BABS3291 Genes, Genomes and Evolution - 2024

Published on the 10 Feb 2024

General Course Information

Course Code : BABS3291
Year : 2024
Term : Term 1
Teaching Period : T1
Is a multi-term course? : No
Faculty : Faculty of Science
Academic Unit : School of Biotechnology and Biomolecular Sciences
Delivery Mode : In Person
Delivery Format : Standard
Delivery Location : Kensington
Campus : Sydney
Study Level : Undergraduate
Units of Credit : 6

Useful Links

[Handbook](#) [Class Timetable](#)

Course Details & Outcomes

Course Description

This course covers cutting edge concepts in genetics, genomics and evolution: genome structure (how genes are organised into genomes), genomics (genome sequencing, assembly and annotation), genome variation and the forces that shape it (mutation, recombination and

genetic drift), molecular phylogenetics (capturing and using patterns of evolution), and applications of genomics (conservation genomics, host-pathogen interactions, genome engineering, and systems biology). Multiple aspects of genome biology will be studied and integrated to understand how genomes function and evolve. Core concepts and methods in genomics, molecular evolution and population genetics will be supported by an integrated set of tutorials, science communication tasks and bioinformatics analysis. Modern research methods will be applied to the analyses of differential gene expression in RNA sequencing datasets.

Course Aims

1. This course will introduce and explore current concepts and methods of genetics as applied in the context of genomics and evolution. Science communication exercises will develop skills to present these concepts to scientific and lay audiences.
2. Large sequencing datasets are the new norm in genomics. The practical component of this course will expose students to the handling and analysis of real genomics data in a research setting.

Relationship to Other Courses

Core foundational courses:

- Builds on Year 2 course Genetics (BABS2204/BABS2264)
- Complements the session 1 courses, Human Molecular Genetics & Disease (BABS3151) and Applied Bioinformatics (BINF3010)

Other courses related to Genes, Genomes and Evolution:

- Molecular Biology of Nucleic Acids (BABS3121)
- Microbial Genetics (MICR3021)
- Molecular Frontiers (BABS3281)
- Animal Behaviour (BIOS3011)
- Conservation Biology and Biodiversity (BIOS3071)
- Population and Community Ecology (BIOS3111)
- Evolution (BIOS3171)

Course Learning Outcomes

Course Learning Outcomes
CLO1 : Describe the main steps, technologies and challenges involved in sequencing, assembling and annotating a whole genome.
CLO2 : Apply molecular evolutionary theory to homology searching, multiple sequence alignment, and molecular phylogenetics, in the context of genome annotation.
CLO3 : Analyse biological data relating to whole genome sequencing and gene annotation, using a variety of commandline, GUI and web tools.
CLO4 : Effectively communicate published scientific research to a non-specialist, peer audience.
CLO5 : Discuss applications of genomics to real-world scientific questions.

Course Learning Outcomes	Assessment Item
CLO1 : Describe the main steps, technologies and challenges involved in sequencing, assembling and annotating a whole genome.	• Genomics Assessment Task 2 • Bioinformatics Assessment Task • Final Exam
CLO2 : Apply molecular evolutionary theory to homology searching, multiple sequence alignment, and molecular phylogenetics, in the context of genome annotation.	• Genomics Assessment Task 2 • Bioinformatics Assessment Task • Final Exam
CLO3 : Analyse biological data relating to whole genome sequencing and gene annotation, using a variety of commandline, GUI and web tools.	• Bioinformatics Assessment Task • Final Exam
CLO4 : Effectively communicate published scientific research to a non-specialist, peer audience.	• Genomics Assessment Task 1 • Bioinformatics Assessment Task
CLO5 : Discuss applications of genomics to real-world scientific questions.	• Genomics Assessment Task 1 • Genomics Assessment Task 2 • Final Exam • Bioinformatics Assessment Task

Learning and Teaching Technologies

Moodle - Learning Management System | Microsoft Teams

Learning and Teaching in this course

The lectures, given by experts in the field, will introduce students to essential concepts and principles in genetics, genomics and evolution, as well as recent developments. The practicals explore some aspects of the material introduced in lectures and extend the discussion to other

relevant topics and skills. Computer-based exercises will provide hands-on exposure to methods, tools and concepts used in genomics. The presentation emphasises developing the ability to communicate and evaluate the value of genome-wide analyses. Effective communication of science is also evaluated through written reports.

This is a third year course that builds on ideas taught in second year genetics (BABS2204/ BABS2264). In developing these ideas, we aim to contextualise the material by using examples of current relevance in the discipline and in society. Emphasis is placed on critical thinking, analytical skills, information literacy and communication because these are qualities that will aid learning in the long term. The objectives and activities of this course are designed to develop UNSW and Science Faculty graduate attributes.

