Figure 1: Performance of our PPSS protocol as a function of the radix b employed in the PIR algorithms. Private search of $q = CTGCAG$ in a genome with $500k$ nucleotides
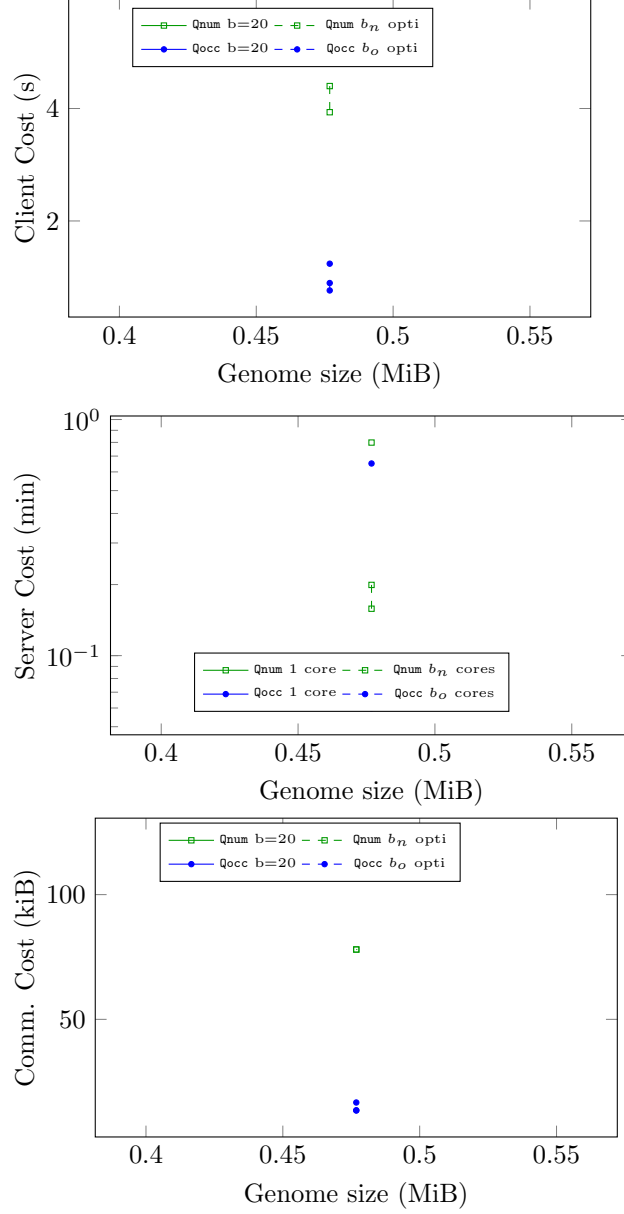
Figure 2: Performance of our PPSS protocol as a function of the genomic document size to find one occurrence of the substring $q = CTGCAG$. Considering each document size in increasing order, the optimal values of radixes b_n and b_o employed during the experiments are $\{13, 17, 21, 26, 14, 17, 20, 21\}$ and $\{27, 14, 17, 20, 24, 28, 17, 18\}$, respectively