

652-301 Genomes and Evolution

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| Credit Points: | 12.500 |
| Level: | Undergraduate |
| Dates & Locations: | 2008, This subject commences in the following study period/s: Semester 2, - Taught on campus. |
| Time Commitment: | Contact Hours: 36 lectures (three hours per week) Total Time Commitment: 120 hours. |
| Prerequisites: | Genetics 652-214 and 652-215. BBIomedSc students: Genetics 652-214, 521-213 and 536-250. |
| Corequisites: | None |
| Recommended Background Knowledge: | None |
| Non Allowed Subjects: | None |
| Core Participation Requirements: | It is University policy to take all reasonable steps to minimise the impact of disability upon academic study and reasonable steps will be made to enhance a student's participation in the University's programs. Students who feel their disability may impact upon their active and safe participation in a subject are encouraged to discuss this with the relevant subject coordinator and the Disability Liaison Unit. |
| Coordinator: | Associate Professor P Batterham |
| Subject Overview: | <p>Upon completion of this subject, students should have:</p> <ul style="list-style-type: none"> # acquired an up-to-date understanding of whole-genome mapping and sequencing projects; # developed a capacity to critically review the written literature and to access web-based databases of genomic information; # understood how genes, gene pools, and genomes change through evolutionary time; # developed a critical appreciation for the methods used to detect and quantify the major evolutionary forces; # comprehended the logic used in inferring evolutionary processes from patterns of genetic variation in space and time; and # appreciated the connections between molecular evolution and conservation biology and phylogenetics. <p>The emphasis of this subject is on the use of molecular markers in genome mapping, in understanding how evolutionary forces shape the gene pool, in dissecting polygenic traits by mapping quantitative trait loci, and in other applications such as phylogenetics and conservation biology.</p> <p>The topics covered will be classical population genetics, the measurement of selection, processes of speciation, conservation genetics, molecular evolution of single-copy and multi-copy genes, phylogenetic reconstruction, development of saturated linkage maps, physical mapping of genomes, whole-genome sequencing projects, mapping quantitative trait loci, comparative genomics, functional genomics, and high-throughput methods for scoring genetic polymorphisms.</p> |
| Assessment: | A written class test during semester (20%); three tutorial assignments of not more than 500 words each due during the semester (30% in total); a 2-hour written examination in the examination period (50%). |
| Prescribed Texts: | None |

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| Breadth Options: | <p>This subject is a level 2 or level 3 subject and is not available to new generation degree students as a breadth option in 2008.</p> <p>This subject or an equivalent will be available as breadth in the future.</p> <p>Breadth subjects are currently being developed and these existing subject details can be used as guide to the type of options that might be available.</p> <p>2009 subjects to be offered as breadth will be finalised before re-enrolment for 2009 starts in early October.</p> |
| Fees Information: | Subject EFTSL, Level, Discipline & Census Date, http://enrolment.unimelb.edu.au/fees |
| Notes: | Students enrolled in the BSc (pre-2008 BSc), BAsc or a combined BSc course will receive science credit for the completion of this subject. |
| Related Course(s): | <p>Bachelor of Arts and Bachelor of Science</p> <p>Bachelor of Arts and Sciences</p> <p>Bachelor of Biomedical Science</p> <p>Bachelor of Science</p> <p>Graduate Diploma in Biotechnology</p> |