Name		ID		Section	

1. Smith–Waterman always aligns full sequences. (True/False)

2. Local alignment ignores negative values during scoring. (True/False)

3. Pairwise alignment is sometimes insufficient to detect weak similarities. (True/False)

4. BLAST uses heuristics instead of full Dynamic Programming. (True/False)

5. Multiple alignment is faster than pairwise alignment. (True/False)

6. If match=+1, mismatch=-1, gap=-2, what is the score of aligning ACG vs AG?

   (a) 0

   (b) 1

   (c) -1

   (d) -2

7. In Smith–Waterman, traceback stops when:

   (a) Top-left reached

   (b) A zero score is reached

   (c) End of sequence reached

   (d) No gaps remain

8. Which method is best for detecting motifs in proteins?

   (a) Global alignment

   (b) Local alignment

   (c) BLAST only

   (d) Multiple alignment only

9. Which scheme favors long gaps?

   (a) Linear penalty

   (b) Affine penalty

   (c) No gap penalty

   (d) Random

10. Time complexity of Smith-Waterman for sequences length m, n is:

    (a) $O(m + n)$

    (b) $O(mn)$

    (c) $O(2^n)$

    (d) $O(n^3)$