**DATA STRUCTURES PROJECT PROPOSAL**

# Sequence Alignment (Global)

# Group Members

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# Description

The program will perform Global Alignment on the given sequence of DNA, RNA or protein. Global alignments, which attempt to align every residue in every sequence, are most useful when the sequences in the query set are similar and of roughly equal size. A general global alignment technique is the **Needleman–Wunsch algorithm**, which is based on dynamic programming.

**Needleman–Wunsch Algorithm**

The Needleman–Wunsch algorithm is an algorithm used in bioinformatics to align protein or nucleotide sequences. The algorithm essentially divides a large problem (e.g. the full sequence) into a series of smaller problems and uses the solutions to the smaller problems to reconstruct a solution to the larger problem. This program will use this algorithm to find the best match between two input strings.

