

Name		ID		Section	
------	--	----	--	---------	--

1. Enumerating all possible alignments is computationally feasible for long sequences. (True/False)
2. The recurrence for global alignment includes left, top, and diagonal neighbors. (True/False)
3. In affine gap penalties, opening a gap is usually costlier than extending it. (True/False)
4. Multiple sequence alignment is computationally more expensive than pairwise alignment. (True/-False)
5. Pairwise alignment is sufficient to detect distant evolutionary relationships.(True/False)
6. BLAST can be used for both protein and nucleotide sequences. (True/False)
7. BLAST always guarantees the optimal alignment. (True/False)
8. If match=+2, mismatch=-1, gap=-2, what is optimal alignment score of A vs A?
  - (a) 2
  - (b) -1
  - (c) -2
  - (d) 0
9. Time complexity of multiple alignment using DP for t sequences of length n:
  - (a)  $O(n^2)$
  - (b)  $O(n^3)$
  - (c)  $O(n^t 2^t)$
  - (d)  $O(2^n)$
10. Which is NOT a limitation of global alignment?
  - (a) Cannot handle variable fragments like introns
  - (b) Cannot detect local similarities
  - (c) Cannot align two sequences of same length
  - (d) Misaligns conserved regions