

## 433-650 Computational Gene Expression

<b>Credit Points:</b>	12.50
<b>Level:</b>	9 (Graduate/Postgraduate)
<b>Dates &amp; Locations:</b>	This subject is not offered in 2009.
<b>Time Commitment:</b>	Contact Hours: Thirty-six hours; Non contact time commitment 84 Hours. Total Time Commitment: Not available
<b>Prerequisites:</b>	Three semesters of programming experience or equivalent.
<b>Corequisites:</b>	None
<b>Recommended Background Knowledge:</b>	None
<b>Non Allowed Subjects:</b>	COMP40023 Computational Gene Expression
<b>Core Participation Requirements:</b>	<p>&lt;p&gt;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.&lt;/p&gt; &lt;p&gt;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: &lt;a href="http://services.unimelb.edu.au/disability"&gt;http://services.unimelb.edu.au/disability&lt;/a&gt;&lt;/p&gt;</p>
<b>Subject Overview:</b>	Topics covered include dynamic programming algorithms; multiple sequence alignment algorithms; hidden Markov models; sequence comparison; data mining for biological data.
<b>Objectives:</b>	On completion of this subject students will be familiar with a range of algorithms used to process biological sequences: to know a variety of techniques for extracting information from biological sequences; and to understand the appropriate application of these algorithms for different applications.
<b>Assessment:</b>	One 3-hour examination (70%) and an assignment of 2000 words equivalent (30%). Both the project work and examination component of assessment must be completed satisfactorily to pass the subject.
<b>Prescribed Texts:</b>	None
<b>Breadth Options:</b>	This subject is not available as a breadth subject.
<b>Fees Information:</b>	Subject EFTSL, Level, Discipline & Census Date, <a href="http://enrolment.unimelb.edu.au/fees">http://enrolment.unimelb.edu.au/fees</a>
<b>Generic Skills:</b>	<p>On successful completion, students should:</p> <ul style="list-style-type: none"> <li># be able to implement the basic algorithms used in processing biological sequences;</li> <li># be able to select appropriate algorithms to process biological sequences;</li> <li># be able to use and critically evaluate the output from software used for processing biological sequences;</li> <li># be able to describe current research issues in Bioinformatics;</li> <li># be able to undertake problem identification, formulation and solution;</li> <li># have a capacity for independent critical thought, rational inquiry and self-directed learning; and</li> <li># have a profound respect for truth and intellectual integrity, and for the ethics of scholarship.</li> </ul>
<b>Related Course(s):</b>	Master of Biomedical Engineering Master of Engineering Science(Biomedical Engineering) Master of Software Systems Engineering