

BIOS 3033 APPLIED BIOINFORMATICS

Credit Points 10

Legacy Code 301406

Coordinator Thomas Jeffries ([https://directory.westernsydney.edu.au/search/name/Thomas Jeffries/](https://directory.westernsydney.edu.au/search/name/Thomas%20Jeffries/))

Description The ability to perform computational experiments and analyse data is a key component for a successful career in the biological sciences. This subject focuses on how biology has been enhanced through advances in technology, genomics, transcriptomics, proteomics and metabolomics in the development of cell phenotype. Using model systems, this subject shows how research biologists use computational cell biology to form hypotheses, mine data, analyse experiments, and synthesise information. Students will apply bioinformatics and engage with next-generation DNA sequencing data. Students will apply web-based bioinformatics toolkits to construct and compare model genomes, transcriptome, proteome and metabolome information to profile cell genotype and phenotype. Students will undertake a project that interprets and communicates research findings in the context of real world applications, legal and ethical frameworks.

School Science

Discipline Biological Sciences

Student Contribution Band HECS Band 2 10cp

Check your fees via the Fees (https://www.westernsydney.edu.au/currentstudents/current_students/fees/) page.

Level Undergraduate Level 3 subject

Restrictions

Successful completion of 120 credit points

Assumed Knowledge

A basic understanding of microbial, animal and plant cell core concepts is desirable.

Learning Outcomes

On successful completion of this subject, students should be able to:

1. Utilise genomics, transcriptomics, proteomics and metabolomics in profiling cell processes and phenotype.
2. Explain how technological advances enable connectivity of omic databases and advances in computational cell modelling.
3. Compare and contrast **omic** features of plant, animal and microbial cells.
4. Describe and annotate genomes, model transcriptomic responses in the context of cellular processes.
5. Develop cellular models through extracting information, managing and organising data
6. Establish the role of in-silico studies underpinning genetic engineering and biotechnology and its application industry and the research sectors.
7. Communicate the findings of investigations within existing legal and ethical frameworks

Subject Content

1. Profiling genomic, transcriptomic, proteomic and metabolomics data in the process of establishing workflow to develop model cell systems.
2. Technologies that enable sequencing of macromolecules, processes and computational resources.
3. Features of genomes, transcriptomes, proteomes and metabolomes, their linkage in the context of computational modelling.
4. Application of bioinformatic tools within an online environment and visual interfaces to acquire, judge, and synthesise biological information.
5. Interrogation of functional pathways and demonstration of in-silico genetic engineering approaches.
6. Professional presentation skills for industry, government, and academia.

Assessment

The following table summarises the standard assessment tasks for this subject. Please note this is a guide only. Assessment tasks are regularly updated, where there is a difference your Learning Guide takes precedence.

Type	Length	Percent	Threshold	Individual/ Group Task
Quiz	2x 60 minutes	30	N	Individual
Portfolio	1000 words or equivalent / 3-7 min Podcast submission	35	N	Individual
Viva Voce	10 minutes including Q&A	35	N	Individual

Teaching Periods

Spring (2024) Hawkesbury

Hybrid

Subject Contact Thomas Jeffries ([https://directory.westernsydney.edu.au/search/name/Thomas Jeffries/](https://directory.westernsydney.edu.au/search/name/Thomas%20Jeffries/))

View timetable (https://classregistration.westernsydney.edu.au/even/timetable/?subject_code=BIOS3033_24-SPR_HW_3#subjects)