Assessments

Assessment Structure

Assessment Item	Weight	Relevant Dates
Genomics Assessment Task 1 Assessment Format: Group	10%	Start Date: Not Applicable Due Date: 01/03/2024 12:00 AM
Genomics Assessment Task 2 Assessment Format: Individual	20%	Start Date: 14/03/2024 02:00 PM Due Date: 14/03/2024 03:00 PM
Bioinformatics Assessment Task Assessment Format: Individual	40%	Start Date: Not Applicable Due Date: 19/04/2024 02:00 PM
Final Exam Assessment Format: Individual	30%	

Assessment Details
Genomics Assessment Task 1

<u>Assessment Overview</u>

In the Genomics Assessment Task 1, you will be asked to present a talk on the RNA sequencing dataset that you choose from a curated list. You will be expected to convey why you think the dataset is interesting and important and to consider the advantages of unbiased genome-wide approaches to the advancement of scientific research.

AIM: Effectively communicate original research to your peers.

TASK: In small groups of approximately four students, you will prepare a 10-minute oral presentation about the RNA-seq dataset that you have chosen and why you think the research is interesting.

ASSESSMENT: You will present your talk as a team, and you will score your peers.

Each presentation will be rated on a scale of 1 (Very Poor), 2 (Poor), 3 (Good), 4 (Very good) to 5 (Excellent).

You will peer mark 4 other randomly allocated students. Peer marks will be based on the mean total grade given, excluding the highest and lowest marks. The final grade will be the mean of the peer and staff marks.

FEEDBACK: Feedback is provided via the marking rubric. Peer and demonstrator markers are also requested to provide some free-text feedback on the best aspects of the presentation plus where there is room for improvement.

<u>Course Learning Outcomes</u>

- CLO4 : Effectively communicate published scientific research to a non-specialist, peer audience.
- CLO5 : Discuss applications of genomics to real-world scientific questions.

<u>Detailed Assessment Description</u>

Genomics Assessment Task 1

Assessment Overview This information is imported from ECLIPS This information is published to public website

In the Genomics Assessment Task 1, you will be asked to present a talk on the RNA sequencing dataset that you choose from a curated list. You will be expected to convey why you think the dataset is interesting and important and to consider the advantages of unbiased genome-wide approaches to the advancement of scientific research.

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TASK: In small groups of approximately four students, you will prepare a 10-minute oral presentation about the RNA-seq dataset that you have chosen and why you think the research is interesting.

ASSESSMENT: You will present your talk as a team, and you will score your peers.

Each presentation will be rated on a scale of 1 (Very Poor), 2 (Poor), 3 (Good), 4 (Very good) to 5 (Excellent).

You will peer mark 4 other randomly allocated students. Peer marks will be based on the mean total grade given, excluding the highest and lowest marks. The final grade will be the mean of the peer and staff marks.

FEEDBACK: Feedback is provided via the marking rubric. Peer and demonstrator markers are also requested to provide some free-text feedback on the best aspects of the presentation plus where there is room for improvement.

Assessment Length

15 minutes

Assignment submission Turnitin type

Not Applicable

Genomics Assessment Task 2

Assessment Overview

TASK: Mid-Term Quiz

In Genomics Assessment Task 2, you will be asked to complete a quiz in multiple-choice answer format. The quiz will incorporate concepts in genetics, genomics and evolution from the lecture material covering Week 1- Week 5, inclusive. Topics may include: The definition of a gene (coding and non-coding genomic units), genome structure (how genes are organised into genomes), gene expression (transcription, splicing and translation), genome variation and the forces that shape it (mutation, recombination and genetic drift).

ASSESSMENT: The quiz will have 3-4 possible answers a-d and you are to select the correct answer. The quiz will be taken during the tutorial in Week 5. Marks will be released to students online.

FEEDBACK: There will be opportunities to discuss the quiz responses with tutors/demonstrators during tutorials.

Course Learning Outcomes

- CLO1 : Describe the main steps, technologies and challenges involved in sequencing, assembling and annotating a whole genome.
- CLO2 : Apply molecular evolutionary theory to homology searching, multiple sequence alignment, and molecular phylogenetics, in the context of genome annotation.
- CLO5 : Discuss applications of genomics to real-world scientific questions.

