**Biotechnology program (English)**

**Third Level /First Semester**

**Answer model of Final writing Exam**

**Bioinformatics course**

**Day of the exam 5-01-2017**

**1. PDB is** **(Two degrees)**

**A. Primary database for macromolecules ☑**

B. can be determined by gel electrophoresis

C. composite database

D. database for three dimensional structure of biological macromolecule

**2. BLOSUM matrices are used for** **(Two degrees)**

A.  Phylogenetic analysis

B. multiple sequence alignment

**C. pairwise sequence alignment ☑**

D. none of these

**3. Which is data retrieving tool?** **(Two degrees)**

**A. ENTREZ ☑**

B. EMBL

C. PHD

D. All of these

**4. Proteomics research can be categorized as (Two degrees)**

**A. structural proteomics and functional proteomics ☑**

B. structural, functional and comparative proteomics

C. functional and comparative proteomics

D. none of these

**5. A cluster analysis is the study of groups of genes that seem to be regulated together. (Two degrees)**

**A. True ☑**

B. False

**6. Examples of irreversible posttranslational covalent modification include acetylation and phosphorylation. (Two degrees)**

A. True

**B. False ☑**

**7. Which of the following statements regarding the proteome is the most correct? (Two degrees)**

A. A large proportion of the proteome is expressed by each cell of a species.

B. Levels of gene expression at the mRNA level generally correlate highly with levels of functional protein.

**C. The proteins produced by a specific cell depend on cell type and environmental conditions. ☑**

D. All of the above.

E. None of these.

**8. A cDNA library: (Two degrees)**

A. Can also be called an expressed sequence tag (EST) library.

B. Consists of coding sequences from genes that are expressed.

C. Is specific to the set of conditions under which the original mRNA was generated.

**D. All of these. ☑**

E. None of these.

**9. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are: The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are: (Two degrees)**

A. RNA editing and alternative splicing.

B. Protein folding and posttranslational covalent modifications.

**C. Alternative splicing and posttranslational covalent modifications. ☑**

D. Posttranslational covalent modification and transcriptional regulation.

E. RNA editing and base modification.

**10. in two dimensional gel electrophoresis: (Two degrees)**

A. Different forms of the same protein will tend to migrate at the same position.

B. Up to about a hundred different proteins can be distinguished from each other.

C. Proteins with similar functions will be located near each other.

D. All of these.

**E. None of these. ☑**

**11. Secondary structure of RNA molecules: (Two degrees)**

**A. Depends on complementary base pairing. ☑**

B. Is generated by covalent bonding between sections of the RNA molecule.

C. Can be described as interactions between portions of the backbone of the molecule.

D. Does not have an impact on function of the molecule.

**12. Which of these would not be a valid reason that use of microarray technology to differentiate between closely related bacterial species and subspecies is important? (Two degrees)**

A. Certain strains of bacteria are more pathogenic than other related strains.

B. Some strains of bacteria are more active in bioremediation than other related strains.

C. Infection by different strains of bacteria may require different therapeutic approaches.

**D. In many cases, critical information about characteristics of a ☑bacterium causing an infection needs to be immediately available.**

E. All of the above are valid reasons.

**13. A multiple sequence alignment of related genes can identify amino acids required for protein function. (Two degrees)**

**A. True ☑**

B. False

**14. Homologous genes: (Two degrees)**

**A. Would be expected to have very similar sequences in related organisms. ☑**

B. Would be expected to be more similar in distantly related organisms than in organisms that are closely related.

C. May have become similar to each other by random mutation.

D. All of these.

E. None of these.

**15. Identification of a gene that does not fit the typical patterns for eukaryotic gene structure would not have a dramatic effect on bioinformatics. (Two degrees)**

A. True

**B. False ☑**

**16. In an analysis of eukaryotic gene, you identify several non-overlapping open reading frames, but they are not all in the same frame. Which explanation makes the most sense? (Two degrees)**

A. By random chance, a second reading frame within the gene also has an open reading frame.

**B. This gene includes introns which are not multiples of three. ☑**

C. This is a mutant allele that has had several small insertions.

D. All of these.

E. None of these.

**17. Which of these would not be an example of sequence element? (Two degrees)**

A. A recognition site for binding of a particular transcription factor.

B. A restriction endonuclease cut site.

**C. An open reading frame. ☑**

D. A stop codon.

E. None of these.

**18. Why might you want to search a database for a protein motif? (Two degrees)**

**A. A specific motif may impart a specific function to the molecule. You could then identify groups of proteins that may have similar functions. ☑**

B. Presence of a specific motif in several proteins indicates that they are likely to be all from the same species.

C. Absence of a specific motif from one of a pair of otherwise similar proteins indicates that they are produced by alternative splicing of the same gene.

D. All of these.

E. None of these.

**19. You have cloned a new gene from your favorite species of experimental organism, which has had very few genes cloned so far. Which of the following techniques would you expect to provide information about the function of this gene? (Two degrees)**

A.Comparison of regulatory sequences to other DNA sequences in this organism.

B. Comparison of regulatory sequences to DNA sequences from other organisms.

C. Comparison of the gene sequence to other DNA sequences in this organism.

**D. Comparison of the gene sequence to DNA sequences from other organisms. ☑**

E. None of these.

**20. What are the advantages of using a protein sequence rather than a DNA sequence when searching the bioinformatics databases? (Two degrees)**

**21. The GenBank is? (Two degrees)**

**22. GenBank provides what information about a gene? (Two degrees)**

**23. What is UniProtKB and what information does it give you? (Two degrees)**

**24. What is FASTA? (Two degrees)**

**25. What information does GeneCards give you about a gene? (Two degrees)**

**26. What information does GeneAtlas give you about a gene? (Two degrees)**

**27. What is PubMed? (Two degrees)**

**28. The term of bioinformatics was coined by (two degrees)**

A. J D Watson

B. Margaret Dayhoff

**C. Pauline Hogeweg ☑**

D. Frederic Sanger

**29. Step wise method for solving problems in computer science is called (two degrees)**

A. flowchart

B. sequential design

C. procedure

**D. algorithm ☑**

**30. The first published completed genome sequence was of (two degrees)**

A. M13 phage

B. T4 Phage

**C. ɸX174 ☑**

D. Lambda phage

**31. *FlyBase* is a (two degrees)**

A. Biodiversity database

**B. model organism database ☑**

C. literature database

D. bio-molecular database

**32. Which of the following is an *E. coli* database (two degrees)**

**A. EcoGene ☑**

B. EcoBase

C. EcoSeq

D. Colgene

**33. Which of the following is a sequence alignment tool (two degrees)**

**A. BLAST ☑**

B. PRINT

C. PROSITE

D. PIR

**34. The first secondary database developed was (two degrees)**

A. PRINTS

**B.PROSITE ☑**

C. PDB

D. PIR

**35. Which is model organism database?**

A. GOLD

B. PROMISE

**C. SGD ☑**

D. SCOP

**With my best wishes and success for all**

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