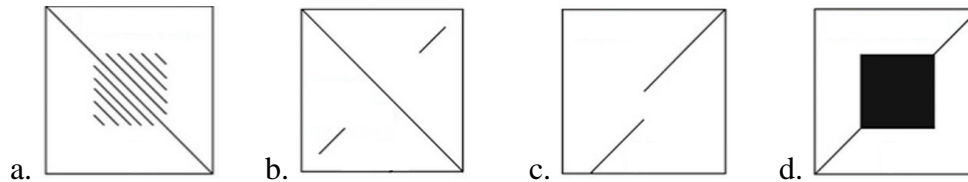# Indraprastha Institute of Information Technology Delhi (IIITD)
Department of Computational Biotechnology

BIO213 – Introduction to Quantitative Biology

Quiz-1 (February 17, 2022)

_____

1. Which of the following dot plots represents the presence of microsatellites in the sequences?

(1 mark)

a.   b.   c.   d.

Correct answer: d

2. Which of the following is the best suited for finding functional domains in a set of protein sequences? (1 mark)
   a. Global alignment
   b. Local alignment
   c. End-free alignment

Correct answer: b

3. Which of the following represents the most diverged sequences? (1 mark)
   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

4. Which of the following is not true for End-free alignment? (1 mark)
   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

5. Consider the following multiple sequence alignment layout   (2 marks)

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

6. Computational complexity of aligning k sequences of length n by dynamic programming and progressive alignment is given by   (2 marks)
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

7. Number of reads covering a position in the genome is referred to as _____, while the degree of overlaps between these reads is termed as _____.   (2 marks)

Correct answer: coverage, linkage

8. tblastx compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.   (2 marks)
a.   True   b. False

Correct answer: a

9. Which of the following is an alignment corresponding to the path shown with bold black border in the image below?   (2 marks)

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

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

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

Correct answer: c

10. Find the score of the following alignment (Match = 4, Mismatch = -1, Gap opening penalty = -2, gap extension penalty = -1)   (2 marks)

ATCGATCGCGCAG
| | | | | |
AT-C - - -A CGCAC

Correct answer: 15

11. The optimal alignment of two similar sequences is usually that _____ number of matches and _____ the number of gaps.   (1mark)
    a. Minimize, maximize
    b. Maximize, minimize
    c. Degrade, upgrade
    d. Upgrade, degrade

Correct answer: b

12. In overlap graphs, nodes represent _____, whereas edges represent _____. (Options: reads, overlaps).   (2 mark)

Correct answer: reads, overlaps

13. Choose the correct option: (1 mark)
    a. Off-springs in Genetic algorithm are generated using mutations and crossover.
    b. Off-springs in Genetic algorithm are generated using Natural selection and crossover.
    c. Off-springs in Genetic algorithm are generated using Natural selection and mutations.

Correct answer: a