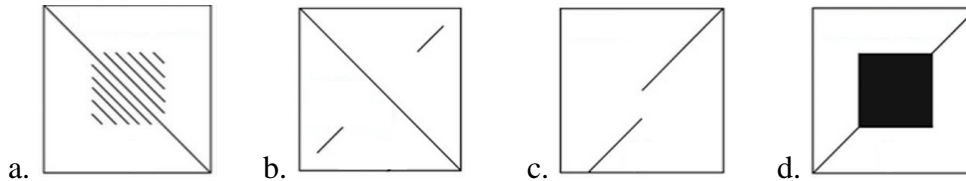# Indraprastha Institute of Information Technology Delhi (IIITD)
Department of Computational Biotechnology

BIO213 – Introduction to Quantitative Biology

Quiz-1

_____

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. How are chimeric fragments (arising due to end-to-end joining of two regular fragments from distinct parts of the target molecule to form a fragment that is not a contiguous part of the target) managed while assembling the genomic fragments? (1 mark)

    Correct answer: Must be recognized as such and removed from the fragment set in a preprocessing stage.

3. blastx is used for   (1 mark)
    a. comparing amino acid sequence against the protein sequence database.
    b. comparing DNA sequence against the translated nucleotide sequence database.
    c. comparing amino acid sequence against the translated nucleotide sequence database.
    d. comparing DNA sequence against the protein sequence database.

    Correct answer: d

4. Which of the following is not an example of basic model for DNA fragment assembly?
    a. RECONSTRUCTION   (1 mark)
    b. MULTICONTIG
    c. Shotgun Sequencing
    d. Shortest Common Superstring

    Correct answer: c

5. Which of the following is an example of transition and transversion respectively?   (2 mark)
    a. $A \rightarrow C$ and $A \rightarrow T$
    b. $C \rightarrow T$ and $G \rightarrow A$
    c. $G \rightarrow C$ and $C \rightarrow T$
    d. $A \rightarrow G$ and $G \rightarrow T$

    Correct answer: d

6. Which of the following does not describe global alignment algorithm? (1 mark)
   a. In initialization step, the first row and first column are subjected to gap penalty.
   b. Scores can be negative.
   c. In trace back step, beginning is with the cell at the lower right of the matrix and it ends at top left cell.
   d. First row and first column are set to zero.

   Correct answer: d

7. Local alignment is suitable for _____ related sequences while Global alignment is preferred for _____ related sequences. (Options: Closely, Distantly) (2 marks)

   Correct answer: Distantly, Closely

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

   ```
   A T C G A T C G C G C A G
   | |           | | | |
   A T - C - - - A C G C A C
   ```

   Correct answer: 15

9. Log odd ratios are calculated using (1 mark)
   a. log odd ratio = $\log_2$(expected/observed)
   b. log odd ratio = $1/\log_2$(expected/observed)
   c. log odd ratio = $\log_2$(observed/expected)
   d. log odd ratio = $1/\log_2$(observed/expected)

   Correct answer: c

10. An overlap is a link if no other fragment completely covers the overlap. (1 mark)
    True or false?

    Correct answer: True

11. In overlap graphs, nodes represent _____, whereas edges represent _____.
    (Options: reads, overlaps). (1 mark)

    Correct answer: reads, overlaps

12. Which of the following is true for all the models for fragment assembly − Shortest common superstring, RECONSTRUCTION and MULTICONTIG?
    a. All three assume that the fragment collection is free of contamination and chimeras.
    b. All three can deal with base call errors.
    c. All three can deal with unknown orientation of the fragments.
    d. All three use distance rather than similarity between the fragments.
    e. All three allow the assembly of contigs in case of low coverage. (1 mark)

    Correct answer: a

13. Which of the following is an alignment resulting from the path shown in the image below?

		A	C	T	G	A	T	T	C	A
	0	-2	-4	-6	-8	-10	-12	-14	-16	-18
A	-2	2	0	-2	-4	-6	-8	-10	-12	-14
C	-4	0	4	2	0	-2	-4	-6	-8	-10
G	-6	-2	2	1	4	2	0	-2	-4	-6
C	-8	-4	0	-1	2	1	-1	-3	0	-2
A	-10	-6	-2	-3	0	4	2	0	-2	2
T	-12	-8	-4	0	-2	2	6	4	2	0
C	-14	-10	-6	-2	-4	0	4	2	6	4
A	-16	-12	-8	-4	-5	-2	2	1	4	8

a.
```
ACTGATTCA
|||||||||
ACGCA-TCA
```

b.
```
ACTG-ATTCA
|| | |||||
AC-GCA-TCA
```

c.
```
ACTG-ATTCA
|| | |||||
AC-GCA-TCA
```

d.
```
ACTG-ATTCA
|| | |||||
AC-GCAT-CA
```

(2 marks)

Correct answer: b or c (both options are the same)

14. Hamiltonian path is a walk that visits each _____ (node/edge) once.   (1 mark)

Correct answer: node

15. 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

16. Which of the following is an example of base call error in DNA?   (1 mark)
   a. Chimera
   b. Insertion
   c. Contamination
   d. Transposition

Correct answer: b