Ontology Matching

OM-2013

Proceedings of the ISWC Workshop

Introduction

Ontology matching[1] is a key interoperability enabler for the semantic web, as well as a useful tactic in some classical data integration tasks dealing with the semantic heterogeneity problem. It takes the ontologies as input and determines as output an alignment, that is, a set of correspondences between the semantically related entities of those ontologies. These correspondences can be used for various tasks, such as ontology merging, data translation, query answering or navigation on the web of data. Thus, matching ontologies enables the knowledge and data expressed in the matched ontologies to interoperate.

The workshop has three goals:

- To bring together leaders from *academia*, *industry* and *user institutions* to assess how academic advances are addressing real-world requirements. The workshop will strive to improve academic awareness of industrial and final user needs, and therefore direct research towards those needs. Simultaneously, the workshop will serve to inform industry and user representatives about existing research efforts that may meet their requirements. The workshop will also investigate how the ontology matching technology is going to evolve.
- To conduct an extensive and rigorous evaluation of ontology matching approaches through the OAEI (Ontology Alignment Evaluation Initiative) 2013 campaign[2]. The particular focus of this year's OAEI campaign is on real-world specific matching tasks as well as on evaluation of interactive matchers. Therefore, the ontology matching evaluation initiative itself will provide a solid ground for discussion of how well the current approaches are meeting business needs.
- To examine similarities and differences from database schema matching, which has received decades of attention but is just beginning to transition to mainstream tools.

The program committee selected 5 submissions for oral presentation and 11 submissions for poster presentation. 23 matching system participated in this year's OAEI campaign.

Further information about the Ontology Matching workshop can be found at: `http://om2013.ontologymatching.org/`.

[1] `http://www.ontologymatching.org/`
[2] `http://oaei.ontologymatching.org/2013`

Acknowledgments. We thank all members of the program committee, authors and local organizers for their efforts. We appreciate support from the Trentino as a Lab (TasLab)[3] initiative of the European Network of the Living Labs[4] at Informatica Trentina SpA[5], the EU SEALS (Semantic Evaluation at Large Scale)[6] project and the Semantic Valley[7] initiative.

Pavel Shvaiko
Jérôme Euzenat
Kavitha Srinivas
Ming Mao
Ernesto Jiménez-Ruiz

October 2013

[3] http://www.taslab.eu
[4] http://www.openlivinglabs.eu
[5] http://www.infotn.it
[6] http://www.seals-project.eu
[7] http://www.semanticvalley.org/index_eng.htm

Organization

Organizing Committee

Pavel Shvaiko, TasLab, Informatica Trentina SpA, Italy
Jérôme Euzenat, INRIA & LIG, France
Kavitha Srinivas, IBM, USA
Ming Mao, eBay, USA
Ernesto Jiménez-Ruiz, University of Oxford, UK

Program Committee

Manuel Atencia, INRIA &LIG, France
Michele Barbera, SpazioDati, Italy
Zohra Bellahsene, LRIMM, France
Chris Bizer, University of Mannheim, Germany
Olivier Bodenreider, National Library of Medicine, USA
Marco Combetto, Informatica Trentina, Italy
Gianluca Correndo, University of Southampton, UK
Isabel Cruz, The University of Illinois at Chicago, USA
Jérôme David, INRIA & LIG, France
AnHai Doan, University of Wisconsin, USA
Alfio Ferrara, University of Milan, Italy
Bin He, IBM, USA
Wei Hu, Nanjing University, China
Ryutaro Ichise, National Institute of Informatics, Japan
Antoine Isaac, Vrije Universiteit Amsterdam & Europeana, Netherlands
Krzysztof Janowicz, University of California, USA
Anja Jentzsch, Wikimedia Deutschland, Germany
Yannis Kalfoglou, Ricoh Europe plc, UK
Anastasios Kementsietsidis, IBM, USA
Patrick Lambrix, Linköpings Universitet, Sweden
Monika Lanzenberger, Vienna University of Technology, Austria
Vincenzo Maltese, University of Trento, Italy
Fiona McNeill, University of Edinburgh, UK
Christian Meilicke, University of Mannheim, Germany
Peter Mork, Noblis, USA
Axel-Cyrille Ngonga Ngomo, University of Leipzig, Germany
Andriy Nikolov, Open University, UK
Leo Obrst, The MITRE Corporation, USA
Heiko Paulheim, University of Mannheim, Germany
Yefei Peng, Google, USA
Andrea Perego, European Commission - Joint Research Centre, Italy
François Scharffe, LIRMM & University of Montpellier, France

Juan Sequeda, University of Texas at Austin, USA
Luciano Serafini, Fondazione Bruno Kessler - IRST, Italy
Umberto Straccia, ISTI-C.N.R., Italy
Ondřej Zamazal, Prague University of Economics, Czech Republic
Cássia Trojahn, IRIT, France
Raphaël Troncy, EURECOM, France
Giovanni Tummarello, Fondazione Bruno Kessler - IRST, Italy
Lorenzino Vaccari, Autonomous Province of Trento, Italy
Ludger van Elst, DFKI, Germany
Shenghui Wang, Vrije Universiteit Amsterdam, Netherlands
Baoshi Yan, LinkedIn, USA
Songmao Zhang, Chinese Academy of Sciences, China

Table of Contents

PART 2 - OAEI Papers

PART 3 - Posters

Rapid Execution of Weighted Edit Distances

Tommaso Soru and Axel-Cyrille Ngonga Ngomo

Department of Computer Science
University of Leipzig
Augustusplatz 10, 04109 Leipzig
{tsoru|ngonga}@informatik.uni-leipzig.de

Abstract. The comparison of large numbers of strings plays a central role in ontology matching, record linkage and link discovery. While several standard string distance and similarity measures have been developed with these explicit goals in mind, similarities and distances learned out of the data have been shown to often perform better with respect to the F-measure that they can achieve. Still, the practical use of data-specific measures is often hindered by one major factor: their runtime. While time-efficient algorithms that allow scaling to millions of strings have been developed for standard metrics over the last years, data-specific versions of these measures are usually slow to run and require significantly more time for the same task. In this paper, we present an approach for the time-efficient execution of weighted edit distances. Our approach is based on a sequence of efficient filters that allow reducing the number of candidate pairs for which the weighted edit distance has to be computed. We also show how existing time-efficient deduplication approaches based on the edit distance can be extended to deal with weighted edit distances. We compare our approach with such an extension of PassJoin on benchmark data and show that we outperform it by more than one order of magnitude.

1 Introduction

The computation of string similarities plays a central role in manifold disciplines, especially in ontology matching and link discovery on the Web of Data[1] [20]. Over the last decades, manifold domain-specific string similarities have been developed for improving the accuracy of automatic techniques that rely on them. For example, the Jaro-Winkler similarity was developed especially to perform well on person names [22]. Still, newer works in machine learning have shown that learning string similarities directly from data can lead to algorithms with a performance superior to that of those which rely on standard similarity measures. Especially, work on link discovery on the Web of Data has shown that data-specific weighted edit distances can lead to higher F-measures [21].

One main problem has yet plagued the approaches which rely on string similarity measures learned from data: their runtime. While dedicated algorithms for

[1] Throughout this paper, we use the expression "link discovery" to mean the discovery of typed relations that link instances from knowledge bases on the Web of Data.

the time-efficient comparison of large volumes of data have been developed over the last years (e.g., PPJoin+ [24], EDJoin [23], PassJoin [12] and TrieJoin [6]), the time-efficient computation of data-specific string similarities has been paid little attention to. Thus, running the data-specific counterparts of standard similarity measures is often orders of magnitude slower. Previous work have circumvented this problem in manifold ways, including the execution of approximations of the data-specific similarity measure. For example, weighted edit distances are sometimes approximated by first computing the edit distance between two strings A and B and only subsequently applying the weight of each of the edit operations [10]. Other approximations can be found in [3, 2].

In this paper, we address the problem of the time-efficient computation of weighted edit distances by presenting a novel approach, REEDED. Our approach uses weight bounds on the input cost matrix to efficiently discard similarity computations that would lead to dissimilar pairs. By these means, REEDED can outperform state-of-the-art approaches for the computation of edit distances by more than one order of magnitude on real datasets. We explain our approach by using an example from link discovery based on the data shown in Table 1. Here, the task is to detect possible pairs $(s, t) \in S \times T$ such that s `owl:sameAs` t, where S is a set of source resources and T is a set of target resources.

This paper is structured as follows: In Section 2, we present preliminaries to our work. Thereafter, we present the REEDED approach for the time-efficient computation of weighted edit distances (Section 3). In Section 4, we evaluate our approach on four datasets and show that we outperform a weighted version of the state-of-the-art approach PassJoin by more than one order of magnitude. Finally, we conclude with Section 6 after giving a brief overview of related work in Section 5.

2 Preliminaries

2.1 Notation and Problem Statement

Let Σ be an alphabet and Σ^* be the set all sequences that can be generated by using elements of Σ. We call the elements of Σ characters and assume that Σ contains the empty character ϵ. The edit distance – or Levenshtein distance – of two strings $A \in \Sigma^*$ and $B \in \Sigma^*$ is the minimum number of edit operations that must be performed to transform A into B [11]. An *edit operation* can be the insertion or the deletion of a character, or the substitution of a character with another one. In a *plain* edit distance environment, all edit operations have a cost of 1. Thus, the distance between the strings "Generalized" and "Generalised" is the same as the distance between "Diabetes Type I" and "Diabetes Type II". Yet, while the first pair of strings is clearly semantically equivalent for most applications, the elements of the second pair bears related yet significantly different semantics (especially for medical applications). To account for the higher probability of edit operations on certain characters bearing a higher semantic difference, weighted edit distances were developed. In a *weighted* edit distance environment, a cost function $cost : \Sigma \times \Sigma \rightarrow [0, 1]$ assigned to each of

the possible edit operations. The totality all of costs can be encoded in a *cost matrix* M. The cost matrix is quadratic and of dimensions $|\Sigma| \times |\Sigma|$ for which the following holds:

$$\forall i \in \{1, \ldots, |\Sigma|\}\ m_{ii} = 0 \tag{1}$$

The entry m_{ij} is the cost for substituting the i^{th} character c_i of Σ with the j^{th} character c_j of the same set. Note that if $c_i = \epsilon$, m_{ij} encode the insertion of c_j. On the other hand, if $c_j = \epsilon$, m_{ij} encode the deletion of c_i.

In most applications which require comparing large sets of strings, string similarities are used to address the following problem: Given a set S of source strings and a set T of target strings, find the set $\mathcal{R}(S, T, \delta_p, \theta)$ of all pairs $(A, B) \in S \times T$ such that

$$\delta_p(A, B) \leq \theta \tag{2}$$

where θ is a distance threshold and δ_p is the plain edit distance. Several scalable approaches have been developed to tackle this problem for plain edit distances [12, 24, 23]. Still, to the best of our knowledge, no scalable approach has been proposed for finding all $(A, B) \in S \times T$ such that $\delta(A, B) \leq \theta$ for weighted edit distances δ. In this paper we address exactly this problem by presenting REEDED. This approach assumes that the computation of weighted edit distances can be carried out by using an extension of the dynamic programming approach used for the plain edit distance.

2.2 Extension of Non-Weighted Approaches

All of the approaches developed to address the problem at hand with the plain edit distance can be easily extended to deal with weighted edit distances for which the dynamic programming approach underlying the computation of the plain edit distance still holds. Such an extension can be carried out in the following fashion: Let

$$\mu = \min_{1 \leq i,j \leq |\Sigma| \wedge i \neq j} m_{ij}. \tag{3}$$

Then, if the weighted edit distance between two strings A and B is d, then at most d/μ edit operations were carried out to transform A into B. By using this insight, we can postulate that for any weighted edit distance δ with cost matrix M, the following holds

$$\forall A \in \Sigma^*\ \forall B \in \Sigma^*\ \delta(A, B) \leq \theta \rightarrow \delta_p(A, B) \leq \frac{\theta}{\mu}. \tag{4}$$

Thus, we can reduce the task of finding the set $\mathcal{R}(S, T, \delta, \theta)$ to that of first finding $\mathcal{R}(S, T, \delta_p, \theta/\mu)$ and subsequently filtering $\mathcal{R}(S, T, \delta_p, \theta/\mu)$ by using the condition $\delta(A, B) \leq \theta$. To the best of our knowledge, PassJoin [12] is currently the fastest approach for computing $\mathcal{R}(S, T, \delta_p, \theta)$ with plain edit distances. We thus extended it to deal with weighted edit distances and compared it with our approach. Our results show that we outperform the extension of PassJoin by more than one order of magnitude.

3 The REEDED Approach

3.1 Overview

Our approach REEDED (Rapid Execution of Weighted Edit Distances) aims to compute similar strings using weighted edit distance within a practicable amount of time. The REEDED approach is basically composed of three nested filters as shown in Figure 1, where each filter takes a set of pairs as input and yields a subset of the input set according to a predefined rule. In the initial step of REEDED, the input data is loaded from S, a source data set, and T, a target data set. Their Cartesian product $S \times T$ is the input of the first length-aware filter. The output of the first filter $\mathcal{L}$ is the input of the second character-aware filter. The weighted edit distance will be calculated only for the pairs that pass through the second filter, i.e. set $\mathcal{N}$. The final result $\mathcal{A}$ is the set of pairs whose weighted edit distance is less or equal than a threshold θ. Note that pairs are processed one by one. This ensures that our algorithm performs well with respect to its space complexity.

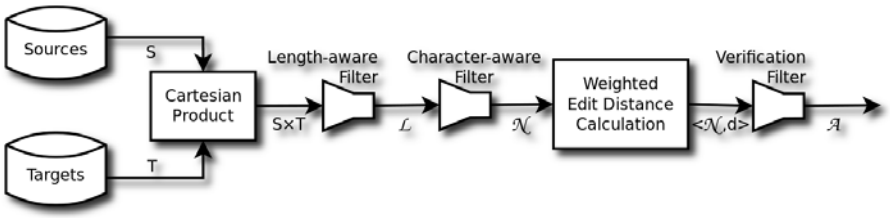


Fig. 1. Flowchart of the REEDED approach.

Table 1. Example data sets.

Sources (S)	Targets (T)
id name	*id name*
s_1 Basal cell carcinoma	t_1 Basal Cell Carcinoma
s_2 Blepharophimosi	t_2 Blepharophimosis
s_3 Blepharospasm	t_3 Blepharospasm
s_4 Brachydactyly type A1	t_4 Brachydactyly Type A1
s_5 Brachydactyly type A2	t_5 Brachydactyly Type A2

3.2 Key Assumption

Similarly to the extensions of plain edit distances for weighted edit distances, REEDED assumes the dynamic programming approach commonly used for computing plain edit distances can be used for computing the weighted edit distance described by the cost matrix M. With respect to M, this assumption translates to the weights in the matrix being such that there is no sequence of two edit operations m_{ij} and $m_{i'j'}$ that is equivalent to a third edit operation $m_{i''j''}$ with

$$m_{i''j''} > m_{ij} + m_{i'j'}. \tag{5}$$

for $(i \neq j) \wedge (i' \neq j') \wedge (i'' \neq j'')$. Formally, we can enforce this condition of the cost matrix M by ensuring that

$$\exists k > 0 \; \forall m_{ij} : k < m_{ij} \leq 2k. \tag{6}$$

Given that the entries in cost matrices are usually bound to have a maximal value of 1, we will assume without restriction of generality that

$$\forall i \in \{1, \ldots, |\Sigma|\} \forall j \in \{1, \ldots, |\Sigma|\} \; i \neq j \rightarrow 0.5 < m_{ij} \leq 1. \tag{7}$$

Thus, in the following, we will assume that $\forall m_{ij} : m_{ij} > 0.5$.

3.3 Length-aware Filter

The *length-aware filter* is the first filter of REEDED. Once the data sets have been loaded, the Cartesian product

$$S \times T = \{\langle s, t\rangle : s \in S, t \in T\} \tag{8}$$

is computed, which in our example corresponds to $\{\langle s_1, t_1\rangle, \langle s_1, t_2\rangle, \ldots, \langle s_5, t_5\rangle\}$. The basic insight behind the first filter is that given two strings s and t with lengths $|s|$ resp. $|t|$, we need at least $||s| - |t||$ edit operations to transform s into t. Now given that each edit operation costs at least μ, the cost of transforming s to t will be at least $\mu||s| - |t||$. Consequently, the rule which the filter relies on is the following:

$$\langle s, t\rangle \in \mathcal{L} \;\Rightarrow\; \langle s, t\rangle \in S \times T \wedge ||s| - |t|| \leq \theta/\mu. \tag{9}$$

In the following, we will set $\tau = \theta/\mu$, where μ is as defined in Equation (3).

In our example, let us assume $\theta = 1$ and $m_{ij} \in (0.5, 1.0]$. Then, $\tau = 2$. If we assume that *S.name* has been mapped to *T.name*, then at the end of this step, 13 of the 25 initial pairs in $S \times T$ are dismissed. The remaining 8 pairs are:

$$\mathcal{L} = \{\langle s_1, t_1\rangle, \langle s_2, t_2\rangle, \langle s_3, t_3\rangle, \langle s_4, t_4\rangle, \langle s_5, t_5\rangle, \langle s_2, t_3\rangle, \langle s_4, t_5\rangle, \langle s_5, t_4\rangle\}. \tag{10}$$

3.4 Character-aware Filter

The second filter is the *character-aware filter* which only selects the pairs of strings that do not differ by more than a given number of characters. The intuition behind the filter is that given two strings s and t, if $|C|$ is the number of characters that do not belong to both strings, we need at least $\lceil |C|/2 \rceil$ operations to transform s into t. As above, the cost of transforming s to t will be at least $\mu\lceil |C|/2 \rceil$. The characters of each string are collected into two sets, respectively C_s for the source string and C_t for the target string. Since s and t may contain more than one occurrence of a single character, characters in C_s and C_t are enumerated. Then, the algorithm computes their exclusive disjunction C:

$$C = C_s \oplus C_t. \tag{11}$$

Finally, the filter performs the selection by applying the rule:

$$\langle s, t \rangle \in \mathcal{N} \iff \langle s, t \rangle \in \mathcal{L} \wedge \left\lceil \frac{|C|}{2} \right\rceil \leq \tau. \tag{12}$$

In our example, a further pair can be dismissed by these means, leading to the set of remaining pairs being as follows:

$$\mathcal{N} = \{\langle s_1, t_1 \rangle, \langle s_2, t_2 \rangle, \langle s_3, t_3 \rangle, \langle s_4, t_4 \rangle, \langle s_5, t_5 \rangle, \langle s_4, t_5 \rangle, \langle s_5, t_4 \rangle\}$$

The pair that is rejected is $\langle s_2, t_3 \rangle$, for which $C = \{h_1, i_1, o_1, i_2, a_1, s_1\}$, which leads to the rule not being satisfied.

3.5 Verification

For all the pairs left in $\mathcal{N}$, the weighted edit distance among is calculated. After that, the third filter selects the pairs whose distance is less or equal than θ.

$$\langle s, t \rangle \in \mathcal{A} \iff \langle s, t \rangle \in \mathcal{N} \wedge \delta(s, t) \leq \theta \tag{13}$$

In our example data sets, the set

$$\mathcal{A} = \{\langle s_1, t_1 \rangle, \langle s_2, t_2 \rangle, \langle s_3, t_3 \rangle, \langle s_4, t_4 \rangle, \langle s_5, t_5 \rangle\} \tag{14}$$

is the final result of the selection. Note that the pairs $\langle s_4, t_5 \rangle$ and $\langle s_5, t_4 \rangle$ are discarded, because their distance (1.2) is greater than the threshold (1.0). [2]

4 Evaluation

The goal of our evaluation was to quantify how well REEDED performs in comparison to the state of the art. We thus compared REEDED with the extension of PassJoin as proposed in [12]. We chose PassJoin because it was shown to outperform other approaches for the efficient computation of edit distances, incl. EDJoin [23] and TrieJoin [6]. Note that we did run an implementation of EdJoin on the DBLP dataset presented below and it required approximately twice the runtime of PassJoin.

[2] A proof of the correctness of REEDED can be found in the extended version of this paper at `http://svn.aksw.org/papers/2013/OM_Reeded/public.pdf`.

4.1 Experimental Setup

We compared the approaches across several distance thresholds on four different datasets that were extracted from real data (see Fig. 2).[3] The first two of these data sets contained publication data from the datasets DBLP and ACM. The third and fourth dataset contained product labels from the product catalogs Google Products and ABT [9]. We chose these datasets because they were extracted from real data sources and because of the different string length distribution across them. By running our experiments on these data sets, we could thus ensure that our results are not only valid on certain string length distributions. As weight matrix we used a *confusion matrix* built upon the frequency of typographical errors presented in [8]. The original confusion matrices report the number of occurrences f for each error:

$$\Phi^S = \{f_{ij} : \text{substitution of } i \text{ (incorrect) for } j \text{ (correct)}\} \tag{15}$$

$$\Phi^I = \{f_{ij} : \text{insertion of } j \text{ after } i\} \tag{16}$$

$$\Phi^D = \{f_{ij} : \text{deletion of } j \text{ after } i\} \tag{17}$$

For insertion and deletion, we calculate the total frequency:

$$\omega_j^I = \sum_i \Phi_{ij}^I \tag{18}$$

$$\omega_j^D = \sum_i \Phi_{ij}^D \tag{19}$$

The weights of our weight matrix are thus defined as:

$$m_{ij} = \begin{cases} 1 - \frac{\Phi_{ij}^S}{2\max(\Phi^S)} & : i \neq \epsilon \wedge j \neq \epsilon \\ 1 - \frac{\omega_j^I - \min(\omega^I)}{2(\max(\omega^I) - \min(\omega^I))} & : i = \epsilon \wedge j \neq \epsilon \\ 1 - \frac{\omega_i^D - \min(\omega^D)}{2(\max(\omega^D) - \min(\omega^D))} & : i \neq \epsilon \wedge j = \epsilon \end{cases} \tag{20}$$

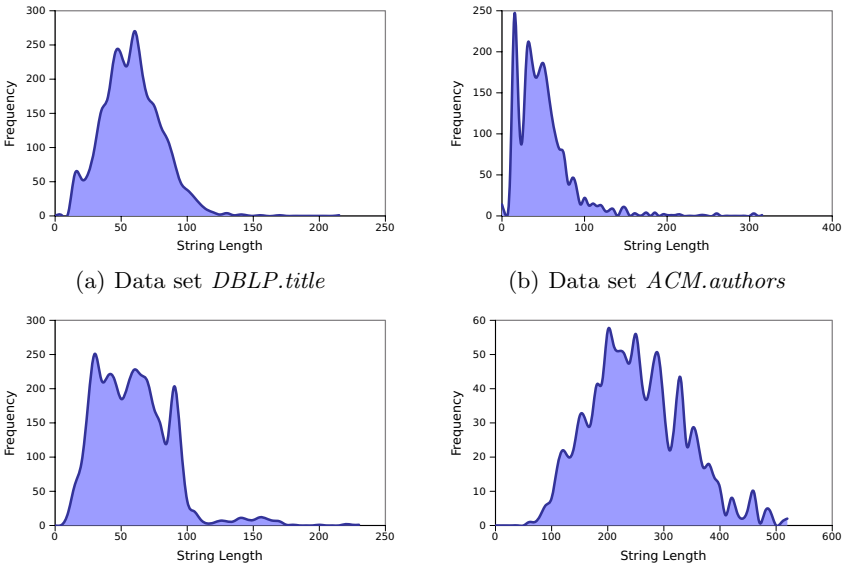
In other words, the higher the probability of an error encoded in m_{ij}, the lower its weight.

All experiments were carried out on a 64-bit server running Ubuntu 10.0.4 with 4 GB of RAM and a 2.5 GHz XEON CPU. Each experiment was run 5 times.

4.2 Results

In Figure 2 we show the string length distribution in the data sets. The results of our experiments are shown in Table 2. Our results show clearly that REEDED

[3] The data used for the evaluation is publicly available at `http://dbs.uni-leipzig.de/en/research/projects/object\_matching/fever/benchmark\_datasets\_for\_entity\_resolution`.



(a) Data set *DBLP.title* (b) Data set *ACM.authors*

(c) Data set *GoogleProducts.name* (d) Data set *ABT.description*

Fig. 2. Distribution of string lengths.

outperforms PassJoin in all experimental settings. On the DBLP dataset (average string length = 56.36), REEDED is already 2 times faster than PassJoin for the threshold 2. For $\theta = 4$, we reach an order of magnitude in difference with runtimes of 25.91 (REEDED) and 246.93 (PassJoin). The runtime of REEDED seems to grow quasi-linearly with increasing values of θ. The results on ACM corroborate the results for the two algorithms. Here, we are 2.16 times faster than PassJoin for $\theta = 2$ and 6.57 times faster for $\theta = 5$. We achieve similar results on the Google Products dataset and are an order of magnitude faster than PassJoin for $\theta = 4$ already. The results we achieve the ABT dataset allow deriving further characteristics of REEDED. Here, the algorithm scales best and requires for $\theta = 5$ solely 1.58 times the runtime it required for $\theta = 1$. This is clearly due to the considerably longer strings contained in this dataset.

We analyzed the results on each of the filters in our approach and measure the reduction ratio (given by $1 - |\mathcal{N}|/|S \times T|$) achieved by the length-aware and character-aware filters. Table 3 shows the set sizes at each filtering step. Both the first and the second filter reduce the number of selected pairs by one or two orders of magnitude for all the datasets. As expected, the length-aware filter is most effective on datasets with large average string lengths. For example, only 1.9% of the Cartesian product of the ABT dataset makes it through the first filter for $\theta = 1$ while the filter allows 6.8% of the DBLP Cartesian product through for $\theta = 1$. One interesting characteristic of the approach is that the size of the $\mathcal{L}$ grows quasi linearly with the value of θ. The character-aware filter

Table 2. Runtime results in seconds.

		PassJoin		REEDED	
Dataset	θ	average	st.dev.	average	st.dev.
DBLP.title	1	10.75	± 0.92	10.38	± 0.35
	2	30.74	± 5.00	15.27	± 0.76
	3	89.60	± 1.16	19.84	± 0.14
	4	246.93	± 3.08	25.91	± 0.29
	5	585.08	± 5.47	37.59	± 0.43
ACM.authors	1	9.07	± 1.05	6.16	± 0.07
	2	18.53	± 0.22	8.54	± 0.29
	3	42.97	± 1.02	12.43	± 0.47
	4	98.86	± 1.98	20.44	± 0.27
	5	231.11	± 2.03	35.13	± 0.35
GoogleProducts.name	1	17.86	± 0.22	15.08	± 2.50
	2	62.31	± 6.30	20.43	± 0.10
	3	172.93	± 1.59	27.99	± 0.19
	4	475.97	± 5.34	42.46	± 0.32
	5	914.60	± 10.47	83.71	± 0.97
ABT.description	1	74.41	± 1.80	24.48	± 0.41
	2	140.73	± 1.40	27.71	± 0.29
	3	217.55	± 7.72	30.61	± 0.34
	4	305.08	± 4.78	34.13	± 0.30
	5	410.72	± 3.36	38.73	± 0.44

seems to have the opposite behavior to the length-aware filter and can discard more string pair on data with small average string lengths. For example, less than 1% of $\mathcal{L}$ makes it through the filter for $\theta = 1$ on the DBLP dataset while 5.1% of $\mathcal{L}$ makes it through the same filter for $\theta = 1$ on ABT.

We also measured the runtime improvement as well as the precision and recall we achieved by combining REEDED with the ACIDS approach and applying this combination to the datasets reported in [21]. The results are shown in Table 4. For the datasets on which the edit distance can be used, the approach achieves a superior precision and recall than state-of-the-art approaches (such as MARLIN [4] and Febrl [5]) which do not rely on data-specific measures. Yet, on more noisy datasets, the approach leads to poorer results. In particular, the edit distance has been shown not to be a good measure when the strings to be compared are too long. Also, the words contained in the source string may be completely different from the words contained in the target string, yet referring to the same meaning. A notable shortcoming of the ACIDS approach is the runtime, wherein the learning system iterated for at least 7 hours to find the weight configuration of the weighted edit distance and optimize the classification [21]. As shown in Table 4, REEDED enhances the execution time of ACIDS reducing the total runtime by 3 orders of magnitude on the DBLP–ACM and the ABT–Buy dataset.

Table 3. Numbers of pairs (s, t) returned by each filter. RR stands for the reduction ratio achieved by the combination of length-aware and character-aware filters.

DBLP.title	$\theta = 1$	$\theta = 2$	$\theta = 3$	$\theta = 4$	$\theta = 5$
$\|S \times T\|$	6,843,456	6,843,456	6,843,456	6,843,456	6,843,456
$\|\mathcal{L}\|$	465,506	832,076	1,196,638	1,551,602	1,901,704
$\|\mathcal{N}\|$	4,320	4,428	5,726	11,382	30,324
$\|\mathcal{A}\|$	4,315	4,328	4,344	4,352	4,426
$RR(\%)$	99.94	99.94	99.92	99.83	99.56
ACM.authors	$\theta = 1$	$\theta = 2$	$\theta = 3$	$\theta = 4$	$\theta = 5$
$\|S \times T\|$	5,262,436	5,262,436	5,262,436	5,262,436	5,262,436
$\|\mathcal{L}\|$	370,538	646,114	901,264	1,139,574	1,374,482
$\|\mathcal{N}\|$	3,820	5,070	24,926	104,482	218,226
$\|\mathcal{A}\|$	3,640	3,708	3,732	3,754	3,946
$RR(\%)$	99.93	99.90	99.53	98.01	95.85
GooglePr.name	$\theta = 1$	$\theta = 2$	$\theta = 3$	$\theta = 4$	$\theta = 5$
$\|S \times T\|$	10,407,076	10,407,076	10,407,076	10,407,076	10,407,076
$\|\mathcal{L}\|$	616,968	1,104,644	1,583,148	2,054,284	2,513,802
$\|\mathcal{N}\|$	4,196	4,720	9,278	38,728	153,402
$\|\mathcal{A}\|$	4,092	4,153	4,215	4,331	4,495
$RR(\%)$	99.96	99.95	99.91	99.63	95.53
ABT.description	$\theta = 1$	$\theta = 2$	$\theta = 3$	$\theta = 4$	$\theta = 5$
$\|S \times T\|$	1,168,561	1,168,561	1,168,561	1,168,561	1,168,561
$\|\mathcal{L}\|$	22,145	38,879	55,297	72,031	88,299
$\|\mathcal{N}\|$	1,131	1,193	1,247	1,319	1,457
$\|\mathcal{A}\|$	1,087	1,125	1,135	1,173	1,189
$RR(\%)$	99.90	99.90	99.89	99.88	99.87

5 Related Work

Our work is mostly related to the rapid execution of similarity functions and link discovery. Time-efficient string comparison algorithms such as PPJoin+ [24], EDJoin [23], PassJoin [12] and TrieJoin [6] were developed for the purpose of entity resolution and were integrated into frameworks such as *LIMES* [15]. In addition to time-efficient string similarity computation approaches for entity resolution, approaches for the efficient computation string and numeric similarities were developed in the area of link discovery. For example, [16] presents an approach based on the Cauchy-Schwarz inequality. The approaches HYPPO [13] and $\mathcal{HR}^3$ [14] rely on space tiling in spaces with measures that can be split into independent measures across the dimensions of the problem at hand. Especially, $\mathcal{HR}^3$ was shown to be the first approach that can achieve a relative reduction ratio r' less or equal to any given relative reduction ratio $r > 1$. Another way to go about computing $\mathcal{R}(S, T, \delta, \theta)$ lies in the use of lossless blocking approaches such MultiBlock [7].

Manifold approaches have been developed on string similarity learning (see, e.g., [19, 4, 3, 2]). [4] for example learns edit distances by employing batch learn-

Table 4. Results for the combination of ACIDS and REEDED. The runtimes in the 2 rows at the bottom are in seconds.

	DBLP–ACM		**DBLP–Scholar**		**ABT–Buy**	
Labeled examples	20	40	20	40	20	40
F-score (%)	88.98	97.92	70.22	87.85	0.40	0.60
Precision (%)	96.71	96.87	64.73	91.88	0.20	0.30
Recall (%)	82.40	99.00	76.72	84.16	100.00	100.00
Without REEDED	27,108	26,316	30,420	30,096	44,172	43,236
With REEDED	14.25	14.24	668.62	668.62	13.03	65.21

ing and SVMs to record deduplication and points out that domain-specific similarities can improve the quality of classifiers. [3, 2] rely on a theory for good edit distances developed by [1] to determine classifiers based on edit distances that are guaranteed to remain under a given classification error. Yet, to the best of our knowledge, REEDED is the first approach for the time-efficient execution of weighted edit distances.

6 Conclusion

In this paper we presented REEDED, an approach for the time-efficient comparison of sets using weighted distances. After presenting the intuitions behind our approach, we proved that it is both correct and complete. We compared our approach with an extension of PassJoin for weighted edit distances and showed that we are more than an order of magnitude faster on 4 different data sets. REEDED is the cornerstone of a larger research agenda. As it enable to now run weighted edit distances on large datasets within acceptable times, it is also the key to developing active learning systems for link discovery that do not only learn link specifications but also similarity measures directly out of the data. As shown in [21], this combination promises to outperform the state of the art, which has relied on standard measures so far. In future work, we will thus combine REEDED with specification learning approaches such as EAGLE [18] and RAVEN [17] and study the effect of weighted edit distances on these approaches.

References

1. Maria-Florina Balcan, Avrim Blum, and Nathan Srebro. Improved guarantees for learning via similarity functions. In *COLT*, pages 287–298, 2008.
2. Aurélien Bellet, Amaury Habrard, and Marc Sebban. Good edit similarity learning by loss minimization. *Machine Learning*, 89(1-2):5–35, 2012.
3. Aurlien Bellet, Amaury Habrard, and Marc Sebban. Learning good edit similarities with generalization guarantees. In *Proceedings of the ECML/PKDD 2011*, 2011.
4. Mikhail Bilenko and Raymond J. Mooney. Adaptive duplicate detection using learnable string similarity measures. In *KDD*, pages 39–48, 2003.

5. Peter Christen. Febrl: a freely available record linkage system with a graphical user interface. In *Proceedings of the second Australasian workshop on Health data and knowledge management - Volume 80*, HDKM '08, pages 17–25, Darlinghurst, Australia, Australia, 2008. Australian Computer Society, Inc.
6. Jianhua Feng, Jiannan Wang, and Guoliang Li. Trie-join: a trie-based method for efficient string similarity joins. *The VLDB Journal*, 21(4):437–461, August 2012.
7. Robert Isele, Anja Jentzsch, and Christian Bizer. Efficient Multidimensional Blocking for Link Discovery without losing Recall. In *WebDB*, 2011.
8. Mark D. Kernighan, Kenneth Ward Church, and William A. Gale. A spelling correction program based on a noisy channel model. In *COLING*, pages 205–210, 1990.
9. Hanna Köpcke, Andreas Thor, and Erhard Rahm. Evaluation of entity resolution approaches on real-world match problems. *PVLDB*, 3(1):484–493, 2010.
10. S. Kurtz. Approximate string searching under weighted edit distance. In *Proc. WSP*, volume 96, pages 156–170. Citeseer, 1996.
11. V. I. Levenshtein. Binary codes capable of correcting deletions, insertions, and reversals. *Doklady Akademii Nauk SSSR 163 (4)*, pages 845–848, 1965.
12. Guoliang Li, Dong Deng, Jiannan Wang, and Jianhua Feng. Pass-join: a partition-based method for similarity joins. *Proc. VLDB Endow.*, 5(3):253–264, November 2011.
13. Axel-Cyrille Ngonga Ngomo. A Time-Efficient Hybrid Approach to Link Discovery. In *OM*, 2011.
14. Axel-Cyrille Ngonga Ngomo. Link Discovery with Guaranteed Reduction Ratio in Affine Spaces with Minkowski Measures. In *ISWC*, pages 378–393, 2012.
15. Axel-Cyrille Ngonga Ngomo. On Link Discovery using a Hybrid Approach. *Journal on Data Semantics*, 1:203 – 217, 2012.
16. Axel-Cyrille Ngonga Ngomo and Sören Auer. LIMES - A Time-Efficient Approach for Large-Scale Link Discovery on the Web of Data. In *IJCAI*, pages 2312–2317, 2011.
17. Axel-Cyrille Ngonga Ngomo, Jens Lehmann, Sören Auer, and Konrad Höffner. RAVEN – Active Learning of Link Specifications. In *Sixth International Ontology Matching Workshop*, 2011.
18. Axel-Cyrille Ngonga Ngomo and Klaus Lyko. Eagle: Efficient active learning of link specifications using genetic programming. In *Proceedings of ESWC*, 2012.
19. E. S. Ristad and P. N. Yianilos. Learning string-edit distance. *Pattern Analysis and Machine Intelligence, IEEE Transactions on*, 20(5):522–532, 1998.
20. Pavel Shvaiko and Jérôme Euzenat. Ontology matching: State of the art and future challenges. *IEEE Trans. Knowl. Data Eng.*, 25(1):158–176, 2013.
21. Tommaso Soru and Axel-Cyrille Ngonga Ngomo. Active learning of domain-specific distances for link discovery. In *Proceedings of JIST*, 2012.
22. William E. Winkler. Overview of record linkage and current research directions. Technical report, BUREAU OF THE CENSUS, 2006.
23. Chuan Xiao, Wei Wang, and Xuemin Lin. Ed-Join: an efficient algorithm for similarity joins with edit distance constraints. *PVLDB*, 1(1):933–944, 2008.
24. Chuan Xiao, Wei Wang, Xuemin Lin, and Jeffrey Xu Yu. Efficient similarity joins for near duplicate detection. In *WWW*, pages 131–140, 2008.

To repair or not to repair: reconciling correctness and coherence in ontology reference alignments

Catia Pesquita[1], Daniel Faria[1], Emanuel Santos[1], and Francisco M. Couto[1]

[1]Dept. de Informática, Faculdade de Ciências, Universidade de Lisboa, Portugal
cpesquita@di.fc.ul.pt

Abstract. A recent development in the field of ontology matching is the alignment repair process, whereby mappings that lead to unsatisfiable classes are removed to ensure that the final alignment is coherent. This process was showcased in the Large Biomedical Ontologies track of OAEI 2012, where two repair systems (ALCOMO and LogMap) were used to create separate coherent reference alignments from the original alignment based on the UMLS metathesaurus. In 2013, the OAEI introduced new reference alignments for this track, created by using the two repair systems in conjunction and manual curation when necessary. In this paper, we present the results of a manual analysis of the OAEI 2013 Large Biomedical Ontologies reference alignments, focused on evaluating the equivalence mappings removed by the repair process as well as those that were replaced by subsumption mappings. We found that up to two-thirds of the removed mappings were correct and that over 90% of the analyzed subsumption mappings were incorrect, since in most cases the correct type of relation was the original equivalence. We discuss the impact that disregarding correctness to ensure coherence can have on practical ontology matching applications, as well as on the evaluation of ontology matching systems.

Keywords: Ontology Matching, Alignment Repair, Reference Alignment, Biomedical Ontologies

1 Introduction

With ontologies growing in size and complexity, the interest in efficient and effective matching methods capable of handling large and heterogeneous ontologies is also on the rise. This is evidenced by the recent introduction of the Large Biomedical Ontologies track in the Ontology Alignment Evaluation Initiative (OAEI) [1], currently the major benchmark for ontology alignment evaluation [2].

The OAEI large biomedical track consists of finding alignments between the Foundational Model of Anatomy (FMA)[3], SNOMED CT [4], and the National Cancer Institute Thesaurus (NCI) [5]. These ontologies are semantically rich and contain tens of thousands of classes.

However, evaluating the matching of very large ontologies is in itself a recognized

challenge [6], since the most common type of ontology matching evaluation relies on the comparison of an alignment produced by an ontology matching system against a reference alignment. For smaller ontologies, reference alignments are manually built, and can then be subject to debugging and quality checking steps [7, 8]. However for very large ontologies this is unfeasible since the number of mappings that need to be manually evaluated grows quadratically with the number of classes in an ontology. Even if some heuristics are used to reduce the search space, the human effort is still too demanding, especially when we are facing ontologies with tens or even hundreds of thousands of classes [9].

Consequently, efforts have been made to create reference alignments in an automated or semi-automated fashion [9–11]. One possible strategy to achieve this is based on existing resources from which the reference alignment can be derived. For the three tasks in the large biomedical track in OAEI, the reference alignments were created by processing UMLS metathesaurus entries. UMLS combines expert assessment with automated methods to connect classes from distinct biomedical ontologies and thesaurii according to their meaning.

However, the produced reference alignments lead to a considerable number of unsatisfiable classes when they are integrated with the input ontologies, and while the integration of FMA with NCI generates only 655 unsatisfiable classes, the integration of SNOMED CT and NCI leads to more than 20,000 unsatisfiable classes [12]. To address this issue, in OAEI 2012, in addition to the original reference alignment, two additional references were created by employing two different techniques to repair the logical inconsistencies of the original alignment, ALCOMO [13] and the repair facility of the ontology matching system LogMap [14, 10] (LogMap-Repair).

Ensuring that the alignment between two ontologies is coherent, i.e., that no class or property is unsatisfiable, has recently become a major focus for ontology matching. This is especially relevant when matching very large ontologies, which typically produce more unsatisfiable classes. To ensure the coherence of the alignment, a system needs to first detect the incoherencies and then repair them, by removing or altering them, in order to improve the coherent alignment with minimum intervention. However, different repair methods can produce different alignments. For instance, Figure 1 depicts three conflicting mappings in the original UMLS reference alignment for FMA-NCI. Each system removed two mappings to solve the inconsistencies caused by the disjoint clauses in NCI, but while ALCOMO removed mappings 2 and 3, LogMap removed 1 and 3. In this case, mapping 2 is correct. However the systems have no way of inferring this from the ontologies and alignment, since there are no mappings between the superclasses. For instance, if Anatomy_Kind was mapped to Anatomical_Entity, then this information could be used to disambiguate between Gingiva and Gum.

The application of these techniques reduced the number of unsatisfiable classes to a few [1]. However, this automated process for repair is rather agressive, removing a significant number of mappings (up to 10%). In an effort to counteract this, in OAEI 2013, the three reference alignments were refined by using the two repair systems in conjunction and manual curation when necessary to ensure all

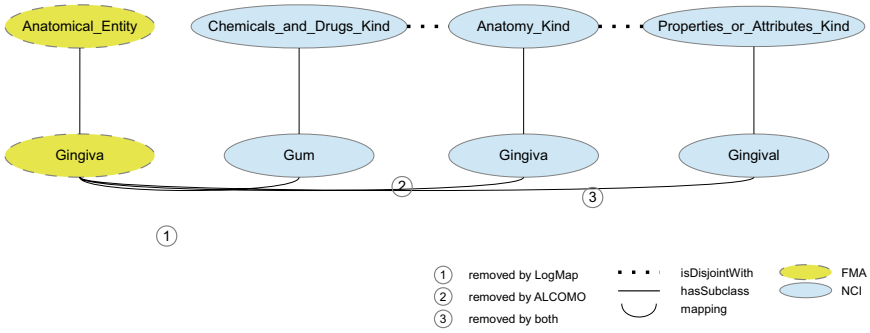


Fig. 1: An example of different repairs made by LogMap and ALCOMO

inconsistencies were solved. This resulted in more complete and fully coherent reference alignments (see Table 1).

Table 1: Reference alignment sizes

Task	Original	LogMap 2012	ALCOMO 2012	Repaired 2013
FMA-NCI	3,024	2,898	2,819	2,931 (13 <, 28 >)
FMA-SNOMED	9,008	8,111	8,132	8,941 (670 <)
SNOMED-NCI	18,844	18,324	N.A.	18,476 (7 <, 540 >)

> and < indicate subsumption mappings

One of the strategies employed to achieve coherence and decrease the number of removed mappings is provided by LogMap. LogMap splits the equivalence mappings into two subsumption mappings and keeps the one that does not violate any logical constraints. This however, may result in mappings that do not reflect the real relationship between classes. Taking again as an example Figure 1, in the repaired alignment in OAEI 2013 all three mappings were replaced by subsumptions: FMA:Gingiva > NCI:Gingival, FMA:Gingiva > NCI:Gingiva and FMA:Gingiva > NCI:Gum. With this solution, the alignment becomes coherent since the relation is directional and the inconsistency is only caused by the disjoint clauses in NCI. However, none of the mappings are correct.
These examples showcase that: 1) different repair techniques produce different repaired alignments; and 2) that solving inconsistencies with subsumption mappings can result in an erroneous alignment. In this paper, we discuss the results of a manual analysis of the OAEI Large Biomedical track reference alignments. We focused our analysis on the differences between the original UMLS and the repaired alignments, in particular on the removed mappings and the ones al-

tered to subsumptions. We also investigated the influence of using the same repair technique to repair both the matching result and to repair the reference alignment.
The paper is organized as follows: Section 2 describes how we conducted our evaluation, Section 3 presents and discusses the evaluation; and finally Section 4 proposes future alternatives for the discussed issues.

2 Methods

To compare the repaired alignments of OAEI 2013 against the original UMLS, we manually evaluated all 41 subsumption mappings in FMA-NCI and 100 randomly chosen subsumption mappings of both FMA-SNOMED and SNOMED-NCI. The evaluation was conducted by two researchers with a biomedical background. We classified each mapping as: correct, incorrect or debatable. We consider mappings correct, not based on their compliance with ontological constraints, but based on their depiction of a real existing relation. For instance, we consider the FMA-NCI mappings between Visceral Pleura, Lung and Thoracic Cavity to be correct even if their integration with the ontologies leads to unsatisfiable classes.
Furthermore, we discerned between mappings where the right relationship would have been equivalence, from those that would have been incorrect with either a subsumption or an equivalence relation. We chose to include a debatable category for those mappings that raised disagreement between the experts, or that they deemed subject to interpretation. For instance, the mappings FMA:Hormone to NCI:Therapeutic_Hormone or SNOMED:Child to NCI:Children.
Our manual evaluation also included the verification of all removed mappings in FMA-NCI and FMA-SNOMED, and of 100 randomly chosen mappings in SNOMED-NCI. These were also classified into the three above-mentioned categories. In addition, we also repaired the original reference alignment with our novel repair technique (AML-Repair) [15] and evaluated the removed mappings.

3 Results and Discussion

Table 2 shows the results of our manual evaluation of the mappings removed or altered from equivalence to subsumption in the repair of the OAEI 2013 Large Biomedical reference alignments. Please note that for the sake of calculating statistics we chose to ignore the debatable removals and alterations.
For FMA-NCI the removal of equivalence mappings is quite successful, with 60 out of 87 removed mappings being correctly so. However, in SNOMED-NCI only half of the mappings were correctly removed, while in FMA-SNOMED this dropped to only 19 out of 65. Regarding the alteration of the mapping relation from equivalence to subsumption, the results are even poorer if more homogeneous between tasks, with 80 to 95% of the alterations being incorrect. Taking into account both removals and alterations, the percentage of correct reparations

ranges from 13% in FMA-SNOMED to 54% in FMA-NCI. Furthermore, considering that the majority of the mappings altered to subsumption by the OAEI 2013 repair are actually equivalences, these alterations do not actually improve the practical quality of the alignment, they just allow the alignment to become coherent without removing the mappings.
To complement this analysis we also repaired the original UMLS reference alignments with our own repair technique (AML-Repair). Compared to the OAEI 2013 repair, AML-Repair makes far more incorrect removals (see Table 3). However, when both removal and alteration are taken into account, AML has a higher percentage of correct repairs in both FMA-SNOMED and SNOMED-NCI.

Table 2: Evaluation of the OAEI 2013 Repair in the Large Biomedical Ontologies track

	Equivalence removal			Alteration to subsumption			
Task	Correct	?	Incorrect	Correct	?	Incorrect	Total correct
FMA-NCI	60	6	27	8	3	30 (26)	54.4 %
FMA-SNOMED	19	1	46	2	5	93 (73)	13.1 %
SNOMED-NCI	42	16	42	4	5	91 (73)	25.7 %

?: Debatable mapping. Numbers in ( ) correspond to mappings where the correct relation is equivalence.

Table 3: Evaluation of AML-Repair in the Large Biomedical Ontologies track

		Equivalence removal			
Task	Size	Correct	?	Incorrect	Total correct
FMA-NCI	2901	48	11	54	47.1%
FMA-SNOMED	8349	19	0	81	19%
SNOMED-NCI	18065	43	6	51	45.7%

?: Debatable mapping.

These results mean that a large percentage of the removed or altered mappings were correct and that both repair techniques are in fact too aggressive.
A fundamental issue here is that different ontologies can have different models of the same subject, and as such, a set of mappings that should be considered correct can render some classes unsatisfiable when the alignment is integrated with the ontologies. For instance, consider the mappings FMA:Fibrillar_Actin = NCI:F-actin and FMA:Actin = NCI:Actin. Both mappings could be considered correct, but when they are integrated with the ontologies they cause an inconsistency. Figure 2 illustrates this issue. Since in FMA F-actin is a subclass of

Actin and in NCI it is a subclass of Actin_Fillament which is disjoint with Actin, the two mappings are in conflict. However, from the biomedical perspective it is arguable that both mappings are correct: F-Actin is the polymer microfilament form of Actin. The OAEI 2013 repair technique solves this issue by changing the relation type in the FMA:Actin=NCI:Actin mapping to subsumption. Since the only constraints violated by the mapping reside in the NCI ontology, by making the mapping one-way, this strategy restores the coherence to the alignment. However, FMA:Actin > NCI:Actin does not represent the true relationship between these classes, which is equivalence.

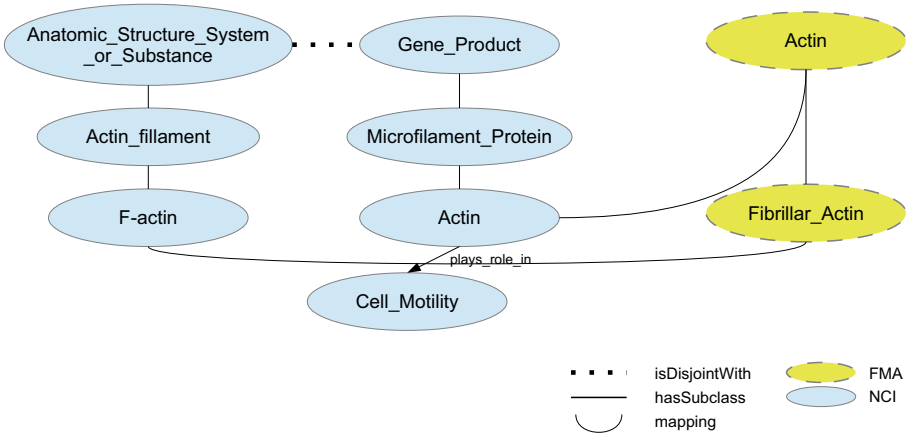


Fig. 2: Two correct mappings causing an inconsistency

So the question is: when creating a reference alignment through automated methods, what is best, an incomplete but coherent reference alignment, or a complete but incoherent one? The answer, we think, depends on the application of the alignment. If the final goal of creating an alignment is to support the integration of two ontologies, then it is necessary to ensure coherence, so that the derived ontology is logically correct and supports reasoning. However, if the goal is supporting the establishment of cross-references between the ontologies to allow navigation between them, then an alignment that does not support linking FMA:Actin to NCI:Actin or reduces the relation to a subsumption would prevent a user from reaching the information that actin plays a role in cell motility. One of the underlying problems is that the existing repair techniques are not guaranteed to remove the incorrect mappings and may erroneously remove correct mappings. The reason for this is that the premise of removing the minimum number of mappings possible (either locally or globally) can fail in cases where there are as many or more incorrect mappings than correct mappings leading to unsatisfiable classes. Indeed, this is exemplified in Figure 1, where ALCOMO erroneously removed the correct mapping. If we evaluated an alignment containing

the correct mapping and not the incorrect ones against the ALCOMO-repaired reference, the alignment would be penalized twice: first for having a mapping not present in the reference, and second for not including the erroneous mapping. This means that, even if the true alignment between two ontologies is coherent, by employing an automated repair technique to create a coherent reference alignment we risk excluding correct mappings, and thus providing a more misleading evaluation than if we used the unrepaired reference alignment.
This problem is amplified by the fact that two repair techniques may remove different mappings and arrive at different coherent alignments of comparable size, as exemplified in Figure 1. Without knowing the true alignment, it is impossible to assess which repair technique produces the more correct alignment. However, if the differences between the techniques are statistically significant, in choosing one technique to repair the reference alignment we may bias the evaluation towards that technique. More concretely, if two matching systems produce a similar unrepaired algorithm but use different repair techniques, the one that uses the same repair technique used to repair the reference alignment is likely to produce better results. This is illustrated in Figure 3, which shows two different repairs with techniques 1 and 2 of the same original reference alignment (A). When technique 1 is used to repair the alignment produced by a matching system, its overlap with the reference alignment repaired by 1 (B) is considerable greater than its overlap with the reference alignment repaired by 2 (C).

Table 4: McNemar's exact test for differences between alignments

Task	ALCOMO - LogMap-Repair	OAEI 2013 Repair - AML-Repair
FMA-NCI	2.80E-4	9.01E-4
FMA-SNOMED	2.97E-09	<1.00E-15
SNOMED-NCI	<1.00E-15	2.08E-08

Values shown are two-sided exact p-values

A related work argued that the differences between repair techniques were on average negligible, by comparing the results of applying LogMap-Repair and ALCOMO to the top three systems that participated in the Large Biomedical track of OAEI 2012 [16]. Although the differences between the repair techniques were indeed generally small in percentage, they reflect differences in tens or even hundreds of mappings and can be significant in the context of the OAEI competition.
To demonstrate that the alignments produced by different repair techniques are statistically different, we performed a McNemar's exact test [17] comparing two sets of reference alignments: the OAEI 2012 reference alignments repaired by LogMap and ALCOMO, and the OAEI 2013 reference alignment with the original UMLS reference alignment repaired by AML-Repair. LogMap and ALCOMO

disagree over 177 mappings and UMLS original and repaired differ in 78 mappings. The results in Table 4 show that there is indeed a statistical difference between these sets of alignments, as the p-values obtained are clearly below the lowest significance intervals typically considered (0.01).
To empirically test the possibility that the repair technique selected to repair the reference alignment may lead to a bias in evaluation, we produced simple lexical-based alignments for the three tasks of the Large Biomedical Ontologies (by using AML on the small overlapping ontology fragments [18]). Then, we repaired these alignments using either LogMap-Repair or AML-Repair, and evaluated the repaired alignments against a set of reference alignments: original (UMLS unrepaired), LogMap-Repair (the original repaired with LogMap, as provided in OAEI 2012), and AML-Repair (the original repaired with AML-repair). The results of this evaluation are shown in Table 5. With the sole exception of the AML + LogMap-Repair in the FMA-SNOMED task, the best evaluation results in each task were obtained when the repair technique used to repair the alignment was the same that was used in the reference. Although the differences between the various reference alignments were relatively small (usually below 1%) they are not irrelevant from the perspective of the OAEI evaluation, as the differences between matching systems are often in this range. Thus, the repair technique used to repair the reference alignment can indeed lead to a biased evaluation. What is more, this encourages systems competing in OAEI to adopt existing repair techniques, rather than try to develop novel and potentially better alternatives.

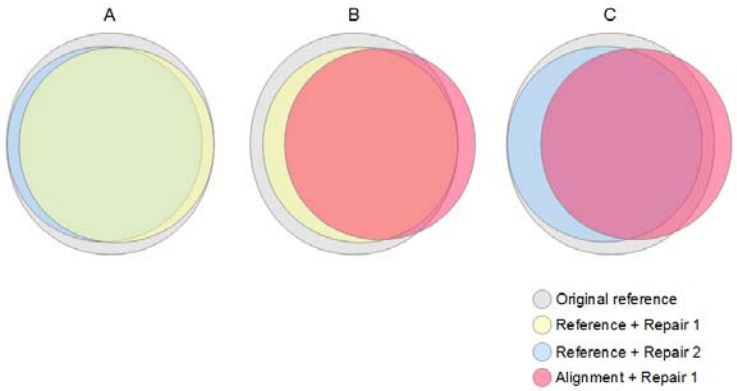


Fig. 3: Comparing a repaired alignment with two different repaired references

We posit that a reference alignment for evaluating ontology matching systems should not exclude potentially correct alignments. As we have shown in Figure 2, it is possible that the true alignment between two ontologies is not coherent. In such cases, repairing the alignment should only be considered if the

Table 5: Influence of different repair techniques on the evaluation of matching systems

Reference	Precision	Recall	F-measure	Size	Correct	Reference
AML + AML-Repair (FMA vs NCI small)						
Original	96.9%	78.8%	87.4%	2457	2382	3024
LogMap-Repair	95.2%	80.7%	87.7%	2457	2339	2898
AML-Repair	95.9%	81.2%	**88.2%**	2457	2356	2901
AML + LogMap-Repair (FMA vs NCI small)						
Original	96.8%	78.8%	87.4%	2461	2383	3024
LogMap-Repair	95.4%	81%	**87.9%**	2461	2347	2898
AML-Repair	95.2%	80.8%	87.7%	2461	2343	2901
AML + AML-Repair (FMA vs SNOMED small)						
Original	95.2%	65.4%	78.9%	6187	5889	9008
LogMap-Repair	86.1%	65.7%	75.2%	6187	5329	8111
AML-Repair	93.2%	69%	**80.2%**	6187	5764	8349
AML + LogMap-Repair (FMA vs SNOMED small)						
Original	94.9%	66.4%	**79.4%**	6298	5978	9008
LogMap-Repair	86.4%	67.1%	76.1%	6298	5439	8111
AML-Repair	89.9%	67.8%	78.1%	6298	5660	8349
AML + AML-Repair (SNOMED vs NCI small)						
Original	92.6%	60.4%	74.8%	12305	11390	18844
LogMap-Repair	91.6%	61.5%	75.1%	12305	11275	18324
AML-Repair	91.5%	62.3%	**75.5%**	12305	11255	18065
AML + LogMap-Repair (SNOMED vs NCI small)						
Original	92.6%	61.3%	75.3%	12474	11550	18844
LogMap-Repair	91.7%	62.4%	**75.7%**	12474	11439	18324
AML-Repair	90.7%	62.6%	75.4%	12474	11312	18065

Best F-score values in bold face

ontologies are to be merged into an integrated resource, as otherwise repairing it implies losing correct mappings. However, even in the cases where the true alignment between two ontologies is expected to be coherent, the use of automatic repair techniques to build a reference alignment is likely to lead to the loss of some correct mappings. Penalizing a system that finds true hard-to-find mappings because these happened to be removed during the repair of the reference alignment is certainly not desirable. The OAEI 2013 reference alignments attempt to minimize the number of mappings removed while still maintaining coherence by replacing equivalence relations with subsumption relations where necessary. But as we have shown, only a small fraction of these relationships are correct as subsumptions. In most cases, the original equivalence relation was correct, and in some other cases the mappings should not exist at all.

On the other hand, using the original (unrepaired) reference alignments is not without issues because these do contain erroneous mappings. Going back to the example in Figure 1, a system that finds only the correct mapping would get a worst result than a system that found the two incorrect mappings if it were evaluated with the original reference alignment. The same would also be true if the system were evaluated with the OAEI 2013 reference alignment, as all three mappings are present in this alignment in the form of subsumptions (assuming the evaluation only considers the presence/absence of mappings and not their relationships).

We propose that a more impartial evaluation could benefit from the fact that existing alignment repair algorithms compute the sets of conflicting mappings as part of their process. Mappings within these sets would be tagged as uncertain, and their presence or absence in the evaluated alignments would not be taken into account when calculating performance metrics. A similar approach has been proposed for cases where only a fraction of the possible mappings have been manually evaluated [19]. Coupling this approach with a satisfiability check on the alignment would allow a more impartial evaluation w.r.t. the repair approach chosen by the matching systems. To illustrate this we have evaluated the AML, AML+AML-Repair and AML+LogMap-Repair alignments for FMA-NCI against an unbiased reference alignment where all conflicting mappings (due to disjointness clauses) have been identified and their presence or absence is not considered in the evaluation. Table 6 presents these results, showing that repaired alignments have a higher precision without losing recall.

Table 6: Evaluaton of different repair techniques against an unbiased reference

Repair Technique	Precision	Recall	F-measure	Size	Correct	Reference
No Repair	95.2%	81.8%	88.2%	1845	1756	2147
AML-Repair	95.9%	81.8%	88.6%	1831	1756	2147
LogMap-Repair	95.7%	81.8%	88.5%	1834	1756	2147

Size and Reference do not include uncertain mappings.

4 Conclusions

As ontologies become more prevalent, large and complex, so must ontology matching systems evolve and with them their evaluation strategies. A recent step in this direction has been the introduction of the large biomedical track in OAEI 2012, where the reference was automatically created by processing an external set of integrated vocabularies and then taking this unrefined alignment and repairing it to diminish its incoherence.
We have found that the repair technique employed to create the OAEI 2013 reference alignment, although less aggressive than the ones used in 2012, still removes a considerable portion of correct mappings and incorrectly alters equivalence mappings to subsumptions. Furthermore, we have shown that alignments repaired with different techniques are significantly different, which can have an impact on the evaluation of ontology matching systems. To decrease the impact of these issues on the evaluation of ontology matching systems, we have proposed an alternative for the evaluation of repaired alignments, where the presence or absence of conflicting mappings is not accounted for. We consider that an alignment between two ontologies should enforce coherence, when the advantages of doing so outweigh the disadvantages, which depends on the application of the alignment and on the ontologies themselves. For instance, if the goal of an alignment is to support integration, then coherence is paramount. However, if the alignment is only intended to support a "lighter" connection between the ontologies (e.g., cross-references), then coverage is likely more relevant than coherence, especially if we consider the error rates of repair techniques. Moreover, when ontologies do not model conflicting views of their domain, then a fruitful alignment between them should be coherent, and ensuring coherence can be a crucial step in filtering out errors. However, when ontologies have incompatible ontological models, their complete integration is impossible and enforcing coherence in their alignment will necessarily remove or alter correct mappings.
How to best integrate ontologies with conflicting views is still a debated question [20], and in some cases the goal might not even be a full-fledged integration. We agree with the opinion expressed in [21] that to solve inherent incompatibilities between ontologies, expert intervention is necessary. However, some incompatibilities are unsolvable, and consequently a full coherent integration of the ontologies is impossible. To promote the usefulness of the alignments there should be room for alignments to contain mappings that violate constraints but are ultimately relevant. A next logical step is to investigate the best approach to support the encoding of these conflicts in the alignment.

Acknowledgements

DF, CP, ES and FMC were funded by the Portuguese FCT through the SOMER project (PTDC/EIA-EIA/119119/2010) and the multi-annual funding program to LASIGE. CP was funded by the FLAD-NSF 2013 Programme under the project "Turning Big Data into Smart Data".

References

1. Eckert, K., Ferrara, A., Hollink, L., Meilicke, C., Nikolov, A., Ritze, D., Shvaiko, P., Grau, B.C., Zapilko, B.: Results of the Ontology Alignment Evaluation Initiative 2012. (2012) 73–115
2. Euzenat, J., Meilicke, C., Stuckenschmidt, H.: Ontology Alignment Evaluation Initiative : six years of experience. Volume 6720. (2011)
3. Rosse, C., Jr, L.V.M.: A reference ontology for biomedical informatics : the Foundational Model of Anatomy. Journal of Biomedical Informatics **36** (2003) 478–500
4. Schulz, S., Cornet, R., Spackman, K.: Consolidating SNOMED CT's ontological commitment. Applied Ontology **6** (2011) 1–11
5. Golbeck, J., Fragoso, G.: The National Cancer Institute's thesaurus and ontology. Web Semantics: Science, Services and Agents on the World Wide Web (2011)
6. Shvaiko, P., Euzenat, J.: Ontology Matching: State of the Art and Future Challenges. IEEE Transactions on Knowledge and Data Engineering **25**(1) (January 2013) 158–176
7. Lambrix, P., Ivanova, V.: A unified approach for debugging is-a structure and mappings in networked taxonomies. Journal of Biomedical Semantics **4**(1) (2013)
8. Beisswanger, E., Hahn, U.: Towards valid and reusable reference alignments - ten basic quality checks for ontology alignments and their application to three different reference data sets. Journal of Biomedical Semantics **3 Suppl 1** (2012) S4
9. Giunchiglia, F., Yatskevich, M., Avesani, P., Shvaiko, P.: A large scale dataset for the evaluation of matching systems. Knowledge Eng. Review (January) (2009)
10. Jiménez-Ruiz, E., Grau, B., Zhou, Y., Horrocks, I.: Large-scale Interactive Ontology Matching: Algorithms and Implementation. ECAI (ii) (2012) 444–449
11. Rosoiu, M., dos Santos, C., Euzenat, J.: Ontology matching benchmarks: generation and evaluation. In: 6th ISWC workshop on ontology matching (OM). (2011)
12. Jiménez-Ruiz, E., Grau, B.C., Horrocks, I.: Exploiting the UMLS Metathesaurus in the Ontology Alignment Evaluation Initiative. E-LKR Workshop (2012) 1–6
13. Meilicke, C.: Alignment incoherence in ontology matching. PhD thesis, University of Mannheim (2011)
14. Jiménez-Ruiz, E., Grau, B.: Logmap: Logic-based and scalable ontology matching. The Semantic WebISWC 2011 (2011)
15. Santos, E., Faria, D., Pesquita, C., Couto, F.: Ontology alignment repair through modularization and confidence-based heuristics. arXiv:1307.5322 (2013)
16. Jiménez-Ruiz, E., Meilicke, C., Grau, B., Horrocks, I.: Evaluating Mapping Repair Systems with Large Biomedical Ontologies. In: 26th International Workshop on Description Logics. (2013)
17. Liddell, F.D.: Simplified exact analysis of case-referent studies: matched pairs; dichotomous exposure. Journal of Epidemiology and Community Health **37**(1) (1983) 82–84
18. Faria, D., Pesquita, C., Santos, E., Palmonari, M., Cruz, I., Couto, F.M.: The AgreementMakerLight Ontology Matching System. In: ODBASE. (2013)
19. Autayeu, A., Maltese, V., Andrews, P.: Recommendations for better quality ontology matching evaluations. In: AISB Workshop on Matching and Meaning. (2010)
20. Schulz, S., Rector, A., Rodrigues, J., Chute, C., Üstün, B., Spackman, K.: Ontology-based convergence of medical terminologies: SNOMED CT and ICD-11. In: eHealth2012. (2012) 89–94
21. Jiménez-Ruiz, E., Grau, B.C., Horrocks, I., Berlanga, R.: Logic-based assessment of the compatibility of UMLS ontology sources. Journal of Biomedical Semantics **2 Suppl 1** (2011) S2

Unsupervised Learning of Link Specifications: Deterministic vs. Non-Deterministic

Axel-Cyrille Ngonga Ngomo[1] and Klaus Lyko[1]

Department of Computer Science
University of Leipzig
Johannisgasse 26, 04103 Leipzig
ngonga@informatik.uni-leipzig.de,
WWW home page: http://limes.sf.net

Abstract. Link Discovery has been shown to be of utter importance for the Linked Data Web. In previous works, several supervised approaches have been developed for learning link specifications out of labelled data. Most recently, genetic programming has also been utilized to learn link specifications in an unsupervised fashion by optimizing a parametrized pseudo-F-measure. The questions underlying this evaluation paper are twofold: First, how well do pseudo-F-measures predict the real accuracy of non-deterministic and deterministic approaches across different types of datasets? Second, how do deterministic approaches compare to non-deterministic approaches? To answer these questions, we evaluated linear and Boolean classifiers against classifiers computed by using genetic programming on six different data sets. We also studied the correlation between two different pseudo-F-measures and the real F-measures achieved by the classifiers at hand. Our evaluation suggests that pseudo-F-measures behave differently on the synthetic and real data sets.

1 Introduction

Over the last years, the importance of Link Discovery (LD) as a research topic has increased significantly. This increase was upheld mainly by the ever-growing size of the Linked Data Web and the scalability and accuracy requirements it brings about. The creation of links between knowledge bases, one of the most important steps in the realization of the vision of the Linked Data Web has profited from this boost of research and seen the development of several LD frameworks and approaches [7, 2, 12, 11, 3]. Two main research focuses played a role so far: (1) the determination of time-efficient algorithms [3, 7, 6] for LD and (2) the development of approaches for the efficient computation of link specifications (also called linkage rules) [8, 4, 10, 9]. In most cases, supervised machine learning approaches were used to tackle the second challenge of LD. Approaches developed so far include batch learning using genetic programming [3], the combination of active learning and of linear and Boolean classifiers [8] as well as the combination of active learning and genetic programming [9]. In addition, unsupervised approaches for learning link specifications have been recently developed [10]. While all these approaches have been shown to achieve good results,

unsupervised approaches obviously trump batch and active learning approaches as they do not require any feedback from the user and can still achieve remarkably good performance. In addition, genetic programming approaches yield the central advantage of being able to exploit the whole spectrum of the link specification grammar provided by the framework in which they were implemented. So far, unsupervised approaches to the discovery of link specifications have only been tested with artificially generated benchmark data and low-noise datasets. Moreover, no deterministic approach for the unsupervised discovery of link specifications has been presented so far, although deterministic approaches such as those presented in [8] counterbalance their limitations in expressiveness by being clearly more time-efficient than approaches based on genetic programming.

The aim of this paper is to experimentally examine the unsupervised discovery of link specifications with respect to two main questions:

1. *Are deterministic approaches able to achieve results comparable to those of genetic approaches?* To address this question, we extended the approach presented in [9] and devised an approach for the unsupervised learning of Boolean and linear classifiers which is loosely based on the RAVEN approach [8]. We refrained from reusing the approach presented in [10] as one of the pseudo-measures we rely on was designed especially to work well with this approach. Consequently, using it could have led to a bias in our results.
2. *How well are pseudo-F-measures suited for unsupervised discovery performed on synthetic and real data sets?* Here, we compared the results achieved by the approaches above on the three OAEI 2010 datasets[1] and on three data sets extracted from real data[2]. In addition to the pseudo-F-measure described in [10] (which we dub $\mathcal{F}_u^\beta$), we devised a supplementary pseudo-F-measure $\mathcal{F}_d^\beta$ which relies more on the standard definition of the F_β-measure. We performed a correlation analysis of the values of $\mathcal{F}_u^\beta$, $\mathcal{F}_d^\beta$ and the F_1 measure and detected a surprisingly different behaviour of these measures across our two groups of data sets.

The rest of this paper is structured as follows: We first give an overview of the approaches and measures we used for our experiments. We then present the results of our experimental setup as well as the results of our experiments. For the sake of reproducibility, we chose to use freely available datasets and made the approaches presented herein freely available at the project website.[3] We conclude with a summary of the implications of our results for the LD community.

2 Approaches

In general, a link specification is a classifier C that assigns each element of the set $S \times T$ to one of the classes of $Y = \{+1, -1\}$, where S is called the set of source

[1] Freely available at `http://oaei.ontologymatching.org/2010/`.
[2] Freely available at `http://dbs.uni-leipzig.de/en/research/projects/object_matching/fever/benchmark_datasets_for_entity_resolution`.
[3] `http://saim.sf.net`

instances, while T is the set of target instances. $(s,t) \in S \times T$ is considered by C to be a correct link when $C(s,t) = +1$. Otherwise, (s,t) is considered not be a potential link. We will assume that the classifier C relies on a complex similarity function σ which consists of a combination of atomic similarity measure σ_i. Each of the atomic similarity measures is associated with a parameter ω_i, which is used in main cases as threshold or weight for σ_i. Supervised approaches to the computation of link specifications use labelled training data $L \subseteq S \times T \times Y$ to maximize an objective function such as the distance from the labelled data items to the boundary of the classifier in the case of Support Vector Machines [1]. The idea behind unsupervised approaches to learning link specifications is that they do not to utilize any training data (i.e., $L = \emptyset$). Instead, they aim to optimize an objective function $\mathcal{F}$. In the following, we present the non-deterministic and the deterministic approaches we utilized in our experiments. We then present two different objective functions that are based on the well-know F_β-measure. These functions build the basis for our evaluation.

