

COMP90014 Algorithms for Functional Genomics

Credit Points:	12.50
Level:	9 (Graduate/Postgraduate)
Dates & Locations:	2010, Parkville This subject commences in the following study period/s: Semester 2, Parkville - Taught on campus.
Time Commitment:	Contact Hours: 36 hours, made up of 24 one-hour lectures (two per week) and 12 one-hour workshops (one per week) Total Time Commitment: 120 hours
Prerequisites:	None
Corequisites:	None
Recommended Background Knowledge:	One semester computer programming, or equivalent experience.
Non Allowed Subjects:	433-450 Computational Sequence Analysis
Core Participation Requirements:	For the purposes of considering request for Reasonable Adjustments under the Disability Standards for Education (Cwth 2005), and Students Experiencing Academic Disadvantage Policy, academic requirements for this subject are articulated in the Subject Description, Subject Objectives, Generic Skills and Assessment Requirements of this entry. The University is dedicated to provide support to those with special requirements. Further details on the disability support scheme can be found at the Disability Liaison Unit website: http://www.services.unimelb.edu.au/disability/
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Subject Overview:	On completion of this subject students should be able to: <ul style="list-style-type: none"> # This subject covers the theory and practice of computational techniques used for analysis and interpretation of functional genomic data. 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 concentrates on current research problems and recently developed computational techniques for analysis and interpretation of these data. Topics covered include machine learning techniques for interpreting genome scan and cell function data, algorithms for assembling and evaluating data from "next generation" sequencing techniques, and other biological modeling and data mining applications. # The subject includes case studies from current research projects.
Objectives:	On completion of this subject students should be able to: <ul style="list-style-type: none"> # Describe current research issues in computational analysis of functional genomics data # Describe the application of classification and clustering techniques to biological data, their strengths and weaknesses # Select the appropriate approach for analyzing wet laboratory data

	# Use a software application for processing gene expression data and critically evaluate the the output
Assessment:	Three assignments during the semester totaling 5,000 words or equivalent (30%), and one 2-hour end-of-semester written examination (70%). Hurdle requirements are a score of at least 35/70 on the examination and 15/30 for 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:	<p>On successful completion students should be able to:</p> <ul style="list-style-type: none"> # Ability to undertake problem identification, formulation, and solution # Ability to utilise a systems approach to complex problems and to design and operational performance # Ability to manage information and documentation # Capacity for creativity and innovation # Ability to communicate effectively, with the engineering team and with the community at large
Related Course(s):	Bachelor of Computer Science (Honours) Master of Biomedical Engineering Master of Software Systems Engineering Postgraduate Certificate in Engineering