

CFA2.6 Course Title: Molecular ecology and population genetics

Modality: Advance Training Course

Dates:

20-24 november 2017

Monday to Friday from 9 until 14. Wednesday and Thursday from 16 to 18:30

Duration:

Lectures: 25h

Laboratory: 0h

Location: DOMAR videoconference room, Torre CACTI, Campus de Vigo, Universidade de Vigo

Academic coordinators:

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Paloma Morán	Universidade de Vigo	paloma@uvigo.es
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Lecturers:

Name	Institution	e-mail
Iria Fernández Silva	Universidade de Vigo	
Miguel Arenas Busto	Universidade de Vigo	

General description:

The course objective is to help students gain a fundamental understanding of population genetic principles and uses of molecular genetic data and theory in areas of behavioral ecology, population ecology, resource management, and evolutionary ecology. The course will be divided into sections that encompass these general areas, with emphasis on marine organism. Each section will cover basic theoretical concepts, statistical methods of inference, using examples and different computer programs.

Contents:

Day 1 (Monday, 9:00-12:00, Iria Fernández)

- Genomes, genetic markers (Brief theory)
- Sampling and acquisition of genetic data: Applications in marine molecular ecology and population genetics (Theory and examples from published articles, including introduction to the article/dataset that we will be using for exercise)
- DNA alignments and genetic diversity (Theory and computer exercise with mtDNA) Presentation of take-home exercise

Day 1 (Monday, 12:00-14:00, Miguel Arenas)

- Phylogenetics and phylogeography I (Theory + Data analysis exercise)

Day 2 (Tuesday, 9:00-12:00, Iria Fernández)

- Populations in equilibrium (Hardy-Weinberg) (Theory)
- Working with genome-wide data: Genome assemblies, SNP data, resequencing genomes (Theory, introduction to article/dataset that we will be using for exercise and computer exercise)
- Metapopulations and genetic structure I (Theory and computer exercise)

Day 2 (Tuesday, 12:00-14:00, Miguel Arenas)

- Phylogenetics and phylogeography II (Theory + Data analysis exercise)

Day 3 (Wednesday, 9:00-12:00, Iria Fernández)

- Metapopulations and genetic structure II (Theory and computer exercises with the same dataset as the day before)

Day 3 (Wednesday, 12:00-14:00, Miguel Arenas)

- Evolutionary parameters. Population size and its variation over time, time to MRCA, rates of evolution, molecular clock, etc. (Brief theory + data analysis exercise)
- Population size and its evolution (Brief theory + data analysis exercise)

Day 3 (Wednesday, 16:00-18:30, Miguel Arenas)

- Computer simulations in population genetics and ecology. The coalescent, forward-in-time simulation and simulation of genetic data (Theory)

Day 4 (Thursday, 9:00-12:00, Iria Fernández)

- Selection and adaptation (Theory)
- Detecting loci under selection (Theory, introduction to article/dataset that we will be using for exercise and computer exercise)

Day 4 (Thursday, 12:00-14:00; 16:00-18:30, Miguel Arenas)

- Migration models (Brief theory)
- Range expansion, range shift, range contraction and habitat fragmentation. Founder events, allele surfing and isolation by distance (Theory + exercise with explicit simulations and data analyses)

Day 5 (Friday, 9:00-12:00, Iria Fernández)

- Adaptation vs. Acclimation - Gene expression analyses (Theory and examples of studies in marine molecular ecology)
- Summary of past lessons questions and answers Discussion on take-home exercise

Day 5 (Friday, 12:00-14:00, Miguel Arenas)

- Demographic/migration model selection with approximate Bayesian computation (Theory + data analysis exercise)
- Estimation of population genetics parameters with approximate Bayesian computation (Theory + data analysis exercise)
- Presentation of the questioner of evaluation (to be filled by the student and delivered after max 2 weeks)

Teaching methodologies:

Software:

Geneious (alignments, genetic diversity)
Arlequin3.5, DnaSP5, MEGA7 (alignments, genetic diversity, phylogenies, genetic differentiation and loci under selection)
BEAST1.8 (Bayesian Evolutionary Analysis Sampling Trees)
SplitsTree4 (Phylogenies)
jModelTest2 (substitution models)
FigTree1.4 (Phylogenies)
STRUCTURE (genetic structure)
LOSITAN (loci under selection)
BAYESCAN (loci under selection)
SPLATCHE2 (Spatial And Temporal Coalescent in a Heterogeneous Environment) R with libraries *lattice*, *MCMCpack*, *ape*, *graphics*, *abc*, *maps*, *fields*

Evaluation system:

Exercises. Quizzes and paper discussions

Brief CV of the lecturers:

Dr. Miguel Arenas is a Principal Investigator of the University of Vigo. His position involves 80% in research and 20% in teaching. He is an expert in evolutionary biology, including models, methods and applications. Indeed, he has investigated the genetic diversity and evolution of some marine organisms. So far his research includes 34 peer-review publications (22 articles in the first quartile and 26 articles as first/last author) and the participation in a variety of national and international research Projects (some of them as principal investigator). He supervised several Master and PhD students.

Dra. Iria Fernández Silva is a Principal Investigator of the University of Vigo. Her research is focused on the study of biodiversity, evolutionary biology and molecular ecology of marine organisms, combining a strong field focus and state-of-the-art genomic methods. Most of her recent research is focused on coral reefs. She has 33 publications and has participated in a variety of national and international projects, some as principal investigator. She has led or participated in +10 international biodiversity surveys and field expeditions across the Atlantic, the Indian and Pacific oceans.