2.1 Non-Deterministic Approach

Algorithm 1 EAGLE

Require: Sets of instances S and T, size of population, number of iterations
  Get property mapping (S, T)
  Generate initial population
  repeat
    Compute $\mathcal{F}$ for all individuals.
    Apply genetic operators to population
  until Number of iterations is reached
  return Overall fittest individual

The non-deterministic approach we evaluated is based on the EAGLE approach presented in [9] and implemented in the LIMES framework [8]. The approach was modified as described in Algorithm 1. We begin by generating a random population of n individuals. Let G^t be the population at the iteration t. To evolve a population to the generation G^{t+1}, the fitness of each individuals $g^t \in G^t$ is computed. For this purpose, the mapping $M(g^t)$ generated by g^t is evaluated and the value $\mathcal{F}(M(g^t))$ is assigned to g^t. These fitness values build the basis for selecting individuals for the genetic operator *reproduction*. EAGLE uses a tournament setting between two selected individuals to decide which one is copied to the next generation g^{t+1}. On randomly selected individuals the operator *mutation* is applied according to a probability called the *mutation rate*. A mutation can affect an individual in three different ways: First, it can alter the thresholds used by the individual. Second, a mutation can alter the property values that are compared by one of the atomic measures on which the classifier relies. Finally, mutations can modify the measures included in the

individuals. The third genetic operator, *crossover*, operates on two parent individuals and builds a new offspring by swapping two random sub-trees of the parent genotypes. The application of these operators is carried out iteratively until a maximal number of iterations is reached. The result of this process is the mapping M that is returned by the best individual. M is postprocessed as follows: Each $s \in S$ such that $\exists t \in T : (s,t) \in M$ is mapped to $\arg\max_{t \in T} \sigma(s,t)$. The postprocessed mapping is finally returned.

2.2 Deterministic Approaches

Algorithm 2 EUCLID

Require: Specification of the datasets S and T
Require: $\Delta_\omega \in]0,1[$
Require: $\gamma > 1$, $\theta > 0$ with $(\gamma, \theta) \in \mathbb{N}^2$
  Get property mapping (S, T)
  bestClassifier = $(1, \ldots, 1)$
  $\Omega = \emptyset$
  for $k = 0 \rightarrow \lfloor 1/\Delta_\omega \rfloor$ **do**
    $\Omega = \Omega \cup \{1 - k\Delta_\omega\}$
  end for
  for $i = 1 \rightarrow n$ **do**
    $\sigma_i^{max} = \arg\max_{\omega \in \Omega, \sigma_i \in \Sigma} \mathcal{F}(\sigma_i \geq \omega)$, $\omega_i^{min} = 0$, $\omega_i^{max} = 1$
  end for
  for $iterations = 1 \rightarrow \theta$ **do**
    $\Delta = \frac{|\omega_i^{max} - \omega_i^{min}|}{\gamma}$
    $C = \arg\max_{i=1}^{n} \mathcal{F}(\omega_i^{min} + k_i\Delta)$
    if $\mathcal{F}(C) > \mathcal{F}$(bestClassifier) **then**
      C = bestClassifier
    else
      bestClassifier = C
    end if
    for $j = 1 \rightarrow n$ **do**
      $\omega_j^{min} = \max(0, \zeta_j)$, $\omega_j^{max} = \min(1, \zeta_j)$
    end for
  end for
  return bestClassifier

Linear and Boolean classifiers have been shown in previous work [8] to also achieve good results on the task of LD. Both types of classifiers can be characterized by a similarity function σ which depends on similarity measures σ_i and parameters ω_i. Linear classifiers $\mathcal{L}$ classify (s,t) as belonging to $+1$ iff $\sum_{i=1}^{n} \omega_i \sigma_i(s,t) \geq 1$. For Boolean classifiers $\mathcal{B}$, the inequality $\bigwedge_{i=1}^{n} \sigma_i(s,t) \geq \omega_i$ must

be fulfilled by the pair (s, t) for it belong to $+1$. In both cases, a classifier can be encoded by the vector $\Omega = (\omega_1, \ldots, \omega_n)$. Determining the best $\mathcal{L}$ or $\mathcal{B}$ would require testing all possible combinations of values $\omega_i \in [0, 1]$, which would be impracticable. The idea behind our algorithm EUCLID (Efficient and Unsupervised Classification for Link Discovery) is to reduce the number of configurations that must be tested by applying a search within the search space whose granularity increases gradually as described in Algorithm 2: We first begin by detecting the right similarity measure for each pair of properties. To achieve this goal, we use the similarity $\sigma_i^{max} = \underset{\omega \in \Omega, \sigma_i \in \Sigma}{\arg\max} \mathcal{F}(\sigma_i \geq \omega)$ for each pair of properties, where $\mathcal{F}(\sigma_i \geq \omega)$ is the value of the pseudo-F-measure (PFM) of the classifier C_0 such that $C_0(s, t) = +1 \iff \sigma_i(s, t) \geq \omega$, $\Omega = \{\omega > 0 \text{ with } \exists k \in \mathbb{N} : \omega = 1 - k\Delta_\omega\}$ is a set of threshold values and Σ is the set of similarity measures implemented by the framework at hand. Note that Δ_ω is the first of the three parameters required by EUCLID.

In a second step, we compute the actual link specification. Given two parameters $\gamma > 1$ and $\theta > 0$, ω_i^{min} and ω_i^{max} are set to 0 and 1 respectively for each of the similarities σ_i. Then the interval ω_i^{min} and ω_i^{max} is split into γ intervals of the same size $\Delta = (|\omega_i^{max} - \omega_i^{min}|/\gamma$. For each of the possible parametrization $\omega_i = \omega_i^{min} + k\Delta$, $k \in \{0, \ldots, \gamma\}$, EUCLID simply runs all of the resulting classifiers C and compute their fitness $\mathcal{F}(C)$. The current overall best classifier $C = (\zeta_1, \ldots, \zeta_n)$ is used as new reference point. ω_{min}^i is set to $\max\{0, \zeta_i - \Delta\}$ and ω_{max}^i to $\min\{\zeta_i + \Delta, 1\}$ while $\gamma := \gamma/2$. This procedure is repeated θ times and the best overall classifier w.r.t. $\mathcal{F}$ is returned.

3 Pseudo-F-measures

We considered two different PFMs for the automatic discovery of link specifications. The first PFM, dubbed $\mathcal{F}_u^\beta$, was proposed by [10] and is based on the F_β measure. Consequently, it is defined as

$$\mathcal{F}_u^\beta = (1 + \beta^2) \frac{\mathcal{P}_u \mathcal{R}_u}{\beta^2 \mathcal{P}_u + \mathcal{R}_u}. \tag{1}$$

Let $M \subseteq S \times T$ be a mapping generated by an algorithm, S be the set of source instances and T be the set of target instances. $\mathcal{P}_u$ is defined as

$$\mathcal{P}_u(M) = \frac{|\{s | \exists t : (s, t) \in M\}|}{\sum\limits_s |\{t : (s, t) \in M\}|}, \tag{2}$$

while $\mathcal{R}_u$ is computed as follows:

$$\mathcal{R}_u(M) = \frac{|M|}{\min(|S|, |T|)}. \tag{3}$$

Note that $\mathcal{R}_u(M)$ can be larger than 1 as $|M|$ can be larger than $min(|S|, |T|)$. While this does not occur in the setup proposed by [10], it seems rather counterintuitive that a recall measure can lead to values beyond 1. We thus specified

the following novel pseudo-recall dubbed $\mathcal{R}_d$:

$$\mathcal{R}_d(M) = \frac{|\{s|\exists t : (s,t) \in M\}| + |\{t|\exists s : (s,t) \in M\}|}{|S| + |T|}. \quad (4)$$

This pseudo-recall computes the ratio how well all source and target instances are covered by the Mapping M. Thus, $\mathcal{R}_d(M) = 1$ if every $s \in S$ is mapped to at least one $t \in T$ and vice versa. We would argue that it is therewith more in line with the original definition of precision and recall. Our pseudo-F-measure $\mathcal{F}_d$ is thus defined as

$$\mathcal{F}_d^\beta(M) = (1+\beta^2)\frac{\mathcal{P}_d(M)\mathcal{R}_d(M)}{\beta^2\mathcal{P}_d(M) + \mathcal{R}_d(M)} \text{ with } \mathcal{P}_d = \mathcal{P}_u. \quad (5)$$

4 Experiments and Results

The goal of our experiments was twofold. First, we wanted to know how deterministic approaches perform in comparison to non-deterministic approaches for the discovery of link specifications. The basic intuition here was that if deterministic approaches can achieve F-scores similar to those of non-deterministic approaches, they should be preferred as they are usually more time-efficient. We thus compared the maximal F-measure achieved by each of our approaches on the six different data sets at hand. Moreover, we wanted to measure how well PFM can predict the real performance of classifiers. Especially, we were interested in knowing whether the predictive power of pseudo-F-measures is as reliable on real data as it has been shown to be on synthetic data. Within this context, we were also interested in knowing which setting of β led to the best real F-measure across the different datasets that we used, as $\beta = 0.1$ was suggested in the past [10]. We thus ran our evaluation using both $\mathcal{F}_u$ and $\mathcal{F}_d$ for β-values between 0.1 and 2.0 using a 0.1 increment. We used two different measures to evaluate the correlation between PFM and F_1. In the following, we present the data, algorithmic parameters and correlation measures used for our experiments. We then present our results and discuss their implications for the next steps of research on link discovery.

4.1 Experimental Setup

In all experiments, we assumed that we knew the perfect mapping between the properties. Each experiment was ran on a single thread of an Ubuntu Linux server running JDK1.7 and was allocated maximally 2GB of RAM. The processors were 2.0GHz quadcore Opterons.

Data We ran our experiments on three synthetic and three real datasets. The synthetic datasets consisted of widely used and well-known Persons1, Persons2 and Restaurant datasets from the OAEI2010 set of benchmark data sets. The real

datasets consisted of the ACM-DBLP, Amazon-Google and Abt-Buy datasets that were extracted from websites or databases and for which a gold standard was created manually as reported in [5]. The ACM-DBLP dataset consists of 2,617 source and 2,295 target publications (gold standard: 2,224 links). The Amazon-Google dataset links 1,363 to 3,226 products (gold standard: 1,300 links). Finally, the Abt-Buy dataset links 1,081 to 1,092 products via 1,097 correct links. All non-RDF datasets were transformed into RDF and all attribute values were set to lower case. Apart from this preprocessing, no other preprocessing step was carried out.

Parametrization of the algorithms Four parameters need to be set to run EAGLE: the number of iterations, the size of the population, the crossover rate and the mutation rate. Similarly to [10], we used 20 iterations with a population of 100 individuals. The crossover and mutation rates were set to 0.6. Given that this approach is not deterministic, we ran the experiments 5 times and present the average values in Section 4.2. Note that the standard deviations for the F-measures were always under 5% of the average value. For EUCLID, we used $\Delta_\omega = 0.1$, $\gamma = 4$, $\theta = 10$.

Correlation Measures To measure the accuracy of the algorithms, we used the standard F_1-measure. We were interested in determining whether the pseudo-F-measures $\mathcal{F}_u^\beta$ and $\mathcal{F}_d^\beta$ can be used practically to predict the F_1 measure achieved by an algorithm and which setting of β was the best to achieve this goal. Thus, we measured the correlation of $\mathcal{F}_u^\beta$ and $\mathcal{F}_d^\beta$ with F_1 across different values of β. We used two different correlation measures: The Pearson and the Spearman correlation. We used the *Pearson* correlation to ensure the comparability of our approach with other correlation studies as this correlation is one of the most commonly used. The main drawback of the Pearson correlation is that it is most reliable at detecting linear correlations between distributions. As there was no reason for assuming a linear relationship between our measures, we opted to also use another correlation measure that do not make any assumption upon the type of correlation between the input distributions. We used the *Spearman correlation* [13], which assesses how well a monotonic function can describe the relationship between the input distributions by comparing the ranks of the values in the two input distribution. For both correlations, we used a 2-tailed significance test with a confidence threshold of 95%.

4.2 Results

We first measured the F_1-scores achieved by our approaches when relying on $\mathcal{F}_d$ (see Figure 1) and $\mathcal{F}_u$ (see Figure 2). Our results indicate that EUCLID is in general slightly superior to EAGLE. Note that the linear classifier in combination with $\mathcal{F}_d$ even outperforms the supervised approaches presented in [5] and [9] on the ACM-DBLP data set. In addition the linear model leads to better results than the Boolean model in most cases (expect on the Restaurant dataset). Our

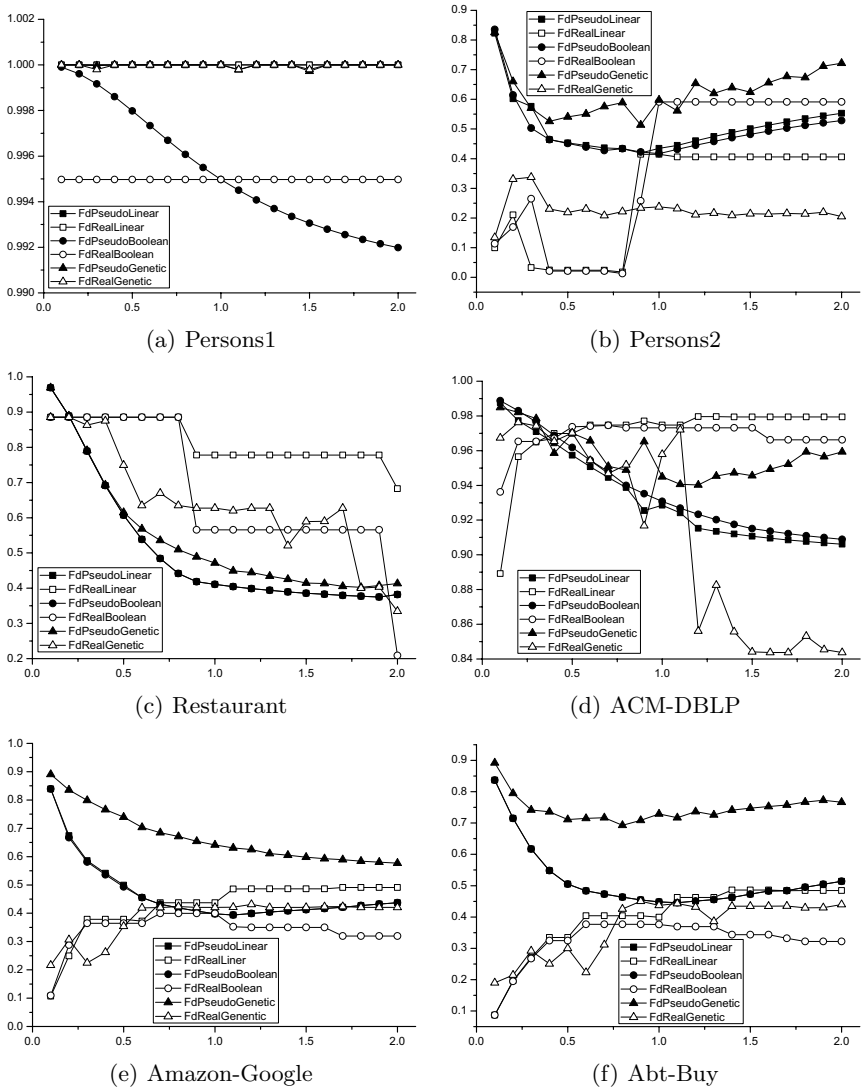
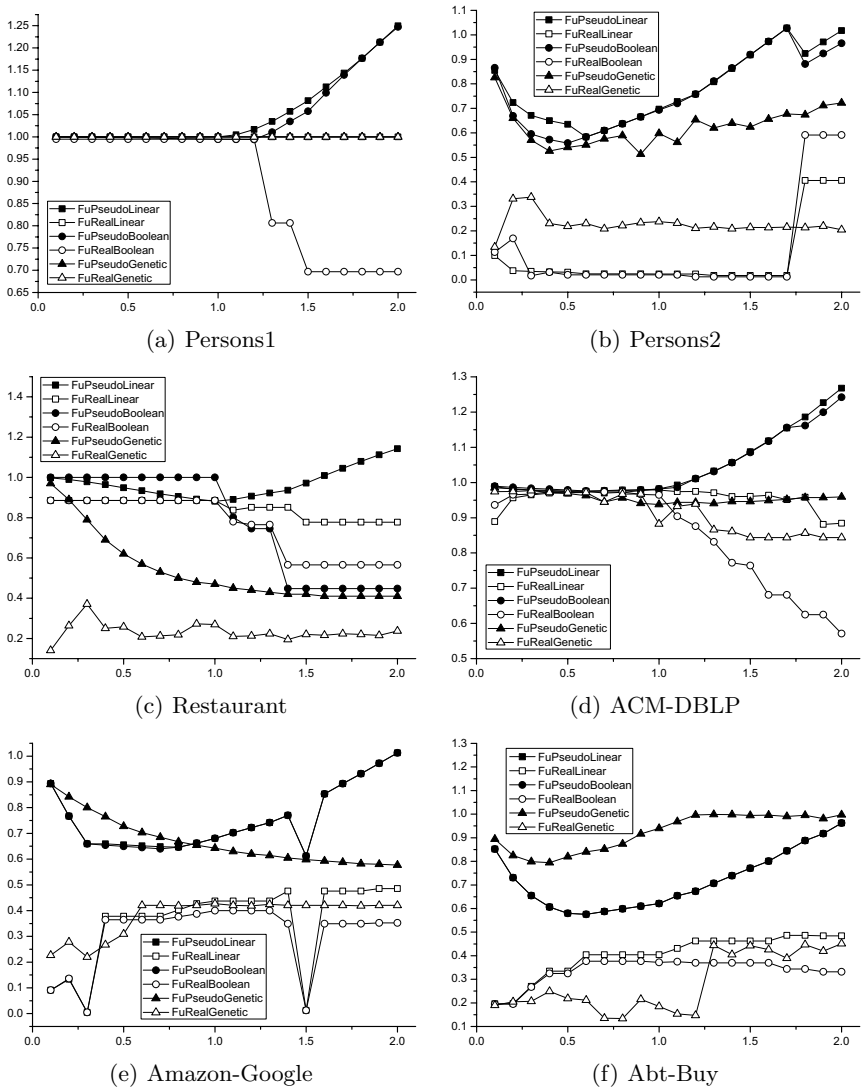


Fig. 1. Evaluation of algorithms based on $\mathcal{F}_d$. The y-axis shows the different F-measures while the x-axis stands for different β-values. Note that "FdPseudo" stands for the pseudo-F-measures achieved by the different classifiers while "FdReal" stands for the real F-measures.

results suggest that $\mathcal{F}_d$ is better suited for EUCLID while $\mathcal{F}_u$ and $\mathcal{F}_d$ tie for EAGLE. With respect to runtime, EUCLID requires between 2.5 and 30s and is therewith between 1 and 2 orders of magnitude faster than EAGLE. Given the significant different in runtimes we observed within our experiments, we suggest



(a) Persons1 (b) Persons2

(c) Restaurant (d) ACM-DBLP

(e) Amazon-Google (f) Abt-Buy

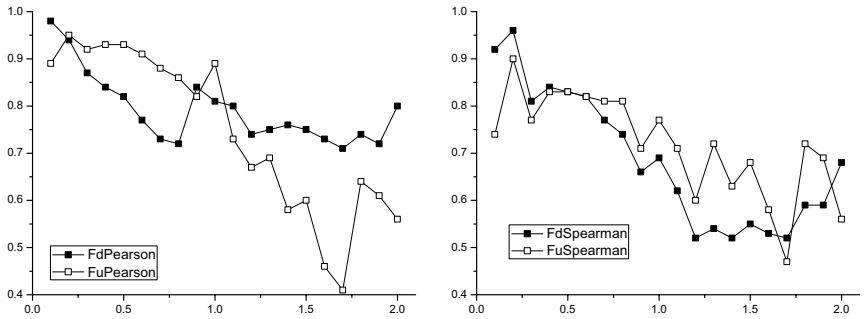
Fig. 2. Evaluation of algorithm based on $\mathcal{F}_u$. The y-axis is the F-measure while the x-axis stands for different β-values. Note that "FuPseudo" stands for the pseudo-F-measures achieved by the different classifiers while "FuReal" stands for the real F-measures.

that the development of specific algorithms for classifiers of a given type can lead to algorithms for the discovery of link specifications that are both time-efficient and highly accurate. The insight we gain is thus a clear *answer to our*

first question: unsupervised deterministic approaches can perform as well as unsupervised approaches on both synthetic and real data.

	Linear		Boolean		Genetic	
	$\mathcal{F}_d$	$\mathcal{F}_u$	$\mathcal{F}_d$	$\mathcal{F}_u$	$\mathcal{F}_d$	$\mathcal{F}_u$
Persons1	**100**	**100**	99.50	99.50	**100**	**100**
Persons2	41.45	40.60	**59.12**	**59.12**	33.77	37.04
Restaurant	**88.56**	**88.56**	**88.56**	**88.56**	**88.56**	**88.56**
ACM-DBLP	**97.96**	97.94	97.46	97.46	97.62	97.71
Amazon-Google	**49.08**	48.55	39.97	39.97	43.11	42.68
Abt-Buy	**48.60**	**48.60**	37.66	37.66	45.03	45.08

Table 1. Maximal F-scores (in %) achieved by the approaches.



(a) Pearson (b) Spearman

Fig. 3. Spearman and Pearson correlation of $\mathcal{F}_u^\beta$ and $\mathcal{F}_d^\beta$ across different values of β measured independently from the algorithm used.

To answer our second question, we first computed the algorithm-independent correlation of $\mathcal{F}_d$ and the F_1 measure as well as the correlation of $\mathcal{F}_u$ and the F_1 measure (see Figure 3). In our experiments, the correlations varied significantly across the different values of β, yet remained positive and significant in 97.5% of the cases (the 2 lowest correlation scores of the Pearson correlation for $\mathcal{F}_u$ were not significant). This means that optimizing $\mathcal{F}_u$ and $\mathcal{F}_d$ for one particular setting of β is a sensible approach towards finding the best classifier for that particular setting of β. We then computed the Pearson and Spearman correlation (see Table 2) between $\mathcal{F}_u$, $\mathcal{F}_d$ and the F_1 measure achieved by the different approaches across different values of β. Our results were somewhat surprising as we detected both significant positive and negative correlations across the different datasets and for both correlations. Interestingly, while the number of

	Linear		Boolean		Genetic	
	$\mathcal{F}_d$	$\mathcal{F}_u$	$\mathcal{F}_d$	$\mathcal{F}_u$	$\mathcal{F}_d$	$\mathcal{F}_u$
Persons1	–	–	–	-0.85*	0.84*	-0.1
Persons2	-0.09	0.54*	-0.12	0.43	-0.43	-0.43
Restaurant	0.73*	-0.71*	0.71*	1*	0.84*	0.16
ACM-DBLP	-0.70*	-0.65*	-0.43	-0.97*	0.46*	0.51*
Amazon-Google	-0.95*	0.49	-0.79*	0.07	-0.88*	-0.03
Abt-Buy	-0.9*	0.27	-0.98*	-0.27	0.38	-0.9*
Persons1	–	–	–	-0.87*	0.99*	-0.1
Persons2	0.02	-0.09	0.21	-0.11	-0.56*	-0.56*
Restaurant	0.85*	-0.54*	0.85*	1*	0.91*	0.15
ACM-DBLP	-0.87*	-0.73*	0.05	-0.95*	0.34	0.47*
Amazon-Google	-0.49*	0.68*	-0.27	-0.22	-0.64*	-0.39
Abt-Buy	-0.37	0.59*	-0.82*	-0.47*	-0.13	-0.49*

Table 2. Pearson and Spearman Correlation of PFM and real F-measures across different β-values. The top section of the table shows the Pearson correlation while the bottom part shows the Spearman correlation. The correlations are not defined for the fields marked with "–" due to at least one of the standard deviations involved being 0. Correlations marked with "*" are significant.

significant positive and negative correlations were relatively balanced for the synthetic data sets, negative correlations seemed to dominate the set of real datasets, thus hinting towards $\mathcal{F}_u$ and $\mathcal{F}_d$ behaving differently depending on the type of data they are confronted with. The negative correlation values suggest that to detect the best values of β for a real dataset automatically, the mapping M which leads to the smallest best value of $\mathcal{F}_d$ across the different values of β should be chosen. This seems rather counter-intuitive and is a hypothesis that requires ampler testing on a larger number of real datasets. Overall, our results show clearly that no β-value achieves a maximal F_1-measure across our data sets. Still, for real datasets, $\mathcal{F}_d$ seems to perform well for $\beta \in [0.8, 1.2]$. Stating such an interval for $\mathcal{F}_u$ is more difficult as the set of β-values that lead to the best mapping is very heterogeneous across the different datasets. Interestingly, this conclusion diverges from that proposed in previous work. The answer to our second question is still clearly that while the predictive power of $\mathcal{F}_u^\beta$ and $\mathcal{F}_d^\beta$ is sufficient for the results to be used in practical settings, significant effort still needs to investigated to create a generic non-parametric PFM that can be used across different datasets and algorithms to predict the F_1-measure reliably .

5 Conclusion

In this paper, we present a first series of experiments to determine how well standard classifier models such as linear and Boolean classifiers perform in com-

parison to classifiers generated by the means of genetic programming in an unsupervised learning setting based on maximizing a PFM. Overall, our results indicate that we are still at the beginning of the search towards the "holy grail" of PFMs. Especially on real data, the maximal PFM achieved by algorithms across different values of β is often negatively correlated with the value of the F_1. The magnitude of this effect is significantly reduced on synthetic data. This difference suggest that there is still a need for benchmark generation methods that allow creating benchmark data sets which reflect real data in a more holistic way. Moreover, our evaluation shows that deterministic classifiers perform as well as or better than non-deterministic approaches while still bearing the main advantage of being significantly more time-efficient. Thus, finding more efficient extension of EUCLID or similar approaches should allow providing users of LD frameworks with accurate link specifications within an interactive setting. Detecting the right parametrization for PFM yet remains an unsolved problem.

References

1. Nello Cristianini and Elisa Ricci. Support vector machines. In *Encyclopedia of Algorithms*. 2008.
2. Aidan Hogan, Axel Polleres, Jrgen Umbrich, and Antoine Zimmermann. Some entities are more equal than others: statistical methods to consolidate linked data. In *Workshop on New Forms of Reasoning for the Semantic Web: Scalable & Dynamic (NeFoRS2010)*, 2010.
3. R. Isele, A. Jentzsch, and C. Bizer. Efficient Multidimensional Blocking for Link Discovery without losing Recall. In *WebDB*, 2011.
4. Robert Isele and Christian Bizer. Learning Linkage Rules using Genetic Programming. In *Sixth International Ontology Matching Workshop*, 2011.
5. Hanna Köpcke, Andreas Thor, and Erhard Rahm. Comparative evaluation of entity resolution approaches with fever. *Proc. VLDB Endow.*, 2(2):1574–1577, 2009.
6. Axel-Cyrille Ngonga Ngomo. A time-efficient hybrid approach to link discovery. In *Proceedings of OM@ISWC*, 2011.
7. Axel-Cyrille Ngonga Ngomo and Sören Auer. Limes - a time-efficient approach for large-scale link discovery on the web of data. In *Proceedings of IJCAI*, 2011.
8. Axel-Cyrille Ngonga Ngomo, Jens Lehmann, Sören Auer, and Konrad Höffner. Raven: Active learning of link specifications. In *Proceedings of the Ontology Matching Workshop (co-located with ISWC)*, 2011.
9. Axel-Cyrille Ngonga Ngomo and Klaus Lyko. Eagle: Efficient active learning of link specifications using genetic programming. In *Proceedings of ESWC*, 2012.
10. Andriy Nikolov, Mathieu D'Aquin, and Enrico Motta. Unsupervised learning of data linking configuration. In *Proceedings of ESWC*, 2012.
11. George Papadakis, Ekaterini Ioannou, Claudia Niedere, Themis Palpanasz, and Wolfgang Nejdl. Eliminating the redundancy in blocking-based entity resolution methods. In *JCDL*, 2011.
12. Jennifer Sleeman and Tim Finin. Computing foaf co-reference relations with rules and machine learning. In *Proceedings of the Third International Workshop on Social Data on the Web*, 2010.
13. C. Spearman. The proof and measurement of association between two things. *The American journal of psychology*, 15:72–101, 1904.

IncMap: Pay as you go Matching of Relational Schemata to OWL Ontologies

Christoph Pinkel[1], Carsten Binnig[2], Evgeny Kharlamov[3], and Peter Haase[1]

[1] fluid Operations AG, D-69190 Walldorf, Germany,
[2] University of Mannheim, D-68131 Mannheim, Germany,
[3] University of Oxford, Oxford, UK

Abstract. Ontology Based Data Access (OBDA) enables access to relational data with a complex structure through ontologies as conceptual domain models. A key component of an OBDA system are mappings between the schematic elements in the ontology and their correspondences in the relational schema. Today, in existing OBDA systems these mappings typically need to be compiled by hand, which is a complex and labor intensive task. In this paper we address the problem of creating such mappings and present *IncMap*, a system that supports a semi-automatic approach for matching relational schemata and ontologies. Our approach is based on a novel matching technique that represents the schematic elements of an ontology and a relational schema in a unified way. *IncMap* is designed to work in a query-driven, pay as you go fashion and leverages partial, user-verified mappings to improve subsequent mapping suggestions. This effectively reduces the overall effort compared to compiling a mappings in one step. Moreover, *IncMap* can incorporate knowledge from user queries to enhance suggestion quality.

1 Introduction

Effective understanding of complex data is a crucial task for enterprises to support decision making and retain competitiveness on the market. This task is not trivial especially since the data volume and complexity keep growing fast in the light of Big Data [1]. While there are many techniques and tools for scalable data analytics today, there is little known on how to find the *right* data.

Today, enterprise information systems of large companies store petabytes of data distributed across multiple – typically relational – databases, each with hundreds or sometimes even thousands of tables (e.g., [2]). For example, an installation of an SAP ERP system comes with tens of thousands of tables [3]. Due to the complexity of data a typical scenario for data analyses today involves a domain expert who formulates an analytical request and an IT expert who has to understand the request, find the data relevant to it, and then translate the request into an executable query. In large enterprises this process may iterate several times between the domain and IT experts, the complexity of data and other factors, and may take up to several weeks.

Ontology-based data access (OBDA) [4] is an approach that has recently emerged to provide semantic access to complex structured relational data. The

core elements of an OBDA system are an *ontology*, describing the application domain, and a set of declarative *mappings*, relating the ontological schema elements (e.g., names of classes and properties) with the relational schema elements (e.g., names of table and attributes) of the underlying data sources. Using the ontology and the mappings, domain experts can access the data directly by formulating queries in terms defined in the ontology that reflects their vocabulary and conceptualization. Using query rewriting techniques, the end-user queries are then translated into queries over the underlying data sources.

Today, most approaches for ontology-based data access focus on the definition of mapping languages and the efficient translation of high-level user queries over an ontology into executable queries over relational data [4,5]. These approaches assume that a declarative mapping of the schema elements of the ontology to the relational elements is already given. So far, in real-world systems [6,7] that follow the ontology-based data access principle, the mappings have to be created manually. The costs for the manual creation of mappings constitute a significant entry barrier for applying OBDA in practice.

To overcome this limitation we propose a novel semi-automatic schema matching approach and a system called *IncMap* to support the creation of mappings directly from relational schemata to ontologies.

We focus on finding one-to-one (direct) correspondences of ontological and relational schema elements, while we also work on extensions for finding more complex correspondences. In order to compute mapping suggestions *IncMap* uses a relational schema, an OWL ontology, a set of user conjunctive queries over the ontology, and user feedback as basic input.

The matching approach of *IncMap* is inspired by the Similarity Flooding algorithm of Melnik et al. [8] that works well for schemata that follow the same modeling principles (e.g., same level of granularity). However, applying the Similarity Flooding algorithm naively for matching schema elements of a relational schema to an OWL ontology results in rather poor quality of the suggested correspondences as we show in our experiments. A major reason is the impedance mismatch between ontologies and relational schemata: While ontologies typically model high-level semantic information, relational schemata describe the syntactical structure on a very low level of granularity.

The contributions of the paper are the following:

- In Section 3, we propose a novel graph structure called *IncGraph* to represent schema elements from both ontologies and relational schemata in a unified way. Therefore, we devise algorithms to convert an ontology as well as a relational schema into their unified *IncGraph* representation. We also briefly discuss techniques to further improve *IncGraph*.
- In Section 4, we present our matching algorithm that we use for matching *IncGraph*s. Its most prominent feature is that *IncMap* can produce the mapping incrementally, query by query. While the original Similarity Flooding algorithm generates correspondences for all schema elements, *IncMap* supports a *pay as you go* matching strategy. For each query we produce only required mappings. *IncMap* leverages the structure of mappings from previ-

ous queries to improve suggestion quality. This effectively reduces the total effort for the user to verify mapping suggestions.
– Section 5 presents an experimental evaluation using different (real-world) relational schemata and ontologies. We see that even in the basic version of *IncMap*, the effort for creating a mapping is up to 20% less than using the Similarity Flooding algorithm in a naive way. In addition, the incremental version of *IncMap* can reduce the total effort by another $50\% - 70\%$.

2 Background

In this section we briefly introduce ontologies [9], relational schemata, and the Similarity Flooding algorithm [8].

Ontologies. An ontology $\mathcal{O}$ specifies a conceptualization of a domain in terms of classes and properties and consists of a set of axioms. Without explanation, ontologies in this paper are OWL ontologies and we will use the following OWL constructs: object and data properties P, and domains $\texttt{Domain}(P)$ and ranges $\texttt{Range}(P)$ of properties. We denote with $\texttt{Class}(\mathcal{O})$ and $\texttt{Property}(\mathcal{O})$ the sets of class and property names, respectively, occurring in the ontology $\mathcal{O}$. For a given ontology $\mathcal{O}$, with $C \in \texttt{Domain}(P)$ we denote the fact that one can derive from $\mathcal{O}$ that the class name C is a domain of the property P. Also, $C' \in \texttt{Range}(P)$ denotes the fact that C' is a range of P and it is derivable from $\mathcal{O}$.

Relational Schemata. A relational schema $\mathcal{R}$ defines a set of relations (tables) T, where each table defines a set of columns c. We also assume that a schema contains foreign keys k that define references between tables.

Similarity Flooding Algorithm. The Similarity Flooding algorithm matches a given schema $\mathcal{S}$ with a schema $\mathcal{S}'$. In the first step, directed labeled graphs $\mathcal{G}(\mathcal{S})$ and $\mathcal{G}(\mathcal{S}')$ are constructed from $\mathcal{S}$ and $\mathcal{S}'$, where the nodes represent the schema elements, and the edges with labels define relationships between the schema elements. There is no exact procedure to construct the graphs from the schemata given in [8]. Thus, the Similarity Flooding algorithm is open for any graph construction process. The second step in the algorithm is to merge $\mathcal{G}(\mathcal{S})$ and $\mathcal{G}(\mathcal{S}')$ into one graph, a so-called pairwise connectivity graph `PCG`. Intuitively, each node of the `PCG` is a pair of nodes, and represents a potential match between schema elements of $\mathcal{S}$ and $\mathcal{S}'$. Then, the `PCG` is enriched with inverse edges and edge weights (propagation coefficients), where the value of the weights is based on the number of outgoing edges with the same label from a given node. This graph is called the induced propagation graph `IPG`. The final step of the algorithm is a fix-point computation to propagate initial similarities by using the structural dependencies represented by the propagation coefficients. The fix-point computation termination is based either on threshold values or the number of iterations. The result is a ranked list of suggested mappings. We refer to [8] for further details.

Algorithm 1: *IncGraph* for constructing graphs from ontologies

INPUT : OWL ontology $\mathcal{O}$
OUTPUT: Graph $\mathcal{G} = (\mathcal{V}, \texttt{Lbl}_\mathcal{V}, \mathcal{E}, \texttt{Lbl}_\mathcal{E})$

Let $\mathcal{G} = (\mathcal{V}, \texttt{Lbl}_\mathcal{V}, \mathcal{E}, \texttt{Lbl}_\mathcal{E})$, $\mathcal{V} = \{n_\top\}$, $\texttt{Lbl}_\mathcal{V} = \{(n_\top, \top)\}$, $\mathcal{E} = \emptyset$, $\texttt{Lbl}_\mathcal{E} = \emptyset$;
foreach $C \in \texttt{Class}(\mathcal{O})$ **do** $\mathcal{V} := \mathcal{V} \cup \{n_C\}$ and $\texttt{Lbl}_\mathcal{E}(n_C) := C$
foreach $P \in \texttt{Property}(\mathcal{O})$ **do**
    $\mathcal{V} := \mathcal{V} \cup \{n_P\}$ and $\texttt{Lbl}_\mathcal{V}(n_P) := P$; Let $C \in \texttt{Domain}(P)$;
    if *P is an object property* **then**
        $\mathcal{E} := \mathcal{E} \cup \{(n_C, n_P)\}$ and $\texttt{Lbl}_\mathcal{V}((n_C, n_P)) :=$ `'ref'`;
        Let $C' \in \texttt{Range}(P)$;
        $\mathcal{E} := \mathcal{E} \cup \{(n_P, n_{C'})\}$ and $\texttt{Lbl}_\mathcal{V}((n_P, n_{C'})) :=$ `'ref'`;
    else if *P is a data property* **then**
        $\mathcal{E} := \mathcal{E} \cup \{(n_C, n_P)\}$ and $\texttt{Lbl}_\mathcal{E}((n_C, n_P)) :=$ `'value'`
return $\mathcal{G}$.

Algorithm 2: *IncGraph* for constructing graphs from relational schemata

INPUT : Relational Schema $\mathcal{R}$
OUTPUT: Graph $\mathcal{G} = (\mathcal{V}, \texttt{Lbl}_\mathcal{V}, \mathcal{E}, \texttt{Lbl}_\mathcal{E})$

Let $\mathcal{V} = \emptyset$, $\texttt{Lbl}_\mathcal{V} = \emptyset$, $\mathcal{E} = \emptyset$, $\texttt{Lbl}_\mathcal{E} = \emptyset$;
foreach *table T in $\mathcal{R}$* **do**
    $\mathcal{V} := \mathcal{V} \cup \{n_T\}$ and $\texttt{Lbl}_\mathcal{V}(n_T) := T$;
    foreach *column c in $\mathcal{R}$* **do**
        $\mathcal{V} := \mathcal{V} \cup \{n_c\}$ and $\texttt{Lbl}_\mathcal{V}(n_c) := c$;
        $\mathcal{E} := \mathcal{E} \cup \{(n_T, n_c)\}$ and $\texttt{Lbl}_\mathcal{E}((n_T, n_c)) :=$ `'value'`
        if *c has a foreign key k to some table T'* **then**
            $\mathcal{V} := \mathcal{V} \cup \{n_k\}$ and $\texttt{Lbl}_\mathcal{V}(n_k) := k$;
            $\mathcal{E} := \mathcal{E} \cup \{(n_T, n_k)\}$ and $\texttt{Lbl}_\mathcal{E}((n_T, n_k)) :=$ `'ref'`
            $\mathcal{E} := \mathcal{E} \cup \{(n_k, n_{T'})\}$ and $\texttt{Lbl}_\mathcal{E}((n_k, n_{T'})) :=$ `'ref'`
return $\mathcal{G}$.

3 The *IncGraph* Model

In this section, we describe the *IncGraph* model used by *IncMap* to represent schema elements of an OWL ontology $\mathcal{O}$ and a relational schema $\mathcal{R}$ in a unified way.

An *IncGraph* model is defined as directed labeled graph $\mathcal{G} = (\mathcal{V}, \texttt{Lbl}_\mathcal{V}, \mathcal{E}, \texttt{Lbl}_\mathcal{E})$. It can be used as input by the original Similarity Flooding algorithm (Section 2) or *IncMap*. $\mathcal{V}$ represents a set of vertices, $\mathcal{E}$ a set of directed edges, $\texttt{Lbl}_\mathcal{V}$ a set of labels for vertices (i.e., one label for each vertex) and $\texttt{Lbl}_\mathcal{E}$ a set of labels for edges (i.e., one label for each edge). A label $l_\mathcal{V} \in \texttt{Lbl}_\mathcal{V}$ represents a name of a schema element whereas a label $l_\mathcal{E} \in \texttt{Lbl}_\mathcal{E}$ is either "ref" representing a so called `ref`-edge or "value" representing a so called `val`-edge.

3.1 *IncGraph* Construction

The goal of the procedures for the basic construction is to incorporate explicit schema information from $\mathcal{O}$ and $\mathcal{R}$ into the *IncGraph* model. Incorporating implicit schema information is discussed in the next section.

Algorithm 1 creates an *IncGraph* model $\mathcal{G}$ for a given ontology $\mathcal{O}$. The algorithm constructs a vertex n_C for each class name $C \in \texttt{Class}(\mathcal{O})$ and a vertex

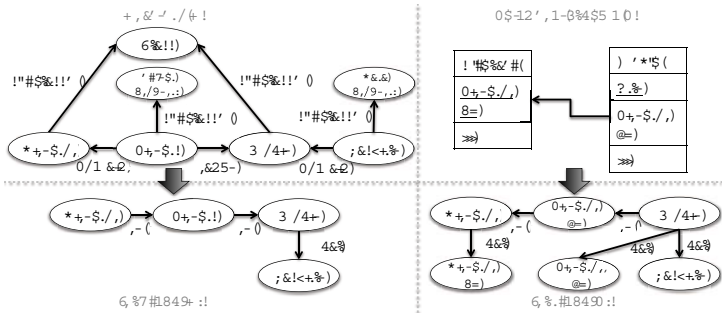


Fig. 1. *IncGraph* Construction Example

n_P for each property name $P \in \texttt{Property}(\mathcal{O})$ using the names of these ontology elements as label in $\texttt{Lbl}_\mathcal{V}$. Directed edges in the *IncGraph* model are created for each domain and range definition in $\mathcal{O}$. The labels $\texttt{Lbl}_\mathcal{E}$ for edges are either "ref" in case of an object property or "value" in case of a data property. For a domain definition in $\mathcal{O}$ the direction of the edge in $\mathcal{G}$ is from the node n_C representing the domain of P to the node n_P representing the property P. For a range definition the direction of the edge in $\mathcal{G}$ is from the node n_P representing object property to the node $n_{C'}$ representing the range of P (i.e., another class). If an object property in $\mathcal{O}$ has no range (respectively, domain) definition, then a directed labeled edge to a node $n_\top$ is added to explicitly model the most general range (respectively, domain), i.e., a top-level concept $\top$ like `Thing`.

Algorithm 2 creates a *IncGraph* model $\mathcal{G}$ for a given relational schema $\mathcal{R}$: The algorithm constructs a vertex n_T for each table and a vertex n_c for each column using the names of these schema elements as labels $\texttt{Lbl}_\mathcal{V}$. Directed edges with the label "value" are created from a node n_T representing a table to a node n_c representing a columns of that table. For columns with a foreign key k an additional node n_k is created. Moreover, two directed edges with the label "ref" are added, which represent a path from node n_T to a node $n_{T'}$ representing the referenced table via node n_k.

Figure 1 shows the result of applying these two algorithms to the ontology $\mathcal{O}$ and the relational schema $\mathcal{R}$ in this figure. Both $\mathcal{O}$ and $\mathcal{R}$ describe the same entities *Directors* and *Movies* using different schema elements. The resulting *IncGraph* models of $\mathcal{O}$ and $\mathcal{R}$ represent the schema structure in a unified way.

3.2 *IncGraph* Annotations

IncGraph is designed to represent both relational schemata and ontologies in a structurally similar fashion because matching approaches such as ours work best when the graph representations on both the source and target side are as similar as possible. However, even in *IncGraph* structural differences remain due to the impedance mismatch and different design patterns used in ontologies and relational schemata, respectively.

We consider this issue by supporting *annotations* in *IncGraph*. Annotations basically are additional `ref`-edges in either the source or target model that can be designed to bridge structural gaps for different design patterns or levels of

granularity. For instance, *shortcut edges* in the relational *IncGraph* model could represent a multi-hop join over a chain of relationship relations. Annotations can be constructed by plug-ins during *IncGraph* construction.

We plan to evaluate the opportunities of different kinds of annotations in future work.

4 The *IncMap* System

In this section, we present our matching approach and system called *IncMap*. *IncMap* takes a source and target *IncGraph* as input, i.e., the *IncGraph*s produced for a relational schema and for an ontology as described in Section 3.

4.1 Overview of *IncMap*

In its basic version, *IncMap* applies the original Similarity Flooding algorithm (with minor adaptions) and thus creates initial mapping suggestions for the *IncGraph* of an ontology $\mathcal{O}$ and a relational schema $\mathcal{R}$. In its extended version, *IncMap* activates inactive `ref`-edges before executing the Similarity Flooding algorithm to achieve better mapping suggestions.

Another extension is the incremental version of *IncMap*. In this version the initial mapping suggestions are re-ranked by *IncMap* in a semi-automatic approach by including user feedback. Re-ranking works iteratively in a query-driven fashion thus increasing the quality of the suggested mappings. In each iteration, *IncMap* applies a version of the Similarity Flooding algorithm (as described before). However, in addition between each iteration user feedback is incorporated.

The idea of user feedback is that the user confirms those mapping suggestions of the previous iteration, which are required to answer a given user query over ontology $\mathcal{O}$. Confirmed suggestions are used as input for the next iteration to produce better suggestions for follow-up queries. This is in contrast to many other existing approaches (including the original Similarity Flooding algorithm) that return a mapping for the complete source and target schema only once.

IncMap is designed as a framework and provides different knobs to control which extensions to use and within each extension which concrete variants to choose (e.g., to select a concrete strategy for activating inactive edges). The goal of this section is to present *IncMap* with all its variants and to show their benefits for different real-world data sets in our experimental evaluation in Section 5. A major avenue of future work is to apply optimization algorithms to find the best configurations of *IncMap* for a given ontology $\mathcal{O}$ and schema $\mathcal{R}$ automatically by searching the configuration space based on the knobs presented before.

4.2 Basic Matching in *IncMap*

As already mentioned, in the basic version of *IncMap*, we simply apply the Similarity Flooding algorithm for the two *IncGraph*s produced for a relational schema $\mathcal{R}$ and for an ontology $\mathcal{O}$ similar to the process as described in Section 2.

As a first step, *IncMap* generates the `PCG` (i.e., a combined graph which pairs similar nodes of both input *IncGraph*s) using an initial lexical matching, which

supports interchangeable matchers as one knob for configuration. One difference is the handling of inactive `ref`-edges in the input *IncGraph*s. For inactive `ref`-edges, which are not handled in the original Similarity Flooding, we apply the following rule when building the `PCG`: if an edge in the `PCG` refers to at least one inactive `ref`-edge in one of the *IncGraph* models, it also becomes inactive in the `PCG`.

In addition, other than in the original Similarity Flooding approach, where propagation coefficients for the `IPG` are ultimately determined during graph construction, our propagation coefficients can be calculated several times when the graph changes with the activation and deactivation of edges. Also, propagation coefficients in *IncMap* are modular and can be changed. In particular, a new weighting formula supported by *IncMap* considers the similarity scores on both ends of an edge in the `IPG`. The intuition behind this is that a higher score indicates better chances of the match being correct. Thus, an edge between two matches with relatively high scores is more relevant for the structure than an edge between one isolated well-scored match and another with a poor score. For calculating the weight $w(e)$ of a directed edge $e = (n_1, n_2)$ from n_1 to n_2 in the `IPG` where l is the label of the edge, we currently use two alternatives:

- *Original Weight as in [8]*: $w(e) = 1/out_l$ where out_l is the number of edges connected to node n_1 with the same label l
- *Normalized Similarity Product*: $w(e) = (score(n_1) * score(n_2))/out_l$.

4.3 Extended *IncMap*: Iterative User Feedback

Query-driven incremental mappings allow to leverage necessary user feedback after each iteration to improve the quality of mapping suggestions in subsequent iterations. One of the reasons why we have chosen Similarity Flooding as a basis for *IncMap* is the fact that user feedback can be integrated by adopting the initial match scores in an `IPG` before the fix-point computation starts.

Though the possibility of an incremental approach has been mentioned already in the Similarity Flooding paper [8], it so far has not been implemented and evaluated. Also, while it is simple to see *where* user feedback could be incorporated in the `IPG`, it is far less trivial to decide *which* feedback should be employed and *how* exactly it should be integrated in the graph. In this paper we focus on leveraging only the most important kind of user feedback, i.e., the previous confirmation and rejection of suggested mappings. We have devised three alternative methods how to add this kind of feedback into the graph.

First, as a confirmed match corresponds to a certain score of 1.0, while a rejected match corresponds to a score of 0.0, we could simply re-run the fix-point computation with adjusted initial scores of confirmed and/or rejected matches. We consequently name this first method *Initializer*. However, there is a clear risk that the influence of such a simple initialization on the resulting mapping is too small as scores tend to change rapidly during the first steps of the fix-point computation.

To tackle this potential problem, our second method guarantees maximum influence of feedback throughout the fix-point computation. Instead of just initializing a confirmed or rejected match with their final score once, we could repeat the initialization at the end of each step of the fix-point computation after

normalization. This way, nodes with definite user feedback influence their neighborhood with their full score during each step of the computation. We therefore call this method *Self-Confidence Nodes*. However, as scores generally decrease in most parts of the graph during the fix-point computation and high scores become more important for the ranking of matches in later fix-point computation steps, this method implies the risk of over-influencing parts of the graph. For example, one confirmed match in a partially incorrect graph neighborhood would almost certainly move all of its neighbors to the top of their respective suggestion lists.

Finally, with our third method, we attempt to balance the effects of the previous two methods. We therefore do not change a confirmed match directly but include an additional node in `IPG` that can indirectly influence the match score during the fix-point computation. We name this method *Influence Nodes*. By keeping the scores of those additional influence nodes invariant we ensure permanent influence throughout all steps of the fix-point computation. Yet, the influence node only indirectly affects the neighborhood of confirmed nodes through the same propagation mechanism that generally distributes scores through the graph.

5 Experimental Evaluation

The main goal of *IncMap* is to reduce the human effort for constructing mappings between existing relational database schemata and ontologies. Mapping suggestions are intended to be used only after they have been validated by a user. Thus, there are two relevant evaluation measures: first, the percentage of the mappings in the reference mappings that *can be represented* by *IncMap*. We specify this percentage for all reference mappings when introducing them. Certain complex mappings (e.g., mappings performing data transformations) cannot be represented by *IncMap*. These complex mappings are rare in all real-world reference mappings we used in this paper. The second and most important measure is the *amount of work* that a user needs to invest to transform a set of mapping suggestions into the correct (intended) mappings. As the latter is the most crucial aspect, we evaluate our approach by measuring the work time required to transform our suggestions into the existing reference mappings.

5.1 Relational Schemata and Ontologies

To show the general viability of our approach, we evaluate *IncMap* in two scenarios with fairly different schematic properties. In addition to showing the key benefits of the approach under different conditions, this also demonstrates how the impact of modular parameters varies for different scenarios.

IMDB and Movie Ontology. As a first scenario, we evaluate a mapping from the schema of well known movie database IMDB[4] to the Movie Ontology [10]. With 27 foreign keys connecting 21 tables in the relational schema and 27 explicitly modeled object properties of 21 classes in the ontology, this scenario is average

[4] http://www.imdb.com

in size and structural complexity. The reference mappings we use to derive correspondences for this scenario[5] has been made available by the -ontop- team [11]. A set of example queries is provided together with these reference mappings. We use these to construct annotations for user queries as well as to structure our incremental, query-by-query experiments. We extract a total of 73 potential correspondences from this mapping, 65 of which can be represented by *IncMap* as mapping suggestions. This corresponds to 89% of the mappings that could be represented in *IncMap*.

MusicBrainz and Music Ontology. The second scenario is a mapping from the MusicBrainz database[6] to the Music Ontology [12]. The relational schema contains 271 foreign keys connecting 149 tables, while the ontology contains 169 explicitly modeled object properties and 100 classes, making the scenario both larger and more densely connected than the previous one. Here we use R2RML reference mappings that have been developed in the project EUCLID.[7] As there were no example queries provided with the mapping in this case, we use example queries provided by the Music Ontology for user query annotations and to structure the incremental experiment runs.

For these reference mappings, two out of 48 correspondences cannot be represented as mapping suggestions by *IncMap* as they require data transformations. This corresponds to 95.8% of the mappings that could be represented in *IncMap*.

5.2 Work Time Cost Model

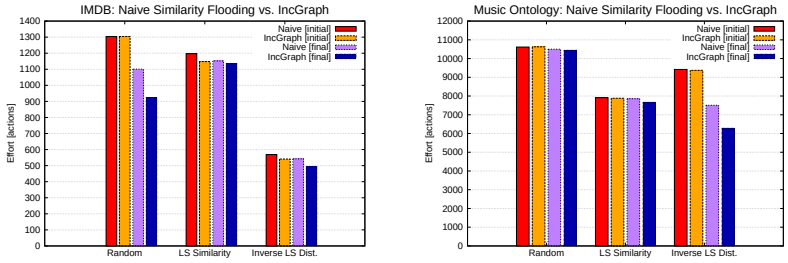
We evaluate our algorithms w.r.t. reducing *work time* (human effort). As the user feedback process always needs to transform mapping suggestions generated by *IncMap* into the correct mappings (i.e. to achieve a precision and recall of 100%), the involved effort is the one distinctive quality measure. To this end, we have devised a simple and straightforward work time cost model as follows: we assume that users validate mappings one by one, either accepting or rejecting them. We further assume that each validation, on average, takes a user the same amount of time $t_{validate}$. The costs for finding the correct correspondence for any concept in this case is identical with the rank of the correct mapping suggestion in the ranked list of mapping suggestions for the concept times $t_{validate}$.

As *IncMap* is interactive by design and would propose the user one mapping suggestion after another, this model closely corresponds to end user reality. We are aware that this process represents a simplification of mapping reality where users may compile some of the mappings by other means for various reasons. Nevertheless, this happens in the same way for any suggestion system and therefore does not impact the validity of our model for the purpose of comparison.

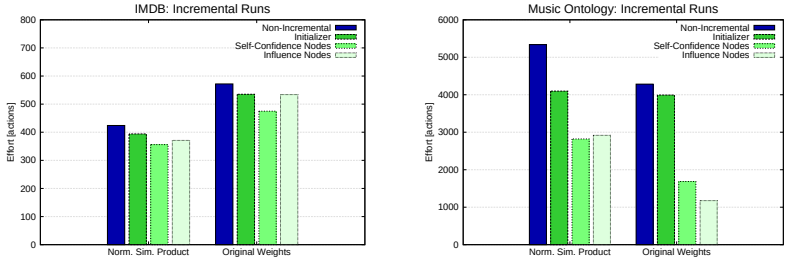
5.3 Experimental Evaluation

Experiment 1 – Naive vs. IncGraph. In our first experiment we compare the effort required to correct the mapping suggestions when the schema and ontol-

[5] https://babbage.inf.unibz.it/trac/obdapublic/wiki/Example_MovieOntology
[6] http://musicbrainz.org/doc/MusicBrainz_Database
[7] http://euclid-project.eu



(a) Naive vs. *IncGraph*



(b) Incremental Evaluation

Fig. 2. Experimental Evaluation

ogy are represented naively, or as *IncGraph*s. Additionally, we vary the lexical matcher used for the initial mapping between randomly assigned scores (minimal base line), Levenshtein similarity and inverse Levenshtein distance. Figure 2(a) shows that *IncGraph* in all cases works better than the naive approach. As *IncMap* reliably improves the mapping for all configurations, it also underlines the ability of *IncMap* to operate in a stable manner with different initial matchers.

Experiment 2 – Incremental Mapping Generation. Finally, we evaluated the best previous configurations incrementally, i.e., leveraging partial mappings. Figure 2(b) illustrates the effects on the total effort. We show total effort for all three incremental methods, for different propagation coefficients. Most significantly, incremental evaluation reduces the overall effort by up to $50\% - 70\%$. More specifically, Self-Confidence Nodes and Influence nodes work much better than the naive Initializer approach.

6 Related Work

Many existing mapping systems rely on two-step mapping procedures: They employ lexical similarity of terms together with structural similarity of the structures ([13,14,15] or [16,17] for surveys). A very few of them rely on variations of Similarity Flooding to perform the latter task. However, to the best of our knowledge, all of these approaches focus on ontology-to-ontology rather than relational schema-to-ontology mappings. RiMOM [18] performs a multi-strategy mapping discovery between ontologies and performs mappings using a variant of the Similarity Flooding algorithm, while it relies on structural similarities of ontologies derived from sub-class and sub-property relationships, rather than connectivity

of classes via properties as we do in order to get a better alignment of relational schemata and ontologies. In Yamm++ [19] the authors used Similarity Flooding and exploit both sub-class and sub-property relationships, and domain and ranges of ontologies, while they did it in a naive way which, as our experimental results showed, does not give good results for relational schemata-to-ontology mappings. Moreover, they use Similarity Flooding to obtain new mappings on top of the ones obtained via linguistic similarities, while we do not derive new mappings but refine the ranking over the linguistically derived ones. There are works on semi-automatic discovery of relational schema-to-ontology mappings, but they use approaches different from ours: For example, [20] transforms relational schemata and ontologies into directed labeled graphs respectively and reuse COMA [21] for essentially syntactic graph matching. Ronto [22] uses a combination of syntactic strategies to discover mappings by distinguishing the types of entities in relational schemata. The authors of [23] exploit structure of ontologies and relational schemata by calculating the confidence measures between virtual documents corresponding to them via the TF/IDF model. All these approaches do not incorporate implicit schema information and do not support an incremental mapping construction in the pay as you go fashion as *IncMap* does. Finally, [24] describes an approach to derive complex correspondences for a relational schema-to-ontology mapping using simple correspondences as input. This work is orthogonal to the approach presented in this paper.

7 Conclusions and Outlook

We presented *IncMap*, a novel semi-automatic matching approach for generating relational schema-to-ontology mappings. Our approach is based on a novel unified graph model called *IncGraph* for ontologies and relational schemata. *IncMap* implements a semi-automatic matching approach to derive mappings from *IncGraph*s using both lexical and structural similarities between ontologies and relational schemata. In order to find structural similarities *IncMap* exploits both explicit and implicit schema information. Moreover, *IncMap* allows to incorporate user queries and user feedback in an incremental way, thus, enabling a pay as you go fashion of the mapping generation. Our experiments with *IncMap* on different real-world relational schemata and ontologies showed that the effort for creating a mapping with *IncMap* is up to 20% less than using the Similarity Flooding algorithm in a naive way. The incremental version of *IncMap* reduces the total effort of mapping creation by another $50\% - 70\%$. As future work we plan to follow three lines: (1) add more implicit schema information (annotations) to the *IncGraph*s, (2) support more complex mappings in *IncMap*, and (3) devise a search strategy over the configuration space to auto-tune *IncMap*.

8 Acknowledgements

This work was supported by the Seventh Framework Program (FP7) of the European Commission under Grant Agreement 318338, the Optique project.

References

1. Beyer, M.A., Lapkin, A., Gall, N., Feinberg, D., Sribar, V.T.: 'Big Data' is Only the Beginning of Extreme Information Management. Gartner rep. G00211490 (2011)
2. Crompton, J.: Keynote talk at the W3C Workshop on Sem. Web in Oil & Gas Industry (2008) http://www.w3.org/2008/12/ogws-slides/Crompton.pdf.
3. SAP HANA Help: http://help.sap.com/hana/html/sql_export.html (2013)
4. Poggi, A., Lembo, D., Calvanese, D., Giacomo, G.D., Lenzerini, M., Rosati, R.: Linking Data to Ontologies. J. Data Semantics **10** (2008) 133–173
5. Kontchakov, R., Lutz, C., Toman, D., Wolter, F., Zakharyaschev, M.: The Combined Approach to Ontology-Based Data Access. In: IJCAI. (2011) 2656–2661
6. Hepp, M., Wechselberger, A.: OntoNaviERP: Ontology-Supported Navigation in ERP Software Documentation. In: International Semantic Web Conference. (2008)
7. Blunschi, L., Jossen, C., Kossmann, D., Mori, M., Stockinger, K.: SODA: Generating SQL for Business Users. PVLDB **5**(10) (2012) 932–943
8. Melnik, S., Garcia-Molina, H., Rahm, E.: Similarity Flooding: A Versatile Graph Matching Algorithm and its Application to Schema Matching. In: ICDE, IEEE Computer Society (2002)
9. Motik, B., Patel-Schneider, P.F., Parsia, B.: OWL 2 Web Ontology Language Structural Specification and Functional-Style Syntax (2012) W3C Rec.
10. Bouza, A.: MO – The Movie Ontology, http://www.movieontology.org (2010)
11. Rodriguez-Muro, M., Calvanese, D.: High Performance Query Answering over DL-Lite Ontologies. In: KR. (2012)
12. Raimond, Y., Giasson, F., (eds): Music Ontology, www.musicontology.com (2012)
13. Jiménez-Ruiz, E., Grau, B.C.: LogMap: Logic-Based and Scalable Ontology Matching. In: International Semantic Web Conference (1). (2011) 273–288
14. Lambrix, P., Tan, H.: SAMBO – A system for aligning and merging biomedical ontologies. J. Web Sem. **4**(3) (2006) 196–206
15. Fagin, R., Haas, L.M., Hernández, M.A., Miller, R.J., Popa, L., Velegrakis, Y.: Clio: Schema Mapping Creation and Data Exchange. In: Conceptual Modeling: Foundations and Applications. (2009) 198–236
16. Shvaiko, P., Euzenat, J.: Ontology Matching: State of the Art and Future Challenges. IEEE Trans. Knowl. Data Eng. **25**(1) (2013) 158–176
17. Rahm, E., Bernstein, P.A.: A Survey of Approaches to Automatic Schema Matching. In: VLDB J. (2001) 334–350
18. Li, J., Tang, J., Li, Y., Luo, Q.: RiMOM: A Dynamic Multistrategy Ontology Alignment Framework. IEEE Trans. Knowl. Data Eng. (2009) 1218–1232
19. Ngo, D., Bellahsene, Z.: YAM++: A Multi-strategy Based Approach for Ontology Matching Task. In: EKAW. (2012) 421–425
20. Dragut, E.C., Lawrence, R.: Composing Mappings Between Schemas Using a Reference Ontology. In: CoopIS/DOA/ODBASE (1). (2004) 783–800
21. Do, H.H., Rahm, E.: COMA – A System for Flexible Combination of Schema Matching Approaches. In: VLDB. (2002) 610–621
22. Papapanagiotou, P., Katsiouli, P., Tsetsos, V., Anagnostopoulos, C., Hadjiefthymiades, S.: Ronto: Relational to Ontology Schema Matching. In: AIS SIGSEMIS BULLETIN. (2006) 32–34
23. Hu, W., Qu, Y.: Discovering Simple Mappings Between Relational Database Schemas and Ontologies. In: ISWC/ASWC. (2007) 225–238
24. An, Y., Borgida, A., Mylopoulos, J.: Inferring Complex Semantic Mappings Between Relational Tables and Ontologies from Simple Correspondences. In: OTM Conferences (2). (2005)

Complex Correspondences for Query Patterns Rewriting

Pascal Gillet, Cassia Trojahn, Ollivier Haemmerlé, and Camille Pradel

IRIT & Université de Toulouse 2, Toulouse, France
pascalgillet@ymail.com,{cassia.trojahn,ollivier.haemmerle,camille.pradel}@irit.fr

Abstract. This paper discusses the use of complex alignments in the task of automatic query patterns rewriting. We apply this approach in SWIP, a system that allows for querying RDF data from natural language-based queries, hiding the complexity of SPARQL. SWIP is based on the use of query patterns that characterise families of queries and that are instantiated with respect to the initial user query expressed in natural language. However, these patterns are specific to the vocabulary used to describe the data source to be queried. For rewriting query patterns, we experiment ontology matching approaches in order to find complex correspondences between two ontologies describing data sources. From the alignments and initial query patterns, we rewrite these patterns in order to be able to query the data described using the target ontology. These experiments have been carried out on an ontology on the music domain and DBpedia ontology.

1 Introduction

Despite the fact that SPARQL is the standard *de facto* language for querying RDF data, its complexity may restrict its use at a large scale, specially for non-expert RDF users. Translating natural language queries into SPARQL ones is the object of researches in both Natural Language Processing and Semantic Web fields. Within the SWIP system [11], users express queries in natural language sentences and pre-written query patterns are instantiated with respect to a syntactic analysis of the initial query. Several possible interpretations of the queries are shown to the user which selects the query he/she is interested in. Unlike other proposals, such as the one in [5, 4], where user queries are limited to keywords, or in [16], where users can express their queries using a visual query language, the originality of SWIP is related to the use of query patterns.

The main principle behind query patterns states that, in real applications, the submitted queries are variations of few typical query families (i.e., the family of queries asking for the *actors playing in movies* or the queries asking for the *members of a musical band*, or the *albums of a musical artist*). On the one hand, the use of patterns avoids exploring the whole ontology to link the semantic entities identified from the keywords since the potential relations are already expressed in the patterns. The process thus benefits from the pre-established families of frequently expressed queries for which real information needs exist.

A query pattern can also be seen as the projection of a subgraph of the underlying knowledge base, used as a mediator for the translation between the query expressed in natural language and the corresponding SPARQL query. On the other hand, one of the main limitations of the query pattern-based approach is that reusing patterns across different data sources can be done in a very limited extent. For each data source to be queried, the corresponding query patterns have to be (manually) built. Rewriting query patterns based on a vocabulary to query patterns based on another vocabulary is a task that can be carried out with the help of ontology alignments.

This paper discusses the use of complex correspondences for automatic query patterns rewriting. While the usefulness of simple correspondences has long been recognised, query rewriting requires more expressive links between ontology entities expressing the true relationships between them. At a lower level of abstraction, ontology alignments have been used to support the task of SPARQL query rewriting [2, 9, 8]. However, query patterns and SPARQL refer to different levels of expressivity in their representations, where query patterns are articulated as a set of subpatterns and rely solely on the $\mathcal{T}$Box of ontologies. Hence, we experiment ontology matching approaches in order to find complex correspondences between two ontologies describing two different data collections. From the complex alignments and source query patterns, we rewrite these patterns in order to be able to query the data collection described using the target ontology. Experiments have been carried out on an ontology on the music domain and DBpedia ontology. As a main outcoming, we have a set of manually validated complex correspondences, from which query patterns can be reused across the data sets described using those ontologies.

The rest of the paper is organised as follows. First, we introduce complex correspondences and query patterns (§2). Then, we present the approach for query pattern rewriting that is based on the use of complex correspondences (§3). Next, the experiments are discussed (§4). Finally, we discuss related work (§5) and conclude the paper (§6).

2 Foundations

2.1 Complex correspondences

Matching two ontologies is the process of generating an alignment between them [6]. An alignment A is directional and refers to a source ontology O and a target ontology O', denoted $A_{O \to O'}$:

Definition 1 (Alignment). *An alignment $A_{O \to O'}$ between two ontologies O and O' is a set of correspondences $A_{O \to O'} = \{c_1, c_2, ..., c_n\}$, where each c_i is a triple $\langle e_i, e'_i, r \rangle$, where:*

- *whether the correspondence is **simple**, then it relates one and only one entity (i.e., a class or a property) e_i of O to one and only one entity e'_i of O' (1:1);*

- *or the correspondence is* ***complex****, and it involves one or more entities in a logical formulation (1:n,m:1,m:n), where e_i refers to a subset of elements $\in O$, and e'_i refers to a subset of elements $\in O'$, and these elements are related using the constructors of a formal language (First-Order Logic or Description Logics);*
- *r is a relation, e.g., equivalence ($\equiv$), more general($\sqsupseteq$), more specific ($\sqsubseteq$), holding between e_i and e'_i;*
- *additionally, a value n (typically in [0,1]) is assigned to c_i indicating the degree of confidence that the relation r holds between the e and e'.*

The correspondence $\langle e_i, e'_i, r\rangle$ is unique in $A_{O\to O'}$. On the other hand, e_i or e'_i may be present in more than one correspondence c_i. The alignment $A_{O\to O'}$ is said *complex* if it contains at least one complex correspondence. In the rest of this paper, a correspondence c_i, which is a triple $\langle e_i, e'_i, r\rangle$ (suffix notation), will be noted $e_i\ r\ e'_i$. For example, $Film \sqsubseteq Work$ is a simple correspondence and asserts that $Film$ in O is more specific than $Work$ in O'. On the other hand, we can have the following two complex correspondences :

$$\forall x, Short\_Film(x) \equiv Film(x) \wedge duration(x, y) \wedge y \leq 59 \quad (1)$$

$$\forall x, Biopic(x) \equiv Film(x) \wedge Celebrity(y) \wedge topic(x, y) \quad (2)$$

(1) asserts that a $Short\_Film$ in O is equivalent to a $Film$ in O' whose duration is less than 59 minutes, and (2) asserts that a *Biopic* (or biographical film) in O is equivalent to a $Film$ in O' whose the topic is about a famous person. We can either use First-Order Logic (FOL) or the constructors of Description Logics (DL) for expressing the complex correspondences. In FOL, a *class* corresponds to a unary predicate with one variable, a *property* to a binary predicate with two variables, and an *instance* to a constant. In DL, a class corresponds to a (atomic) concept, a property to a role, and an instance to an individual. We can equally transpose logical statements from DL to FOL, and conversely, as long as the DL fragment is always respected. In particular, we take advantage of the expressivity allowed by $\mathcal{SHOIN}$, describing the following DL operators: $\neg C$ (negation of concepts), $C \sqcap C$ (intersection or conjunction of concepts), $C \sqcup C$ (union or disjunction of concepts), $\exists R.C$ (existential restriction), $\forall R.C$ (universal restriction), $\leq nR$ (at most restriction), $\geq nR$ (at least restriction). For instance, the formula (1) becomes (3) and the formula (2) becomes (4) :

$$Short\_Film \equiv Film \sqcap \exists duration. \leq 59 \quad (3)$$

$$Biopic \equiv Film \sqcap \exists topic.Celebrity \quad (4)$$

In a (complex) correspondence formula expressed in FOL, a variable may occur in several entities in left and right operands. Intuitively, two classes referring to the same single variable are bound and are first connected by a simple correspondence (with a subsumption relation, otherwise there is no need for an additional complex correspondence to characterise the entities involved). For instance, the formulas (1) and (2) are *consistent* only if $Court\_metrage \sqsubseteq Film$ and $Biopic \sqsubseteq Film$, respectively. The use of DL in (4) requires to explicitly assert the simple correspondence $Biopic \sqsubseteq Film$ first, as we do not know if $Biopic$ is a specialisation or rather a generalisation of $Film$ or $Celebrity$ otherwise.

2.2 Query patterns

A pattern p^O targetting an ontology O is composed of an RDF graph which is the prototype of a relevant family of queries. A pattern can be composed of several subpatterns sp_i, such as $p^O = \{sp_1, sp_2, ..., sp_n\}$. Subpatterns are assigned minimal and maximal cardinalities, making these subgraphs optional or repeatable when generating the final SPARQL query. Formally, a query pattern can be defined as follows [12]:

Definition 2 (Query pattern). *Let G be a graph and v a vertex of the graph, we denote by $G\backslash v$ the graph deprived of the vertex v and all the arcs incident to the vertex. A query pattern p is a triple (G, Q, SP) such as :*

- *G is a RDF connected graph that describes the general structure of the pattern and represents a family of requests;*
- *Q is a subset of elements in G, called qualifier elements; these are typical of the pattern and will be taken into account during the association of the user request to the pattern in question. A qualifier element is either a vertex (class or data type), or an arc (object or data property) in G;*
- *SP is the set of subpatterns sp in p such that $\forall sp = (SG, v, card_{min}, card_{max}) \in SP$, we have:*
  - *SG is a subgraph of G and v is a vertex of SG (and thus of G), such as $G\backslash v$ is not connected (v is a joint vertex in G, also called junction vertex) and admits $SG\backslash v$ as a connected component (i.e. all the vertices in this connected component belong to the subpattern subpattern's graph);*
  - *At least one vertex or an arc of SG is a qualifier element;*
  - *$card_{min}, card_{max} \in \mathbb{N}$ et $0 \leq card_{min} \leq card_{max}$; are respectively the minimum and maximum cardinality of sp that define the optional and repeatable characteristics of sp.*

Figure 2.2 shows an example of a query pattern which deals with the events, and the performers involved, where musical works have been performed (or conversely) with the corresponding artist(s) and release date. The pattern is composed of three subpatterns named *live*, *artist* and *date*. All of them are optional, and only the subpatterns *live* and *artist* are repeatable: it is considered that a musical work can have only one release date, but a musical work may be the work of several artists and can be performed many times.