Detailed Assessment Description

Title: Genomics Assessment Task 2

TASK: Mid-Term Quiz

In Genomics Assessment Task 2, you will be asked to complete a quiz in multiple-choice answer format. The quiz will incorporate concepts in genetics, genomics and evolution from the lecture material covering Week 1- Week 5, inclusive. Topics may include: The definition of a gene (coding and non-coding genomic units), genome structure (how genes are organised into genomes), gene expression (transcription, splicing and translation), genome variation and the forces that shape it (mutation, recombination and genetic drift).

ASSESSMENT: The quiz will have 30 questions with 3-4 possible answers a-d and you are to select the correct answer. The quiz will take 45 minutes and will be be taken during the practical in Week 5. Marks will be released to students online.

FEEDBACK: There will be opportunities to discuss the quiz responses with tutors/demonstrators during tutorials.

Assessment Length

45 minutes

Assignment submission Turnitin type

Not Applicable

Bioinformatics Assessment Task

Assessment Overview

AIM: You will learn how to perform, manage and write up analysis of real data using real bioinformatics tools.

TASK: The main laboratory component for BABS3291 is a term-long online bioinformatics practical, supported by computer labs and tutorials. You will work through step-by-step guides for differential gene expression analyses of an RNA sequencing dataset you choose from a curated list. Emphasis throughout the project will be on transferable bioinformatics skills and exposure to a variety of potential methods and environments.

SUBMISSION: Submission will be as a single document online.

ASSESSMENT: You will submit a project report in the last week of the course. The assignment is

divided into 2 parts: A and B.

In part A (30%), you will describe the analyses you have chosen to perform, describe your methods, results and conclusions.

In part B (10%), you will discuss, in no more than 500 words, potential future directions for your sequencing analyses, drawing on techniques and knowledge from the Lecture content and related research articles of your choice.

the general format of a short research paper covering methods, results and interpretation of results in part A and discussion and future directions in Part B.

Marks will be awarded for presentation, clarity in description of methods and results, quality of figures, and scientific insight. Grading is rubric-guided.

FEEDBACK: Report marks are released to you online on an official release date. Formative feedback is given during development of the material in practical classes and tutorials, through interaction with instructors and demonstrators.

<u>Course Learning Outcomes</u>
- CLO1 : Describe the main steps, technologies and challenges involved in sequencing, assembling and annotating a whole genome.
- CLO2 : Apply molecular evolutionary theory to homology searching, multiple sequence alignment, and molecular phylogenetics, in the context of genome annotation.
- CLO3 : Analyse biological data relating to whole genome sequencing and gene annotation, using a variety of commandline, GUI and web tools.
- CLO4 : Effectively communicate published scientific research to a non-specialist, peer audience.
- CLO5 : Discuss applications of genomics to real-world scientific questions.

<u>Detailed Assessment Description</u>

Title: Bioinfomatics Asessment task 3- Practical Report

AIM: You will learn how to perform, manage and write up analysis of real data using real bioinformatics tools.

TASK: The main laboratory component for BABS3291 is a term-long online bioinformatics practical, supported by computer labs and tutorials. You will work through step-by-step guides for differential gene expression analyses of an RNA sequencing dataset you choose from a curated list. Emphasis throughout the project will be on transferable bioinformatics skills and

exposure to a variety of potential methods and environments.

SUBMISSION: Submission will be as a single document online.

ASSESSMENT: You will submit a project report in the last week of the course. The assignment is divided into 2 parts: A and B.

In part A (30%), you will describe the analyses you have chosen to perform, describe your methods, results and conclusions.

In part B (10%), you will discuss, in no more than 500 words, potential future directions for your sequencing analyses, drawing on techniques and knowledge from the Lecture content and related research articles of your choice.

the general format of a short research paper covering methods, results and interpretation of results in part A and discussion and future directions in Part B.

Marks will be awarded for presentation, clarity in description of methods and results, quality of figures, and scientific insight. Grading is rubric-guided.

FEEDBACK: Report marks are released to you online on an official release date. Formative feedback is given during development of the material in practical classes and tutorials, through interaction with instructors and demonstrators.

<u>Assessment Length</u>

Maximum of 2000 words

<u>Assignment submission Turnitin type</u>

Not Applicable

Final Exam

<u>Assessment Overview</u>

This exam is a long response format. You will be asked to choose your question from a list of possible questions and write a short essay on that aspect of the study of Genomics. Possible questions will be offered from each of three sections:
Genes and Genomics, Molecular Evolution, Applications of Genomics.

The exam takes place at a set time during the official examination period and can be completed

online. Mark/grade will be released to students on official assessment results release date, with feedback available via inquiry with the course convenor.

