

## SAMPLE MID-TERM

There are a total of 130 points possible for this exam. To get a perfect you just need to get 100 points.

### Question 1 (40pts)

In many of the sequence alignment problems that we encountered we used dynamic programming algorithms to solve them optimally. A key characteristic of dynamic programming formulations is the notion of optimal substructure. Answer the following questions:

1. Define the optimal substructure property for generic dynamic programming formulations.
2. Describe how this substructure property is manifested itself in the context of global sequence alignment.
3. Describe two different approaches to decompose the problem of global sequence alignment using this optimal substructure property.

### Question 2 (10pts)

Describe an algorithm to compute the global sequence alignment between two sequences using an alphabet-weight scoring matrix in which the spaces at the end (but not at the beginning) of the alignment are free.

### Question 3 (40pts)

Answer the following questions regarding multiple sequence alignments:

1. Describe two different methods for evaluating the quality of a multiple sequence alignment.
2. Describe the center-star method for computing a multiple sequence alignment.
3. What can you say about the quality of the solutions produced by the center-star method? Discuss the relation between the center-star solution and the optimal solutions of the methods described in the first part of this question.
4. What are the advantages and disadvantages of the motif-based approaches for computing multiple sequence alignments?