Indraprastha Institute of Information Technology Delhi (IIITD)
Department of Computational Biotechnology

BIO213 – Introduction to Quantitative Biology

Quiz-1

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1. Vertical and horizontal frame shifts in a dot plot show
   a. Palindromic sequences
   b. Microsatellites
   c. Insertion and deletions
   d. Repeating elements

Correct answer: c (1 mark)

2. Which of the following the best suited for finding functional domains in a set of protein sequences?
   a. Global alignment
   b. Local alignment
   c. End-free alignment

Correct answer: b (1 mark)

3. Which of the following is not true for End-free alignment?
   a. The first row and column are initialized to zero for allowing indels/gaps at the ends without penalty
   b. The minimum value in a cell can be zero
   c. It is essentially used for building genome fragments out of shorter sequencing data
   d. Traceback starts with the best score in an end column or an end row.

Correct answer: b (1 mark)

4. Which of the following is represents the most divergent sequences?
   a. BLOSUM 80 and PAM 120
   b. BLOSUM 62 and PAM 1
   c. BLOSUM 62 and PAM 250
   d. BLOSUM 45 and PAM 250

Correct answer: d (1 mark)

5. Consider the following multiple sequence alignment layout

   a. ```
      WW
      WA
      GW
      AG
      NW
      WA
      ```
   b. ```
      WG
      WA
      WG
      WA
      WG
      AW
      ```

Which of the above (a or b) is more likely to have a higher log-odd ratio for the event W→G?

a. a
b. b

Correct answer: a (2 mark)

6. BLAST often produces several short HSPs rather than a single aligned region.
   a. True
   b. False

Correct answer: a (1 mark)

7. Sequencing reads are in general contaminated with _____ DNA.

Correct answer: Vector/host DNA (1 mark)

8. Computational complexity of aligning k sequences of length n by dynamic programming and progressive alignment is given by
   a. $O(k^2n^2)$ and $O(2^kn^k)$, respectively.
   b. $O(2^kn^k)$ and $O(k^2n^2)$, respectively.
   c. $O(n^2)$ and $O(7n^k)$, respectively.
   d. $O(7n^k)$ and $O(n^2)$, respectively.

Correct answer: b (1 mark)

9. Number of reads covering a position in the genome is referred to as _____, while the degree of overlaps between these reads is termed as _____.

Correct answer: Coverage, Linkage (2 marks)

10. Which of the following helps in finding the shortest common string using the overlap graph?
    a. Hamiltonian path
    b. Genetic algorithm
    c. Greedy algorithm
    d. RECONSTRUCTION model
    e. None of the above

Correct answer: c (1 mark)

11. Which of the following has been built on the logic of dot plot?
    a. FASTA
    b. BLAST
    c. MULTICONTIG

Correct answer: a (1 mark)

12. In an affine gap penalty model, if the gap opening penalty is -20, gap extension penalty is -4 and gap length is 8, the gap score will be _____.

Correct answer: -48 (2 mark)

13. tblastx compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.
   a. True
   b. False
 Correct answer: a (1 mark)

14. Which of the following is an alignment corresponding to the path shown with bold black border in the image below?

   a. B-ANDMASTERS
      TWIN---S-E-T

   b. B-ANDMASTERS
      TWIN---S-ET-

   c. -BANDMASTERS
      TWIN---S-E-T

 Correct answer: a (2 mark)

15. Which of the following does not describe local alignment algorithm?
   a. Score can be negative
   b. Negative score is set to 0
   c. First row and first column are set to 0 in initialization step
   d. In traceback step, beginning is with the highest score, it ends when 0 is encountered

 Correct answer: a (1 mark)

16. The optimal alignment of two similar sequences is usually that _____ number of matches and _____ the number of gaps.

a. Minimize, maximize
b. Maximize, minimize
c. Degrade, upgrade
d. Upgrade, degrade

Correct answer: b (1 mark)