Seat No: _____ Enrollment No: _____

PARUL UNIVERSITY

FACULTY OF APPLIED SCIENCE

M.Sc./IMSC Winter 2019 Examination

Semester: 3/9 **Date: 02/12/2019**
Subject Code: 11202201 **Time: 02:00 pm to 04:30 pm**
Subject Name: Bioinformatics and Biostatistics **Total Marks: 60**

Instructions:
1. All questions are compulsory.
2. Figures to the right indicate full marks.
3. Make suitable assumptions wherever necessary.
4. Start new question on new page.

Q.1. A) Essay type/ Brief note (4x2) (Each of 04 marks) **(08)**
(a) Describe Multiple Sequence Alignment (MSA) in detail with examples
(b) Write a note on methods of Secondary Structure Prediction

Q.1. B) Answer the following questions (Any two)
(a) Short note/ Brief note (2x2)/ Schematically label the figures (2x2) (Each of 02 marks) **(04)**
1. Write a brief note on FASTA
2. Genome mapping
(b) Types of Biological databases **(04)**
(c) Protein docking **(04)**

Q.2. A) Answer the following questions.
(a) Short note/ Brief note (2x2)/ Fill in the blanks. (Each of 02 marks) **(04)**
1. Swiss-Prot
2. MEGA software
(b) Homology modeling and its working **(04)**

Q.2. B) Answer the following questions (Any two)
(a) Short note/ Multiple choice questions. (Each of 01 marks) **(03)**
1. The alignment procedure that tries to align the entire sequence is
a) multiple sequence alignment c) pair-wise alignment
b) global alignment d) local alignment
2. The procedure of aligning two sequences by searching for patterns that is in the same order in the sequences
a) sequence alignment c) pair-wise alignment
b) multiple sequence alignment d) all of these
3. International Human Genome project was initiated by
a) National Institute of Health (NIH) b) Celera genomics
c) US Department of Energy (DoE) d) NIH and US DoE
(b) Computer Aided Drug Design (CADD) in Drug discovery **(03)**
(c) Describe gene prediction program **(03)**

Q.3. A) Essay type/ Brief note (4x2) (Each of 04 marks) **(08)**
(a) Write a note on Protein 3D Structure Prediction
(b) Write a note on Genome Annotation

Q.3. B) Answer the following questions (Any two)
(a) Short note/ Brief note (2x2)/ Schematically label the figures (2x2) (Each of 02 marks) **(04)**
1. Global and local alignment
2. Dynamic programming
(b) Brief note on Threading method in protein secondary structure prediction **(04)**
(c) PDB and its access to public domain **(04)**

Q.4. A) Answer the following questions.
(a) Short note/ Brief note (2x2)/ Fill in the blanks. (Each of 02 marks) **(04)**
1. Blast2GO
2. SWISS PDB-Viewer
(b) Short note on Bioinformatics online tools **(04)**

Q.4. B) Answer the following questions (Any two)
(a) Short note/ Multiple choice questions. (Each of 01 marks) **(03)**
1. GROMOS
2. E-value
3. Dendogram
(b) Short note on CATH database **(03)**
(c) Short note Human Genome Project **(03)**