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No. of Printed Pages : 2

SEAT No._____

[25]

SARDAR PATEL UNIVERSITY
EXTERNAL EXAMINATION AM
DATE – 01/11/18 DAY- Thursday TIME 10:00 TO 1:00 pm
Course- US05CBNF05 SUBJECT: BIOINFORMATICS
CLASS- T.Y.B.Sc V Sem TITLE--- BIOINFORMATICS APPLICATION-I
TOTAL MARKS: 70

Q1- Select the correct from the following Multiple Choice: [1 X 10] [10]

(i) **_____ was the first organism to have its entire genome sequenced.**
a) The fruit fly b) *E. Coli* c) *Homo sapiens* d) *Haemophilus influenza*

(ii) **Gene duplication has been found to be one of the major reasons for genome expansion in eukaryotes. In general, what would be the selective advantage of gene duplication?**
a) If one gene copy is non-functional, a backup is available.
b) Larger genomes are more resistant to spontaneous mutations
c) Duplicated genes will make more of the protein product.
d) Gene duplication will lead to new species evolution.

(iii) **The human genome contains approximately how many base pairs?**
a) three thousand b) three million
c) three billion d) three trillion

(iv) **Funding for the Human Genome Project comes from the**
a) NIH b) DOE c) NIH and DOE d) NIH, DOE and ELSI

(v) **What would be a likely explanation for the existence of pseudogenes?**
a) gene duplication b) gene duplication and mutation events
c) unequal crossing over d) evolutionary pressure

(vi) **Each ds DNA has ..... frame in ORF.**
a) 10 b)3 c) 6 d) 2

(vii) **Block is**
a) Sequence with indel b) sequence with mismatch only
c) Sequence with match only d) sequence with gaps only

(viii) **Well-conserved regions in multiple sequence alignments**
a) reflect areas of structural importance. b) reflect areas of functional importance
c) reflect areas of both functional and structural importance
d) reflect areas likely to be of functional and/or structural importance.

(ix) **Why are colour schemes important in creating and analysing sequence alignments?**
a) They look pretty.
b) To make clearer printouts and presentations.
c) To allow you to distinguish conserved residues and residue groups more easily
d) To allow you to detect active sites of proteins

(x) **Meaning of {} bracket in pattern**
a)All codes b) codes except present in the bracket
c) None of the code d) any code

Q2 Answer the following in brief (any ten) [2X10]

(i) Why comparative genomics is important?

[P.T.O.]

(ii) Differentiate conservative and replicative mode of transposition.
(iii) Explain restriction mapping and its important.
(iv) Differentiate nuclear genome and mitochondrial genome.
(v) Explain the significance and limitation of shotgun method of genome sequencing.
(vi) Give the importance of sequence logo.
(vii) Diagrammatically explain structure of gene in eukaryotes.
(viii) What is promoter and its utility in gene expression
(ix) Explain <[EST]-{DW}-2(X)-R-{C}
(x) What are sequence motifs? Give examples.
(xi) How minisatellites differ from microsatellites?
(xii) Explain the basic concept of Hidden Markov Model.

LONG QUESTIONS

Q3 Write a short note on (10)
i) Transposons ii) Alternative splicing
iii) Pseudo genes iv) Repeat regions

OR

Q3 Explain in detail about prokaryotic genome organization and how it differ from eukaryotic genome? (10)

Q4 Discuss the method and significance of genome sequencing. (10)

OR

Q4 Elaborate the aims, objectives and application of Human Genome Project. (10)

Q5(a) What is ORF? Discuss the basic algorithm for gene identification. (05)
Q5(b) Write a short note on ANN. (05)

OR

Q5 Explain the structure of prokaryotic gene structure and different methods for its prediction. (10)

Q6 Write a short note on the following: (any 2)
i) Profile ii) Block iii) pattern (10)

OR

Q6(a) What is sequence logo? Explain its importance. (05)
Q6(b) How HMM model can be used for multiple sequence alignment. (05)

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