Qz.kraft

Topic Name : ABIN_quiz_1
Total MCQs : 3
Total Subjective Questions : 10
Instructor Name : Dr. Debarka Sengupta
Quiz Creation Date : 8/9/2023
Total Score : 20

MCQ:

(Total MCQ Score: 3)

1. What is the hamming distance between ATGCACTA and AGTCATTA? (Score: 1)

   A. 1

   B. 2

   C. 3

   D. 4

   Answer:
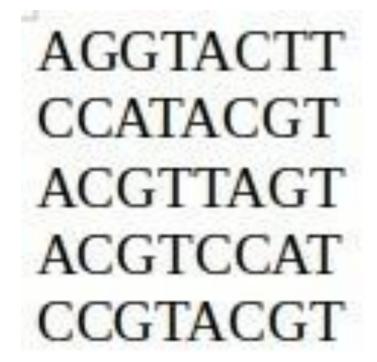   3

2. How many unique possible 3mer can be formed? (Score: 1)

   A. 16

   B. 64

   C. 256

   D. 1024

   Answer:
   64

3. Below, you have five motif of five sequences. What is the motif score of the consensus sequence? (Score: 1)

AGGTACTT
CCATACGT
ACGTTAGT
ACGTCCAT
CCGTACGT

   A. 31

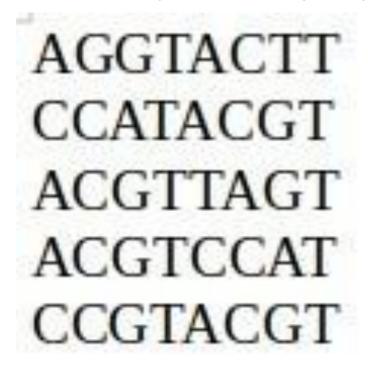   B. 25

C. 28

D. 37

Answer:
31

SUBJECTIVE:

1. **Which enzyme is responsible for transcription? (Score: 1)**

   Answer:
   RNA polymerase

2. **Write the consensus sequence for the below aligned 5 sequence? (Score: 1)**

   AGGTACTT
   CCATACGT
   ACGTTAGT
   ACGTCCAT
   CCGTACGT

   Answer:
   ACGTACGT

(Total Subjective Score: 17)

3. **What does the height of each letter at each position on the MOTIF logo reflect? (Score: 1)**

   Answer:
   The height of each letter at each position of a motif logo reflects the frequency of that specific nucleotide or amino acid residue at that position within the sequence alignment used to create the motif logo.

4. **Does the choice of initial values affect the Gibbs Sampling algorithm? Please explain why (Score: 2)**

   Answer:
   The choice of initial values or starting points in the Gibbs Sampling algorithm can have a significant impact on its performance and the quality of the results obtained. The choice of initial values in Gibbs Sampling can affect convergence speed and few other parameters.

5. **What is the time complexity of the BruteForceMotifSearch for each set of starting positions? Here, 't' represents the number of sample DNA sequences, 'n' represents the length of each DNA sequence, and 'l' represents the length of the motif (l-mer).**

   (Score: 1)

   Answer:
   $l(n - l + 1)^t = O(ln^t)$

6. **What are the advantages of the Median String Problem over the normal Motif Finding Problem? (Score: 1)**

Answer:
The Median String Problem requires examination of a relatively lower number of combinations.

7. **Outline the steps involved in the Gibbs Sampling Algorithm? (Score: 4)**

   Answer:
   1. Randomly choose starting positions s = (s1,...,st) and form the set of l-mers associated with these starting positions.

   2. Randomly choose one of the t sequences.

   3. Create a profile P from the other t – 1 sequences.

   4. For each position in the removed sequence, calculate the probability that the l-mer starting at that position was generated by P.

   5. Choose a new starting position for the removed sequence at random based on the probabilities calculated in Step 4.

   6. Repeat steps 2-5 until there is no improvement.

8. **Outline the steps involved in the Median String Search Algorithm? (Score: 4)**

   Answer:
   MedianStringSearch (DNA, t, n, l):

   bestWord <- AAA...A

   bestDistance <- ∞

   for each l-mer s from AAA...A to TTT...T

   if TotalDistance(s,DNA) < bestDistance

   bestDistance<-TotalDistance(s,DNA)

   bestWord <- s

   return bestWord

9. **What is the difference between local and global alignment? (Score: 1)**

   Answer:
   1. Global alignment aligns entire sequences from start to end, whereas local alignment finds the best matching subsequence within sequences, allowing gaps at the beginning or end.
   2. Global alignment is suitable for aligning two closely related sequences whereas local alignment can be used for aligning more divergent or distantly related sequences.

10. **What is the biological significance of a Motif? (Score: 1)**

    Answer:
    The biological significance of a motif lies in its function as a conserved sequence or pattern within biomolecules, aiding in regulatory, structural, or functional roles critical for cellular processes, evolution, and disease mechanisms.