Course Learning Outcomes

- CLO1 : Describe the main steps, technologies and challenges involved in sequencing, assembling and annotating a whole genome.
- CLO2 : Apply molecular evolutionary theory to homology searching, multiple sequence alignment, and molecular phylogenetics, in the context of genome annotation.
- CLO3 : Analyse biological data relating to whole genome sequencing and gene annotation, using a variety of commandline, GUI and web tools.
- CLO5 : Discuss applications of genomics to real-world scientific questions.

Detailed Assessment Description

Title: Assessment 4 - Final Exam

This exam is a long response format. You will be asked to choose your question from a list of possible questions and write a short essay on that aspect of the study of Genomics. Possible questions will be offered from each of three sections:

Genes and Genomics, Molecular Evolution, Applications of Genomics.

The examination will be based upon lecture material (weeks 1-10) and will consist of nine short essay questions in three sections. The topics include: The complexity of the genome, population genetics & molecular evolution, emerging technologies in genomics and their applications. Students must answer ONE question from EACH SECTION (3 in total). Details will be released via Moodle/Teams.

The exam takes place at a set time during the official examination period and can be completed online. Mark/grade will be released to students on official assessment results release date, with feedback available via inquiry with the course convenor.

Assessment Length

2 hours

Assignment submission Turnitin type

This assignment is submitted through Turnitin and students do not see Turnitin similarity reports.

General Assessment Information

Grading Basis

Standard

Requirements to pass course

You will be expected to attend all practical classes, 80% of tutorials and 50% of TEAMS lectures live to pass the course.

Course Schedule

Teaching Week/Module	Activity Type	Content
Week 0 : 5 February - 11 February	Other	Orientation week
Week 1 : 12 February - 18 February	Lecture	• Course introduction (CK + RW) • Genes, genomes and evolution (CK) • Gene duplications & gene families (CK)
	Laboratory	Intro to Unix and High Performance Computing on Katana
	Tutorial	Dataset Research
Week 2 : 19 February - 25 February	Lecture	• Mobile DNA (CK) • Retrotransposons (CK) • Sex Chromosomes (PW)
	Laboratory	Exploring Online Genetic Resources - SRA and Ensembl
	Tutorial	Q&A Prac
Week 3 : 26 February - 3 March	Lecture	• Microchromosomes (PW) • Mutation and genetic variation (MT) • Selection and fitness landscapes (MT)
	Laboratory	Using FASTQC for Data Quality report
	Tutorial	Assignment 1 Talks
Week 4 : 4 March - 10 March	Lecture	• Genetic drift and population size (MT) • Molecular clocks (MT) • Epigenomics (KS)
	Laboratory	Using Trimmomatic for Trimming and Filtering
	Tutorial	Prac Q&A
Week 5 : 11 March - 17 March	Lecture	• Transcription (SB) • Splicing (RW) • Translation (RW)
	Laboratory	Assignment 2 Quiz
	Tutorial	The complexity of the genome (JM)
Week 6 : 18 March - 24 March	Online Activity	Flexibility week
Week 7 : 25 March - 31 March	Lecture	• Short-read sequencing (JB) • Long-read sequencing (ID)
	Laboratory	Using Kallisto for Pseudoalignment
Week 8 : 1 April - 7 April	Lecture	• High content imaging (JL) • Single cell sequencing (FL)
	Laboratory	Identifying Differentially Expressed Genes
	Tutorial	Ramaciotti Tour and work on Prac report
Week 9 : 8 April - 14 April	Lecture	• Epigenomics technology (FVM • Tuning of Immunity (SG) • Human genomics (VH)
	Laboratory	Work on Prac Report
	Tutorial	Sequencing Technology (JB)
Week 10 : 15 April - 21 April	Lecture	• Network genomics (FV) • Genomics for conservation (JBr) • Cancer Genomics (FVM)
	Laboratory	Work on Prac Report
	Tutorial	Work on Prac Report

Attendance Requirements

Students are strongly encouraged to attend all classes and review lecture recordings.

General Schedule Information

You will have 3 (1 hour) lectures per week, one 2 hour practical and one 2 hour tutorial per week.

Course Resources

Prescribed Resources

There is no textbook set for this course because the topics covered are diverse and no single book covers all the material adequately. Lecturers will suggest additional reading material throughout the course. Recommended texts include:

- Mattick, J., & Amaral, P. (2022). RNA, the Epicenter of Genetic Information (1st ed.). CRC Press. https://doi.org/10.1201/9781003109242
- Susan Holmes and Wolfgang Huber (2019). Modern Statistics for Modern Biology.
- Lesk (2017). Introduction to Genomics. Oxford University Press, Oxford.
- Lesk (2008). Introduction to Bioinformatics. Oxford University Press, Oxford.
- Higgs & Attwood (2005). Bioinformatics and Molecular Evolution. Blackwell Science, Oxford.
- Page & Holmes (1998). Molecular Evolution: A Phylogenetic Approach. Blackwell Science, Oxford.

