ASSIGNMENT1: ABSTRACT&INTRODUCTION1

  \*In this paper  we propose a new method that generates pairwise sequence alignments for more accurate template-based modeling.  using machine learning for accurate template-based protein structure prediction

\*problem is homology search methods have been able to detect remote homologs, although sometimes sufficiently accurate structure models cannot be obtained because the quality of the sequence alignment generated by homology detection program is poor.

\*The proposed method trains a machine learning model using the structural alignment , Thus, when calculating sequence alignments, instead of a fixed substitution matrix, this method dynamically predicts a substitution score from the trained model.

\* Template structures are the structures of homologous proteins, often found with homology detection methods. Currently, template-based modeling methods are the most practical because the predicted models are much more accurate if we can find good templates and protein sequence alignments

\*In essence, alignment quality is crucial to template-based modeling. Thus far, a method’s ability to detect remote homologs has been prioritized because models cannot be generated without a template.