**Week 1**

1. There is a unique longest common subsequence of the strings CTCGAT and TACGTC. What is it?

**TCGT**

1. True or False: There are some coin denominations for which **GreedyChange** does not solve the Change Problem (i.e., does not find a minimum number of coins making change).

**True**

False

1. Imagine a hypothetical world in which there are two amino acids, X and Z, having respective masses 2 and 3. How many linear peptides can be formed from these amino acids having mass equal to 25? (Remember that the order of amino acids matters.)

**465**

1. True or False: Not all recursive algorithms are inefficient.

**True**

False

1. Consider the following adjacency list of a DAG:

a -> b: 5 a -> c: 6 a -> d: 5

b -> c: 2 b -> f: 4

c -> e: 4 c -> f: 3 c -> g: 5

d -> e: 6 d -> f: 8

e -> g: 2

f -> g: 1

What is the longest path in this graph? Give your answer as a sequence of nodes separated by spaces. (Note: a, b, c, d, e, f, g is a topological order for this graph.)

**a d f g**

1. Here is the adjacency list of a graph with six nodes and ten edges:

a -> b, c, d, e, f b -> c, f c -> d d -> e -> d, f f ->

Which of the following are topological orderings of the nodes in this graph? (Select all that apply.)

**a, b, c, e, d, f**

**a, e, b, c, f, d**

**a, b, e, c, f, d**

a, b, e, d, c, f

a, b, e, f, d, c

a, b, c, d, e, f

1. True or False: The dynamic programming algorithm we introduced for finding a longest path in a DAG has runtime proportional to the number of edges in the graph.

**True**

False

**Week 2**

1. Consider the following alignment:

TCGAC--ATT

CC---GAA-T

What is the score of this alignment if the match score is 1, the mismatch penalty is 1, and the indel penalty is 2?

**-10**

1. Consider the following alignment:

TACTATTT**ACAGTAGACAC**GT

AACAGAC-**ATAC-AGATAC**CT

What is the score of the bold portion of this alignment as a *local* alignment if the match score is 1, the mismatch penalty is 3, and the indel penalty is 1?

**-3**

1. Say that the match score is 1, the mismatch penalty is 1, and the indel penalty is 1. What is the maximum score of a fitting alignment of GATACACT and ACGACCACAGATACCGCTATTCACTATATCGTT? (Hint: don't make this problem too difficult.)

**5**

1. Say that the match score is 1, the mismatch penalty is 0, and the indel penalty is 2.

Score the following overlap alignment.

AGTACATCAGAGGAGTT-ACATACTAACG

             AGTTCACAGGCTA-CGTACAGATATTACGACAGGCAGA

**8**

1. What type of alignment should you use if you are interested in aligning short regions of two strings?

Global alignment

**Local alignment**

Fitting alignment

Overlap alignment

**Week 3**

1. Consider the following alignment:

TCGAC--ATT

CC---GAA-T

What is the score of this alignment if the match score is 1, the mismatch penalty is 1, and the indel penalty is affine with a gap opening penalty of 4 and a gap extension penalty of 1?

**-13**

1. True or False: Using a three-level Manhattan is quicker than using a Manhattan with long indel edges to solve the Alignment with Affine Gap Penalties Problem.

**True**

False

1. True or False: Different longest paths in an alignment graph may have different middle nodes.

**True**

False

1. There is a unique multiple longest common subsequence of CGGAACTGGT, TGAGACGGTA, and TGCGACGGCT. What is it?

**GGACGGT**

1. True or False: Optimal pairwise alignments of three strings always can be assembled into an optimal 3-way alignment.

True

**False**

**Week 4**

1. True or False: genome rearrangements can be thought of as genomic earthquakes.

**True**

False

[Mutations are genomic erosion.]

1. Compute the number of steps required by **GreedySorting** to sort the following permutation (i.e., to transform it into the identity permutation.)

(-16 -20 +12 +18 -14 -17 -15 -6 -8 -19 -11 +13 -10 +4 -5 -2 +7 -3 +1 -9)

**29**

1. Compute the number of breakpoints in the following permutation.

(+6 -12 -9 +17 +18 -4 +5 -3 +11 +19 +20 +10 +8 +15 -14 -13 +2 +7 -16 -1)

**18**

1. What is the maximum number of breakpoints that a single reversal can eliminate?

**2**

**Week 5**

1. Given the genome containing the circular chromosomes (+1 +2 +3 +4)(+5 +6)(+7+8+9), which of the following is a genome resulting from a 2-break on this genome? (Select all that apply.)

**(+1 +2 +3 +4)(+5 -9 -8 -7 +6)**

(+1 +2 +3 +4 +5 +6 +7 +8 +9)

**(+1 +2 +3 +4)(-5 +6) (+7 +8 +9)**

(+1 +2)(+3 +4)(+5 +6)(+7 +8)(+9)

1. What is the maximum number of cycles that the breakpoint graph of two genomes with 97 synteny blocks can have?

**97**

1. Say that genomes P and Q share 200 synteny blocks. P has 15 circular chromosomes, Q has 37 circular chromosomes, and the 2-break distance between P and Q is 57. How many red-blue alternating cycles are there in the breakpoint graph of P and Q?

**143** [d(P,Q) = n – c 🡪 c = n - d(P,Q) = 200 – 57]

1. Give the number of shared 3-mers of TGGCCTGCACGGTAG and GGACCTACAAATGGC. Please make sure that you consult the definition of shared *k*-mers from the epilogue in the interactive text (include reverse complements).

**7**

1. True or False: Evidence suggests that there are rearrangement hotspots in the human genome.

**True**

False

1. True or False: It is possible to prove a scientific theory in the same way that one would prove a mathematical theorem.

True

**False**