SARDAR PATEL UNIVERSITY
EXTERNAL EXAMINATION
DATE – 20/11/19 DAY- Wednesday          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)     **ELSI was established as part of the Human Genome Project to:**
        a) study the ethical, legal, and social implications of mapping the human genome
        b) educate society about the opportunities and challenges of the new genetics
        c) create new technologies that will accelerate the sequencing process
        d) a and b

(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)   **Alignment of more than two sequences is**
        a) Pair wise alignment           c) Multiple sequence alignment
        b) Matrix                        d) None of the above

(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)    **Which of the following regular expressions would be matched by sequence DWILKDG?**
        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) D-M-x-[ILV]-x{2}-G              b) [DN]-W-x-[ILV]-[RKH]-x-G
        c) [DN]-W-x{2}-[ILV]-G             d) D-W-I-[ILMV]-x-K-[GA]

**Q2**  Answer the following in brief (any ten)  [2X10]
(i)  Why comparative genomics is important?
(ii)  What are jumping genes? Explain
(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 Profiles are created?
(xii)  Explain the basic model of Hidden Markov Model.

**LONG QUESTIONS**

**Q3**  Write a short note on  (10)
|  |  |  |
|---|---|---|
| i) | Exons | 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 methods 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.

**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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