

COMP90014 Algorithms for Functional Genomics

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| Credit Points: | 12.50 |
| Level: | 9 (Graduate/Postgraduate) |
| Dates & Locations: | This subject is not offered in 2014. |
| Time Commitment: | Contact Hours: 36 hours, comprising of one 2-hour lecture and one 1-hour workshop per week Total Time Commitment: 200 hours |
| Prerequisites: | None |
| Corequisites: | None |
| Recommended Background Knowledge: | One semester of computer programming or equivalent experience. |
| Non Allowed Subjects: | |
| 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: | email: sloc@unimelb.edu.au (mailto:sloc@unimelb.edu.au) |
| Subject Overview: | <p>AIMS</p> <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 the computational techniques used in genomics analysis, with an emphasis on functional genomics.</p> <p>This subject is a core subject in the MSc (Bioinformatics), and is an elective in the Master of Science (Computer Science) 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> <p>INDICATIVE CONTENT</p> <p>The subject covers key algorithms used in genomics analyses, and their application. Topics include: computational analysis of microarray data; classification and clustering, and their application to functional genomics analysis; detecting variants in genomic data; next generation sequencing for DNA; next generation sequencing for RNA.</p> |
| Learning Outcomes: | <p>INTENDED LEARNING OUTCOMES (ILO)</p> <p>On completion of this subject the student is expected to:</p> <ol style="list-style-type: none"> 1 Describe and apply key algorithms used in the analysis of genomics data 2 Describe next generation DNA sequencing, and compare and contrast it with the application of next generation sequencing to RNA (RNA-seq) 3 Describe the application of machine learning techniques to gene expression data, and their strengths and weaknesses 4 Understand the uses and limitations of bioinformatics software tools which use these algorithms, and apply these tools to practical data analysis 5 Describe the limitations of current methods in functional genomics |

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| Assessment: | Project work includes two research reports, worth 15% each, spread evenly over the semester (30% in total). The total expected time commitment for project assessments is approximately 35 - 40 hours. A 3-hour written examination at the end of the semester (70%). Hurdle requirement: 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: | Having completed this unit the student is expected to have the following skills: <ul style="list-style-type: none"> # Read the current literature in functional genome analysis. # Describe current research issues in computational analysis of functional genomics data. # Investigate current genomics software tools, understand their principles and limitations, and apply them appropriately. |
| Notes: | <p>LEARNING AND TEACHING METHODS</p> <p>The subject will be delivered through a combination of lectures, group discussion, and tutorials. The assigned project work is also a key feature in the learning process.</p> <p>INDICATIVE KEY LEARNING RESOURCES</p> <p>Students will have access to lecture notes and audio recording of the lectures. Papers drawn from the current literature are posted to the LMS for each topic. Students are expected to find and read additional papers from the literature relevant to their assignments.</p> <p>CAREERS / INDUSTRY LINKS</p> <p>The subject provides an in-depth introduction to the two main approaches to functional genomics current today. As such the subject provides a foundation for applied and research careers in bioinformatics. Guest lectures are given by practitioners in the field.</p> |
| 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 |
| Related Majors/Minors/ Specialisations: | Computer Science Master of Engineering (Biomedical) Master of Engineering (Software with Business) Master of Engineering (Software) |