Bioinformatics (COMP0082)

Description

Aims:
The overall aim of this module is to introduce machine learning students to the field of bioinformatics (computational biology) and show how machine learning techniques can be employed in this area. The module is aimed at students who have no previous knowledge of biology and so the aim of Part 1 of the course is to give a basic introduction to molecular biology as a background for bioinformatics. Part 2 will concentrate on classical bioinformatics applications, particularly those which make good use of pattern recognition and machine learning methods. Part 3 will cover more recent bioinformatics areas, including gene expression analysis and systems biology.

Learning outcomes:
On successful completion of the module, a student will be able to:
1. Have a basic knowledge of modern molecular biology and genomics;
2. Understand the advantages and disadvantages of different machine learning techniques in bioinformatics and how the relative merits of different approaches can be evaluated by correct benchmarking techniques;
3. Understand how theoretical approaches can be used to model and analyse complex biological systems;

Content:
Part 1: Basic molecular biology (6 lectures):
- Introduction to Basic Cell Chemistry: Cell chemistry and macromolecules. Biochemical pathways e.g. Glycolysis. Protein structure and functions;

Key information

Year 2019/20
Credit value 15 (150 study hours)
Delivery PGT L7, Campus-based
Reading List View on UCL website
Tutor Prof David Jones
Term Term 2
Timetable View on UCL website

Assessment

- Written examination (main exam period): 85%
- Coursework: 15%

Find out more

For more information about the department, programmes, relevant open days and to browse other modules, visit ucl.ac.uk

Disclaimer: All information correct as of August 2019. Please note that aspects of the module may be subject to change. UCL will make best efforts to inform applicants of major changes.
- Recombinant DNA Technology: Restriction enzymes. Hybridisation techniques. Gene cloning. Polymerase chain reaction;
- Genomics and Structural Genomics: Genes, genomes, mapping and DNA sequencing;

Part 2:
- Biological Databases: Overview of the use and maintenance of different databases in common use in biology;
- Gene Prediction: Methods for analysing genomic DNA to identify genes. Techniques: neural networks and HMMs;
- Detecting Distant Homology: Methods for inferring remote relationships between genes and proteins. Techniques: dynamic programming, HMMs, hierarchical clustering;
- Protein Structure Prediction: Methods for predicting the secondary and tertiary structure of proteins. Techniques: neural networks, SVMs, genetic algorithms and stochastic global optimization;

Part 3:
- Systems Biology: biological networks, -omics technologies and data representation;

Requisites:
In order to be eligible to select this module, a student must be registered on a programme for which it is a formally-approved option or elective choice AND must (i) be familiar with the principles of techniques such as neural networks, Support Vector Machines, and Hidden Markov Models; and (ii) able to program machine learning applications using a standard machine learning framework such as Matlab.

Undergraduate students must have also taken at least one introductory machine learning module prior to starting this module. Suitable qualifying modules are COMP0078, COMP0088, COMP0090 or COMP0142.
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