

Course Unit	Bioinformatics	Field of study	Informatics
Bachelor in	Biology and Biotechnology	School	School of Agriculture
Academic Year	2019/2020	Year of study	3
Type	Semestral	Semester	1
Workload (hours)	162	Contact hours	T 30 TP - PL 30 TC - S - E - OT 4 O -
Level	1-3	ECTS credits	6.0
Code	9029-510-3101-00-19		

T - Lectures; TP - Lectures and problem-solving; PL - Problem-solving, project or laboratory; TC - Fieldwork; S - Seminar; E - Placement; OT - Tutorial; O - Other

Name(s) of lecturer(s) Altino Branco Choupina, Sérgio Alípio Domingues Deusdado

Learning outcomes and competences

At the end of the course unit the learner is expected to be able to:

1. Develop strategies for the approach in silico of biological information processing.
2. Implement and to modificate software in the field of biological tools and databases.
3. Be capable of proficiently use bioinformatics tools, available in public domain, for the analysis and annotations of biological information.
4. Use statistical approaches to analyze large quantities of biological data and predict structures and functions of biomolecules.
5. Use bioinformatics in the optimization of biotechnological productions.
6. Dominate bioinformatics tools to develop proteins structure models and simulation.

Prerequisites

Before the course unit the learner is expected to be able to:
Basic computer science knowledge. Molecular biology and genetics principles. Statistics.

Course contents

Biological data. Biological data bases. Bioinformatics on-line in WWW. Bioinformatic tools to analyse, align and predict biological sequences. Programming oriented to bioinformatics. Probabilistic analysis og biological sequences. Optimization. Microarrays. Phylogenetics. 3D models of proteins.

Course contents (extended version)

1. Technology of databases and acquisition of biological data.
2. Biological Databases (DNA, RNA and proteins).
3. Bioinformatics on the WWW.
4. Software tools for analysis and prediction of biological sequences.
5. Principles of programming focused on biological computing (Perl).
6. Analysis of sequences: patterns, alignments, profiles, motifs.
7. Probabilistic and statistical models for analysis and prediction of genes.
 - Markov Models.
 - Dynamic Programming.
 - Data Mining.
 - Process of extraction of knowledge.
8. Optimization.
 - Neural Networks.
 - CBR and Genetic Algorithms.
 - Integrating Databases and Bioinformatic Services.
 - Networks and high-performance computing (parallel computing)
9. Microarrays.
10. Bioinformatics and Phylogeny.
11. Modeling and computer simulation of the structure and function of proteins.

Recommended reading

1. An Introduction to Bioinformatics Algorithms (Computational Molecular Biology), Neil C. Jones and Pavel A. Pevzner, 2004.
2. Bioinformatics: Sequence and Genome Analysis, David W. Mount, 2004.
3. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Third Edition by Andreas D. Baxeavanis and B. F. Francis Ouellette, 2004.
4. Biological Sequence Analysis : Probabilistic Models of Proteins and Nucleic Acids by Richard Durbin, Sean R. Eddy, Anders Krogh, and Graeme Mitchison, 2004.
5. Beginning Perl for Bioinformatics by James Tisdall , 2001. Structural Bioinformatics by Philip E. Bourne and Helge Weissig, 2003.

Teaching and learning methods

Lectures - 2 lessons per week for 1 hour. Theoretical approach using the multimedia and audiovisual means. Provision of study materials via the e-learning resources. Practical classes - 1 lesson weekly for 2 hours. Realization of practical laboratory work, with the equipment available in the laboratory of computer science.

Assessment methods

- Alternative 1 - (Regular, Student Worker) (Final, Supplementary, Special)
 - Final Written Exam - 50%
 - Practical Work - 50%

Language of instruction

Portuguese

Electronic validation

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09-11-2019	11-11-2019	11-11-2019	11-11-2019