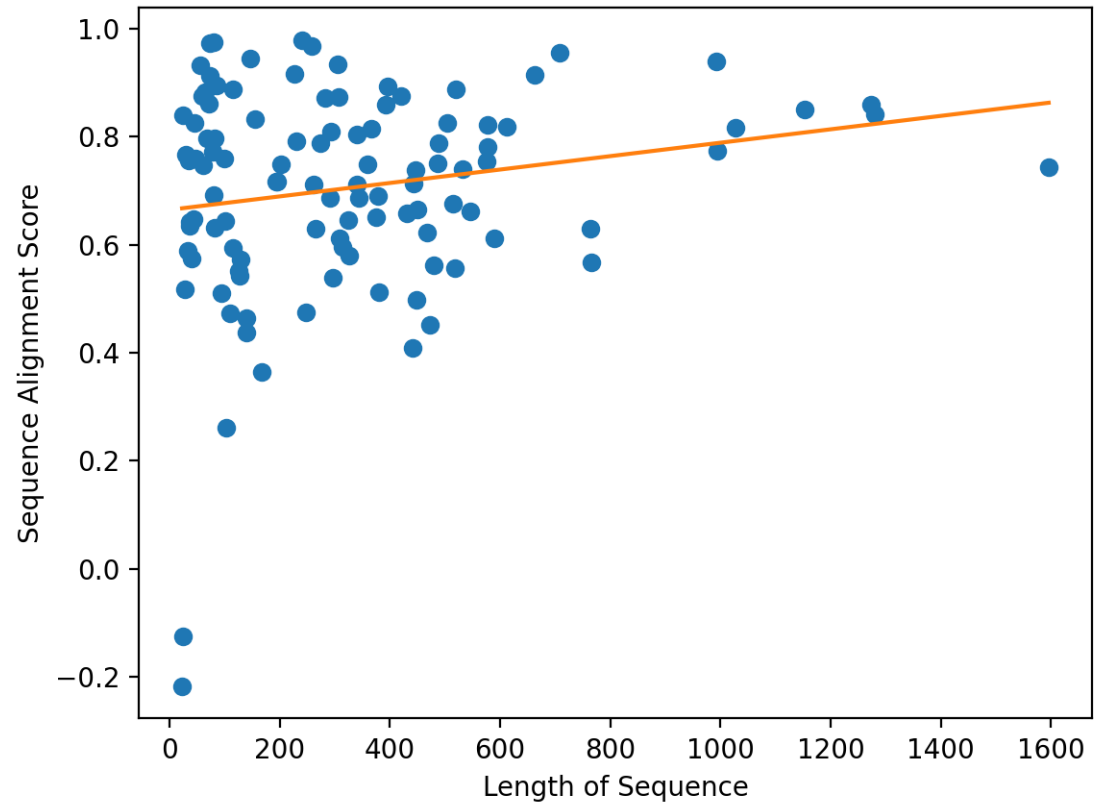# 4 Results

Figure 3 : The average sequence alignment score normalized by the length
of the sequence, for each sequence length.

