MS203-15 Patterns and Populations

23/24

Department
> Warwick Medical School

Level
> Undergraduate Level 2

Module leader
> Sascha Ott

Credit value
> 15

Module duration
> 10 weeks

Assessment
> 100% coursework

Study locations
> University of Warwick main campus, Coventry Primary
> field trip location: FSC Dale Fort (https://www.field-studies-council.org/locations/dalefort/)

Description

Introductory description

This module focuses on how complex biological systems can be described and analysed using mathematical and computational approaches. For example, (1) new sequencing data is revealing insight into the connectivity in gene regulation; and (2) mathematical models underly key concepts in population and community ecology. Such information is critical as we look to understand the effects of the Anthropocene on species' genetic diversity and extinction.
The module will be compulsory for second year Integrated Natural Sciences (INS) students. It is a continuation of MSci Integrated Natural Sciences 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 Natural Sciences 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, 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.

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Block 1 (weeks 1 - 4): Genes and gene network analysis of high-throughput sequencing data. How to handle data, detect and correct biases, and assure data quality. How to extract differential expression and gene network information.

Block 2 (weeks 5 - 7): Ecology and evolution in populations, communities, and ecosystems. Using the sequencing and data analysis tools developed in Block 1 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
The module ends with a field trip to collect data and perform statistical analysis.

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 transcriptomics data and their representation (Block 1)
- interpret and apply data to understand network interactions in ecology and evolution of biological systems (Blocks 1-2)
- Apply statistical knowledge to estimate uncertainties in analysis (Blocks 1-2)
- Apply concepts such as species interactions and feedback to ecological systems (Block 2)
- Present concisely, appropriately and effectively on topics discussed in class (Blocks 1-2)
- Synthesise biological concepts related to network interaction (Blocks 1-2)
- Understand how to use the literature to deepen understanding (Block 1-2)
- Evaluate biological data using different techniques and able to critique the appropriateness of each methodology

Indicative reading list

Michael Begon & Colin R. Townsend. Ecology: From Individuals to Ecosystems. 5th Ed.

Interdisciplinary

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

Subject specific skills

Knowledge of key methods in bioinformatics, data handling and analysis. Knowledge how to apply analysis tools to extract quantitative data from nucleotide reads of biological samples. Knowledge about how to interpret data in the context of ecological and evolutionary theory.

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
Lectures	8 sessions of 1 hour (5%)
Practical classes	7 sessions of 2 hours (9%)
Fieldwork	5 sessions of 8 hours (27%)
Private study	58 hours (39%)
Assessment	30 hours (20%)
Total	150 hours

Private study description

Reading around topics and learning tools to perform analyses. Also includes deepening understanding of statistical approaches.

Costs

No further costs have been identified for this module.

Assessment

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

Assessment group A

	Weighting	**Study time**	**Eligible for self-certification**

Assessment component

Block 1 Presentation	25%	7 hours	Yes (waive)

Presentation related to bioinformatic analysis

Reassessment component is the same

Assessment component

Bioinformatic data analysis	25%	8 hours	Yes (extension)

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

Reassessment component is the same

Assessment component

Block 2 presentation	25%	7 hours	Yes (extension)

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

Reassessment component is the same

Assessment component

Field trip report	25%	8 hours	Yes (extension)

Students complete data analysis, evaluation and interpretation of data, based on the field trip.

Reassessment component is the same

Feedback on assessment

Oral feedback on presentations and for first report.

Availability

Courses

This module is Core for:

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