CSE 463 - Introduction to Bioinformatics
January 2021 Term
Class Test # 4 Time: 20 minutes (+5 minutes submission)
[Please write your answers in single page. Multiple pages of answers will not be accepted]

1. Following are the (3, 1) read pairs providing full coverage, in a sequence assembly problem. All the read pairs are from the same strand:

    { AGC|GCT, AGC|GCT, CAG|AGC, CAG|TGC, GCA|CAG, GCA|CTG, TGC|GCA }

    Using appropriate approach, can you recover the original sequence?   **(10)**

2. The figure below shows an HMM with two states α and β. Given that the HMM emitted the string GC, draw the Viterbi graph. Use log-scores (base 10), rather than straight probability scores.   **(10)**