# COMP90016 Computational Genomics

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| **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<br>Total Time Commitment: 120 hours |
| **Prerequisites:** | None |
| **Corequisites:** | None |
| **Recommended Background Knowledge:** | One semester of computer programming or equivalent experience |
| **Non Allowed Subjects:** | 433-451 Computational Genomics |
| **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: <a href="http://services.unimelb.edu.au/disability">http://services.unimelb.edu.au/disability</a> |
| **Contact:** | Dr Linda Stern<br>email: **stern@unimelb.edu.au (mailto:adrianp@unimelb.edu.au)** |
| **Subject Overview:** | Topics covered include:<br># Computational issues in physical mapping of DNA, in genome annotation, and in analyzing gene expression data<br># Motif extraction; methods for determining phylogenetic trees<br># RNA structure determination<br># And protein structure determination |
| **Objectives:** | On completion of this subject students should be able to:<br># Describe current research issues in bioinformatics<br># Describe the most commonly used approaches to processing genomic data, their theoretical underpinnings, and their strengths and limitations<br># Outline a variety of algorithms used for processing genomic data<br># Select algorithms appropriate to a given application<br># Critically evaluate the results obtained using different bioinformatics techniques to process genomic data<br># Write a simple bioinformatics computer program and use bioinformatics programming libraries<br># Describe the role of information theory in analysis of biological data |
| **Assessment:** | Four assignments spread over the semester, totaling 5,000 words or equivalent (30%) 2-hour end-of-semester written examination (70%) Hurdle requirement: Students must obtain a mark of at least 35/70 for the exam and 15/30 for the assignments |
| **Prescribed Texts:** | None |

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| **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:<br># Ability to undertake problem identificaiton, formulation and solution<br># Ability to utilise a systems approach to complex problems and to design an operational performance<br># Ability tomanage information and docmentation<br># Capacity for creativity and innovation<br># Ability to communicate effectively with both the engineering team and the community at large |
| **Related Course(s):** | Master of Biomedical Engineering<br>Master of Engineering in Distributed Computing<br>Master of Philosophy - Engineering<br>Master of Science (Bioinformatics)<br>Master of Science (Computer Science)<br>Master of Software Systems Engineering<br>Ph.D.- Engineering<br>Postgraduate Certificate in Engineering |
| **Related Majors/Minors/ Specialisations:** | Computer Science<br>Master of Engineering (Biomedical)<br>Master of Engineering (Software) |