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**BR—331—2016**

**FACULTY OF COMPUTER STUDIES**

**M.Sc. (Second Year) (Fourth Semester) EXAMINATION**

**NOVEMBER/DECEMBER, 2016**

**(CBCS Course)**

**COMPUTER SCIENCE**

**Paper CS-403 Elective—III**

**(Introduction to Bioinformatics)**

**(Tuesday, 22-11-2016)**

**Time : 2.00 p.m. to 5.00 p.m.**

*Time—Three Hours*

*Maximum Marks—75*

*N.B. :—* (i) All questions are compulsory.

(ii) Write answers brief and to the point.

(iii) Draw neat and labelled diagrams wherever necessary.

1. Attempt any *three* of the following : 15

(a) What is Bioinformatics ? Explain the applications of bioinformatics.

(b) What is data retrieval ? Explain data retrieval tool.

(c) Explain genetic and physical maps of genome.

(d) Explain any *one* method of sequence alignment.

(e) What is FASTA ? Explain FASTA algorithm.

2. Answer the following (any *three*) : 15

(a) What is Drug ? Explain types of drug.

(b) Explain the drug discovery technology.

(c) Explain the approach of drug design.

(d) Explain any *three* databases used in bioinformatics.

3. Solve the following (any *three*) : 15

(a) What is searching on web ? Explain any *one* tool for searching.

(b) What is Genome ? Explain gene in detail.

(c) Explain biological motivation of alignment problems.

(d) Distinguish between FASTA and BLAST algorithm.

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4. Answer the following (any *three*) : 15
- (a) Discuss the areas which are influencing drug discovery.
  - (b) Explain G-protein coupled receptors as drug targets.
  - (c) Explain the role of computer in drug designing method.
  - (d) Explain in detail data mining of biological databases.
5. Write short notes on any *three* : 15
- (a) Human Genome Project
  - (b) Gene Family
  - (c) Target Validation
  - (d) STS maps
  - (e) Prokaryotic Genomes.

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