Chapter 8
Bioinformatics

1. Which of the following are the members database of InterPro?
(A) SCOP **(B)** HAMAP
(C) PIRSF **(D)** Pfam

2. Which of the following are correct methods along with their formulas to calculate the similarities between two hierarchical clustering?
(A) Min: Sim(C1,C2) = Min Sim(Pi,Pj) such that Pi ∈ C1 & Pj ∈ C2
(B) Max: Sim(C1,C2) = Sim(Pi,Pj) such that Pj ∈ C1 & Pi ∈ C2
(C) Ward's method: sim(C1,C2) = ∑ (dist(Pi, Pj))²/|C1|*|C2|, where Pi ∈ C1 & Pj ∈ C2
(D) Group average: sim(C1,C2) = ∑ sim(Pi, Pj)/|C1|*|C2|

3. Which of the following are examples of Homology and similarity tool?
(A) BLAST **(B)** EMBOSS
(C) SSEARCH **(D)** PROSPECT

4. Literature database includes
(A) MEDLINE **(B)** PDB
(C) PDS **(D)** PubMED

5. Sequence alignment helps scientists
(A) to align non-conserved sequence motifs.
(B) to trace out evolutionary relationship.
(C) to infer the function of newly synthesized genes.
(D) to product new members of gene families.

6. Which of the following are correct about GenBank DNA Sequence Entry?
(A) The information is organized into fields, each with an identifier, shown as the first text on each line
(B) In some entries, these identifiers may be abbreviated to two letters, e.g., RF for reference
(C) Some identifiers may have additional subfields
(D) The CDS subfield in the field FEATURES does not offer the amino acid sequence

7. Submission to GENBANK are made using
(A) Bankit **(B)** Bankin
(C) Entrez **(D)** Sequin

8. Which of the following is a nucleotide sequence database?
(A) EMBL **(B)** GenBank
(C) PROSITE **(D)** SWISS PROT

9. Which of the following is a data retrieving tool?

(A) ENTREZ **(B)** EMBL
(C) PHD **(D)** DBGET

10. Information of all known nucleotide and protein sequences are available on
(A) EMBL **(B)** DDBJ
(C) NCBI's Gene Bank **(D)** SWISS PROT

Answer Key
1. (B), (C), (D)
2. (A), (C), (D)
3. (A), (C)
4. (A), (D)
5. (B), (C), (D)
6. (A), (B), (C)
7. (A), (D)
8. (A), (B)
9. (A), (D)
10. (A), (B), (C)