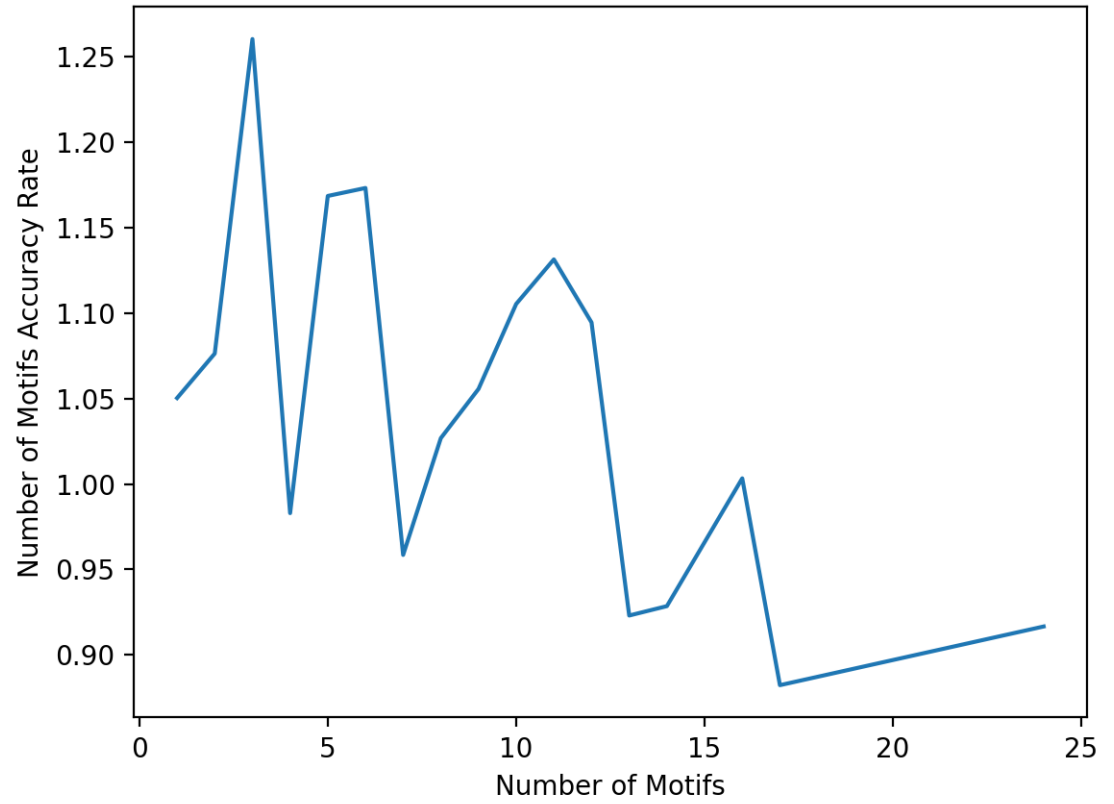The score matrix gave 1 point for match, -1 for mismtach, and -2 for gap.

Figure 4: The ration between predicted number of motifs and the true number of motifs, for each number of motifs.
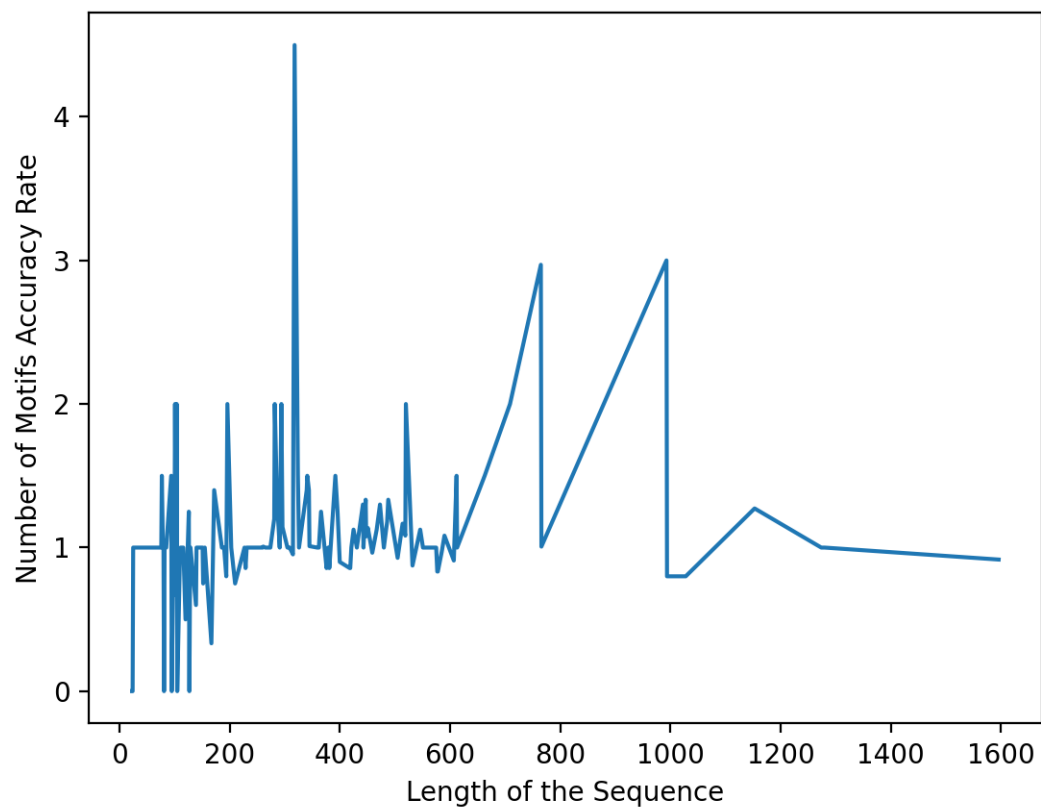
Figure 5: The ratio between predicted number of motifs and the true number of motifs, for each sequence length.