3 Patterns rewriting approach

The rewriting approach takes as input a complex alignment $A_{O \to O'}$ and a set P=$\{p_1^O,...,p_n^O\}$ of query patterns p_i^O, and outputs a set P'=$\{p_1^{O'},...,p_n^{O'}\}$ of query patterns $p_j^{O'}$. The intuition is that every subgraph from the input patterns has potentially a (complex) correspondence associating its entities to entities in the target ontology. We consider that the subpattern is the relevant unit of semantic information constituting the patterns. Each subpattern is ideally replaced with

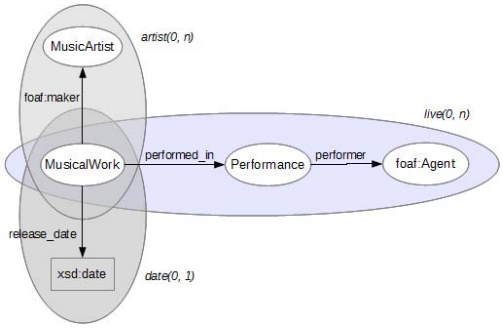


Fig. 1. Query pattern asking for events and their performers, where musical works have been performed (or conversely), with the corresponding artist(s) and release date.

an *equivalent* subgraph corresponding to a logical statement relating concepts and properties of the target ontology. This statement is the target part of the correspondence, if any in the alignment, in which the source part *matches* the initial subpattern. But the subpatterns and the correspondences in the alignment may not have the same granularity (correspondences can be either simple or can relate smaller subgraphs). Thus, we define an algorithm that is similar to a Depth-First Search algorithm (DFS) for traversing and searching graph data structures in the input query patterns. It starts at the largest subgraph, i.e. the subpattern, and recursively explores its subgraphs (i.e. subpattern > RDF triples > classes and properties), until a correspondence is found for the considered subgraph (in which case, the target graph is written to the subpattern being outputted) or a class or property is reached. If at the end of this process, there are entities that have not been translated, the whole subpattern will be discarded[1]. The operation is repeated for each subpattern in the input patterns.

The approach is inherently limited by the use of ontology alignment, which is itself an incomplete process. The subpattern is the indivisible expression of a need for information: it can be rewritten by chunks but if it is not fully rewritten at the end of the process, it is discarded. Thus, the conservation of the semantics of original patterns directly depends on the completeness of the input alignment (coverage of the source ontology, quality of correspondences, etc.). We consider that some loss of (semantic) information is acceptable, and that it can be filled with other techniques (for instance, by interacting with the user). However, it is out of the scope of this paper. Figure 3 illustrates the rewriting of the pattern depicted in Figure 2.2 (with the input alignment given later in §4.3, Table 1). The subpattern named *live* is rewritten to *live'*, following the complex correspondence #6 in the alignment. The subpattern named *artist* is rewritten to *artist'*, following the complex correspondence #2 in the alignment (in this case, only the first term of the disjunction $artist \sqcup author \sqcup creator \sqcup musicComposer$ appears in the resulting subpattern, for the sake of simplicity and readability).

[1] In this case, the pattern is still connected, i.e. there is a chain connecting each pair of vertices.

Finally, the subpattern named *date* could not be directly rewritten since there is no correspondence for this subgraph. Instead, the property *release_date* is rewritten to *releaseDate*, following a simple correspondence, and the data type *xsd:date* remains *xsd:date*.

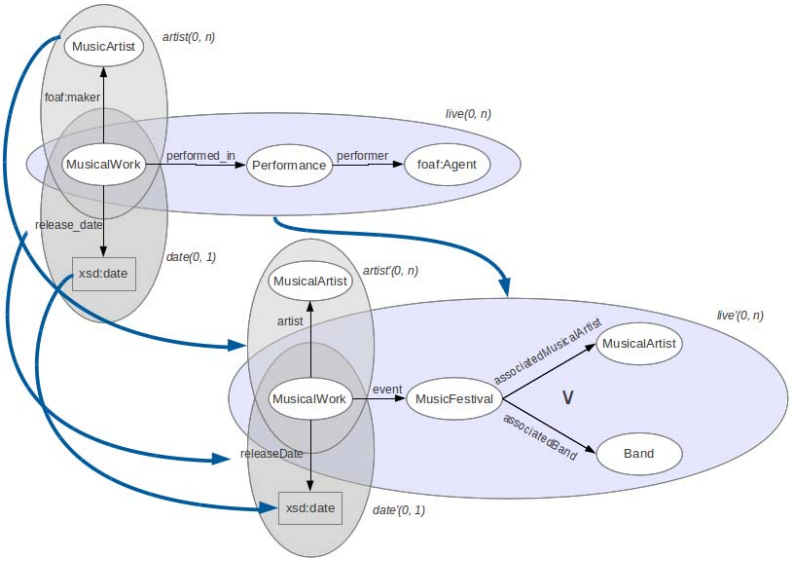


Fig. 2. Example of query pattern rewriting.

4 Experiments and discussion

4.1 Data sets

SWIP provides two sets of query patterns, one for the MusicBrainz collection described in terms of the Music ontology[2] (containing 249 $\mathcal{T}$Box entities), and another for querying the $\mathcal{A}$Box of the Cinema IRIT[3] ontology (containing 300 $\mathcal{T}$Box entities). We have carried out our experiments using the Music ontology and DBpedia 3.8[4] ontology (containing 2213 entities), in order to rewrite query patterns targeting MusicBrainz collection into patterns targeting DBpedia. The music set of patterns is composed of 5 query patterns and 19 subpatterns.

4.2 Preliminary experiments

In a first series of experiments, we used a set of simple correspondences for rewriting patterns. These correspondences come from a merge of alignments generated

[2] `http://musicontology.com/`
[3] `http://ontologies.alwaysdata.net/cinema`
[4] `http://wiki.dbpedia.org/Ontology?v=181z`

by OAEI 2012 matching systems (the reader can refer to [7] for details). Overall, 67% of the entities in the Music ontology were covered in the alignment. 25 out of 60 entities in the query patterns for this ontology could be replaced by a target entity (coverage of 41%). In terms of subpatterns, only 2 out of the 19 subpatterns could be fully rewritten using the alignment. Although we have found a handmade (reference) alignment between Music and DBpedia ontologies[5], we could not use it because it is mostly composed by correspondences linking classes only, using subsumption relations, and few equivalences could be inferred from them. Despite the fact that the quality of the alignment from the matchers was not measured, these first experiments highlighted the limitations in replacing individually the entities in the patterns. Nevertheless, we needed to accurately assess this deficiency and to know to what extent we could rewrite query patterns. It turned out that simple correspondences are not sufficient to capture all the meaningful relations between entities of two related ontologies.

4.3 Complex correspondences

Very few systems are able to find complex correspondences. First, we tried the tool described in [14], which finds complex correspondences using a set of predefined patterns. Besides the two ontologies to align, this tool takes an alignment as input. We used the tool on the pair Music-DBpedia, with (i) the handmade alignment between Music and DBpedia ontologies, and (ii) the merged alignment from the matchers used in the preliminary experiments (§4.2). In both cases, few correct correspondences could be identified. We tried then the successor of this tool described in [15], which benefits of natural language processing techniques instead of requiring an input alignment, and we obtained similar results.

Hence, we manually created a set of 28 complex correspondences (along 11 simple ones) for the pair Music-DBpedia, guided by the query patterns for Music[6]. A subset of them is presented in Table 1. The idea behind using complex correspondences is that every subgraph pattern has potentially a (complex) correspondence in the target ontology. Given that the subpattern is the relevant unit of semantic information constituting the patterns, we isolated them, and for each of them, we tried to find an equivalent logical statement relating concepts and properties of the target ontology. For constructing the complex correspondence set, we used as basis a set of simple correspondences (the left operand refers to an entity of the Music ontology, and the right operand refers to an entity of the DBpedia ontology): MusicalManifestation $\sqsubseteq$ MusicalWork, MusicalWork $\equiv$ MusicalWork*, MusicArtist $\equiv$ MusicalArtist*, Performance $\sqsubseteq$ Event, Performer $\equiv$ MusicalArtist, foaf:Group $\sqsupset$ Band, MusicGroup $\equiv$ Band*, SoloMusicArtist $\sqsubseteq$ MusicalArtist, Track $\sqsubseteq$ MusicalWork, Track $\equiv$ Song, and Record $\sqsubseteq$ MusicalWork[7].

For each correspondence, we identified the complex correspondence patterns that characterise it, from the patterns proposed in the literature: *Class*

[5] `http://knoesis.org/projects/BLOOMS/#Resources_for_Download`

[6] The resulting alignment do not cover all possible correspondences between Music-DBpedia, but a subset of them where entities appear in the query patterns.

[7] Correspondences with an asterisk were discovered using OAEI matchers.

#1	**CAV** MusicalManifestation ⊓ ∃release_type.album ≡ Album
#2	**CAT ≡ OR** MusicManifestation ⊓ ∃foaf:maker.MusicArtist ≡ MusicalWork ⊓ (∃artist.owl:Thing ⊔∃author.Person ⊔ ∃creator.Person ⊔ ∃musicComposer.MusicalArtist)
#3	**CAV ⊑ CAT** MusicalManifestation ⊓ ∃release_type.live ⊑ MusicalWork ⊓ ∃recordedIn.PopulatedPlace
#4	**CAV + CAT ⊐ CAT** MusicalManifestation ⊓ ∃release_type.soundtrack ⊓ ∃composer.foaf:Agent ⊐ Film ⊓ ∃musicComposer.MusicalArtist
#5	**PC ≡ OR** MusicGroup ⊓ ∃bio:event(bio:Birth ⊓ ∃bio:date.xsd:dateTime) ≡ Band ⊓ (∃formationDate.xsd:date ⊔ ∃formationYear.xsd:gYear ⊔ ∃activeYearsStartYear.xsd:gYear)
#6	**PC ≡ CAT(OR)** MusicalWork ⊓ ∃performed_in(Performance ⊓ ∃performer.foaf:Agent) ≡ MusicalWork ⊓ ∃event(Event ⊓ (∃associatedMusicalArtist.MusicalArtist ⊔ ∃associatedBand.Band))
#7	**CAT ≡ CAT** Track ⊓ ∃duration.xsd:decimal ≡ MusicalWork ⊓ ∃runtime.Time
#8	**CAT ≡ OR + CAT-1** foaf:Agent ⊓ ∃member_of.foaf:Group ≡ Person ⊓ (∃bandMember.Band ⊔ ∃formerBandMember.Band)
#9	**AND + PC ≡ AND(CAT-1)** Membership ⊓ (∃event:agent.foaf:Agent ⊓ ∃group.foaf:Group ⊓ ∃event:time.(event: TemporalEntity ⊓ (∃tl:start.xsd:date ⊓ ∀ tl:end.¬xsd:date)) ≡ Person ⊓ (∃bandMember.Band ⊓ ∀ formerBandMember.¬Band)
#10	**AND(PC) ≡ AND** Membership ⊓ ∃event:agent.foaf:Agent ⊓ ∃event:time.(event:TemporalEntity ⊓ ∃tl:start.xsd:date) ≡ Event ⊓ (∃pastMember.Person ⊓ ∃startDate.xsd:date)
#11	**PC ≡ CAT** SoloMusicArtist ⊓ ∃bio:event(bio:Birth ⊓ ∃bio:date.xsd:dateTime) ≡ MusicalArtist ⊓ ∃birthDate.xsd:date
#12	**CAT ≡ OR(CAT)** foaf:Agent ⊓ ∃collaborated_with.foaf:Agent ≡ (Artist ⊓ ∃associatedAct.Artist) ⊔ (Person ⊓ ∃partner.Person)

Table 1. 12 out of 28 handmade complex correspondences between Music and DBpedia ontologies.

by Attribute Type [14] (CAT), *Class by Inverse Attribute Type* [14] (CAT-1), *Class by Attribute Value* [14] (CAV), *Attribute Value Restriction* [18] (AVR), equivalent to CAV, *Property Chain* [14] (PC), *Aggregation* [18] (AGR), equivalent to PC, *Inverse Property* [15] (IP), *Union* [18] (OR), and *Intersection* [18] (AND). Although no new pattern was discovered, stating that, for our case, the patterns proposed in the literature cover all types of generated correspondences, several of our correspondences are in fact compositions of them (Table 1). For instance, the left operand in the correspondence #4 is an assembly of the patterns CAV and CAT. In the scope of this paper, however, we do not define any algebra which would describe how patterns can be composed or associated to represent the structure of complex correspondences (definition of basic properties and laws such as associativity, commutativity and distributivity). We have also manually generated 52 multilingual complex correspondences (along 13 simple correspondences) for the Cinema and DBpedia ontologies. For instance, the correspondence expressing the relation between the artists that are awarded the Cesar Award in Cinema (source ontology) and DBpedia (target ontology) : $Artiste \sqcap \exists estRecompenseA.CesarDuCinema \equiv Artist \sqcap \exists cesarAward(Award \sqcap \exists event.FilmFestival)$.

4.4 Rewriting SPARQL queries and query patterns

From the set of complex correspondences for the pair Music-DBpedia and the query patterns for Music, we applied our approach (§3) for rewriting Music patterns in terms of the DBpedia vocabulary. Before rewriting patterns, we evaluated the use of these correspondences for rewriting SPARQL queries. For doing so, we defined a set of rules for translating a complex correspondence pattern into RDF graph patterns (Table 2). These rules are intended to be used for guiding the process of SPARQL rewriting. Following these rules, we managed to rewrite the 25 first SPARQL queries from the benchmark training data in QALD 2013[8]. The training data include 100 natural language questions for MusicBrainz with the corresponding SPARQL queries, as well as the answers these queries retrieve. The queries have been rewritten in order to interrogate DBpedia.

ID	**Formal pattern**	**SPARQL rewriting rule**
CAT	A ≡ ∃R.B	?x a A → { ?x R B }
CAT-1	A ≡ B ⊓ ∃R-.T	?x a A → { ?x a B . ?y R ?x }
CAV	A ≡ ∃R.{...}	?x a A → { ?x R "..."^^*ex:dataType* }
AVR	A ≡ B ⊓ ∃R.{...}	?x a A → { ?x a B . ?x R *SomeValue* . }
PC	R ≡ P.(A ⊓ ∃Q)	?x R ?y → { ?x P A . A Q ?y }
IP	R- ⊑ P	?x R ?y → ?y P ?x
OR	A ≡ B ⊓ (∃R.T ⊔ ∃Q.T)	?x a A → {?x a B . {B R ?y} UNION {B Q ?z}}
AND	A ≡ B ⊓ (∃R.T ⊓ ∃Q.T)	?x a A → {?x a B . ?x R ?y ; Q ?z .}

Table 2. Complex correspondence patterns and SPARQL rewriting rules.

As an example, consider the query in Table 3 asking if there are *members of the Ramones who are not named Ramone* (question #25) over MusicBrainz, and the same query rewritten for DBpedia. The MusicBrainz result answers *false*, while the DBpedia result asserts the opposite. The DBpedia request is not less correct: if we return the actual query solutions (SELECT) instead of testing whether or not the query pattern has a solution (ASK), we find that Clem Burke in DBpedia was a member of The Ramones under the name "Elvis Ramone", while the MusicBrainz data set directly refers to him with this alias. In fact, both sets of instances do not fully intersect and they are not necessarily/correctly interlinked[9]. From this point of view, 18 of the 25 rewritten queries are correct and *consistent* with the queries for MusicBrainz: they do not necessarily give the same results, but they do answer the same question. 3 of these 18 results give the same number of solutions with exactly the same literals. 5 out of the 7 remaining results give no solution at all (no instance). And finally, the 2 last results are not fully correct since the complex correspondences ahead are not correct themselves. For instance, $MusicalManifestation \sqcap \exists release\_type.live \sqsubseteq MusicalWork \sqcap \exists recordedIn.PopulatedPlace$ turns out to be erroneous since the albums which have been recorded in a recording studio are equally selectable

[8] Open challenge on Multilingual Question Answering over Linked Data: `http://greententacle.techfak.uni-bielefeld.de/~cunger/qald/index.php?x=task1&q=3`

[9] `http://wiki.dbpedia.org/Interlinking?v=vn`

within the property *recordedIn*: we wrongly thought it was reserved for live performances only. Thus, these results allowed us to validate our complex correspondences and remove those that prove to be incorrect.

ASK	ASK
WHERE {	WHERE {
?band foaf:name 'Ramones' .	?band foaf:name 'Ramones'**@en** .
?artist foaf:name ?artistname .	?artist foaf:name ?artistname .
?artist mo:member_of ?band .	**{?band dbo:bandMember ?artist}**
	UNION
	{?band dbo:formerBandMember ?artist} .
FILTER (NOT regex(?artistname,"Ramone"))	FILTER (NOT regex(?artistname,"Ramone"))
}	}

Table 3. DBpedia rewritten query (right) from MusicBrainz query (left). Namespace prefix bindings were ommitted (*dbo* refers to dbpedia and *mo* to music).

Next, we rewrote the Music query patterns in terms of the DBpedia vocabulary. Using the 11 simple correspondences and the 28 complex correspondences, we achieved a rewriting percentage of 90% of the Music patterns: on the 19 subgraphs (subpatterns) identified in the patterns for Music, we were able to transform 17 of them. For the Cinema patterns, we were able to rewrite 45 out of 51 subpatterns from the Cinema IRIT query patterns. Then, the patterns rewritten from Music were injected in the SWIP system along the DBpedia data set, in order to demonstrate the relevance of rewriting query patterns in the whole process. We managed to run five queries from QALD and originally intended to MusicBrainz. The generated SPARQL queries are (semantically) correct as long as (i) the correspondences involved do not apply any disjunction of terms, which is not currently supported in SWIP (in this case, only the most likely term is kept), and (ii) the source and target in the correspondences involved have the same information level (basically, equivalence).

5 Related work

Rewriting query patterns using complex correspondences is the novel aspect of this paper. With respect to complex correspondence generation, different approaches have emerged in the literature in the last years. A common approach is based on complex correspondence patterns [18, 17, 14, 15] (§4.3). Walshe [19] proposes refining elementary correspondences by identifying which correspondence pattern best represents a given correspondence. Following a different strategy, Qin *et al.* [13] propose an iterative process that combines terminological, structural, and instance-based matching approaches for mining *frequent queries*, from which complex matching rules (represented in FOL) are generated. Nunes *et al.* [10] present a two-phase instance-based technique for complex datatype property matching, where the first phase identifies simple property matches and the second one uses a genetic programming approach to detect complex matches. Recently, Arnold [1] uses state-of-the-art matchers for generating initial correspondences

that are further (semi-automatically) enriched by using linguistic, structural and background knowledge-based strategies. Although different strategies have been proposed, very few matchers for generating complex correspondences are available or use EDOAL, an expressive alignment language [3], for representing them. With respect to query patterns rewriting, the problem can be seen, at a lower level of abstraction, as a problem of SPARQL rewriting. Correndo *et al.* [2] propose a set of SPARQL rewriting rules exploiting both (complex) ontology alignments and entity co-reference resolution. Zheng *et al.* [20] propose to rewrite SPARQL queries from different contexts, where context mappings provide the articulation of the data semantics for the sources and receivers. Makris *et al.* [9, 8] present the SPARQL-RW rewriting framework that applies a set of predefined (complex) correspondences. They define a set of correspondence types that are used as basis for the rewriting process (i.e., *Class Expression*, *Object Property Expression*, *Datatype Property*, and *Individual*). However, the way the set of complex correspondences is established is not described. Our naive approach for rewriting query patterns is close to these SPARQL rewriting proposals in the sense of using complex correspondences. One of the difficulties is the lack of established ways for automatically identifying them. Although m:n complex correspondences are proposed at conceptual level, few concrete examples are available in the literature. Most of our correspondences are n:m. As most proposals, we start from a set of (automatically) discovered simple correspondences. Finally, our method is applied in an applicative context of rewriting patterns for a question answering system over RDF data.

6 Conclusions and future work

This paper has discussed the use of complex correspondences for rewriting query patterns, aiming at reusing query families across data sets that overlap. Although we could not fully evaluate the rewriting process mainly due to the fact that SWIP does not treat pattern disjunctions, we were able to validate our approach on a subset of manually validated complex correspondences. This opens several opportunities for future work. First, the structure of query patterns in SWIP could evolve so that they match the structure of the complex correspondences we have established. In particular, SWIP would benefit from the disjunction of subpatterns or specification of instances in patterns. Second, we plan to represent our complex correspondences using EDOAL. Third, we plan to formalise the composition of complex correspondence patterns, which are thereby the building blocks to obtain richer correspondences, following a grammar defining a set of rules for rewriting logical statements in FOL or DL. The grammar must define the properties of pattern precedence, transitivity, associativity, commutativity, and distributivity. Finally, we plan to propose an approach for (multilingual) complex correspondence generation, exploiting specially the $\mathcal{A}$Box of ontologies.

References

1. P. Arnold. Semantic enrichment of ontology mappings: Detecting relation types and complex correspondences. In *25th GI-Workshop on Foundations of Databases*, 2013.
2. G. Correndo, M. Salvadores, I. Millard, H. Glaser, and N. Shadbolt. SPARQL Query Rewriting for Implementing Data Integration over Linked Data. In *1st International Workshop on Data Semantics (DataSem 2010)*, March 2010.
3. J. David, J. Euzenat, F. Scharffe, and C. Trojahn. The Alignment API 4.0. *Semantic Web*, 2(1):3–10, 2011.
4. S. Elbassuoni and R. Blanco. Keyword search over rdf graphs. In *Proceedings of the 20th ACM International Conference on Information and Knowledge Management*, CIKM '11, pages 237–242. ACM, 2011.
5. S. Elbassuoni, M. Ramanath, R. Schenkel, and G. Weikum. Searching RDF Graphs with SPARQL and Keywords. *IEEE Data Eng. Bull.*, 33(1):16–24, 2010.
6. J. Euzenat and P. Shvaiko. *Ontology Matching*. Springer-Verlag, Berlin, Heidelberg, 2007.
7. P. Gillet, C. Trojahn, and O. Haemmerlé. Réécriture de patrons de requêtes à l'aide d'alignements d'ontologies. In *Atelier Qualité et Robustesse dans le Web de Données, IC*, 2013.
8. K. Makris, N. Bikakis, N. Gioldasis, and S. Christodoulakis. SPARQL-RW: transparent query access over mapped RDF data sources. In *15th International Conference on Extending Database Technology*, pages 610–613. ACM, 2012.
9. K. Makris, N. Gioldasis, N. Bikakis, and S. Christodoulakis. Ontology mapping and SPARQL rewriting for querying federated RDF data sources. In *2010 Conference on On the Move to Meaningful Internet Systems*, pages 1108–1117, 2010.
10. B. Nunes, A. Mera, M. Casanova, K. Breitman, and L. A. Leme. Complex Matching of RDF Datatype Properties. In *6th Workshop on Ontology Matching*, 2011.
11. C. Pradel, O. Haemmerlé, and N. Hernandez. A Semantic Web Interface Using Patterns: The SWIP System. In *Graph Structures for Knowledge Representation and Reasoning*, LNCS, pages 172–187. Springer Berlin Heidelberg, 2012.
12. C. Pradel, O. Haemmerlé, N. Hernandez, et al. Des patrons modulaires de requêtes sparql dans le système swip. *23es Journées d'Ingénierie des Connaissances*, 2012.
13. H. Qin, D. Dou, and P. LePendu. Discovering executable semantic mappings between ontologies. In *OTM International Conference*, pages 832–849, 2007.
14. D. Ritze, C. Meilicke, O. Sváb-Zamazal, and H. Stuckenschmidt. A pattern-based ontology matching approach for detecting complex correspondences. In *4th Workshop on Ontology Matching*, 2009.
15. D. Ritze, J. Völker, C. Meilicke, and O. Sváb-Zamazal. Linguistic analysis for complex ontology matching. In *5th Workshop on Ontology Matching*, 2010.
16. A. Russell and P. R. Smart. Nitelight: A graphical editor for sparql queries. In *Poster and Demo Session at the 7th International Semantic Web Conference*, 2008.
17. F. Scharffe. *Correspondence Patterns Representation*. PhD thesis, University of Innsbruck, Innsbruck, 2009.
18. F. Scharffe and D. Fensel. Correspondence patterns for ontology alignment. In *Knowledge Engineering: Practice and Patterns*, pages 83–92. Springer, 2008.
19. B. Walshe. Identifying complex semantic matches. In *9th International Conference on The Semantic Web: Research and Applications*, pages 849–853, 2012.
20. X. Zheng, S. E. Madnick, and X. Li. SPARQL Query Mediation over RDF Data Sources with Disparate Contexts. In *WWW Workshop on Linked Data on the Web*, 2012.

Results of the Ontology Alignment Evaluation Initiative 2013*

Bernardo Cuenca Grau[1], Zlatan Dragisic[2], Kai Eckert[3], Jérôme Euzenat[4], Alfio Ferrara[5], Roger Granada[6,7], Valentina Ivanova[2], Ernesto Jiménez-Ruiz[1], Andreas Oskar Kempf[8], Patrick Lambrix[2], Andriy Nikolov[9], Heiko Paulheim[3], Dominique Ritze[3], François Scharffe[10], Pavel Shvaiko[11], Cássia Trojahn[7], and Ondřej Zamazal[12]

[1] University of Oxford, UK
{berg,ernesto}@cs.ox.ac.uk
[2] Linköping University & Swedish e-Science Research Center, Linköping, Sweden
{zlatan.dragisic,valentina.ivanova,patrick.lambrix}@liu.se
[3] University of Mannheim, Mannheim, Germany
{kai,heiko,dominique}@informatik.uni-mannheim.de
[4] INRIA & LIG, Montbonnot, France
Jerome.Euzenat@inria.fr
[5] Università degli studi di Milano, Italy
alfio.ferrara@unimi.it
[6] Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, Brazil
roger.granada@acad.pucrs.br
[7] IRIT & Université Toulouse II, Toulouse, France
cassia.trojahn@irit.fr
[8] GESIS – Leibniz Institute for the Social Sciences, Cologne, Germany
andreas.kempf@gesis.org
[9] Fluid operations, Walldorf, Germany
andriy.nikolov@fluidops.com
[10] LIRMM, Montpellier, France
francois.scharffe@lirmm.fr
[11] TasLab, Informatica Trentina, Trento, Italy
pavel.shvaiko@infotn.it
[12] University of Economics, Prague, Czech Republic
ondrej.zamazal@vse.cz

Abstract. Ontology matching consists of finding correspondences between semantically related entities of two ontologies. OAEI campaigns aim at comparing ontology matching systems on precisely defined test cases. These test cases can use ontologies of different nature (from simple thesauri to expressive OWL ontologies) and use different modalities, e.g., blind evaluation, open evaluation and consensus. OAEI 2013 offered 6 tracks with 8 test cases followed by 23 participants. Since 2010, the campaign has been using a new evaluation modality which provides more automation to the evaluation. This paper is an overall presentation of the OAEI 2013 campaign.

* This paper improves on the "Preliminary results" initially published in the on-site proceedings of the ISWC workshop on Ontology Matching (OM-2013). The only official results of the campaign, however, are on the OAEI web site.

1 Introduction

The Ontology Alignment Evaluation Initiative[1] (OAEI) is a coordinated international initiative, which organizes the evaluation of the increasing number of ontology matching systems [11, 14]. The main goal of OAEI is to compare systems and algorithms on the same basis and to allow anyone for drawing conclusions about the best matching strategies. Our ambition is that, from such evaluations, tool developers can improve their systems.

Two first events were organized in 2004: (i) the Information Interpretation and Integration Conference (I3CON) held at the NIST Performance Metrics for Intelligent Systems (PerMIS) workshop and (ii) the Ontology Alignment Contest held at the Evaluation of Ontology-based Tools (EON) workshop of the annual International Semantic Web Conference (ISWC) [28]. Then, a unique OAEI campaign occurred in 2005 at the workshop on Integrating Ontologies held in conjunction with the International Conference on Knowledge Capture (K-Cap) [3]. Starting from 2006 through 2012 the OAEI campaigns were held at the Ontology Matching workshops collocated with ISWC [12, 10, 5, 7–9, 1]. In 2013, the OAEI results were presented again at the Ontology Matching workshop[2] collocated with ISWC, in Sydney, Australia.

Since 2011, we have been promoting an environment for automatically processing evaluations (§2.2), which has been developed within the SEALS (Semantic Evaluation At Large Scale) project[3]. SEALS provided a software infrastructure, for automatically executing evaluations, and evaluation campaigns for typical semantic web tools, including ontology matching. For OAEI 2013, almost all of the OAEI data sets were evaluated under the SEALS modality, providing a more uniform evaluation setting.

This paper synthetizes the 2013 evaluation campaign and introduces the results provided in the papers of the participants. The remainder of the paper is organised as follows. In Section 2, we present the overall evaluation methodology that has been used. Sections 3-10 discuss the settings and the results of each of the test cases. Section 11 overviews lessons learned from the campaign. Finally, Section 12 concludes the paper.

2 General methodology

We first present the test cases proposed this year to the OAEI participants (§2.1). Then, we discuss the resources used by participants to test their systems and the execution environment used for running the tools (§2.2). Next, we describe the steps of the OAEI campaign (§2.3-2.5) and report on the general execution of the campaign (§2.6).

2.1 Tracks and test cases

This year's campaign consisted of 6 tracks gathering 8 test cases and different evaluation modalities:

[1] http://oaei.ontologymatching.org
[2] http://om2013.ontologymatching.org
[3] http://www.seals-project.eu

The benchmark track (§3): Like in previous campaigns, a systematic benchmark series has been proposed. The goal of this benchmark series is to identify the areas in which each matching algorithm is strong or weak by systematically altering an ontology. This year, we generated a new benchmark based on the original bibliographic ontology.

The expressive ontology track offers real world ontologies using OWL modelling capabilities:

- **Anatomy (§4):** The anatomy real world test case is about matching the Adult Mouse Anatomy (2744 classes) and a small fragment of the NCI Thesaurus (3304 classes) describing the human anatomy.
- **Conference (§5):** The goal of the conference test case is to find all correct correspondences within a collection of ontologies describing the domain of organizing conferences. Results were evaluated automatically against reference alignments and by using logical reasoning techniques.
- **Large biomedical ontologies (§6):** The Largebio test case aims at finding alignments between large and semantically rich biomedical ontologies such as FMA, SNOMED-CT, and NCI. The UMLS Metathesaurus has been used as the basis for reference alignments.

Multilingual

- **Multifarm(§7):** This test case is based on a subset of the Conference data set, translated into eight different languages (Chinese, Czech, Dutch, French, German, Portuguese, Russian, and Spanish) and the corresponding alignments between these ontologies. Results are evaluated against these alignments.

Directories and thesauri

- **Library(§8):** The library test case is a real-word task to match two thesauri. The goal of this test case is to find whether the matchers can handle such lightweight ontologies including a huge amount of concepts and additional descriptions. Results are evaluated both against a reference alignment and through manual scrutiny.

Interactive matching

- **Interactive(§9):** This test case offers the possibility to compare different interactive matching tools which require user interaction. Its goal is to show if user interaction can improve matching results, which methods are most promising and how many interactions are necessary. All participating systems are evaluated on the conference data set using an oracle based on the reference alignment.

Instance matching (§10): The goal of the instance matching track is to evaluate the performance of different tools on the task of matching RDF individuals which originate from different sources but describe the same real-world entity. Both the training data set and the evaluation data set were generated by exploiting the same configuration of the RDFT transformation tool. It performs controlled alterations of an initial data source generating data sets and reference links (i.e. alignments). Reference links were provided for the training set but not for the evaluation set, so the evaluation is blind.

Table 1 summarizes the variation in the proposed test cases.

test	formalism	relations	confidence	modalities	language	SEALS
benchmark	OWL	=	[0 1]	blind+open	EN	√
anatomy	OWL	=	[0 1]	open	EN	√
conference	OWL-DL	=, <=	[0 1]	blind+open	EN	√
large bio	OWL	=	[0 1]	open	EN	√
multifarm	OWL	=	[0 1]	open	CZ, CN, DE, EN, ES, FR, NL, RU, PT	√
library	OWL	=	[0 1]	open	EN, DE	√
interactive	OWL-DL	=, <=	[0 1]	open	EN	√
im-rdft	RDF	=	[0 1]	blind	EN	

Table 1. Characteristics of the test cases (open evaluation is made with already published reference alignments and blind evaluation is made by organizers from reference alignments unknown to the participants).

2.2 The SEALS platform

In 2010, participants of the Benchmark, Anatomy and Conference test cases were asked for the first time to use the SEALS evaluation services: they had to wrap their tools as web services and the tools were executed on the machines of the developers [29]. Since 2011, tool developers had to implement a simple interface and to wrap their tools in a predefined way including all required libraries and resources. A tutorial for tool wrapping was provided to the participants. It describes how to wrap a tool and how to use a simple client to run a full evaluation locally. After local tests are passed successfully, the wrapped tool had to be uploaded on the SEALS portal[4]. Consequently, the evaluation was executed by the organizers with the help of the SEALS infrastructure. This approach allowed to measure runtime and ensured the reproducibility of the results. As a side effect, this approach also ensures that a tool is executed with the same settings for all of the test cases that were executed in the SEALS mode.

2.3 Preparatory phase

Ontologies to be matched and (where applicable) reference alignments have been provided in advance during the period between June 15^{th} and July 3^{rd}, 2013. This gave potential participants the occasion to send observations, bug corrections, remarks and other test cases to the organizers. The goal of this preparatory period is to ensure that the delivered tests make sense to the participants. The final test base was released on July 3^{rd}, 2013. The data sets did not evolve after that.

2.4 Execution phase

During the execution phase, participants used their systems to automatically match the test case ontologies. In most cases, ontologies are described in OWL-DL and serialized in the RDF/XML format [6]. Participants can self-evaluate their results either by comparing their output with reference alignments or by using the SEALS client to compute

[4] `http://www.seals-project.eu/join-the-community/`

precision and recall. They can tune their systems with respect to the non blind evaluation as long as the rules published on the OAEI web site are satisfied. This phase has been conducted between July 3^{rd} and September 1^{st}, 2013.

2.5 Evaluation phase

Participants have been encouraged to provide (preliminary) results or to upload their wrapped tools on the SEALS portal by September 1^{st}, 2013. For the SEALS modality, a full-fledged test including all submitted tools has been conducted by the organizers and minor problems were reported to some tool developers, who had the occasion to fix their tools and resubmit them.

First results were available by September 23^{rd}, 2013. The organizers provided these results individually to the participants. The results were published on the respective web pages by the organizers by October 1^{st}. The standard evaluation measures are usually precision and recall computed against the reference alignments. More details on evaluation measures are given in each test case section.

2.6 Comments on the execution

The number of participating systems has regularly increased over the years: 4 participants in 2004, 7 in 2005, 10 in 2006, 17 in 2007, 13 in 2008, 16 in 2009, 15 in 2010, 18 in 2011, 21 in 2012, 23 in 2013. However, participating systems are now constantly changing. In 2013, 11 (7 in 2012) systems have not participated in any of the previous campaigns. The list of participants is summarized in Table 2. Note that some systems were also evaluated with different versions and configurations as requested by developers (see test case sections for details).

System	AML	CIDER-CL	CroMatcher	HerTUDA	HotMatch	IAMA	LilyIOM	LogMap	LogMapLite	MaasMtch	MapSSS	ODGOMS	OntoK	RiMOM2013	ServOMap	SLINT++	SPHeRe	StringsAuto	Synthesis	WeSeE	WikiMatch	XMap	YAM++	Total=23
Confidence	√	√	√				√	√		√		√	√	√	√	√				√		√	√	14
benchmarks	√	√	√	√	√	√		√	√	√	√	√	√	√	√			√	√	√	√	√	√	20
anatomy	√	√		√	√	√		√	√	√	√	√			√			√		√	√	√	√	17
conference	√	√	√	√	√	√		√	√	√	√	√	√	√	√			√	√	√	√	√	√	20
multifarm	√	√		√	√	√		√	√	√	√	√	√	√				√	√	√	√		√	17
library	√			√	√	√		√	√			√			√			√				√	√	11
interactive	√			√				√												√				4
large bio	√			√	√	√		√	√	√		√			√		√	√				√	√	13
im-rdft							√	√						√		√								4
total	7	4	2	7	6	6	1	8	6	5	4	6	3	4	5	1	1	6	3	5	4	5	6	106

Table 2. Participants and the state of their submissions. Confidence stands for the type of results returned by a system: it is ticked when the confidence is a non boolean value.

Only four systems participated in the instance matching track, where two of them (LogMap and RiMOM2013) also participated in the SEALS tracks. The interactive track also had the same participation, since there are not yet many tools supporting user intervention within the matching process. Finally, some systems were not able to pass some test cases as indicated in Table 2. SPHeRe is an exception since it only participated in the largebio test case. It is a special system based on cloud computing which did not use the SEALS interface this year.

The result summary per test case is presented in the following sections.

3 Benchmark

The goal of the benchmark data set is to provide a stable and detailed picture of each algorithm. For that purpose, algorithms are run on systematically generated test cases.

3.1 Test data

The systematic benchmark test set is built around a seed ontology and many variations of it. Variations are artificially generated, and focus on the characterization of the behavior of the tools rather than having them compete on real-life problems.

Since OAEI 2011.5, they are obtained by discarding and modifying features from a seed ontology. Considered features are names of entities, comments, the specialization hierarchy, instances, properties and classes. Full description of the systematic benchmark test set can be found on the OAEI web site.

This year, we used a version of the benchmark test suite generated by the test generator described in [13] from the usual bibliography ontology. The biblio seed ontology concerns bibliographic references and is inspired freely from BibTeX. It contains 33 named classes, 24 object properties, 40 data properties, 56 named individuals and 20 anonymous individuals. The test case was not available to participants: participants could test their systems with respect to last year data sets, but they have been evaluated against a newly generated test. The tests were also blind for the organizers since we did not looked into them before running the systems.

We also generated and run another test suite from a different seed ontology, but we decided to cancel the evaluation because, due to the particular nature of the seed ontology, the generator was not able to properly discard important information. We did not run scalability tests this year.

The reference alignments are still restricted to named classes and properties and use the "=" relation with confidence of 1.

3.2 Results

We run the experiments on a Debian Linux virtual machine configured with four processors and 8GB of RAM running under a Dell PowerEdge T610 with 2*Intel Xeon Quad Core 2.26GHz E5607 processors and 32GB of RAM, under Linux ProxMox 2 (Debian). All matchers where run under the SEALS client using Java 1.7 and a maximum heap size of 6GB. No timeout was explicitly set.

Reported figures are the average of 5 runs. As has already been shown in [13], there is not much variance in compliance measures across runs. This is not necessarily the case for time measurements so we report standard deviations with time measurements.

From the 23 systems listed in Table 2, 20 systems participated in this test case. Three systems were only participating in the instance matching or largebio test cases. XMap had two different system versions.

A few of these systems encountered problems (marked * in the results table): LogMap and OntoK had quite random problems and did not return results for some tests sometimes; ServOMap did not return results for tests past #261-4; MaasMatch did not return results for tests past #254; MapSSS and StringsAuto did not return results for tests past #202 or #247. Besides the two last systems, the problems where persistent across all 5 runs. MapSSS and StringsAuto alternated between the two failure patterns. We suspect that some of the random problems are due to internal or network timeouts.

Compliance Concerning F-measure results, YAM++ (.89) and CroMatcher (.88) are far ahead before Cider-CL (.75), IAMA (.73) and ODGOMS (.71). Without surprise, such systems have all the same profile: their precision is higher than their recall.

With respect to 2012, some systems maintained their performances or slightly improved them (YAM++, MaasMatch, Hertuda, HotMatch, WikiMatch) while other showed severe degradations. Some of these are explained by failures (MapSSS, ServOMap, LogMap) some others are not explained (LogMapLite, WeSeE). Matchers with lower performance than the baseline are those mentioned before as encountering problems when running tests. This is a problem that such matchers are not robust to these classical tests. It is noteworthy, and surprising, that most of the systems which did not complete all the tests were systems which completed them in 2012!

Confidence accuracy Confidence-weighted measures reward systems able to provide accurate confidence values. Using confidence-weighted F-measures does not increase the evaluation of systems (beside edna which does not perform any filtering). In principle, the weighted recall cannot be higher, but the weighted precision can. In fact, only edna, OntoK and XMapSig have an increased precision. The order given above does not change much with the weighted measures: IAMA and ODGOMS pass CroMatcher and Cider-CL. The only system to suffer a dramatic decrease is RiMOM, owing to the very low confidence measures that it provides.

For those systems which have provided their results with confidence measures different from 1 or 0, it is possible to draw precision/recall graphs in order to compare them; these graphs are given in Figure 1. The graphs show the real precision at n% recall and they stop when no more correspondences are available; then the end point corresponds to the precision and recall reported in the Table 3.

The precision-recall curves confirm the good performances of YAM++ and CroMatcher. CroMatcher achieves the same level of recall as YAM++ but with consistently lower precision. The curves show the large variability across systems. This year, systems seem to be less focussed on precision and make progress at the expense of precision. However, this may be an artifact due to systems facing problems.

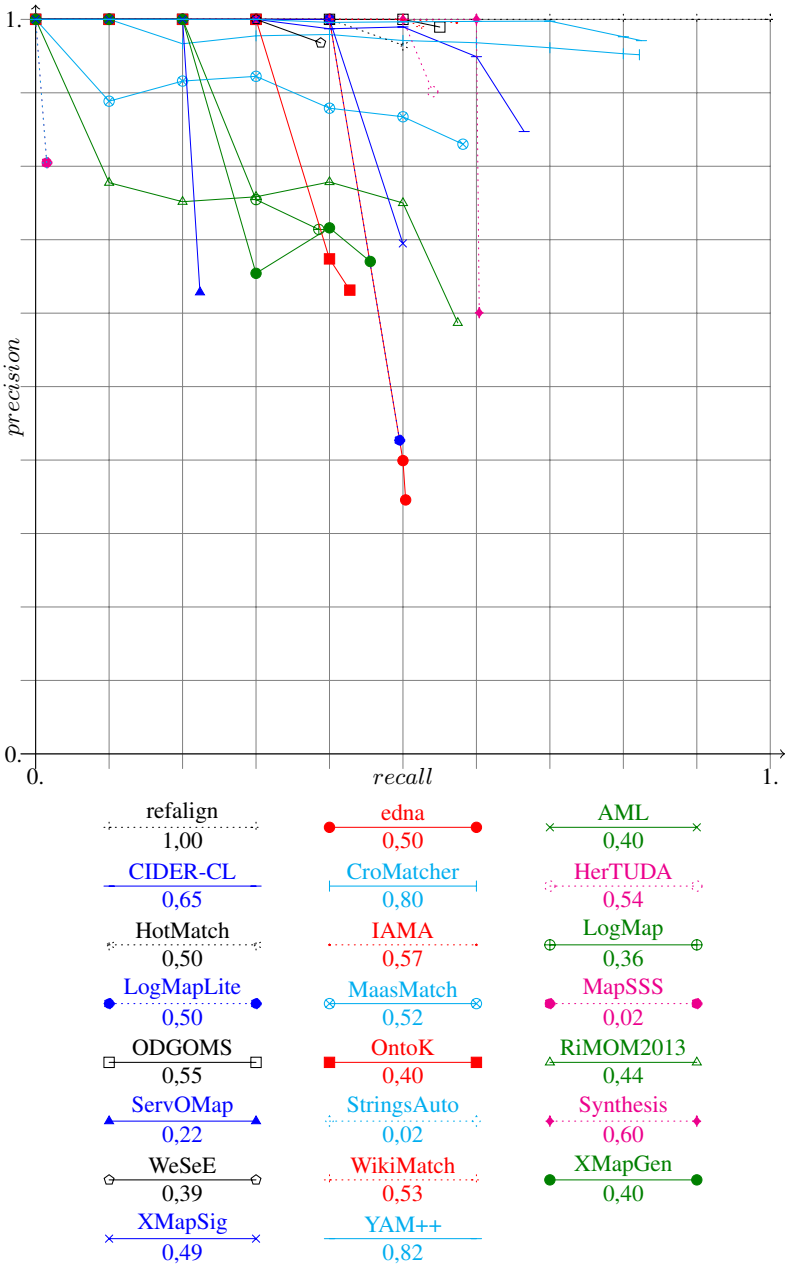


Fig. 1. Precision/recall graphs for benchmarks. The alignments generated by matchers are cut under a threshold necessary for achieving $n\%$ recall and the corresponding precision is computed. Systems for which these graphs are not meaningful (because they did not provide graded confidence values) are drawn in dashed lines.

Runtime There is a large discrepancy between matchers concerning the time spent to match one test run, i.e., 94 matching tests. It ranges from less than a minute for LogMapLite and AML (we do not count StringsAuto which failed to perform many tests) to nearly three hours for OntoK. In fact, OntoK takes as much time as all the other matchers together. Beside these large differences, we also observed large deviations across runs.

We provide (Table 3) the average F-measure point provided per second by matchers. This makes a different ordering of matchers: AML (1.04) comes first before Hertuda (0.94) and LogMapLite (0.81). None of the matchers with the best performances come first. This means that, for achieving good results, considerable time should be spent (however, YAM++ still performs the 94 matching operations in less than 12 minutes).

3.3 Conclusions

Regarding compliance, we observed that, with very few exceptions, the systems performed always better than the baseline. Most of the systems are focussing on precision. This year there was a significant number of systems unable to pass the tests correctly. On the one hand, this is good news: this means that systems are focussing on other test cases than benchmarks. On the other hand, it exhibits system brittleness.

Except for a very few exception, system run time performance is acceptable on tests of that size, but we did not perform scalability tests like last year.

	biblio2 (2012)			biblioc			time		
Matching system	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.	Time(s)	St. Dev.	pt F-m./s
edna	0.46	0.48	0.50	0.35	0.41	0.50			
	(0.61)	(0.55)		(0.58)	(0.54)				
AML				1.00	0.57	0.40	**55**	±6	**1.04**
CIDER-CL				0.85	0.75	0.67	844	±19	0.09
				(0.84)	(0.66)	(0.55)			
CroMatcher				0.95	**0.88**	0.82	1114	±21	0.08
				(0.75)	(0.68)	(0.63)			
Hertuda	0.93	0.67	0.53	0.90	0.68	0.54	72	±6	0.94
Hotmatch	0.99	0.68	0.52	0.96	0.68	0.50	103	±6	0.66
IAMA				0.99	0.73	0.57	102	±10	0.72
LogMap	1.00	0.64	0.47	0.72	0.53	0.42	123	±7	0.43
		(0.59)	(0.42)		(0.51)	(0.39)			
LogMapLt	0.95	0.66	0.50	0.43	0.46	0.50	57	±7	0.81
MaasMtch (*)	0.6	0.6	0.6	0.84	0.69	0.59	173	±6	0.40
	(0.93)	(0.65)	(0.5)	(0.66)	(0.50)	(0.41)			
MapSSS (*)	1.00	**0.86**	0.75	0.84	0.14	0.08	81	±44	0.17
ODGOMS				0.99	0.71	0.55	100	±6	0.71
				(0.98)	(0.70)	(0.54)			
OntoK				0.63	0.51	0.43	10241	±347	0.00
				(0.69)		(0.40)			
RiMOM2013				0.59	0.58	0.58	105	±34	0.55
				(0.49)	(0.19)	(0.12)			
ServOMap (*)	1.00	0.67	0.5	0.53	0.33	0.22	409	±33	0.08
StringsAuto (*)				0.84	0.14	0.08	56	±38	0.25
Synthesis				0.60	0.60	0.60	659	±11	0.09
WeSeE	1.00	0.69(0.68)	0.52	0.96	0.55	0.39	4933	±40	0.01
Wikimatch	0.97	0.67(0.68)	0.52	0.99	0.69	0.53	1845	±39	0.04
XMapGen				0.66	0.54	0.46	594	±5	0.09
					(0.52)	(0.44)			
XMapSig				0.70	0.58	0.50	612	±11	0.09
				(0.71)	(0.59)				
YAM++	0.96	**0.89**	0.82	0.97	**0.89**	0.82	702	±46	0.13
	(1.00)	(0.72)	(0.56)	(0.84)	(0.77)	(0.70)			

Table 3. Results obtained by participants on the biblio benchmark test suite aggregated with harmonic means (values within parentheses are *weighted* version of the measure reported only when different).

4 Anatomy

The anatomy test case confronts matchers with a specific type of ontologies from the biomedical domain. We focus on two fragments of biomedical ontologies which describe the human anatomy[5] and the anatomy of the mouse[6]. This data set has been used since 2007 with some improvements over the years.

4.1 Experimental setting

We conducted experiments by executing each system in its standard setting and we compare precision, recall, F-measure and recall+. The measure recall+ indicates the amount of detected non-trivial correspondences. The matched entities in a non-trivial correspondence do not have the same normalized label. The approach that generates only trivial correspondences is depicted as baseline *StringEquiv* in the following section.

This year we run the systems on a server with 3.46 GHz (6 cores) and 8GB RAM allocated to the matching systems. This is a different setting compared to previous years, so, runtime results are not fully comparable across years. The evaluation was performed with the SEALS client. However, we slightly changed the way how precision and recall are computed, i.e., the results generated by the SEALS client vary in some cases by 0.5% compared to the results presented below. In particular, we removed trivial correspondences in the `oboInOwl` namespace like

```
http://...oboInOwl#Synonym = http://...oboInOwl#Synonym
```

as well as correspondences expressing relations different from equivalence. Using the Pellet reasoner we also checked whether the generated alignment is coherent, i.e., there are no unsatisfiable concepts when the ontologies are merged with the alignment.

4.2 Results

In Table 4, we analyze all participating systems that could generate an alignment in less than ten hours. The listing comprises of 20 entries sorted by F-measure. Four systems participated each with two different versions. These are AML and GOMMA with versions which use background knowledge (indicated with suffix "-bk"), LogMap with a lightweight version LogMapLite that uses only some core components and XMap with versions XMapSig and XMapGen which use two different parameters. For comparison purposes, we run again last year version of GOMMA. GOMMA and HerTUDA participated with the same system as last year (indicated by * in the table). In addition to these two tools we have eight more systems which participated in 2012 and now participated with new versions (HotMatch, LogMap, MaasMatch, MapSSS, ServOMap, WeSeE, WikiMatch and YAM++). Due to some software and hardware incompatibilities,

[5] `http://www.cancer.gov/cancertopics/cancerlibrary/terminologyresources/`

[6] `http://www.informatics.jax.org/searches/AMA_form.shtml`

YAM++ had to be run on a different machine and therefore its runtime (indicated by **) is not fully comparable to that of other systems. Thus, 20 different systems generated an alignment within the given time frame. Four participants (CroMatcher, RiMOM2013, OntoK and Synthesis) did not finish in time or threw an exception.

Matcher	Runtime	Size	Precision	F-measure	Recall	Recall+	Coherent
AML-bk	43	1477	0.95	0.94	0.93	0.82	√
GOMMA-bk*	11	1534	0.92	0.92	0.93	0.81	-
YAM++	62**	1395	0.94	0.90	0.87	0.66	-
AML	15	1315	0.95	0.89	0.83	0.54	√
LogMap	13	1398	0.92	0.88	0.85	0.59	√
GOMMA*	9	1264	0.96	0.87	0.80	0.47	-
StringsAuto	1444	1314	0.90	0.83	0.78	0.43	-
LogMapLite	7	1148	0.96	0.83	0.73	0.29	-
MapSSS	2040	1296	0.90	0.83	0.77	0.44	-
ODGOMS	1212	1102	0.98	0.82	0.71	0.24	-
WikiMatch	19366	1027	0.99	0.80	0.67	0.15	-
HotMatch	300	989	0.98	0.77	0.64	0.14	-
StringEquiv	-	946	*1.00*	0.77	0.62	0.00	-
XMapSig	393	1192	0.86	0.75	0.67	0.13	-
ServOMap	43	975	0.96	0.75	0.62	0.10	-
XMapGen	403	1304	0.81	0.75	0.69	0.19	-
IAMA	10	845	*1.00*	0.71	0.55	0.01	-
CIDER-CL	12308	1711	0.65	0.69	0.73	0.31	-
HerTUDA*	117	1479	0.69	0.68	0.67	0.15	-
WeSeE	34343	935	0.62	0.47	0.38	0.09	-
MaasMatch	8532	2011	0.36	0.41	0.48	0.23	-

Table 4. Comparison, ordered by F-measure, against the reference alignment, runtime is measured in seconds, the "size" column refers to the number of correspondences in the generated alignment.

Nine systems finished in less than 100 seconds, compared to 8 systems in OAEI 2012 and 2 systems in OAEI 2011. This year, 20 out of 24 systems generated results compared to last year when 14 out of 18 systems generated results within the given time frame. The top systems in terms of runtimes are LogMap, GOMMA, IAMA and AML. Depending on the specific version of the systems, they require between 7 and 15 seconds to match the ontologies. The table shows that there is no correlation between quality of the generated alignment in terms of precision and recall and required runtime. This result has also been observed in previous OAEI campaigns.

Table 4 also shows the results for precision, recall and F-measure. In terms of F-measure, the two top ranked systems are AML-bk and GOMMA-bk. These systems use specialised background knowledge, i.e., they are based on mapping composition techniques and the reuse of mappings between UMLS, Uberon and FMA. AML-bk and GOMMA-bk are followed by a group of matching systems (YAM++, AML, LogMap, GOMMA) generating alignments that are very similar with respect to precision, recall and F-measure (between 0.87 and 0.91 F-measure). LogMap uses the general (biomedical) purpose UMLS Lexicon, while the other systems either use Wordnet or no back-

ground knowledge. The results of these systems are at least as good as the results of the best system in OAEI 2007-2010. Only AgreementMaker using additional background knowledge could generate better results than these systems in 2011.

This year, 8 out of 20 systems achieved an F-measure that is lower than the baseline which is based on (normalized) string equivalence (StringEquiv in the table).

Moreover, nearly all systems find many non-trivial correspondences. An exception are IAMA and WeSeE which generated an alignment that is quite similar to the alignment generated by the baseline approach.

From the systems which participated last year WikiMatch showed a considerable improvement. It increased precision from 0.86 to 0.99 and F-measure from 0.76 to 0.80. The other systems produced very similar results compared to the previous year. One exception is WeSeE which achieved a much lower F-measure than in 2012.

Three systems have produced an alignment which is coherent. Last year two systems produced such alignments.

4.3 Conclusions

This year 24 systems (or system variants) participated in the anatomy test case out of which 20 produced results within 10 hours. This is so far the highest number of participating systems as well as the highest number of systems which produce results given time constraints for the anatomy test case.

As last year, we have witnessed a positive trend in runtimes as the majority of systems finish execution in less than one hour (16 out of 20). The AML-bk system improves the best result in terms of F-measure set by a previous version of the system in 2010 and makes it also the top result for the anatomy test case.

5 Conference

The conference test case introduces matching several moderately expressive ontologies. Within this test case, participant results were evaluated against reference alignments (containing merely equivalence correspondences) and by using logical reasoning. The evaluation has been performed with the SEALS infrastructure.

5.1 Test data

The data set consists of 16 ontologies in the domain of organizing conferences. These ontologies have been developed within the OntoFarm project[7].

The main features of this test case are:

– *Generally understandable domain.* Most ontology engineers are familiar with organizing conferences. Therefore, they can create their own ontologies as well as evaluate the alignments among their concepts with enough erudition.

[7] http://nb.vse.cz/~svatek/ontofarm.html

– *Independence of ontologies.* Ontologies were developed independently and based on different resources, they thus capture the issues in organizing conferences from different points of view and with different terminologies.
– *Relative richness in axioms.* Most ontologies were equipped with OWL DL axioms of various kinds; this opens a way to use semantic matchers.

Ontologies differ in their numbers of classes, of properties, in expressivity, but also in underlying resources.

5.2 Results

We provide results in terms of $F_{0.5}$-measure, F_1-measure and F_2-measure, comparison with baseline matchers, precision/recall triangular graph and coherency evaluation.

Evaluation based on reference alignments We evaluated the results of participants against blind reference alignments (labelled as *ra2* on the conference web-page). This includes all pairwise combinations between 7 different ontologies, i.e. 21 alignments.

These reference alignments have been generated as a transitive closure computed on the original reference alignments. In order to obtain a coherent result, conflicting correspondences, i.e., those causing unsatisfiability, have been manually inspected and removed by evaluators. As a result, the degree of correctness and completeness of the new reference alignment is probably slightly better than for the old one. However, the differences are relatively limited. Whereas the new reference alignments are not open, the old reference alignments (labeled as *ra1* on the conference web-page) are available. These represent close approximations of the new ones.

Table 5 shows the results of all participants with regard to the new reference alignment. $F_{0.5}$-measure, F_1-measure and F_2-measure are computed for the threshold that provides the highest average F_1-measure. F_1 is the harmonic mean of precision and recall where both are equally weighted; F_2 weights recall higher than precision and $F_{0.5}$ weights precision higher than recall. The matchers shown in the table are ordered according to their highest average F_1-measure. This year we employed two baselines matcher. *edna* (string edit distance matcher) is used within the benchmark test case and with regard to performance it is very similar as previously used *baseline2*; *StringEquiv* is used within the anatomy test case. These baselines divide matchers into three groups. Group 1 consists of matchers (YAM++, AML-bk –AML standing for AgreementMakerLight–, LogMap, AML, ODGOMS, StringsAuto, ServOMap, MapSSS, HerTUDA, WikiMatch, WeSeE-Match, IAMA, HotMatch, CIDER-CL) having better (or the same) results than both baselines in terms of highest average F_1-measure. Group 2 consists of matchers (OntoK, LogMapLite, XMapSigG, XMapGen and SYNTHESIS) performing better than baseline *StringEquiv* but worse than *edna*. Other matchers (RIMOM2013, CroMatcher and MaasMatch) performed worse than both baselines. CroMatcher was unable to process any ontology pair where conference.owl ontology was included. Therefore, the evaluation was run only on 15 test cases. Thus, its results are just an approximation.

Performance of matchers from Group 1 regarding F_1-measure is visualized in Figure 2.

Matcher	Prec.	$F_{0.5}$-m.	F_1-m.	F_2-m.	Rec.	Size	Inc. Al.	Inc-dg
YAM++	0.78	0.75	0.71	0.67	0.65	12.524	0	0.0%
AML-bk	0.82	0.74	0.64	0.57	0.53	9.714	0	0.0%
LogMap	0.76	0.70	0.63	0.57	0.54	10.714	0	0.0%
AML	0.82	0.73	0.63	0.55	0.51	9.333	0	0.0%
ODGOMS1_2	0.70	0.66	0.62	0.57	0.55	11.762	13	6.5%
StringsAuto	0.74	0.68	0.60	0.53	0.50	11.048	0	0.0%
ServOMap_v104	0.69	0.64	0.58	0.53	0.50	11.048	4	2.0%
MapSSS	0.77	0.68	0.58	0.50	0.46	9.857	0	0.0%
ODGOMS1_1	0.72	0.65	0.57	0.51	0.47	9.667	9	4.4%
HerTUDA	0.70	0.63	0.56	0.49	0.46	9.857	9	5.3%
WikiMatch	0.70	0.63	0.55	0.48	0.45	9.762	10	6.1%
WeSeE-Match	0.79	0.67	0.55	0.46	0.42	8	1	0.4%
IAMA	0.74	0.65	0.55	0.48	0.44	8.857	7	4%
HotMatch	0.67	0.62	0.55	0.50	0.47	10.524	9	5.0%
CIDER-CL	0.72	0.64	0.55	0.48	0.44	22.857	21	19.5%
edna	*0.73*	*0.64*	*0.55*	*0.48*	*0.44*			
OntoK	0.72	0.63	0.54	0.47	0.43	8.952	7	3.9%
LogMapLite	0.68	0.62	0.54	0.48	0.45	9.952	7	5.4%
XMapSiG1_3	0.68	0.61	0.53	0.47	0.44	10.714	0	0.0%
XMapGen1_4	0.64	0.59	0.53	0.48	0.45	18.571	0	0.0%
SYNTHESIS	0.73	0.63	0.53	0.45	0.41	8.429	9	4.8%
StringEquiv	*0.76*	*0.64*	*0.52*	*0.43*	*0.39*			
RIMOM2013*	0.55	0.53	0.51	0.48	0.47	56.81	20	27.1%
XMapSiG1_4	0.75	0.62	0.50	0.41	0.37	8.048	1	0.8%
CroMatcher	0.56	0.53	0.49	0.45	0.43			
XMapGen	0.70	0.59	0.48	0.40	0.36	12	1	0.4%
MaasMatch	0.27	0.30	0.36	0.44	0.53			

Table 5. The highest average $F_{[0.5|1|2]}$-measure and their corresponding precision and recall for each matcher with its F_1-optimal threshold (ordered by F_1-measure). Average size of alignments, number of incoherent alignments and average degree of incoherence. The mark * is added when we only provide lower bound of the degree of incoherence due to the combinatorial complexity of the problem.

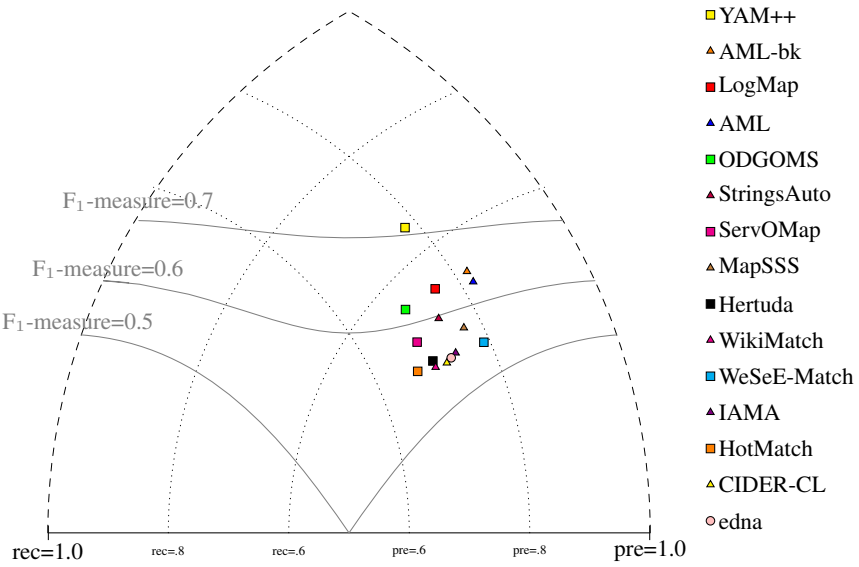


Fig. 2. Precision/recall triangular graph for the conference test case. Dotted lines depict level of precision/recall while values of F_1-measure are depicted by areas bordered by corresponding lines F_1-measure=0.[5|6|7].

Comparison with previous years Ten matchers also participated in this test case in OAEI 2012. The largest improvement was achieved by MapSSS (precision from .47 to .77, whereas recall remains the same, .46) and ServOMap (precision from .68 to .69 and recall from .41 to .50).

Runtimes We measured the total time of generating 21 alignments. It was executed on a laptop under Ubuntu running on Intel Core i5, 2.67GHz and 8GB RAM. In all, there are eleven matchers which finished all 21 tests within 1 minute or around 1 minute (AML-bk: 16s, ODGOMS: 19s, LogMapLite: 21s, AML, HerTUDA, StringsAuto, HotMatch, LogMap, IAMA, RIMOM2013: 53s and MaasMatch: 76s). Next, four systems needed less than 10 minutes (ServOMap, MapSSS, SYNTHESIS, CIDER-CL). 10 minutes are enough for the next three matchers (YAM++, XMapGen, XMapSiG). Finally, three matchers needed up to 40 minutes to finish all 21 test cases (WeSeE-Match: 19 min, WikiMatch: 26 min, OntoK: 40 min).

In conclusion, regarding performance we can see (clearly from Figure 2) that YAM++ is on the top again. The next four matchers (AML-bk, LogMap, AML, ODGOMS) are relatively close to each other. This year there is a larger group of matchers (15) which are above the edna *baseline* than previous years. This is partly because a couple of previous system matchers improved and a couple of high quality new system matchers entered the OAEI campaign.

Evaluation based on alignment coherence As in the previous years, we apply the Maximum Cardinality measure to evaluate the degree of alignment incoherence, see

Table 5. Details on this measure and its implementation can be found in [21]. We computed the average for all 21 test cases of the conference test case for which there exists a reference alignment. In one case, RIMOM2013, marked with an asterisk, we could not compute the exact degree of incoherence due to the combinatorial complexity of the problem, however we were still able to compute a lower bound for which we know that the actual degree is higher. We do not provide numbers for CroMatcher since it did not generate all 21 alignments. For MaasMatch, we could not compute the degree of incoherence since its alignments are highly incoherent (and thus the reasoner encountered exceptions).

This year eight systems managed to generate coherent alignments: AML, AML-bk, LogMap, MapSSS, StringsAuto, XMapGen, XMapSiG and YAM++. Coherent results need not only be related to a specific approach ensuring the coherency, but it can be indirectly caused by generating small and highly precise alignments. However, looking at Table 5 it seems that there is no matcher which on average generate too small alignments. In all, this is a large important improvement compared to previous years, where we observed that only four (two) systems managed to generate (nearly) coherent alignments in 2011-2012.

6 Large biomedical ontologies (largebio)

The Largebio test case aims at finding alignments between the large and semantically rich biomedical ontologies FMA, SNOMED-CT, and NCI, which contains 78,989, 306,591 and 66,724 classes, respectively.

6.1 Test data

The test case has been split into three matching problems: FMA-NCI, FMA-SNOMED and SNOMED-NCI; and each matching problem in 2 tasks involving different fragments of the input ontologies.

The UMLS Metathesaurus [4] has been selected as the basis for reference alignments. UMLS is currently the most comprehensive effort for integrating independently-developed medical thesauri and ontologies, including FMA, SNOMED-CT, and NCI. Although the standard UMLS distribution does not directly provide "alignments" (in the OAEI sense) between the integrated ontologies, it is relatively straightforward to extract them from the information provided in the distribution files (see [18] for details).

It has been noticed, however, that although the creation of UMLS alignments combines expert assessment and auditing protocols they lead to a significant number of logical inconsistencies when integrated with the corresponding source ontologies [18].

To address this problem, in OAEI 2013, unlike previous editions, we have created a unique refinement of the UMLS mappings combining both Alcomo (mapping) debugging system [21] and LogMap's (mapping) repair facility [17], and manual curation when necessary. This refinement of the UMLS mappings, which does not lead to unsatisfiable classes[8], has been used as the Large BioMed reference alignment. Objections

[8] For the SNOMED-NCI case we used the OWL 2 EL reasoner ELK, see Section 6.4 for details.

have been raised on the validity (and fairness) of the application of mapping repair techniques to make reference alignments coherent [24]. For next year campaign, we intend to take into consideration their suggestions to mitigate the effect of using repair techniques. This year reference alignment already aimed at mitigating the fairness effect by combining two mapping repair techniques, however further improvement should be done in this line.

6.2 Evaluation setting, participation and success

We have run the evaluation in a high performance server with 16 CPUs and allocating 15 Gb RAM. Precision, Recall and F-measure have been computed with respect to the UMLS-based reference alignment. Systems have been ordered in terms of F-measure.

In the largebio test case, 13 out of 21 participating systems have been able to cope with at least one of the tasks of the largebio test case. Synthesis, WeSeEMatch and WikiMatch failed to complete the smallest task with a time out of 18 hours, while MapSSS, RiMOM, CIDER-CL, CroMatcher and OntoK threw an exception during the matching process. The latter two threw an out-of-memory exception. In total we have evaluated 20 system configurations.

6.3 Tool variants and background knowledge

There were, in this test case, different variants of tools using background knowledge to certain degree. These are:

- XMap participates with two variants. XMapSig, which uses a sigmoid function, and XMapGen, which implements a genetic algorithm. ODGOMS also participates with two versions (v1.1 and v1.2). ODGOMS-v1.1 is the original submitted version while ODGOMS-v1.2 includes some bug fixes and extensions.
- LogMap has also been evaluated with two variants: LogMap and LogMap-BK. LogMap-BK uses normalisations and spelling variants from the general (biomedical) purpose UMLS Lexicon[9] while LogMap has this feature deactivated.
- AML has been evaluated with 6 different variants depending on the use of repair techniques (R), general background knowledge (BK) and specialised background knowledge based on the UMLS Metathesaurus (SBK).
- YAM++ and MaasMatch also use the general purpose background knowledge provided by WordNet[10].

Since the reference alignment of this test case is based on the UMLS Metathesaurus, we did not included within the results the alignments provided by AML-SBK and AML-SBK-R. Nevertheless we consider their results very interesting: AML-SBK and AML-SBK-R averaged F-measures higher than 0.90 in all 6 tasks.

We have also re-run the OAEI 2012 version of GOMMA. The results of GOMMA may slightly vary w.r.t. those in 2012 since we have used a different reference alignment.

[9] http://www.nlm.nih.gov/pubs/factsheets/umlslex.html
[10] http://wordnet.princeton.edu/

System	FMA-NCI		FMA-SNOMED		SNOMED-NCI		Average	#
	Task 1	Task 2	Task 3	Task 4	Task 5	Task 6		
LogMapLt	7	59	14	101	54	132	61	6
IAMA	13	139	27	217	98	206	117	6
AML	16	201	60	542	291	569	280	6
AML-BK	38	201	93	530	380	571	302	6
AML-R	18	194	86	554	328	639	303	6
GOMMA_{2012}	39	243	54	634	220	727	320	6
AML-BK-R	42	204	121	583	397	635	330	6
YAM++	93	365	100	401	391	712	344	6
LogMap-BK	44	172	85	556	444	1,087	398	6
LogMap	41	161	78	536	433	1,232	414	6
ServOMap	140	2,690	391	4,059	1,698	6,320	2,550	6
SPHeRe (*)	*16*	*8,136*	*154*	*20,664*	*2,486*	*10,584*	7,007	6
XMapSiG	1,476	-	11,720	-	-	-	6,598	2
XMapGen	1,504	-	12,127	-	-	-	6,816	2
Hertuda	3,403	-	17,610	-	-	-	10,507	2
ODGOMS-v1.1	6,366	-	27,450	-	-	-	16,908	2
HotMatch	4,372	-	32,243	-	-	-	18,308	2
ODGOMS-v1.2	10,204	-	42,908	-	-	-	26,556	2
StringsAuto	6,358	-	-	-	-	-	6,358	1
MaasMatch	12,409	-	-	-	-	-	12,409	1
# Systems	**20**	**12**	**18**	**12**	**12**	**12**	**5,906**	**86**

Table 6. System runtimes (s) and task completion. GOMMA is a system provided in 2012. (*) SPHeRe times were reported by the authors. SPHeRe is a special tool which relies on the utilization of cloud computing resources.

6.4 Alignment coherence

Together with Precision, Recall, F-measure and Runtimes we have also evaluated the coherence of alignments. We report (1) the number of unsatisfiabilities when reasoning with the input ontologies together with the computed mappings, and (2) the ratio of unsatisfiable classes with respect to the size of the union of the input ontologies.

We have used the OWL 2 reasoner MORe [2] to compute the number of unsatisfiable classes. For the cases in which MORe could not cope with the input ontologies and the mappings (in less than 2 hours) we have provided a lower bound on the number of unsatisfiable classes (indicated by $\geq$) using the OWL 2 EL reasoner ELK [20].

In this OAEI edition, only three systems have shown mapping repair facilities, namely: YAM++, AML with (R)epair configuration and LogMap. Tables 7-10 show that even the most precise alignment sets may lead to a huge amount of unsatisfiable classes. This proves the importance of using techniques to assess the coherence of the generated alignments.

6.5 Runtimes and task completion

Table 6 shows which systems (including variants) were able to complete each of the matching tasks in less than 18 hours and the required computation times. Systems have

been ordered with respect to the number of completed tasks and the average time required to complete them. Times are reported in seconds.

The last column reports the number of tasks that a system could complete. For example, 12 system configurations were able to complete all six tasks. The last row shows the number of systems that could finish each of the tasks. The tasks involving SNOMED were also harder with respect to both computation times and the number of systems that completed the tasks.

6.6 Results for the FMA-NCI matching problem

Table 7 summarizes the results for the tasks in the FMA-NCI matching problem. LogMap-BK and YAM++ provided the best results in terms of both Recall and F-measure in Task 1 and Task 2, respectively. IAMA provided the best results in terms of precision, although its recall was below average. Hertuda provided competitive results in terms of recall, but the low precision damaged the final F-measure. On the other hand, StringsAuto, XMapGen and XMapSiG provided a set of alignments with high precision, however, the F-measure was damaged due to the low recall of their alignments. Overall, the results were very positive and many systems obtained an F-measure higher than 0.80 in the two tasks.

Efficiency in Task 2 has decreased with respect to Task 1. This is mostly due to the fact that larger ontologies also involve more possible candidate alignments and it is harder to keep high precision values without damaging recall, and vice versa.

6.7 Results for the FMA-SNOMED matching problem

Table 8 summarizes the results for the tasks in the FMA-SNOMED matching problem. YAM++ provided the best results in terms of F-measure on both Task 3 and Task 4. YAM++ also provided the best Precision and Recall in Task 3 and Task 4, respectively; while AML-BK provided the best Recall in Task 3 and AML-R the best Precision in Task 4.

