Pseudo Code, Snapshots, and Assumptions for Hw #3

Bridget Mohn and Eric Wilson

For every pair of sequences in the given multiple sequence alignment

Count the number of time each amino acid occurs

Add the count to the proper place in the Counts dictionary

Count the number of times each aligned pair occurs

Add the count to the proper place in the Counts dictionary

Calculate the P() of each amino acid

Calculate the P() of each aligned amino acid pair

Calculate/Create the Amino Acid Substitution Matrix

Compare our matrix with BLOSUM 62 Amino Acid Substitution Matrix

Calculate the Correlation Coefficient between the two matrices