

### Assignment-3

This assignment is to gain experience in implementing dynamic programming to solve selected problems in computational biology such as sequence alignment and to implement the Burrows-Wheeler transform (BWT) on a string.

(i) Write a program to perform global alignment for the two DNA sequences using the Needleman-Wunsch algorithm. Print the best alignment as output, along with its score.

(ii) Write a program to perform Burrows-Wheeler transform on a string (will be referred to as BWT(s)). Also implement a module to generate the original string given the BWT(s).

Example input files are provided uploaded along with the assignment and the file names are align\_nw.inp, bwt.inp.

- Provide a document (README.txt) of the steps involved in your implementation.
- Use comments appropriately in your code to make it more readable.
- Provide details on how to run it and software requirements.

PS:

- (a) In case of availability, you can use intrinsic functions such as “sort” to arrange the strings lexically (for the BWT problem).
- (b) You can work in a group of 2.