Overall, the results were less positive than in the FMA-NCI matching problem and only YAM++ obtained an F-measure greater than 0.80 in the two tasks. Furthermore, 9 systems failed to provide a recall higher than 0.4. Thus, matching FMA against SNOMED represents a significant leap in complexity with respect to the FMA-NCI matching problem.

As in the FMA-NCI matching problem, efficiency also decreases as the ontology size increases. The most important variations were suffered by SPHeRe, IAMA and GOMMA in terms of precision.

6.8 Results for the SNOMED-NCI matching problem

Table 9 summarizes the results for the tasks in the SNOMED-NCI matching problem. LogMap-BK and ServOMap provided the best results in terms of both Recall and F-measure in Task 5 and Task 6, respectively. YAM++ provided the best results in terms of precision in Task 5 while AML-R in Task 6.

Task 1: small FMA and NCI fragments							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
LogMap-BK	45	2,727	0.95	0.91	0.88	2	0.02%
YAM++	94	2,561	0.98	0.91	0.85	2	0.02%
GOMMA$_{2012}$	40	2,626	0.96	0.91	0.86	2,130	20.9%
AML-BK-R	43	2,619	0.96	0.90	0.86	2	0.02%
AML-BK	39	2,695	0.94	0.90	0.87	2,932	28.8%
LogMap	41	2,619	0.95	0.90	0.85	2	0.02%
AML-R	19	2,506	0.96	0.89	0.82	2	0.02%
ODGOMS-v1.2	10,205	2,558	0.95	0.89	0.83	2,440	24.0%
AML	16	2,581	0.95	0.89	0.83	2,598	25.5%
LogMapLt	8	2,483	0.96	0.88	0.81	2,104	20.7%
ODGOMS-v1.1	6,366	2,456	0.96	0.88	0.81	1,613	15.8%
ServOMap	141	2,512	0.95	0.88	0.81	540	5.3%
SPHeRe	16	2,359	0.96	0.86	0.77	367	3.6%
HotMatch	4,372	2,280	0.96	0.84	0.75	285	2.8%
Average	2,330	2,527	0.90	0.81	0.75	1,582	15.5%
IAMA	14	1,751	0.98	0.73	0.58	166	1.6%
Hertuda	3,404	4,309	0.59	0.70	0.87	2,675	26.3%
StringsAuto	6,359	1,940	0.84	0.67	0.55	1,893	18.6%
XMapGen	1,504	1,687	0.83	0.61	0.48	1,092	10.7%
XMapSiG	1,477	1,564	0.86	0.60	0.46	818	8.0%
MaasMatch	12,410	3,720	0.41	0.46	0.52	9,988	98.1%

Task 2: whole FMA and NCI ontologies							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
YAM++	366	2,759	0.90	0.87	0.85	9	0.01%
GOMMA$_{2012}$	243	2,843	0.86	0.85	0.83	5,574	3.8%
LogMap	162	2,667	0.87	0.83	0.79	10	0.01%
LogMap-BK	173	2,668	0.87	0.83	0.79	9	0.01%
AML-BK	201	2,828	0.82	0.80	0.79	16,120	11.1%
AML-BK-R	205	2,761	0.83	0.80	0.78	10	0.01%
Average	1,064	2,711	0.84	0.80	0.77	9,223	6.3%
AML-R	194	2,368	0.89	0.80	0.72	9	0.01%
AML	202	2,432	0.88	0.80	0.73	1,044	0.7%
SPHeRe	8,136	2,610	0.85	0.80	0.75	1,054	0.7%
ServOMap	2,690	3,235	0.73	0.76	0.80	60,218	41.3%
LogMapLt	60	3,472	0.69	0.74	0.81	26,442	18.2%
IAMA	139	1,894	0.90	0.71	0.58	180	0.1%

Table 7. Results for the FMA-NCI matching problem.

As in the previous matching problems, efficiency decreases as the ontology size increases. For example, in Task 6, only ServOMap and YAM++ could reach an F-measure higher than 0.7. The results were also less positive than in the FMA-SNOMED matching problem, and thus, the SNOMED-NCI case represented another leap in complexity.

Task 3: small FMA and SNOMED fragments							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
YAM++	100	6,635	0.98	0.84	0.73	13,040	55.3%
AML-BK	93	6,937	0.94	0.82	0.73	12,379	52.5%
AML	60	6,822	0.94	0.82	0.72	15,244	64.7%
AML-BK-R	122	6,554	0.95	0.80	0.70	15	0.06%
AML-R	86	6,459	0.95	0.80	0.69	14	0.06%
LogMap-BK	85	6,242	0.96	0.79	0.67	0	0.0%
LogMap	79	6,071	0.97	0.78	0.66	0	0.0%
ServOMap	391	5,828	0.95	0.75	0.62	6,018	25.5%
ODGOMS-v1.2	42,909	5,918	0.86	0.69	0.57	9,176	38.9%
Average	8,073	4,248	0.89	0.55	0.44	7,308	31.0%
$GOMMA_{2012}$	54	3,666	0.92	0.54	0.38	2,058	8.7%
ODGOMS-v1.1	27,451	2,267	0.88	0.35	0.22	938	4.0%
HotMatch	32,244	2,139	0.87	0.34	0.21	907	3.9%
LogMapLt	15	1,645	0.97	0.30	0.18	773	3.3%
Hertuda	17,610	3,051	0.57	0.29	0.20	1,020	4.3%
SPHeRe	154	1,577	0.92	0.27	0.16	805	3.4%
IAMA	27	1,250	0.96	0.24	0.13	22,925	97.3%
XMapGen	12,127	1,827	0.69	0.24	0.14	23,217	98.5%
XMapSiG	11,720	1,581	0.76	0.23	0.13	23,025	97.7%

Task 4: whole FMA ontology with SNOMED large fragment							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
YAM++	402	6,842	0.95	0.82	0.72	$\geq$57,074	$\geq$28.3%
AML-BK	530	6,186	0.94	0.77	0.65	$\geq$40,162	$\geq$19.9%
AML	542	5,797	0.96	0.76	0.62	$\geq$39,472	$\geq$19.6%
AML-BK-R	584	5,858	0.94	0.74	0.62	29	0.01%
AML-R	554	5,499	0.97	0.74	0.59	7	0.004%
ServOMap	4,059	6,440	0.86	0.72	0.62	$\geq$164,116	$\geq$81.5%
LogMap-BK	556	6,134	0.87	0.71	0.60	0	0.0%
LogMap	537	5,923	0.89	0.71	0.59	0	0.0%
Average	2,448	5,007	0.83	0.59	0.48	40,143	19.9%
$GOMMA_{2012}$	634	5,648	0.41	0.31	0.26	9,918	4.9%
LogMapLt	101	1,823	0.88	0.30	0.18	$\geq$4,393	$\geq$2.2%
SPHeRe	20,664	2,338	0.61	0.25	0.16	6,523	3.2%
IAMA	218	1,600	0.75	0.23	0.13	$\geq$160,022	$\geq$79.4%

Table 8. Results for the FMA-SNOMED matching problem.

6.9 Summary results for the top systems

Table 10 summarizes the results for the systems that completed all 6 tasks of the Large BioMed Track. The table shows the total time in seconds to complete all tasks and averages for Precision, Recall, F-measure and Incoherence degree. The systems have been ordered according to the average F-measure.

Task 5: small SNOMED and NCI fragments							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
LogMap-BK	444	13,985	0.89	0.77	0.68	≥40	≥0.05%
LogMap	433	13,870	0.90	0.77	0.67	≥47	≥0.06%
ServOMap	1,699	12,716	0.93	0.76	0.64	≥59,944	≥79.8%
AML-BK-R	397	13,006	0.92	0.76	0.65	≥32	≥0.04%
AML-BK	380	13,610	0.89	0.76	0.66	≥66,389	≥88.4%
AML-R	328	12,622	0.92	0.75	0.63	≥36	≥0.05%
YAM++	391	11,672	0.97	0.75	0.61	≥0	≥0.0%
AML	291	13,248	0.89	0.75	0.64	≥63,305	≥84.3%
Average	602	12,003	0.92	0.72	0.60	32,222	42.9%
LogMapLt	55	10,962	0.94	0.70	0.56	≥60,427	≥80.5%
GOMMA_{2012}	221	10,555	0.94	0.68	0.54	≥50,189	≥66.8%
SPHeRe	2,486	9,389	0.92	0.62	0.47	≥46,256	≥61.6%
IAMA	99	8,406	0.96	0.60	0.44	≥40,002	≥53.3%

Task 6: whole NCI ontology with SNOMED large fragment							
System	Time (s)	# Mappings	Scores			Incoherence	
			Prec.	F-m.	Rec.	Unsat.	Degree
ServOMap	6,320	14,312	0.82	0.72	0.64	≥153,259	≥81.0%
YAM++	713	12,600	0.88	0.71	0.60	≥116	≥0.06%
AML-BK	571	11,354	0.92	0.70	0.56	≥121,525	≥64.2%
AML-BK-R	636	11,033	0.93	0.69	0.55	≥41	≥0.02%
LogMap-BK	1,088	12,217	0.87	0.69	0.58	≥1	≥0.001%
LogMap	1,233	11,938	0.88	0.69	0.57	≥1	≥0.001%
AML	570	10,940	0.93	0.69	0.55	≥121,171	≥64.1%
AML-R	640	10,622	0.94	0.68	0.54	≥51	≥0.03%
Average	1,951	11,581	0.88	0.67	0.55	72,365	38.3%
LogMapLt	132	12,907	0.80	0.66	0.56	≥150,773	≥79.7%
GOMMA_{2012}	728	12,440	0.79	0.63	0.53	≥127,846	≥67.6%
SPHeRe	10,584	9,776	0.88	0.61	0.47	≥105,418	≥55.7%
IAMA	207	8,843	0.92	0.59	0.44	≥88,185	≥46.6%

Table 9. Results for the SNOMED-NCI matching problem.

YAM++ was a step ahead and obtained the best average Precision and Recall. AML-R obtained the second best Precision while AML-BK obtained the second best Recall.

Regarding mapping incoherence, LogMap-BK computed, on average, the mapping sets leading to the smallest number of unsatisfiable classes. The configurations of AML using (R)epair also obtained very good results in terms mapping coherence.

Finally, LogMapLt was the fastest system. The rest of the tools, apart from ServoMap and SPHeRe, were also very fast and only needed between 11 and 53 minutes to complete all 6 tasks. ServOMap required around 4 hours to complete them while SPHeRe required almost 12 hours.

System	Total Time (s)	Average			
		Prec.	F-m.	Rec.	Inc. Degree
YAM++	2,066	0.94	0.82	0.73	14%
AML-BK	1,814	0.91	0.79	0.71	44%
LogMap-BK	2,391	0.90	0.78	0.70	*0%*
AML-BK-R	1,987	0.92	0.78	0.69	*0%*
AML	1,681	0.93	0.78	0.68	43%
LogMap	2,485	0.91	0.78	0.69	*0%*
AML-R	1,821	0.94	0.78	0.67	*0%*
ServOMap	15,300	0.87	0.77	0.69	52%
GOMMA_{2012}	1,920	0.81	0.65	0.57	29%
LogMapLt	371	0.87	0.60	0.52	34%
SPHeRe	42,040	0.86	0.57	0.46	21%
IAMA	704	0.91	0.52	0.39	46%

Table 10. Summary results for the top systems (values in italics are not absolute 0 but are caused by rounding).

6.10 Conclusions

Although the proposed matching tasks represent a significant leap in complexity with respect to the other OAEI test cases, the results have been very promising and 12 systems (including all system configurations) completed all matching tasks with very competitive results.

There is, however, plenty of room for improvement: (1) most of the participating systems disregard the coherence of the generated alignments; (2) the size of the input ontologies should not significantly affect efficiency, and (3) recall in the tasks involving SNOMED should be improved while keeping the current precision values.

The alignment coherence measure was the weakest point of the systems participating in this test case. As shown in Tables 7-10, even highly precise alignment sets may lead to a huge number of unsatisfiable classes. The use of techniques to assess mapping coherence is critical if the input ontologies together with the computed mappings are to be used in practice. Unfortunately, only a few systems in OAEI 2013 have shown to successfully use such techniques. We encourage ontology matching system developers to develop their own repair techniques or to use state-of-the-art techniques such as Alcomo [21], the repair module of LogMap (LogMap-Repair) [17] or the repair module of AML [26], which have shown to work well in practice [19].

7 MultiFarm

For evaluating the ability of matching systems to deal with ontologies in different natural languages, the MultiFarm data set has been proposed [22]. This data set results from the translation of 7 Conference test case ontologies (cmt, conference, confOf, iasted, sigkdd, ekaw and edas), into 8 languages (Chinese, Czech, Dutch, French, German, Portuguese, Russian, and Spanish, in addition to English). The 9 language versions result in 36 pairs of languages. For each pair of language, we take into account the alignment direction (cmt_{en}→confOf_{de} and cmt_{de}→confOf_{en}, for instance, as two matching

tasks), what results in 49 alignments. Hence, MultiFarm contains 36×49 matching tasks.

7.1 Experimental setting

For the 2013 evaluation campaign, we have used a subset of the whole MultiFarm data set, omitting all the matching tasks involving the edas and ekaw ontologies (resulting in $36 \times 25 = 900$ matching tasks). In this sub set, we can distinguish two types of matching tasks: (i) those test cases where two different ontologies have been translated in different languages, e.g., cmt→confOf, and (ii) those test cases where the same ontology has been translated in different languages, e.g., cmt→cmt. For the test cases of type (ii), good results are not necessarily related to the use of specific techniques for dealing with ontologies in different natural languages, but on the ability to exploit the fact that both ontologies have an identical structure (and that the reference alignment covers all entities described in the ontologies).

This year, 7 systems (out of 23 participants, see Table 2) use specific cross-lingual[11] methods : CIDER-CL, MapSSS, RiMOM2013, StringsAuto, WeSeE, WikiMatch, and YAM++. This maintains the number of participants implementing specific modules as in 2012 (ASE, AUTOMSv2, GOMMA, MEDLEY, WeSeE, WikiMatch, and YAM++), counting on 4 new participants (some of them, extensions of systems participating in previous campaigns). The other systems are not specifically designed to match ontologies in different languages nor do they use any component for that purpose. CIDER-CL uses textual definitions of concepts (from Wikipedia articles) and computes co-occurrence information between multilingual definitions. MapSSS, StringsAuto and RiMOM2013[12] apply translation, using Google Translator API, before the matching step. In particular, RiMOM2013 uses a two-step translation: a first step for translating labels from the target language into the source language and a second step for translating all labels into English (for using WordNet). WeSeE uses the Web Translator API and YAM++ uses Microsoft Bing Translation, where both of them consider English as pivot language. Finally, WikiMatch exploits Wikipedia for extracting cross-language links for helping in the task of finding correspondences between the ontologies.

7.2 Execution setting and runtime

All systems have been executed on a Debian Linux virtual machine configured with four processors and 20GB of RAM running under a Dell PowerEdge T610 with 2*Intel

[11] We have revised the definitions of multilingual and cross-lingual matching. Initially, as reported in [22], MultiFarm was announced as a benchmark for multilingual ontology matching, i.e., *multilingual* in the sense that we have a set of ontologies in 8 languages. However, it is more appropriate to use the term *cross-lingual* ontology matching. Cross-lingual ontology matching refers to the matching cases where each ontology uses a different natural language (or a different set of natural languages) for entity naming, i.e., the intersection of sets is empty. It is the case of the matching tasks in MultiFarm.

[12] These 3 systems have encountered problems for accessing Google servers. New versions of these tools were received after the deadline, improving, for some test cases, the results reported here.

Xeon Quad Core 2.26GHz E5607 processors and 32GB of RAM, under Linux ProxMox 2 (Debian). The runtimes for each system can be found in Table 11. The measurements are based on 1 run. We can observe large differences between the time required for a system to complete the 900 matching tasks. While RiMOM requires around 13 minutes, WeSeE takes around 41 hours. As we have used this year a different setting from the one in 2012, we are not able to compare runtime measurements over the campaigns.

7.3 Evaluation results

Overall results Before discussing the results per pairs of languages, we present the aggregated results for the test cases within type (i) and (ii) matching task. Table 11 shows the aggregated results. Systems not listed in this table have generated empty alignments, for most test cases (ServOMap) or have thrown exceptions (CroMatcher, XMapGen, XMapSiG). For computing these results, we do not distinguish empty and erroneous alignments. As shown in Table 11, we observe significant differences between the results obtained for each type of matching task (specially in terms of precision). Most of the systems that implement specific cross-lingual techniques – YAM++ (.40), WikiMatch (.27), RiMOM2013 (.21), WeSeE (.15), StringsAuto (.14), and MapSSS (.10) – generate the best results for test cases of type (i). For the test cases of type (ii), systems non specifically designed for cross-lingual matching – MaasMatch and OntoK – are in the top-5 F-measures together with YAM++, WikiMatch and WeSeE. Concerning CIDER-CL, this system in principle is able to deal with a subset of languages, i.e., DE, EN, ES, and NL.

Overall (for both types i and ii), in terms of F-measure, most systems implementing specific cross-lingual methods outperform non-specific systems: YAM++ (.50), WikiMatch (.22), RiMOM (.17), WeSeE (.15) – with MaasMatch given its high scores on cases (ii) – and StringsAuto (.10).

Comparison with previous campaigns In the first year of evaluation of MultiFarm, we have used a subset of the whole data set, where we omitted the ontologies edas and ekaw, and suppressed the test cases where Russian and Chinese were involved. Since 2012, we have included Russian and Chinese translations, but still have not included edas and ekaw. In the 2011.5 intermediary campaign, 3 participants (out of 19) used specific techniques – AUTOMSv2, WeSeE, and YAM++. In 2012, 7 systems (out of 24) implemented specific techniques for dealing with ontologies in different natural languages – ASE, AUTOMSv2, GOMMA, MEDLEY, WeSeE, WikiMatch, and YAM++. This year, as in 2012, 7 participants out of 21 use specific techniques: 2 of them have been participating since 2011.5 (WeSeE and YAM), 1 since 2012 (WikiMatch), 3 systems (CIDER-CL, RiMOM2013 and MapSSS) have included cross-lingual approaches in their implementations, and 1 new system (StringsAuto) has participated.

Comparing 2012 and 2013 results (on the same basis), WikiMatch improved precision for both test case types – from .22 to .34 for type (i) and .43 to .65 for type (ii) – preserving its values of recall. On the other hand, WeSeE has decreased both precision – from .61 to .22 – and recall – from .32 to .12 – for type (i) and precision – from .90 to .56 – and recall – from .27 to .09 – for type (ii).

			Different ontologies (i)			Same ontologies (ii)		
	System	Runtime	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.
Cross-lingual	CIDER-CL	110	.03	.03	.04	.18	.06	.04
	MapSSS	2380	.27	.10	.07	.50	.06	.03
	RiMOM2013	13	.52	.21	.13	.87	.14	.08
	StringsAuto	24	.30	.14	.09	.51	.07	.04
	WeSeE	2474	.22	.15	.12	.56	.16	.09
	WikiMatch	1284	.34	.27	.23	.65	.18	.11
	YAM++	443	.51	**.40**	.36	.91	**.60**	.50
Non specific	AML	7	.14	.04	.03	.35	.03	.01
	HerTUDA	46	.00	.01	1.0	.02	.03	1.0
	HotMatch	17	.00	.00	.00	.41	.04	.02
	IAMA	15	.15	.05	.03	.58	.04	.02
	LogMap	18	.18	.05	.03	.35	.03	.01
	LogMapLite	6	.13	.04	.02	.25	.02	.01
	MaasMatch	70	.01	.02	.03	.62	**.29**	.19
	ODGOMS	44	.26	**.10**	.06	.47	.05	.03
	OntoK	1602	.01	.01	.05	.16	.16	.15
	Synthesis	67	.30	.05	.03	.25	.04	.03

Table 11. MultiFarm aggregated results per matcher, for each type of matching task – types (i) and (ii). Runtime is measured in minutes (time for completing the 900 matching tasks).

Language specific results Table 12 shows the results aggregated per language pair, for the the test cases of type (i). For the sake of readability, we present only F-measure values. The reader can refer to the OAEI results web page for more detailed results on precision and recall. As expected and already reported above, the systems that apply specific strategies to match ontology entities described in different natural languages outperform the other systems. For most of these systems, the best performance is observed for the pairs of language including Dutch, English, German, Spanish, and Portuguese: CIDER-CL (en-es .21, en-nl and es-nl .18, de-nl .16), MapSSS (es-pt and en-es .33, de-en .28, de-es .26), RiMOM2013 (en-es .42, es-pt .40, de-en .39), StringsAuto (en-es .37, es-pt .36, de-en .33), WeSeE (en-es .46, en-pt .41, en-nl .40), WikiMatch (en-es .38, en-pt, es-pt and es-fr .37, es-ru .35). The exception is YAM++ which generates its best results for the pairs including Czech : cz-en and en-pt .57, cz-pt .56, cz-nl and fr-pt .53. For all specific systems, English is present in half of the top pairs.

For non-specific systems, most of them cannot deal at all with Chinese and Russian languages. 7 out of 10 systems generate their best results for the pair es-pt (followed by the pair de-en). Again, similarities in the language vocabulary have an important role in the matching task. On the other hand, although it is likely harder to find correspondences between cz-pt than es-pt, for some systems Czech is on pairs for the top-5 F-measure (cz-pt, for AML, IAMA, LogMap, LogMapLite and Synthesis). It can be explained by the specific way systems combine their internal matching techniques (ontology structure, reasoning, coherence, linguistic similarities, etc).

	AML	CIDER-CL	HerTUDA	HotMatch	IAMA	LogMap	LogMapLite	MaasMatch	MapSSS	ODGOMS	OntoK	RiMOM2013	StringsAuto	Synthesis	WeSeE	WikiMatch	YAM++
cn-cz		.00	.01								.01	.12				.12	.36
cn-de		.00	.01					.00			.01	.18				.15	.37
cn-en		.01	.01								.01	.25				.16	.43
cn-es		.00	.01	.01				.00			.01	.17				.24	.19
cn-fr		.01	.01	.01				.01			.01	.17			.01	.10	.42
cn-nl		.00	.01	.01				.00			.01	.16				.19	.31
cn-pt		.01	.01								.01	.10				.18	.32
cn-ru		.00	.01	.01						.00	.01				.01	.23	.34
cz-de	.10	.00	.01		.10	.09	.09	.01	.14	.13	.01	.24	.22	.11	.02	.26	.48
cz-en	.04	.00	.01		.12	.05	.04	.02	.25	.24	.01	.25	.29	.06	.08	.18	.57
cz-es	.11	.00	.01		.11	.11	.11	.02	.18	.18	.03	.24	.22	.14	.09	.29	.19
cz-fr	.01	.00	.01	.01	.01	.01	.01	.01	.15	.07	.02	.17	.17	.02	.04	.22	.52
cz-nl	.04	.00	.01		.05	.04	.04	.01	.12	.12	.03	.32	.18	.04	.01	.23	.53
cz-pt	.12	.01	.01		.13	.13	.13	.01	.18	.20	.02	.24	.23	.16	.04	.25	.56
cz-ru		.01	.01								.01					.25	.48
de-en	.20	.12	.01		.21	.22	.20	.05	.28	.30	.01	.39	.33	.22	.33	.32	.50
de-es	.07	.15	.01		.07	.09	.06	.02	.26	.24	.01	.31	.29	.08	.28	.29	.19
de-fr	.05	.01	.01		.04	.04	.04	.02	.08	.06	.01	.29	.23	.04	.32	.26	.44
de-nl	.05	.16	.01		.04	.04	.04	.04	.17	.21	.01	.30	.19	.05	.31	.27	.40
de-pt	.07		.01		.08	.07	.07	.02	.13	.11	.02	.27	.18	.09	.34	.26	.41
de-ru		.00	.01	.01				.01			.01					.31	.47
en-es	.06	.21	.01		.05	.15	.04	.03	.33	.30	.01	.42	.37	.05	.46	.38	.23
en-fr	.06		.01	.01	.10	.06	.04	.05	.17	.15	.01	.32	.29	.04	.32	.33	.50
en-nl	.07	.18	.01		.07	.07	.10	.05	.22	.24	.02	.35	.24	.08	.40	.32	.52
en-pt	.06		.01		.06	.06	.06	.02	.18	.19	.02	.36	.30	.07	.41	.37	.57
en-ru		.00	.01					.00			.01					.24	.50
es-fr	.03		.01		.06	.06	.01	.03	.17	.14	.02	.36	.29	.02	.25	.37	.20
es-nl		.18	.01					.02	.07	.03	.01	.29	.15		.34	.32	.16
es-pt	.29		.01		.29	.24	.23	.05	.33	.33	.04	.40	.36	.25	.33	.37	.25
es-ru		.00	.01								.02					.35	.19
fr-nl	.12	.00	.01	.01	.12	.13	.12	.06	.16	.13	.03	.30	.26	.15	.24	.34	.46
fr-pt	.01		.01	.01	.01			.04	.10	.11		.26	.19		.34	.28	.53
fr-ru		.01	.01					.00			.01					.33	.46
nl-pt	.01		.01		.02	.01	.01	.02	.03	.04	.01	.15	.07	.02	.31	.27	.51
nl-ru		.00	.01					.01			.01					.33	.44
pt-ru		.00	.01					.00			.01					.29	.47

Table 12. MultiFarm results per pair of languages, for the test cases of type (i). In this detailed view, we distinguished empty alignments, represented by empty cells, from wrong ones (.00)

7.4 Conclusion

As expected, systems using specific methods for dealing with ontologies in different languages work much better than non specific systems. However, the absolute results

are still not very good, if compared to the top results of the original Conference data set (approximatively 75% F-measure for the best matcher). For all specific cross-lingual methods, the techniques implemented in YAM++, as in 2012, generate the best alignments in terms of F-measure (around 50% overall F-measure for both types of matching tasks). All systems privilege precision rather than recall. Although we count this year on 4 new systems implementing specific cross-lingual methods, there is room for improvements to achieve the same level of compliance as in the original data set.

8 Library

The library test case was established in 2012[13]. The test case consists of matching of two real-world thesauri: The Thesaurus for the Social Sciences (TheSoz, maintained by GESIS) and the Standard Thesaurus for Economics (STW, maintained by ZBW). The reference alignment is based on a manually created alignment from 2006. As additional benefit from this test case, the reference alignment is constantly improved by the maintainers by manually checking the generated correspondences that have not yet been checked and that are not part of the reference alignment[14].

8.1 Test data

Both thesauri used in this test case are comparable in many respects. They have roughly the same size (6,000 resp. 8,000 concepts), are both originally developed in German, are today both multilingual, both have English translations, and, most important, despite being from two different domains, they have significant overlapping areas. Not least, both are freely available in RDF using SKOS[15]. To enable the participation of all OAEI matchers, an OWL version of both thesauri is provided, effectively by creating a class hierarchy from the concept hierarchy. Details are provided in the report of the 2012 campaign [1]. As stated above, we updated the reference alignment with all correct correspondences found during the 2012 campaign, it now consists of 3161 correspondences.

8.2 Experimental setting

All matching processes have been performed on a Debian machine with one 2.4GHz core and 7GB RAM allocated to each system. The evaluation has been executed by using the SEALS infrastructure. Each participating system uses the OWL version.

To compare the created alignments with the reference alignment, we use the Alignment API. For this evaluation, we only included equivalence relations (skos:exactMatch). We computed precision, recall and F_1-measure for each matcher. Moreover, we measured the runtime, the size of the created alignment and checked

[13] There has already been a library test case from 2007 to 2009 using different thesauri, as well as other thesaurus test cases like the food and the environment test cases.

[14] With the reasonable exception of XMapGen, which produces almost 40.000 correspondences.

[15] `http://www.w3.org/2004/02/skos`

whether a 1:1 alignment has been created. To assess the results of the matchers, we developed three straightforward matching strategies, using the original SKOS version of the thesauri:

- MatcherPrefDE: Compares the German lower-case preferred labels and generates a correspondence if these labels are completely equivalent.
- MatcherPrefEN: Compares the English lower-case preferred labels and generates a correspondence if these labels are completely equivalent.
- MatcherPref: Creates a correspondence, if either MatcherPrefDE or MatcherPrefEN or both create a correspondence.
- MatcherAllLabels: Creates a correspondences whenever at least one label (preferred or alternative, all languages) of an entity is equivalent to one label of another entity.

8.3 Results

Of all 21 participating matchers (or variants), 12 were able to generate an alignment within 12 hours. CroMatcher, MaasMatch, RiMOM2013, WeSeE and WikiMatch did not finish in the time frame, OntoK had heap space problems and CiderCL, MapSSS and Synthesis threw an exception. The results can be found in Table 13.

Matcher	Precision	F-Measure	Recall	Time (ms)	Size	1:1
ODGOMS	0.70	0.76	0.83	27936433	3761	-
YAM++	0.69	0.74	0.81	731860	3689	-
MatcherPref	0.91	0.74	0.63	-	2190	-
ServOMap	0.70	0.74	0.78	648138	3540	-
AML	0.62	0.7	0.88	39366	4433	-
MatcherPrefDE	0.98	0.73	0.58	-	1885	-
MatcherAllLabels	0.61	0.72	0.88	-	4605	-
LogMap	0.78	0.70	0.64	98958	2622	-
LogMapLite	0.65	0.70	0.77	20312	3775	-
HerTUDA	0.52	0.67	0.92	11228741	5559	-
HotMatch	0.73	0.65	0.58	12128682	2494	√
MatcherPrefEN	0.88	0.57	0.42	-	1518	-
XmapSig	0.80	0.45	0.32	2914167	1256	-
StringsAuto	0.77	0.30	0.19	1966012	767	√
IAMA	0.78	0.08	0.04	18599	166	-
XmapGen	0.03	0.06	0.37	3008820	38360	-

Table 13. Results of the Library test case (ordered by F-measure).

The best systems in terms of F-measure are ODGOMS and YAM++. These matchers also have a higher F-measure than MatcherPref. ServOMap and AML are below this baseline but better than MatcherPrefDE and MatcherAllLabels. A group of matchers including LogMap, LogMapLite, HerTUDA and HotMatch are above the MatcherPrefEN baseline. Compared to last year evaluation with the updated reference alignment, the matchers clearly improved: in 2012, no matcher was able to beat MatcherPref and MatcherPrefDE, only ServOMapLt was better than MatcherAllLabels. Today, two

matchers outperformed all baselines; further two matchers outperformed all baselines but MatcherPref. This is remarkable, as the matchers are still not able to consume SKOS and therefore neglect the distinction between preferred and alternative labels. The baselines are tailored for very high precision by design, while the matchers usually have a higher recall. This is reflected in the F-measure, where the highest value increased from 0.72 to 0.76 by almost 5 percentage points since last year. The recall mostly increased, e.g. YAM++ from 0.76 to 0.81 (without affecting the precision negatively, which also increased from 0.68 to 0.69).

Like in the previous year, an additional intellectual evaluation of the alignments established automatically was done by a domain expert to further improve the reference alignment. Unsurprisingly, the matching tools predominantly detected matches based on the character string. This included the term alone as well as the term's context. Especially in the case of short terms, this could easily lead to wrong correspondences, e.g., "tea" $\neq$ "team", "sheep" $\neq$ "sleep". Except for its sequence of letters the term's context was not taken into account.

This sole attention to the character string was a main source of error in cases in which on the term as well as on the context level similar terminological entities appeared, e.g., "Green revolution" subject category: "Development Politic" $\neq$ "permanent revolution" subject category: "Political Developments and Processes".

Additionally, identical components of a compound frequently lead to incorrect correspondences, e.g., "prohibition of interest" $\neq$ "prohibition of the use of force". Moreover, terms in different domains might look similar, but in fact have very different meanings. An illustrative example is "Chicago Antitrust Theory" $\neq$ "Chicago School", where indeed the same Chicago is referenced, but without any effect on the (dis-)similarity of both concepts.

8.4 Conclusion

The overall performance improvement is encouraging in this test case. While it might not look impressive to beat simple baselines as ours at first sight, it is actually a notable achievement. The baselines are not only tailored for very high precision, benefitting from the fact that in many cases a consistent terminology is used, they also exploit additional knowledge about the labels. The matchers are general-purpose matchers that have to perform well in all OAEI test cases. Nonetheless, there does not seems to be matchers who understand SKOS in order to make use of the many concept hierarchies provided on the Web.

Generally, matchers still rely too much on the character string of the labels and the labels of the concepts in the immediate vicinity. During the intellectual evaluation process, it became obvious that a multitude of incorrect matches could be prevented if the subject categories, respectively the thesauri's classification schemes be matched beforehand. In many cases, misleading candidate correspondences could be discarded by taking these higher levels of the hierarchy into account. It could be prevented, for example, to build up correspondences between personal names and subject headings. A thesaurus, however, is not a classification system. The disjointness of two subthesauri is therefore not easy to establish, let alone to detect by automatic means. Nonetheless,

thesauri oftentimes have their own classification schemes which partly follow classification principles. We believe that further exploiting this context knowledge could be worthwhile.

9 Interactive matching

The interactive matching test case was evaluated at OAEI 2013 for the first time. The goal of this evaluation is to simulate interactive matching [23], where a human expert is involved to validate mappings found by the matching system. In the evaluation, we look at how user interaction may improve matching results.

For the evaluation, we use the conference data set 5 with the ra1 alignment, where there is quite a bit of room for improvement, with the best fully automatic, i.e., non-interactive matcher achieving an F-measure below 80%. The SEALS client was modified to allow interactive matchers to ask an oracle, which emulates a (perfect) user. The interactive matcher can present a correspondence to the oracle, which then tells the user whether the correspondence is right or wrong.

All matchers participating in the interactive test case support both interactive and non-interactive matching. This allows us to analyze how much benefit the interaction brings for the individual matchers.

9.1 Results

Overall, five matchers participated in the interactive matching test case: AML and AML-bk, Hertuda, LogMap, and WeSeE-Match. All of them implement interactive strategies that run entirely as a post-processing step to the automatic matching, i.e., take the alignment produced by the base matcher and try to refine it by selecting a suitable subset.

AML and AML-bk present all correspondences below a certain confidence threshold to the oracle, starting with the highest confidence values. They stop adding references once the false positive rate exceeds a certain threshold. Similarly, LogMap checks all questionable correspondences using the oracle. Hertuda and WeSeE-Match try to adaptively set an optimal threshold for selecting correspondences. They perform a binary search in the space of possible thresholds, presenting a correspondence of average confidence to the oracle first. If the result is positive, the search is continued with a higher threshold, otherwise with a lower threshold.

The results are depicted in Table 14. Please note that the values in this table slightly differ from the original values in the conference test case, since the latter uses micro average recall and precision, while we use macro averages, so that we can compute significance levels using T-Tests on the series of recall and precision values from the individual test cases. The reason for the strong divergence of the results for WeSeE to the conference test case results is unknown. Altogether, the biggest improvement in F-measure, as well as the best overall result (although almost at the same level as AML-bk), is achieved by LogMap, which increases its F-measure by four percentage points. Furthermore, LogMap, AML and AML-bk show a statistically significant increase in recall as well as precision, while all the other tools except for Hertuda show a significant

	AML	AML-bk	Hertuda	LogMap	WeSeE
Non-Interactive Results					
Precision	0.88	0.88	0.77	0.83	0.57
F-measure	0.69	0.71	0.62	0.68	0.49
Recall	0.59	0.61	0.53	0.62	0.46
Interactive Results					
Precision	[1]**0.91**	[1]**0.91**	**0.79**	[1]**0.90**	[1]**0.73**
F-measure	[1]**0.71**	[1]**0.73**	0.58	[1]**0.73**	0.47
Recall	[5]**0.61**	[5]**0.63**	0.50	[5]**0.64**	0.40
Average Number of Interactions					
Positive	1.43	1.57	1.95	2.57	1.67
Negative	5.14	5.05	10.33	1.76	3.81
Total	6.57	6.67	12.33	4.33	5.48

Table 14. Results of the interactive matching test case. The table reports both the results with and without interaction, in order to analyze the improvement that was gained by adding interactive features. Improvements of the interactive variants over the non-interactive variants are shown in bold. Statistically significant differences are marked with $^{5}(p < 0.05)$ and $^{1}(p < 0.01)$. Furthermore, we report the average number of interactions, showing both the positive and negative examples presented to the oracle.

increase in precision. The increase in precision is in all cases however higher than the increase of recall. It can be observed for AML, AML-bk and LogMap that a highly significant increase in precision also increases F-measure at a high significance level, even if the increase in recall is less significant.

At the same time, LogMap has the lowest number of interactions with the oracle, which shows that it also makes the most efficient use of the oracle. In a truly interactive setting, this would mean that the manual effort is minimized. Furthermore, it is the only tool that presents more positive than negative examples to the oracle.

On the other hand, Hertuda and WeSeE even show a decrease in recall, which cannot be compensated by the increase in precision. The biggest increase in precision (17 percentage points) is achieved by WeSeE, but on an overall lower level than the other matching systems. Thus, we conclude that their strategy is not as efficient as those of the other participants.

Compared to the results of the non-interactive conference test case, the best interactive matcher (in terms of F-measure) is slightly below the best matcher (YAM++) with a F-measure value of 0.76 (using macro averages). Except for YAM++, the interactive versions of AML-bk, AML and LogMap achieve better F-measure scores than all non-interactive matchers.

9.2 Discussion

The results show that current interactive matching tools mainly use interaction as a means to post-process an alignment found with fully automatic means. There are, however, other interactive approaches that can be thought of, which include interaction at an earlier stage of the process, e.g., using interaction for parameter tuning [25], or determining anchor elements for structure-based matching approaches using interactive

methods. The maximum F-measure of 0.73 achieved shows that there is still room for improvement.

Furthermore, different variations of the evaluation method can be thought of, including different noise levels in the oracle's responses, i.e., simulating errors made by the human expert, or allowing other means of interactions than the validation of single correspondences, e.g., providing a random positive example, or providing the corresponding element in one ontology, given an element of the other one.

So far, we only compare the final results of the interactive matching process. In [23], we have introduced an evaluation method based on *learning curves*, which gives insights into how quickly the matcher converges towards its final result. However, we have not implemented that model for this year's OAEI, since it requires more changes to the matchers (each matcher has to provide an intermediate result at any point in time).

10 Instance matching

The instance matching track aims at evaluating the performance of different matching tools on the task of matching RDF individuals which originate from different sources but describe the same real-world entity [16].

10.1 RDFT test cases

Starting from the experience of previous editions of the instance matching track in OAEI [15], this year we provided a set of RDF-based test cases, called RDFT, that is automatically generated by introducing controlled transformations in some initial RDF data sets. The controlled transformations introduce artificial distortions into the data, which include data value transformations as well as structural transformations. RDFT includes blind evaluation. The participants are provided with a list of five test cases. For each test case, we provide training data with the accompanying alignment to be used to adjust the settings of the tools, and contest data, based on which the final results will be calculated. The evaluation data set is generated by exploiting the same configuration of the RDFT transformation tool used for generating training data.

The RDFT test cases have been generated from an initial RDF data set about well-known computer scientists data extracted from DBpedia. The initial data set is composed by 430 resources, 11 RDF properties and 1744 triples. Some descriptive statistics about the initial data set are available online. Starting from the initial data set, we provided the participants with five test cases, where different transformations have been implemented, as follows:

- **Testcase 1: value transformation.** Values of 5 properties have been changed by randomly deleting/adding chars, by changing the date format, and/or by randomly change integer values.
- **Testcase 2: structure transformation.** The length of property path between resources and values has been changed. Property assertions have been split in two or more assertions.
- **Testcase 3: languages.** The same as Testcase 1, but using French translation for comments and labels instead of English.

	tescase01			tescase02			tescase03			tescase04			tescase05		
system	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.	Prec.	F-m.	Rec.
LilyIOM	1.00	**1.00**	0.99	0.74	0.74	0.74	0.94	0.93	0.92	0.71	0.72	0.73	0.71	0.58	0.49
LogMap	0.97	0.80	0.69	0.79	0.88	0.99	0.98	0.84	0.73	0.95	0.80	0.70	0.92	0.74	0.62
RiMOM2013	1.00	**1.00**	1.00	0.95	0.97	0.99	0.96	**0.98**	0.99	0.94	**0.96**	0.98	0.93	**0.96**	0.99
SLINT+	0.98	0.98	0.98	1.00	**1.00**	1.00	0.94	0.92	0.91	0.91	0.91	0.91	0.87	0.88	0.88

Table 15. Results for the RDFT test cases.

- **Testcase 4: combined.** A combination of value and structure transformations using French text.
- **Testcase 5: cardinality.** The same as Testcase 4, but now part of the resources have none or multiple matching counterparts.

10.2 RDFT results

An overview of the precision, recall and F_1-measure results for the RDFT test cases is shown in Table 15.

All the tools show good performances when dealing with singular type of data transformation, i.e., Testcases 1-3, either value, structural, and language transformations. Performances drop when different kinds of transformations are combined together, i.e., Testcases 4-5, except for RiMOM2013, which still has performances close to 1.0 for both precision and recall. This suggests that a possible challenge for instance matching tools is to work in the direction of improving the combination and balancing of different matching techniques in a single, general-purpose, configuration scheme.

In addition to precision, recall and F_1-measure results, we performed also a test based on the similarity values provided by participating tools. In particular, we selected the provided mappings by different thresholds on the similarity values, in order to monitor the behavior of precision and recall[16]. Results of this second evaluation are shown in Figure 3.

Testing the results when varying the threshold used for mapping selection is useful to understand how robust are the mappings retrieved by the participating tools. In particular, RiMOM2013 is the only tool which has very good results with all the threshold values that have been tested. This means that the retrieved mappings are generally correct and associated with high levels of similarity. Other tools, especially LilyIOM and LogMap, retrieve a high number of mappings which are associated with low levels of confidence. In such cases, when we rely only on mappings between resources that are considered very similar by the tool, the quality of results becomes lower.

Finally, as a general remark suggested from the result analysis, we stress the opportunity of working toward two main goals in particular: one one side, on the integration of different matching techniques and the need of conceiving self-adapting tools, capable of self-configuring the most suitable combination of matching metrics according to the nature of data heterogeneity that needs to be handled; on the other side, the need for

[16] This experiment is partially useful in the case of SLINT+, where the similarity values are not in the range [0,1] and are not necessarily proportional to the elements similarity.

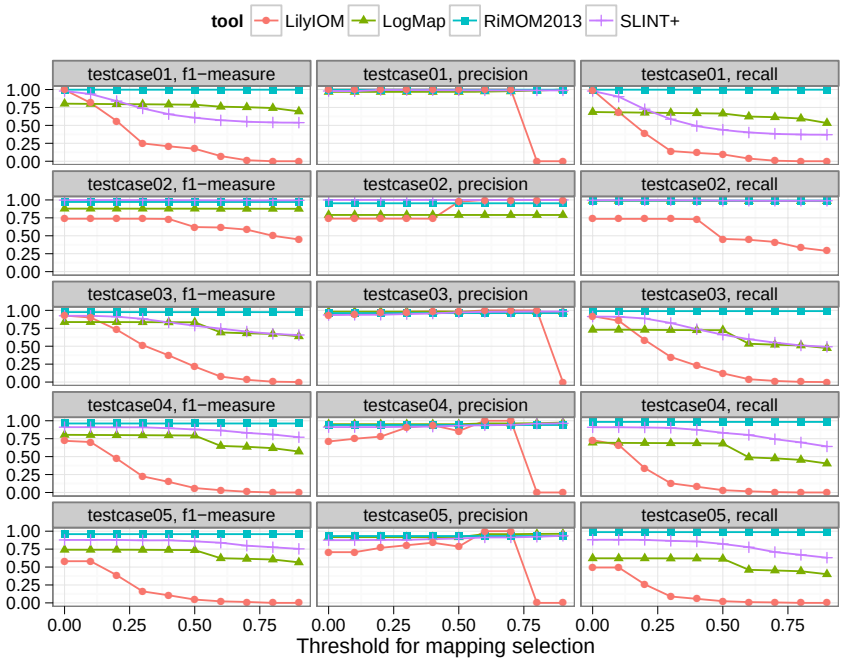


Fig. 3. Evaluation test based on the similarity values.

tools capable of providing a degree of confidence which could be used for measuring the reliability of the provided mappings.

11 Lesson learned and suggestions

There are, this year, very few comments about the evaluation execution:

A) This year indicated again that requiring participants to implement a minimal interface was not a strong obstacle to participation. Moreover, the community seems to get used to the SEALS infrastructure introduced for OAEI 2011. This might be one of the reasons for an increasing participation.
B) Related to the availability of the platform, participants checked that their tools were working on minimal tests and discovered in September that they were not working on other tests. For that reason, it would be good to set the preliminary evaluation results by the end of July.
C) Now that all tools are run in exactly the same configuration across all test cases, some discrepancies appear across such cases. For instance, benchmarks expect only class correspondences in the name space of the ontologies, some other cases expect something else. This is a problem, which could be solved either by passing parameters to the SEALS client (this would make its implementation heavier) or by post processing results (which may be criticized).
D) [24] raised and documented objections (on validity and fairness) to the way reference alignments are made coherent with alignment repair techniques. Appropriate measures should be taken to mitigate this.
E) Last years we reported that we had many new participants. The same trend can be observed for 2013.
F) Again and again, given the high number of publications on data interlinking, it is surprising to have so few participants to the instance matching track.

12 Conclusions

OAEI 2013 saw an increased number of participants and most of the test cases performed on the SEALS platform. This is good news for the interoperability of matching systems.

Compared to the previous years, we observed improvements of runtimes and the ability of systems to cope with large ontologies and data sets (testified by the largebio and instance matching results). This comes in addition to progress in overall F-measure, which is more observable as the test case is more recent. More preoccupying was the lack of robustness of some systems observed in the simple benchmarks. This seems to be due to an increased reliance on the network and networked resources that may time-out systems.

As usual, most of the systems favour precision over recall. In general, participating matching systems do not take advantage of alignment repairing system and return sometimes incoherent alignments. This is a problem if their result has to be taken as input by a reasoning system. They do not generally use natural language aware strategies, while the multilingual tests show the worthiness of such an approach.

A novelty of this year was the evaluation of interactive systems, included in the SEALS client. It brings interesting insight on the performances of such systems and should certainly be continued.

Most of the participants have provided a description of their systems and their experience in the evaluation. These OAEI papers, like the present one, have not been peer reviewed. However, they are full contributions to this evaluation exercise and reflect the hard work and clever insight people put in the development of participating systems. Reading the papers of the participants should help people involved in ontology matching to find what makes these algorithms work and what could be improved. Sometimes participants offer alternate evaluation results.

The Ontology Alignment Evaluation Initiative will continue these tests by improving both test cases and testing methodology for being more accurate. Matching evaluation still remains a challenging topic, which is worth further research in order to facilitate the progress of the field [27]. Further information can be found at:

`http://oaei.ontologymatching.org`.

Acknowledgements

We warmly thank the participants of this campaign. We know that they have worked hard for having their matching tools executable in time and they provided insightful papers presenting their experience. The best way to learn about the results remains to read the following papers.

We are very grateful to STI Innsbruck for providing the necessary infrastructure to maintain the SEALS repositories.

We are also grateful to Martin Ringwald and Terry Hayamizu for providing the reference alignment for the anatomy ontologies and thank Elena Beisswanger for her thorough support on improving the quality of the data set.

We thank Christian Meilicke for help with incoherence evaluation within the conference and his support of the anatomy test case.

We also thank for their support the other members of the Ontology Alignment Evaluation Initiative steering committee: Yannis Kalfoglou (Ricoh laboratories, UK), Miklos Nagy (The Open University (UK), Natasha Noy (Stanford University, USA), Yuzhong Qu (Southeast University, CN), York Sure (Leibniz Gemeinschaft, DE), Jie Tang (Tsinghua University, CN), Heiner Stuckenschmidt (Mannheim Universität, DE), George Vouros (University of the Aegean, GR).

Bernardo Cuenca Grau, Jérôme Euzenat, Ernesto Jimenez-Ruiz, Christian Meilicke, and Cássia Trojahn dos Santos have been partially supported by the SEALS (IST-2009-238975) European project in the previous years.

Ernesto and Bernardo have also been partially supported by the Seventh Framework Program (FP7) of the European Commission under Grant Agreement 318338, "Optique", the Royal Society, and the EPSRC projects Score!, ExODA and MaSI^3.

Cássia Trojahn dos Santos and Roger Granada are also partially supported by the CAPES-COFECUB Cameleon project number 707/11.

References

1. José Luis Aguirre, Bernardo Cuenca Grau, Kai Eckert, Jérôme Euzenat, Alfio Ferrara, Robert Willem van Hague, Laura Hollink, Ernesto Jiménez-Ruiz, Christian Meilicke, An-

driy Nikolov, Dominique Ritze, François Scharffe, Pavel Shvaiko, Ondrej Sváb-Zamazal, Cássia Trojahn, and Benjamin Zapilko. Results of the ontology alignment evaluation initiative 2012. In *Proc. 7th ISWC ontology matching workshop (OM), Boston (MA US)*, pages 73–115, 2012.

2. Ana Armas Romero, Bernardo Cuenca Grau, and Ian Horrocks. MORe: Modular combination of OWL reasoners for ontology classification. In *Proc. 11th International Semantic Web Conference (ISWC), Boston (MA US)*, pages 1–16, 2012.
3. Benhamin Ashpole, Marc Ehrig, Jérôme Euzenat, and Heiner Stuckenschmidt, editors. *Proc. K-Cap Workshop on Integrating Ontologies*, Banff (Canada), 2005.
4. Olivier Bodenreider. The unified medical language system (UMLS): integrating biomedical terminology. *Nucleic Acids Research*, 32:267–270, 2004.
5. Caterina Caracciolo, Jérôme Euzenat, Laura Hollink, Ryutaro Ichise, Antoine Isaac, Véronique Malaisé, Christian Meilicke, Juan Pane, Pavel Shvaiko, Heiner Stuckenschmidt, Ondrej Sváb-Zamazal, and Vojtech Svátek. Results of the ontology alignment evaluation initiative 2008. In *Proc. 3rd ISWC ontology matching workshop (OM), Karlsruhe (DE)*, pages 73–120, 2008.
6. Jérôme David, Jérôme Euzenat, François Scharffe, and Cássia Trojahn dos Santos. The alignment API 4.0. *Semantic web journal*, 2(1):3–10, 2011.
7. Jérôme Euzenat, Alfio Ferrara, Laura Hollink, Antoine Isaac, Cliff Joslyn, Véronique Malaisé, Christian Meilicke, Andriy Nikolov, Juan Pane, Marta Sabou, François Scharffe, Pavel Shvaiko, Vassilis Spiliopoulos, Heiner Stuckenschmidt, Ondrej Sváb-Zamazal, Vojtech Svátek, Cássia Trojahn dos Santos, George Vouros, and Shenghui Wang. Results of the ontology alignment evaluation initiative 2009. In *Proc. 4th ISWC ontology matching workshop (OM), Chantilly (VA US)*, pages 73–126, 2009.
8. Jérôme Euzenat, Alfio Ferrara, Christian Meilicke, Andriy Nikolov, Juan Pane, François Scharffe, Pavel Shvaiko, Heiner Stuckenschmidt, Ondrej Sváb-Zamazal, Vojtech Svátek, and Cássia Trojahn dos Santos. Results of the ontology alignment evaluation initiative 2010. In *Proc. 5th ISWC ontology matching workshop (OM), Shanghai (CN)*, pages 85–117, 2010.
9. Jérôme Euzenat, Alfio Ferrara, Robert Willem van Hague, Laura Hollink, Christian Meilicke, Andriy Nikolov, François Scharffe, Pavel Shvaiko, Heiner Stuckenschmidt, Ondrej Sváb-Zamazal, and Cássia Trojahn dos Santos. Results of the ontology alignment evaluation initiative 2011. In *Proc. 6th ISWC ontology matching workshop (OM), Bonn (DE)*, pages 85–110, 2011.
10. Jérôme Euzenat, Antoine Isaac, Christian Meilicke, Pavel Shvaiko, Heiner Stuckenschmidt, Ondrej Svab, Vojtech Svatek, Willem Robert van Hage, and Mikalai Yatskevich. Results of the ontology alignment evaluation initiative 2007. In *Proc. 2nd ISWC ontology matching workshop (OM), Busan (KR)*, pages 96–132, 2007.
11. Jérôme Euzenat, Christian Meilicke, Pavel Shvaiko, Heiner Stuckenschmidt, and Cássia Trojahn dos Santos. Ontology alignment evaluation initiative: six years of experience. *Journal on Data Semantics*, XV:158–192, 2011.
12. Jérôme Euzenat, Malgorzata Mochol, Pavel Shvaiko, Heiner Stuckenschmidt, Ondrej Svab, Vojtech Svatek, Willem Robert van Hage, and Mikalai Yatskevich. Results of the ontology alignment evaluation initiative 2006. In *Proc. 1st ISWC ontology matching workshop (OM), Athens (GA US)*, pages 73–95, 2006.
13. Jérôme Euzenat, Maria Rosoiu, and Cássia Trojahn dos Santos. Ontology matching benchmarks: generation, stability, and discriminability. *Journal of web semantics*, 21:30–48, 2013.
14. Jérôme Euzenat and Pavel Shvaiko. *Ontology matching*. Springer-Verlag, Heidelberg (DE), 2nd edition, 2013.
15. Alfio Ferrara, Andriy Nikolov, Jan Noessner, and François Scharffe. Evaluation of instance matching tools: The experience of OAEI. *Journal of Web Semantics*, 21:49–60, 2013.

16. Alfio Ferrara, Andriy Nikolov, and François Scharffe. Data linking for the semantic web. *International Journal on Semantic Web and Information Systems*, 7(3):46–76, 2011.
17. Ernesto Jiménez-Ruiz and Bernardo Cuenca Grau. LogMap: Logic-based and scalable ontology matching. In *Proc. 10th International Semantic Web Conference (ISWC), Bonn (DE)*, pages 273–288, 2011.
18. Ernesto Jiménez-Ruiz, Bernardo Cuenca Grau, Ian Horrocks, and Rafael Berlanga. Logic-based assessment of the compatibility of UMLS ontology sources. *J. Biomed. Sem.*, 2, 2011.
19. Ernesto Jiménez-Ruiz, Christian Meilicke, Bernardo Cuenca Grau, and Ian Horrocks. Evaluating mapping repair systems with large biomedical ontologies. In *Proc. 26th Description Logics Workshop*, 2013.
20. Yevgeny Kazakov, Markus Krötzsch, and Frantisek Simancik. Concurrent classification of EL ontologies. In *Proc. 10th International Semantic Web Conference (ISWC), Bonn (DE)*, pages 305–320, 2011.
21. Christian Meilicke. *Alignment Incoherence in Ontology Matching*. PhD thesis, University Mannheim, 2011.
22. Christian Meilicke, Raúl García Castro, Frederico Freitas, Willem Robert van Hage, Elena Montiel-Ponsoda, Ryan Ribeiro de Azevedo, Heiner Stuckenschmidt, Ondrej Sváb-Zamazal, Vojtech Svátek, Andrei Tamilin, Cássia Trojahn, and Shenghui Wang. MultiFarm: A benchmark for multilingual ontology matching. *Journal of web semantics*, 15(3):62–68, 2012.
23. Heiko Paulheim, Sven Hertling, and Dominique Ritze. Towards evaluating interactive ontology matching tools. In *Proc. 10th Extended Semantic Web Conference (ESWC), Montpellier (FR)*, pages 31–45, 2013.
24. Catia Pesquita, Daniel Faria, Emanuel Santos, and Francisco Couto. To repair or not to repair: reconciling correctness and coherence in ontology reference alignments. In *Proc. 8th ISWC ontology matching workshop (OM), Sydney (AU)*, page this volume, 2013.
25. Dominique Ritze and Heiko Paulheim. Towards an automatic parameterization of ontology matching tools based on example mappings. In *Proc. 6th ISWC ontology matching workshop (OM), Bonn (DE)*, pages 37–48, 2011.
26. Emanuel Santos, Daniel Faria, Catia Pesquita, and Francisco Couto. Ontology alignment repair through modularization and confidence-based heuristics. *CoRR*, abs/1307.5322, 2013.
27. Pavel Shvaiko and Jérôme Euzenat. Ontology matching: state of the art and future challenges. *IEEE Transactions on Knowledge and Data Engineering*, 25(1):158–176, 2013.
28. York Sure, Oscar Corcho, Jérôme Euzenat, and Todd Hughes, editors. *Proc. ISWC Workshop on Evaluation of Ontology-based Tools (EON), Hiroshima (JP)*, 2004.
29. Cássia Trojahn dos Santos, Christian Meilicke, Jérôme Euzenat, and Heiner Stuckenschmidt. Automating OAEI campaigns (first report). In *Proc. ISWC Workshop on Evaluation of Semantic Technologies (iWEST), Shanghai (CN)*, 2010.

Oxford, Linköping Mannheim, Grenoble, Milano, Porto Alegre, Toulouse, Köln,
Walldorf, Montpellier, Trento, Prague
November 2013

AgreementMakerLight Results for OAEI 2013

Daniel Faria[1], Catia Pesquita[1], Emanuel Santos[1],
Isabel F. Cruz[2], and Francisco M. Couto[1]

[1] LASIGE, Dept Informatics, Faculty of Sciences of the University of Lisbon, Portugal
[2] ADVIS Lab, Dept Computer Science, University of Illinois at Chicago, USA

Abstract. AgreementMakerLight (AML) is an automated ontology matching framework based on element-level matching and the use of external resources as background knowledge. This paper describes the configuration of AML for the OAEI 2013 competition and discusses its results.
Being a newly developed and still incomplete system, our focus in this year's OAEI were the anatomy and large biomedical ontologies tracks, wherein background knowledge plays a critical role. Nevertheless, AML was fairly successful in other tracks as well, showing that in many ontology matching tasks, a lightweight approach based solely on element-level matching can compete with more complex approaches.

1 Presentation of the system

1.1 State, purpose, general statement

AgreementMakerLight (AML) is an automated ontology matching framework derived from the AgreementMaker system [2, 4]. It was developed with the main goal of tackling very large ontology matching problems such as those in the life science domain, which AgreementMaker cannot handle efficiently.

The key design principles of AML were efficiency and simplicity, although flexibility and extensibility—which are key features of AgreementMaker—were also high on the list [5]. Additionally, AML drew upon the knowledge accumulated in AgreementMaker by reusing, adapting, and building upon many of its components. Finally, one of the main paradigms of AML is the use of external resources as background knowledge in ontology matching.

AML is primarily focused on lexically rich ontologies in general and on life sciences ontologies in particular, although it can be adapted to many other ontology matching tasks, thanks to its flexible and extensible framework. However, due to its short development time (eight months), it does not include components for instance matching or translation yet, and thus cannot handle all ontology matching tasks.

1.2 Specific techniques used

The AML workflow for the OAEI 2013 can be divided into six steps, as shown in Fig. 1: ontology loading, baseline matching and profiling, background knowledge matching (optional), extension matching and selection, property matching (conditional), and repair (optional).

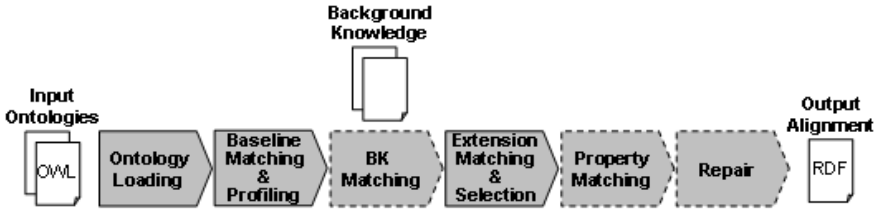


Fig. 1. The AgreementMakerLight Workflow for the OAEI 2013.

Ontology Loading In the ontology loading step, AML reads and processes each of the input ontologies and stores the information necessary for the subsequent steps in its own data structures.
First, AML reads the localName, labels and synonym properties of all classes, normalizes them, and enters them into the *Lexicon* [5] of that ontology. Then, it derives new synonyms for each name in the *Lexicon* by removing leading and trailing stop words [8], and by removing name sections within parenthesis. After class names, AML reads the class-subclass relationships and the disjoint clauses and stores them in the *RelationshipMap* [5]. Finally, AML reads the name, type, domain, and range of each property and stores them in the *PropertyList*.
Note that AML currently does not store or use comments, definitions, or instances.

Baseline Matching and Profiling In the baseline matching and profiling step, AML employs an efficient weighted string-equivalence algorithm, the *Lexical Matcher* [5], to obtain a baseline class alignment between the input ontologies. Then, AML profiles the matching problem by assessing the size (i.e., number of classes) of the input ontologies, the cardinality of the baseline alignment, and the property/class ratio.
Regarding size, AML divides matching problems into three size categories (small, medium or large), which will affect decisions and thresholds during the background knowledge matching and the extension matching and selection steps.
Regarding cardinality, AML also considers three categories (near-one, medium and high), which will determine how selection is performed during the extension matching and selection step.
As for the property/class ratio, it determines whether AML will match properties during the property matching step.

Background Knowledge Matching For the OAEI 2013, AML employs three sources of background knowledge: Uberon [6], UMLS [1] and WordNet [10]. When using background knowledge, AML tests how well each source fits the matching problem by comparing the coverage of its alignment with the coverage of the baseline alignment.
The *Uberon Matcher* uses the Uberon ontology (in OWL) and a table of pre-processed Uberon cross-references (in a text file). Each input ontology is matched both against the Uberon ontology using the *Lexical Matcher* and directly against the cross-reference

table, and AML determines which form of matching is best (giving priority to the cross-references, since they are more reliable). When Uberon is a good fit for the matching problem, it is selected as the only source of background knowledge and is used to extend the *Lexicons* of the input ontologies [8]. When it is a reasonable fit, its alignment is merged with the baseline alignment.
The *UMLS Matcher* uses a pre-processed version of the MRCONSO table from the UMLS Metathesaurus (in a text file). Each input ontology is matched against the whole UMLS table, then AML decides whether to use a single UMLS source (by comparing the coverage of all sources) or the whole table. When UMLS is a good fit for the matching problem, its alignment is used exclusively, and the extension matching and selection step is skipped. Otherwise, if it is a reasonable fit, its alignment is merged with the baseline alignment.
The *WordNet Matcher* queries the WordNet database for synonyms of each name in the *Lexicons* of the input ontologies, using the Jaws API CITATION. These synonyms are used to create temporary extended *Lexicons*, which are matched with the *Lexical Matcher*. Because WordNet is prone to induce errors, AML uses it only to extend the baseline alignment, meaning that it matches only previously unmatched classes.

Extension Matching and Selection The extension matching and selection step comprises two matching sub-steps that alternate with two selection sub-steps. First, AML employs a word-based similarity algorithm, the *Word Matcher* [5], to extend the current alignment globally, followed by a selection algorithm to reduce the alignment to the desired cardinality. Then AML employs the *Parametric String Matcher* [5], which implements the *Isub* string similarity metric [11], to extend the resulting alignment locally (i.e., by matching the children, parents and siblings of already matched class pairs). This is followed by a final selection sub-step.
When the matching problem is profiled as 'large', the *Word Matcher* is skipped because it is too memory intensive to be used globally, and its local use is subsumed by that of the *Parametric String Matcher* [3].
In the interactive matching track, AML employs an interactive selection algorithm, which asks the user for feedback about mappings in case of conflict or below a given similarity threshold, until a given number of negative answers is reached.

Property Matching In the property matching step, AML matches the ontology properties. AML compares the properties' types, domains and ranges, looking for mappings in the class alignment when the domains/ranges are classes. Then, if the properties have attributes in common, AML measures the word-based similarity between their names (as per the *Word Matcher* [5]), employing also WordNet when background knowledge is turned on.

Repair In the repair step, AML employs a heuristic repair algorithm [9] to ensure that the final alignment is coherent with regard to disjoint clauses. The repair algorithm was used by default in all OAEI tracks, except for the Large Biomedical Ontologies track where we ran AML both with and without repair.

1.3 Link to the system and parameters file

The AML system and the alignments it produced for the OAEI 2013 are available at the SOMER project page (http://somer.fc.ul.pt/).

2 Results

2.1 Benchmark

AML had a very high precision (100%) but a fairly low recall (40%) in the Benchmark track, returning empty alignments in several of the tests. This is a consequence of AML's simple framework, which is exclusively based on element-level matching and does not handle instances. Nevertheless, it was interesting to note that AML had the highest F-measure/time ratio, which attests to its efficiency.

2.2 Anatomy

The AML Anatomy results are shown in Table 1. AML ran in this track both with and without background knowledge (AML-BK and AML respectively). In the case of this track, AML-BK selects Uberon exclusively as the source of background knowledge, and uses it for *Lexicon* extension. Thus, the only difference between AML and AML-BK is that the latter has *Lexicons* enriched with Uberon synonyms.

Table 1. AgreementMakerLight results in the Anatomy track.

Configuration	Precision	Recall	F-Measure	Recall+
AML	95.4%	82.7%	88.6%	54.5%
AML-BK	95.4%	92.9%	94.2%	81.7%

The results of AML-BK were very good, with a fairly high precision, and the highest recall, F-measure and recall+ in this year's evaluation. However, the AML results without background knowledge were also good, ranking fourth overall in F-measure, and second if we exclude the systems using Uberon. In fact, we believe that the AML results are near-optimal for a strategy based solely on element-level matching, and that background knowledge is required to obtain substantial improvements. The impact and quality of the Uberon cross-references is clear when we note that AML-BK gained 10% recall over AML without any loss in precision. Finally, it is also noteworthy that AML was one of only two systems to produce coherent alignments.

2.3 Conference

The AML Conference results with reference alignment 1 are shown in Table 2 (the results with reference alignment 2 are slightly worst for all systems, but do not affect their ranking). AML ran in this track with and without background knowledge, with

Table 2. AgreementMakerLight results in the Conference track with reference alignment 1.

Configuration	Precision	Recall	F-Measure
AML	87%	56%	68%
AML-BK	87%	58%	70%

AML-BK using WordNet as the only source of background knowledge (to match both classes and properties).

The results of both AML-BK and AML were good, having the highest precision of this year's evaluation and ranking second and tied for third in terms of F-measure, respectively. An important part of the success of AML in this task was the property matching algorithm, which found 9 and 11 property mappings with 100% precision, with and without background knowledge respectively.

2.4 Multifarm

As we expected, the performance of AML in the Multifarm track was poor, with F-measures of only 4% and 3% when comparing different ontologies and the same ontologies respectively. Participation in this track was beyond our scope, as AML does not handle translations or employ structural-level matching, which are essential for success in this track.

2.5 Library

The results of AML in the Library track were reasonable, as it ranked 4th in terms of F-measure (with 73%) and had the second highest recall of this year's OAEI (87.7%). Nevertheless, there is clearly room for improvement regarding precision, which was significantly lower than that of other top systems (62.5%) likely due to the fact that AML does not take the language of labels into account. Indeed, the results of AML were very similar to the MatcherAllLabels benchmark.

2.6 Interactive Matching

The AML Interactive Matching results are shown in Table 3. AML ran with the same configurations used in the Conference track, except that in this track the selection algorithm employed is interactive, rather than automatic.

Table 3. AgreementMakerLight results in the Interactive Matching track.

Configuration	Precision	Recall	F-Measure	Interactions
AML	91%	60.7%	71.5%	138
AML-BK	91.2%	62.7%	73%	140

The results show that AML's interactive selection algorithm was effective, gaining both precision and recall in comparison with the conference results. Nevertheless, this

algorithm is far from optimized, and it should be possible to reduce the number of user interactions without sacrificing F-measure.

2.7 Large Biomedical Ontologies

The AML Large Biomedical Ontologies results are shown in Table 4. AML ran in this track with six different configurations: without background knowledge (AML); with background knowledge (AML-BK); with specialized background knowledge (AML-SBK); and in all three cases with (-R) and without repair. AML-BK selects Uberon in all six tasks of this track (although never for *Lexicon* extension) and selects WordNet only in the SNOMED-NCI small task. AML-SBK is given access to UMLS, and selects it exclusively for all six tasks.
Our goals in testing all these configurations were: to assess the impact of using domain background knowledge both unrelated (Uberon) and directly related (UMLS) to the reference alignments; to assess the effect of using repair on the quality of the results; and to contribute to improve the quality of the reference alignments.

Table 4. Summary AgreementMakerLight results in the Large Biomedical Ontologies track.

Configuration	Precision	Recall	F-Measure	Incoherence
AML	92.6%	68.3%	78.3%	43.1%
AML-R	93.9%	66.6%	77.6%	0.028%
AML-BK	90.8%	70.9%	79.2%	44.2%
AML-BK-R	92.1%	69.2%	78.5%	0.027%
AML-SBK	96.2%	96.1%	96.2%	55%
AML-SBK-R	97.6%	92.5%	95%	0.015%

The results of AML-SBK were very good, with a marked advantage over all other systems in this year's evaluation. This is unsurprising given that AML-SBK derived its alignments from UMLS using an automatic strategy that is likely analogous to that used to build the reference alignments in the first place. This evidently gives AML-SBK an advantage over systems that do not use UMLS. Note, however, that the strategy employed by AML is a general-purpose strategy for reusing preexisting mappings and cross-references, which is used for both UMLS and Uberon. The only issue is that the reference alignments were also automatically derived from UMLS, which makes the evaluation of AML-SBK positively biased.
The results of AML-BK were also good, ranking second overall in recall and F-measure if we exclude the systems that used UMLS. However, in this case the evaluation of AML-BK is negatively biased by the reference alignments. The reason for this is that AML-BK uses Uberon, and many of the mappings derived from Uberon are not present in UMLS despite being correct. This is particularly evident in the FMA-NCI matching problem with whole ontologies, where the contribution of Uberon (based on cross-references which are manually curated) was approximately neutral, decreasing the precision as substantially as it increased the recall (in relation to AML). Perhaps extending the reference alignments by compiling mappings from multiple reliable data sources

such as Uberon could enable a fairer evaluation of the systems competing in this track, and make the tasks less trivial for systems using background knowledge.
The use of repair led to clearly more coherent alignments, as all AML configurations with repair obtained very low degrees of unsatisfiability. However, in terms of quality of the results, the use of repair led to a minor increase in F-measure in some cases, but a substantial decrease in others, and thus had a negative effect overall. This is tied to yet another bias in the reference alignments, caused by the fact that they were automatically repaired [7]. Employing a repair strategy that differs from that used to build the reference alignments can be more penalizing than not doing any repair at all, since for each different decision a repair algorithm makes, it will remove a "correct" mapping and keep an "incorrect" one, whereas without repair we would only have the latter. The problem is that such decisions are essentially arbitrary regarding correctness.

3 General comments

3.1 Comments on the results

On the whole, the results of AML (without background knowledge) were interesting, and show that, for many ontology matching tasks, a lightweight approach based solely on element-level matching can compete with more complex approaches. It is worth highlighting that AML was among the quickest systems in all tracks, and thus had a consistently high F-measure/time ratio in all tracks except for Multifarm. However, the results in the Multifarm track, and to a lesser degree those in the Benchmark track, remind us that AML is still a system in development.
The results of AML-BK (and SBK) show that using suitable background knowledge is critical in specialized domains such as the biomedical, but can be advantageous even for more typical matching problems (such as those in the Conference track).

3.2 Discussions on the way to improve the proposed system

Implementing efficient and effective structural-level matching algorithms will be critical to improve the performance of AML overall. Language handling and translation will also be important to expand the scope of AML, and allow it to tackle tasks such as those in the Multifarm track. Finally, the inclusion of more sources of background knowledge will undoubtedly contribute to improve the performance of AML in tasks beyond the biomedical domain.

4 Conclusion

The participation of AML in the OAEI 2013 was a success overall, with very good results in the Anatomy, Conference, Interactive Matching and Biomedical Ontologies tracks, and reasonable results in the Library track. These results validate the background knowledge paradigm of AML, and demonstrate the effectiveness of a lightweight ontology matching strategy based solely on element-level matching. Nevertheless, it is also

clear from the results that AML is not a complete ontology matching system yet, and that it can benefit from the addition of new tools to its base strategy.
Regarding its namesake, AML was able to build upon the success AgreementMaker had in the Anatomy track in previous OAEI competitions, and was able to transpose this success to the Large Biomedical Ontologies track.

Acknowledgments

DF, CP, ES and FMC were funded by the Portuguese FCT through the SOMER project (PTDC/EIA-EIA/119119/2010) and the multi-annual funding program to LASIGE. CP was also funded by the FLAD-NSF 2013 PORTUGAL-U.S. Research Networks Program through the project "Turning Big Data into Smart Data". The research of IFC was partially supported by NSF Awards IIS-0812258, IIS-1143926, IIS-1213013, and CCF-1331800, by a UIC Area of Excellence Award, and by a IPCE Civic Engagement Research Fund Award.

