

STAT817 Bioinformatics

Time: Semester 2, Tuesdays 4-6 pm E7B-164
 Fridays 3-4 pm E4B 308 (Statistics Computing Laboratory)
 or W5C-211 (Tutorial)

Lecturers: Professor Graham Wood E4A-511 9850-8553
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Unit home page:

http://www.efs.mq.edu.au/PG/coursework/units/Stat_postgraduate_units/stat/stat817

Brief Description: Bioinformatics addresses problems related to the storage, retrieval and analysis of information about biological structure. This unit will provide a broad-ranging study of this application of quantitative methods in biology. Topics studied will be selected from: data sources, data retrieval, quantitative methods in genome science, proteome science, population genetics, evolutionary genetics and animal and plant breeding. A suitable preparation in statistics and in biology is strongly recommended.

Topics:

- Basic notions in biology
- Population genetics
- Web-based data sources, data retrieval and tools
- The analysis of single and multiple DNA or protein sequences
- Hidden Markov Models and their applications
- Evolutionary models
- Phylogenetic trees
- Microarray analysis
- Functional genomics
- Use of R in bioinformatics applications

Text: R. Durbin, S. Eddy, A. Krogh and G. Mitchison “Biological Sequence Analysis” Cambridge University Press, 1998.

References:

1. Warren J. Ewens and Gregory R. Grant, Statistical methods in bioinformatics, An introduction, Statistics for Biology and Health, Springer-Verlag, New York, 2001.
2. Kenneth Lange, Mathematical and statistical methods for genetic analysis, Statistics for Biology and Health, Springer-Verlag, New York, 2002.
3. Pak Sham, Statistics in human genetics, Arnold, 1998.
4. D.J. Balding, M. Bishop and C. Cannings, Handbook of statistical genetics, John Wiley and Sons (2001).

Assessment:	Assignments	20%
	Project and presentation	20%
	Final examination	60%

Syllabus

Week	Tuesday	Friday	Lecturer
1	Basic notions in biology		SB
2	Population genetics		SB
3	The analysis of single DNA or protein sequences	NCBI database1	SB
4	Data sources and retrieval - use of the NCBI biological database,	NCBI database2	SB GW
5	The analysis of a multiple DNA or protein sequences		SB
6/7	Evolutionary models, Phylogenetic tree estimation		GW
8	Hidden Markov models and their applications	HMM Software	GW
9	Linkage and Functional Genomics	LODs	SB
10/11	Microarray analysis	GeneSpring R-Bioconductor	GW
12	Use of R in bioinformatics		GW
13	Class project presentations		SB GW