Due February 24, 2006 (in class)

CENG 465 – Assignment #1

Problem 1: (5*5 = 25 points) Determine the alignment score for each of the following sequence alignments:

   a. Global alignment: match score = +1, mismatch score = 0, gap penalty = -1
      TGTACGGCTATA
      TC---CGCCT-TA

   b. Global alignment: match score = +1, mismatch score = 0, gap penalty = -1
      ---TCTGTACGCGATCATGT
      TAGC-GTCCGATAT-A---

   c. Global alignment: match score = +1, mismatch score = -1, gap opening penalty = -2, gap extension penalty = -1
      AGATAGAAACTGATATATA
      AGA-A-A-ACAGAG-T---

   d. Global alignment: match score = +1, mismatch score = -1, gap opening penalty = -2, gap extension penalty = -1
      AGATAGAAACTGATATATA
      AG---AAAACAGAGT----

   e. Semiglobal alignment: match score = +1, mismatch score = -1, gap opening penalty = -2, gap extension penalty = -1
      AGATAGAAACTGATATATA
      AG---AAAACAGAGT----

Problem 2: (25 points) Using the Needleman and Wunsch global alignment method, construct the dynamic programming score table for the following two sequences, using the following scoring parameters: match score = +1, mismatch score = 0, gap penalty = -1.

   ACAGTCGAAACG
   ACCGTCCCG

What is the optimal global alignment between these sequences?
Problem 3: (25 points) Using the Smith-Waterman method, construct the dynamic programming score table for a local alignment of the following two sequences:

ACGTATCGCGTATA
GATGCTCTCGGAAA

What is the best local alignment between these two sequences?

Problem 4: (5*5 = 25 points) Explain the following terms briefly:

1. Central Dogma
2. Genome
3. Ortholog
4. Paralog
5. Protein Secondary Structure