References

1. O. Bodenreider. The Unified Medical Language System (UMLS): integrating biomedical terminology. *Nucleic Acids Res*, 32(Database issue):267–270, 2004.
2. I. F. Cruz, F. Palandri Antonelli, and C. Stroe. AgreementMaker: Efficient Matching for Large Real-World Schemas and Ontologies. *PVLDB*, 2(2):1586–1589, 2009.
3. I. F. Cruz, F. Palandri Antonelli, C. Stroe, U. Keles, and A. Maduko. Using AgreementMaker to Align Ontologies for OAEI 2009: Overview, Results, and Outlook. In *ISWC International Workshop on Ontology Matching (OM)*, volume 551 of *CEUR Workshop Proceedings*, pages 135–146, 2009.
4. I. F. Cruz, C. Stroe, F. Caimi, A. Fabiani, C. Pesquita, F. M. Couto, and M. Palmonari. Using AgreementMaker to Align Ontologies for OAEI 2011. In *ISWC International Workshop on Ontology Matching (OM)*, volume 814 of *CEUR Workshop Proceedings*, pages 114–121, 2011.
5. D. Faria, C. Pesquita, E. Santos, M. Palmonari, I. F. Cruz, and F. M. Couto. The AgreementMakerLight Ontology Matching System. In *OTM Conferences - ODBASE*, pages 527–541, 2013.
6. C. J. Mungall, C. Torniai, G. V. Gkoutos, S. Lewis, and M. A. Haendel. Uberon, an Integrative Multi-species Anatomy Ontology. *Genome Biology*, 13(1):R5, 2012.
7. C. Pesquita, D. Faria, E. Santos, and F. M. Couto. Using AgreementMaker to Align Ontologies for OAEI 2011. In *ISWC International Workshop on Ontology Matching (OM)*, CEUR Workshop Proceedings, page To appear, 2013.
8. C. Pesquita, C. Stroe, D. Faria, E. Santos, I. F. Cruz, and F. M. Couto. What's in a "nym"? Synonyms in Biomedical Ontology Matching. In *International Semantic Web Conference (ISWC)*, page To appear, 2013.
9. E. Santos, D. Faria, C. Pesquita, and F. M. Couto. Ontology alignment repair through modularization and confidence-based heuristics. arXiv:1307.5322, 2013.
10. B. Spell. Java API for WordNet Searching (JAWS). http://lyle.smu.edu/∼tspell/jaws/, 2009.
11. G. Stoilos, G. Stamou, and S. Kollias. A string metric for ontology alignment. In *International Semantic Web Conference (ISWC)*, pages 624–637, 2005.

Monolingual and Cross-lingual Ontology Matching with CIDER-CL: evaluation report for OAEI 2013

Jorge Gracia[1] and Kartik Asooja[1,2]

[1] Ontology Engineering Group, Universidad Politécnica de Madrid, Spain
jgracia@fi.upm.es
[2] Digital Enterprise Research Institute, National University of Ireland, Galway, Ireland
kartik.asooja@deri.org

Abstract. CIDER-CL is the evolution of CIDER, a schema-based ontology alignment system. Its algorithm compares each pair of ontology entities by analysing their similarity at different levels of their ontological context (linguistic description, superterms, subterms, related terms, etc.). Then, such elementary similarities are combined by means of artificial neural networks. In its current version, CIDER-CL uses SoftTFIDF for monolingual comparisons and Cross-Lingual Explicit Semantic Analysis for comparisons between entities documented in different natural languages. In this paper we briefly describe CIDER-CL and comment its results at the Ontology Alignment Evaluation Initiative 2013 campaign (OAEI'13).

1 Presentation of the system

CIDER-CL is the evolution of CIDER (Context and Inference baseD alignER) [7], now incorporating cross-lingual capabilities. In order to match ontology entities, CIDER-CL extracts their ontological context and enriches it by applying lightweight inference rules. Then, elementary similarity comparisons are performed to compare different features of the ontological contexts. Such elementary comparisons are combined by means of artificial neural networks (ANNs) [9] to produce a final similarity value between the compared entities. The use of ANNs saves a lot of effort on manual tuning and allows to quickly adapt the system into different domains (as far as there are reference alignments available for them).

In its current version, the aligner has been re-implemented to include more features in the comparisons and to add new metrics for similarity computation. In particular, cross-lingual capabilities have been added by including the use of Cross-Lingual Explicit Semantic Analysis (CL-ESA) [10] between entities documented in different natural languages. Further, the previous metrics for monolingual comparison (based on Vector Space Modelling [8]) have been changed by the SoftTFIDF metric [3]. CIDER-CL is not intended to be used with large ontologies, particularly in the cross-lingual case (CL-ESA computation is quite costly in terms of time).

1.1 State, purpose, general statement

According to the high level classification given in [5], our method is a *schema-based* system (opposite to others which are instance-based, or mixed), because it relies mostly

on schema-level input information for performing ontology matching. CIDER-CL can operate in two modes: (i) as an *ontology aligner*, taking two ontologies as input and giving their alignment as output, and (ii) as a *similarity service*, taking two ontology entities as input and giving the similarity value between them as output. In the first case the input to CIDER-CL are two OWL ontologies and a threshold value and the output is an RDF file expressed in the *alignment format*[3], although it can be easily translated into another formats such as EDOAL[4].

The type of alignment that CIDER-CL obtains is *semantic equivalence*. In its current implementation the following languages are covered: English (EN), Spanish (ES), German (DE), and Dutch (NL).

1.2 Specific techniques used

In this section we briefly introduce the monolingual and cross-lingual metrics used by CIDER-CL, as well as the overall architecture of the ontology aligner.

SoftTFIDF. SoftTFIDF [3] is a hybrid string similarity measure that combines TF-IDF, a token-based similarity widely used in information retrieval [8], with an edit-based similarity such as Jaro-Winkler [11] (although any other could be used instead).

Typically, string comparisons to compute TF-IDF weights are based on exact matching (after some normalisation or tokenisation step). The idea of SoftTFIDF is to use an edit distance instead to support a higher degree of variation between the terms. In particular, we use Jaro-Winkler similarity with a 0.9 threshold, above which two strings are consider equal. SoftTFIDF measure has proved to be very effective when comparing short strings [3]. In our case, the corpus used by SoftTFIDF is dynamically created with the lexical information coming from the two compared ontologies (extracting their labels, comments, and URI fragments).

CL-ESA. For cross-lingual ontology matching we propose the use of CL-ESA [10], a cross-lingual extension of an approach called Explicit Semantic Analysis [6] (ESA). ESA allows comparing two texts semantically with the help of explicitly defined concepts. This method uses the co-occurrence information of the words from the textual definitions of the concepts using, for instance, the Wikipedia articles. In short, ESA extends a simple bag of words model to a *bag of concepts* model. Some reports [2] have demonstrated the good behaviour of CL-ESA for certain tasks such as cross lingual information retrieval.

To compare two texts in different languages semantically, Wikipedia-based CL-ESA represents the two texts as vectors in a vector space that has the Wikipedia titles (articles) as dimensions, each vector in its own language specific Wikipedia. The magnitude of each title/dimension is the associativity weight of the text to that title. To quantify this associativity, the textual content of the Wikipedia article is utilized. This weight can be calculated by using different methods, for instance, TF-IDF score.

[3] http://alignapi.gforge.inria.fr/format.html
[4] http://alignapi.gforge.inria.fr/edoal.html

For implementing CL-ESA, we followed an information retrieval-based approach by creating a Lucene inverted index of the Wikipedia extended abstracts that exist in all the considered languages i.e., EN, ES, NL, and DE. To create the weighted vector of concepts, the term is searched over the index of the respective languages to retrieve the top associated Wikipedia concepts and the Lucene ranking scores are taken as the associativity weights of the concepts to the term. We used DBpedia URIs [1] as the pivot between cross-lingual Wikipedia spaces and to identify a Wikipedia concept no matter the language.

Scheme of the Aligner. Briefly explained, the alignment process is as follows (see Figure 1):

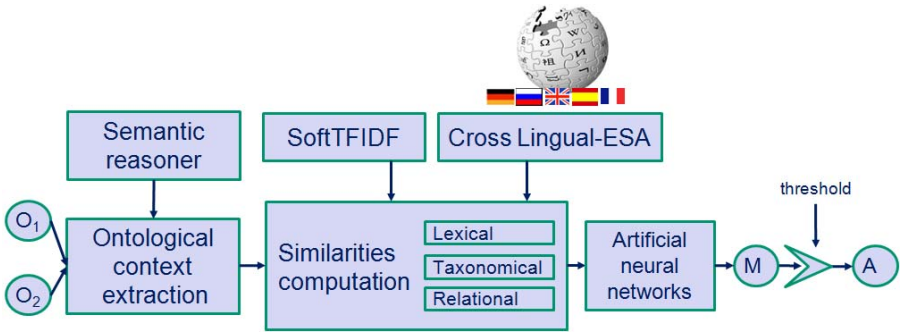


Fig. 1. Scheme of the matching process.

1. First, the ontological context of each ontology term is extracted. This process is enriched by applying a lightweight inference mechanism[5], in order to add more semantic information that is not explicit in the asserted ontologies.
2. Second, similarities are computed between different parts of the ontological context. In particular, ten different features are considered: *labels, comments, equivalent terms, subterms, superterms, direct subterms, direct superterms* (both for classes and properties) and *properties, direct properties*, and *related classes* (for classes) or *domains, direct domains*, and *ranges* (for properties).
3. Third, the different similarities are combined within an ANN to provide a final similarity degree. CIDER-CL uses four different neural networks (*multilayer perceptrons* in particular) for computing monolingual and cross-lingual similarities between classes and properties, respectively.
4. Finally, a matrix (M in Figure 1) with all similarities is obtained. The final alignment (A) is then extracted from it, finding the highest rated one-to-one relationships among terms and filtering out the ones below the given threshold.

[5] Typically transitive inference, although RDFS or more complex rules can be also applied, at the cost of processing time.

Implementation. Some datasets used in OAEI campaigns are open and the reference alignments available for download. We have used part of such data to train our system. In particular, we chose a subset of the OAEI'11 benchmark track to train our neural networks for the monolingual case. We used the whole dataset but excluding cases 202 and 248-266, which present a total absence or randomization of labels and comments (however their variations, 248-2, 248-4, etc., were not excluded). Also the reference alignments of the conference track, which are also open, were added to the training data set.

The use of the benchmark track for adjusting the ANNs is motivated by the fact that it covers many possible situations and variations well, such as presence or absence of certain ingredients (labels, comments, etc.) or the effect of aligning at different granularity levels (flattened/expanded hierarchies), etc. Further, we add also data of the conference track to include training data coming from "real world" ontologies.

For the cross-lingual case, we trained the neural networks with a subset of the ontologies of the OAEI'13 Multifarm track (in EN, ES, DE, and NL): cmt, conference, confOf, and sigkdd. Comparisons were run among the different ontologies in the different languages, excluding comparisons between the same ontologies. Due to the slow performance of CL-ESA, we decided to perform an attribute selection analysis to discover which features have more predictive power. As result, we limited the system to compute these features for classes: *labels, subterms, direct superterms, direct subterms*, and *properties*; while for properties they were limited to: *labels, subterms*, and *ranges*.

CIDER-CL has been developed in Java, extending the Alignment API [4]. To create and manipulate neural networks we use Weka[6] data mining framework. For SoftTFIDF we use SecondString[7] and for CL-ESA we use the implementation developed by the Monnet project[8], which is available in GitHub as open source[9].

1.3 Adaptations made for the evaluation

The weights and the configuration of the neural networks remained constant for all the tests and tracks of OAEI'13, as well as the threshold. In particular we selected a threshold of 0.0025. The intention of such a small value was to promote recall over precision (while filtering out some extremely low values). Therefore, later filtering can be made to perform a threshold analysis as the organisers of some OAEI tracks do (e.g., conference track).

Some minor technical adaptations were needed to integrate the system into the Seals platform, like solving compatibility issues with the libraries used by the Seals wrapper.

1.4 Link to the system and parameters file

The version of CIDER-CL used for this evaluation (v1.1) was uploaded to the Seals platform: http://www.seals-project.eu/ . More information can be found at CIDER-CL's website http://www.oeg-upm.net/files/cider-cl .

[6] http://www.cs.waikato.ac.nz/ml/weka/
[7] http://secondstring.sourceforge.net/
[8] http://www.monnet-project.eu/
[9] https://github.com/kasooja/clesa

1.5 Link to the set of provided alignments (in align format)

The resultant alignments will be provided by the Seals platform: http://www.seals-project.eu/

2 Results

For OAEI'13 campaign, CIDER-CL participated in all the Seals-based tracks[10]. In the following, we report the results of CIDER-CL for benchmark, conference, anatomy, and multifarm tracks. For the other tracks, the system was not fit for the type of evaluation (e.g., interactive track) or could not complete the task (e.g., library). Details about the test ontologies, the evaluation process, and the complete results for all tracks can be found at the OAEI'13 website[11].

2.1 Benchmark

This year, a blind test set was generated based on a seed ontology of the bibliographic domain. Out of the 21 systems participating in this track, CIDER-CL was within the three best systems in terms of F-measure. In particular, the obtained results were:

Precision(P)=0.85, Recall(R)=0.67 and F-Measure(F)=0.75

Compare to the F=0.41 of edna, a simple edit distance-based baseline. In addition, confidence-weighted measures were also computed for those systems that provided a confidence value. In almost all cases the results were worse, as it was also the case of CIDER-CL: P=0.84, R=0.55, and F=0.66

Also the time spent in the evaluation was calculated. CIDER-CL took 844$\pm$19 seconds, which was slower than most of the systems (the median value was 173 sec) although still far from the slowest one (10241$\pm$347 sec).

2.2 Conference

In this track, several ontologies from the conference domain were matched, resulting in 21 alignments. In this case the organisers explored different thresholds and selected the best achievable results. This test is not blind and the participants have the reference alignments at their disposal before the evaluation phase.

Two reference alignments were used in this track: the original reference alignment (ra1) and its transitive closure (ra2). Two baselines (edna and string equivalence) were computed for comparison. Notice that the results for CIDER-CL in this track are merely illustrative and should not be taken as a proper test, due to the fact that part of the training data of its neural networks came from the conference track reference alignments (i.e., training and test data coincide partially).

Out of the 25 systems participating in this track (some of them were variations of the same system), CIDER-CL performance was close to the average. The results were:

[10] http://oaei.ontologymatching.org/2013/seals-eval.html
[11] http://oaei.ontologymatching.org/2013

test ra1 (original): P = 0.75, R = 0.47, and F = 0.58 with threshold= 0.14
test ra2 (entailed): P = 0.72, R = 0.44, and F = 0.55 with threshold= 0.08

CIDER-CL was in the group of systems that performed better than the two baselines for ra2 and between the two baselines for ra1. The results for ra1 illustrates an improvement with respect to the results obtained by its previous version (CIDER v0.4) for the same test at OAEI'11 (F=0.53). The runtime was also registered: CIDER-CL took less than 10 minutes for computing the 21 alignments. The other systems ranged from 1 minute to more than 40.

2.3 Anatomy

This year, the current version of CIDER-CL completed the task and gave results for the first time. In fact, in previous editions of OAEI, CIDER gave time-outs and the tool did not finish the task, due to the big size of the involved ontologies. The results are:

P = 0.65, R = 0.73, F = 0.69, R+ = 0.31

These results are below the average of the overall results (F-Measure ranging from 0.41 to 0.94, with a median value of 0.81). An "extended recall" (R+) was also computed, that is, the amount of detected non-trivial correspondences (that do not have the same normalized label). For this metric CIDER-CL behaved better than the median value (0.23). In terms of running time, CIDER-CL was the third slowest system (12308 sec) in this track, after discarding those that gave time-out.

2.4 Multifarm

This track is based on the alignment of ontologies in nine different languages: EN, DE, ES, NL, CZ, RU, PT, FR, and CN. All pairs of languages (36 pairs) were considered in the evaluation. A total of 900 matching tasks were performed. There were 21 participants in this track, 7 of them implementing specific cross-lingual modules as it was the case of CIDER-CL.

The organisers divided the results in two types: comparisons between different ontologies (type i) and comparisons between the same ontologies (type ii). The result summary published by the organisers aggregates the individual results for all the language pairs. In the case of CIDER-CL this hampers direct comparisons with other systems, owing to the fact that CIDER-CL only covers a subset of languages (EN, DE, ES, NL) and non produced alignments in other languages penalised the overall results. For this reason we have filtered the language specific results to consider only such subset of languages. The averaged results for CIDER-CL are:

type i (different ontologies): P = 0.16, R = 0.19, F = 0.17
type ii (same ontologies): P = 0.82 , R = 0.16, F = 0.26

For type ii, CIDER-CL got the 4th best result overall in terms of F-Measure and the 3rd best result in the set of systems implementing specific cross-lingual techniques (the results for such systems ranged from F = 0.12 to F = 0.44 for the referred subset of

languages). On the other hand, for type i CIDER-CL was in 8th position out of the 21 participants, although in the last place among the set of systems implementing cross-lingual techniques (F-measure of the other techniques ranged from 0.17 to 0.35).

3 General comments

The following subsections contain some remarks and comments about the results obtained and the evaluation process.

3.1 Comments on the results

CIDER-CL obtained good results for the benchmark track (third place out of 21 participants). This shows that our system performs well for domains in which the system could be trained with available reference data. Also that SoftTFIDF is suitable for ontology matching. In contrast, the results for the anatomy track were relatively poor. This shows that creating a general purpose aligner based on our technique is not immediate. Adding more training data from other domains would help to solve this.

The results from the multilingual track are rather modest, but the fact that even the best systems scored low illustrates the difficulty of the problem. We consider that the use of CL-ESA is promising for cross-lingual matching, but it will require more study and adaptation to achieve better results.

3.2 Discussions on the way to improve the proposed system

More reference alignments from "real world" ontologies will be used in the future for training the ANNs, in order to cover more domains and different types of ontologies. Regarding the cross-lingual matching, there is still room for continuing improving the use of CL-ESA to that end. We plan also to combine this novel technique with other ones such as machine translation.

Time response in CIDER-CL is still an issue and has to be further improved. In fact CIDER-CL works well with small and medium sized ontologies but not with large ones. Partitioning and other related techniques will be explored in order to solve this.

3.3 Comments on the OAEI 2013 test cases

The variety of tracks and the improvements introduced along the years makes the campaign very useful to test the performance of ontology aligners and analyse their strengths and weaknesses. Nevertheless, we miss blind tests cases in more tracks, which would allow a fair comparison between systems.

4 Conclusion

CIDER-CL is a schema-based alignment system that compares the ontological context of each pair of terms in the aligned ontologies. Several elementary comparisons are

computed and combined by means of artificial neural networks. Monolingual and cross-lingual metrics are used in the matching.

We have presented here some results of the participation of CIDER-CL at OAEI'13 campaign. The results vary depending on the track, from the good results in the benchmark track to the relatively limited behaviour in anatomy, for instance. We confirmed that the proposed technique, based on ANNs, is suitable in conjunction with SoftTFIDF metric for monolingual ontology matching. The use of CL-ESA metric for cross-lingual matching is promising but requires more study.

Acknowledgments. This work is supported by the Spanish national project BabeLData (TIN2010-17550) and the Spanish Ministry of Economy and Competitiveness within the Juan de la Cierva program.

References

1. C. Bizer, J. Lehmann, G. Kobilarov, S. Auer, C. Becker, R. Cyganiak, and S. Hellmann. DBpedia - a crystallization point for the web of data. *Web Semantics: Science, Services and Agents on the World Wide Web*, 7(3):154–165, Sept. 2009.
2. P. Cimiano, A. Schultz, S. Sizov, P. Sorg, and S. Staab. Explicit versus latent concept models for cross-language information retrieval. In *Proceedings of the 21st international jont conference on Artifical intelligence*, IJCAI'09, pages 1513–1518, San Francisco, CA, USA, 2009. Morgan Kaufmann Publishers Inc.
3. W. W. Cohen, P. Ravikumar, and S. E. Fienberg. A comparison of string distance metrics for name-matching tasks. In *Proc. Workshop on Information Integration on the Web (IIWeb-03) @ IJCAI-03, Acapulco, Mexico*, pages 73–78, Aug. 2003.
4. J. Euzenat. An API for ontology alignment. In *3rd International Semantic Web Conference (ISWC'04), Hiroshima (Japan)*. Springer, November 2004.
5. J. Euzenat and P. Shvaiko. *Ontology matching*. Springer-Verlag, 2007.
6. E. Gabrilovich and S. Markovitch. Computing semantic relatedness using wikipedia-based explicit semantic analysis. In *In Proceedings of the 20th International Joint Conference on Artificial Intelligence*, pages 1606–1611, 2007.
7. J. Gracia, J. Bernad, and E. Mena. Ontology matching with CIDER: Evaluation report for OAEI 2011. In *Proc. of 6th Ontology Matching Workshop (OM'11), at 10th International Semantic Web Conference (ISWC'11), Bonn (Germany)*, volume 814. CEUR-WS, Oct. 2011.
8. V. V. Raghavan and M. S. K. Wong. A critical analysis of vector space model for information retrieval. *Journal of the American Society for Information Science*, 37(5):279–287, 1986.
9. M. Smith. *Neural Networks for Statistical Modeling*. John Wiley & Sons, Inc., New York, NY, USA, 1993.
10. P. Sorg and P. Cimiano. Exploiting wikipedia for cross-lingual and multilingual information retrieval. *Data Knowl. Eng.*, 74:26–45, Apr. 2012.
11. W. E. Winkler. String comparator metrics and enhanced decision rules in the Fellegi-Sunter model of record linkage. In *Proceedings of the Section on Survey Research*, pages 354–359, 1990.

CroMatcher - Results for OAEI 2013

Marko Gulić[1], Boris Vrdoljak[2]

[1] Faculty of Maritime Studies, Rijeka, Croatia
marko.gulic@pfri.hr
[2] Faculty of Electrical Engineering and Computing, Zagreb, Croatia
boris.vrdoljak@fer.hr

Abstract. CroMatcher is an ontology matching system based on terminological and structural matchers. The most important part of the system is automated weighted aggregation of correspondences produced by using different basic ontology matchers. This is the first year CroMatcher has been involved in the OAEI campaign. The results obtained this year will certainly help in finding and resolving shortcomings in the system before the next campaign.

1 Presentation of the system

CroMatcher is an automatic ontology matching system for determining correspondences between entities of two different ontologies. There are several terminological and structural basic matchers in CroMatcher. The system is based on a weighted aggregation that automatically determines the importance of each basic matcher according to the produced correspondences. As this is the first time the CroMatcher has taken part in the OAEI campaign, CroMatcher is fully prepared only for benchmark test set.

1.1 State, purpose, general statement

CroMatcher is a system that executes several basic matchers and then aggregates the results obtained by these matchers. The system does not use any external resource. After the execution of terminological basic matchers, the automatic weighted aggregation is executed. The results of certain terminological basic matcher are included into the common results depending on their importance. The importance of certain basic matcher is determined automatically within weighted aggregation. Then, the several iterative structural matchers are executed (e.g. if the child entities are similar, the parent entities are similar too). To find correspondences with structural matchers, the common results of terminological matchers are used. After the execution of structural basic matchers, the automatic weighted aggregation is executed too. At the end of matching process, the weighted aggregation is executed for the terminological and structural common results. Finally, the method of final alignment (choosing the relevant correspondences between entities of two ontologies) is executed. This method iteratively takes the best correspondences between two

certain entities into the final alignment. Each entity can be related just to one entity of other ontology.

1.2 Specific techniques used

In this section, the main components of the CroMatcher will be described in details. The workflow and the main components of the system can be seen in the Fig. 1. The CroMatcher consists of the following components:

1. **Data extraction from ontologies** - the information of every entity is extracted from given ontologies. After extraction of all data about certain entity, all textual data is normalized by tokenizing into set of tokens, and removing stop words.

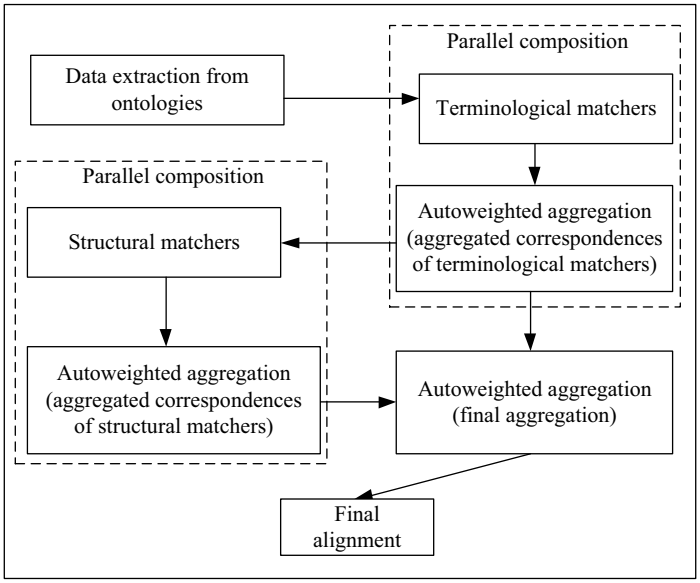


Fig. 1. The workflow and the main components of the Cromatcher

2. **Terminological matchers:**

- Matcher that compares ID and annotations' text of two entities (classes or properties) with the bi(tri)gram matcher (tests how many bi(tri)grams, i.e. (substrings of length 2, 3) are the same within two names, e.g. FTP and FTPServer have 2 bigrams - FT and TP) [1]
- Matcher that compares only label (or entity's ID if the entity does not have label) of two entities (classes or properties) with the bi(tri)gram matcher
- Matcher that compares textual profiles of two entities with TF/IDF [2] and cosine similarity [3]. A profile of class entity contains annotations of actual class entity (and all sub classes) and annotations of every property whose domain is actual class. A profile of property entity contains annotations of actual property entity and all sub properties.

- Matcher that compares individuals of two entities with TF/IDF and cosine similarity. An individual of class entity contains individual values of actual class entity and individual values of all subclasses. An individual of property entity contains individual values of its range class entities.
- Matcher that compares extra individuals of two entities with TF/IDF and cosine similarity. An extra individual of class entity contains individual values of first super class of actual class entity. An extra individual of property entity contains individual values of its domain and range class entities.
- Matcher that compares some general data about the entities. A general data of class entity contains number of object (data) properties, number of restrictions and number of sub (super) class entities. A general data of property entity contains number of sub (super) property entities, number of domain class entities. More similar the general data, there is the greater correspondence between entities.

3. Structural matchers:

- Matcher that compares the similarity between super entities (classes or properties) of currently compared entities. If the super entities are similar, compared entities are similar too. The matcher is executed iteratively and it ends when the correspondence value of compared entities stops changing. In each step, the new correspondence value of compared entities is calculated by summing 50% of the previous similarity value and 50% of the similarity value between super entities.
- Matcher that compares the similarity between sub entities (classes or properties) of currently compared entities. If the sub entities are similar, the compared entities are similar too. The matcher is executed iteratively and it ends when the correspondence value of compared entities stops changing. In each step, the new correspondence value of compared entities is calculated by summing 50% of the previous similarity value and 50% of the similarity value between sub entities.
- Matcher that compares the similarity between properties (and its range classes) that have the currently compared classes as their domain. A part of matcher for similarity between properties compares domain classes of properties.
- Matcher that compares the similarity between range classes of currently compared properties.

4. Autoweighted aggregation for parallel composition of basic matchers:

After the execution of terminological and structural matchers, the results of these matchers have to be aggregated together. In our system, we used a parallel composition of matchers for integration of multiple matchers. The main problem in parallel composition is how to aggregate the results obtained by every basic matcher. Weighted aggregation is one of the methods for aggregation of matchers [4]. This method determines a weighted sum of similarity values of the basic matchers and needs relative weights which should correspond to the expected importance of the basic matchers. The problem is how to determine the importance of every basic matcher. Our automatic Autoweight method proposed in [5] automatically defines the importance of various basic matchers in order to improve overall performance of the matching system. In this method, the importance of certain basic matcher is specified

by determining the importance of individual best correspondences (greatest correspondences between two entities in both directions of mapping, as those correspondences are the most relevant) within the results obtained by that matcher. The importance of a certain correspondence found within the results of a basic matcher is higher when the same correspondence is found within a smaller number of other basic matchers. The method that finds the same correspondences as all other methods does not provide any new significant information for the matching process.

5. **Process of final alignment:**

At the end, the selection of relevant correspondences, for inclusion in the final alignment, is executed iteratively. The final alignment includes only the greatest correspondences between $entity_{1i}$ (first ontology) and $entity_{2j}$ (second ontology). A correspondence between $entity_{1i}$ and $entity_{2j}$ is the greatest correspondence only if it has the greatest value among all correspondences in which the $entity_{1i}$ (or $entity_{2j}$) is included. Threshold for these greatest correspondences is set to 0.15. We consider that this threshold is sufficient because the final alignment included only those correspondences that are the greatest for both compared entities.

1.3 Link to the system and parameters file

A system can be downloaded from the http://www.seals-project.eu (tool identifier: e0fe95d5-943e-4652-bc53-5b36b712c9cb, version: 1.0).

2 Results

In this section, the evaluation results of CroMatcher matching system executed on the SEALS platform are presented.

2.1 Benchmark

In OAEI 2013, benchmark includes one blind test (biblio). In Table 1 the result obtained by running the CroMatcher ontology system can be seen.

Test set	Recall	Precision	F-Measure	Time (s)
Benchmark	0.82	0.95	0.88	1114

Table 1. CroMatcher result for benchmark track

2.2 Anatomy, conferences, multifarm, library, large biomedical ontologies and instance matching

This is the first year CroMatcher has been involved in the OAEI campaign and the focus was on benchmark track. Therefore, the system had problems with other tracks because we did not manage to test the system for other tracks before the evaluation due the lack of time. This year, the ontology matching system had to finish matching

the anatomy ontologies within 10 hours, and our system has not finished even after 30 hours therefore we need to speed up the system before the next OAEI campaign. In the conference track, our system was partially evaluated because it could not process several ontologies. In the multifarm, library, large biomedical ontologies, our system gave an "OutOfMemory" exception so we need to solve that problem too before the next evaluation. Regarding the instance matching, we did not participate in this track.

3 General comments

As we stated before, this is the first time the CroMatcher system participates in the OAEI campaign. We are very pleased that our ontology matching system was evaluated on the SEALS platform because this way we could compare our system with existing systems. There are many different test cases and we think that these test cases will help us to improve our system in the future.

3.1 Comments on the results

Our system shows great results in benchmark track. Considering the fact that the benchmark track contains the largest number of ontologies in which the different parts are missing, we can conclude that our system performs well but only while matching small ontologies like these in the benchmark track. While matching big ontologies (thousands of entities), our system is quite slow and it cannot handle big ontologies yet.

3.2 Discussions on the way to improve the proposed system

We will have to find faster measure than TF/IDF to compare different documents of entities. Also, we will have to store the data about the entities in a separate file instead in the java objects in order to reduce the usage of memory in the system.

4 Conclusion

The CroMatcher ontology matching system and its results of evaluation on different OAEI track were presented in this paper. The evaluation results show that CroMatcher successfully matches small ontologies but it has problems dealing with ontologies that have a large number of entities. We will try to solve this problem and prepare the system to be competitive in all OAEI tracks next year.

References

1. Euzenat, J., Shvaiko, P.: Ontology matching. Springer, 2007.

2. Salton, G., McGill, M.H.: Introduction to Modern Information Retrieval. McGraw-Hill, New York (1983)
3. Baeza-Yates, R., Ribeiro-Neto B.: Modern Information Retrieval. Addison-Wesley, Boston (1999)
4. Do, H., Rahm, E.: COMA - a system for flexible combination of schema matching approaches. In Proc. 28th International Conference on VLDB, pages 610-621, 2002.
5. Gulić, M., Magdalenić, I., Vrdoljak, B.: Automatically Specifying Parallel Composition of Matchers in Ontology Matching Process. In: Barriocanal, E. G., Cebeci, Z., Okur, M. C., Öztürk, A. (eds.) MTSR 2011. Communications in Computer and Information Science, vol. 240, pp. 22-33. Springer, Berlin Heidelberg (2011)

IAMA Results for OAEI 2013

Yuanzhe Zhang[1], Xuepeng Wang[1], Shizhu He[1],
Kang Liu[1], Jun Zhao[1], and Xueqiang Lv[2]

[1] Institute of Automation, Chinese Academy of Sciences, China
{yzzhang, xpwang, shizhu.he, kliu, jzhao}@nlpr.ia.ac.cn
[2] Beijing Key Laboratory of Internet Culture and Digital Dissemination Research
lxq@bistu.edu.cn

Abstract. This paper presents the results of IAMA on OAEI 2013. IAMA (Institute of Automation's Matcher) is an ontology matching system with the capability to deal with large scale ontologies. IAMA is designed to find out the correspondences between two ontologies by using multiple similarity measures. Candidate filtering technique is adopted when processing ontologies at large scale.

1 Presentation of the system

1.1 State, purpose, general statement

Large amount of ontologies has been published since the semantic web emerged. However, managing the heterogeneity among various ontologies is still a problem [1]. For example, many ontologies describe the same entity (i.e., class or property) using different terminologies, while the entities having the same name belonging to different ontologies may refer to disparate objects. Finding the matching between different ontologies is still challenging. Ontology matching, as a solution to the aforementioned problem, has received great interests in these years.

The principal goal of IAMA is to discover equivalent entities rapidly between different ontologies. We use efficient terminology matching techniques and do not turn to any external resource at this stage. IAMA is able to match classes and properties of two input ontologies. The system could achieve qualified results, though neglecting the structural information. The Matching process takes little time to cope with small ontologies. When processing large scale ontologies, IAMA could still, with the help of candidate filtering, yield the alignment in reasonable time. We tend to make an universal and extensible system, so more matching methods could be conveniently incorporated in the future.

1.2 Specific techniques used

IAMA employs various similarity measures to take advantage of the available information in the ontologies. The entities in two ontologies are pairwise compared, and lexical similarities and structural similarities are calculated respectively. In the current version, only 1:1 alignment is considered.

Let O_1 and O_2 denote the two input ontologies, and e_1 is an entity in O_1. Each entity e_2 in $O2$ has a similarity with $e1$ indicated as $sim(e1, e_2)$. We are able to find out the maximum value as $sim(e_1, \hat{e})$. If $sim(e_1, \hat{e})$ is greater than a predetermined threshold t_1, entity pair (e_1, $\hat{e}$) will be added to the alignment. In the following paragraphs, we will present the used similarity measures in our system.

Lexical Similarity

The system extracts local names, labels, and comments of the entities in the two input ontologies as lexical features. For most situations, the lexical information is effective.

Local Name similarity measures the similarity between the names of two entities. We get rid of the spaces and other punctuations because the entity name is comprised of multiple words or contains hyphens at times. All the letters are turned to lower case simultaneously. *Label Similarity* measures the similarity between the labels. Not all the entities have labels, and many entities have a label exactly the same as its local name. *Comment Similarity* measures the similarity between the comments. A comment of an entity is usually a brief descriptive sentence, which is helpful when the two ontologies name their entities with quite different style. Both labels and comments are processed as local names, thereby treated as a single word.

IAMA uses Levenshtein [2] distance, which is proved competent in [3], to calculate lexical similarities. For the three lexical similarities mentioned above, we do not take them equally. Each similarity is assigned a weight intuitively. Local name similarity has a greater weight than label similarity, while comments similarity has the lowest weight.

Individual Similarity

Between the classes that have individuals, *Individual Similarity* is additionally calculated. The names of individuals that belong to a class are extracted to a set of string. Assume S_1 and S_2 are two sets, then the similarity between them is computed as follows:

$$sim(S_1, S_2) = 2 \times \frac{\#(S_1 \cap S_2)}{\#S_1 + \#S_2} \tag{1}$$

For example, if c_1 is a class in ontology O_1, and c_2 is a class in ontology O_2. The names of the individuals belonging to c_1 is a set of string $i_1 = \{s_1, s_2, s_3\}$, and similarly we get $i_2 = \{s_2, s_3, s_4, s_5\}$. The individual similarity $sim_i(c_1, c_2)$ is:

$$sim_i(c_1, c_2) = 2 \times \frac{\#(i_1 \cap i_2)}{\#i_1 + \#i_2} = 2 \times \frac{2}{3+4} = 0.571$$

IAMA adopts the maximum value of all the similarities as the final similarity of the entity pair. It is worth noting that other similarities such as superclass similarity, subclass similarity, domain similarity and range similarity are also tested in our earlier attempts. But they contributed little considering the time increased. They could be added easily if needed, which makes IAMA extensible.

Candidate Filtering

Pairwise compare is time consuming. In most cases, calculating similarities for every entity pair is unnecessary. *Candidate Filtering* helps to find out a few promising entity pairs in advance, thus saving running time dramatically.

Assume the two input ontologies are O_1 and O_2, and O_2 has more entities than O_1. For each entity in O_1, we attempt to find out potential entities in O_2 to construct a candidate set. The idea is implemented as follow. First, the lexical information in the bigger ontology O_2, namely name, label and comment is tokenized and indexed by Lucene[3]. Second, we construct search query for each entity in O_1. For instance, the lexical information of an entity in O_1 is "Reference", "Reference", "Base class for all entries". We split it into index tokens, and every single token is searched in the constructed index, yielding top-k entities as a candidate set. Last, our system calculates the final similarity values pairwise.

The time used for indexing and searching is acceptable. For large input ontologies, candidate filtering improves the matching speed substantially. Take anatomy track for example, the difference can be seen in Table 1. The experiment is conducted on a computer with 4.7GHz Intel i5 CPU (4 core) and 8GB RAM.

	Precision	F-Measure	Recall	Runtime (ms)
IAMA without candidate filtering	0.994	0.719	0.563	117,503
IAMA with candidate filtering	0.995	0.713	0.555	5,376

Table 1. The impact of candidate filtering in Anatomy track

Candidate filtering could still miss some potential entity pairs though negligible. IAMA defined an alterable trigger threshold $t2$, which is set to 500 empirically. Only both the two ontologies have more than 500 entities, candidate filtering is employed.

1.3 Adaptations made for the evaluation

There are two key parameters in IAMA (i.e., $t1$ and $t2$). Specifically, if the final similarity of an entity pair is greater than $t1$, the pair will be added to the alignment. $t2$ is the trigger threshold of candidate filtering component as mentioned before. In the version to participate in OAEI 2013, $t1$ is set to 0.9 and $t2$ is set to 500.

1.4 Link to the system and parameters file

The latest version of IAMA can be seen on https://github.com/YuanzheZhang/IAMA.

2 Results

This section presents the results of IAMA achieved in OAEI 2013. Our system mainly focuses on benchmark, anatomy, conference, and large biomedical ontologies. We do not provide multilingual support for the moment.

[3] http://lucene.apache.org

2.1 benchmark

The goal of the benchmark data set is to provide a stable and detailed picture of each algorithm[4]. The benchmark test library consists of several test suits. The test suites are generated from the usual bibliography ontology this year, and they are blind to participants. Table 2 shows the results of benchmark track. Pt F-m./s means the average F-measure point provided per second.

Precision	F-Measure	Recall	Time (s)	pt F-m./s
0.99	0.73	0.57	102	0.72

Table 2. Results for Benchmark track

Our system acquired its best results in this track. Concerning F-measure, IAMA ranked fourth in the 21 systems. The comparison with other top systems is shown in Table 3

System	Precision	F-Measure	Recall	Time (s)	pt F-m./s
YAM++	0.97	0.89	0.82	702	0.13
CroMatcher	0.95	0.88	0.82	1,114	0.08
CIDER-CL	0.85	0.75	0.67	844	0.09
IAMA	0.99	0.73	0.57	102	0.72
ODGOMS	0.99	0.71	0.55	100	0.71

Table 3. Comparison with other top systems in Benchmark track

2.2 anatomy

The task of anatomy track is to find the alignment between the Adult Mouse Anatomy and a part of the NCI Thesaurus. These two ontologies describe the mouse anatomy and the human anatomy respectively. The results of our system on anatomy are shown in Table 4.

Runtime	Size	Precision	F-Measure	Recall	Recall	Coherent
10	845	0.996	0.713	0.555	0.014	-

Table 4. Results for Anatomy track

Since both the two ontologies have the scale larger than 500 entities, candidate filtering is employed. As a result, IAMA finishes this track in 10 seconds. Only two systems are faster than IAMA. The simple use of lexical similarity generates mostly trivial correspondences, leading the low recall+ measure.

2.3 conference

Conference track contains sixteen ontologies from the conference organization domain. There are two versions of reference alignment. The original reference alignment is labeled as *ra1*, and the new reference alignment, generated as a transitive closure computed on the original reference alignment, is labeled as *ra2*. Table 5 shows the results of our system in this track.

	Precision	F-Measure	Recall
ra1	0.78	0.59	0.48
ra2	0.74	0.55	0.44

Table 5. Results for Conference track

IAMA finishes the conference track in 53 seconds. Candidate filtering has not been activated.

2.4 multifarm

The MultiFarm data set contains ontologies in eight different languages. These ontologies are translated from conference track. IAMA does not design a multilingual method specifically, thus obtained relatively poor results. We managed to utilize language detection and translation API. Unfortunately, it increased the processing time of our system and led to other problems. In the next version, IAMA will adopt specialized method to deal with multilingual ontologies. The results are presented in Table 6.

Average Precision	Average F-Measure	Average Recall
0.30	0.05	0.03

Table 6. Results for MultiFarm track

2.5 library

The task of library track is to match two real-world thesaurus, namely STW and TheSoz. IAMA does not provide particular method aiming at this track. The results can be seen in Table 7. IAMA does not apply particular method for this track.

Precision	F-Measure	Recall
0.78	0.04	0.08

Table 7. Results for Library track

2.6 large biomedical ontologies

Large Biomedical track challenges matching tools by offering large scale ontologies. The task of this track is to find alignments between Foundational Model of Anatomy (FMA), SNOMED CT, and the National Cancer Institute Thesaurus (NCI). IAMA finishes the task in reasonable time owe to the use of candidate filtering. Table 8 shows the results.

Task 1: Small FMA and NCI fragments				
P	F	R	#Mappings	Runtime (s)
0.979	0.733	0.585	1,751	14
Task 2: Whole FMA and NCI ontologies				
P	F	R	#Mappings	Runtime (s)
0.901	0.708	0.582	1,894	139

Task 3: Small FMA and SNOMED fragments				
P	F	R	#Mappings	Runtime (s)
0.962	0.236	0.134	1,250	27
Task 4: Whole FMA and SNOMED ontologies				
P	F	R	#Mappings	Runtime (s)
0.749	0.227	0.134	1,600	218

Task 5: Small SNOMED and NCI fragments				
P	F	R	#Mappings	Runtime (s)
0.965	0.604	0.439	8,406	99
Task 6: Whole SNOMED and NCI ontologies				
P	F	R	#Mappings	Runtime (s)
0.917	0.593	0.439	8,843	207

Table 8. Results for Large Biomedical track

IAMA is one of the fifteen systems that are able to complete all six tasks, and provides the best results in terms of precision in task 1 and task 2. Furthermore, our system finishes all the tasks in 704 seconds, only slower than LogMapLt (371 seconds). The average results are shown in Table 9.

Precision	F-Measure	Recall	Incoherence	Total time (s)
0.912	0.517	0.386	46.4%	704

Table 9. The average results for Large Biomedical track

3 General comments

3.1 Comments on the results

IAMA achieved qualified results in its first participation in OAEI. The results for benchmark, conference, and large biomedical track is better. Since the system does not design specific method to handle MultiFarm and library track, the results are relatively poor. It is evident that IAMA got relatively high precision but low recall. The reason is that the threshold $t1$ is fixed to a high value of 0.9. Candidate filtering, as already mentioned, cuts down the recall as well.

3.2 Discussions on the way to improve the proposed system

IAMA remains much to be improved. First, the system does not take advantage of structural information, which is beneficial when lack of lexical information. We tried to calculate structural similarity like subclass similarity and superclass similarity, but did not receive expected results. The hierarchy information is also remained to be exploited. Second, predetermining all the parameters loses the flexibility. The influence of parameter $t1$ can be seen in Table 10. The experiment is conducted on a computer with 4.7GHz Intel i5 CPU (4 core) and 8GB RAM. A self-adjust mechanism is to be employed in the future. Third, the system lacks the ability to match ontologies in different languages. The next version will support multi-language inputs. We expect the optimized system would become an eligible universal ontology matching system.

	Precision	F-Measure	Recall
$t1$=0.7	0.800	0.752	0.710
$t1$=0.8	0.945	0.783	0.668
$t1$=0.9	0.995	0.719	0.563

Table 10. Impact of parameter $t1$ in anatomy track (without candidate filtering)

4 Conclusion

This paper has reported the results of IAMA in OAEI 2013. The results reflect that IAMA has the ability to deal with a majority of ontologies, including large ones. On the other hand, for those disadvantages exposed, we discuss the possible solutions. By and large, IAMA achieved reasonable results for its first participation in OAEI, and it is promising to be much improved in the future.

Acknowledgement

This work was supported by the National Natural Science Foundation of China (No. 61070106,61272332,61202329) and the Opening Project of Beijing Key Laboratory of Internet Culture and Digital Dissemination Research(ICDD201201).

References

1. P Shvaiko and Jérôme Euzenat. Ontology matching: State of the art and future challenges. *Knowledge and Data Engineering, IEEE Transactions on*, (99), 2012.
2. Vladimir I Levenshtein. Binary codes capable of correcting deletions, insertions and reversals. In *Soviet physics doklady*, volume 10, page 707, 1966.
3. Giorgos Stoilos, Giorgos Stamou, and Stefanos Kollias. A string metric for ontology alignment. In *The Semantic Web–ISWC 2005*, pages 624–637. Springer, 2005.
4. José Luis Aguirre, Bernardo Cuenca Grau, Kai Eckert, Jérôme Euzenat, Alfio Ferrara, Robert Willem van Hague, Laura Hollink, Ernesto Jimenez-Ruiz, Christian Meilicke, Andriy Nikolov, et al. Results of the ontology alignment evaluation initiative 2012. In *Proc. 7th ISWC workshop on ontology matching (OM)*, pages 73–115, 2012.

LogMap and LogMapLt results for OAEI 2013

Ernesto Jiménez-Ruiz, Bernardo Cuenca Grau, Ian Horrocks

Department of Computer Science, University of Oxford, Oxford, UK

Abstract. We present the results obtained in the OAEI 2013 campaign by our ontology matching system LogMap and its 'lightweight" variant called LogMapLt. The LogMap project started in January 2011 with the objective of developing a scalable and logic-based ontology matching system. This is our fourth participation in the OAEI and the experience has so far been very positive.

1 Presentation of the system

LogMap [11, 12] is a highly scalable ontology matching system with built-in reasoning and inconsistency repair capabilities. LogMap also supports (real-time) user interaction during the matching process, which is essential for use cases requiring very accurate mappings. LogMap is one of the few ontology matching system that (1) can efficiently match semantically rich ontologies containing tens (and even hundreds) of thousands of classes, (2) incorporates sophisticated reasoning and repair techniques to minimise the number of logical inconsistencies, and (3) provides support for user intervention during the matching process. LogMap is also available as a "lightweight" variant called LogMapLt, which essentially only applies (efficient) string matching techniques.

LogMap relies on the following elements, which are keys to its favourable scalability behaviour (see [11, 12] for details).

Lexical indexation. An inverted index is used to store the lexical information contained in the input ontologies. This index is the key to efficiently computing an initial set of mappings of manageable size. Similar indexes have been successfully used in information retrieval and search engine technologies [4].

Logic-based module extraction. The practical feasibility of unsatisfiability detection and repair critically depends on the size of the input ontologies. To reduce the size of the problem, we exploit ontology modularisation techniques. Ontology modules with well-understood semantic properties can be efficiently computed and are typically much smaller than the input ontology (e.g. [7]).

Propositional Horn reasoning. The relevant modules in the input ontologies together with (a subset of) the candidate mappings are encoded in LogMap using a Horn propositional representation. Furthermore, LogMap implements the classic Dowling-Gallier algorithm for propositional Horn satisfiability [8, 10]. Such encoding, although incomplete, allows LogMap to detect unsatisfiable classes soundly and efficiently.

Axiom tracking and greedy repair. LogMap extends Dowling-Gallier's algorithm to track all mappings that may be involved in the unsatisfiability of a class. This extension is key to implementing a highly scalable repair algorithm.

Semantic indexation. The Horn propositional representation of the ontology modules and the mappings are efficiently indexed using an interval labelling schema [1] — an optimised data structure for storing directed acyclic graphs (DAGs) that significantly reduces the cost of answering taxonomic queries [6, 17]. In particular, this semantic index allows us to answer many entailment queries over the input ontologies and the mappings computed thus far as an index lookup operation, and hence without the need for reasoning. The semantic index complements the use of the propositional encoding to detect and repair unsatisfiable classes.

1.1 Adaptations made for the 2013 evaluation

The new version of LogMap also integrates MORe [2, 3] as OWL 2 reasoner. MORe is a modular reasoner which combines a fully-fledged (and slower) reasoner with a profile specific (and more efficient) reasoner.

LogMap's algorithm described in [11–13] has also been adapted to meet the requirements of the new interactive matching track which uses an *Oracle* as expert user.

LogMap aims at making a reduced number of calls to the Oracle, i.e.: only those borderline mappings that cannot be clearly included or excluded with automatic heuristics. For each call to the Oracle, LogMap applies conflict and ambiguity based heuristics (see [12] for details) to reduce the remaining number of calls (i.e. mappings).

Additionally, the interactive algorithm described in [12] has been slightly extended to include object and data properties in the process.

1.2 Link to the system and parameters file

LogMap is open-source and released under GNU Lesser General Public License 3.0.[1] Latest components and source code are available from the LogMap's Google code page: `http://code.google.com/p/logmap-matcher/`.

LogMap distributions can be easily customized through a configuration file containing the matching parameters.

LogMap, including support for interactive ontology matching, can also be used directly through an AJAX-based Web interface: `http://csu6325.cs.ox.ac.uk/`. This interface has been very well received by the community, with more than 900 requests processed so far coming from a broad range of users.

1.3 Modular support for mapping repair

Only very few systems participating in the OAEI 2013 competition implement repair techniques. As a result, existing matching systems (even those that typically achieve very high precision scores) compute mappings that lead in many cases to a large number of unsatisfiable classes.

We believe that these systems could significantly improve their output if they were to implement repair techniques similar to those available in LogMap. Therefore, with

[1] `http://www.gnu.org/licenses/`

Table 1: Results for Benchmark track.

System	biblio 2012			biblioc		
	P	R	F	P	R	F
LogMap	1.00	0.47	0.64	0.73	0.42	0.53
LogMapLt	0.95	0.50	0.66	0.43	0.50	0.46

Table 2: Results for Anatomy track.

System	P	R	F	Time (s)
LogMap	0.918	0.846	0.881	13
LogMapLt	0.962	0.728	0.829	7

the goal of providing a useful service to the community, we have made LogMap's ontology repair module (LogMap-Repair) available as a self-contained software component that can be seamlessly integrated in most existing ontology matching systems [14].

2 Results

In this section, we present a summary of the results obtained by LogMap and LogMapLt in the OAEI 2013 campaign. Please refer to `http://oaei.ontologymatching.org/2013/results/index.html` for complete results.

2.1 Benchmark track

Ontologies in this track have been synthetically generated. The goal of this track is to evaluate the matching systems in scenarios where the input ontologies lack important information (e.g., classes contain no meaningful URIs or labels) [9].

Table 1 summarises the average results obtained by LogMap and LogMapLt. Note that the computation of candidate mappings in LogMap and LogMapLt heavily relies on the similarities between the vocabularies of the input ontologies; hence, there is a direct negative impact in the cases where the labels are replaced by random strings.

2.2 Anatomy track

This track involves the matching of the Adult Mouse Anatomy ontology (2,744 classes) and a fragment of the NCI ontology describing human anatomy (3,304 classes). The reference alignment has been manually curated [19], and it contains a significant number of non-trivial mappings.

Table 2 summarises the results obtained by LogMap and LogMapLt. LogMap ranked 3rd among the systems not using specialised background knowledge. Regarding mapping coherence, only two tools (including LogMap) generated coherent alignments. The evaluation was run on a server with 3.46 GHz (6 cores) and 8GB RAM.

Table 3: Results for Conference track.

System	RA1 reference			RA2 reference			Time (s)
	P	R	F	P	R	F	
LogMap	0.80	0.59	0.68	0.76	0.54	0.63	24
LogMapLt	0.73	0.50	0.59	0.68	0.45	0.54	21

Table 4: Results for Library track.

System	P	R	F	Time (s)
LogMap	0.777	0.645	0.705	99
LogMapLt	0.646	0.771	0.703	20

2.3 Conference track

The Conference track uses a collection of 16 ontologies from the domain of academic conferences [18]. These ontologies have been created manually by different people and are of very small size (between 14 and 140 entities). The track uses two reference alignments RA1 and RA2. RA1 contains manually curated mappings between 21 ontology pairs, while RA2 also contains composed mappings based on the alignments in RA1.

Table 3 summarises the average results obtained by LogMap and LogMapLt. The last column represents the total runtime on generating all 21 alignments. Tests were run on a laptop with Intel Core i5 2.67GHz and 8GB RAM. LogMap ranked 3rd and produced coherent alignments.

2.4 Multifarm track

This track is based on the translation of the OntoFarm collection of ontologies into 9 different languages [16]. Both LogMap and LogMapLt, as expected, obtained poor results since they do not implement specific multilingual techniques.

2.5 Library track

The library track involves the matching of the STW thesaurus (6,575 classes) and the TheSoz thesaurus (8,376 classes). Both of these thesauri provide vocabulary for economic and social sciences. Table 4 summarises the results obtained by LogMap and LogMapLt. The track was run on a computer with one 2.4GHz core with 7GB RAM and 2 cores. LogMap ranked 5th in this track.

2.6 Interactive matching track

The interactive track is based on the conference track and it uses the RA1 reference alignment as Oracle. Table 5 summarizes the obtained results by LogMap with and without the interactive mode activated. LogMap with interactivity (LogMap-Int) improved both the average Precision and Recall wrt LogMap with the interactive mode

Table 5: Results for Interactive track.

System	RA1 reference			Calls	Time (s)
	P	R	F		
LogMap	0.80	0.59	0.68	0	24
LogMap-Int	0.90	0.64	0.73	91	27

Table 6: Summary results for the Large BioMed track

System	Total Time (s)	P	R	F	Inc. Degree.
LogMap-BK	2,391	0.904	0.700	0.785	0.013%
LogMap	2,485	0.910	0.689	0.780	0.015%
LogMapLt	371	0.874	0.517	0.598	34.1%

deactivated, and it only performed 91 calls to the Oracle along the 21 matching tasks (i.e. less than 5 questions per ontology pair).

Not that, although LogMap-Int ranked 1st in the interactive matching track, it could not outperform the best tool in the conference track, which obtained a F-measure of 0.74 (wrt the RA1 reference alignment). Nevertheless, there is still room for improvement and we aim at implementing more sophisticated matching and interactive techniques.

2.7 Large BioMed track

This track consists of finding alignments between the Foundational Model of Anatomy (FMA), SNOMED CT, and the National Cancer Institute Thesaurus (NCI). These ontologies are semantically rich and contain tens of thousands of classes. UMLS Metathesaurus [5] has been selected as the basis for the track reference alignments.

In this track LogMap has been evaluated with two variants: LogMap and LogMap-BK. LogMap-BK uses normalisations and spelling variants from the general (biomedical) purpose UMLS Lexicon,[2] while LogMap has this feature deactivated.

Table 6 summarises the results obtained by LogMap and LogMapLt. The table shows the total time in seconds to complete all tasks in the track and averages for Precision, Recall, F-measure and Incoherence degree. The track was run on a server with 16 CPUs and allocating 15GB RAM.

Regarding mapping coherence, only two tools (including LogMap and its variant LogMap-BK) generated almost coherent alignments. LogMap-BK ranked 3rd among the systems not using specialised background knowledge and 1st among the systems computing almost coherent alignments. LogMapLt was the fastest to complete all tasks.

[2] `http://www.nlm.nih.gov/pubs/factsheets/umlslex.html`

Table 7: Results for Instance matching track.

System	RDFT		
	P	R	F
LogMap	0.922	0.746	0.812

2.8 Instance matching

This year only LogMap participated in the Instance Matching track. The dataset was based on dbpedia ontology[3] and included controlled transformations in the data (i.e. value and structure transformations).

Table 7 summarises the average results obtained by LogMap. The results are quite promising considering that LogMap does not implement sophisticated instance matching techniques. Furthermore, LogMap outperformed one of the participating tools specialised in instance matching.

Adaptations to the original dataset The original provided dataset was preprocessed in order to be properly interpreted by the OWL API and to avoid inconsistencies when reasoning. Next we summarise the performed changes:

- *Added import of dbpedia:* The dataset (ABOX) is based on dbpedia, however, the dbpedia ontology was not included as TBOX. Hence the OWL API was interpreting the instance entities of the dataset as "annotations" and not as "OWL named individuals". Furthermore, by adding dbpedia TBOX to the datasets, an OWL 2 reasoner could be used to infer the corresponding class type for each instance.
- *Minor changes to dbpedia:* The integration of the provided dataset (ABOX) and dbpedia (TBOX) resulted in an inconsistent knowledge base. The inconsistencies were due to some data property assertion axioms pointing to the incorrect datatype and a functional datatype property which was used in two or more data property assertion axioms with the same subject. To avoid these inconsistencies dbpedia was slightly modified by removing the range and the functionality of the corresponding data properties.
- *Added additional object properties:* The dataset also references the object properties "curriculum", "places" and "label" which are not included in the dbpedia ontology. Hence, these properties has been explicitly declared as OWL object properties.
- *Removal of invalid characters:* the dataset also included some characters that could not be processed by the OWL API and Protégé (e.g. \u).

3 General comments and conclusions

3.1 Comments on the results

LogMap, apart from Benchmark and Multifarm tracks for which does not implement specific techniques, has been one of the top systems in the OAEI 2013. Furthermore,

[3] `http://dbpedia.org/`

it has also been one of the few systems implementing repair techniques and providing (almost) coherent mappings in all tracks.

LogMap's main weakness relies on the fact that the computation of candidate mappings is based on the similarities between the vocabularies of the input ontologies; hence, there is a direct negative impact in the cases where the ontologies are lexically disparate or do not provide enough lexical information (e.g. Benchmark and Multifarm).

3.2 Discussions on the way to improve the proposed system

LogMap is now a stable and mature system that has been made available to the community. There are, however, many exciting possibilities for future work. For example we aim at exploiting background knowledge to be competitive in the Multifarm track and to improve the performance in the other tracks.

3.3 Comments on the OAEI test cases

The number and quality of the OAEI tracks is growing year by year. However, there is always room for improvement:

Comments on the OAEI instance matching track. I consider the 2012 IIMB Instance Matching track more challenging, from the logical point of view, than the current task. The IIMB dataset included a TBOX and the controlled transformations also involved changes on the instance class types. Thus the application of logic based techniques had an important impact since lexically similar instances belonging to two disjoint class types should not be matched.

Comments on the OAEI interactive matching track. The new interactive track has been a very important step forward in the OAEI, however, larger and more challengings tasks should be included. For example, matching tasks (e.g. anatomy and largebio) where the number of questions to the expert user or Oracle may be critical. Furthermore, it is quite unlikely that the expert user will be perfect, thus, the interactive matching track should also consider the evaluation of several Oracles with different error rates such as the evaluation performed in [12].

Comments on the OAEI largebio track. One of the objectives of the largebio track is the creation of a "silver standard" reference alignment by harmonising the output of the different participating systems. In the next OAEI campaign it would be very interesting to actively use this "silver standard" in the construction of the track's reference alignment.

3.4 Comments on the OAEI 2013 measures

Although the *mapping coherence* is a measure already used in the OAEI we consider that is not given yet the required weight in the evaluation. Thus, developers focus on creating matching systems that maximize the F-measure but they disregard the impact of the generated output in terms of logical errors. As a result, even highly precise mappings lead to a large number of unsatisfiable classes.

Thus, we encourage ontology matching system developers to develop their own repair techniques or to use state-of-the-art techniques such as Alcomo [15] and LogMap-Repair (see Section 1.3), which have shown to work well in practice [14].

Acknowledgements

This work was supported by the Seventh Framework Program (FP7) of the European Commission under Grant Agreement 318338, "Optique", the Royal Society, and the EPSRC projects Score!, ExODA and MaSI^3.

References

1. Agrawal, R., Borgida, A., Jagadish, H.V.: Efficient management of transitive relationships in large data and knowledge bases. In: ACM SIGMOD Conf. on Management of Data. pp. 253–262 (1989)
2. Armas Romero, A., Cuenca Grau, B., Horrocks, I.: MORe: Modular Combination of OWL Reasoners for Ontology Classification. In: Int'l Sem. Web Conf. (ISWC). pp. 1–16 (2012)
3. Armas Romero, A., Cuenca Grau, B., Horrocks, I., Jiménez-Ruiz, E.: MORe: a Modular OWL Reasoner for Ontology Classification. In: OWL Reasoning Evaluation (ORE) (2013)
4. Baeza-Yates, R.A., Ribeiro-Neto, B.A.: Modern Information Retrieval. ACM Press / Addison-Wesley (1999)
5. Bodenreider, O.: The unified medical language system (UMLS): integrating biomedical terminology. Nucleic Acids Research 32, 267–270 (2004)
6. Christophides, V., Plexousakis, D., Scholl, M., Tourtounis, S.: On labeling schemes for the Semantic Web. In: Int'l World Wide Web (WWW) Conf. pp. 544–555 (2003)
7. Cuenca Grau, B., Horrocks, I., Kazakov, Y., Sattler, U.: Modular reuse of ontologies: Theory and practice. J. Artif. Intell. Res. 31, 273–318 (2008)
8. Dowling, W.F., Gallier, J.H.: Linear-time algorithms for testing the satisfiability of propositional Horn formulae. J. Log. Prog. 1(3), 267–284 (1984)
9. Euzenat, J., Rosoiu, M.E., dos Santos, C.T.: Ontology matching benchmarks: Generation, stability, and discriminability. J. Web Sem. 21, 30–48 (2013)
10. Gallo, G., Urbani, G.: Algorithms for testing the satisfiability of propositional formulae. J. Log. Prog. 7(1), 45–61 (1989)
11. Jiménez-Ruiz, E., Cuenca Grau, B.: LogMap: Logic-based and Scalable Ontology Matching. In: Int'l Sem. Web Conf. (ISWC). pp. 273–288 (2011)
12. Jiménez-Ruiz, E., Cuenca Grau, B., Zhou, Y., Horrocks, I.: Large-scale interactive ontology matching: Algorithms and implementation. In: European Conf. on Artif. Intell. (ECAI). pp. 444–449 (2012)
13. Jiménez-Ruiz, E., Grau, B.C., Horrocks, I.: LogMap and LogMapLt results for OAEI 2012. In: Proceedings of the 7th International Workshop on Ontology Matching (2012)
14. Jimenez-Ruiz, E., Meilicke, C., Cuenca Grau, B., Horrocks, I.: Evaluating mapping repair systems with large biomedical ontologies. In: 26th Description Logics Workshop (2013)
15. Meilicke, C.: Alignment Incoherence in Ontology Matching. Ph.D. thesis, University of Mannheim (2011)
16. Meilicke, C., Castro, R.G., Freitas, F., van Hage, W.R., Montiel-Ponsoda, E., de Azevedo, R.R., Stuckenschmidt, H., Šváb-Zamazal, O., Svátek, V., Tamilin, A., Trojahn, C., Wang, S.: MultiFarm: a benchmark for multilingual ontology matching. J. Web Sem. (2012)
17. Nebot, V., Berlanga, R.: Efficient retrieval of ontology fragments using an interval labeling scheme. Inf. Sci. 179(24), 4151–4173 (2009)
18. Šváb, O., Svátek, V., Berka, P., Rak, D., Tomášek, P.: OntoFarm: towards an experimental collection of parallel ontologies. In: Int'l Sem. Web Conf. (ISWC). Poster Session (2005)
19. Zhang, S., Mork, P., Bodenreider, O.: Lessons learned from aligning two representations of anatomy. In: Conf. on Princliples of Knowledge Representation and Reasoning (KR) (2004)

Summary of the MaasMatch participation in the OAEI-2013 campaign

Frederik C. Schadd, Nico Roos

Maastricht University, The Netherlands
{frederik.schadd, roos}@maastrichtuniversity.nl

Abstract. This paper summarizes the results of the third participation of the MaasMatch system in the Ontology Alignment Evaluation Initiative (OAEI) competition. Several additions were made to the MaasMatch system with the intent of rectifying its limitations, as observed during the previous OAEI campaign. The extent of the additions and their effect on the individual dataset will be elaborated.

1 Presentation of the system

MaasMatch is a ontology mapping system with the initial focus of fully utilizing the information located in the concept names, labels and descriptions in order to produce a mapping between two ontologies. This was achieved through the utilization of syntactic similarities and virtual documents, which can also be used as a disambiguation method for the improvement of lexical similarities [3,4]. The results of the benchmark track in the OAEI 2012 competition [1] substantiated the evident conclusion that when the naming and annotation features of an ontology are not present or distorted, the system produces unsatisfactory mappings. Several additions have been made to rectify this issue, the details of which are presented in the next subsection.

1.1 Specific techniques used

The current version of MaasMatch utilizes a wider spectrum of similarity techniques than past versions. The overall setup in which these are used can be seen in Figure 1.

When given two input ontologies, these are parsed into an OWL format to allow further processing. For each configured similarity measure the pairwise similarities between the ontology concepts are computed, which are then combined into a similarity cube. The different similarity values are then aggregated, such that these can be used as initial vertex weights for the similarity flooding procedure [2]. The vertex weights are propagated until they converge, with a limit of 10 iteration configured to deal with situation where the values do not converge. However, in our own preliminary evaluations we found that on average only 4 iterations were needed until the values converged. Using the resulting vertex weights the results alignment is extracted.

The previous version of MaasMatch utilized four similarity measures which rely on the names, labels and comments of the concept definitions. One of which is a syntactical similarity (Jaccard), two a type of structural similarity (Name-Path, Virtual Document

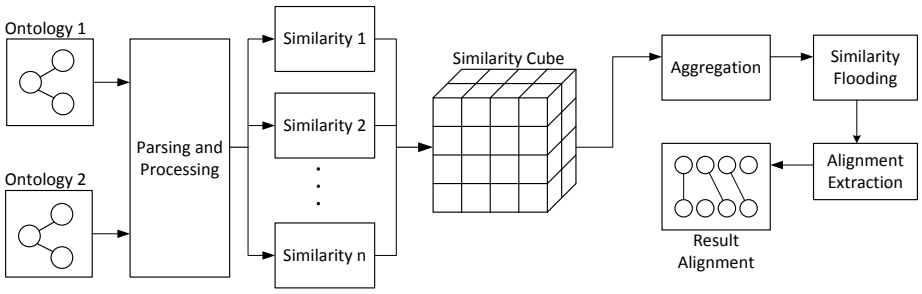


Fig. 1. Visualization of the MaasMatch architecture.

Similarity) and one a lexical similarity. The details of these can be found in the report paper of the previous year [4].

The aim of this year's development was to increase the utilization of other ontology feature, with the hope that the resulting system will be more robust to distortions and produce alignments of better quality. To achieve this, the system now also utilizes a internal structural similarity and a instance similarity, while also a similarity flooding procedure after the aggregation step in order to discover additional mappings.

When comparing classes, the internal structural similarity gathers all properties whose inferred domains correspond with the given classes. Then the a maximum correspondence between these two sets of properties are computed according to the similarities between the data-types of the properties. Comparing properties involves a combinations of two similarities. First, the data-types of the properties themselves are compared. Second, the other properties in the immediate neighbourhood are compared using the maximum correspondence of the two property sets.

The instance similarity compares the asserted instances of concepts using information retrieval techniques. For classes, all instances that are asserted to belong to their corresponding class are gathered, where all values that are asserted in each of these instances are collected in a document. For properties, all values that are asserted using these properties are gathered in a document instead. The similarity between classes and properties is then determined by the similarity of their instance documents.

It is important to note that with the attempt of making the system more robust by adding more similarities and procedures, the runtime of the system will be negatively impacted, especially since the full similarity cube is computed. Also, the similarity flooding procedure entails the process of computing a pairwise connectivity graph of the two input ontologies. This means that, given two large input ontologies, the resulting graph will have many nodes and vertices, which will have to be stored in memory. Hence, the memory requirements for large matching tasks will be quite high. Given both of these issues, future endeavours will likely entail some methodologies to reduce the memory requirements and the amount of comparisons between concepts.

1.2 Adaptations made for the evaluation

For this year's evaluation we have re-introduced a alignment cut-off based on preliminary evaluations, since not all tracks perform a thresholding procedure during the evaluation, yielding results that do not reflect the alignment quality. For the similarity flooding procedure the vertex weights are updated using the increment method C [2]. We also added secondary matcher, based on our anchor-profile approach [5], to the bridge for the evaluation using partial input alignments. Unfortunately, this year's competition did not run this specific sub-track, meaning that we were not able to observe its performance in the field. The functionality however is still available.

1.3 Link to the system and parameters file

MaasMatch and its corresponding parameter file is available on the SEALS platform and can be downloaded at http://www.seals-project.eu/tool-services/browse-tools.

2 Results

This section presents the evaluation of the OAEI2013 results achieved by MaasMatch. Evaluations utilizing ontologies exceeding the supported complexity range, such as the Library track, will be excluded from the discussion for the sake of brevity.

2.1 Benchmark

The benchmark track consists of synthetic datasets, where an ontology is procedurally altered in various ways and to different extents, in order to see under what circumstances a system can still produce good results. Table 1 displays the results on the two evaluated datasets:

Test Set	Precision	F-Measure	Recall
biblio2	0.6	0.6	0.6
biblioc	0.84	0.69	0.59

Table 1. Harmonic means of the benchmark test sets.

Overall, we can see an improvement over last year's performance [4]. While in the previous year the highest achieved f-measure was at 0.6 among the different sets, this year this is actually the lowest achieved f-measure, with the system scoring significantly higher on the *biblioc* set.

Unfortunately, according to the experimenter the system did not produce any output for the tasks 254 and higher. Upon hearing about this issue, we evaluated the tool locally using the SEALS client to replicate the issue, using both the client from last year and the current 'v4i' version. With both evaluation clients, MaasMatch ran normally and

produced output for all tasks of the test sets. Furthermore, we also observed that other systems, namely LogMap, ServOMap and MapSSS, also had these issues, even though these and also MaasMatch performed without error in last year's competition. From this we must conclude that this error stems from the SEALS platform, and given a proper evaluation the MaasMatch system could have performed much higher.

In addition to this evaluation, another benchmark run was performed using the *onlira* ontology, with the intention of performing an evaluation for which the participants do have access to the dataset in advance. While the results of this evaluation will likely not be published, due to many participating systems not being able to cope with the matching task, it is interesting to see how well MaasMatch performed with this base ontology:

Test Set	Precision	F-Measure	Recall
onlira	0.94	0.74	0.61

Table 2. Harmonic means of the benchmark test set using the onlira base ontology.

From Table 2 we can see that the performance of MaasMatch is consistent with the performance of the standard benchmark set, with a higher emphasis on precision than recall.

2.2 Anatomy

The anatomy dataset consists of a single matching task, which aligns a biomedical ontology describing the anatomy of a human to an ontology describing the anatomy of a mouse. Unique aspects about this ontology are their large sizes and the fact that they contains specialized vocabulary which is not often found in non-domain specific thesauri. Table 3 displays the results of this dataset.

Test Set	Precision	F-Measure	Recall
mouse-human	0.359	0.409	0.476

Table 3. Results of the anatomy data set.

This year we can observe a drop in performance, specifically with regard to the recall of the alignment. The most likely reason behind this is that this dataset does not contain the features that the newly added similarities use, namely instances and properties, such that the distinction between the positive and negative correspondences becomes smaller. The overall similarity values will be lower, since two similarities will not produce any positive values, such that it is more likely that correct correspondences will be dismissed due to their similarity value being lower than the re-introduced threshold.

2.3 Conference

The confidence data set consists of numerous real-world ontologies describing the domain of organizing scientific conferences. The results of this track can be seen in Table 4.

Test Set	Precision	F-Measure	Recall
ra1	0.29	0.38	0.54
ra2	0.29	0.37	0.53

Table 4. Results of the conference data set.

Similarly tot he anatomy dataset, we observe that the additions to the system had a detrimental effect to the alignment quality, in this case with more pronounced effects on the precision. Similarly to the anatomy track, this dataset also does not contain instances, yielding the instance similarity redundant. However, properties are present, yielding the interesting observation that while the internal structural similarity showed itself to be of positive influence on the benchmark dataset, its basic intuition which it exploits is not applicable to the conference dataset.

