1. Given two DNA sequences \( S \) and \( iS \) that are each other’s inverse (for example 5’-GATCAT-3’ and 5’-TACTAG-3’), what does their dotplot look like?

![Dotplot Options](image)

- A)
- B)
- C)
- D)

2. Which of the following statements on the Needleman and Wunsch algorithm for pairwise sequence alignment is true?

A) The Needleman-Wunsch algorithm is always better in aligning homologous sequences than a multiple sequence alignment

B) The Needleman-Wunsch algorithm provides the single best alignment.

C) The alignment is optimal (as measured by the alignment score), but there might be many equally optimal pathways/traces through the scoring table.

D) The Needleman and Wunsch algorithm computes the best local alignment

E) None of the above

3. The figure below shows a small fragment of a protein. From this figure, is it possible to define which extremity is the N-terminal, and which extremity is the C-terminal?

![Protein Fragment](image)

- a) Yes: 1 is Nter, 2 is Cter
- b) No: there is not enough information
- c) Yes, 1 is Cter and 2 is Nter
- d) No: Nter and Cter are only defined for nucleic acids
- e) No: we would need to know the sequence of this protein fragment
4) Which combination of program / substitution matrix will most likely give you the best alignment between two sequences that are highly similar?

A) BLAST / Blosum45
B) Needleman-Wunsch / Blosum45
C) BLAST / Blosum90
D) Needleman-Wunsch / Blosum90

5) We want to find the best alignment(s) between the protein sequences WWYCTY and WCYTY. The scoring scheme S is defined as follows: S(i,i) = 10, S(i,j) = 0 otherwise. There is a gap penalty of -2N, where N is the length of the gap (gaps at the beginning are considered, see below). The score Sbest and the number N of optimal alignments are (show your final dynamic programming matrix for full credit):

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A) Sbest = 40, N = 1
B) Sbest = 35, N = 1
C) Sbest = 35, N = 2
D) Sbest = 36, N = 2
E) Sbest = 37, N = 1

6. How many possible alignments of length M, with no gaps, can you form when you compare two sequences of length N and M, with N > M?

A) 1
B) N-M
C) N-M+1
D) M
E) N

7. We want to find the best alignment(s) between the DNA sequences AGTATCT and AGATGTC. The scoring scheme S is defined as follows: S(i,j) = 2 if i = j, and S(i,j) = 0 otherwise. There is a gap penalty of -2N, where N is the length of the gap (penalty for the first position counts; see table below). What is the value at the position marked (?)

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A) -2
B) 0
C) 2
D) -1
E) 1