Code No: R05322301 | **R05** | **Set No. 2**

III B.Tech II Semester Examinations,December 2010
BIOINFORMATICS
Bio-Technology

Time: 3 hours   Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Write short notes on:

    (a) Telnet.
    (b) WWW.   [8+8]

2. Describe the following:

    (a) DOT MATRIX sequence alignment
    (b) String similarity.   [8+8]

3. How we can relate the contributions of Alfred Russel Wallace & Hennins to homology.   [16]

4. Describe in brief about EXPASY and state usefulness in research.   [16]

5. Write short notes on:

    (a) Shot gun approach.
    (b) Clone contig approach.   [8+8]

6. What is Swissprot? Discuss the bioinformatics tools available in it. [16]

7. Discuss the applications of PDB files with one example.   [16]

8. How would you construct phylogenetic trees using clustal programs? Explain briefly.

                                                                     [16]

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1

Code No: R05322301 | **R05** | **Set No. 4**

III B.Tech II Semester Examinations,December 2010
BIOINFORMATICS
Bio-Technology

Time: 3 hours
Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Write short notes on:

   (a) Telnet.
   (b) WWW. [8+8]

2. What is Swissprot? Discuss the bioinformatics tools available in it. [16]

3. Describe the following:

   (a) DOT MATRIX sequence alignment
   (b) String similarity. [8+8]

4. How we can relate the contributions of Alfred Russel Wallace & Hennins to homology. [16]

5. Write short notes on:

   (a) Shot gun approach.
   (b) Clone contig approach. [8+8]

6. How would you construct phylogenetic trees using clustal programs? Explain briefly.

   [16]

7. Describe in brief about EXPASY and state usefulness in research. [16]

8. Discuss the applications of PDB files with one example. [16]

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Code No: R05322301　　　　　**R05**　　　　**Set No. 1**

III B.Tech II Semester Examinations,December 2010
BIOINFORMATICS
Bio-Technology

Time: 3 hours　　　　　　　　　　　　　　　　　　Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. How would you construct phylogenetic trees using clustal programs? Explain briefly.

　　　　　　　　　　　　　　　　　　　　　　　　　　　　　[16]

2. Write short notes on:

　(a) Telnet.

　(b) WWW.　　　　　　　　　　　　　　　　　　　　　[8+8]

3. How we can relate the contributions of Alfred Russel Wallace & Hennins to homology.　　　　　　　　　　　　　　　　　　　　　　　　[16]

4. Discuss the applications of PDB files with one example.　　　　[16]

5. Describe in brief about EXPASY and state usefulness in research.　　[16]

6. Describe the following:

　(a) DOT MATRIX sequence alignment

　(b) String similarity.　　　　　　　　　　　　　　　　　[8+8]

7. Write short notes on:

　(a) Shot gun approach.

　(b) Clone contig approach.　　　　　　　　　　　　　　　[8+8]

8. What is Swissprot? Discuss the bioinformatics tools available in it.　　[16]

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3

Code No: R05322301 | **R05** | **Set No. 3**

III B.Tech II Semester Examinations,December 2010
BIOINFORMATICS
Bio-Technology

Time: 3 hours   Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Describe in brief about EXPASY and state usefulness in research. [16]

2. Write short notes on:

   (a) Telnet.
   (b) WWW. [8+8]

3. Describe the following:

   (a) DOT MATRIX sequence alignment
   (b) String similarity. [8+8]

4. How we can relate the contributions of Alfred Russel Wallace & Hennins to homology. [16]

5. Write short notes on:

   (a) Shot gun approach.
   (b) Clone contig approach. [8+8]

6. Discuss the applications of PDB files with one example. [16]

7. What is Swissprot? Discuss the bioinformatics tools available in it. [16]

8. How would you construct phylogenetic trees using clustal programs? Explain briefly.

[16]

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