

**QUIZ 2 - COMPUTATIONAL BIOLOGY LA04**

Jumlah questions: 15

Estimasi pengerjaan: 27menit

Nama instruktur: Williams Sandjaya

Nama

Kelas

Tanggal

1. 1. Which of the following is not a variant of BLAST?

- a) BLASTN
- b) BLASTP
- c) BLASTX
- d) TBLASTNX

a) D

b) A

c) B

d) C

2. Which of the following is not correct about BLAST?

- a) The BLAST web server has been designed in such away as to simplify the task of program selection
- b) The programs are organized based on the type of query sequences
- c) The programs are organized based on the type of nucleotide sequences, or nucleotide sequence to be translated
- d) BLAST is not based on heuristic searching methods

a) A

b) C

c) D

d) B

3. Which of the following is not a benefit or a factual of FASTA over BLAST?

- a) FASTA scans smaller window sizes
- b) It gives more sensitive results
- c) It gives less sensitive results
- d) It gives results with a better coverage rate for homologs

a) B

b) C

c) D

d) A

4. Which of the following is not one of the requirements for implementing algorithms for sequence database searching?

- a) Size of the dataset
- b) Sensitivity
- c) Specificity
- d) Speed

a) A

b) B

c) C

d) D

5. Which of the given statements is incorrect about Database Types?
- a) Relational databases are more useful in the development of biological databases
 - b) The tables in relational database are carefully indexed and cross-referenced with each other, sometimes using additional tables, so that each item in the database has a unique set of identifying features
 - c) The relational database orders data in tables made up of rows giving specific items in the database, and columns giving the features as attributes of those items
 - d) The two principal types of DBs are the relational and object-oriented databases

a) A

b) C

c) B

d) D

6. Which of the following does not describe local alignment?
- a) A local alignment aligns a substring of the query sequence to a substring of the target sequence
 - b) A local alignment is defined by maximizing the alignment score, so that deleting a column from either end would reduce the score, and adding further columns at either end would also reduce the score
 - c) Local alignments have terminal gaps
 - d) The substrings to be examined may be all of one or both sequences; if all of both are included then the local alignment is also global

a) A

b) C

c) D

d) B

7. Which of the following is untrue regarding the gap penalty used in dynamic programming?
- a) Gap penalty is subtracted for each gap that has been introduced
 - b) Gap penalty is added for each gap that has been introduced
 - c) The gap score defines a penalty given to alignment when we have insertion or deletion
 - d) Gap open and gap extension has been introduced when there are continuous gaps (five or more)

a) C

b) B

c) A

d) D

8. Which of the following does not describe global alignment algorithm?
- a) In initialization step, the first row and first column are subject to gap penalty
 - b) Score 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

a) A

b) C

c) D

d) B

9. Which of the following does not describe global alignment algorithm?
- a) It attempts to align every residue in every sequence
 - b) It is most useful when the aligning sequences are similar and of roughly the same size
 - c) It is useful when the aligning sequences are dissimilar
 - d) It can use Needleman-Wunsch algorithm

a) D

b) C

c) B

d) A

10. The higher is the score in the alignment _____
- a) the more significant is the alignment
 - b) or the less it resembles alignments in related proteins
 - c) the less significant is the alignment
 - d) the less it aligns with the related protein sequence

a) C

b) B

c) A

d) D

11. Which of the following is untrue regarding dynamic programming algorithm?
- a) The method compares every pair of characters in the two sequences and generates an alignment
 - b) The output alignment will include matched and mismatched characters and gaps in the two sequences that are positioned so that the number of matches between identical or related characters is the maximum possible
 - c) The dynamic programming algorithm provides a reliable computational method for aligning DNA and protein sequences
 - d) This doesn't allow making evolutionary predictions on the basis of sequence alignments

a) A

b) B

c) D

d) C

12. Phylogenetic analysis of a set of sequences that aligns _____ is straightforward because the positions that correspond in the sequences can be readily identified in a _____ of the sequences.
- a) very well, multiple sequence alignment
 - b) in a haphazard manner, multiple sequence alignment
 - c) in a distorted way, multiple sequence alignment
 - d) very well, self alignment

a) A

b) C

c) D

d) B

13. Two more recent uses of phylogenetic analysis are to analyze _____ and to trace the evolutionary history of specific genes. Which of the following could not be the correct blank?
- a) gene families
 - b) genomes
 - c) proteomes
 - d) physical separation methods

a) B

b) D

c) A

d) C

14. To use molecular data to reconstruct evolutionary history requires making a number of reasonable assumptions. Which of the following is incorrect about it?
- a) The molecular sequences used in phylogenetic construction are homologous
 - b) The molecular sequences used in phylogenetic construction share a common origin
 - c) Phylogenetic divergence cannot be bifurcating
 - d) Parent branch splits into two daughter branches at any given point

a) D

b) B

c) A

d) C

15. Which of the following is incorrect regarding the terminologies of phylogenetics?
- a) The connecting point where two adjacent branches join is called a node
 - b) Node represents an inferred ancestor of extant taxa
 - c) At the tips of the branches are long lost species or sequences
 - d) The lines in the tree are called branches

a) C

b) D

c) A

d) B