BRAC University
Department of Computer Science and Engineering

CSE 443: Bioinformatics-I (B)

Quiz 04: Summer 2025 Time: 15 Minutes Marks: 15

Name		ID		Section	

Q1. The Baum-Welch algorithm computes: (A) Most likely path (B) Probability of observed sequence (C) Train parameters (D) None

Q2. The DP table for Viterbi with 2 states, length n has dimension: (A) $n \times n$ (B) $2 \times n$ (C) $k \times k$ (D) $n \times k^2$

Q3. For sequence "CG", island: $P(C) = 0.35, P(G) = 0.35$; background: $0.2, 0.2$. Which is favored? (A) Background (B) Island (C) Equal (D) Cannot say

Q4. If two Viterbi paths tie, backpointer chooses: (A) Random (B) Arbitrary fixed (C) Both (D) Fewer switches

Q5. In genomics, CpG islands modeled by HMMs because: (A) Random bases (B) Distinct emissions vs background (C) Not probabilistic (D) Too short

Q6. Which parameter governs observing a base? (A) Initial (B) Transition (C) Emission (D) None

Q7. With flat emissions (0.25 each), path depends only on: (A) Emissions (B) Transitions (C) Both (D) None

Q8. Which algorithm trains CpG HMM from unlabeled data? (A) Baum-Welch (B) Viterbi (C) Forward (D) Greedy

Q9. In log-space, multiplication becomes: (A) Addition (B) Subtraction (C) Division (D) Max

Q10. If sequence has far more G/C than A/T, Viterbi prefers: (A) Background (B) Island (C) Equal (D) Cannot say

Q11. In Viterbi recurrence $V_t(j) = \max_i[V_{t-1}(i) \cdot a_{ij}] \cdot b_j(x_t)$, a_{ij} is: (A) Emission prob (B) Transition prob (C) Initial prob (D) Sequence prob

Q12. If $P(B \to I) = 0.01$, the HMM will: (A) Switch often (B) Rarely switch (C) Never switch (D) Switch half the time

Q13. Which algorithm computes total probability of sequence? (A) Forward (B) Viterbi (C) Needleman-Wunsch (D) BLAST

Q14. The output of Viterbi on genomic DNA is: (A) Base counts (B) Segmentation into states (C) Protein coding seq (D) GC content

Q15. Why not just count GC% instead of HMMs? (A) Ignores transitions (B) Harder to compute (C) Requires training (D) GC% higher in background