

2005/06 Taught Postgraduate Module Catalogue

BIOL5160M

The Bioinformatics of Transcriptomics and Proteomics

15 credits

Module manager Dr. D. R. Westhead

Taught Semester 2 [View Timetable](#)

Year running 2005/06

Pre-requisite qualifications

BIOL5510M or equivalent knowledge of biochemistry and molecular biology.

Basic statistical knowledge (descriptive statistics, t-tests, Chi-squared)

(revision material will be provided if necessary)

This module is mutually exclusive with

BIOL5530M

This module is not approved as an Elective

Objectives

On completion of this module, students should be able to:

1. explain the main experimental methods and theoretical basis of high throughput gene (transcriptome) and protein (proteome) expression measurement, and interaction proteomics;
2. use publicly available databases of these data;
3. explain the informatics issues associated with storage, archiving and exchange of these data, and describe current efforts to implement international standards and data models;
4. use database software employing the above standards to store 'private' data;
5. explain the most important statistical methods of analysis for these data, and select and use methods appropriate to particular biological problems;
6. integrate the results of these analyses with genome annotations (including Gene Ontology descriptions), and other sequence analysis methods (e.g. promoter analysis);
7. explain current efforts to use these data in constructing gene interaction networks and the relevance of these methods in systems biology;
8. and, synthesise a coherent opinion on the use and value of these technologies in cutting edge genome-enabled research.

Syllabus

Expression measurement using microarrays and other technologies; Proteomics, 1D/2D gels, mass spectroscopy, protein chips; Protein interactions, yeast 2 hybrid systems; Data models, meta-data and data exchange for microarrays, proteomics and interaction data; Public databases, creation of private databases; Analysis of raw data, gel and microarray image analysis, microarray normalisation. Multivariate statistical methods and application to microarray data; Integrating with genome sequence data, gene function and the use of Gene Ontology descriptions, promoter analysis, discovery of cis elements and sequence pattern discovery. Gene interaction networks, reconstruction problems, systems biology. Research papers in all the above areas.

Teaching methods

Lectures: 6 x 1 hour;
Practical classes: 3 x 3 hours;
Problem-based learning: 10 x 2 hours.

Private study

3 hours reading per lecture: 18 hours;
Problem-based learning activities: 60 hours;
Coursework (essay): 37 hours.

Progress monitoring

Progress will be monitored in problem-based learning sessions, where student groups will make presentations, and which will occur weekly throughout the module.

Methods of assessment

No written examination.
Seminar on problem-based learning results: 40%;
Essay (1500-3000 words) based on (a) current research paper(s): 60%.

Reading list

The [reading list](#) is available from the Library website