**Reg. No. \_\_\_\_\_\_\_\_**

**Karunya University**

**(Karunya Institute of Technology and Sciences)**

(Declared as Deemed to be University under Sec.3 of the UGC Act, 1956)

**End Semester Examination – April/May 2010**

**Subject Title:** biocomputing Time: 3 hours

**Subject Code: 09BI219 Maximum Marks: 100**

#### **Answer ALL questions**

**PART – A** (10 x 1 = 10 MARKS)

1. What is parallelism?

2. Give the full form for FORTRAN.

3. Define a scoring matrix.

4. What is MFOLD?

5. List a gene expression analysis tool.

6. Give the full form of ANOVA.

7. What does the letter “Y” denote in a protein sequence?

8. Which force is stabilizing the α – helix structure of protein?

9. What is OTU in phylogenetics?

10. List a character based method of evolutionary tree prediction.

**PART – B (5 x 3 = 15 MARKS)**

11. What is Flyn taxonomy?

12. Outline few salient features of RNA secondary structure.

13. What is image processing and normalization?

14. Outline the significance of nearest neighbor joining method.

15. What is molecular clock theory?

**PART – C (5 x 15 = 75 MARKS)**

16. Write short notes on:

a. Ncube C and SEQUENT (10)

b. Role of paragon XP/S in parallel computing (5)

(OR)

17. What is parallel computing? Give a detailed account on different networks involved in processor organization. (3+12)

18. Write short notes on:

a. Significance of Grail – II in gene prediction (10)

b. Energy plots in RNA structure prediction (5)

(OR)

19. What is the significance of promoters in gene expression? Discuss in brief the promoter prediction in E.coli. (5+10)

20. Give a detailed account on various statistical techniques adopted in the analysis of microarray technologies.

(OR)

21. What is a microarray? Explain in brief the various microarray technologies for gene analysis.

(3+12)

[P.T.O]

22. Describe about various methods adopted for protein secondary structure prediction. Add a note on of β-pleated structure of proteins. (10+5)

(OR)

23. Write short notes on:

a. Applications of neural networks in bioinformatics (8)

b. Contact potential method (7)

24. Write short notes on:

a. Phylogram and cladogram with a neat labeled sketch (8)

b. Maximum likelihood method in phylogenetics (7)

(OR)

25. What is the principle of distance based methods? Explain in detail the steps involved in UPGMA and NJ methods in phylogenetic analysis. (3+12)