Recommended Resources

Moodle site for this course.

TEAMS site for this course.

BABS3291 Course manual.

Library website and resources: http://info.library.unsw.edu.au/ PubMed: http://www.ncbi.nlm.nih.gov/pubmed

Ensembl: http://www.ensembl.org/index.html Kalllisto: https://pachterlab.github.io/kallisto/about

DESeq2:

ELISE - Take this online tutorial if you have not already done it. http://subjectguides.library.unsw.edu.au/elise

Various computer rooms around campus provide PCs for student use. Software for the pracs should be available on these machines via MyAccess.

Additional Costs

None

Course Evaluation and Development

The course will be evaluated via discussion and feedback during practicals and Tutorials. Responses to MyExperience surveys are taken seriously, and suggestions considered for incorporation into subsequent years. All constructive feedback is valuable and greatly appreciated.

Staff Details

Position	Name	Email	Location	Phone	Availability	Equitable Learning Services Contact	Primary Contact
Convenor	Cecile King		Room 420C, Level 4 Biological Sciences Building North, D26	+61 2 9348 0789	Term 1 week days	No	Yes
	Robert Weatheritt					No	No

Other Useful Information

Academic Information

Upon your enrolment at UNSW, you share responsibility with us for maintaining a safe, harmonious and tolerant University environment.

You are required to:

- Comply with the University's conditions of enrolment.
- Act responsibly, ethically, safely and with integrity.
- Observe standards of equity and respect in dealing with every member of the UNSW community.
- Engage in lawful behaviour.
- Use and care for University resources in a responsible and appropriate manner.
- Maintain the University's reputation and good standing.

For more information, visit the UNSW Student Code of Conduct Website.

Academic Honesty and Plagarism

Referencing is a way of acknowledging the sources of information that you use to research your assignments. You need to provide a reference whenever you draw on someone else's words, ideas or research. Not referencing other people's work can constitute plagiarism.
Further information about referencing styles can be located at https://student.unsw.edu.au/referencing

Academic integrity is fundamental to success at university. Academic integrity can be defined as a commitment to six fundamental values in academic pursuits: honesty, trust, fairness, respect, responsibility and courage. At UNSW, this means that your work must be your own, and others' ideas should be appropriately acknowledged. If you don't follow these rules, plagiarism may be detected in your work.
Further information about academic integrity, plagiarism and the use of AI in assessments can be located at:

- The Current Students site,
- The ELISE training site, and
- The Use of AI for assessments site.

The Student Conduct and Integrity Unit provides further resources to assist you to understand your conduct obligations as a student: https://student.unsw.edu.au/conduct

Submission of Assessment Tasks

Penalty for Late Submissions
UNSW has a standard late submission penalty of:

- 5% per day,
- for all assessments where a penalty applies,
- capped at five days (120 hours) from the assessment deadline, after which a student cannot submit an assessment, and
- no permitted variation.

Any variations to the above will be explicitly stated in the Course Outline for a given course or assessment task.

Students are expected to manage their time to meet deadlines and to request extensions as early as possible before the deadline.

Special Consideration

If circumstances prevent you from attending/completing an assessment task, you must officially apply for special consideration, usually within 3 days of the sitting date/due date. You can apply by logging onto myUNSW and following the link in the My Student Profile Tab. Medical documentation or other documentation explaining your absence must be submitted with your application. Once your application has been assessed, you will be contacted via your student email address to be advised of the official outcome and any actions that need to be taken from there. For more information about special consideration, please visit: https://student.unsw.edu.au/special-consideration

Important note: UNSW has a "fit to sit/submit" rule, which means that if you sit an exam or submit a piece of assessment, you are declaring yourself fit to do so and cannot later apply for Special Consideration. This is to ensure that if you feel unwell or are faced with significant circumstances beyond your control that affect your ability to study, you do not sit an examination or submit an assessment that does not reflect your best performance. Instead, you should apply for Special Consideration as soon as you realise you are not well enough or are otherwise unable to sit or submit an assessment.

Faculty-specific Information

Additional support for students

- [The Current Students Gateway](#)
- [Student Support](#)
- [Academic Skills and Support](#)
- [Student Wellbeing, Health and Safety](#)
- [Equitable Learning Services](#)
- [UNSW IT Service Centre](#)
- Science EDI Student [Initiatives](#), [Offerings](#) and [Guidelines](#)