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1. What is the effect of adding pseudocounts in profile estimation?
 - (a) Increases zero probabilities
 - (b) Prevents zero probabilities
 - (c) Decreases motif length
 - (d) Ignores rare nucleotides
2. Which of these is NOT a reason for failure in motif search algorithms?
 - (a) Too few input sequences
 - (b) Incorrect motif length
 - (c) High motif conservation
 - (d) Excessive noise in data
3. What is the profile probability of the k-mer "ATG" given profile: A: [0.3, 0.1, 0.4] C: [0.2, 0.2, 0.3] G: [0.2, 0.4, 0.1] T: [0.3, 0.3, 0.2] ?
4. Gibbs Sampling always converges to the same motif set regardless of initial position. [True / False]
5. In a profile matrix, summing probabilities per position gives 1. [True / False]
6. A k-mer that matches the consensus exactly will always have the highest profile probability. [True / False]
7. The information content is highest when profile probabilities are uniform. [True / False]

8. Which of the following is an advantage of Gibbs Sampling?
- (a) Deterministic output
 - (b) No need for initialization
 - (c) Avoids local optima by stochastic updates
 - (d) Uses only consensus strings
9. How many candidate 6-mers exist in 20 sequences of length 100?
10. High entropy means low conservation in motif positions. [True / False]
11. The total score of a motif set is based on total mismatches from consensus. [True / False]
12. The motif length k must be known or assumed before applying motif finding algorithms. **JUSTIFY.**[True / False]
13. Gibbs sampling updates all motifs in each iteration. [True / False]
14. What is the expected count of 'T' at position 1 with probability 0.8 in 10 sequences?
15. Which 3-mer is most probable under profile A:[0.6,0.1,0.7], T:[0.1,0.7,0.1]?
- (a) ATA
 - (b) TAT
 - (c) ATT
 - (d) TAA