2.4 Multifarm

The Multifarm data set is based on ontologies from the OntoFarm data set, that have been translated into a set of different languages in order to test the multi lingual capabilities of a specific system. The results of MaasMatch on this track can bee seen in Table 5.

	cn-cz	cn-de	cn-en	cn-es	cn-fr	cn-nl	cn-pt	cn-ru	cz-de	cz-en	cz-es	cz-fr	cz-nl	cz-pt	cz-ru	de-en	de-es	de-fr
P	.13	.11	.12	.13	.12	.11	.14	.13	.15	.16	.15	.15	.16	.16	.10	.20	.15	.16
F	.12	.11	.12	.13	.12	.11	.13	.12	.14	.16	.15	.14	.15	.15	.10	.19	.14	.15
R	.12	.10	.11	.12	.11	.10	.12	.12	.14	.15	.14	.13	.14	.14	.10	.18	.14	.14
	de-nl	de-pt	de-ru	en-es	en-fr	en-nl	en-pt	en-ru	es-fr	es-nl	es-pt	es-ru	fr-nl	fr-pt	fr-ru	nl-pt	nl-ru	pt-ru
P	.20	.15	.12	.18	.20	.19	.18	.14	.19	.17	.22	.12	.17	.19	.12	.15	.12	.12
F	.19	.14	.12	.17	.19	.18	.17	.14	.18	.16	.21	.12	.17	.18	.12	.14	.12	.11
R	.18	.14	.11	.16	.18	.17	.17	.13	.17	.15	.20	.11	.16	.17	.11	.14	.11	.11

Table 5. Results of the multifarm dataset.

Compared to the results of the previous year [1], we can see an overall improvement on nearly every task. While in the previous year a very large portion of the tasks resulted in an f-measure of 0.1 or below, this year we can see that in all tasks MaasMatch produced an alignment with an f-measure of .1 or greater. While we can observe

that the addition of language independent similarities did aid the performance of our system, further development is still required in order to reliably produce alignments of significant quality.

3 General comments

3.1 Comments on the results

This year we have observed mixed results for MaasMatch. While the performance of some tracks has seen improvements thanks to our modifications (benchmark, multifarm), these came at a cost of performance in other tracks (conference, anatomy).

3.2 Discussions on the way to improve the proposed system

This year we added a wider range of similarities in order to make the system more robust. Unfortunately, this caused a detriment in performance for mapping tracks which did not contain the ontology features which the new similarities exploit. From this, we can conclude that an important improvement to our system would be the automatic detection of ontology features and automatic selection of appropriate similarities.

Furthermore, the runtime of MaasMatch is too high in order to realistically tackle huge mapping tasks. This is mostly due to the computation of the full similarity cube. To remedy this, another addition could be some kind of partitioning method, such that larger mapping tasks also become feasible.

We did see improvements in the multifarm dataset. However, this was achieved without any preprocessing step on the ontologies. An obvious improvement on this end would be the addition of a preprocessing step which automatically detects the natural language in which the ontology is written and translating it to a standard lingua-franca, for instance English.

3.3 Comments on the OAEI 2013 procedure

This year's run on the benchmark trajectory saw numerous systems, including MaasMatch, consistently having troubles producing alignments. While the participants have been notified before the results publication of this issue, they were left with only a limited amount of time to address the issue, while the organizers did not investigate the issue themselves at all. This is especially troubling since our own local evaluations using the SEALS clients did not result in these errors, giving a strong indication that the problem lies within the SEALS infrastructure, thus unfairly casting the affected systems in a negative light. We suggest to re-introduce a three week testing period to the evaluation procedure, similar to the 2011 OAEI competition. That way participants can be notified sufficiently early about potential technical issues and giving them enough time to address these.

3.4 Comments on the OAEI 2013 measures

The evaluation of ontology mapping quality is commonly done using the standard measures of precision, recall and f-measure, these methods do not take into account the confidence values associated with the individual correspondences. Recently, two techniques have seen deployment to take the confidences into account, being thresholding and confidence weighted measures. While these developments are appreciated, it is important to communicate which of these techniques have been applied in the evaluation process in order to facilitate the accurate replication of evaluation results.

4 Conclusion

This paper describes the 2013 participation of MaasMatch in the OAEI campaign. We briefly describes the overall setup of the system and the new techniques which were added to it for this evaluation. Those techniques were mainly aimed at improving the robustness of the system by utilizing a more varied range of ontological features. While this main goal has been achieved, evidenced by higher performances in the benchmark and multifarm evaluation, this surprisingly came to the detriment in performance in the remaining tracks, where the newly exploited types of features are not present in the test ontologies. We conclude that, now that MaasMatch possesses a varied spectrum of similarities, there needs to be computation step before the similarity calculation, which analyses the input ontologies with regards to its features. According to this analysis, only appropriate similarities would then be selected for the mapping procedure.

References

1. J.L. Aguirre, B.C. Grau, K. Eckert, J. Euzenat, A. Ferrara, R.W. van Hague, L. Hollink, E. Jimenez-Ruiz, C. Meilicke, A. Nikolov, D. Ritze, P. Shvaiko, O. Svab-Zamazal, C. Trojahn, and B. Zapilko. Results of the ontology alignment evaluation initiative 2012. In *Proc. of the 7th ISWC workshop on ontology matching*, pages 73–115, 2012.
2. Sergey Melnik, Hector Garcia-Molina, and Erhard Rahm. Similarity flooding: A versatile graph matching algorithm and its application to schema matching. In *Data Engineering, 2002. Proceedings. 18th International Conference on*, pages 117–128. IEEE, 2002.
3. F.C. Schadd and N. Roos. Coupling of wordnet entries for ontology mapping using virtual documents. In *Proceedings of The Seventh International Workshop on Ontology Matching (OM-2012) collocated with the 11th International Semantic Web Conference (ISWC-2012)*, pages 25–36, 2012.
4. F.C. Schadd and N. Roos. Maasmatch results for oaei 2012. In *Proceedings of The Seventh ISWC International Workshop on Ontology Matching*, pages 160–167, 2012.
5. F.C. Schadd and N. Roos. Anchor-profiles for ontology mapping with partial alignments. In *Proceedings of the 12th Scandinavian AI conference (SCAI)*, 2013. Accepted paper.

StringsAuto and MapSSS Results for OAEI 2013

Michelle Cheatham and Pascal Hitzler

Kno.e.sis Center, Wright State University, Dayton, OH, USA
{cheatham.7, pascal.hitzler}@wright.edu

Abstract. StringsAuto and MapSSS are two closely related ontology alignment systems. The StringsAuto matcher seeks to explore the limits of a syntactic-only approach to alignment. The MapSSS system then expands on this work by embedding the syntactic matching of StringsAuto within a more complete alignment system that also makes use of semantic and structural information. In this paper we describe the basic operation of the two systems and discuss their performance in the OAEI 2013 evaluation.

1 Presentation of the system

1.1 State, purpose, general statement

The vast majority of ontology alignment systems use some form of string similarity metric. Our overall goal with StringsAuto and MapSSS is to explore the importance of the choice of a particular string metric. StringsAuto consists *only* of string metrics, while MapSSS uses strategically chosen string metrics within the context of a more fully-featured alignment system.

In [1] we analyzed the performance of eleven string similarity metrics (TF-IDF, Soft TF-IDF, Jaccard, Soft Jaccard, Exact Match, Longest Common Substring, Jaro Winkler, Levenstein, Monge Elkan, N-gram, and Stoilos) on different types of ontologies (standard, biomedical, and multi-lingual). In addition, we experimented with the use of common string pre-processing methods (tokenization, normalization, stemming, stop word removal, synonyms, and translations). StringsAuto grew out of this work. Its purpose is to investigate string similarity metrics as applied to ontology alignment. In particular, it is of interest to compare the performance of this system to that of the very basic string-based matchers used as baselines for some of the OAEI tracks.

The MapSSS system was involved in previous OAEI evaluations. The three S's in MapSSS stand for syntactic, semantic, and structural, which are the three types of metrics used by the system. This year MapSSS has been augmented with a different semantic metric, based on Google queries, and modified to use the same syntactic metric selection strategy as StringsAuto. We are interested in comparing the performance of this version to that of previous years.

1.2 Specific techniques used

Based on the results of the string metric analysis in [1], we produced a set of guidelines for choosing string metrics and preprocessing strategies based on the characteristics of

the ontologies to be aligned and whether precision or recall is of primary concern. More information can be found in the referenced paper.

- Precision
  - Less than two words per label: **Jaro-Winkler 1, 1**
  - Two or more words per label
    - Synonyms: **Soft Jaccard .2, .5 with Levenstein .9 base metric**
    - No synonyms: **Soft Jaccard 1, 1 with Levenstein .8 base metric**
- Recall
  - Less than two words per label: **TF-IDF .8, .8**
  - Two or more words per label
    - Synonyms: **Soft TF-IDF .5, .8 with Jaro-Winkler .8 base metric**
    - Different Languages: **Soft TF-IDF 0, .7 with Jaro-Winkler .9 base metric**
    - Other: **Soft TF-IDF .8, .8 with Jaro-Winkler .8 base metric**

StringsAuto simply chooses two metrics based on these heuristics: one that prioritizes precision and another that focuses on recall. Each of these metrics is run (in series) and the resulting alignment is used as-is. When a metric is run, every label in the first ontology is compared to every label in the second ontology, and the results of the similarity metric are stored in a matrix. The stable marriage algorithm is then run over the matrix, and any matches greater than a threshold value are included in the alignment. If either entity involved in a match has already been used in the alignment, that match is ignored. This means that all alignments generated are 1:1 and the recall-centric metric cannot override the precision-centric method.

MapSSS uses the same syntactic metric selection strategy as StringsAuto. In addition, it uses a semantic metric based on Google queries. When considering two labels, A from the first ontology and B from the second, this metric queries Google for the phrase A definition. It then searches the snippets on the first page of results for B. If B is found, the metric returns true, otherwise it returns false. If this metric returns true in both directions (i.e. googleMetric(A, B) and googleMetric(B, A) are both true) then the mapping is added to the alignment. Finally, MapSSS also contains a structural metric. If all of the entities in the direct neighborhood of two classes are mapped to one another, then those classes are mapped. This approach is sometimes called "flooding." The structural metric is run repeatedly until no new mappings are created.

1.3 Adaptations made for the evaluation

No significant adaptations were made for the OAEI evaluation. In particular, the heuristics used to select the string similarity metrics do not break cleanly along the different OAEI tracks. Some possibly relevant details of these alignment systems include:

- Neither alignment system attempts to align properties or instances; only classes are considered. Our previous work has shown that string similarity metrics perform particularly poorly on property labels.

– The systems determine the language of an ontology by randomly selecting a sample of ten entity labels and sending them to Google Translate. This assumes each ontology involves predominately one language.
– To determine if an ontology has embedded synonyms, the alignment systems look for tags involving the word "synonym." This is to some extent tailored to the anatomy track of the OAEI.
– The semantic metric within MapSSS uses the Google API. There is a limit on the number of queries that can be submitted using this API each day, as well as a monthly cap. This causes problems for some of the larger ontology alignment problems within the OAEI evaluation. We attempted to cache the query results to alleviate this problem, but the SEALS server configuration made this unworkable (we would need to be able to write to a file during execution and have this file available during subsequent runs of the program).

1.4 Link to the system and parameters file

StringsAuto is available at http://pascal-hitzler.de/resources/Strings.zip and MapSSS is available at http://pascal-hitzler.de/resources/MapSSS.zip.

2 Results

Development and testing of StringsAuto and MapSSS focused primarily on the conference, anatomy, and multiform test sets, but we present results for all tracks in which alignments were produced.

2.1 anatomy

StringsAuto achieved an f-measure of 0.835 on this test set (see Table 1). This placed it 7th out of 21 participating systems. In particular, the results produced by StringsAuto were significantly better than those of StringsEquiv, a basic string equality matcher.

Interestingly, the performance of MapSSS did not differ greatly from StringsAuto. When compared to the performance of the 2012 version of MapSSS, we see that the precision has dropped while the recall has increased slightly. Notably, the recall+ measure is significantly higher with the current version, which makes use of a string similarity metric specifically chosen to enhance recall and semantic information gleaned from Google queries.

2.2 conference

The (ra2) results of StringsAuto and MapSSS on the conference track are shown in Table 2. StringsAuto outperformed both StringsEquiv and edna (an edit distance metric with a threshold of .82). Overall, StringsAuto was 6th out of 27 alignment systems in terms of f-measure, while edna was 11th and StringsEquiv was 22nd. The 2013 version of MapSSS significantly outperformed its predecessor but fell slightly short of StringsAuto.

Table 1. Anatomy Track Results

Alignment System	F-measure	Precision	Recall	Recall+
StringsEquiv	.766	.997	.622	0
StringsAuto	.835	.899	.779	.433
MapSSS 2013	.828	.898	.768	.443
MapSSS 2012	.831	.935	.747	.337

Table 2. Conference Track Results

Alignment System	F-measure	Precision	Recall
StringsEquiv	.52	.76	.39
edna	.55	.73	.44
StringsAuto	.60	.74	.50
MapSSS 2013	.58	.77	.46
MapSSS 2012	.46	.47	.46

2.3 multifarm

There was a problem running both StringsAuto and MapSSS on the multifarm test set. While both systems were able to produce alignments, they had to fall back to their non-translating versions due to a problem reaching the Google Translate service from the OAEI test server. We attempted to fix this during the evaluation by caching the results of the translation queries, but this did not work, possibly due to write restrictions on the server itself (we need to be able to write to a file that will persist between different executions of the program). Here we report both the results achieved during the evaluation and the results we get when we run StringsAuto on a local computer. In addition, the code used to generate the StringsAuto results is available from http://pascal-hitzler.de/resources/Strings.zip and the actual alignments produced on the multifarm test cases are available http://pascal-hitzler.de/resources/Multifarm2013alignments.zip.

Table 3. Multifarm Track Results

	Different			Same		
Alignment System	F-measure	Precision	Recall	F-measure	Precision	Recall
StringsAuto	.14	.30	.09	.07	.51	.04
MapSSS	.10	.27	.07	.06	.50	.03
StringsAuto (corrected)	.30	.42	.23	.36	.92	.23

2.4 library

MapSSS did not produce alignments for this track, likely due to the size of the thesauri causing the system to exceed the Google API query limit.

StringsAuto finished below the reference (string equality) matchers on this test. StringsAuto could very probably be improved by recognizing all of the labels as synonyms (as it does for the anatomy benchmark). Another potential issue is that StringsAuto might have decided that either or both of the ontologies was entirely in German due to its sampling technique, and then attempted to translate all of the labels in that ontology (even the ones already in English).

Table 4. Library Track Results

Alignment System	F-measure	Precision	Recall
StringsAuto	.302	.774	.188

2.5 large biomedical ontologies

In this track StringsAuto was only able to complete one out of the six tasks (FMA-NCI), and MapSSS was not able to complete any of them (again due to the Google API query limit).

The results of StringsAuto on the FMA-NCI task were not very good. The system achieved an f-measure of 0.667 (based on a precision of 0.838 and a recall of 0.554). This placed the system 20th out of 23. It is odd that the performance here is so different than on the anatomy track. Similar to the problem on the library track, it is likely this is partially due to StringAuto's inability to recognize multiple labels for a single entity as synonyms. The synonym extraction method should be adapted to include this information.

It might be surprising that StringsAuto was unable to complete more of the tasks in this track. While in theory a matcher that only does string comparisons of labels should scale very well, StringsAuto uses a global (m x n) matrix to store all of the pair-wise similarity values and runs the stable marriage algorithm over this data. This obviously runs into memory limitations for large ontologies. In the future it might make sense to choose mappings based on a simple local maximum (with a threshold).

3 General comments

3.1 Comments on the results

Despite some technical problems, the performance of StringsAuto compared to that of the base string matchers shows that a careful selection of string similarity metrics leads to a significant performance increase in ontology alignment systems. In fact, StringsAuto finished in the top third of all alignment systems in both the anatomy and conference tracks. This shows that a significant amount of semantic information within some ontologies is contained in the labels themselves, and string similarity metrics are therefore an important component of ontology alignment systems.

The lackluster performance of MapSSS when compared with StringsAuto was somewhat surprising. Further research will be needed to improve the utility of the Google-based semantic similarity metric. We have begun looking into leveraging other general sources of information, including wikilinks[1] and Wikipedia. It would be interesting to perform an comprehensive analysis of these type of metrics similar to the one done for string similarity metrics in [1].

3.2 Discussions on the way to improve the proposed system

While StringsAuto is basically a proof-of-concept alignment system, it could be extended in several ways that would improve its performance on the OAEI evaluation. In particular, it could be adapted to treat multiple labels for a single entity as synonyms and to avoid the use of a global data structure so that larger ontology pairs could be aligned.

The main problem with MapSSS is due to the Google API query limit. This is also a problem with Bing, according to their terms of service. To mitigate this issue, we need to identify another general information source that does not have such a limit or only invoke this metric in a more limited way.

3.3 Comments on the OAEI 2013 procedure

It would be convenient to provide a way to run all of the language pairs in the multifarm test set with a single command and produce the same results published by the organizers of that track (i.e. the precision, recall and f-measure separated into the "same" and "different" ontology categories).

3.4 Proposed new measures

It might be interesting to see some details about the alignments produced by the various tools. For instance, were there some mappings identified by all of the alignment systems? Were there some that were missed by all systems? This might provide insights that improve the performance of ontology alignment systems in general. It might also highlight any controversial mappings remaining in the reference alignments.

4 Conclusion

We have described two related ontology alignment systems, StringsAuto and MapSSS, which explore the role that string similarity metrics play in ontology alignments. The results of these matchers on the OAEI evaluation are significantly better than the baseline string similarity matchers, and in some cases perform quite well when compared to all other alignment systems. The disappointing performance of the Google-based semantic similarity metric used in MapSSS indicates the need for further research in this area.

[1] http://www.iesl.cs.umass.edu/data/wiki-links

Acknowledgements

This work was supported by the National Science Foundation under award 1354778 "EAGER: Collaborative Research: EarthCube Building Blocks, Leveraging Semantics and Linked Data for Geoscience Data Sharing and Discovery." Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

References

1. M. Cheatham and P. Hitzler. String similarity metrics for ontology alignment. In *Proceedings of the 12th International Semantic Web Conference (ISWC 2013), Sydney, NSW, Australia, October 21-25, 2013*, Heidelberg, 2013. Springer.

ODGOMS - Results for OAEI 2013*

I-Hong Kuo[1,2], Tai-Ting Wu[1,3]

[1] Industrial Technology Research Institute, Taiwan
[2] yihonguo@itri.org.tw
[3] taitingwu@itri.org.tw

Abstract. ODGOMS is a multi-strategy ontology matching system which consists of elemental level, structural level, and optimization level strategies. When it starts to match ontologies, it first exploits appropriate string-based and token-based similarity computing strategies to find preliminary aligned results, and then it filters these results and merges them by using the optimization strategies. Despite ODGOMS uses simple matching logic, the results show that it is competitive with other well known ontology matching tools.

1 Presentation of the system

1.1 State, purpose, general statement

ODGOMS (Open Data Group Ontology Matching System) is an ontology matching system exploited by our looking forward research plan in the company. The target of mentioned above research plan is to offer people an user-friendly integrated interface to search and to browse linked open data on the internet.

The main idea of ODGOMS is to exploit simple but useful matching and merging strategies to produce robust aligned results. All strategies used in the system can be grouped into three groups that are elemental level strategies, structural level strategies, and optimization level strategies.

We have submitted two versions of ODGOMS which are version 1.1 and version 1.2 to participate in OAEI 2013 campaign. Of the two the latter is better than the former. This is because the latter has fixed some bugs existed in the former and has added some new features. Since ODGOMS version 1.2 is the latest version of the system, we only describe the contents of it in the following sections.

1.2 Specific techniques used

ODGOMS focuses on developing individual ontology matching modules for different matching aspects and on finding an appropriate way to merge all matching modules.

* Supported by the looking-forward research plan in Industrial Technology Research Institute. The mentioned above plan is named "Data Refining for LOD Using Linked Data Integration Technology."

Each matching module of ODGOMS can be exploited individually by setting filter threshold and the positions of input ontologies. The system architecture of ODGOMS is shown in Fig. 1.

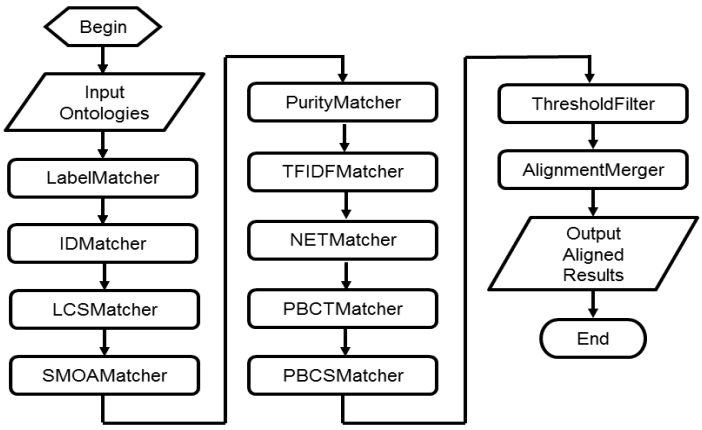


Fig. 1. System architecture of ODGOMS

The workflow of ODGOMS shown in Fig. 1 is described as follows. It first reads input ontologies into the memory, then it runs all matching modules individually which are LabelMatcher, IDMatcher, LCSMatcher, SMOAMatcher, PurityMatcher, TFIDFMatcher, NETMatcher, PBCTMatcher, and PBCSMatcher. After that it uses a filtering module named ThresholdFilter to filter all aligned results stored in each matching module, and merges them in an special order by exploiting an optimizating module named AlignmentMerger. At last, it outputs the integrated aligned results. All modules are divided into three groups which are elemental level modules, structural level modules, and optimization level modules. The detailed description of mentioned above modules are described as follows.

1.2.1 Elemental Level Modules

LabelMatcher For each entity in the first input ontology, this module finds a best matched entity in the second input ontology that has at least one common label (e.g. rdfs:label), and stores them as aligned results. Please note that it deletes non-English and non-Numeric characters from the labels of input entities and transforms the labels into lowercase characters before it starts to match entities.

IDMatcher The matching procedure of this module is the same as that of LabelMatcher, except that it finds a best matched entity in the second input ontology for each entity in the first input ontology that has identical ID (e.g. rdf:ID).

LCSMatcher It finds a best matched entity with highest LCS [5] (Longest Common Subsequence) similarity in the second ontology for each entity in the first input ontology and stores them as aligned results. When it computes the LCS similarity of

two input entities, it first delete non-English and non-Numeric characters from all labels (e.g. rdf:ID, rdfs:label, rdfs:comment) of the input entities. Then it computes the LCS similarities of each pair of labels between the input entities and considers the highest similarity as the final similarity of the input two entities. The LCS similarity of two input labels can be computed using the following equation:

$$LCS\ Similarity(A, B) = \frac{2 \times LCSlen(A, B)}{Length(A) + Length(B)}$$

In above equation, A and B mean the input labels, function LCSlen(A,B) returns the length of longest common subsequence between A and B, and functions Length(A) and Length(B) returns the lengths of A and B respectively.

SMOAMatcher The matching procedure of this module is the same as that of LCSMatcher, except that it replaces the LCS similarity computing scheme with the SMOA [4] similarity computing scheme.

PurityMatcher The matching procedure of this module is similar to that of LabelMatcher and IDMatcher, except that it deletes all useless English stopwords (such as words "has") of all labels within the classes and properties in the input ontologies before it starts to match ontologies. It can find interesting aligned results such as the mapping of labels "has_an_Email" versus "email".

TFIDFMatcher This module matches only classes from different input ontologies based on the TF-IDF [1] Cosine similarity [2] computing scheme. The idea of exploiting text-mining techniques (such as TF-IDF representation) in the system is inspired by YAM++ version 2012 [6]. The matching procedure of this module is described as follows. For each class in the first input ontology, it computes the TF-IDF Cosine similarities of the class and all classes in the second ontology. Then it chooses the best matched class with highest similarity in the second ontology, and stores them as aligned results. When it tries to compute the TF-IDF Cosine similarity of two input classes, it first splits the all labels (e.g. rdf:ID and rdfs:label) of input classes into two English token sets, and then it computes the TF-IDF values of each token within the two token sets respectively. Please note that the TF value of a token means the frequency of this token appears in the token set, and the IDF value of a token means the inverted frequency of this token appears in all token sets that all classes hold in the ontology. After that, it normalizes the TF-IDF values of two token sets, considers them as two normalized TF-IDF vectors, and finally computes the Cosine similarity of these two TF-IDF vectors.

NETMatcher It finds a best matched class with highest NET (named-entity transformation) similarity in the second ontology for each class in the first input ontology and stores them as aligned results. When it tries to compute the NET similarity of two input classes, it first deletes non-English and non-Numeric characters of all labels (e.g. rdf:ID and rdfs:label) of input classes and splits them into tokens. Please note that if there are n tokens and n is no less than 2, then at least n-1 tokens leads by capital English character or numeric character. Then it computes the input classes' NET similarity using the following equation:

$$NETSimilarity(A, B) = \frac{commonPrefix((A \cup B) - (A \cap B)) + commonTokens(A \cap B)}{n}$$

In above equation, A and B mean the token sets belong to different input classes, function commonTokens returns the total common tokens of input token sets, function commonPrefix returns the average of total common prefix characters versus total characters of all tokens within different input token sets. This module can find interesting aligned results such as the mappings of tokens "OWL" versus "Web Ontology Language" or "PCMembers" versus "Program Community Members", etc.

1.2.2. Structural Level Modules

There are two structural level matching modules, PBCTMatcher and PBCSMatcher in the system now. The former computes classes' integrated similarities using token-based computing scheme and the latter computes them using string-based ones. The ideas of the above matching modules are derived from the matcher NameAndPropertyAlignment of Alignment API 4.5 [3].

PBCTMatcher The full name of it is Property-based Class Token Matcher. For each class in the first input ontology, it finds a best matched class with highest integrated similarity in the second input ontology. It computes input classes' integrated similarities by combining the input classes' similarities and their properties' similarities using the following equation:

$$Integrated\ Similarity = \begin{cases} 0.5 \times CS_{tfidf} + 0.5 \times PS_{tfidf} & if\ PS \geq 0.5 \\ 0 & if\ PS < 0.5 \end{cases}$$

In the above equation, CS_{tfidf} means the TF-IDF Cosine similarity between the input classes, and PS_{tfidf} means the TF-IDF Cosine similarity between the belonged properties of input classes. The computing procedure of TF-IDF Cosine similarity is the same as that of TFIDFMatcher.

PBCSMatcher The full name of it is Property-based Class String Matcher. It's like PBCTMatcher, except it computes input classes' integrated similarities using LCS (Longest Common Subsequence) similarity computing scheme rather than using TF-IDF similarity computing scheme in PBCTMatcher.

1.2.3. Optimization Level Modules

ThresholdFilter It filters the stored aligned results in each matching module according to the default filter threshold, respectively. Each aligned result whose similarity is lower than the specified filter threshold is deleted from the original matching module.

AlignmentMerger It merges all stored aligned results of each matching module by a special order. The merging type of AlignmentMerger is called Absorb. That means when it merges the aligned results of two matching modules, it preserves all aligned results of the former and filters any aligned results of the latter which is partly or

completely overlapped in the former. A merging example of AlignmentMerger is given in Fig. 2.

Fig. 2. A merging example of AlignmentMerger.

In Fig. 2, AlignmentMerger is to merge the aligned results of the matching modules A_1 and A_2. Let $C_{i,j}$ be the j_{th} object in ontology i. If the aligned results in A_1 are { $<C_{1,1},C_{2,1}>$, $<C_{1,2},C_{2,4}>$ } and the ones in A_2 are { $<C_{1,2},C_{2,5}>$, $<C_{1,3},C_{2,8}>$ }. Because $<C_{1,2},C_{2,5}>$ in A_2 is partly overlapped with $<C_{1,2},C_{2,4}>$ in A_1, the merged aligned results are thus { $<C_{1,1},C_{2,1}>$, $<C_{1,2},C_{2,4}>$, $<C_{1,3},C_{2,8}>$ }.

1.3 Adaptations made for the evaluation

ODGOMS uses the same parameters to run each experiment in all tracks of OAEI 2013. The parameters are divided into two groups as follows.

The first group of parameters includes the default filter thresholds used by module ThresholdFilter in the system, which are set to be 1.0 for modules LabelMatcher, IDMatcher, and SMOAMatcher, 0.87 for modules LCSMatcher, PurityMatcher, and NETMatcher, 0.8 for module PBCSMatcher, 0.781 for module TFIDFMatcher, and 0.3 for module PBCTMatcher, respectively.

The second group of parameters includes the merging order used by module AlignmentMerger in the system. The mentioned above merging order is : LabelMatcher, IDMatcher, LCSMatcher, SMOAMatcher, PurityMatcher, TFIDFMatcher, NETMatcher, PBCTMatcher, and PBCSMatcher.

1.4 Link to the system and parameters file

The readers can download execution files of all versions of ODGOMS from our Google SkyDrive download position[1], and test them using SEALS client 4.1. Please refer to SELAS client tutorial[2] to learn more testing examples.

2 Results

In this section, the OAEI 2013 official results of ODGOMS are listed in from Table 1 to Table 5, and they can be find on the OAEI 2013 website too.

Since some tasks in Largebio track are time-consuming and ODGOMS cannot finish those tasks in 18 hours, we have run ODGOMS for three lightweight tasks of Largebio track by SEALS client 4.1 at local side, and have listed the results in Table 6. The mentioned above experiments are executed on a PC with Intel Core i7-3770S CPU (3.10GHz), 4GB RAM, and Ubuntu 12.04 LTS (64-bit version).

1ODGOMS download position: http://goo.gl/SKkhnU
2http://oaei.ontologymatching.org/2013/seals-eval.html#tutorial

2.1 Benchmark

The official results of ODGOMS version 1.2 released from OAEI 2013 website are listed in Table 1.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
Benchmark – biblioc	**0.99**	**0.55**	**0.71**	**100**
Benchmark – biblioc (weighted)	**0.98**	**0.54**	**0.70**	**100**

Table 1. The results for Benchmark track.

2.2 Anatomy

The official results of ODGOMS version 1.2 released from OAEI 2013 website are listed in Table 2.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
Anatomy Testsuite	**0.979**	**0.712**	**0.824**	**1,212**

Table 2. The results for Anatomy track.

2.3 Conference

The official results of ODGOMS version 1.2 released from OAEI 2013 website are listed in Table 3. In Table 3, the pre-test results (ra1) are listed in the first row, and the blind-test results (ra2) are listed in the second row.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
Conference Testsuite (ra1)	**0.74**	**0.60**	**0.66**	**19**
Conference Testsuite (ra2)	**0.7**	**0.55**	**0.62**	**19**

Table 3. The results for Conference track.

2.4 Multifarm

The official results of ODGOMS version 1.2 released from OAEI 2013 website are listed in Table 4.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
Multifarm – Different ontologies (i)	**0.26**	**0.06**	**0.10**	**2,640**
Multifarm – Same ontologies (ii)	**0.47**	**0.03**	**0.05**	

Table 4. The results for Multifarm track.

The results show that the F-Measures of the MultiFarm track are not good. We think the reasons for these results are that ODGOMS is not designed to match ontologies which are written in completely different languages yet.

2.5 Library

The official results of ODGOMS version 1.1 (not version 1.2 in this track) released from OAEI 2013 website are listed in Table 5. In this track, ODGOMS got the highest F-measures of all attended systems. By the way, in our local test the results of ODGOMS version 1.2 is slightly better than it of version 1.1.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
Library Testsuite	**0.698**	**0.830**	**0.758**	**27,936**

Table 5. The results for Library track.

2.6 Largebio

We run ODGOMS for three small tasks of Largebio track by SEALS client 4.1 at local side. The results are listed in Table 6. In Table 6, the F-Measures are identical to the official results released on OAEI 2013 website except the execution time of the former are faster than the latter. The results of SNOMED-NCI (small) are not shown in the official results on OAEI 2013 website since its execution time exceeded the maximum limit of 18 hours.

Test Datasets	Precision	Recall	F-Measure	Execution Time(s)
FMA-NCI (small)	**0.953**	**0.831**	**0.888**	**6,578**
FMA-SNOMED (small)	**0.862**	**0.570**	**0.686**	**30,046**
SNOMED-NCI (small)	**0.873**	**0.622**	**0.726**	**245,434**

Table 6. The results for Largebio track.

3 General Comments

3.1 Comments on the results

The official results of OAEI 2013 show that ODGOMS is competitive with other well known ontology matching systems in all OAEI tracks, especially in Library track it got the highest F-measures of all attended systems. The worst performance is happened in Multifarm track. The reason is that ODGOMS is not designed to deal with purely multilingual ontology matching problems yet.

3.2 Discussions on the way to improve the proposed system

ODGOMS exploits simple string-matching schemes and text-mining techniques to match ontologies now. It suffers from the following two problems. The first one is that it cannot optimize the results for each matching question automatically. The second one is that it cannot perfectly deal with purely multilingual ontology matching problems.

In order to solve the above two problems, we are extending the new abilities into the system as follows. For the first problem, we will apply machine learning technologies into the system so that it can find the best parameters that can be used in the system automatically when it deals with different ontology matching questions. And for the second problem, we will add the off-line translation ability between foreign languages and English into the system so that it doesn't need the help of on-line translation API (e.g. Microsoft On-Line Translation API).

4 Conclusion

It's the first time ODGOMS attended OAEI campaign. Although it got good results in almost all OAEI 2013 tracks, but it still suffers from some problems such as time-consuming and multilingual problems. The further research topics would be extend the machine learning and multilingual abilities into the system. We hope the performance of it can be improved when it attends the OAEI campaign next year.

References

1. Gerard Salton and Chris Buckley. Term Weighting Approaches in Automatic Text Retrieval. Information Processing and Management, 24 (5): 513-523, 1988.
2. Amit Singhal. Modern Information Retrieval: A Brief Overview. Bulletin of the IEEE Computer Society Technical Committee on Data Engineering, 24 (4): 35-43, 2001.
3. Jerome David, Jerome Euzenat, Francois Scharffe, and Cassia Trojahn dos Santos. The Alignment API 4.0. Semantic Web Journal, 2 (1): 3-10, 2011.
4. Giorgos Stoilos, Giorgos Stamou, and Stefanos Kollias. A String Metric for Ontology Alignment. Lecture Notes in Computer Science (LNCS), 3729: 624-637, 2005.
5. L. Bergroth, H. Hakonen, and T. Raita. A Survey of Longest Common Subsequence Algorithms. SPIRE (IEEE Computer Society) 00: 39-48, 2000.
6. DuyHoa Ngo and Zohra Bellahsene. YAM++ - Results for OAEI 2012. In Seventh International Workshop on Ontology Matching (OM 2012): 226-233, 2012.

RiMOM2013 Results for OAEI 2013

Qian Zheng[1], Chao Shao[1], Juanzi Li[1], Zhichun Wang[2] and Linmei Hu[1]

[1] Tsinghua University, China {zy,shaochao,ljz}keg.tsinghua.edu.cn
[2] Beijing Normal University, Beijing, China zcwang@bnu.edu.cn

Abstract. This paper presents the results of RiMOM2013 in the Ontology Alignment Evaluation Initiative (OAEI) 2013. We participated in three tracks of the tasks: Benchmark, IM@OAEI2013 , and Multifarm. We first describe the basic framework of our matching System (RiMOM2013); then we describe the alignment process and alignment strategies of RiMOM2013, and then we present specific techniques used for different tracks. At last we give some comments on our results and discuss some future work on RiMOM2013.

1 Presentation of the system

Recently, ontology is increasingly seen as an apocalyptic factor for enabling interoperability between heterogeneous systems and Semantic Web applications. Ontology Aligning is required for combining distributed and motley ontologies. Developing ontology alignment systems has become an essential issue of recent ontology research.

RiMOM2013 is named after RiMOM(Risk Minimization based Ontology Mapping) which is a multi-strategy ontology alignment system and was firstly developed in 2007 [1][2]. RiMOM implements several different matching strategies that have been defined based on different ontological information. For different ontology mapping tasks, RiMOM can automatically select and combine multiple strategies to generate accurate alignment results. RiMOM has evolved all the time since 2007, and RiMOM2013 is developed based on RiMOM and has several new characteristics that will be described in following subsections.

1.1 State, purpose, general statement

As shown in Fig. 1, the whole system is consists of three layers: *User Interface layer, Control layer and Component layer. In the User Interface layer*, RiMOM2013 provides an interface to allow customizing the matching procedure: including selecting preferred components, setting the parameters for the system, choosing to use translator tool or not. In semi-automatic ontology matching, the task layer stores parameters of the alignment tasks, and controls the execution process of components in the component layer. In component layer, we define six groups of executable components, including preprocessor, matcher, aggregator, evaluator, postprocessor and other utilities. In each group, there are several instantiated components. For a certain alignment task, user can select appropriate components and execute them in desired sequence.

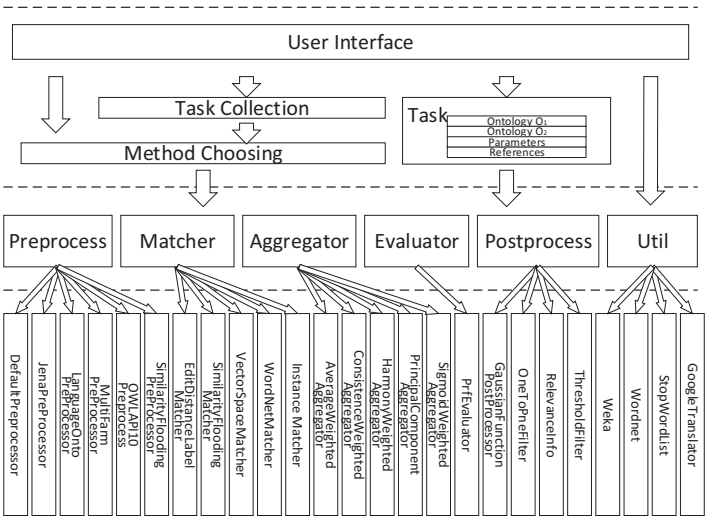


Fig. 1. Framework of RiMOM2013

1.2 Specific techniques used

This year we participate in three tracks of the campaign: Benchmark, Multifarm, and Instance Matching. We will describe specific techniques used in different tracks as follows:

Benchmark

For benchmark track, we use five matching methods: Similarity preprocessor, Similarity matcher, Similarity Flooding preprocessor, Similarity Flooding matcher, and Similarity Aggregator.

We use Edit Distance method and WordNet 2.0 to calculate the similarity between labels of entities, then for each entity pair we combine these two similarities to an aggregated similarity.

Experiments are did on five different flooding methods based on similarity flooding[3]: Property Only Method(POM), Hierarchy Method(HM), Common Relation Me thod(CRM), RDFGraphOfSchema Method(RGSM) and Nothing Method(NM). These five methods are used to generate the initial graph only for the next step. In POM we add entity pairs which have superclass relationship; And in HM, we add entity pairs which have subclass and super property; In CRM, first we check the relationship between each two entities, then we add entity pairs which have domain relationship or range relationship. In RGSM, we add these pairs either contented in HM and CRM. And for NM, we add all entity pairs into initialize graph.

In the next two steps we use the similarity flooding method to flood the similarities in the graph, and because the map is usually gargantuan, we use a threshold filter to prune the pairs whose similarity smaller than threshold when after the flooding process.

Next we use Aggregator to combine these similarities: EditDistance similarity, WordNet 2.0 similarity, similarity Flooding result similarity. The experiment reflects that the

only single task list without aggregator and other similarities(EditDistance and WordNet 2.0) gains the best result.

Multifarm

The multifarm track is designed to test the aligning systems' ability on multi-lingual dataset[4]. The multifarm data is composed of a set of ontologies translated in seven different languages and the corresponding alignments between these ontologies. Each entity in one ontology requested to be matched with related entity in different language ontology.

The nodus makes this task difficult is that there is restricted information in each entity, which usually only has label information like "writes contribution", and the label of its range property of this entity is "contribution", the label of its domain property of this entity is "author", which when translated into same language usually got same or almost same result like "autor" in Spanish.

In the first preprocess step in multifarm task, we use google translate tool to make two different language into same language, such as when we do the "en-cn" alignment task, we translate the Chinese label to English, and when we do the "cn-es" alignment task, we translate Spanish label into Chinese. Particularly, when either the source ontology or target ontology's language is Russian, we translate them both into English.

In the second preprocess step, we use google translate tool to make two different entities's label all in English for the purpose of use wordnet 2.0 in order to calculate the sentence similarity.

Next we use Aggregator to combine these two similarities for each label pair, the experiment reflects that the edit-distance contributes more in the combined-similarity.

Instance Matching

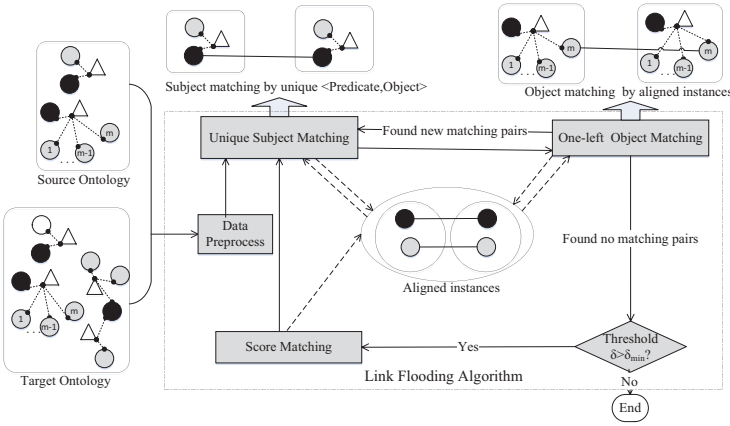


Fig. 2. Framework of instance matching system

For instance matching task, we propose an algorithm called Link Flooding Algorithm inspired by [5] , which includes four main modules, namely Data Preprocess, Unique

Subject Matching, One-left Object Matching and Score Matching. Before going into the details, we first define ontology Ont as a set of RDF triples $< s, p, o >$ (Subject, Predicate, Object), and instance Ins as a set of many RDF triples having the same Subject. Since an instance's subject could be another's object, we consider instance matching in three situations: subject and subject alignment, subject and object alignment and object and object alignment.

In the first module called data preprocess, we purify the data including transferring the data sets which are multilingual to be uniform in English. Additionally, we unify the format of data, for example, the date expressed as "august, 01, 2013" or "August, 01, 2013" is transformed to "08, 01, 2013". We also do a lot of other operations like removing special characters to clean the data. The second module achieves instance matching through one unique $< p, o >$ for the two instances to be aligned. For example, if in source ontology, only one instance, INS_X has $< p, o >$ as $< birthday, "01, 08, 2013" >$, then in target ontology, instances containing <birthday,"01, 08, 2013"> are concluded to be aligned with INS_X. Consequently, one instance in source ontology can be matched with arbitrary number of instances in target ontology. In the third module, we obtain object and object alignment via all of the aligned subjects. In detail, if two aligned instances have a same predicate both having m objects, of which $m-1$ are aligned, then the "one-left" object is aligned. The last module is named Score Matching where we consider two instances aligned if the weighted average score of their comments, mottos, birthDates ,and almaMaters is above a certain threshold. In this task, we take the edit distance as score measure of similarity. We illustrate the algorithm in Fig. 2.

We first input source ontology and target ontology into the algorithm, as shown in the picture, the black circles represent the subjects of the RDF triples, the gray circles represent the objects of the RDF triples, and the white triangles represent the predicate[6]. We then clean the data set with the module Data Preprocess. Next, we generate some initial instance matching pairs as seeds through Unique Subject Matching. As we mentioned previously, one instance's subject could be another's object, we can input the seeds to One-left Object Matching to get more matching pairs. With those new detected matching pairs, we reapply Unique Subject Matching to acquire more new matching pairs. So, we can iteratively run these two modules until we can not find any new matching pairs. After that, we need to run the Score Matching module with a high threshold to get new pairs with high confidence, thus we can repeat previous operation namely iteratively running Unique Subject Matching and One-left Object Matching module with little error. Later, we reduce the threshold step by step, where in each step newfound pairs are input into the repeated previous operation to control error propagation. Lastly, we output all of the matching pairs if the threshold is below the minimum threshold or all the instances in target ontology are aligned.

1.3 Adaptations made for the evaluation

Deploying the system on seals platform by a network bears three main challenges. Firstly, the input source can not download as a file, we can hardly see the information and structure inherently. Secondly, without the input string path, we can not determine which task and which size of the dataset are now using. Lastly, with the calling the

interface we provide by seals platform, some XML reader problems occur and make the process interrupt, then we have no choice but to discard the XML read and load component to make the system executable, but in multifarm task, we found that there is some difference between the result generated by our local pc and by seals platform, there may have some undiscoverable problems when we turn RiMOM2013 as a unvarying-purpose system.

1.4 Link to the system and parameters file

The RiMOM2013 system can be found at
`http://keg.cs.tsinghua.edu.cn/project/RiMOM/`

2 Results

As introduced before, RiMOM2013 participates in three tracks in OAEI 2013. In the following section, we present the results and related analysis for the individual OAEI 2013 tracks below.

2.1 benchmark

There are two test set this year, biblio and finance, and for each dataset there are 94 align tasks. We divide these tasks into four groups, 101, 20x, 221-247 and 248-266. We got good result on 221-247 and the result turns bad on 248-266, compared with the 2010's result, the evaluate fashion is changed this year, and there is some error during the system docking mission, when we try to use a XML loader to implement circuit-customize, the incompatible problem occurred and because of we do not know the exactly version of the tool seals platform called, we have to write the program imitation separately and make them inflexible. As RiMOM2013 is an dynamic system, these problem more or less affected our implementation.

DataSet	Precision	Recall	F1-measure
101	0.84	1.00	0.91
20x	0.57	0.52	0.53
221-247	0.71	1.00	0.82
248-266	0.46	0.48	0.45

Table 1. Benchmark Result of biblio-dataset

2.2 multifarm

There are 36 language pairs in multifarm data set, these pairs is combined with 8 languages: Chinese(cn), Czech(cz), Dutch(nl), French(fr), German(de), Portuguese(pt), Russian(ru), Spanish(es). And permutate depend on lexicographical order. Results are show in Table. 1.

Result is shown in Table 2 and this result is from OAEI2013 result page. It is notable that our system got the minimum runtime among the multilingual matchers, which is not put in this table. Although we got the third rank in multifarm task, we still have to mention that our system basically is a translation based system and the connection with the translator's supplier is not that good. Otherwise, we could have made it much better. We have proven it locally with no edas and ekaw ontologies, getting F1 as 0.49.

Language Pair	F1-measure	Language Pair	F1-measure	Language Pair	F1-measure
cn-cz	0.120	cz-nl	0.320	en-pt	0.360
cn-de	0.180	cz-pt	0.240	en-ru	NaN
cn-en	0.250	cz-ru	NaN	es-fr	0.360
cn-es	0.170	de-en	0.390	es-nl	0.290
cn-fr	0.170	de-es	0.310	es-pt	0.400
cn-nl	0.160	de-fr	0.290	es-ru	NaN
cn-pt	0.100	de-nl	0.300	fr-nl	0.300
cn-ru	NaN	de-pt	0.270	fr-pt	0.260
cz-de	0.240	de-ru	NaN	fr-ru	NaN
cz-en	0.250	en-es	0.420	nl-pt	0.150
cz-es	0.240	en-fr	0.320	nl-ru	NaN
cz-fr	0.170	en-nl	0.350	pt-ru	NaN

Table 2. Multifarm Result by Seals

The table shows that the worst results all happened in Chinese tasks, because the basic tool we use in all multifarm fashion is translate tool, we use both google translator and bing's translator to initialize the label set before we calculate the WordNet similarity, edit-distance similarity and vector space similarity.

Because of the fact that information in each multifarm's tasks is qualified, involuntarily, we got the limit on result, the highest F1 we got is 0.605 which is Czech ontology and English ontology 's alignment on local machine.

2.3 instance matching

The result for Instance Matching 2013 is shown in Table 3.

As we can see from the table, we achieve high values for all measures in all five testcases, especially in testcase1 and 3. Furthermore, the official result shows that we win first prize in IM@OAEI2013. We confidently believe our algorithm, Link Propagation Algorithm is effective for instance matching. We owe our results to each module of the algorithm and further explain the results more specifically.

For testcase1, the Score Matching module exploits weighted average score, therefore avoiding emphasizing some particular information of instances. The reasons why we attain best performance in testcase1 also include little change in target ontology. In testcase2, with almost only link information, we needn't employ last module Score Matching. Nevertheless, it achieves comparative performance, reflecting the power of

link information, in other words, the power of Link Flooding Algorithm. Though testcase 3, 4 and 5 have few initial links, we can find new matching pairs through Score Matching. Although only a few matching pairs are found, we can detect lots of new pairs by iteratively running Unique Subject Matching and One-left Object Matching.

TestCase	Precision	Recall	F1-measure
testcase01	1.00	1.00	1.00
testcase02	0.95	0.99	0.97
testcase03	0.96	0.99	0.98
testcase04	0.94	0.98	0.96
testcase05	0.93	0.99	0.96

Table 3. Instance Matching Result

3 General comments

3.1 Discussions on the way to improve the proposed system

We have got no split new method implemented during the benchmark task, and there also have much information in these tasks that we need to make them outcrop. And we have not run the RiMOM2013 on anatomy, conference, Library, etc. For anatomy, since many technical terms emerge as labels in ontologies, we should add some manually labelling step to generate the reference alignment result but the problem is how to determine a result pair is matched or not if we have not any biological knowledge. For multifarm, because the multifarm dateset is translated from conference collection, if we do the experiment on conference before multifarm, there may be a credible auxiliary information between each entity pair during the multifarm experiment.

3.2 Comments on the OAEI 2013 measures

The results show that in schema level matching, using description information gain the better matching result, by contrast, in instance level's matching, using linking information got the better result, because in instance level, the types of relationship between each entity is diverse, and in schema level is drab.

4 Conclusion

In this paper, we present the result of RiMOM2013 in OAEI 2013 Campaign. We participate in three tracks this year, including Benchmark, Multifarm and Instance Matching. We presented the architecture of RiMOM2013 framework and described specific techniques we used during this campaign. In our project, we design a new framework to do the ontology alignment task. We focus on the instance matching task and propose three new method in instance matching tasks. The results show that our project can both deal with multi-lingual ontology on schema level and do well on instance level, and this will be paid attention in the community.

5 Acknowledgement

The work is supported by NSFC (No. 61035004), NSFC-ANR(No. 61261130588), 863 High Technology Program (2011AA01A207), FP7-288342, and THU-NUS NExT Co-Lab.

References

1. Li, J., Tang, J., Li, Y., Luo, Q.: RiMOM: a dynamic multistrategy ontology alignment framework. IEEE Trans. Knowl. Data Eng. (2009) 1218–1232
2. Wang, Z., Zhang, X., Hou, L., Zhao, Y., Li, J., Qi, Y., Tang, J.: RiMOM results for oaei 2010. In: OM'10. (2010)
3. Melnik, S., Garcia-Molina, H., Rahm, E.: Similarity Flooding: A versatile graph matching algorithm and its application to schema matching. In: ICDE'02. (2002) 117–128
4. Meilicke, C., Garcia-Castro, R., Freitas, F., van Hage, W.R., Montiel-Ponsoda, E., de Azevedo, R.R., Stuckenschmidt, H., Svb-Zamazal, O., Svtek, V., Tamilin, A., dos Santos, C.T., Wang, S.: Multifarm: A benchmark for multilingual ontology matching. J. Web Sem. (2012) 62–68
5. Wang, Z., Li, J., Wang, Z., Tang, J.: Cross-lingual knowledge linking across wiki knowledge bases. In: WWW'12. (2012) 459–468
6. Nguyen, K., Ichise, R., Le, B.: SLINT: a schema-independent linked data interlinking system. In: OM'12. (2012)

ServOMap Results for OAEI 2013

Amal Kammoun[1] and Gayo Diallo[1]

ERIAS, INSERM U897, University of Bordeaux, France
first.last@isped.u-bordeaux2.fr

Abstract. We briefly present in this paper ServOMap, a large scale ontology matching system, and the performance it achieved during the OAEI 2013 campaign. This is the second participation in the OAEI campaign.

1 Presentation of the system

ServOMap [1] is a large scale ontology matching system designed on top of the ServO Ontology Server system [2], an idea originally developed in [3]. It is able to handle ontologies which contain several hundred of thousands entities. To deal with large ontologies, ServOMap relies on an indexing strategy for reducing the search space and computes an initial set of candidates based on the terminological description of entities of the input ontologies.

New components have been introduced since the 2012 version of the system. Among them:

- The use of a set of string distance metrics to complement the vectorial based similarity of the IR library we use[1],
- An improved contextual similarity computation thanks to the introduction of a Machine Learning strategy,
- The introduction of a general purpose background knowledge, WordNet [4], to deal with synonymy issues within entities' annotation,
- The use of a logical consistency check component.

In 2013, ServOMap participated in the entities matching track and does not implemented a specific adaptation for the **Interactive Matching** and **Multifarm** tracks.

1.1 State, purpose, general statement

ServOMap is designed with the purpose of facilitating interoperability between different applications which are based on heterogeneous knowledge organization systems (KOS). The heterogeneity of these KOS may have several causes including their language format and their level of formalism. Our system relies on Information Retrieval (IR) techniques and a dynamic description of entities of different KOS for computing the similarity between them. It is mainly designed for meeting the need of matching large scale ontologies. It has proven to be efficient for tackling such an issue during the 2012 OAEI campaign.

[1] http://lucene.apache.org/

1.2 Specific techniques used

ServOMap has a set of components highly configurable. The overall workflow is depicted on figure 1. It includes three steps briefly described in the following. Typically, the input of the process is two ontologies which can be described in OWL, RDF(S), SKOS or OBO. ServOMap provides a set of weighted correspondences [5] between the entities of these input ontologies.

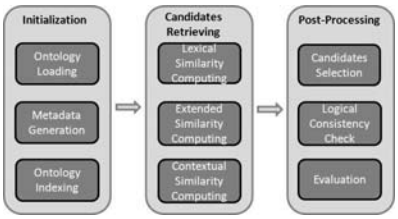


Fig. 1. ServOMap matching process.

Initialization Step. During the initialization step, the **Ontology Loading** component has in charge of processing the input ontologies. For each entity (concept, property, individual), a virtual document from the set of annotations is generated for indexing purpose. These annotations include the ID, labels, comments and, if the entity is a concept, information about it properties. For an individual, the values of domain and range are considered as well.

Metadata Generation. A set of metrics are computed. They include the size of input ontologies in term of concepts, properties and individuals, the list of languages denoting the annotations of entities (labels, comments), etc. Determining the size helps adapting latter the matching strategy. Indeed, besides detecting an instances matching case, we distinguish this year small (less than 500 concepts) from large ontologies. Detecting the set of languages allows using latter the appropriate list of stopwords.

Ontology Indexing. With ServOMap we consider an ontology as a corpus of semantic document to process. Therefore, the purpose of the indexing module is to build an inverted index for each input ontology from the virtual documents generated previously. The content of each virtual document is passed through a set of filters: stopwords removal, non alphanumeric characters removal, lowercasing and stemming labels, converting numbers to characters. In addition, labels denoting concepts are enriched by their permutation. This operation is applied to the first 4 words of each label. For instance, after enriching the term '*Bone Marrow Donation*' we obtain the set {*Bone Marrow Donation, Marrow Bone Donation, Marrow Donation Bone, Donation Marrow Bone, Donation Bone Marrow*}.

Further, two strategies are used for indexing, *exact* and *relaxed* indexing. Exact indexing allows high precise retrieving. In this case, before the indexing process, all words for each label are concatained by removing spaces between them. In addition,

for optimization purpose, the possibility is offered to index each entity with information about its siblings, descendants and ancestors.

Candidates Retrieving. The objective is to compute a set of candidates mappings M $= \bigcup(M_{exact}, \mathrm{M}_{relaxed}, \mathrm{M}_{context}, \mathrm{M}_{prop})$.

Lexical Similarity Computing. Let's assume that after the initializing step we have two indexes I_1 and I_2 corresponding respectively to the input ontologies O_1 and O_2. The first step for candidates retrieving is to compute the initial set of candidates mappings constituted by only couple of concepts and denoted by M_{exact}. This set is obtained by performing an exact search, respectively over I_1 using O_2 as search component and over I_2 using O_1. To do so, a query which takes the form of a virtual document is generated for each concept and sent to the target index. The search is performed through the IR library which use the usual *tf.idf* score. We select the best K results having a score greater than a given threshold θ. The obtained couples are filtered out in order to keep only those satisfying *the lexical similarity condition*. This condition is checked as follows.

For each filtered couple (c_1, c_2), two lexical descriptions are generated. They are constituted respectively by ID and labels of c_1 and its direct ancestors (Γ_1), ID and labels of c_2 and its direct ancestors (Γ_2).

We compute a similarity Sim_{lex}=*f*($\alpha \times ISub(\Gamma_1, \Gamma_2)$, $\beta \times QGram(\Gamma_1, \Gamma_2)$, $\gamma \times Lev(\Gamma_1, \Gamma_2)$), where I-Sub, QGram and Lev denote respectively the ISUB similarity measure [6], the QGram and Levenshtein distance. Coefficients α, β and γ are chosen empirically for OAEI 2013. All couples with Sim_{lex} greater than a threshold are selected. Finally, M_{exact} is the intersection of the two set of selected couples obtained after the search performed on the two indexes.

The same process is repeated in order to compute the set $\mathrm{M}_{relaxed}$ from the concepts not yet selected with the exact search. A similar strategy for computing M_{exact} is used for computing the similarity between the properties of the input ontologies. This generates the M_{prop} set. Here, the description of a property includes its domain and range.

Extended Similarity Computing. In order to deal with synonym issue, from the set of concepts not selected after the previous phase, we use the WordNet dictionary for retrieving alternative labels for concepts to be mapped. The idea is to check whether a concept in the first ontology is denoted by synonym terms in the second one. All couples in this case are retrieved as possible candidates.

Contextual Similarity Computing. The idea is to acquire new candidates mappings, $\mathrm{M}_{context}$, among those couples which have not been selected in the previous steps. To do so, we rely on the structure of the ontology by considering that the similarity of two entities depends on the similarity of the entities that surround them. In 2013, we have introduced a Machine Learning strategy which uses M_{exact} as basis for training set using the WEKA tool [7]. Indeed, according to our tests, candidates mappings from M_{exact} use to be highly accurate. Therefore, retrieving candidates using contextual similarity is transformed as a classification problem. Each new couple is to be classified as *correct* or *incorrect* according to candidates already in M_{exact}.

We use 5 similarity measures (Levenshtein, Monge-Elkan, QGram, Jackard and BlockDistance) to compute the features of the training set. For each couple (c_1, c_2) $\in M_{exact}$, we compute the 5 scores using the ID and labels associated to c_1 and c_2 and denote this entry as *correct*. We complete M_{exact} by randomly generating new couples assumed to be incorrect. To do so, for each couple (c_1, c_2) in M_{exact}, we compute the 5 scores for (c_1, *ancestor*(c_2)), (*ancestor*(c_1), c_2), (*descendant*(c_1), c_2) and (c_1, *descendant*(c_2)) and denote them as *incorrect*. The *ancestor* and *descendant* functions retrieve the super-concepts and sub-concepts of a given concept. We use the J48 decision tree algorithm of Weka for generating the classifier.

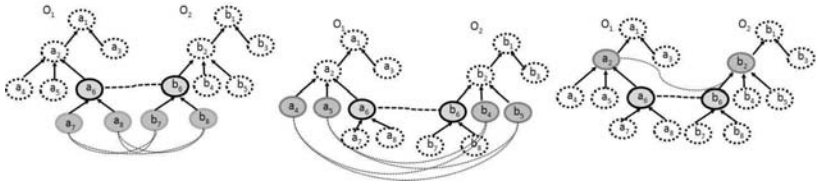


Fig. 2. Strategy for contextual based candidates generation. For each couple of M_{exact}, the similarity of the surrounding concepts are looked up.

We build the dataset to classify as follows. The exact set is used to learn new candidates couples according to the strategy depicted on figure 2 by assuming here for instance that (a_6, b_6) $\in M_{exact}$. For each couple of M_{exact}, the idea is to retrieve possible couples not already in M_{exact} among the sub-concepts ((a_7, b_7), (a_7, b_8), (a_8, b_8), (a_8, b_7) in figure 2), the super-concepts and the siblings. For each candidate couple (c_1, c_2), if the score

$$s = f(getScoreDesc(), getScoreAsc(), getScoreSib())$$

is greater than a fixed threshold, then we compute the 5 similarity scores for (c_1, c_2). The functions getScoreDesc(), getScoreAsc(), getScoreSib() compute respectively a score for (c_1, c_2) from its descendants, ancestors and siblings concepts. The obtained dataset is classified using the previously built classifier.

Post-Processing Step . This step involves enriching the set of candidates mapping (mainly incorporating those couples having all their sub-concepts mapped), the selection of the final candidates from the set M and performing inconsistency check. We have implemented a new filtering algorithm for selecting the best candidates based on their scores and we perform consistency check as already implemented in the 2012 version (disjoints concepts, criss-cross). Further, we use the repair facility of the LogMap system [8] to perform logical inconsistency check. Finally, we have implemented an evaluator for computing the usual Precision/Recall/F-measure for the generated final mappings if a reference alignment is provided.

1.3 Adaptations made for the evaluation

ServOMap is configured to adapt its strategy to the size of the input ontologies. Therefore, as mentioned earlier, two categories are considered: input ontology with size less than 500 concepts and ontology with size greater than 500 concepts. For large ontologies, our tests showed that exact search is sufficient for generating concepts mappings of OAEI test cases, while for small one relaxed and extended search is needed.

Further, according to the performance achieved by our system in OAEI 2012 [9], the focus of this year was more to improve the recall than optimizing the computation time. From technical point of view, the previous version of ServOMap was based on the following third party components: the JENA framework for processing ontologies and the Apache Luncene API as IR library. We have moved from JENA framework to the OWLAPI library for ontology processing, in particular for handling in an efficient manner complex domain and range axioms and taking into account wider formats of input ontologies. In addition, a more recent version of the IR library is used for the actual version. However, in order to have a compatible SEALS client, we have downgraded the version of the Apache Lucene API used for the evaluation. This leaded to a less robust system for the 2013 campaign as some components have not been fully adapted.

1.4 Link to the system and parameters file

The wrapped SEALS client for ServOMap version used for the OAEI 2013 edition is available at http://lesim.isped.u-bordeaux2.fr/ServOMap. The instructions for testing the tool is described in the tutorial dedicated to the SEALS client[2].

1.5 Link to the set of provided alignments

The results obtained by ServOMap during OAEI 2013 are available at http://lesim.isped.u-bordeaux2.fr/ServOMap/oaei2013.zip/.

2 Results

We present in this section the results obtained by running the ServOMap system with the SEALS client. As the uploaded version does not implement multilingual and interactive matching features, the results of the corresponding tracks are not described here.

2.1 Benchmark

In the OAEI 2013 campaign, the Benchmark track includes only the bibliography test case in a blind mode. The experiments are performed on a Debian Linux virtual machine configured with four processors and 8GB of RAM. ServOMap finished the task in about 7mn. Because of some issues in processing tests set from #261-4 to #266, the results of ServOMap has been affected and decreased compared to 2012.

[2] http://oaei.ontologymatching.org/2013/seals-eval.html

Test set	H-Precision	H-Recall	H-F-score
biblioc	0.63	0.22	0.33

Table 1. ServOMap results on the Benchmark track

2.2 Anatomy

The Anatomy track consists of finding an alignment between the Adult Mouse Anatomy (2,744 classes) and a part of the NCI Thesaurus (3,304 classes). The evaluation is performed on a server with 3.46 GHz (6 cores) and 8GB RAM. Table 2 shows the results and runtime of ServOMap.

Test set	Precision	Recall	F-score	Runtime (s)
Anatomy	0.961	0.618	0.752	43

Table 2. ServoMap results on the Anatomy track

2.3 Conference

The conference track contains 16 ontologies from the same domain (conference organization). These ontologies are in English and each ontology must be matched against each other. The match quality was evaluated against an original (ra1) as well as entailed reference alignment (ra2). ServoMap increased its performance in term of F-measure by 0.07. The table 3 shows the results obtained on this track.

Test set	Precision	Recall	F-score
Conference (ra1)	0.73	0.55	0.63
Conference (ra2)	0.69	0.5	0.58

Table 3. ServOMap results on the Conference track

2.4 Library

The library track is about matching two thesauri, the STW and the TheSoz thesaurus. They provide a vocabulary for economic respectively social science subjects and are used by libraries for indexation and retrieval. Thanks to the use of a new API for processing ontologies, ServOMap was able to handle directly the two thesauri of the library track without any adaptation. ServOMap performed the task in a longer time (4 compared to 2012 edition of OAEI, however by increasing the F-measure.

Test set	Precision	Recall	F-score	Runtime (s)
Library	0.699	0.783	0.739	648

Table 4. ServoMap results on the Library track

2.5 Large biomedical ontologies

The Large BioMed track consists of finding alignments between the Foundational Model of Anatomy (FMA), SNOMED CT, and the National Cancer Institute Thesaurus (NCI). There are 6 sub tasks corresponding to different sizes of input ontologies (small fragment and whole ontology for FMA and NCI and small and large fragments for SNOMED CT). The results obtained by ServOMap are depicted on Table 5.

Test set	Precision	Recall	F-score	Runtime (s)
Small FMA-NCI	0.951	0.815	0.877	141
Whole FMA-NCI	0.727	0.803	0.763	2,690
Small FMA-SNOMED	0.955	0.622	0.753	391
Whole FMA- Large SNOMED	0.861	0.620	0.721	4,059
Small SNOMED-NCI	0.933	0.642	0.761	1,699
Whole NCI- Large SNOMED	0.822	0.637	0.718	6,320

Table 5. ServOMap results on Large BioMed Track

3 General comments

This is the second time that we participate in the OAEI campaign. While we participated with two configurations of our system to the 2012 edition of the campaign, respectively with ServOMap-lt and ServOMap, this year a unique version has been submitted. Several changes have been introduced. We moved from JENA to OWLAPI for processing ontologies and a more recent version of the Apache Lucene API that is used as IR tool. This last change introduced some issues on having a wrapped tool compatible with the Seals client. Therefore, the uploaded version of ServOMap uses a downgraded version of Lucene to be able to run correctly with the client. This resulted of a degraded performance and less robust system compared to that obtained with the actual version of our tool. Further, the uploaded version has not been optimized in term of computation time. This affected particularly the runtime for the Large BioMed Track.

3.1 Comments on the results

The evaluated ServOMap version for OAEI 2013 shows a significant improvement for the conference and library track. We have increased our recall in several tasks without loosing enough in term of precision. Overall, We notice that, the introduction of string similarity measures and inconsistency repair facility affected the computation

time. However, ServOMap confirmed its ability to cope with very large dataset but also shows that it relies heavily on the terminological richness of the input ontologies.

4 Conclusion

We have briefly described the ServOMap ontology matching system and presented the results achieved during the 2013 edition of the OAEI campaign. Several components, including Machine Learning based contextual similarity computing, have been added to the previous version. In the vein of the last year participation, the performance achieved by ServOMap are still very interesting and places it among the best system for large scale Ontology matching. Future work will include improving the strategy of contextual similarity computing and focusing on a more efficient semantic filtering component of candidate mappings. Further, we will investigate interactive and multilingual matching issues.

5 Acknowledgments

This work has been partly supported by the EU FP7 ARITMO project. We also thank the organizers of OAEI with providing test dataset and the evaluation infrastructure.

References

1. M. Ba and G. Diallo. Large-scale biomedical ontology matching with servomap. *IRBM*, 34(1):56 – 59, 2013. Digital Technologies for Healthcare.
2. Gayo Diallo. Efficient building of local repository of distributed ontologies. In *IEEE Proceedings of the SITIS'2011 International Conference.*, pages 159–166, November 2011.
3. Gayo Diallo. *An ontology-based architecture for structured and unstructured data management*. PhD thesis, Université Joseph Fourier - Grenoble 1, December 2006. Original Title: Une Architecture á base d'Ontologies pour la Gestion Unifiées des Données Structurées et non Structurées.
4. George A. Miller. Wordnet: A lexical database for english. *COMMUNICATIONS OF THE ACM*, 38:39–41, 1995.
5. Pavel Shvaiko and Jérôme Euzenat. Ontology matching: State of the art and future challenges. *IEEE Trans. Knowl. Data Eng.*, 25(1):158–176, 2013.
6. Giorgos Stoilos, Giorgos Stamou, and Stefanos Kollias. A string metric for ontology alignment. In Y. Gil, editor, *Proceedings of the International Semantic Web Conference (ISWC 05)*, volume 3729 of *LNCS*, pages 624–637. Springer-Verlag, 2005.
7. Mark Hall, Eibe Frank, Geoffrey Holmes, Bernhard Pfahringer, Peter Reutemann, and Ian H. Witten. The weka data mining software: An update. *SIGKDD Explor. Newsl.*, 11(1):10–18, November 2009.
8. Ernesto Jimenez Ruiz, Bernardo Cuenca Grau, Yujiao Zhou, and Ian Horrocks. Large-scale interactive ontology matching: Algorithms and implementation. In *Proceedings of the 20th European Conference on Artificial Intelligence (ECAI)*, pages 444–449. IOS Press, 2012.
9. José-Luis Aguirre, Kai Eckert, Jérôme Euzenat, Alfio Ferrara, Willem Robert van Hage, Laura Hollink, Christian Meilicke, Andriy Nikolov, Dominique Ritze, and François Scharffe et al. Results of the ontology alignment evaluation initiative 2012. In Pavel Shvaiko, Jérôme Euzenat, Anastasios Kementsietsidis, Ming Mao, Natasha Fridman Noy, and Heiner Stuckenschmidt, editors, *OM*, volume 946 of *CEUR Workshop Proceedings*. CEUR-WS.org, 2012.

SLINT+ Results for OAEI 2013 Instance Matching

Khai Nguyen[1] and Ryutaro Ichise[2]

[1] The Graduate University for Advanced Studies, Japan
nhkhai@nii.ac.jp
[2] National Institute of Informatics, Japan
ichise@nii.ac.jp

Abstract. The goal of instance matching is to detect identity resources, which refer to the same real-world object. In this paper, we introduce SLINT+, a novel interlinking system. SLINT+ detects all identity linked data resources between two given repositories. SLINT+ does not require the specifications of RDF predicates and labeled matching resources. SLINT+ performs competitively at OAEI instance matching campaign this year.

1 Presentation of the system

The problem of detecting instances co-referring to the same real-world object is positively important in data integration. It is useful for reducing the heterogeneity and warranting the consistency of data. The asynchronous development of linked data increasingly requires the specific linked data instance matching algorithms to connect existing instances and newly added instances.

In linked data, the differences of data representation appear not only in object values, but also in RDF predicates, which specify the meaning of objects properties. This issue is popularly found in different data repositories or even the same repository but different domains. Also, it separates the current solutions into two groups: schema-dependent and schema-independent. The first approach uses the descriptions of RDF predicate as the guide for matching while the second approach does not. In addition, the schema-independent approach consists of two minor branches: supervised learning and unsupervised learning, which involve with using or not using the labeled data of identity instances.

We develop SLINT [3] and its extension SLINT+ [2]. These systems are schema-independent and training-free. SLINT+ is used for instance matching track of OAEI 2013.

1.1 State, purpose, general statement

SLINT+ is a flexible schema-independent linked data interlinking system. SLINT+ can interlink various data sources, and is independent on the schema of data sources. By detecting appropriate predicate alignments without supervised learning, SLINT+ does not require expensive curation on data examples.

