COMP90016 Computational Genomics

Credit Points:	12.5
Level:	9 (Graduate/Postgraduate)
Dates & Locations:	2016, Parkville This subject commences in the following study period/s: Semester 1, Parkville - Taught on campus.
Time Commitment:	Contact Hours: 36 hours, comprised of one 2-hour lecture and one 1-hour workshop per week. Total Time Commitment: 200 hours
Prerequisites:	One semester programming or equivalent experience.
Corequisites:	None
Recommended Background Knowledge:	One semester of computer programming or equivalent experience.
Non Allowed Subjects:	None
Core Participation Requirements:	For the purposes of considering request for Reasonable Adjustments under the Disability Standards for Education (Cwth 2005), and Student Support and Engagement Policy, academic requirements for this subject are articulated in the Subject Overview, Learning Outcomes, Assessment and Generic Skills sections of this entry. It is University policy to take all reasonable steps to minimise the impact of disability upon academic study, and reasonable adjustments will be made to enhance a student's participation in the University's programs. Students who feel their disability may impact on meeting the requirements of this subject are encouraged to discuss this matter with a Faculty Student Adviser and Student Equity and Disability Support: http://services.unimelb.edu.au/disability
Coordinator:	Dr Jan Schroeder
Contact:	Dr Jan Schroeder email: **jsch@unimelb.edu.au (jsch)**
Subject Overview:	**AIM** The study of genomics is on the forefront of biology. Current laboratory technologies generate huge amounts of data. Computational analysis is necessary to make sense of these data. This subject covers a broad range of approaches to the computational analysis of genomic data. Students learn the theory behind the different approaches to genomic analysis, preparing them to use existing methods appropriately and positioning them to develop new ways to analyse genomic data. The subject is a core subject in the MSc (Bioinformatics), and is an elective in the Master of Information Technology and the Master of Engineering. It can also be taken by PhD students and by undergraduate students, subject to the approval of the lecturer. **INDICATIVE CONTENT** This subject covers computational analysis of genomic data, from the perspective of information theory. Topics include information theoretic analysis of genomic sequences; sequence comparison, including heuristic approaches and multiple sequence alignment; and approaches to motif finding and genome annotation, including probabilistic modelling and visualization, computational detection of RNA families, and current challenges in protein structure determination. Practical work includes writing bioinformatics applications programs and preparing a research report that uses existing bioinformatics web resources.
Learning Outcomes:	**INTENDED LEARNING OUTCOMES (ILO)** On completion of this subject the student is expected to:

1 Describe and analyse critically the most commonly used computational approaches to processing genomic data and their theoretical underpinnings
2 Describe current research issues in bioinformatics
3 Outline a variety of algorithms used for processing genomic data and describe in some detail their operation and strengths and limitations
4 Select algorithms appropriate to a given bioinformatics application
5 Write simple bioinformatics computer programs and use bioinformatics programming libraries
6 Describe the role of information theory in analysis of biological data.

Assessment:	Programming Assignment 1, requiring approximately 13 - 15 hours of work, due in week 4 (10%), addresses Intended Learning Outcomes (ILOs) 5 and 6 Programming Assignment 2, requiring approximately 13 - 15 hours of work, due in week 6 (10%), addresses Intended Learning Outcomes (ILOs) 5 and 6 Programming Assignment 3, requiring approximately 13 - 15 hours of work, due in week 9 (10%), addresses ILOs 5 and 6 Programming Assignment 4, requiring approximately 13 - 15 hours of work, due in week 11 (10%) addresses Intended Learning Outcomes (ILOs) 5 and 6. A 2.5-hour written examination at the end of the semester (60%) addresses ILOs 1-4 & 6. Hurdle requirement: To pass the subject students must obtain at least: 50% overall 30/60 on the end-of-semester examination 20/40 on the project work.
Prescribed Texts:	None
Breadth Options:	This subject is not available as a breadth subject.
Fees Information:	Subject EFTSL, Level, Discipline & Census Date, http://enrolment.unimelb.edu.au/fees
Generic Skills:	On completion of this subject students should have the following skills: # Ability to undertake problem identification, formulation and solution # Ability to utilise a systems approach to complex problems and to design an operational performance # Ability to manage information and documentation # Capacity for creativity and innovation # Ability to communicate effectively with both the engineering team and the community at large.
Notes:	**LEARNING AND TEACHING METHODS** The subject will be delivered through a combination of lectures, group discussion, and supervised laboratory. The assigned project work is also a key feature in the learning process. **INDICATIVE KEY LEARNING RESOURCES** Students will have access to lecture notes and audio recording of the lectures. Papers drawn from the current literature are posted on the LMS for each topic. **CAREERS / INDUSTRY LINKS** The subject provides an overview of computational genomics, and as such is a foundation for applied and research careers in bioinformatics. Guest lectures are given by practitioners in the field.
Related Course(s):	Doctor of Philosophy - Engineering Master of Philosophy - Engineering Master of Science (Bioinformatics) Master of Science (Computer Science)
Related Majors/Minors/ Specialisations:	Computer Science Computer Science Master of Engineering (Biomedical with Business) Master of Engineering (Biomedical) Master of Engineering (Software)