

Math 6390 – Bioinformatics
January 31, 2002
Due February 14, 2002

The goal of this assignment is to implement the Needleman-Wunch Algorithm for global alignment in a computer program.

The program should be able

- To accept different weights for substitutions, insertions, and deletions
- Be able to add a gap penalty
- Compute the distance matrix
- Perform a traceback
- Print the optimal alignment(s)

Turn in the following:

1. A printout of the code
2. A sample run for a simple alignment with the weights (1 for a mismatch, 0 for a match)
3. A sample run for the alignment for the sequences on page 82 of the text with the same weights as above.
4. Add a gap penalty and align the sequences on page 82.
5. An alignment for the sequence on page 82 with your own choice of weights.