The principle of SLINT+ is similar to previous data interlinking systems. There are two main phases in the interlinking process of SLINT+: candidate generation and

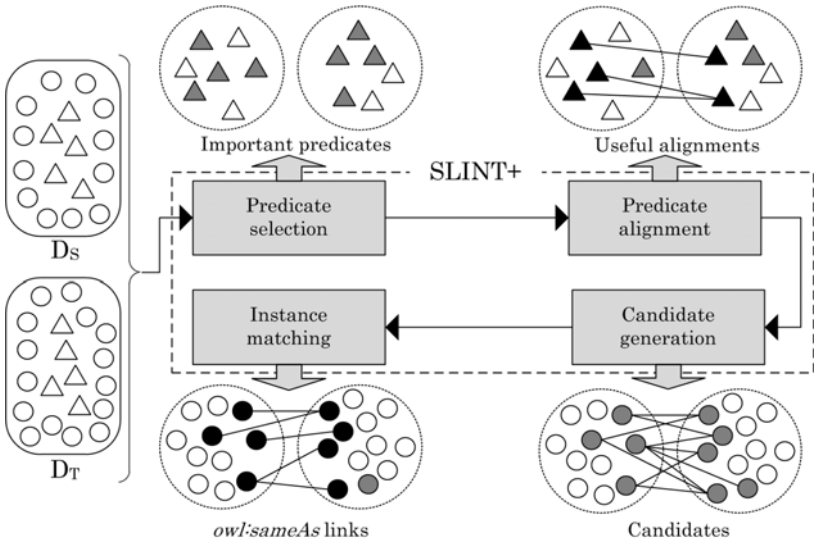


Fig. 1. The interlinking process of SLINT+

instance matching. The first phase separates similar instances into different groups in order to reduce the number of the pending pairs. The second phase will determine which candidate is really identity. With the schema-independent goal, we add two steps into SLINT+: predicate selection and predicate alignment. The mission of these new steps is to find the predicate alignments specifying the same properties of instances.

1.2 Specific techniques used

The architecture of SLINT+ is depicted in Fig.1. D_S and D_T are the source and target data. The predicate selection step finds the important predicate by some statistical measures based on RDF objects involving with each predicate. The predicate alignment step matches important predicates and selects the reasonable alignments. This step can be recognized as an instance-based ontology matching task. The candidate generation step picks up similar instances, which are predicted to be identity. The final step, instance matching, compares suggested candidates and produces the interlinking result. In the following sections, we describe the details of each step in order of the process.

1.2.1 Predicate selection

This is the first step of the interlinking process. It collects the important predicates of each input data sources. Important predicates are expected to be used by a large portion of instances and stored specific information of each instance. Thus, an important predicate should have high frequency and diver RDF objects.

We use coverage and discriminability as the metrics to evaluate the importance level of each predicate. These metrics are the extensions from [4]. Equation (1) and (2) in turn

are the formulas of coverage $Cov(p_k)$ of predicate p_k and its discriminability $Dis(p_k)$. The notation $< s, p, o >$ stands for subject, predicate, and object of a RDF triple. x, D, and f are the instance, data source, and frequency of RDF object, respectively.

$$Cov(p_k) = \frac{|\{x|x \in D, \exists t =< s, p_k, o >\in x\}|}{|D|} \tag{1}$$

$$\begin{aligned} Dis(p_k) &= \frac{Var(p_k) \times H(p_k)}{Var(p_k) + H(p_k)} \\ Var(p_k) &= \frac{|O_{p_k}|}{|\{t|\exists x \in D, t =< s, p_k, o >\in x\}|} \\ H(p_k) &= -\sum_{o_i \in O_{p_k}} \frac{f(o_i)}{\sum_{o_j \in O_{p_k}} f(o_j)} \times \log \frac{f(o_i)}{\sum_{o_j \in O_{p_k}} f(o_j)} \\ O_{p_k} &= \{o|\exists x \in D, t =< s, p_k, o >\in x\} \end{aligned} \tag{2}$$

A predicate is important if its coverage, discriminability, and the harmonic means of them are greater than given thresholds α, β, and γ, respectively. We select two sets of important predicates, from two input data sources. In the next step, we align these sets and find the useful predicate alignments.

1.2.2 Predicate alignment

In this step, we firstly group the predicates by their type. The type of a predicate is determined by the dominant type of its RDF objects. There are five predicate types used in SLINT+: string, URI, double, integer, and date. Secondly, we combine the type-similar predicates of source and target data to get raw predicate alignments. Confidence is the evidence for evaluating the usefulness of raw alignments. The confidence is estimated using the intersection of all RDF objects described by the predicates of each alignment. Equation (3) describes the confidence of the alignment between predicates p_i and p_j.

$$\begin{aligned} conf(p_i, p_j) &= \frac{|R(O_{p_i}) \cap R(O_{p_j})|}{|R(O_{p_i}) \cup R(O_{p_j})|} \\ O_{p_i} &= \{o|\exists x \in D_S, < s, p_i, o >\in x\} \\ O_{p_j} &= \{o|\exists x \in D_T, < s, p_j, o >\in x\} \end{aligned} \tag{3}$$

By using function R, the string, URI, and double are compared indirectly. For string and URI, R collects lexical words from given texts and links. For double, R rounds the values into two decimal points precision. For the remaining types, R uses the original values without transformation.

Only useful alignments whose confidence is greater than a threshold will be kept for the next steps. This threshold is computed by averaging the confidence of non-trivial alignments. An alignment is considered as non-trivial if its confidence is higher than threshold ϵ, a small value. In the next steps, useful alignments will be used as the specification for comparing instances.

1.2.3 Candidate generation

The goal of candidate generation is to limit the number of instances to be compared. SLINT+ performs a very fast comparison for each pair of instances. The result of this comparison is a rough similarity between instances. It is consolidated from their shared RDF objects, without any consideration for each predicate alignment. That is, two compared RDF objects can associate with two predicates having no alignments selected. Equation (4) is the rough similarity of instances x_S and x_T. In this equation, A is the set of filtered predicate alignments; R is the preprocessing procedure, as used in predicate alignment step; $w(O, S)$ and $w(O, T)$ are the weight of shared value O in each data source D_S and D_T, respectively. The weight of string and URI values is estimated by the TF-IDF score while that of remaining types is fixed to 1.0.

$$
\begin{aligned}
rough(x_S, x_T) = & \sum_{O \in R(O_S) \cap R(O_T)} w(O, D_S) \times w(O, D_T) \times sum(p_S) \times sum(p_T) \\
& O_k = \{o | \exists x \in D_k, < s, p_k, o > \in x\} \\
& sum(p_S) = \sum_{(p_S, p) \in A} conf(p_S, p) \\
& sum(p_T) \sum_{(p, p_T) \in A} conf(p, p_T)
\end{aligned}
\tag{4}
$$

Although the rough similarity is computed for each pair of instances, in technical aspect, it can easily be accumulated by passing through each repository only one time in combination with matrix representation for all rough similarities.

Candidates are the pairs whose similarity satisfies two conditions. First, it must be higher than the average similarity of all others λ, because not every instance in source data has the identities in target data. Second, it must be relatively higher than the similarity of the others, in which each instance of the current pair participating. In addition, we multiply the maximum similarity with a damping factor ζ to avoid the single pairing assumption.

1.2.4 Instance matching

For each candidate, we re-compute the similarity and then select identity pairs based on this measure. The similarity of two instances is calculated from the shared values in RDF objects, which are described by each pair of useful predicate alignments. The confidence of each alignment is used as the weight for the similarity. Concretely, the similarity function is given in equation (5). In this equation, R is similar with the previous steps; and $corr$ is the similarity function for RDF objects declared by p_S and p_T. $corr$ function works variously for different type of data. For string and URI, it computes the TF-IDF cosine similarity. For double and integer, it returns the inverted disparity. For date, it simply performs the exact matching.

$$sim(x_S, x_T) = \frac{1}{W} \times \sum_{<p_S,p_T>\in A} conf(p_S, p_T) \times corr(R(O_S), R(O_T)),$$
$$O_k = \{o | \exists x \in D_k, < s, p_k, o > \in x\} \quad (5)$$
$$W = \sum_{<p_S,p_T>\in A} conf(p_S, p_T)$$

Similar to selecting candidate in the previous step, we use η and θ as the same functions and estimations with λ and ζ in the candidate generation step.

The instance matching step closes the standard interlinking process of SLINT+. Next, we describe the configuration for participating OAEI 2013 instance matching.

1.3 Adaptations made for the evaluation

The instance matching track this year requests participant to connect instances between DBpedia and an anonymous synthesis repository. There are five test cases with different difficulty levels. To simplify the experiment, our aim is not using different parameters for each test case. Therefore, we select the configuration that conciliate the results and use it for all test cases. We installed the parameters of SLINT+ by testing the system on training data. We set α, β, γ to 0.01, ϵ = 0.01, ζ = 0.20 and θ = 0.75. We slightly modify the use of η and θ. Instead of using average value of similarities, we permanently set η and λ to 0.

We use BM25 weighting scheme as an alternative for TF-IDF modified cosine in computing the string similarity in instance matching step. To improve the quality of string matching, we remove the words whose frequency is under 0.25.

In addition, we use some unsupervised transformation on the data before inputting to the system. For test case #2, we leverage the information stored in linked instances. In order to obtain adequate properties for matching, we recover the hidden data by dereferencing the linked instances provided in RDF objects. For test case #3, #4, and #5, we use machine translation to get the English version of French strings stored in the target data. SLINT+ currently does not support multilingual matching. Translation from other languages into English is a prerequisite.

1.4 Link to the system, parameters file, and provided alignments

SLINT+ is available to be downloaded at http://ri-www.nii.ac.jp/SLINT/oaei2013.html. We also provide the parameters and the set of alignments for OAEI 2013 instance matching on this page.

2 Results

In this section, we report the experiment result of SLINT+. The results of candidate generation and instance matching are separately reported. To evaluate the final result

Table 1. Candidate generation result

Test case	Number of candidates	Pair completeness	Reduction ratio
#1	2675	0.995	0.986
#2	3602	1.000	0.994
#3	5000	0.995	0.971
#4	5438	0.987	0.968
#5	7177	0.991	0.967

Table 2. Instance matching result

Test case	Recall	Precision	F1
#1	0.979	0.979	0.979
#2	0.998	1.000	0.999
#3	0.913	0.935	0.924
#4	0.909	0.912	0.910
#5	0.880	0.875	0.878

Table 3. Total runtime

Test case	Runtime (in millisecond)
#1	409
#2	421
#3	342
#4	283
#5	353

of data interlinking process, we use the conventional measures: Recall, Precision, and F1 score. To evaluate candidate generation, we use Pair completeness and Reduction ratio [4]. Pair completeness expresses how many actual identity pairs are selected to the candidate set. Reduction ratio is the compression level of instance matching pool comparing with all possible instances pairs between given data sources. We also report the runtime of SLINT+. The experiment was conducted on a computer running with core 2 quad 2.66 GHz CPU, 4 GB of RAM, and Windows 7 64 bit version.

The result of candidate generation, instance matching, and time consumption are given in Table 1, Table 2, and Table 3, respectively.

The results of candidate generation are very good when reserving at least 98.7% of correct alignments and nearly 100% on test case #2. In addition, the largest number of candidate is only 7177, which reduces 96.7% of total instance pairs.

The final results of SLINT+ are generally good. Comparing Recall and Pair completeness on each test, they are similar on test case #1 and #2 and about 7% different on remaining test cases. In addition, SLINT+ performs a stable interlinking since the precision and recall are equivalent for all test cases.

The main reason for the lower result on test case #3, #4, and #5 comes from the transformation of string values. We temporarily used machine translation to convert strings from French to English before conducting the matching process. A better translation strategy may boost the Recall of SLINT+ on these test cases.

The runtime of SLINT+ is very short. It takes about 350 milliseconds for SLINT+ to finish each test case. This is a promising indication for designing a scalable system based on SLINT+ in the future.

3 General comments

3.1 Comments on the OAEI 2013 test cases

Comparing with recent years, the test cases of this time are more interesting and challenging. It is very reasonable when OAEI organizers publish the offline data for keeping the same input for all participants. In addition, it is effective that the test cases can inspect the advantages of each system.

The test cases for this year assume that every instance in source data has an identical one in target data. In our opinion, it could be more efficient if there is a test case that does not imply this assumption. Besides that, the various sizes of data can help evaluate the performance of participants.

3.2 Comments on the OAEI 2013 measures

Since most interlinking systems generate potentially identity instances before matching, we suggest to evaluate this step in separation with instance matching, as also was recommended in [1]. There are many recognized measures in assessing the quality of this step, such as recall, and reduction ratio as we reported in this paper.

4 Conclusion

We introduced SLINT+, a schema-independent and training-free linked data interlinking system. SLINT+ performs four steps interlinking including predicate selection, predicate alignment, candidate generation, and instance matching. SLINT+ gives a promising result at the campaign this year.

Implementing a graph matching algorithm is our objective in improving SLINT+. Since linked data is basically a graph, leveraging linking characteristics between instances will result more confident matching quality. Improving SLINT+ to a scalable system is also our current goal.

References

1. Euzenat J (2012). A modest proposal for data interlinking evaluation. In: ISWC'12 7th Workshop on Ontology Matching, pp. 234.
2. Nguyen K, Ichise R, Le B (2012). Interlinking linked data sources using a domain-independent system. In: 2nd Joint International Semantic Technology, pp.113-128, LNCS 7774.
3. Nguyen K, Ichise R, Le B (2012). SLINT: A schema-independent linked data instance matching system. In: ISWC'12 7th Workshop on Ontology Matching, pp. 1-12.
4. Song D, Heffin J (2011). Automatically generating data linkages using a domain-independent candidate selection approach. In: ISWC' 11, pp. 649-664.

System for Parallel Heterogeneity Resolution (SPHeRe) results for OAEI 2013

Wajahat Ali Khan, Muhammad Bilal Amin, Asad Masood Khattak, Maqbool Hussain, and Sungyoung Lee

Department of Computer Engineering
Kyung Hee University
Seocheon-dong, Giheung-gu, Yongin-si, Gyeonggi-do, Republic of Korea, 446-701
{wajahat.alikhan, mbilalamin, asad.masood, maqbool.hussain, sylee}@oslab.khu.ac.kr

Abstract. SPHeRe is an ontology matching system that utilizes cloud infrastructure for matching large scale ontologies and focus on alignment representation to be stored in the Mediation Bridge Ontology (MBO). MBO is the mediation ontology that stores all the alignments generated between the matched ontologies and represents it in a manner that provides maximum metadata information. SPHeRe is a new initiative therefore it only participates in the large biomedical ontologies track of the OAEI 2013 campaign. The objectives of SPHeRe system participation in OAEI is to shift focus of ontology matching community towards areas such as cloud utilization, effective mapping representation, and flexible and extendable design of the matching system.

1 Presentation of the system

Ontology mappings enables accessibility of information by aligning the resources in ontologies belonging to diverse organizations [3]. These also resolves semantic heterogeneities among data sources. Mainly two steps are required to overcome semantic heterogeneity: Matching resources to determine alignments and interpreting those alignments according to application requirements [5].

We have started developing SPHeRe system in 2013 and its an ongoing project. The objectives of SPHeRe system are performance [2], accuracy, mapping representation, and flexible and extendible design of the system.

1.1 State, purpose, general statement

SPHeRe system target a complete package of a system with main objectives as accuracy, mapping representation, and flexible and extendible system. Its precision is on the higher side in large biomedical ontologies track, that shows its potential of improving the accuracy. It is based on different algorithms such as String Matching Bridge, Synonym Bridge, Child Based Structural Bridge (CBSB), Property Based Structural Bridge (PBSB), and Label Bridge. We plan to include further bridge algorithms in next version of the proposed system by incorporating new matching techniques.

Parallelism has been overlooked by ontology matching systems. SPHeRe avails this opportunity and provides a solution by: (i) creating and caching serialized subsets of

candidate ontologies with single-step parallel loading; (ii) lightweight matcher-based and redundancy-free subsets result in smaller memory footprints and faster load time; and (iii) implementing data parallelism based distribution over subsets of candidate ontologies by exploiting the multicore distributed hardware of cloud platform for parallel ontology matching and execution [2].

Mapping representation is another aspect of SPHeRe system which is not covered in this paper. We have followed OAEI alignment representation format, but we consider mapping representation as an important dimension to be worked by ontology matching research community. The more expressive the alignments should be, the easy its expert verification and the more will be confidence level in transformation process.

1.2 Specific techniques used

SPHeRe system is based on bridge algorithms run in the parallel execution environment to generate alignments to be stored in the MBO as shown in Fig. 1. Matcher Library components stores all the bridge algorithms to be run on the parallel execution environment represented by Parallel Matching Framework. Communication between these two components is regulated by SPHeRe Execution Control module that behaves as a controller. The alignments are stored in the MBO; generated by the bridge algorithms stored in Matcher Library that are run by the Parallel Matching Framework.

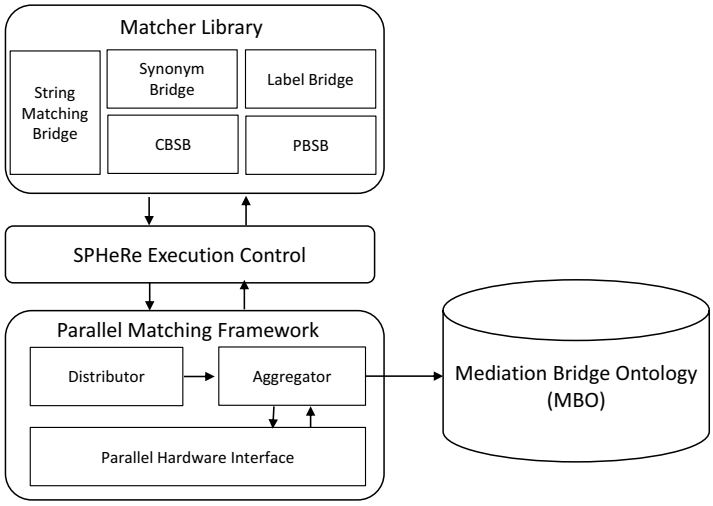


Fig. 1. SPHeRe System Working Model

String Matching Bridge provides matching results by finding similar concepts based on string matching techniques in the matching ontologies. Mainly the algorithm is based on applying edit distance technique [4] of string matching. For any two concepts C_i and

C_j of the ontologies O_i and O_j respectively, edit distance is applied to find matching value, $SimScore \longleftarrow C_i$. EditDistance ($C_j$). A threshold $Threshold$ value of n is set for matching in String Matching Bridge algorithm to limit the number of impure mappings.

Label Bridge uses the labels of the source and target concepts for matching. Initially, concept labels are normalized e.g. using stop word elimination, then list of the source concept labels are matched with list of the target concept labels. The source and target concepts label list $LabelList_i$ and $LabelList_j$ are matched using (($LabelList_i \cap LabelList_j$) $\neq \phi$). If any label in the lists matches, the source and target concepts are stored in the MBO as mappings.

Synonym Bridge is based on finding the similarity between concepts using wordnet [1]. The relationship is identified based on matching the synonyms of the concepts accessed using wordnet. Initially synonyms of source $List_l$:= C_i.GetSynonymWordnetList() and target $List_m$:= C_j.GetSynonymWordnetList() concepts are extracted using wordnet; where C_i and C_j are the source and target concepts respectively. The number of common synonyms $MatchedItems$ is found for calculating the matching value $SimScore$. If its value is less than the threshold then this alignment is discarded, otherwise stored in the MBO.

Child Based Structural Bridge (CBSB) bridge generates mappings between source and target ontologies based on matching children of the concepts. Initially, children of source C_i and target C_j concepts are accessed as lists $ChildList_i$ and $ChildList_j$ respectively. The number of common children in the lists is identified as $MatchChildren$. Finally the matching value $SimScore$ is calculated and compared with the threshold $Threshold$ that is assigned value n. The matching value is calculated using $SimScore \longleftarrow MatchedChildren$ / Average($ChildList_i$, $ChildList_j$). Property Based Structural Bridge (PBSB) uses String Matching Bridge techniques to match properties of source and target concepts for finding similar properties. This information is utilized as in CBSB for matching the source and target ontologies concepts based on their properties. These bridge algorithms are run on a parallel execution environment for better performance of the system.

Multiphase design of SPHeRe system is represented in Fig. 2(taken from [2]) that describes the parallelism inclusion in ontology matching process for better performance. The first phase of the system is ontology loading and management, in which the source and target ontologies are loaded in parallel by multithreaded ontology load interface (OLI). The main tasks of OLI includes; parallel loading of source and target ontologies, parsing for object model creation, and finally ontology model serialization and de-serialization. This is an important phase for data parallelism over multi-threaded execution into the second phase of distribution and matching [2].

Serialized subsets of source and target ontologies are loaded in parallel by multithreaded ontology distribution interface (ODI). ODI is responsible for task distribution of ontology matching over parallel threads (Matcher Threads). ODI currently implements size-based distribution scheme to assign partitions of candidate ontologies to be matched by matcher threads. In a single node, matcher threads correspond to the number of available cores for the running instance. In multi-nodes, each node performs its own parallel loading and internode control messages which are used to communicate

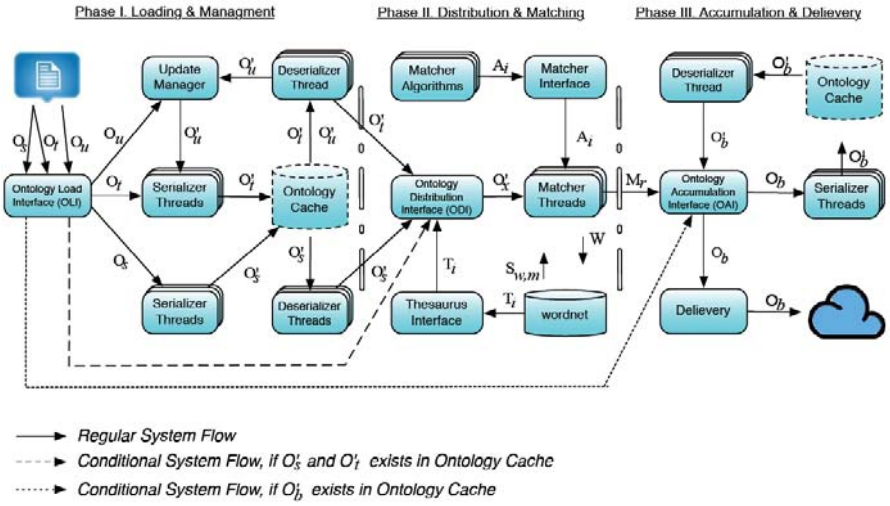


Fig. 2. Performance of SPHeRe System [2]

regarding the ontology distribution and matching algorithms. Matched results provided by matcher threads are submitted to accumulation and delivery phase for the MBO creation and delivery [2].

Ontology Aggregation Interface (OAI) accumulates matched results provided by matcher threads. OAI is responsible for MBO creation by combining matched results as mappings and delivering MBO via cloud storage platform. OAI provides a thread-safe mechanism for all matcher threads to submit their matched results. After the completion of all matched threads, OAI invokes MBO creation process which accumulates all the matched results in a single MBO instance [2]. In case of multi-node distribution, OAI also accumulates results from remote nodes after completion of their local matcher threads. This is a summary version of the performance oriented ontology matching process of SPHeRe system, extracted from [2], that provides a detailed version of the overall process.

1.3 Link to the system and parameters file

https://sites.google.com/a/bilalamin.com/sphere/results

1.4 Link to the set of provided alignments (in align format)

https://sites.google.com/a/bilalamin.com/sphere/results

2 Results

SPHeRe is deployed in multi-node configuration on virtual instances (VMs) over a tri-node private cloud equipped with commodity hardware. Each node is equipped with Intel(R) Core i7(R) CPU, 8GB memory with Xen Hypervisor. Jena API is utilized for its inferencing capabilities. As SPHeRe is using cloud infrastructure therefore initially we have only targeted large biomedical ontologies track. The results are as follows:

2.1 Large biomedical ontologies

SPHeRe is a cloud based ontology matching system that provides the facility to user for matching large scale ontologies without changing their hardware specifications. Figure 3 shows the results of our proposed system in large biomedical ontologies track. It has shown better precision values in almost all the tracks except task 4, while the recall of the system needs to be improved.

Tasks	**Time (s)**	**#Mappings**	**Scores**			**Incoherence Analysis**	
			Precision	Recall	F-Measure	Unsat.	Degree
Task 1	16	2359	0.960	0.772	0.856	367	3.6%
Task 2	8136	2610	0.846	0.753	0.797	1054	0.7%
Task 3	154	1577	0.916	0.162	0.275	805	3.4%
Task 4	20664	2338	0.614	0.160	0.254	6523	3.2%
Task 5	2486	9389	0.924	0.469	0.623	≥ 46256	≥ 61.6%
Task 6	10584	9776	0.881	0.466	0.610	≥ 105,418	≥ 55.7%

Fig. 3. SPHeRe Large Biomedical Ontologies Track Results

3 General comments

3.1 Comments on the results

Performance and precision are the strengths of our system. The design of proposed system also adds to its strength as it is a extendible and reusbale system. Recall is the main weakness of our system, but with the addition of new matching techniques as bridge algorithms can improve this aspect and therefore accuracy can be improved. Extendibility allows adoption of new bridge algorithms easily into the proposed system.

3.2 Discussions on the way to improve the proposed system

New bridge algorithms incorporating new matching techniques is the next line of plan for the proposed system. Object oriented and ontology alignment design patterns are to be implemented for matching different tracks of OAEI campaign. We also tend to include instance based matching, and incorporate change management techniques in the system.

4 Conclusion

SPHeRe system is a new initiative that relies on parallel execution of matcher bridge algorithms for achieving better performance and accuracy. The system is still working on improving the accuracy by incorporating more matcher bridge algorithms to increase the recall value of the system. Performance of the proposed system is better as compare to other system due to running large biomedical ontologies on a single system in appropriate time.

References

1. Wordnet a lexical database for english. http://wordnet.princeton.edu/, last visited in October 2013
2. Amin, M.B., Batool, R., Khan, W.A., Huh, E.N., Lee, S.: Sphere: A performance initiative towards ontology matching by implementing parallelism over cloud platform. In: Journal of Supercomputing. Springer, in Press
3. Li, L., Yang, Y.: Agent-based ontology mapping and integration towards interoperability. Expert Systems 25(3), 197–220 (2008)
4. Navarro, G.: A guided tour to approximate string matching. ACM computing surveys (CSUR) 33(1), 31–88 (2001)
5. Pavel, S., Euzenat, J.: Ontology matching: state of the art and future challenges. Knowledge and Data Engineering, IEEE Transactions on (25), 158–176 (2013)

SYNTHESIS: Results for the Ontology Alignment Evaluation Initiative (OAEI) 2013

Antonis Koukourikos[1, 2], George Vouros[2], Vangelis Karkaletsis[1]

[1]Institute of Informatics & Telecommunications, NCSR "Demokritos", Greece
[2]Department of Digital Systems, University of Piraeus, Greece

Abstract. The paper presents the SYNTHESIS platform, a system for automatic ontology alignment. The system supports the model-based synthesis of different individual matching methods under a co-operational framework. The configuration that has been tested over the datasets provided by the OAEI 2013 tracks incorporates four matching methods. The paper provides a brief description of the system, presents the results acquired over the various OAEI 2013 Campaign tracks and discusses the system's strengths and weaknesses, as well as, future work that will target the observed issues.

1 Presentation of the System

1.1 State, Purpose, General Statement

Given the plethora of the different proposed approaches to ontology alignment, as well as, the variations between them in terms of the types and different facets of information they exploit, the usage (or not) of various external resources and services [1], it is evident that we need effective methods for synthesizing different matching methods.

The present paper describes a specific configuration of the SYNTHESIS platform, a system for ontology matching that combines different methods under a model-based synthesis framework [2]. The objective of SYNTHESIS is to compute coherent alignments, taking advantage of the distinct and complementary advantages of various matching methods. Subsequently we present the generic synthesis process, as well as, the individual methods integrated in the current version of the system. We proceed to present the results of SYNTHESIS over the different test sets of the OAEI 2013 campaign, and the conclusions regarding its performance, its strengths and weaknesses, and the focal points that should be taken into account for the improvement of the system.

1.2 Specific Matching Techniques Used

This section describes briefly the method for synthesizing different matching methods that is employed by SYNTHESIS. Furthermore, it describes the individual matching methods incorporated in the configuration of the system that participated in the OAEI 2013 campaign.

Synthesis. The design and initial implementation of the described matching method is described in [2]. In this work, the synthesis of different matching methods is treated as a coordination problem, aiming to maximize the welfare of the interacting entities (agents). In this setting, each agent corresponds to a specific ontology element and to an individual matching method. Each agent is responsible to decide on a correspondence for its element to a target ontology, also in coordination with the other agents, so as to preserve the semantics of specifications. An agent is characterized by: (a) its state and (b) its utility function. The state ranges in the set of those elements in the target ontology that the matching method of the agent assesses to correspond to the agent's element. A specific assignment to the state variable represents an agent's decision on a specific correspondence. Nevertheless the utility of an agent for a specific correspondence depends on the states of neighboring agents. Specifically, the utility of an agent is specified to take into account structural constraints derived from subsumption relations among classes in the source ontology. These constraints represent dependencies between agents' decisions, and must be satisfied in order for the computed correspondences to preserve the semantics of ontological specifications and ensure the coherence of the correspondences.

Actually, neighbor agents of an agent *A* are those agents that correspond to the same ontology element but to different alignment methods, as well as those agents that correspond to ontology elements that are subsumed by the ontology element of *A*.

Agents are organized in graphs where they run the max-sum algorithm [3] to compute a joined set of correspondences (i.e. an alignment) so as to maximize the sum of their utilities.

SYNTHESIS is actually a generic platform that can be configured to incorporate any number of individual matching methods.

Methods incorporated in the current version of the system. The configuration of SYNTHESIS that was used for the OAEI 2013 campaign incorporates four, most of them fairly standard, matching methods. These are described in the following subsections.

COCLU. This is a string matching technique. It is realized by a partition-based clustering algorithm, which divides the examined data (strings in our cases) into clusters and searches over the created clusters using a greedy heuristic [4]. The clusters are represented as Huffman trees, incrementally constructed as the algorithm generates and updates the clusters by processing one string at a time. The decision for adding a newly encountered string in a given cluster is based on a score function, defined as the difference of the summed length of the coded string tokens that are members of the cluster and the corresponding length of the tokens in the cluster when the examined string is added to the cluster. The implementation incorporated into SYNTHESIS exploits and compares the local names, labels and comments of the examined classes.

VSM. This is a Vector Space Models-based method [5], computing the similarity between two documents. In the case of mapping tasks, the pseudo-documents to be compared are constructed as follows: Each document corresponds to a class or property and

comprises words in the vicinity of that element, i.e. all words found in (a) local name, label and comments of the class; (b) the local name, label and comments for each of the class' properties; and lexical information for its related classes, as defined in [5]. The produced documents are represented as vectors of weighted index words. Each weight is the number of words' occurrence in the document. We apply cosine similarity to measure the similarity between two vectors.

CSR. The CSR method [6] computes subsumption relationships between pairs of classes belonging in two distinct ontologies. The method treats the mapping problem as a classification task, exploiting class properties and lexical information derived from labels, comments, properties and instantiations of the compared classes. Each pair of classes is represented as a feature vector, which has a length equal to the number of distinct features of the ontologies. The classifier is trained using information of both ontologies, considering each ontology in isolation.

LDM Alignment. This new method is conceived as part of a Linked Data management system, which uses unstructured textual information from the Web, in the form of extracted relation triples, in order to perform various processes related to the whole spectrum of managing and maintaining Linked Data repositories, such as Ontology Alignment and Enrichment, Repository Population, Linkage to external repositories, and Content and Link Validation [7]. The method performs web searches, using lexical information from the local names, labels and instances of the compared classes. The web documents returned from the web searches are pre-processed in order to derive their textual information, and relation tuples are extracted from each document. The sets of relation tuples associated with each class are compared, and classes' similarity is assessed.

1.3 Adaptations Made for the Evaluation

After some preliminary runs of the system with the datasets provided by the OAEI campaign, it became evident that the main flaws of the system had to do with its inability to handle ontologies of large size (in terms of the number of elements in the ontology). This is due to the current implementation of the generic synthesis process and to the complexity of the methods incorporated in SYNTHESIS.

In order to produce a system of acceptable efficiency, we introduced a dynamic method allocation component in SYNTHESIS. The component performs a shallow analysis of the input ontologies, in terms of their size and their structure. After several runs with different method combinations for the campaign datasets, the following allocation strategy was adopted: the CSR and LDM methods were excluded when the source ontology included more than 300 classes and properties. Furthermore, CSR was excluded if the examined ontologies were relatively flat, that is if the hierarchy of classes was not deeper that three subsumption levels.

While the motivation for the introduction of this component was to obtain meaningful results for as many OAEI tracks possible, we aim to expand on the idea of dynamically invoking different sets of mapping methods, depending on the specific alignment

task at hand. To this end, the method allocation component can become more intricate and analytic, and be able to select a specific configuration of mapping methods from a much larger pool, ensuring that the system has reasonable execution times while also preserving its performance in terms of precision and recall.

1.4 Link to the System and Parameters File

http://users.iit.demokritos.gr/~kukurik/SYNTHESIS.zip

1.5 Link to the set of provided alignments

http://users.iit.demokritos.gr/~kukurik/results.zip

2 Results

The subsections that follow provide an overview and a brief analysis of the results achieved by SYNTHESIS in the various tracks included in the OAEI 2013 Campaign. SYNTHESIS was packaged and executed following the setup defined by the SEALS platform and using the provided SEALS client executable JAR.

2.1 Benchmark

The following table summarizes the results obtained for the benchmark track, and specifically the bibliography test set.

Bibliographic Dataset		
Average Runtime	H-mean Precision	H-mean Recall
5217 msec	0.576	0.603

We furthermore obtained results for the finance test set, as it was provided via the SEALS platform. These results are summarized below:

Finance Dataset		
Average Runtime	H-mean Precision	H-mean Recall
974454 msec	0.504	0.605

2.2 Anatomy

SYNTHESIS was not able to finish its execution within a reasonable timeframe for this dataset.

2.3 Conference

The following table summarizes the results obtained for the conference dataset of the 2013 campaign, as they were obtained via the SEALS client. The accumulative results are as follows:

Conference Dataset		
Average Runtime	H-mean Precision	H-mean Recall
5245 msec	0.799	0.484

2.4 Multifarm

The current version of SYNTHESIS does not directly address the mapping of ontologies expressed in different languages. However, due to the fact that the synthesis approach somehow matches ontologies by respecting their hierarchical structure, the results obtained show a fairly acceptable precision. The following table summarizes the results reported for this track.

Precision	Recall	F-measure
Different Ontologies		
0.30	0.03	0.05
Same Ontologies		
0.25	0.03	0.04

2.5 Library

SYNTHESIS was not able to finish its execution within a reasonable timeframe for this dataset.

2.6 Large biomedical ontologies

SYNTHESIS was not able to finish its execution within a reasonable timeframe for this dataset.

3 General Comments

3.1 Comments on the results

As evidenced by the obtained results, the main advantages of SYNTHESIS can be summarized to the following:

- SYNTHESIS manages to balance the precision and recall throughout different datasets, even with the fairly simple matching methods running for many pairs of ontologies.

- When adequate lexical information is available, i.e. when classes' names and comments were not suppressed, SYNTHESIS is able to exploit it and produce very good results.
- The constraints taken into account by agents, enables SYNTHESIS to compute coherent alignments.

In contrast, the main drawbacks of SYNTHESIS are:

- The generic synthetic approach implemented in SYNTHESIS, does not scale well with respect to ontology size. While its runtime for small and medium size ontologies is quite satisfactory, when dealing with large or very large ontologies, the system requires a significantly bigger execution time.
- Scalability is significantly affected also by the performance of the individual matching methods incorporated in the OAEI 2013 system configuration.
- The current configuration of SYNTHESIS is sensitive to the lack of adequate lexical information for the ontology elements. In the test cases where information like local class names and labels were suppressed, the results were significantly worse. This is due to the inclusion of mainly lexical-based matching methods in the current configuration of the method.

3.2 Discussions on the ways to improve the current system

The drawbacks of the current configuration of SYNTHESIS directly lead to the main points that can be improved in the future. More specifically, the main problem in various tracks of the campaign was the fact that SYNTHESIS was not able to complete its execution within an acceptable timeframe. This motivates us to examine different scalability techniques and incorporate them in the system. The actions to improve scalability can refer to the performance of the individual methods used, as well as, the actual process of synthesizing the different methods under Synthesis.

Another important step towards improving SYNTHESIS is to design and incorporate a more intricate method for choosing individual mapping methods. This is an improvement step on itself, but it is a prerequisite for being able to introduce additional methods in Synthesis and use the ones more appropriate for a specific alignment task.

The ultimate goal is to incorporate methods that exploit different types of information available (lexical, semantic, structural) at various settings (e.g. ontologies in different languages), by performing a pre-processing step to detect the characteristics of an alignment tasks, and use the most appropriate methods for constructing the agents that will be part of the synthesis process.

4 Conclusion

The participation in the OAEI 2013 has provided significant input for the evaluation and evolution of our system. The major conclusion was the system's inability to handle ontologies of large size, which will be the focus during the immediate next steps of our research. The more detailed feedback provided by the organizers of each track was also

of particular importance, as it provided further insights for the functionality and the requirements of an alignment system.

5 References

1. P. Shvaiko and J. Euzenat, “Ontology Matching: State of the Art and Future Challenges”, IEEE Transactions on Knowledge and Data Engineering 2013, pp. 158-176.
2. V. Spiliopoulos and George A. Vouros, "Synthesizing Ontology Alignment Methods Using the Max-Sum Algorithm", IEEE Transactions on Knowledge and Data Engineering, vol. 24(5), pp. 940-951, May, 2012.
3. A. Farinelli, A. Rogers, A. Petcu, and N.R. Jennings, “Decentralised coordination of low-power embedded devices using the max-sum algorithm”, in Proc. Of the 7th International Conference on Autonomous Agents and Multiagent Systems (AAMAS 2008), Estoril, Portugal, 2008
4. K. Kotis, A. Valarakos, and G.A. Vouros, “AUTOMS: Automating Ontology Mapping through Synthesis of Methods”, in Proceedings of the OAEI (Ontology Alignment Evaluation Initiative) 2006 contest, Ontology Matching International Workshop, Athens, Georgia, USA, 2006
5. V. Spiliopoulos, A.G. Valarakos, G.A. Vouros, and V. Karkaletsis, “SEMA: Results for the ontology alignment contest OAEI 2007”, OAEI (Ontology Alignment Evaluation Initiative) 2006 contest, Ontology Matching International Workshop, Busan, Korea, 2007
6. V. Spiliopoulos, G.A. Vouros, and V. Karkaletsis, “On the discovery of subsumption relations for the alignment of ontologies”, Web Semantics: Science, Services and Agents on the World Wide Web, Volume 8(1), pp. 69-88, March 2010
7. A. Koukourikos, V. Karkaletsis, and G.A. Vouros, “Exploiting unstructured web information for managing linked data spaces”, in Proceedings of the 17th Panhellenic Conference on Informatics (PCI '13), Thessaloniki, Greece, September 2013

WeSeE-Match Results for OAEI 2013

Heiko Paulheim[1] and Sven Hertling[2]

[1] University of Mannheim
Data and Web Science Group
heiko@informatik.uni-mannheim.de
[2] Technische Universitt Darmstadt
Knowledge Engineering Group
hertling@ke.tu-darmstadt.de

Abstract. *WeSeE-Match* is a simple, element-based ontology matching tool. Its basic technique is invoking a web search engine request for each concept and determining element similarity based on the similarity of the search results obtained. Multi-lingual ontologies are translated using a standard web based translation service. Furthermore, it implements a simple strategy for selecting candidate mappings interactively.

1 Presentation of the system

1.1 State, purpose, general statement

The idea of *WeSeE-Match* is to use information on the web for matching ontologies. When developing the algorithm, we were guided by the way a human would possibly solve a matching task. Consider the following example from the OAEI anatomy track[1]: one element in the reference alignment are the two classes with labels *eyelid tarsus* and *tarsal plate*, respectively. As a person not trained in anatomy, one might assume that they have something in common, but one could not tell without doubt.

For a human, the most straight forward strategy in the internet age would be to search for both terms with a search engine, look at the results, and try to figure out whether the websites returned by both searches talk about the same thing. Implicitly, what a human does is identifying relevant sources of information on the web, and analyzing their contents for similarity with respect to the search term given. This naive algorithm is implemented in *WeSeE-Match*.

Furthermore, *WeSeE-Match* uses a basic method for interactive matching, which tries to adaptively set the threshold for selecting the final alignment from the set of candidates.

1.2 Specific techniques used

The core idea of our approach is to use a web search engine for retrieving web documents that a relevant for concepts in the ontologies to match. For getting search terms

[1] http://oaei.ontologymatching.org/2013/anatomy/

from ontology concepts (i.e., classes and properties), we use the labels, comments, and URI fragments of those concepts as search terms. The search results of all concepts are then compared to each other. The more similar the search results are, the higher the concepts' similarity score.

To search for websites, we use URI fragments, labels, and comments of each concept as search strings, and perform some pre-processing, i.e., splitting camel case and underscore separated words into single words, and omitting stop words. For every search result, all the titles and summaries of web pages provided by the search engine are put together into one *describing document*. This approach allows us to parse only the search engine's answer, while avoiding the computational burden of retrieving and parsing all websites in the result sets. The answer provided by the search engine contains titles and excerpts from the website (i.e., some sentences surrounding the occurance of the search term in the website). Therefore, we do not use *whole* websites, but ideally only *relevant parts* of those web sites, i.e., we exploit the search engine both for information retrieval and for information extraction.

For each concept c, we perform a single search each for the fragment, the label, and the comment (if present), thus, we generate up to three documents $doc_{fragment}(c)$, $doc_{label}(c)$, and $doc_{comment}(c)$. The similarity score for each pair of concepts is then computed as the maximum similarity over all of the documents generated for those concepts:

$$sim(c_1, c_2) := max_{i,j \in \{fragment, label, comment\}} sim^*(doc_i(c_1), doc_j(c_2)) \quad (1)$$

For computing the similarity sim^* of two documents, we compute a TF-IDF score, based on the complete set of documents retrieved for all concepts in both ontologies.

Using the TF-IDF measure for computing the similarity of the documents has several advantages. First, stop words like *and*, *or*, and so on are inherently filtered, because they occur in the majority of documents. Second, terms that are common in the domain and thus have little value for disambiguating mappings are also weighted lower. For example, the word *anatomy* will occur quite frequently in the anatomy track, thus, it has only little value for determining mappings there. On the other hand, in the library track, it will be a useful topic identifier and thus be helpful to identify mappings. The TF-IDF measure guarantees that the word *anatomy* gets weighted accordingly in each track.

The result is a score matrix with elements between 0 and 1 for each pair of concepts from both ontologies. For each row and each column where there is a score exceeding τ, we return that pair of concepts with the highest score as a mapping. Furthermore, the filter chain explained in [2] is used, which removes mappings for datatype properties with different ranges, as well as mappings that refer to any imported ontologies.

For multi-lingual ontologies, we first translate the fragments, labels, and comments to English as a pivot language [4]. The translated concepts are then processed as described above.

While the threshold is set to fixed values for the standard tracks in the evaluation, we use an interactive method of selecting the threshold in the interactive track. We use a binary search for selecting the threshold, as discussed in [6], using the following algorithm:

1. Set τ to the average threshold of all candidates. Set $\tau_{min} = 0$, $\tau_{max} = 1$.
2. Present a candidate that has a confidence of τ (or the candidate whose confidence is closest to τ) to the oracle.
3. If the candidate is correct, set τ to $\tau_{min} + (\tau_{max} - \tau_{min}/2)$, τ_{min} to the previous value of τ, Otherwise set set τ to $\tau_{max} - (\tau_{max} - \tau_{min}/2)$, τ_{max} to the previous value of τ
4. If $\tau_{max} > \tau_{min}$, go to 2.
5. Select the final candidates: all candidates with a threshold above τ plus all candidates that are rated positive by the oracle minus all candidates that are rated negative by the oracle.

Given that the ordering of candidates is optimal, i.e., all wrong candidates have a lower confidence score than all correct candidates, that algorithm will yield a threshold τ that separates correct from incorrect candidates.

1.3 Adaptations made for the evaluation

The 2012 version of *WeSeE-Match* [5] used Microsoft Bing as a search engine, as well as the Microsoft Translator API. In order to create a matching system that does not use any services which require payment, we decided to make the following changes for the 2013 evaluation campaign:

- The Bing web search was replaced by JFreeWebSearch[2], which encapsulates the free FAROO web search API[3].
- The Microsoft Translator API was replaced by the Web Translator API[4].

The other new feature for this year's evaluation was the inclusion of the interactive post-processing method. The same code for handling interactive matching was also used in the *Hertuda* matching system [3] for the OAEI 2013 evaluation campaign.

The parameter τ was set to 0.42 for multi-lingual and to 0.51 for mono-lingual matching problems in the non-interactive tracks.

1.4 Link to the system and parameters file

The system is available from `http://www.ke.tu-darmstadt.de/resources/ontology-matching/wesee-match/`.

2 Results

2.1 benchmark

The results from the benchmark track are not surprising. For those problems where labels, URI fragments and/or comments are present and contain actual terms, i.e., they

[2] `http://www.ke.tu-darmstadt.de/resources/jfreewebsearch`
[3] `http://www.faroo.com/`
[4] `http://sourceforge.net/projects/webtranslator/`

are not replaced by random strings, *WeSeE-Match* provides reasonable results. As soon as those strings are removed, the F-measure of *WeSeE-Match* drops, since no other evaluation (e.g., ontology structure) is used by *WeSeE-Match*.

The evaluation of runtime also reveals that *WeSeE-Match* is one of the slowest matching systems participating in the campaign. This is due to the fact that the search engine used restricts the usage to one request per second. Thus, *WeSeE-Match* spends a lot of idle time to fulfill that requirement.

2.2 anatomy and conference

On anatomy, *WeSeE-Match* is one of the worst performing matchers, suffering both in precision in recall. It is in particular interesting to see the drop from last year's performance (F-measure 0.829) to this year's (F-measure 0.47), where the only significant change was the use of a different search engine. This shows that the choice of the web search engine in search-engine based matching can make a huge difference in the results.

In the conference track, the differences to last year are not that significant, ending at a comparable F-measure of 0.55, which makes *WeSeE-Match* an average matcher in the conference track.

2.3 multifarm

For multifarm, the F-measure has dropped from 0.41 in OAEI 2012 to 0.15 in OAEI 2013. As discussed above, the performance on the English-only conference track, which underlies multifarm, has remained stable, so this is mainly an effect of the use of a different translation engine. Again, it becomes obvious that the choice of a different translation engine clearly influences the results.

In detail, the 2012 version of *WeSeE-Match* was capable of matching Chinese and Russian ontologies, because these languages were supported by the Microsoft Translator API, but not the Web Translator API. Furthermore, the results for Czech are significantly below the 2012 results, which shows a suboptimal support for that language in the Web Translator API. For the other languages, the results have remained on a similar level.

2.4 library and large biomedical ontologies

Since *WeSeE-Match* is not optimized for scalability (in particular, necessary waiting times to avoid blocking from search engine providers slow down the matcher), it could not be run on those larger tracks due to time limits. However, the approach does in principle scale up to larger ontologies as well. In the OAEI 2012 campaign, for example, *WeSeE-Match* was capable of completing the library track, when the time limit was set to one week instead of one day [1].

Table 1. Thresholds and results in the interactive track. The table depicts the best possible threshold and the F-measure that is achieved with that threshold, as well as the threshold chosen and the F-measure achieved by *WeSeE-Match*. In cases where an interval of thresholds leads to the same result, we report the average of that interval.

	best possible selection				actual selection			
Test case	Threshold	Precision	Recall	F-measure	Threshold	Precision	Recall	F-Measure
cmt-conference	0.14	0.438	0.467	0.452	0.03	0.304	0.467	0.368
cmt-confOf	0.15	0.385	0.313	0.345	0.26	0.714	0.313	0.435
cmt-edas	0.94	0.889	0.615	0.727	1.00	0.778	0.538	0.636
cmt-ekaw	0.90	0.625	0.455	0.526	0.19	0.500	0.455	0.476
cmt-iasted	0.66	0.800	1.000	0.889	1.00	0.800	1.000	0.889
cmt-sigkdd	0.14	0.786	0.917	0.846	0.23	0.769	0.833	0.800
conf-confOf	0.97	0.583	0.467	0.519	1.00	0.714	0.333	0.455
conf-edas	0.95	0.583	0.412	0.483	1.00	1.000	0.118	0.211
conf-ekaw	0.12	0.333	0.480	0.393	0.18	0.538	0.280	0.368
conf-iasted	0.15	0.500	0.357	0.417	0.79	1.000	0.214	0.353
conf-sigkdd	0.28	0.818	0.600	0.692	0.78	0.750	0.600	0.667
confOf-edas	1.00	0.643	0.474	0.545	1.00	0.778	0.368	0.500
confOf-ekaw	0.11	0.619	0.650	0.634	1.00	0.667	0.600	0.632
confOf-iasted	0.90	0.571	0.444	0.500	1.00	1.000	0.333	0.500
confOf-sigkdd	0.69	0.667	0.571	0.615	0.19	0.500	0.429	0.462
edas-ekaw	0.60	0.526	0.435	0.476	1.00	1.000	0.130	0.231
edas-iasted	0.28	0.500	0.421	0.457	0.19	0.500	0.105	0.174
edas-sigkdd	0.95	0.875	0.467	0.609	1.00	0.875	0.467	0.609
ekaw-iasted	0.57	0.429	0.600	0.500	1.00	0.556	0.500	0.526
ekaw-sigkdd	0.81	0.875	0.636	0.737	1.00	1.000	0.273	0.429
iasted-sigkdd	0.94	0.647	0.733	0.688	1.00	0.667	0.133	0.222

2.5 interactive

The interactive matching component in *WeSeE-Match* – which is the same as in Hertuda – tries to find an optimal threshold via binary search for selecting the final mapping, as discussed above. Table 1 depicts the results. For comparison, we also show the optimal threshold that could have been selected in theory.[5]

It can be observed that the thresholds chosen by our algorithm are most often far from the optimum, which is also reflected in the F-measure achieved. In most cases, the selected threshold is higher than the optimal, i.e., the selection is biased towards precision. In fact, 1.0 is often chosen as a threshold. The reason is that that mapping elements such as `conference#Conference = eads#Conference`, which naturally re-

[5] There are cases where the F-measure achieved by the actual selection is higher. This is due to the fact that in a post-processing step, all information obtained from the oracle is exploited by removing the wrong mappings and including the correct ones, even if they do not fall into the interval defined by the final threshold selection. Furthermore, in some cases, the precision is lower despite a higher threshold. This is due to the fact that the interactive track uses a slightly different reference alignment than the original conference track, on which the optimal thresholds have been determined.

ceive a confidence score of 1.0, are rated wrong by the oracle, so that our binary search approach sets the threshold τ to the maximum possible, i.e., 1.0.

In general, while our interactive approach would work well for ideally sorted candidates, its performance with real confidence scores provided by *WeSeE-Match* (and also Hertuda) are not satisfying. Thus, using a greedy algorithm here is maybe not the best choice, and other means to determine an optimal threshold, such as estimating the F-measure based on user interaction, as discussed in [6], may be a better option for future versions.

3 Conclusion

In this paper, we have discussed the results of the 2013 version of *WeSeE-Match*. It can be observed that the choice for free services instead of commercial ones has changed the performance of *WeSeE-Match* for the worse. The trade-off between the use of commercial services and high-quality results is not easy to address.

Furthermore, it can be seen that a naive greedy approach for selecting a threshold parameter interactively does not provide satisfying results, which calls for more sophisticated methods.

References

1. Jos Luis Aguirre, Kai Eckert, Jrme Euzenat, Alfio Ferrara, Willem Robert van Hage, Laura Hollink, Christian Meilicke, Andriy Nikolov, Dominique Ritze, Francois Scharffe, Pavel Shvaiko, Ondrej Svab-Zamazal, Cssia Trojahn, Ernesto Jimnez-Ruiz, Bernardo Cuenca Grau, and Benjamin Zapilko. Results of the ontology alignment evaluation initiative 2012. In *Seventh International Workshop on Ontology Matching (OM 2012)*, 2012.
2. Thanh Tung Dang, Alexander Gabriel, Sven Hertling, Philipp Roskosch, Marcel Wlotzka, Jan Ruben Zilke, Frederik Janssen, and Heiko Paulheim. Hotmatch results for oeai 2012. In *Seventh International Workshop on Ontology Matching (OM 2012)*, 2012.
3. Sven Hertling. Hertuda results for oeai 2012. In *Seventh International Workshop on Ontology Matching (OM 2012)*, 2012.
4. Michael Paul, Hirofumi Yamamoto, Eiichiro Sumita, and Satoshi Nakamura. On the importance of pivot language selection for statistical machine translation. In *2009 Annual Conference of the North American Chapter of the Association for Computational Linguistics, Companion Volume: Short Papers*, pages 221–224, 2009.
5. Heiko Paulheim. Wesee-match results for oeai 2012. In *Seventh International Workshop on Ontology Matching (OM 2012)*, 2012.
6. Heiko Paulheim, Sven Hertling, and Dominique Ritze. Towards evaluating interactive ontology matching tools. In *Lecture Notes in Computer Science*, 2013.

XMapGen and XMapSiG Results for OAEI 2013

Warith Eddine Djeddi and Mohamed Tarek Khadir

LabGED, Computer Science Department, University Badji Mokhtar, Annaba, Algeria
{djeddi, khadir}@labged.net

Abstract. The XMapGen and XMapSig systems are flexible and self-configuring matching tools using different strategies for combining multiple similarity measures into a single aggregated metric with the final aim of improving the ontology alignment quality of large scale ontologies. XMapGen and XMapSig are two variants of XMap++. The results obtained by the two ontology matching tools within the 9th edition of the Ontology Alignment Evaluation Initiative (OAEI 2013) campaign are therefore presented.

1 Presentation of the system

We present a fully automatic general purpose ontology alignment tools called XMapGen (eXtensible Mapping using Genetic) and XMapSig (eXtensible Mapping using Sigmoid), a new and lighter implementations of their ancestor XMap++ [1]. XMapGen and XMapSig include several matchers. These matchers calculate similarities between the terms from the different source ontologies. The matchers implement strategies based on linguistic matching, structure-based strategies and strategies that use auxiliary information in the thesaurus WordNet to enhance the alignment process. XMapGen uses Genetic Algorithm (GA) as a machine learning-based method to ascertain how to combine multiple similarity measures into a single aggregated metric with the final aim of improving the ontology alignment quality. XMapSig uses sigmoid function [4] for combining the corresponding weights for different semantic aspects, reflecting their different importance. This year, XMapGen and XMapSig participate in five tracks including Benchmark, Conference, Library, Anatomy and Large Biomedical Ontologies tracks.

1.1 State, purpose, general statement

XMapGen and XMapSig are a scalable ontology alignment tools capable of matching English language ontologies described in different OWL languages (i.e., OWL Lite, OWL DL, and OWL Full). The major principle of the matching strategy in XMapGen and XMapSig approaches is combining multiple similarity measures into a single similarity metric using weights determined by intelligent strategies in order to skip over the burden of manual selection. Despite the impressive strategy in adding GA, aligning medium-sized and large-scale ontologies is still very time consuming and computationally expensive. This inspires us to consider the use of a particular parallel matching on multiple cores or machines for dealing with the scalability issue on ontology matching.

1.2 Specific techniques used

In this section, the workflow of XMap++ and its main components is briefly described and shown in Fig.1. Both systems XMapGen and XMapSig calculate three different basic measures to create three similarity matrixes. String-based, semantic and structural methods are the three different categories of measuring similarities.

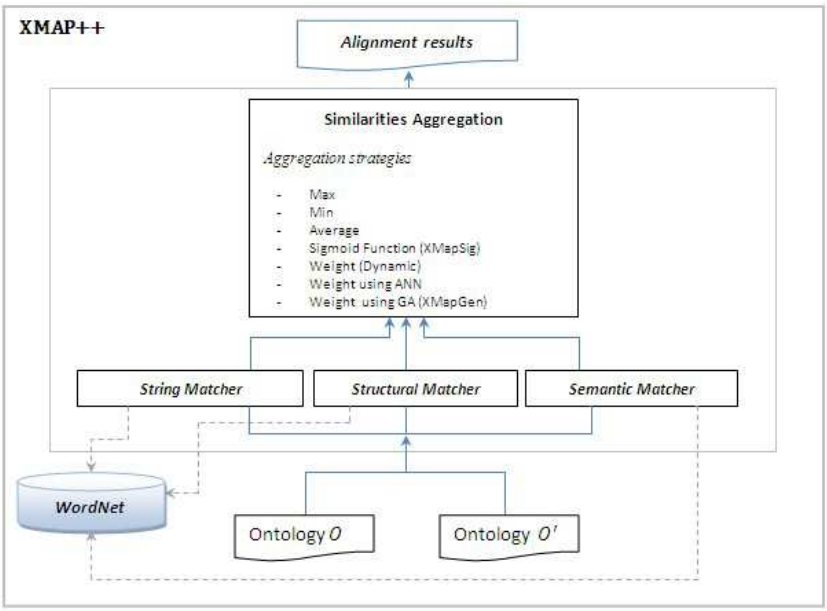


Fig. 1. Sketch of Architecture for XMAP++.

In XMap++ approach, a generic workflow for a given ontology matching scenario is as follows:

1. Matching inputs are two ontologies, source O and target $O^{'}$ parsed by an Ontology Parser component;
2. The ***String Matcher*** based on linguistic matching compares the textual descriptions of the concepts associated with the nodes (labels, names) of each ontology;
3. The ***Linguistic matcher*** jointly aims at identifying words in the input strings, relaying on WordNet [5] which provide additional information towards unveiling mappings in cases where features such as labels are missing or in cases where names are replaced by random strings. These matching techniques may provide incorrect match candidates, structural matching is used to correct such match candidates based on their structural context. In order to deal with lexical ambiguity, we introduce the notion of *scope* belonging to a concept which represents the context where it is placed. In our approach, the similarity between two entities of different ontologies is evaluated not only by investigating the semantics of the entities

names, but also taking into account the local context, through which the effective meaning is described. In particular, the neighborhood of a term (immediate parent and children in the *is-a* hierarchy). Increasing the radius means enlarging the scope (i.e. this area) and, consequently, the set of neighbour concepts that intervene in the description of the context. The value of linguistic methods is added to the linguistic matcher or the structure matcher in order to enhance the semantic ambiguity during the comparison process of entity names;

4. The ***structural matcher*** aligns nodes based on their adjacency relationships. The relationships (e.g., *subClassOf* and *is-a*) that are frequently used in the ontology serve, at one hand, as the foundation of the structural matching. On the other hand, the structural rules are used to extract the ontological context of each node, up to a certain depth (radius). This context includes some of its neighbours, where each of them is associated a weight representing the importance it has when evaluating the contextual node. The XMap++ algorithm values the semantic relation between two concepts while taking in consideration the types of cardinality constraints (e.g. *OWLAllValuesFrom*, *OWLSomeValuesFrom*, *OWLMinCardinality*, *OWL-Cardinality*, *OWLMaxCardinality*, *Same_as* or *Kind_of*) and values between their properties (e.g. *OWLMaxCardinality* $>=1$). Alignment suggestions are then determined by combining and filtering the results generated by one or more matchers;

5. The three matchers perform similarity computation in which each entity of the source ontology is compared with all the entities of the target ontology, thus producing three similarity matrices, which contain a value for each pair of entities. After that, an aggregation operator is used to combine multiple similarity matrices computed by different matchers to a single aggregated $n * m$ similarity matrix, where n is the number of element in the source ontology and m is the number of elements in the target ontology. We refer to [1] for more detail about the pruning and splitting techniques on data matrices for two couple of entities;

6. XMap++ uses three types of aggregation operator; these strategies are *aggregation*, *selection* and *combination*. The *aggregation* reduces the similarity cube to a matrix, by aggregating all matcher's results matrices into one. This *aggregation* is defined by five strategies: *Max*, *Min*, *Average*, *sigmoid function* and *Weighted*. The *Max* strategy is an optimistic one, selecting the highest similarity value calculated by any matcher. Contrary, the *Min* strategy selects the lowest value. *Average* evens out the matcher results, calculating the average. The *sigmoid* method combines multiple results using a sigmoid methods, which is essentially a smoothed threshold function [4]. In order to satisfy a different importance of matcher results, *Weighted* computes the weighted sum of the results, according to user defined weights or automatic defined weights using a dynamic strategy [3], using an Artificial Neural Network (ANN) (Djeddi and Khadir, 2013) or using Genetic Algorithm (GA);

7. Finally, these values are filtered using a selection according to a defined threshold and the desired cardinality. In our algorithm, we adopt the *1-1* cardinality to find the optimal solution in polynomial time.

1.3 Adaptations made for the evaluation

Several technical adaptations were required for integrating the system into the Seals platform, such as:

- Updating some libraries (e.g., Alignment API) or changing the way some parameters are communicated.
- To deal with large ontologies, XMapGen and XMapSig conducted specific experiments to see whether a matching system can exploit a multi-core architecture [6] to speed up the matching process. We adapted parallel matching to the use of threading to distribute the jobs of two matchers (Classes matcher and Properties matcher) on all available CPU cores on only one machine.
- There are two factors that directly impact to the systems' performance. The first ones relates to matching by machine learning model. The training data and selected similarity metrics as learning attributes are important. A simple solution for this issue is proposed by selecting the most appropriate similarity metrics and training data according to their correlation with expert's assessment. The second issue relates to the threshold used as a filter in the selection module. Different tests require different thresholds.
- In XMap++, the aim of the *Structural Matcher* is to correct such match candidates based on their structural context. The structural approach matches the nodes based on their adjacency relationships. XMapGen and XMapSig exploit only the superclass-subclass relationships (subsumption relationships) that are frequently used in ontologies when the total number of entities is bigger than 1500 entities in each ontology. *We restrict the contextual similarity computing; only the value of the semantic relation between two concepts without taking in consideration the types of cardinality constraints and values between their properties*, because if the ontologies became larger, the efficiency of the automatic alignment methods decreases considerably, in term of execution time, and memory size.

2 Results

Evaluation results of XMapGen and XMapSig in the OAEI 2013 campaign are here evaluated and discussed. We participated in five tracks: *Benchmarks*, *Conference*, *Library*, *Anatomy* and *Large Biomedical* Ontologies. Detailed results and descriptions about the used computation environments are provided on the OAEI 2013 result page.

2.1 Benchmark

In this track, there are multiple match tasks per sub-track where one source ontology is compared with a number of systematically modified target ontologies. According to Table 1, it is shown that approximately 4% is the percentage improvement of XMapSig versus XMapGen. The recall low values are explained by the fact that ontological entities with scrambled labels, lexical similarity becomes ineffective. For two algorithms, structural similarity stems from lexical similarity hence scrambling the labels makes the alignment more challenging. This trend of reduction in precision, recall and f-measure which can be observed throughout the test cases from 248 till 266.

Table 1. Results for Benchmark track.

System	biblioc		
	P	R	F
XMapSig	0.70	0.50	0.58
XMapGen	0.66	0.46	0.54

2.2 Anatomy

The Anatomy track consists of finding an alignment between the Adult Mouse Anatomy (2744 classes) and a part of the NCI Thesaurus (3304 classes) describing the human anatomy. XMapSig achieves a good F-Measure value of ≈75% in an acceptable amount of time (393 sec.) (see Table 2). In a separate configuration using genetic algorithm (XMapGen) we could increase the recall to ≈2% but the precision is decreased of ≈5%, due to running the structural matcher in a lightweight version (restriction of the contextual similarity). XMapGen needs around 403 minutes to compute the alignment. We plan to use bio medical lexical databases like Unified Medical Language System (UMLS) for improving the recall.

Table 2. Results for Anatomy track.

System	Precision	F-Measure	Recall	Time(s)
XMapSig	0.856	0.753	0.673	393
XMapGen	0.808	0.747	0.695	403

2.3 Conference

The Conference track uses a collection of 16 ontologies from the domain of academic conferences. Most ontologies were equipped with OWL DL axioms of various kinds; this opens a useful way to test our semantic matchers. The match quality was evaluated against an original (ra1) as well as entailed reference alignment (ra2). As the Table 3 shows, for both evaluations we achieved F-Measure values better than the Baseline1 results (57% for ra1 and 53% for ra2) when using XMapGen1_4. Also with XMapSig1_3 we achieved F-Measure values better than the Baseline1 results (58% for ra1 and 53% for ra2).

Table 3. Results for Conference track.

System	RA1 Reference			RA2 Reference		
	P	R	F	P	R	F
XMapSig1_3	0.72	0.48	0.58	0.68	0.44	0.53
XMapGen1_4	0.68	0.49	0.57	0.64	0.45	0.53

2.4 Library

The library track involves the matching of the STW thesaurus (6,575 classes) and the Soz thesaurus (8,376 classes). Both of these thesauri provide vocabulary for economic and social sciences. Table 4 summarizes the results obtained by XMapGen and XMapSig. The mapping quality achieved by XMapSig on the library track is not as positive as on the other tracks. XMapSig attains a precision of 0.79 and a recall of 0.31. Possible reasons may be the absence of domain and range definitions (in fact, of properties in general), as for anatomy, and the presence of multi-lingual labels. As XMapSig does not respect languages, this may lead to false positives. XMapSig requires $\approx$ 48 min and 34 sec. It is mainly due to the fact that our approach uses the notion of context with a value of radius not fixed as an input parameter at the starting of the matching task. So the algorithm looks at all the depth for the compared ontologies which involve the creation of a matrix with $M > 1.3$ billion pairs.

XMapGen could perform worse in terms of precision (0.031) and obtained higher for recall than XMapSig (0.37). The low of precision is due to a problem in the training of the genetic algorithm. We fixed this problem with an improved version delivered after deadline (precision and recall performance was different). In this paper we decided to present (see Table 4), only the results generated with the official version of our tool (before the deadline of the contest), and not the one generated with an improved version (fixing the training problem of GA) submitted after the deadline.

Table 4. Results for Library track.

System	Precision	Recall	F-Measure	Time(s)
XMapSig	0.799	0.318	0.455	2914
XMapGen	0.031	0.371	0.057	3008

2.5 Large biomedical ontologies

This data set consists of several large scale ontologies, containing up to tens of thousands of concepts. Our two systems were only capable to match the small task for FMA-NCI and FMA-SNOMED. The large ones are not finished in time due to the high computational complexity. We found the NCI thesaurus very time consuming for context based mapping as its concepts have many siblings. Among the varying evaluation methods, XMapGen and XMapSig produced fairly consistent alignments when matching the FMA and NCI ontologies, all resulting in f-measures of approximately 0.60 (See Table 5). However, the results of the completed tasks indicate that our system is already capable of producing alignments of high quality in this domain, thus improving its efficiency, for instance by applying the complete functionalities of XMap++ , should result in an overall satisfying performance during the next evaluation. As not expected from our two systems, they could perform the alignment in less than 3 hours 25 min of Small FMA-SNOMED fragments with high precision and low recall (See Table 6).

Table 5. Results for the Large BioMed track: FMA-NCI tasks

Task 1: Small FMA and NCI fragments					
System	Size	Precision	Recall	F-Measure	Time(s)
XMapSig	1564	0.864	0.461	0.602	1477
XMapGen	1687	0.833	0.479	0.608	1504

Table 6. Results for the Large BioMed track: FMA-SNOMED tasks

Task 3: Small FMA and SNOMED fragments					
System	Size	Precision	Recall	F-Measure	Time(s)
XMapSig	1581	0.760	0.134	0.228	11720
XMapGen	1827	0.694	0.142	0.236	12127

3 General comments

3.1 Comments on the results and future improvements

As previously stated, the aim of this development experience was not to deliver a tool to compete with others in terms of precision and recall. Instead, we aimed at the development of a new and stable version of XMap++ using new and state-of-the-art technologies and alignment methods. Additionally, to tackle the large ontology matching problem we improved the runtime of the algorithm using a divide-and-conquer approach that can partition the execution of the matchers into small threads was improved and joins their results after each similarity calculation. A direct comparison between the XMapGen and XMapSig shows that the addition of GA does not has a negative effect on the algorithm but, on the contrary, leads to slightly better results, especially in terms of recall. In most track, XMapSig supplies high precision than XMapGen. Whereas using Genetic Algorithm (XMapGen) performs quite high in terms of recall than using sigmoid function (XMapSig). The reason is behind the using of the sigmoid function and the weight for linguistic matcher. Therefore, for a high value of the linguistic weight, some important properties of classes founded by XMapSig may be omitted, as the weight of linguistic matcher is high and the algorithm focuses more on the linguistic level (names of classes) than the structural level (properties and their restrictions). This problem can be resolved by using a sigmoidal function, which increases proportionally the important similarity of the structural matcher, to be considered in the final calculation of two classes similarities. Finally we participated in the OAEI 2013 with two variants with the aim to analyze the strength and the weakness of each strategy (Sigmoid and Genetic) at the goal for combing them in one ontology alignment task.

3.2 Discussions on the way to improve the proposed system

Some probable approaches to improving our tools are listed as follows:

1. Adopt more flexible strategies in defining the way for automatic threshold rather than manually tuning. Developing dynamic strategies for setting the correct threshold value for each compared ontologies and not one for all;

2. Take comments and Instance information of ontology into account, especially when the name of concept is meaningless;
3. Matching larger ontologies still takes significantly longer time when parsing ontologies with Alignment API. We plan to solve this problem using an ontology parser which permits to load multiple ontologies in parallel via threading;
4. Usage of background knowledge based on the UMLS Meta-thesaurus to have high recall when aligning ontologies from the biomedical science domain.

3.3 Comments on the OAEI 2013 procedure

As a first participation, we found the OAEI procedure very convenient and the organizers very supportive. The use of Seals allows objective assessments. The OAEI test cases are various and this leads to comparison on different levels of difficulty, which is very interesting. We found that SEALS platform is a very valuable tool to compare the performance of our system with the others.

4 Conclusion

Our system participated to the campaign with two versions (XMapGen and XMapSig) of our approach, corresponding to different strategies of weights aggregation. Generally, according to our results in OAEI 2013, our two systems delivered fair results comparatively to other participants. The preliminary results were quite good to encourage us to continue seeking better solutions. It seems that both systems XMapGen and XMapSig can efficiently match semantically rich ontologies containing tens (and even hundreds) of thousands of classes. We confirm that the addition of Genetic Algorithm (GA) keeps the performance and, furthermore, eliminates the necessity of tuning the weights manually. Moreover, the learning framework is very flexible: many combinations of matchers and parameters may be used in the future, various types of training models (Resilient propagation, Levenberg marquardt, Backpropagation, Anneal, Radial or Manhatan method, etc.) and new metrics.

References

1. Djeddi, W., Khadir, M.T.: Ontology alignment using artificial neural network for large-scale ontologies. In the International Journal of Metadata, Semantics and Ontologies (IJMSO), Vol.8, No.1, pp.75-92 (2013)
2. Djeddi, W., Khadir, M.T.: Introducing artificial neural network in ontologies alignment process. In the Journal Control and Cybernetics, Vol. 41, No. 4, pp.743-759 (2012)
3. Djeddi, W., Khadir, M.T. : A dynamic multistrategy ontology alignment framework based on semantic relationships using WordNet. In Proc of the 3rd International Conference on Computer Science and its Applications (CIIA11), 1315 December, Saida, Algeria, pp.149154 (2012)
4. Djeddi, W., Khadir, M.T.: XMAP: a novel structural approach for alignment of OWL-full ontologies. In Proc. of the International Conference on Machine and Web Intelligence (ICMWI), pp.347-352 (2010)
5. Fellbaum, C. : WordNet: An Electronic Lexical Database, MIT Press, Cambridge, MA (1998)
6. Gross, A., Hartung, M., Kirsten, T. and Rahm, E. : On matching large life science ontologies in parallel. In , in Lambrix, P. and Kemp, G.J.L. (Eds), DILS, Springer, pp.35-49 (2010)

YAM++ – Results for OAEI 2013

DuyHoa Ngo, Zohra Bellahsene

University Montpellier 2, LIRMM
{duyhoa.ngo, bella}@lirmm.fr

Abstract. In this paper, we briefly present the new YAM++ 2013 version and its results on OAEI 2013 campaign. The most interesting aspect of the new version of YAM++ is that it produces high matching quality results for large scale ontology matching tasks with good runtime performance on normal hardware configuration like PC or laptop without using any powerful server.

1 Presentation of the system

YAM++ - (not) Yet Another Matcher is a flexible and self-configuring ontology matching system for discovering semantic correspondences between entities (i.e., classes, object properties and data properties) of ontologies. This new version YAM++ 2013 has a significant improvement from the previous versions [6, 5] in terms of both effectiveness and efficiency, especially for very large scale tasks. The YAM++'s general architecture is not changed much. However, most of its algorithms have been updated/added by the new effective ones. For example, we have implemented a **disk-based** method for storing the temporary information of the input ontology during the indexing process in order to save main memor space. Consequently, the new version YAM++ 2013 has improved both the matching quality and time performance in large scale ontology matching tasks. This year, YAM++ participates in **six tracks** including **Benchmark**, **Conference**, **Multifarm**, **Library**, **Anatomy** and **Large Biomedical Ontologies** tracks. However, due to limitation of time and person, we have not upgrade YAM++ to participate to **Interactive matching evaluation** and **Instance Matching** tasks.

