Pseudocode Lab 7

1. Check that the file containing the reference protein sequence (reference. fasta) opens.

2. Check whether the file containing the comparative protein sequences (comparison. fasta) opens.

3. Using get_id_and_sequence, read the reference protein id and sequence from the file containing the reference protein.

4. Using string_to_protein_sequence, convert the reference sequence (which is a string) to a protein sequence.

5. While reading comparison id/sequence pairs from the file containing the comparison proteins is successful (using get_id_and_sequence).

- using string_to_protein_sequence, convert the current comparison sequence (which is a string) to a protein sequence.

- To construct an NWAlignment Direction data structure, use the needleman_wunsch function.

- To generate a Comparison data structure, call create comparison with the proper parameters.

- As parameters, pass the result of the previous step and the id of the current comparison sequence to print_comparison.