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

BIO213 – Introduction to Quantitative Biology

Quiz-3 (May 06, 2022)

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Duration: 20 mins   **Total marks: 20**

Question 1. A coiled peptide chain held in place by hydrogen bonding between peptide bonds in the same chain is?
a) Primary structure
b) α-helix
c) β-pleated sheets
d) Tertiary structure   **(1 mark)**

Question 2. Which of the following is untrue about template selection step in homology modeling of proteins?
a) The first step in protein structural modeling is to select appropriate structural templates.
b) This forms the foundation for rest of the modeling process.
c) Heuristic alignment search programs are used.
d) The template selection involves searching the non-redundant protein database for homologous proteins with determined structures. **(2 marks)**

Question 3. A major design consideration in a microarray experiment is the incorporation of replicates. Select which one/s of the following statement/s are consequences of not including replicates in your experiment:
a) The number of false-positive errors in detecting differentially expressed genes will increase.
b) The number of false-negative errors in detecting differentially expressed genes will increase.
c) No statistical analysis of the significance of the observed changes will be possible.
d) All of the above. **(2 marks)**

Question 4. Which of the following is not a conformational search method?
a) Monte Carlo
b) Genetic Algorithm
c) Simulated annealing
d) Maximum parsimony **(2 marks)**

Question 5. Which of following is not a measure to reduce computational complexity of *Ab initio* modelling?
a) Torsion angles are restricted to a finite set of values.
b) Protein sequence is searched against fold database to look for regions of structural similarity.
c) Only the polar hydrogens are given importance.
d) Bulky side chains are replaced by single pseudo-atoms. **(2 marks)**

Question 6. Which of the following is the correct sequence of steps involved in RNA-seq analysis?
a) Library preparation, sequencing, quantification, read mapping, differential expression analysis
b) Quantification, library preparation, sequencing, read mapping, differential expression analysis
c) Library preparation, sequencing, read mapping, quantification, differential expression analysis
d) Quality check, library preparation, sequencing, read mapping, differential expression analysis
(2 marks)

Question 7. Which of the following is true with respect to RNA-seq differential gene expression analysis?
1. The chances of finding false positives increases with increasing number of genes.
2. For 30000 genes and p-value of 0.05, one would expect 1500 genes to have p-value<0.05 by chance.
3. p-value is adjusted using methods like false discovery rate.

a) 1 and 2
b) 1 and 3
c) 2 and 3
d) All of these
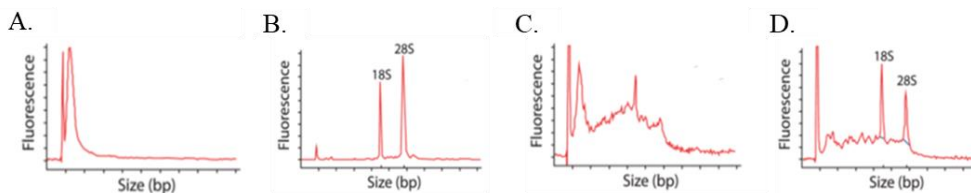e) None of these   **(2 marks)**

Question 8. Which of the following is not the method that can be used for validation of the modelled protein structure?
a) Ramachandran plot
b) ERRAT
c) Rosetta
d) ANOLEA   **(1 mark)**

Question 9. Which of the following indicates the best and the worst quality RNA?

a) Best- A, Worst- D
b) Best- B, Worst- A
c) Best- B, Worst- C
d) Best- A, Worst- D   **(2 marks)**

Question 10. Which of the following are the common problems associated with next-generation RNA sequencing experiments?
1. Sample contamination due to the presence of other types of nucleotide sequences.
2. Low confidence bases.
3. Adaptor contamination.
4. Sequence bias due to the presence of high GC content.   **(2 marks)**

a) 1, 2, 3
b) 1, 3, 4
c) 2 and 3
d) None of these
e) All of these

Question 11. Which of the following statistical tests are used if the data does not follow the normal distribution?
a) T-test and ANOVA
b) Wilcoxon test and ANOVA
c) ANOVA and Kruskal−Wallis test

d) Kruskal−Wallis test and Wilcoxon test   **(2 marks)**