## **Course contents for Bioinformatics**

- 1. Faculty: FLSB
- 2. Course Code:
- 3. Course Title: Bioinformatics
- 4. Number of Credits: Two
- 5. Course objectives:

This course is planned and structured keeping in mind that this might be the first exposure to computational biology for most of the students. Besides providing a basic understanding of the subject, various aspects of data analyses will be described. Classes will be conducted on networkenabled computers to acquaint students with the computational tools and applications utilized for analyzing biological systems. Practical sessions and extensive project work will be conducted to provide bioinformatics hands-on experience.

# 6. Minimum prerequisites for taking this course, if any:

Basic understanding of biomolecules, evolution and molecular biology will be assumed. Good computational skills are desired.

### 7. Course structure with units, if applicable:

- a. Sequence alignments and database searching
- b. Evolutionary relationships and phylogenetic analyses
- c. Predicting protein secondary and tertiary structures

### 8. Reading suggestions:

- a. Understanding Bioinformatics, MarketaZvelebil and Jeremy O. Baum
- b. Blast, by Korf, Yandell and Bedell, O'Reilly Media

c. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids by Durbin, Eddy,

Krogh, Mitchison, Cambridge University Press

d. NCBI bookshelf, Sequence - Evolution - Function, Computational Approaches in Comparative

Genomics, by Koonin and Y Galperin, http://www.ncbi.nlm.nih.gov/books/NBK20260/

- e. Bioinformatics, Paul H. Dear
- f. Biological Computation, Ehud Lamm and Ron Unger
- g. Bioinformatics Methods and Protocols, Stephen Misener and Stephen A. Krawetz
- h. Evolutionary Bioinformatics, Donald R. Forsdyke

### 9. Evaluation:

Mid-semester Written Examination	: 40% Marks
End-semester Written Examination	: 40% Marks
Quiz/Assignment/ Presentation (oral/poster)	: 20% Marks