

MODULE: CMP-6034B: Algorithms for Bioinformatics**ASSIGNMENT TITLE: Program for alignment of two biological sequences**

DATE SET	:	Week 5 (Thursday)
DATE & TIME OF SUBMISSION	:	Week 10 Thursday 15.00/ Demo Friday 13.00-15.00.
RETURN DATE	:	Week 12
ASSIGNMENT VALUE	:	40%
SET BY	:	Dr. Steven Hayward
CHECKED BY	:	Mr Anthony Duncan

Aim:

To make the student familiar with dynamic programming algorithm.
To develop skills in programming in a Bioinformatics context.
To consolidate knowledge taught in lectures.

Learning outcomes:

Improved understanding of dynamic programming algorithm.
To learn the concepts involved in biological sequence alignment.

Relationship to formative assessment

This assignment is based on the work done in the first three lab exercises.

Description of the assignment:

To implement the dynamic programming method for pairwise alignment of two biological sequences. The basic program should be able to perform the global alignment of two sequences using a substitution matrix, and a linear gap penalty using dynamic programming. The program should be able to display an optimal alignment and its associated score. Extra marks will be awarded for programs that have features beyond this basic requirement – see Marksheet. In particular extra marks will be awarded to those programs that are able to be used to teach the principles of dynamic programming for sequence alignment, i.e. a pedagogical tool for teaching the principles of dynamic programming. The program can be written in any language.

Assessment - more details are in Marksheet

Marks will be awarded for the following criteria:

Satisfying the basic requirement (see above).

Features and versatility of program beyond the usual Needleman and Wunsch approach.

How well your implementation can be used to teach the principles of dynamic programming.

Quality of design and code.

Quality of your demonstration and understanding of algorithm.

Required:

A full submission should consist of:

- 1) A short report explaining the program's features. Include a screenshot of the program that you will show in your demo – this will help the marker associate your report with your demo. (1 side maximum)
- 2) Program + Demo.

Handing in procedure:

Please hand in the hard-copy of the **report at the hub by Thursday 19/03/2020 before 15:00.**

Please submit electronic copies of source code and other supporting files to Blackboard by this deadline.

You will be asked to demo your program on Friday 20/03/2020 13.00-15.00.

CMP-6034B Marksheet: Program for alignment of two biological sequences

Student name		Student N°	
Marker name			
Basic working program for global alignment of two biological sequences using the Needleman and Wunsch algorithm (max: 40%)			
Implementation of extra features and other forms of sequence alignment. Marks awarded for: Being able to find all optimal alignments (10%) Affine gap penalty (10%) Semi global or local (5%) GUI (10%) Pedagogy (15%)			
Design and code 5%			
Demo 5%			
Additional comments			
		Mark	/100