

COMP90014 Algorithms for Functional Genomics

Credit Points:	12.50
Level:	9 (Graduate/Postgraduate)
Dates & Locations:	This subject is not offered in 2013.
Time Commitment:	Contact Hours: 36 hours, comprising of one 2-hour lecture and one 1-hour workshop per week Total Time Commitment: 120 hours
Prerequisites:	None
Corequisites:	None
Recommended Background Knowledge:	One semester of computer programming or equivalent experience
Non Allowed Subjects:	Students cannot enrol in and gain credit for this subject and: 433-450 Computational Sequence Analysis
Core Participation Requirements:	<p><p>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.</p> <p>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</p></p>
Contact:	Dr Linda Stern email: stern@unimelb.edu.au (mailto:stern@unimelb.edu.au)
Subject Overview:	<p>Technological advances in obtaining high throughput data from functioning cells have stimulated the development of new computational approaches to functional genomics and systems biology. This subject covers the theory and practice of two of the most widely used computational techniques used for analysis and interpretation of functional genomic data: microarray analysis and RNA-seq (next generation sequencing for RNA). This subject concentrates on current research problems and recently developed computational techniques for analysis. This subject is a core subject in the MSc(Bioinformatics), and is an elective in the Master and 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.</p>
Objectives:	<p>On completion of this subject students should be able to:</p> <ul style="list-style-type: none"> # Compare and contrast the two major computational approaches to analysing functional genomics data. # Describe the application of machine learning techniques to microarray data, and their strengths and weaknesses. # Describe next generation DNA sequencing, and compare and contrast it with the application of next generation sequencing to RNA (RNA-seq). # Describe the limitations of current methods in functional genomics. # Critically analyse the role of laboratory methods for functional genomic analysis in clinical medicine. # Outline the use of computation in gene assembly and describe the limitations of existing methods.

Assessment:	Project work includes three research reports spread evenly over the semester, totalling 3,000 words or equivalent (30%). The assignments address ILOs 4, 5, and 6. A 2-hour written examination at the end of the semester (70%) addresses ILOs 1-6. To pass the subject students must obtain at least: 50% overall 35/70 on the end-of-semester examination 15/30 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 successful completion students should be able to: <ul style="list-style-type: none"> # Read the current literature in functional genome analysis. # Describe the two major approaches to functional genomic analysis used today, including their limitations. # Describe current research issues in computational analysis of functional genomics data.
Related Course(s):	Master of Biomedical Engineering Master of Philosophy - Engineering Master of Science (Bioinformatics) Master of Science (Computer Science) Master of Software Systems Engineering Ph.D.- Engineering Postgraduate Certificate in Engineering
Related Majors/Minors/ Specialisations:	Computer Science Master of Engineering (Biomedical) Master of Engineering (Software)