Name		ID		Section	

1. What is the minimum number of mismatches between "AAGTC" and any k-mer in "CTTAAGTCTG"?

2. How many distinct 6-mers are in a 1000 bp genome?

3. What is the Hamming distance between 'ATCG', 'ATGG', 'ATGA', 'ATGA' and the consensus 'ATGA'?

4. The greedy search can be trapped in suboptimal motif configurations.[True / False]

5. The sum of probabilities in each profile position may exceed 1 and we need normalization to handle that.[True / False]

6. A motif with lower information content is typically more conserved.[True / False]

7. A profile matrix must be recomputed after each motif update.[True / False]

8. Reverse complements are unnecessary when searching for motifs on single-stranded DNA.[True / False]

9. Which step in Gibbs sampling introduces randomness?

   (a) Profile update
   (b) Resampling one motif instance
   (c) Scoring motifs
   (d) Initial motif selection

10. A profile matrix for one position is: A=2, C=1, G=1, T=0. What is the probability of G (with pseudo-counts)?

11. What is the profile probability of k-mer 'ATA' in profile A:[0.6,0.1,0.7], T:[0.1,0.7,0.1] is?

12. Skew diagrams help predict transcription start sites.[True / False]

13. Motif instances are always perfectly identical in practice.[True / False]

14. The RandommizedMotifSearch algorithm always finds the global optimum.[True / False]

15. In motif search, sequences can contain multiple motifs of the same pattern.[True / False]