MD2A2-30 MD2A2-30 Integrated Science: Patterns and Populations

21/22

Department
> Warwick Medical School

Level
> Undergraduate Level 2

Module leader
> Anne Straube

Credit value
> 30

Module duration
> 10 weeks

Assessment
> 100% coursework

Study location
> University of Warwick main campus, Coventry

Description

Introductory description

MD2A2-30 - Integrated Science: Patterns and Populations

The module is a continuation of MSci Integrated Science Year 1 laboratory modules that focus on molecules, cells and organisms to further increase scale to population level. The programme extends the first year of the degree using more advanced methods and analysis, but retaining the Integrated Science ethos, solving problems by drawing freely from the methods and mindsets of more than one discipline.

Module aims

The module will focus primarily on computational methods to analyse data, model interactions and spatial patterns and link changes at the DNA and transcriptional level to outcomes in spatial developmental patterns, species interaction and population ecology. The students will be equipped to extract quantitative data from raw sequencing reads and images, derive network information and mathematical models to describe multidimensional patterns and complex multi-species interactions.

Outline syllabus

This is an indicative module outline only to give an indication of the sort of topics that may be covered. Actual sessions held may differ.

This is an indicative module outline only to given an indication of the sort of topics that may be covered. Actual sessions held may differ:

Week 1: Introduction to term-long data analysis project, e.g. segmentation of butterfly wing patterns and extraction of size, shape, colour and texture information

Block 1 (weeks 2 - 4): Genes and gene networks
Analysis of new generation sequencing data. How to determine binding sites of gene regulators. How to handle data, bias correction of data. How to extract differential expression and gene network information. Introduction to spatial transcriptomics

Block 2 (weeks 5 - 7): Developmental patterning
Feedback loops, Morphogen gradients and how to model them as one-dimensional patterns. How to set positions in a developing organism and how are gene networks built to support this. Robustness, i.e. how to interpret noisy expression patterns to discreet phenotypic outputs. How do you get the right number of extremities, on example of polydactyly. Large scale and multidimensional patterns - evolution and environmental constraints, e.g. environmental impact on butterfly spot size and how this is regulated.

Block 3 (weeks 8 -10): Ecology and evolution in populations, communities, and ecosystems
Using the sequencing and data analysis tools developed in weeks 2-4 to characterise real-world communities. Investigate feedback(s) across scales, how species interactions scale-up to influence ecosystem properties and vice versa how ecosystems drive or constrain the evolution of species

Learning outcomes

By the end of the module, students should be able to:

- Utilise software packages for analysing sequencing data (Block 1)
- Comprehend concepts underlying spatial transcriptomics and their representation (Block 1)
- Generate data (Block 1), interpret (Block 2), and apply (Block 3) network interactions to study the ecology and evolution of biological systems
- Apply model fitting approaches to experimental data (Blocks 2 and 3)
- Apply statistical knowledge to estimate uncertainties in analysis (Blocks 1, 2 and 3)
- Apply concepts such as species interactions and feedbacks to ecological systems (Block 3)
- Use sequencing data to infer information about species evolution (Block 3)
- Present concisely, appropriately and effectively on topics discussed in class (Blocks 1, 2 and 3)
- Synthesise biological concepts related to network interaction. In particular, students are expected to being together different elements of the course to show how the concepts are integrated (Blocks 1, 2 and 3)
- Understand how to use the literature to deepen understanding (Blocks 1, 2 and 3)

- Understand fundamental concepts underlying biological networks, including feedback, hysteresis, and robustness
- Apply statistical techniques to a variety of biological data (Block 1: sequencing; Block 2: dynamic; Block 3: applications to ecology and evolution)
- Evaluate biological data using different techniques and able to critique the appropriateness of each methodology

Interdisciplinary

The students will apply computational, mathematical, physical methods to understand and describe complex biological phenomena.

Subject specific skills

Knowledge of key methods in bioinformatics, data handling and analysis.
Knowledge of approaches to model linear and multidimensional gradients resulting in robust pattern formation.
Knowledge of how genetic variance impacts the spread of infectious disease within same species and different species.
Knowledge how to develop analysis tools to extract quantitative data from images and nucleotide reads of biological samples.

Transferable skills

Students will be able to demonstrate integrated thinking across the Sciences.
Oral presentations on quantitative methods applied to biological problems.

Study

Study time

Type	Required
Seminars	20 sessions of 1 hour (7%)
Practical classes	20 sessions of 3 hours (20%)
Fieldwork	4 sessions of 5 hours (7%)
Assessment	200 hours (67%)
Total	300 hours

Private study description

No private study requirements defined for this module.

Costs

Category	Description	Funded by	Cost to student
Other	Costs for field trip and sequencing of environmental samples	Department	£0.00

Assessment

You do not need to pass all assessment components to pass the module.

Assessment group A

	Weighting	Study time
Image analysis assignment	25%	50 hours

Students work (in groups of 2-3) on a term-long project to extract quantitive data from a collection of images. The submission is a report on the process and extracted information, commented code and a user guide.

Presentations in Block 1	10%	20 hours

Oral presentation in block 1 on a topic set by block lead

Assignment Block 1	15%	30 hours

Students complete data analysis, evaluation and interpretation tasks based on techniques taught in the block.

Presentations in Block 2	10%	20 hours

Oral presentation in block 2 on a topic set by block lead

Assignment Block 2	15%	30 hours

Students complete data analysis, evaluation and interpretation tasks based on techniques taught in the block.

Presentations in Block 3	10%	20 hours

Oral presentation in block 3 on a topic set by block lead

Assignment Block 3	15%	30 hours

Students complete data analysis, evaluation and interpretation tasks based on techniques taught in the block.

Feedback on assessment

If a student is ill on the day of a scheduled oral presentation for the group, we will waive one of the presentations and recalculate the mark for the remaining components. The remaining students in the group can continue with the presentation and will be marked. If a student is not available for a

second presentation, we will reschedule their presentation, potentially purely for assessment purposes with the respective block lead. Students will receive feedback from peers and the block lead on oral presentations.

The Assignments will be marked by block leads and moderated by module lead and written feedback will be provided.

Availability

Courses

This module is Core for:

- Year 2 of UMDA-CF10 Undergraduate Integrated Natural Sciences (MSci)