Course Outline

BINF3020
Computational Bioinformatics
Teaching Period 2 2011

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Course Staff

Staff Name	Role	Email	Phone
Mike Bain	Course Convenor	mike at cse.unsw.edu.au	56935

Staff Name	Day/Time	Location
Mike Bain	Monday 1400-1500	K17 401H

Course Details

Course Code:	BINF3020
Course Title:	Computational Bioinformatics
Units of Credit:	6
Course WebSite:	http://www.cse.unsw.edu.au/~bi3020/
Handbook Entry:	http://www.handbook.unsw.edu.au/undergraduate/courses/2011/BINF3020.html

Course Summary

This course explores the computational basis of bioinformatics and complements and extends understanding of bioinformatics tools and resources acquired in other courses.

Course Aims

BINF3020 builds on the foundations laid in BINF1001 and BINF3010, and covers a range of core and advanced topics and current research areas in bioinformatics. The course demonstrates the application of computational, mathematical and statistical methods to problems in modern life sciences, through examples in the analysis of nucleotide and protein sequence, gene expression and function, networks of interaction and systems modelling.

As a result of successfully completing this course students will have a working knowledge of key topics in computational bioinformatics, and will be able to demonstrate their knowledge both by describing aspects of the topics and by solving problems related to the topics. They will have practical experience with the topics covered in the assignments undertaken.

Student Learning Outcomes

As a result of successfully completing this course students will be able to work independently and in collaboration on advanced-level topics in bioinformatics. By the end of the subject, students should be able to:

1. Reproduce, explain and apply the major methods of pairwise and multiple sequence analysis in bioinformatics
2. Define key computational and statistical concepts in bioinformatics approaches to pairwise and multiple sequence analysis
3. Define Hidden Markov models, describe their associated algorithms, and discuss their application to

biological sequence analysis
4. Define and apply methods of clustering and classification in analysis of genome- scale data
5. Express and apply key concepts from graph theory to model biological networks
6. Research and explain the use of selected modelling approaches to represent biological processes and their application in systems biology
7. Discuss and present the range of open source development environments available to bioinformatics software developers and use at least one of these environments in their own software development projects

This course contributes to the development of the following graduate capabilities:

Graduate Capability	Acquired in
scholarship: understanding of their discipline in its interdisciplinary context	1-7
scholarship: capable of independent and collaborative enquiry	1-7
scholarship: rigorous in their analysis, critique, and reflection	1-7
scholarship: able to apply their knowledge and skills to solving problems	1-7
scholarship: ethical practitioners	7
scholarship: capable of effective communication	2,6,7
scholarship: information literate	6
scholarship: digitally literate	1-7
leadership: enterprising, innovative and creative	6,7
leadership: capable of initiating as well as embracing change	5-7
leadership: collaborative team workers	6,7
professionalism: capable of independent, self-directed practice	2,6,7
professionalism: capable of lifelong learning	1-7
professionalism: capable of operating within an agreed Code of Practice	7
global citizens: capable of applying their discipline in local, national and international contexts	7
global citizens: culturally aware and capable of respecting diversity and acting in socially just/responsible ways	1-5,7
global citizens: capable of environmental responsibility	1-7

Assumed Knowledge

Before commencing this course, students should:

- have a basic knowledge of mathematical, computational and biological concepts, including basic probability, statistics, logic, computational complexity, basic biology and bioinformatics
- be able to program in a number of programming and scripting languages such as C or Java, Perl, etc. and access and operate bioinformatics tools and resources

These are assumed to have been acquired in the courses COMP1917, COMP1927, MATH1131, MATH1231, MATH1081, BINF1001 or equivalent alternatives.

Teaching Rationale

This course is taught to establish the link between the topics being covered and the current state of the art in bioinformatics research, with emphasis on proper theoretical foundations coupled with practical experience based on sound computational approaches, designed to engage active learning in lectures and assignments.

Teaching Strategies

- Lectures introduce concepts, show examples and are supplemented by computer assignments that require students to implement algorithms discussed in lectures, design solutions to practical problems, and analyse software environments and published research
- Group assignments and class presentations assess research, teamwork, leadership and communication skills

Assessment

Details of assessment items

Assessment component	Description	Marks available	Due date
Mid-semester exam	Covers material up to week 5	15	Week 7
Final exam	Covers potentially all material, but with emphasis on material not covered in mid-semester exam	40	Exam period

Assignment 1	Design, implement, test and evaluate a protein sequence evolution simulator and optimal alignment system, with a written report	20	Three parts, due end of weeks 3, 6 and 8
Assignment 2	Group assignment to select an open source development environment (e.g., BioPerl, BioJava), use and evaluate it, and present results to the class to critically assess how this resource can assist in bioinformatics software development.	10	Week 11
Assignment 3	Group assignment to research into and apply a method of modelling a biological system and present a summary of the group's findings in a written report.	15	Week 13

Note: all dates subject to change !

The course mark will be the sum total of the component marks.

Programming assignments will be marked on the ability of the software to generate correct output with both provided and new test input. Reports and class presentations will be marked on content, organization and quality of writing and oral presentation skills.

Assignments involving software construction or other written material will require submission via `give`. Presentations will be during scheduled class times.

Late submission penalties for assignments will be given as part of each specification.

Academic Honesty and Plagiarism

Plagiarism is defined as "using the words or ideas of others and presenting them as your own". UNSW and CSE treat plagiarism as academic misconduct, which means that it carries penalties as severe as being excluded from further study at UNSW. There are several on-line sources to help you understand what plagiarism is and how it is dealt with at UNSW:

- Learning Centre: Plagiarism and Academic Integrity
- MyUNSW: Plagiarism and Academic Misconduct
- CSE: Addendum to UNSW Plagiarism Guidelines
- CSE: Yellow Form (whose terms you have agreed to)

Make sure that you read and understand these. Ignorance is not accepted as an excuse for plagiarism.

Course Schedule

Schedule of topics, organised by week:

Week	Topic
01	Optimal methods of sequence alignment
02	Heuristic methods of sequence alignment
03	Hidden Markov Models 1
04	Hidden Markov Models 2
05	Statistics of sequence alignment
06	Multiple sequence alignment and analysis
07	Gene expression and functional genomics
08	Regulatory networks
09	Networks as Graphs
10	Systems biology modelling 1
11	Systems biology modelling 2
12	Biomedical ontologies and data integration

Note: topics and dates subject to change !

Resources for Students

Texts and recommended readings:

The course has a recommended textbook (copies available through the UNSW bookshop):

- "An Introduction to Bioinformatics Algorithms", Neil C. Jones and Pavel A. Pevzner, MIT Press, 2004..

A number of bioinformatics textbooks are available through the UNSW library for reference reading. One starting point for assistance is the University library catalogue. Pointers to other resources will be given during the course.

Course Evaluation and Development

This course is evaluated each session using the CATEI system.

In the previous offering of this courses, students noted that more feedback would be welcome, and more "hands-on" examples.

Based on their comments, we plan to give more comments on assessed material, and implement an eLearning tutorial on one of the main topics.