1.1 State, purpose, general statement

In YAM++ approach all useful information of entities such as terminological, structural or contextual, semantic and extensional are exploited. For each type of extracted information, a corresponding matching module has been implemented in order to discover as many as possible candidate mappings.

The major drawback of the previous version **YAM++ 2012** [5], despite the fact that it achieved good results and high ranking at almost tracks, is very low time performance, especially for the **Large Biomedical Ontologies** tracks. After carefully studying this issue, we realize that our algorithms for pre-processing and indexing the input ontologies lead to a high complexity of $O(n^2)$, where n is the size of the ontology. Additionally, the semantic verification component did not work well for the very large scale ontology matching task.

In the current version **YAM++ 2013**, the flaws mentioned above have been significantly fixed. Firstly, we have revised our algorithms for pre-processing and indexing the input ontologies and now they are with $O(\|n\|+\|v\|)$ complexity, where n and v are the number of nodes and edges of a Directed Acyclic Graph transformed from the ontology. Moreover, we have implemented a **disk-based** method for storing the temporary information of the input ontologes during the indexing process. This method allows us save a significant space of main memory. this makes possible run YAM++ with very large scale ontology matching in a personal computer with ordinary configuration (using 1G JVM only).

Secondly, we have introduced different inconsistent alignment patterns in order to detect as much as possible conflict set. Then, a new and fast approximate algorithm has been implemented to find the nearly optimization solution, which corresponds to the final consistent alignment.

1.2 Specific techniques used

In this section, we will briefly describe the workflow of YAM++ and its main components, which are shown in Fig.1.

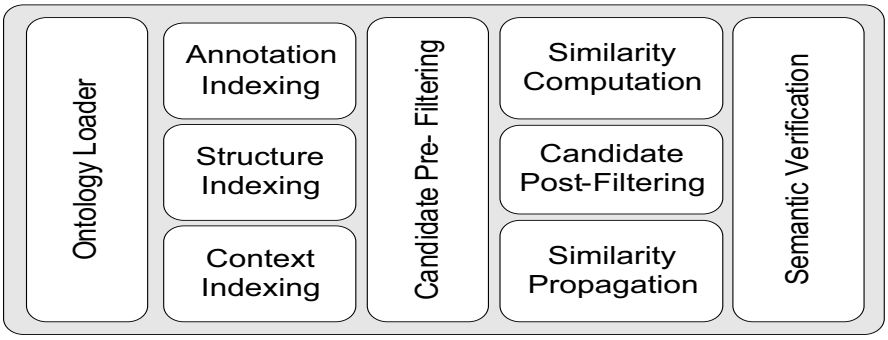


Fig. 1: Main components of YAM++ system

In YAM++ approach, a generic workflow for a given ontology matching scenario is as follows.

1. Input ontologies are loaded and parsed by a **Ontology Loader** component;
2. Information of entities in ontologies are indexed by the **Annotation Indexing**, the **Structure Indexing** and **Context Indexing** components;
3. **Candidates Pre-Filtering** component filters out all possible pairs of entities from the input ontologies, whose descriptions are highly similar;
4. The candidate mappings are then passed into **Similarity Computation** component, which includes: (i) the **Terminological Matcher** component that produces a set of mappings by comparing the annotations of entities; (ii) the **Instance-based Matcher** component that supplements new mappings through shared instances between ontologies and (iii) the **Contextual Matcher**, which is used to compute the similarity value of a pair of entities by comparing their context profiles. In YAM++,

the matching results of the **Terminological Matcher**, the **Contextual Matcher** and the **Instance-based Matcher** are combined to have a unique set of mappings. We call them element level matching result.

5. The **Similarity Propagation** component then enhances element level matching result by exploiting structural information of entities; We call the result of this phase structure level matching result.
6. The **Candidate Post-Filtering** component is used to combine and select the potential candidate mappings from element and structure level results.
7. Finally, the **Semantic Verification** component refines those mappings in order to eliminate the inconsistent ones.

Let us now to present the specific features of each component.

Ontology Loader To read and parse input ontologies, YAM++ uses OWLAPI open source library. In addition, YAM++ makes use of (i) Pellet[1] - an OWL 2 Reasoner in order to discover hidden relations between entities in small ontology and (ii) ELK[2] reasoner for large ontology. In this phase, the whole ontology is loaded in the main memory.

Annotation Indexing In this component, all annotations information of entities such as ID, labels and comments are extracted. The languages used for representing annotations are considered. In the case where input ontology use different languages to describe the annotations of entities, a multilingual translator (**Microsoft Bing**) is used to translate those annotations to English. Those annotations are then normalized by tokenizing into set of tokens, removing stop words, and stemming. Next, the resulting tokens are indexed in a table for future use.

Structure Indexing In this component, the main structure information such as IS-A and PAR-OF hierarchies of ontology are stored. In particular, YAM++ assigns a compressed bitset values for every entity of the ontology. Through the bitset values of each entity, YAM++ can fast and easily gets its ancestors, descendants, etc. A benefit of this method is to easily access to the structure information of ontology and minimize memory for storing it. After this step, the loaded ontology can be released to save main memory.

Context Indexing In this component, we define a context profile of an entity as a set of three text corpora: (i) Entity Description includes annotation of the entity itself; (ii) Ancestor Description comprises the descriptions of its ancestor and (iii) Descendant Description comprises the descriptions of its descendant. Indexing those corpora is We performed by **Lucene** indexing engine.

Candidates Pre-Filtering The aim of this component is to reduce the computational space for a given scenario, especially for the large scale ontology matching tasks. In YAM++, two filters have been designed for the purpose of performing matching process efficiently.

[1] http://clarkparsia.com/pellet/
[2] http://www.cs.ox.ac.uk/isg/tools/ELK/

– A **Description Filter** is a search-based filter, which filters out the candidate mappings before computing the real similarity values between the description of entities. Firstly, the descriptions of all entities in the bigger size ontology are indexed by **Lucene** search engine. For each entity in the smaller size ontology, three multiple terms queries corresponding to three description included in its context profile will be performed. The **top-K** algorithm based on ranking score of those queries is used to select the most similar entities.
– A **Label Filter** is used to fast detect candidate mappings, where the labels of entities in each candidate mapping are similar or differ in maximum two tokens. The intuition is that if two labels of two entities differ by more than three tokens, any string-based method will produce a low similarity score value. Then, these entities are highly unmatched.

Similarity Computation The three matcher described in this component are the same as in the **YAM++ 2012** version. For more detail, we refer readers to our papers: **Terminological Matcher** [7], **Instance-based Matcher** [6]. A slight modification at the **Contextual Matcher** is that we use algorithm described in [8] for small ontology matching, whereas we use the **Lucene** ranking score for large scale ontology matching.

Similarity Propagation This component is similar to the **Structural Matcher** component described in YAM++ 2012 version. It contains two similarity propagation methods namely Similarity Propagation and Confidence Propagation.

– The **Similarity Propagation** method is a graph matching method, which inherits the main features of the well-known **Similarity Flooding** algorithm [2]. The only difference is about transforming an ontology to a directed labeled graph. This matcher is not changed from the first YAM++ version to the current version. Therefore, for saving space, we refer to section **Similarity Flooding** of [6] for more details.
– The **Confidence Propagation** method principle is as follows. Assume $\langle a_1, b_1, \equiv, c_1\rangle$ and $\langle a_2, b_2, \equiv, c_2\rangle$ are two initial mappings, which are maybe discovered by the element level matcher (i.e., the terminological matcher or instance-based matcher). If a_1 and b_1 are ancestors of a_2 and b_2 respectively, then after running confidence propagation, we have $\langle a_1, b_1, \equiv, c_1 + c_2\rangle$ and $\langle a_2, b_2, \equiv, c_2 + c_1\rangle$. Note that, confidence values are propagated only among collection of initial mappings.

In YAM++, the aim of the **Similarity Propagation** method is discovering new mappings by exploiting as much as possible the structural information of entities. This method is used for a small scale ontology matching task, where the total number of entities in each ontology is smaller than 1000. In contrary, the **Confidence Propagation** method supports a **Semantic Verification** component to eliminate inconsistent mappings. This method is mainly used in a large scale ontology matching scenario.

Candidates Post-Filtering The aim of the **Mappings Combination and Selection** component is to produce a unique set of mappings from the matching results obtained by the terminological matcher, instance-based matcher and structural matcher. In this component, a **Dynamic Weighted Aggregation** method have been implemented. Given an ontology matching scenario, it automatically computes a weight value for each matcher and establishes a threshold value for selecting the best candidate mappings. The main idea of this method can be seen in [6] for more details.

Semantic Verification After running the similarity or confidence propagation on overall candidate mappings, the final achieved similarity values reach a certain stability. Based on those values, YAM++ is able to remove inconsistent mappings with more certainty. There are two main steps in the **Semantic Verification** component such as (i) identifying inconsistent mappings, and (ii) eliminating inconsistent mappings.

In order to identify inconsistencies, several semantic conflict patterns have been designed in YAM++ as follows (see [4] for more detail):

- Two mappings $\langle a_1, b_1\rangle$ and $\langle a_2, b_2\rangle$ are crisscross conflict if a_1 is an ancestor of a_2 in ontology O_1 and b_2 is an ancestor of b_1 in ontology O_2.
- Two mappings $\langle a_1, b_1\rangle$ and $\langle a_2, b_2\rangle$ are disjointness subsumption conflict if a_1 is an ancestor of a_2 in ontology O_1 and b_2 disjoints with b_1 in ontology O_2 and vice versa.
- A property-property mapping $\langle p_1, p_2\rangle$ is inconsistent with respect to alignment A if $\{Doms(p_1) \times Doms(p_2)\} \cap A = \emptyset$ and $\{Rans(p_1) \times Rans(p_2)\} \cap A = \emptyset$ then (p_1, p_2), where $Doms(p)$ and $Rans(p)$ return a set of domains and ranges of property p.
- Two mappings $\langle a, b_1\rangle$ and $\langle a, b_2\rangle$ are duplicated conflict if the cardinality matching is 1:1 (for a small scale ontology matching scenario) or the semantic similarity $SemSim(b_1, b_2)$ is less than a threshold value θ (for a large scale matching with cardinality 1:m).

Two methods, i.e., complete and approximate diagnosis are used in order to eliminate inconsistent mappings. We use complete version Alcomo [3] for small scale. In term of approximate version for large scale, we transform this task into a **Maximum Weighted Vertex Cover** problem. A modification of **Clarkson** algorithm [1], which is a **Greedy** approach. The idea of this method is that it iteratively removes the mapping with the smallest cost, which is computed by a ratio of its current confidence value to number of its conflicts.

1.3 Adaptations made for the evaluation

Before running the matching process, YAM++ analyzes the input ontologies and adapts itself to the matching task. In particular, if the annotations of entities in input ontologies are described by different languages, YAM++ automatically translates them in English. If the number of entities in input ontologies is smaller than 1000, YAM++ is switched to small scale matching regime, otherwise, it runs with large scale matching regime. The main difference between the two regimes lies in the **Similarity Propagation** and **Semantic Verification** components as we discussed above.

1.4 Link to the system and parameters file

A SEALS client wrapper for YAM++ system and the parameter files can be download at: http://www2.lirmm.fr/d̃ngo/YAMplusplus2013.zip. See the instructions in tutorial from SEALS platform[3] to test our system.

[3] http://oaei.ontologymatching.org/2013/seals-eval.html

1.5 Link to the set of provided alignments (in align format)

The results of all tracks can be downloaded at: http://www2.lirmm.fr/d̃ngo/ YAMplus-plus2013Results.zip.

2 Results

In this section, we present the evaluation results obtained by running YAM++ with SEALS client with **Benchmark**, **Conference**, **Multifarm**, **Library**, **Anatomy** and **Large Biomedical Ontologies** tracks. All experiments are executed by YAM++ with SEALS client version 4.1 beta and JDK 1.6 on PC Intel 3.0 Pentium, 3Gb RAM, Window XP SP3.

2.1 Benchmark

In OAEI 2013, Benchmark includes 5 blind tests for both organizers and participants. Those tests are regeneration of the bibliography test set. Table 1 shows the avergae results of YAM++ running on the Benchmark dataset.

Test set	H-mean Precision	H-mean Recall	H-mean Fmeasure
Biblio	0.97	0.82	0.89

Table 1: YAM++ results on pre-test Benchmark track

2.2 Conference

Conference track now contains 16 ontologies from the same domain (conference organization) and each ontology must be matched against every other ontology. This track is an open+blind, so in the Table 2, we can only report our results with respect to the available reference alignments

Test set	H-mean Precision	H-mean Recall	H-mean Fmeasure
Conference ra1	0.80	0.69	0.74
Conference ra2	0.78	0.65	0.71

Table 2: YAM++ results on Conference track

2.3 MultiFarm

The goal of the MultiFarm track is to evaluate the ability of matcher systems to deal with multilingual ontologies. It is based on the OntoFarm dataset, where annotations of entities are represented in different languages such as: English (en), Chinese (cn), Czech (cz), Dutch (nl), French (fr), German (de), Portuguese (pt), Russian (ru) and Spanish (es). YAM++'s results are showed in the Fig. 2

2.4 Anatomy

The Anatomy track consists of finding an alignment between the Adult Mouse Anatomy (2744 classes) and a part of the NCI Thesaurus (3304 classes) describing the human anatomy. Table 3 shows the evaluation result and runtime of YAM++ on this track.

Test	Pr	Fm	Re	Test	Pr	Fm	Re	Test	Pr	Fm	Re	Test	Pr	Fm	Re
cn-cz	0.71	0.56	0.46	cz-en	0.81	0.7	0.62	de-nl	0.73	0.6	0.5	es-nl	0.66	0.13	0.07
cn-de	0.75	0.58	0.48	cz-es	0.68	0.14	0.08	de-pt	0.73	0.61	0.52	es-pt	0.76	0.23	0.13
cn-en	0.74	0.59	0.49	cz-fr	0.78	0.69	0.61	de-ru	0.77	0.62	0.52	es-ru	0.69	0.15	0.08
cn-es	0.58	0.16	0.1	cz-nl	0.76	0.65	0.57	en-es	0.72	0.18	0.1	fr-nl	0.77	0.68	0.61
cn-fr	0.77	0.62	0.52	cz-pt	0.77	0.67	0.59	en-fr	0.81	0.72	0.65	fr-pt	0.79	0.72	0.67
cn-nl	0.71	0.57	0.48	cz-ru	0.77	0.63	0.53	en-nl	0.79	0.68	0.6	fr-ru	0.77	0.66	0.58
cn-pt	0.7	0.57	0.49	de-en	0.82	0.71	0.62	en-pt	0.8	0.7	0.62	nl-pt	0.77	0.7	0.64
cn-ru	0.75	0.57	0.46	de-es	0.68	0.14	0.08	en-ru	0.79	0.66	0.57	nl-ru	0.76	0.65	0.57
cz-de	0.76	0.63	0.54	de-fr	0.76	0.65	0.57	es-fr	0.71	0.15	0.09	pt-ru	0.75	0.65	0.57

Fig. 2: YAM++ results on MultiFarm track

Test set	Precision	Recall	Fmeasure	Run times
Anatomy	0.944	0.869	0.905	62 (s)

Table 3: YAM++ results on Anatomy track

2.5 Library

The library track is a real-word task to match the STW (6575 classes) and the TheSoz (8376 classes) thesaurus. Table 4 shows the evaluation result and runtime of YAM++ against an existing reference alignment on this track.

Test set	Precision	Recall	Fmeasure	Run times
Library	0.692	0.808	0.745	411 (s)

Table 4: YAM++ results on Library track

2.6 Large Biomedical Ontologies

This track consists of finding alignments between the Foundational Model of Anatomy (FMA), SNOMED CT, and the National Cancer Institute Thesaurus (NCI). There are 9 sub tasks with different size of input ontologies, i.e., small fragment, large fragment and the whole ontologies. Table 5 shows the evaluation results and run times of YAM++ on those sub tasks.

3 General comments

This is the third time YAM++ participates to the OAEI campaign. We found that SEALS platform is a very valuable tool to compare the performance of our system with the others. Besides, we also found that OAEI tracks covers a wide range of heterogeneity in ontology matching task. They are very useful to help developers/researchers to develop their semantic matching system.

3.1 Comments on the results

The current version of YAM++ has shown a significant improvement both in terms of matching quality and runtime with respect to the previous version. In particular, the

Test set	Precision	Recall	Fmeasure	Run times
Small FMA - NCI	0.976	0.853	0.910	94 (s)
Whole FMA - NCI	0.899	0.846	0.872	366 (s)
Small FMA - SNOMED	0.982	0.729	0.836	100 (s)
Whole FMA - SNOMED	0.947	0.725	0.821	402 (s)
Small SNOMED - NCI	0.967	0.611	0.749	391 (s)
Whole SNOMED - NCI	0.881	0.601	0.714	713 (s)

Table 5: YAM++ results on Large Biomedical Ontologies track

H-mean Fmeasure value of all the very large scale dataset (i.e., Library, Biomedical ontologies) has been improved.

4 Conclusion

In this paper, we have presented our ontology matching system called YAM++ and its evaluation results on different tracks on OAEI 2013 campaign. The experimental results are promising and show that YAM++ is able to work effectively and efficiently with real-world ontology matching tasks. In near future, we continue improving the matching quality and efficiency of YAM++. Furthermore, we plan to deal with instance matching track also.

References

[1] Kenneth L. Clarkson. A modification of the greedy algorithm for vertex cover. *Information Processing Letters*, pages 23 – 25, 1983.

[2] Sergey Melnik el at. Similarity flooding: A versatile graph matching algorithm and its application to schema matching. In *ICDE*, pages 117–128, 2002.

[3] Christian Meilicke. Alignment incoherence in ontology matching. In *PhD.Thesis, University of Mannheim, Chair of Artificial Intelligence*, 2011.

[4] DuyHoa Ngo. Enhancing ontology matching by using machine learning, graph matching and information retrieval techniques. In *PhD.Thesis, University Montpellier II*, 2012.

[5] DuyHoa Ngo and Zohra Bellahsene. Yam++ results for oaei 2012. In *OM*, 2012.

[6] DuyHoa Ngo, Zohra Bellahsene, and Remi Coletta. Yam++ results for oaei 2011. In *OM*, 2011.

[7] DuyHoa Ngo, Zohra Bellahsene, and Konstantin Todorov. Opening the black box of ontology matching. In *ESWC*, pages 16–30, 2013.

[8] DuyHoa Ngo, Zohra Bellasene, and Remi Coletta. A generic approach for combining linguistic and context profile metrics in ontology matching. In *ODBASE Conference*, 2011.

Collective Ontology Alignment

Jason B. Ellis, Oktie Hassanzadeh, Kavitha Srinivas, and Michael J. Ward

IBM T.J. Watson Research,
P.O. Box 704, Yorktown Heights, NY 10598
{jasone,hassanzadeh,ksrinivs,MichaelJWard}@us.ibm.com

1 Introduction

Enterprises are captivated by the promise of using big data to develop new products and services that provide new insights into their customers and businesses. However, there are significant challenges leveraging data across heterogeneous data stores, including making those data accessible and usable by non-experts. We designed a novel system called Helix which employs a combination of user-driven and automated techniques to bootstrap the building of a unified semantic model over virtualized data. Such a uniform semantic model allows users to query across data stores transparently, without needing to navigate a maze of data silos, data formats, and query languages.

In this poster, we discuss a specific aspect of Helix: the method by which it facilitates ontology alignment. Such alignments are very noisy and manually fixing the issues is a laborious process, especially when all the work must be done prior to putting the system into use. Instead, Helix proposes to engage users progressively in the process of ontology alignment through the course of their everyday use of the system. We do this by framing ontology alignment as a guided data exploration and integration task.

2 Guided Exploration, Linking, and Sharing

Helix provides a uniform user interface for heterogeneous data exploration and linking. This interface abstracts the underlying differences among data stores and data representations, with the goal of allowing the user to focus on their task rather than the technology. This interface engages users in the data alignment process through three key features:

1. Guided navigation - search and navigate to locate results of interest, assisted by suggestions based on semantic and schematic links
2. Saving results - save results of interest and share those results with others
3. Guided linking - users select two saved results and Helix guides them through ontology alignment. The resulting linked data can be saved, shared, and used in future links. (see Figure 1)

Through this process, users are creating ontology alignments by finding data of interest, aligning it, and saving/sharing what they find useful. In this way,

Fig. 1. Helix Front Page with two results selected for linking.

everyone who uses Helix is contributing to the alignment of the underlying data sources and can leverage the work of others.

Currently, sharing happens by one user explicitly sending saved results to another. However, we are building a recommender system that will automatically show relevant results to users through the course of their work, allowing them to more readily reuse ontology alignments.

Previous work has proposed systems that perform analysis and "pay-as-you-go" integration in specific domains using semantic technologies [2]. However, such systems typically leave the user out of the ontology mapping process. Helix explicitly engages users in linking the data they are interested in.

This work is also related to research on making it easier for non-expert users to query standard database management systems, particularly those that take an *exploratory search* approach [3]. Explorator offers a somewhat similar user experience, allowing users to explore RDF data through a process involving search, faceted navigation, and set operations [1]. By contrast, Helix allows users to navigate heterogeneous data and build complex queries through a process of progressively linking saved results. It also assists users through semantic & schematic guidance, linkage discovery, and (ultimately) recommendations.

References

1. de Araújo, S., Schwabe, D.: Explorator: a tool for exploring RDF data through direct manipulation. In: Linked Data on the Web WWW Workshop (2009)
2. Lopez, V., Kotoulas, S., Sbodio, M.L., Stephenson, M., Gkoulalas-Divanis, A., Mac Aonghusa, P.: QuerioCity: a linked data platform for urban information management. In: ISWC'12: Proceedings of the 11th international conference on The Semantic Web. Springer-Verlag (Nov 2012)
3. White, R.W., Drucker, S.M., Marchionini, G., Hearst, M., schraefel, m.c.: Exploratory search and HCI. In: CHI '07 extended abstracts. pp. 2877–2880. ACM Press, New York, New York, USA (2007)

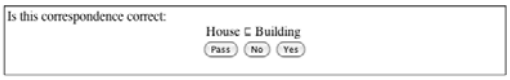
Uncertainty in crowdsourcing ontology matching

Jérôme Euzenat

INRIA & LIG, France

Matching crowdsourcing There may be several motivations for crowdsourcing ontology matching, i.e., relying on a crowd of workers for establishing alignments [2]. It may be for matching itself or for establishing a reference alignment against which matchers are evaluated. It may also be possible to use crowdsourcing as complement to a matcher, either to filter the finally provided alignment or to punctually provide hints to the matcher during its processing.

The ideal way of crowdsourcing ontology matching is to design microtasks (t) around alignment correspondences and to ask workers (w) if they are valid or not.



$c_w(t) = \sqsubseteq \equiv$
House $\sqsubseteq$ Building

Uncertainty Most of the crowdsourcing philosophy relies on the idea that microtasks have one single solution that workers are good at finding (even if this requires more skilled workers).

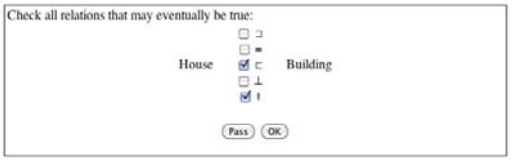
The experience acquired in ontology matching shows that, because concepts are underdefined, there may not be one unique answer to a matching microtask. Moreover, we know that "experts" do not necessary have coinciding opinions [3].

One way to deal with this problem is to take into account uncertainty from the beginning and to know how to deal with uncertainty instead of trying to cast it into certainty.

We base our approach on the principle that workers may not know for certain what the answer is, but they may know for certain that it is among a set of alternatives. Representing this set is a way to deal with uncertainty.

Disjunctive crowdsourcing One first idea is, instead of asking people what the answer is (is this correspondence correct), asking them what could be an answer. For that purpose it is necessary to ask them choosing between several alternative relations.

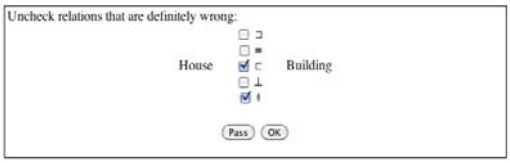
Using jointly exhaustive and pairwise disjoint (JEPD) relations (R) is a proper way to ask such questions. Moreover, uncertainty may be represented within alignments through algebras of relations [1].



$dc_w(t) = \{\sqsubseteq, \between\} \equiv$
House $\sqsubseteq$ Building
$\vee$ House $\between$ Building

This will require slightly more work from workers, but they will not require them to choose between alternatives when they do not see any clear correct one.

Complement crowdsourcing One further possibility, instead of asking people what could be an answer is to ask them what is definitely *not* an answer. In this second setting, it may be easier for people to provide meaningful information without needing to commit to one particular answer.



$$cc_w(t) = \{\sqsubseteq, \not\between\} \equiv$$
$$\neg(\mathsf{House} \sqsubseteq \mathsf{Building})$$
$$\wedge\neg(\mathsf{House} \not\between \mathsf{Building})$$

Complement crowdsourcing is logically the complement of disjunctive crowdsourcing. However, we conjecture that this will make workers adopt a cautious attitude, discarding only relations that they really think are wrong.

Summary This is related to the consensus between experts [3]. In the initial case, if they do not choose the same relation, they disagree. In the two latter schemes, as long as the intersection between their choices are not disjoint, they do not disagree, but express disjunctive opinions.

With a population W of workers, classical crowdsourcing asks if one relation is true or what is the relation between two entities. So, the result of the task c_w is a single relation. Disjunctive crowdsourcing asks which relations could hold, hence, $dc_w \subseteq R$. Similarly, complement crowdsourcing asks which relations do not hold, hence $cc_w \subseteq R$. We conjecture that:

$$\forall w \in W, \overline{cc_w}(t) \supseteq dc_w(t) \supseteq \{c_w(t)\}$$

This would have the good feature to provide better opportunity for consensus because:

$$\cap_{w \in W} \overline{cc_w}(t) \supseteq \cap_{w \in W} dc_w(t) \supseteq \cap_{w \in W} \{c_w\}(t)$$

It would be an interesting experiment to check if these modalities allow for less conflicts and more accurate alignments. We could test the hypothesis that if it is better to ask users to choose one relation between two entities or to discard nonapplyable relations among all the possible ones.

References

1. Jérôme Euzenat. Algebras of ontology alignment relations. In *Proc. 7th international semantic web conference (ISWC), Karlsruhe (DE)*, pages 387–402, 2008.
2. Cristina Sarasua, Elena Simperl, and Natalya Noy. CrowdMAP: crowdsourcing ontology alignment with microtasks. In *Proc. 11th ISWC*, volume 7649 of *Lecture notes in computer science*, pages 525–541, 2012.
3. Anna Tordai, Jacco van Ossenbruggen, and Bob Wielinga. Let's agree to disagree: on the evaluation of vocabulary alignment. In *Proc. 6th International Conference on Knowledge Capture (K-CAP)*, pages 65–72, Banff (CA), 2011.

Mix'n'Match: Iteratively Combining Ontology Matchers in an Anytime Fashion

Simon Steyskal[1,2] and Axel Polleres[3,1]

[1] Siemens AG, Siemensstrasse 90, 1210 Vienna, Austria
[2] Vienna University of Technology, 1040 Vienna, Austria
[3] Vienna University of Economics & Business, 1020 Vienna, Austria

1 The Mix'n'Match Framework

Mix'n'Match is a framework to combine different ontology matchers in an iterative fashion for improved combined results: starting from an empty set of alignments, we aim at iteratively supporting in each round, matchers with the combined results of other matchers found in previous rounds, aggregating the results of a heterogeneous set of ontology matchers, cf. Fig.1.

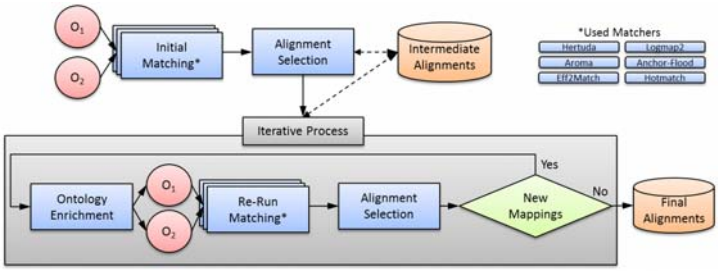


Fig. 1. Framework of Mix'n'Match

Alignment Combination: The combination of the alignments, especially the choice of those which are used for the enrichment step is based on majority votes. By only accepting alignments which were found by a majority of heterogeneous matching tools we aim to ensure a high precision of the found alignments and therefore try to emulate reference alignments as e.g. provided by iterative approval through a human domain expert. Although Mix'n'Match would support the definition of an alignment confidence threshold as additional parameter (i.e, only allowing alignments over a specific threshold to pass) we set this threshold per default to 0 in our experiments: since the calculation of confidence values is not standardized across matchers and some matchers only produce boolean confidence values, e.g. [3]). Other result aggregation methods may be conceivable here, like taking the individual performance of off-the-shelf matchers on specific matching tasks into account [2, 4], but since this approach would lead to a more inflexible alignment process this issue needs more detailed investigations in future versions of Mix'n'Match.

Ontology Enrichment: After mixing of the alignments, enrichment of the ontologies takes place; since most ontology matchers do not support refernce alignments (as specified by the OAEI alignment format[4]), we implement enrichment by simple URI replacement to emulate such reference alignments found in each matching round: for every pair of matched entities in the set of aggregated alignments, a merged entity URI is created and will replace every occurrence of the matched entities in both ontologies. This approach is motivated by the assumption that if two entities were stated as equal by the majority of ontology matchers, their URI can be replaced by an unified URI, stating them as equal in the sense of URIs as global identifiers. Note that, despite the fact that most matchers seem to ignore URIs as unique identifiers of entities, our experiments showed that URI replacement was effective in boosting the confidence value of such asserted alignments in almost all considered matchers.

Intermediate Results and Anytime Behavior: We collect the intermediate results of every finished off-the-shelf matcher in every iteration. Furthermore we keep track of every alignment found so far together with the number of individual matchers which have found this alignment in any previous matching round. This offers the possibility to interrupt the matching process at any time, retrieving only those alignments which have been found by the majority of the ontology matchers at the time the interruption has taken place. In contrast to other ontology matchers which offer this anytime behavior like MapPSO [1], we are not only restricted to gather alignment results of the last finished matching iteration, but also use the alignment results of already finished off-the-shelf matchers in the current matching round.

Evaluation Results To test our approach, we based our evaluations on OAEI evaluation tracks (*Benchmark, Conference, Anatomy*) and retrieved very promising results, typically outperforming the single matchers combined within the Mix'n'Match framework in terms of F-measure. For detailed evaluation results we refer our readers to an extended report accompanying this poster, available at `http://www.steyskal.info/om2013/extendedversion.pdf`.

References

1. J. Bock, J. Hettenhausen. Discrete particle swarm optimisation for ontology alignment. *Information Sciences*, 192:152–173, 2012.
2. I.F. Cruz, F. Palandri Antonelli, C. Stroe. Efficient selection of mappings and automatic quality-driven combination of matching methods. In *Int'l Workshop on Ontology Matching (OM)*, CEUR volume 551, pages 49–60. Citeseer, 2009.
3. M. Seddiqui Hanif, M. Aono. An efficient and scalable algorithm for segmented alignment of ontologies of arbitrary size. *J. Web Sem.*, 7(4):344–356, 2009.
4. A. Nikolov, M. d'Aquin, E. Motta. Unsupervised learning of link discovery configuration. In *ESWC2012*, pages 119–133. Springer, 2012.

[4] `http://alignapi.gforge.inria.fr/format.html`

An Ontology Mapping Method Based on Support Vector Machine

Jie Liu,Linlin Qin, Hanshi Wang

College of Information and Engineering, Capital Normal University, Beijing 100048, P.R.China

Correspondence should be addressed to Jie Liu, liujxxxy@126.com

Abstract. Ontology mapping has been applied widely in the field of semantic web. In this paper a new algorithm of ontology mapping were achieved. First, the new algorithms of calculating four individual similarities (concept name, property, instance and structure) between two concepts were mentioned. Secondly, the similarity vectors consisting of four weighted individual similarities were built, and the weights are the linear function of *harmony* and *reliability*, and the linear function can measure the importance of individual similarities. Here, each of ontology concept pairs was represented by a similarity vector. Lastly, Support Vector Machine (SVM) was used to accomplish mapping discovery by training the similarity vectors. Experimental results showed that, in our method, *precision*, *recall* and *f-measure* of ontology mapping discovery reached 95%, 93.5% and 94.24%, respectively. Our method outperformed other existing methods.

Introduction: In this paper, our study mainly is to discover the mapping[1] between concepts belonging to the different ontologies respectively. The proposed algorithm about ontology mapping in this paper mainly focuses on the following two points:

1. Using new methods of calculating individual similarities (concept name, property, instance and structure).
2. Proposing the methods of similarity aggregation using SVM to classify the similarity vectors which reflect the similarities of concept pairs. Here, the elements of a similarity vector consist of the weighted individual similarities, and the weight of an individual similarity is the linear function of *harmony*[2] and *reliability*[3].

To evaluate the method proposed in this paper, we used the benchmark tests in OAEI ontology matching campaign 2012 as data sets, and got precision, recall and f-measure of the different ontology mapping algorithms by experiment.

The algorithms of ontology mapping: The process from calculating similarities to discovering ontology mapping is shown as Fig.1. In Fig.1, O_1, O_2 are two ontologies. Firstly, four individual similarities were computed; secondly, the similarity vectors consisting of four weighted individual similarities were built, and the weights were decided by both of harmony and reliability. Here, each of concept pairs between two ontologies was represented by a similarity vector; lastly, SVM was used to accomplish mapping discovery by classifying the similarity vectors.

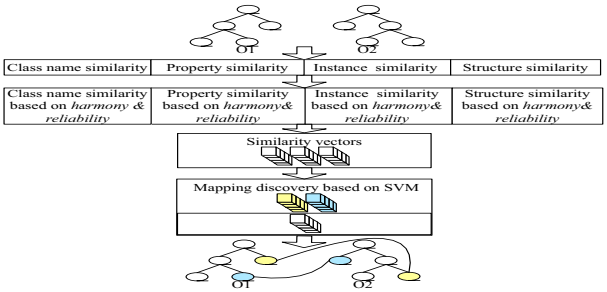


Fig.1. Process of ontology mapping

Experiment Design: Ontology mapping methods related to similarity calculation have been discussed in many studies, and *precision*, *recall* and *f-measure* are usually used to evaluate mapping results. Experimental steps are as follows:

(1) For all ontological concept pairs, the four individual similarities would be calculated; (2)These similarities would be aggregated and mappings between ontologies would be extracted by using 11 methods such as "*Neural network*", "*Sigmoid*", "*Harmony*", "*Reliability*" and so on;(3) For our approach, after four individual similarities and their respective harmony and reliability were worked out, similarity vectors consisting of our weighted individual similarities would be built, and the weights are the linear function of harmony and reliability, and ontology mappings would be extracted by SVM;(4)For all ontology pairs, precision, recall and f-measure of ontology mapping discovery would be calculated in every methods.

Result: Precision, recall and f-measure in our approach reach 0.95,0.935 and 0.9424, respectively, and are the highest, which can validate that the results of mapping discovery are more accurate after harmony and reliability is joined into SVM, and also can show that our approach outperforms than others dramatically.

Conclusions: This study is an effective approach to resolve the problem about ontology mapping in the Semantic Web. Future work will focus on studying the mapping algorithms between uncertain ontologies.

ACKNOWLEDGMENTS

This paper is supported by the National Nature Science Foundation (No.61371194, 61303105).

REFERENCES

1. P.Shvaiko, and J.Euzenat. Ontology Matching: State of the Art and Future Challenges. Knowledge and Data Engineering, IEEE Transactions on, 2013, 25(1): 158-176.
2. Ming Mao, Yefei Peng, and Michael Spring. An Adaptive Ontology Mapping Approach with Neural Network based Constraint Satisfaction , Journal of Web Semantics, Volume 8, Issue 1 (2010), page 14-25
3. Mahboobeh Houshmand, Mahmoud Naghibzadeh, Saeed Araban. Reliability-based Similarity Aggregation in Ontology Matching[C]. 2010 IEEE International Conference on Intelligent Computing and Intelligent Systems, Xiamen, China: IEEE, 2010: 744-749.

PLATAL - A Tool for Web Hierarchies Extraction and Alignment

Bernardo Severo[1], Cassia Trojahn[2], and Renata Vieira[1]

[1] Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, Brazil
[2] Université Toulouse 2 & IRIT, Toulouse, France

Abstract. This paper presents PLATAL, a modular and extensible tool for extraction of hierarchical structures from web pages which can be automatically aligned and also manually edited via a graphical interface. Evaluation of alignments can be carried out using standard measures.

1 Introduction

Web sites are rich sources of information for a range of applications. Tools for automatically extracting structured content from these sources and for comparing content across web sites are valuable resources. For helping in these tasks, we propose PLATAL (**Plat**form of **Al**ignment), a modular and extensible tool that provides an integrated environment for extraction of web hierarchies and alignment creation, edition and evaluation. The main motivation behind PLATAL is to assist users in the complete alignment cycle of two web hierarchies. Differently from other matching tools offering a visual environment, like OLA [1], Prompt [3], Homer [5], Yam++ [2] and SOA-based tool [4], PLATAL offers novel functionalities: the possibility of automatically extracting hierarchical structures from the web together with a centralised visual tool for alignment manipulation.

2 PLATAL modules

PLATAL is a standalone tool composed of four modules: (1) *hierarchy extraction module*, which extracts fragments from HTML pages using XPath expressions; (2) *automatic alignment module*, which implements a set of terminological (prefix, suffix, edit-distance) and structural matching techniques (similarity of parents and children entities) for generating equivalence correspondences; (3) *manual alignment module*, which allows users to edit or create alignments; and (4) *evaluation module*, which takes two alignments and computes precision, recall and F-measure measures. These modules operate independently of each other and alternative implementations can be added instead. Figure 1 shows a screenshot of automatic alignment creation. After loading two hierarchies, each hierarchy will be displayed in the respective section. Then, users can select one or more alignment processes and start them ('Start Alignment Process'). If at least one method founds one correspondence between two entities, the user can see it by

selecting the source or target entity in the hierarchies (field 'Correspondences'). Alignments can be exported in the Alignment format[3] ('Save').

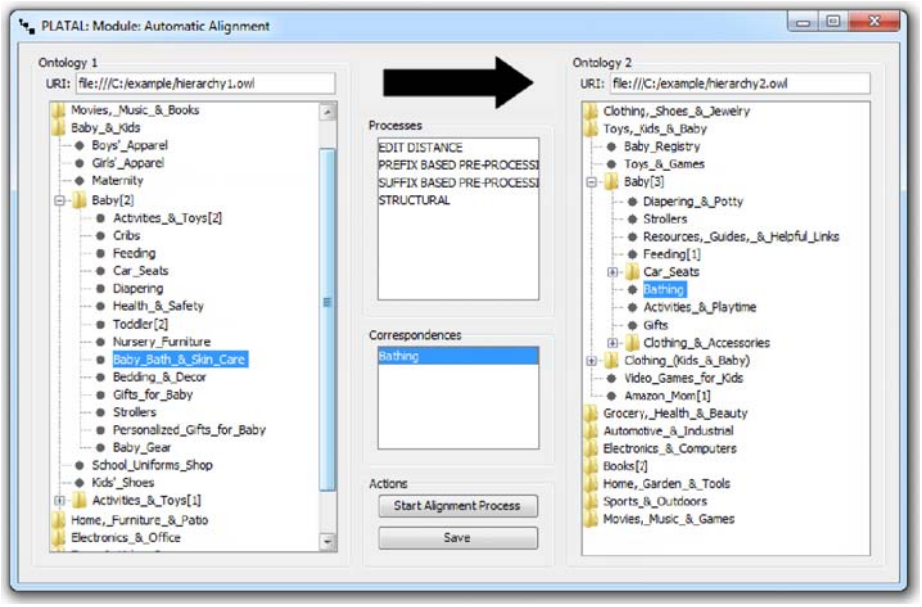


Fig. 1. Automatic Alignment Module screenshot.

3 Conclusions and future work

We have presented a visual tool for extraction, alignment and evaluation of web hierarchies. To the best of our knowledge, there is no publicly available environment integrating all these features together. As future work, we plan to improve the visualisation of alignments, develop a web-based version, allow parametrisation and customisation of alignment techniques through the user interface, and add a multilingual ontology matching module.

References

1. J. Euzenat, D. Loup, M. Touzani, and P. Valtchev. Ontology Alignment with OLA. In *3rd EON Workshop*, pages 59–68, 2004.
2. D. H. Ngo and Z. Bellahsene. YAM++ : (not) Yet Another Matcher for Ontology Matching Task. In *BDA*, France, 2012.
3. N. F. Noy and M. A. Musen. PROMPT: Algorithm and Tool for Automated Ontology Merging and Alignment. In *17h AAAI*, pages 450–455, 2000.
4. K. W. Onn, V. Sabol, M. Granitzer, W. Kienreich, and D. Lukose. A visual soa-based ontology alignment tool. In *OM*, 2011.
5. O. Udrea, R. Miller, and L. Getoor. Homer: Ontology visualization and analysis. In *Demo session ISWC*, 2007.

[3] http://alignapi.gforge.inria.fr/format.html

Is my ontology matching system similar to yours? ⋆

Ernesto Jiménez-Ruiz, Bernardo Cuenca Grau, Ian Horrocks

Department of Computer Science, University of Oxford, Oxford UK

Abstract. In this paper we extend the evaluation of the OAEI 2012 Large BioMed track, which involves the matching of the semantically rich ontologies FMA, NCI and SNOMED CT. Concretely, we report about the differences and similarities among the mappings computed by the participant ontology matching systems.

1 Introduction

The quality of the mappings computed by an ontology matching system in the Ontology Alignment Evaluation Initiative (OAEI) [2, 1] is typically measured in terms of precision and recall with respect to a reference set of mappings. Additionally, the OAEI also evaluates the coherence of the computed mappings [1].

However, the differences and similarities among the mappings computed by different systems have often been neglected in the OAEI.[1] In this paper we provide a more fine-grained comparison among the matching systems participating in the OAEI 2012 Large BioMed track;[2] concretely *(i)* we have harmonised (i.e. voted) the computed mapping sets, and *(ii)* we provide a graphical representation of the similarity of these sets.

2 Mapping harmonization

We have considered the mappings voted (i.e. included in the output) by at least one ontology matching system. Figure 1 shows the harmonization (i.e. voting) results for the FMA-NCI and FMA-SNOMED matching problems. Mappings have received at most 11 and 8 votes (i.e. number of participating systems[3]), respectively. For example, in the FMA-NCI matching problem, 3,719 mappings have been voted by at least 2 systems.

Figure 1 also shows the evolution of F-score, Precision and Recall for the different harmonized mapping sets. As expected the maximum recall (respectively precision) is reached with the minimum (respectively maximum) number of votes. For example, the maximum recall in the FMA-SNOMED problem is 0.81, which shows the difficulty of identifying correct mappings in this matching problem.

The harmonized mapping sets with the best trade-off between precision and recall have been selected as the *representative mapping sets* of the participating ontology matching systems. For the FMA-NCI matching problem we have selected the mappings sets with (at least) 3, 4 and 5 votes, while in the FMA-SNOMED matching problem we have selected the sets with (at least) 2 and 3 votes (see dark-grey bars in Figure 1).

⋆ This research was financed by the Optique project with the grant agreement FP7-318338.

[1] As far as we know, only in the 2007 Anatomy track some effort was done in this line: `http://oaei.ontologymatching.org/2007/results/anatomy/`

[2] Results available at: `http://www.cs.ox.ac.uk/isg/projects/SEALS/oaei/`

[3] Systems with several variants have only been considered once in the voting process.

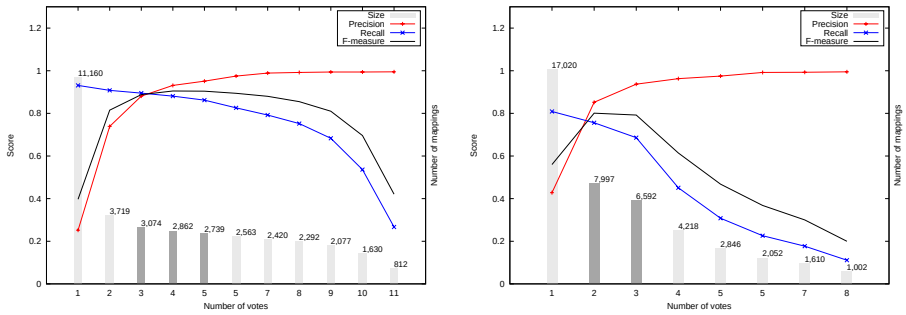


Fig. 1: Harmonisation in the FMA-NCI (left) and FMA-SNOMED (right) problems

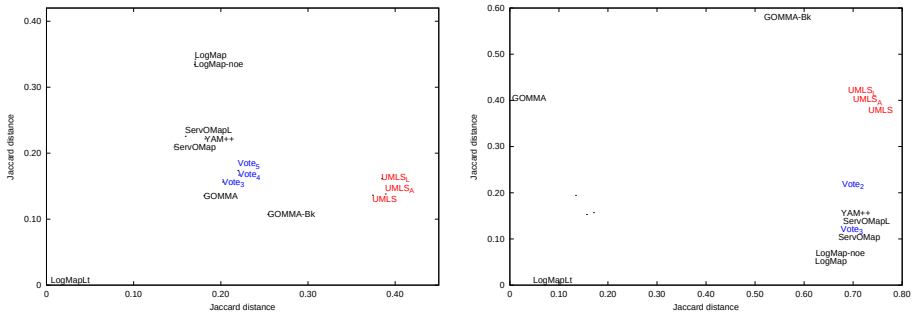


Fig. 2: Mapping similarity in the FMA-NCI (left) and FMA-SNOMED (right) problems

3 Mapping similarity among systems

We have compared the similarity among *(i)* the representative mapping sets from the harmonisation (see Section 2), *(ii)* the UMLS-based reference mappings of the track, and *(iii)* the mapping sets computed by the top-8 ontology matching systems in the FMA-NCI and FMA-SNOMED matching problems [1]. To this end we have calculated the *jaccard distance* $(|\mathcal{M}_A \cup \mathcal{M}_B| - |\mathcal{M}_A \cap \mathcal{M}_B|)/|\mathcal{M}_A \cup \mathcal{M}_B|$, which ranges from 0 (*the same*) to 1 (*different*), between each pair ($\mathcal{M}_A$ and $\mathcal{M}_B$) of the mapping sets from *(i)-(iii)*, and represented such distances in a two-dimensional scatterplot (see Figure 2). System names which are distant to each other indicate that their computed mappings differ to a large degree. For example, in Figure 2 (right), the mappings computed by LogMapLt and GOMMA are very different with respect to the mappings computed by other systems, as well as with respect to the harmonized and reference mapping sets.

References

1. Aguirre, J., et al.: Results of the Ontology Alignment Evaluation Initiative 2012. In: Ontology Matching Workshop. Vol-946 of CEUR Workshop Proceedings (2012)
2. Euzenat, J., Meilicke, C., Stuckenschmidt, H., Shvaiko, P., Trojahn, C.: Ontology alignment evaluation initiative: Six years of experience. J. Data Sem. 15, 158–192 (2011)

Ontological Quality Control in Large-scale, Applied Ontology Matching

Catherine Legg, Samuel Sarjant
The University of Waikato, New Zealand

Email: clegg@waikato.ac.nz, sarjant@waikato.ac.nz

Abstract. To date, large-scale applied ontology mapping has relied greatly on label matching and other relatively simple syntactic features. In search of more holistic and accurate alignment, we offer a suite of partially overlapping ontology mapping heuristics which allows us to *hypothesise* matches and test them against the knowledge in our source ontology (OpenCyc). We thereby automatically align our source ontology with 55K concepts from Wikipedia with 93% accuracy.

1. Introduction

We have developed a method of specifically *ontological* quality control in ontology mapping which combines a suite of partially overlapping mapping heuristics with common-sense knowledge in OpenCyc. Our approach differs from previous largely label-matching approaches (Suchanek et al, 2008, Ponzetto and Navigli, 2009) in its use of knowledge, and also from previous knowledge-based approaches (Shvaiko and Euzenat, 2005, Sabou et al, 2006), in treating potential matches as *hypotheses*, and testing them more iteratively and open-endedly than previously accomplished.

2. Iterative Mapping Process

Concept to Wikipedia article mapping is governed by a *priority queue* which iteratively evaluates potential mappings ordered via continuously updated weightings. The process begins with concept-to-article mappings (**Table 1**), then verifies these using article-to-concept heuristics. The weight of each potential mapping is equal to the product of weights produced by the two sets of heuristics.

Table 1. Heuristics that map between source ontology concepts and Wikipedia articles.

Concept → Article	**Example**
TITLE MATCHING	`Batman-TheComicStrip` → {*Batman (comic strip)*:1.0}
SYNONYM MATCHING	`ComputerWorm` → {*Worm*:1.0, *Computer worm*:0.39, ... (+5 more)}
CONTEXT-RELATED SYNONYM MATCHING	`ComputerWorm` → {*Computer worm*:1.0, *Worm*:0.59,... (+4 more)}
Article → Concept	**Example**
TITLE MATCHING	*Dog* → {`Dog`:1.0, `HotDog`:1.0}
LABEL MATCHING	*Dog* → {`Dog`:1.0, `HotDog`:0.995, `CanineAnimal`:0.03, `CanineTooth`:0.03}

A final quality control measure is the 'consistency check' between information on concept and the mapped article. Most Wikipedia first sentences are conventionally structured as: '*X* is/was/are/were a/an/the *Y*', where *Y* is links to articles typically

representing appropriate classes. The mapping weight is multiplied by the proportion of assertions not rejected using OpenCyc's disjointness knowledge.

Example 1: *"**Bill Laswell** is an American [[bassist]], [[record producer|producer]] and [[record label]] owner."* Only three of the four assertions in this sentence are kept: `BillLaswell` is a `UnitedStatesPerson`, `BassGuitarist`, and `Producer`. `BillLaswell` cannot be a `RecordCompany` because OpenCyc knows a person cannot be a company.

Example 2: The concept `Basketball-Ball` initially maps as follows (*Basketball:*1.0, *Basketball (ball)*:0.95, *College basketball:*0.02). The second candidate is the correct one, as the first refers to the team sport. The algorithm attempts to map its first choice *Basketball* back to `Basketball-Ball`, which succeeds but also creates a new potential reverse mapping *Basketball* → `Basketball`. Consistency checking now tests "`Basketball-Ball` is a `TeamSport`", which fails, removing this potential mapping. The next highest reverse-mapping is *Basketball* → `Basketball`, which is found to be consistent, so a mapping is recorded for that. The process now backtracks to hypothesising the second-best option from the original list: *Basketball (ball)*:0.95, which also successfully reverse-maps and is consistent, creating a new (correct) mapping. It is worth emphasising how similar the two 'basketball concepts' are by standard semantic relatedness measures, and thus the subtlety our methods are capable of.

3. Results and Conclusions

The algorithm identified 54,987 mappings of OpenCyc concepts to Wikipedia articles. Applying manual analysis to a random 300 mappings, 266 were judged 'True' (88.5%), 21 'False' (7%) and 13 (4.3%) were assigned 'B' for 'Broader term' (the mapping was largely correct but one side generalised the other). Thus 93% of our mappings were either 'True' or highly related. Although YAGO reports 95% accuracy, what is being rated is not mapping joins between Wordnet and Wikipedia, but the truth of assertions in infoboxes. Although our efforts so far lack the scale of projects such as YAGO, we suggest they have a role to play in long-term development towards maximum accuracy in this field. We offer our results at: `http://bit.ly/10MlLjl`.

References

Euzenat, J. and Shvaiko, P. (2007). *Ontology Matching*. Springer-Verlag.

Ponzetto, S.P., and Navigli, R. (2009). Large-Scale Taxonomy Mapping for Restructuring and Integrating Wikipedia, *IJCAI 2009*, Pasadena, California, pp. 2083-2088.

Sabou, M., D'Aquin, M., Motta, E. (2006). Using the Semantic Web as Background Knowledge for Ontology Mapping, *OM-2006*, Athens, GA, USA.

Shvaiko, P. and Euzenat, J. (2005). A Survey of Schema-based Matching Approaches. *Journal on Data Semantics* **4**.

Suchanek, F. M., Kasneci, G., and Weikum, G. (2008). Yago: A Large Ontology from Wikipedia and WordNet. *Elsevier Journal of Web Semantics* **6**(3), 203-217.

Variations on Aligning Linked Open Data Ontologies

Valerie Cross, Chen Gu, Xi Chen, Weiguo Xia, Peter Simon

Computer Science and Software Engineering Department
Miami University, Oxford, OH 45056
crossv@muohio.edu

Traditional OA systems are not as suitable for aligning LOD ontology schemas; for example, equivalence relations are limited among LOD concepts so that OA systems for LOD ontology alignment also find subclass and superclass relations. Four recent approaches for LOD ontology alignment are BLOOMS (BL) [1] and BLOOMS+ [2], AgreementMaker (AM) [3], WikiMatch (WM) [4], and Holistic Concept Mapping (HCM) [5]. Table 1 briefly compares these systems for aligning LOD ontologies.

Table 1. Recent OA systems for aligning LOD ontology schemas

OA system	Mapping type	Knowledge Source	Data Structure	Algorithms	Experiment description
BL/BL+	Equivalence, subclass	Wikipedia category hierarchy	Concept category trees in a forest	Tree overlap using node depth, contextual similarity on superconcepts	LOD reference alignments, Proton mappings to DBpedia, Geonames, Freebase.
AM	Equivalence, subclass, superclass	WordNet, other LOD ontologies, i.e.,DBpedia or FOAF	Lexicon for a concept	Advanced Similarity Matcher, inferencing on import concept	LOD reference alignments
WM	Equivalence	Wikipedia articles	sets of articles	Jaccard index on article sets	OAEI 2011.5 conference track, multifarm dataset
HCM	Equivalence, similar to, disjoint	Wikipedia category hierarchy	Concept category trees in a forest.	IR tf-idf on comment, label keyword, topic sets ppjoin with Jaccard	Concepts from triples of Billion Triple Challenge dataset, expert evaluation

Unlike the Ontology Alignment Evaluation Initiative (OAEI), no standard reference alignment exists for LOD ontologies. Researchers [4] had experts develop a benchmark, the LOD reference alignments between ontology schema pairs taken from eight LOD ontologies: AKT Reference (A), BBC program(B), DBpedia (D), FOAF(F), Geonames(G), Music(M), SIOC (S), and the Semantic Web Conference (W) because of their substantial LOD coverage domain diversity, and publicly available schemas. Experts produced both subclass and equivalence mappings between the pairs listed in Table 2. BLOOMS and AM are compared in the last two columns [3] since WM or HCM produce only equivalence mappings and few of these

exist in the LOD reference alignments. Both BLOOMS and AM use inferencing to produce some subclass mappings, BLOOMS using post-processing with the Jena reasoner and AM using its own inferencing techniques. To understand this influence, we performed an analysis on the LOD reference alignment for each pair to see the percentage of its mappings inferrable from its equivalence mappings, given in column 1. The * for M, B indicates an analysis was not possible since many BBC concepts could not be found directly in its file or even when opening the file using Protégé.

Table 2. LOD reference alignment pairs

Pair	% inferable	# mappings	BLOOMS		AM	
			Prec	Recall	Prec	Recall
F, D	87%	225	0.67	0.73	0.72	0.80
G, D	71%	41	0	0	0.26	0.68
M, D	20%	645	0.39	0.62	0.62	0.40
W, D	29%	519	0.70	0.40	0.58	0.35
M, B	*	528	0.63	0.78	0.48	0.16
S, F	27%	22	0.55	0.64	0.56	0.41
W, A	58%	366	0.42	0.59	0.48	0.43

BLOOMS has better recall except for F,D and G,D. F,D has 87% inferable mappings from its three equivalence relations. AM's use of other LOD ontologies and WordNet contributes to finding more correct mappings. For the G,D pair BLOOMS does not find the only equivalence relation SpatialThing = Place so that Jena cannot produce any of the inferable mappings. AM finds this mapping, likely from the comment field for SpatialThing including the word 'places.' AM finds 68% (recall) of the reference alignment mappings, very close to the 71% inferable mappings. Of the five remaining pairs, AM has better precision for M,D with the smallest percentage of inferable mappings. BLOOMS with Wikipedia finds more correct mappings since very few are from inferable relations. AM's lower recall corresponds with fewer inferable relations, but those that it does find are more likely correct with its 0.62 precision

References

1. Jain, P., Hitzler, P., Sheth, A. P., Verma, K., and Yeh, P. Z.: Ontology Alignment for Linked Open Data. In: Proceedings of the International Semantic Web Conference (ISWC) (2010)
2. Jain, P., Yeh, P. Z, Verma, K., Vasquez, G., Damova, M., Hitzler, P., and Sheth, A. P.: Contextual Ontology Alignment of LOD with an Upper Ontology:A Case Study with Proton. In Proceedings of the Extended Semantic Web Conference (ESWC) (2011)
3. Cruz, I., Palmonari, M., Caima, F., and Stroe, C.: Towards "On the Go" Matching of Linked Open Data Ontologies. In: Workshop on Discovering Meaning On the Go in Large Heterogeneous Data (LHD), The 22nd International Joint Conference on Artificial Intelligence (IJCAI-11) (2011)
4. Hertling, S. and Paulheim, H.: WikiMatch – Using Wikipedia for Ontology Matching, in: Seventh International Workshop on Ontology Matching (OM 2012) (2012)
5. Grutze, T., Bohm, C.. Naumann, F.: Holistic and Scalable Ontology Alignment for Linked Open Data. In: Workshop on Linked Data on the Web (LDOW) at WWW (2012)

LOD4STAT: a scenario and requirements

Pavel Shvaiko[1], Michele Mostarda[2], Marco Amadori[2], and Claudio Giuliano[2]

[1] TasLab, Informatica Trentina S.p.A., Trento, Italy
[2] Fondazione Bruno Kessler - IRST, Trento, Italy

Abstract. In this short paper we present a scenario and requirements for ontology matching posed by a statistical eGovernment application, which aims at publishing its data (also) as linked open data.

Introduction. Our application domain is *eGovernment*. By eGovernment we mean an area of application for information technologies to modernize public administration by optimizing work of various public institutions and by providing citizens and businesses with better and new services. More specifically, we focus on statistical applications for eGovernment. The driving idea is to capitalize on the statistical information in order to increase knowledge of the Trentino region. Releasing statistical data (with disclosure control) as linked open data aims at simplifying access to resources in digital formats, at increasing transparency and efficiency of eGovernment services, etc. The main challenge is the realization of a knowledge base, which is natively enabled to work with RDBMS tables. Despite this approach has been tailored specifically to the statistical database domain, there is substantial room for generalization. In this view, there was a number of initiatives aiming at releasing governmental data as linked open data to be taken into account: in GovWILD [1] links were established automatically with specifically developed similarity measures, while in [2], the alignment was done semi-automatically with Google Refine. The currently available matching techniques can be well used for automating this process [3].

Scenario. Figure 1 shows the key component, called Statistical Knowledge Base (SKB), of the LOD4STAT system-to-be. The SKB aims at enabling its users to query statistical data, metadata and relations across them without requiring specific knowledge of the underlying database. Users can issue queries, such as *find all data related to population age and employment for the municipality of Trento*. Specifically, user query is analyzed in order to extract concepts out of labels. Then, these are matched at run time against the SKB. For the query example, the term *population age* is connected to *Registry Office*, while *employment* is connected to *Social Security*. The system returns a set of tables, metadata and entities from the Registry Office (with information about population and age) and from the Social Security (with information about employment) containing data for the city of Trento and will suggest possible joins between columns.

The SKB is an interconnected aggregation of ontologies (interpreted in a loose sense), such as WordNet, DBpedia, ESMS[1] what allows both multi-classification and multiple views on data. These ontologies have to be matched among them to enable navigation across them through the respective correspondences. The SKB is also able to export query results in several formats, such as RDF Data Cube and JSON-Stat. The SKB is represented by three (horizontal) layers. The upper layer is a collection of ontologies specific to the statistics domain, e.g., ESMS. The middle layer is composed

[1] http://epp.eurostat.ec.europa.eu/portal/page/portal/statistics/metadata

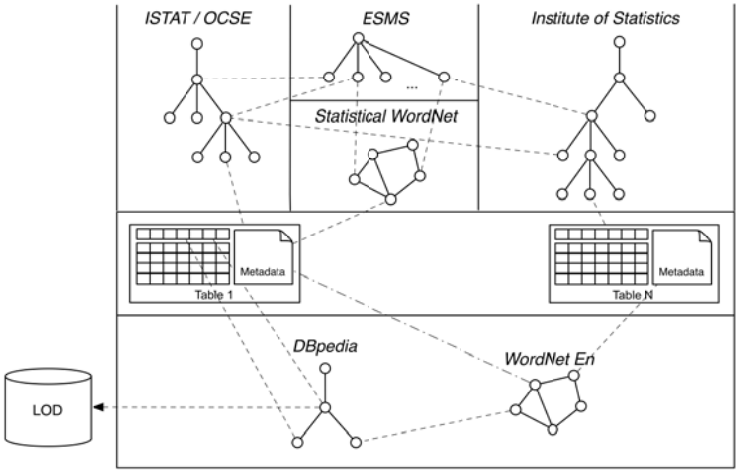


Fig. 1: LOD4STAT: the statistical knowledge base component.

of relational tables associated with metadata. The lower layer is composed of a collection of general purpose ontologies, e.g., WordNet, DBpedia. Table columns are to be matched to the entities of the involved ontologies. Notice that SKB allows for the definition of explicit connections between columns of different tables that can be joined together. Every time an alignment is updated the respective data is updated accordingly.

Requirements. There are several key requirements posed by this application, such as: *performance* - answer queries within 3s., as suggested by the UI interaction practice; *availability* - service up by 99% of time, no more than 15mins. downtime per day during working hours. These requirements put only constraints on run time matching needed between the user query and the SKB ontologies. Matching results can be approximate, though their correctness is preferred over completeness. For what concerns design time matching inside the SKB, it can be performed at design time semi-automatically with sound and complete alignment when any of these knowledge sources evolve. Notice that statistical disclosure control methods use weights associated to the table columns, and it should be possible to inherit them through the respective alignments.

Conclusions and future work. In this short paper we have presented a scenario and requirements for ontology matching within a statistical eGovernment application. We note that such requirements in part have a transversal character, such as for run time query matching and design time matching between the ontologies of the system. However, there are also peculiarities related to the use of alignments, such as support for statistical disclosure control. Future work includes formalization, implementation and evaluation of the system in order to be brought to production.

Acknowledgments. The work has been supported by the Autonomous Province of Trento, Italy.

References

1. C. Böhm, M. Freitag, A. Heise, C. Lehmann, A. Mascher, F. Naumann, V. Ercegovac, M. Hernández, P. Haase, and M.l Schmidt. GovWILD: integrating open government data for transparency. In *Proceedings of WWW*, pages 321–324, 2012.
2. F. Maali, R. Cyganiak, and V. Peristeras. A publishing pipeline for linked government data. In *Proceedings of ESWC*, pages 778–792, 2012.
3. P. Shvaiko and J. Euzenat. Ontology matching: state of the art and future challenges. *TKDE*, 25(1):158–176, 2013.

Interlinking and Visualizing Linked Open Data with Geospatial Reference Data

Abdelfettah Feliachi[1], Nathalie Abadie[1], Fayçal Hamdi[2], and Ghislain Auguste Atemezing[3]

[1] IGN, COGIT, 73 Avenue de Paris, 94165 Saint-Mandé, France
[2] CEDRIC, CNAM, F-75141 Paris Cedex 03, France
[3] EURECOM, Multimedia Department, Campus SophiaTech, France

1 Context and purposes

An increasing number of thematic datasets are published as RDF graphs and linked to other datasets by identifying equivalent resources in other relevant datasets. Among the set of properties usually used as data linking criteria, geolocation (addresses, locations, coordinates) remains one of the most commonly used.

However, resources that actually refer to complex topographic features are generally described by very simple geolocation properties, such as a position defined by coordinates (long, lat). On the other hand, geographic reference datasets provide more precise geometric information about geographic features. Interlinking thematic linked open datasets with geographic reference datasets would enable us to take advantage of both information sources to link independent thematic datasets and create rich cartographic applications for data visualization.

This data linking task is generally performed by comparing properties values of each resource of a given data set, with homologous properties of the resources described in other datasets [3]. In the field of geographic databases, data matching is also performed by comparing properties, and especially complex geometries (curves, lines, polygons) that are used to represent the shape and the location of geographic features. This task is usually based on distance measures chosen according to the type of the geometric primitives that must be compared [1, 2, 4, 5]. We aim at combining both approaches to link both thematic and geographical reference data and exploit the generated links in a data visualization application.

2 Approach and use case

In order to take advantage of existing data linking tools, we have converted geographic shape data and stored them into a RDF triple store. This task has been achieved by using the Datalift[4] platform that also enables to perform the linking process with external published datasets, through the use of Silk[5] linking tool. Our linking approach is mainly based on geolocation properties comparison.

[4] `http://datalift.org/`
[5] `https://www.assembla.com/spaces/silk/wiki/Silk_Workbench`

Thus we have added to Silk more GIS distance measures for computing the shortest distance between any geometric primitive and simple position locations used in thematic datasets.

The result of this interlinking process is a list of `owl:sameAs` links between entities of each datasets, at a given threshold. These links are used to extend the geographic reference data set with information queried on the fly from the external thematic datasets through the visualization interface. We have applied this approach on a geographical reference dataset about buildings and data about historical monuments extracted from French DBpedia[6], on the area of Paris.

Fig. 1. DBpedia points locating historical monuments linked with polygons describing buildings in a geographic reference dataset.

3 Conclusion

The use of links between thematic and reference data could be further investigated to enable data visualization at different level of detail, and visual detection errors during matching process of geodata.

References

1. Mustire, S. et Devogele, T. Matching networks with different levels of detail. GeoInfor-matica, paratre en 2008
2. Olteanu, A.-M. Appariement de donnes spatiales par prise en compte de connaissances imprcises. Thse de doctorat. Universit de Marne-La-Valle, 2008
3. Scharffe, F., Euzenat, J.: Mthodes et outils pour lier le Web des donnes. RFIA 2010: Re-connaissance des Formes et Intelligence Artificielle (2010)
4. Voltz, S. An Iterative Approach for Matching Multiple Representations of Street Data. In : Proceedings of ISPRS Workshop, Multiple representation and interoperability of spatial data, Hanovre (Allemagne), 22-24 fvrier 2006, p. 101-110
5. Walter, V. et Fritsch, D. Matching Spatial datasets: Statistical Approach. International Journal of Geographical Information Science, 1999, 13(5), p. 445-473

[6] `http://fr.dbpedia.org`

Matching Geospatial Instances

Heshan Du[1], Natasha Alechina[1], Michael Jackson[1], Glen Hart[2]

[1] University of Nottingham
[2] Ordnance Survey of Great Britain

The work presented in this paper extends our work on matching formal and informal geospatial ontologies [1], aimed to realize the synergistic use of authoritative and crowd-sourced geospatial information. A geospatial instance is an object which has a certain and verifiable location (geometry, topographic footprint), as well as a meaningful label (for example, Victoria Shopping Centre in Nottingham, UK). The source of examples in this paper are: The OpenStreetMap (OSM) [2] and the Ordnance Survey of Great Britain (OSGB) [3].

Different geospatial instances may have the same purely lexical information and the same classification in terms of an ontology, but different locations. For example, there may be several restaurants called 'Prezzo Ristorante' in the same city. Therefore, when matching geospatial instances, it is essential to use location information. However, few of existing ontology matching or data interlinking methods can match spatial instances effectively.

There is also a choice in representing objects such as shopping centres as a collection of parts or as a single instance. For example, Victoria Centre is represented as a collection of shops and other businesses in OSGB and as a single instance in OSM. In order to produce a meaningful correspondence between instances in OSGB and in OSM, we propose to use 'partOf' relation (mereological partOf in geometry and having similar labels). If for two instances a and b we get 'partOf' relations in both directions, we generate a hypothesis that a and b belong to 'sameAs'.

Here we propose a new method for establishing 'sameAs' and 'partOf' relations between geospatial instances from different ontologies. In crowd-sourced data, there is an increased possibility of error in measurement, and tendency to simplify shapes of buildings. For this reason, in our method we use buffers to compare geometries of instances. The size of the buffer (intuitively, 'the margin of error' σ) is a parameter which can be arrived at experimentally or within reason set arbitrarily. Intuitively the optimal value of σ corresponds to the maximal deviation between two representations of the same object in two different data sets. In the case of OSGB and OSM data for Nottingham, this is experimentally determined as 20m. The new method has four steps.

Step 1: Extracting geometry sets. An ABox contains facts (geometry, lexical and semantic classification information) about geospatial instances. We extract a set of geometries, G_i, from all the spatial instances in each ABox A_i, $i = 1, 2$.

Step 2: Matching geometry sets. For two sets of geometries, G_1, G_2, a level of tolerance α and tolerance for the second best β, we generate the best two candidate matches for each geometry in G_1 if they exist in G_2, and the best two candidate matches for each geometry in G_2 if they exist in G_1. The candidates are

selected by comparing minimal buffers. The buffer of a geometry g, $\mathit{buffer}(g, \sigma) = \{p : \exists p' \in g.\ \mathit{distance}(p, p') \leq \sigma\}, (\sigma > 0)$. For two geometries g and h, the minimal buffer of h containing g is $\mathit{buffer}(h, \sigma)$ such that $g \subseteq \mathit{buffer}(h, \sigma)$ and for all $\sigma' < \sigma$, $g \not\subseteq \mathit{buffer}(h, \sigma')$. For any geometry g, the minimal buffer α ($\alpha \leq \sigma$) of its best candidate o_1 ($g \subseteq \mathit{buffer}(o_1, \alpha)$) is the smallest among those of all the candidates. We generate a 'buffered part of' (BPT) relation between each geometry and its candidates, i.e. $(g, o_1) \in BPT(\sigma)$.

Step 3: Comparing labels. We use string comparison, including equality, inclusion, abbreviation and edit distance to check whether the labels, such as names or addresses, of two instances are similar. If there is no pair of labels of spatial instances s_1, s_2 that are similar, then their lexical information is incompatible, $(s_1, s_2) \in LF$. Otherwise, their lexical information is compatible, $(s_1, s_2) \in LT$.

For every pair of spatial instances s_1, s_2, if $(g_1, g_2) \in BPT(\alpha)$ (where g_i is the geometry of s_i, $i = 1, 2$) and $(s_1, s_2) \in LT$, then $(s_1, s_2) \in \mathit{partOf}$ possibly holds, and we will add it to the initial instance mapping M.

Step 4: Verifying initial instance mapping M using semantic classification information. It is part of ontology (ABox and TBox) matching process, presented in [1].

We implement the method described above as part of GeoMap [1]. From the studied area (2km sq) of Nottingham city centre, 713 geospatial individuals of 47 types are added to OSGB Buildings and Places ontology from the OSGB Address Layer 2 and the OSGB Topology Layer [3], 253 geospatial individuals of 39 types are added into OSM ontology automatically from the building layer of OSM data. The ground truth instance mapping is obtained from manually matching all the instances in the two ontologies. It contains 286 'partOf' relations, and 73 'sameAs' relations can be inferred. The data used is available on `http://www.cs.nott.ac.uk/~hxd/GeoMap.html`. We compare the performance of our method with LogMap [4] and KnoFuss [5]. The precisions of mappings produced by GeoMap, LogMap and KnoFuss are 1, 0.24 and 0.18 respectively, and the recalls are 0.95, 0.38, 0.25 respectively. The precision and recall of GeoMap are much higher, mainly because LogMap and KnoFuss cannot make effective use of location information.

References

1. Du, H., Alechina, N., Jackson, M., Hart, G.: Matching Formal and Informal Geospatial Ontologies. In: Geographic Information Science at the Heart of Europe. Lecture Notes in Geoinformation and Cartography. Springer (2013) 155–171
2. OpenStreetMap: http://www.openstreetmap.org (2012)
3. Ordnance Survey: http://www.ordnancesurvey.co.uk/oswebsite (2012)
4. Jiménez-Ruiz, E., Grau, B.C.: LogMap: Logic-Based and Scalable Ontology Matching. In: International Semantic Web Conference (1). (2011) 273–288
5. Nikolov, Andriy and Uren, Victoria and Motta, Enrico: KnoFuss: a Comprehensive Architecture for Knowledge Fusion. In: Proceedings of the 4th International Conference on Knowledge Capture. (2007) 185–186