

# MAST30033 Statistical Genomics

<b>Credit Points:</b>	12.5															
<b>Level:</b>	3 (Undergraduate)															
<b>Dates &amp; Locations:</b>	This subject is not offered in 2016.															
<b>Time Commitment:</b>	Contact Hours: 48 hours: 24 x one-hour lectures (2 lectures per week), 12 x two-hour practice classes (1 per week). Total Time Commitment: Not available															
<b>Prerequisites:</b>	<p>One of:</p> <table border="1"> <thead> <tr> <th>Subject</th> <th>Study Period Commencement:</th> <th>Credit Points:</th> </tr> </thead> <tbody> <tr> <td>MAST30032 Biological Modelling and Simulation</td> <td>Semester 1</td> <td>12.5</td> </tr> <tr> <td>MAST20005 Statistics</td> <td>Semester 2</td> <td>12.5</td> </tr> </tbody> </table> <p>And:</p> <table border="1"> <thead> <tr> <th>Subject</th> <th>Study Period Commencement:</th> <th>Credit Points:</th> </tr> </thead> <tbody> <tr> <td>GENE20001 Principles of Genetics</td> <td>Semester 1</td> <td>12.5</td> </tr> </tbody> </table> <p>Or equivalent knowledge of genetics.</p>	Subject	Study Period Commencement:	Credit Points:	MAST30032 Biological Modelling and Simulation	Semester 1	12.5	MAST20005 Statistics	Semester 2	12.5	Subject	Study Period Commencement:	Credit Points:	GENE20001 Principles of Genetics	Semester 1	12.5
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MAST20005 Statistics	Semester 2	12.5														
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GENE20001 Principles of Genetics	Semester 1	12.5														
<b>Corequisites:</b>	None															
<b>Recommended Background Knowledge:</b>	None															
<b>Non Allowed Subjects:</b>	None															
<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>Contact:</b>	dbalding@unimelb.edu.au															
<b>Subject Overview:</b>	<p>This subject introduces the biology and technology underlying modern genomics data, features of the resulting data types including the frequency and patterns of error and missingness, and the statistical methods used to analyse them. It will include hands-on data analysis using R software. The material covered will evolve as genomics technology and practice change, and will span the following four areas: introduction to genomics technology and the resulting data (approx 25% of course), population genetics (approx 20% of course) including stochastic models and statistical inference, association analysis (approx 40% of course) including tests of association and major sources of confounding, and heritability and prediction (approx 15% of course) both in human genetics and for animal and plant breeding.</p>															
<b>Learning Outcomes:</b>	<p>On completion of this subject, students should have:</p> <ul style="list-style-type: none"> <li># Ability to explain the key genomics assays, their purpose and the strengths and limitations of the data generated.</li> <li># An understanding of the role of population genetics theory in interpreting genomics data.</li> <li># Ability to perform a range of association analyses using SNP and sequence data.</li> </ul>															

	<ul style="list-style-type: none"> <li># Awareness of the major problems in association analyses that can lead to false inferences.</li> <li># An understanding of the strengths and weaknesses of SNP-based heritability relative to traditional measures of heritability.</li> <li># Ability to explain the use of statistical models in predicting phenotype from genomic data, and the uses and limitations of genomic prediction.</li> </ul>
<b>Assessment:</b>	Four computer-based assignments handed out and discussed during computer lab classes, completed in students' own time, and due the following week. Submissions will include computer code, results generated (numerical and graphical) plus sections of text interpreting the results (total 10 pages per assignment) due in weeks, 2, 5, 8 and 11 (12.5% per assignment). A 2-hour written exam due during the examination period (50%).
<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>In addition to learning specific skills that will assist students in their future careers in science, they will have the opportunity to develop generic skills that will assist them in any future career path. In particular</p> <ul style="list-style-type: none"> <li># computer-based data handling and statistical analysis of large data sets using the R software (students are expected to have some skills at entry but the subject will take them to a higher level)</li> <li># ability to read, understand, modify and use short computer programs</li> <li># time-management: completing assignments according to deadlines while making judgments about time required for different parts of the assignment.</li> </ul>
<b>Related Majors/Minors/Specialisations:</b>	Computational Biology Science-credited subjects - new generation B-SCI and B-ENG.