## 6 SEM TDC ZOO M 4

2016

(May)

ZOOLOGY

(Major)

Course: 604

## ( Biotechnology and Bioinformatics )

Full Marks: 48
Pass Marks: 19

Time: 2 hours

The figures in the margin indicate full marks for the questions

Answer Question No. 1 and any three from the rest

- 1. (a) Choose and write the correct answer for the following: 1×3=3
  - (i) HTML/FTP/SMTP/HTTP is used to assess data using www.
  - (ii) FASTA is a DNA and RNA/DNA and protein/RNA and protein sequence alignment software package.
  - (iii) The biological tool of genetic engineering linkers contains target sites for the action of one/one or two/one or more restriction enzymes.

(b) Fill in the blanks:

 $1 \times 2 = 2$ 

- (i) The first somatic hybrid between Nicotiana glauca and N. \_\_\_\_ was achieved by P. S. Carlson et al (1972).
- (ii) \_\_\_\_ compares an amino acid query sequence against protein sequence database.
- (c) Write short notes on the fellowing:

31/2×2=7

- (i) Cloning vectors
- (ii) Scope of bioinformatics
- 2. What is genetic engineering? Describe briefly the application of genetic engineering in medicine and agriculture. 2+5+5=12
- 3. What is human genome project? Write the salient goals of human genome project. Give an account of the application and future challenges of human genome project. 2+5+5=12
- 4. What are genomics and proteomics? Write briefly role of internet in bioinformatics.

3+3+6=12

5. What is phylogenetic analysis? Describe the steps in evaluation of phylogeny and constructing phylogenetic trees. 2+5+5=12

- 6. Write short notes on any three of the following: 4×3=12
  - (a) Primary and secondary databases
  - (b) Transgenic animals
  - (c) DNA sequencing
  - (d) BLAST
  - (e) IPR

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