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- What does the minimum in a skew diagram suggest?
  - Point of maximum G content
  - Origin of replication
  - Transcription termination site
  - Random sequence noise
- Which algorithm starts with one k-mer and builds the motif profile iteratively?
  - Gibbs Sampling
  - Greedy Motif Search
  - Randomized Motif Search
  - Naive Exact Search
- Given the DNA string 'CATTCCGGA', what is the skew at position 5?
- What is the consensus string for the matrix: A: [2,0,1] C: [1,3,1] G: [0,1,2] T: [1,0,0]?
- What function quantifies the dissimilarity of motif instances from a consensus?
  - Information content
  - Likelihood
  - Hamming distance
  - Entropy
- Which of the following improves Greedy motif search accuracy?
  - Using pseudocounts
  - Ignoring reverse complements
  - Reducing number of sequences
  - Decreasing motif length

7. In a profile matrix, counts at one position are A:2, C:1, G:1, T:0. What is the probability of A (with pseudocounts +1)?
8. Reverse complements are essential for identifying motifs on both DNA strands.[True / False]
9. The sum of all nucleotide probabilities at any position in a profile matrix equals 1. [True / False]
10. Skew diagrams are symmetric with respect to reverse strands.[True / False]
11. The consensus string is always a substring of one of the input sequences.[True / False]
12. What is the profile probability of k-mer 'ATG' given profile: Position 1: A=0.2, C=0.3, G=0.2, T=0.3 Position 2: A=0.3, C=0.2, G=0.3, T=0.2 Position 3: A=0.5, C=0.1, G=0.2, T=0.2?
13. Which of the following is an advantage of Gibbs Sampling?
- (a) Always finds global optimum
  - (b) Runs in constant time
  - (c) Can escape local optima via randomness
  - (d) Requires no initialization
14. The origin of replication is typically located at the first base of the genome.[True/False]
15. Adding pseudocounts reduces the influence of small sample size in profile estimation.[True/False]