

# Appendix A

## Genome Sequence Alignment : Terminology

**Affine gap penalty** : Cost associated with introducing or extending gaps in sequences

**Dynamic programming** : A programming methodology which uses the properties of overlapping subproblems and optimal substructures

**Global Sequence Alignment** : A group of sequence alignment problems where the entire sequence needs to be optimally aligned with another

**Heuristics** : A method in Computer Science where the most appropriate solution to a problem is chosen based on certain rules

**Local Sequence Alignment** : A group of sequence alignment problems where subsequences within given sequences need to be optimally aligned

**Needleman-Wunsch algorithm** : A well-known global alignment algorithm

**Scoring Matrix** : A matrix which gives the scores for each pair of bases in during the calculation of a similarity score

**Similarity matrix** : The matrix used to find the optimal alignment in the Smith-Waterman algorithm

**Similarity score** : The sum of scores for all character alignments in any two given sequences

**Smith-Waterman algorithm** : A well-known local alignment algorithm