



LUND UNIVERSITY  
Faculty of Science

# Previous GENECO courses

## Abbreviations:

G: organised or coorganised by GENECO

LS: organised by the Life-science program at Lund university

SLL: organised by SciLifeLab

## 2018

High-Dimensional Data Analysis in Ecology and Evolutionary Biology Using R  
2-4 May, 28 May – 1 June 2018, Lund

High-Dimensional Data Analysis in Ecology and Evolutionary Biology Using R (28 May-1 June: G)

*This workshop is intended for researchers who have interest in analysing high-dimensional data (many continuous variables, or dissimilarity matrices from other types of data). The workshop introduces participants to linear model methods incorporating randomized residual permutation procedures, which allow analysis of high-dimensional data with high statistical power. Emphasis is placed on evaluation of linear model effects for high-dimensional data, how to calculate effect sizes, comparison of models, comparison of covariance structure, and the resampling methods that make these objectives possible. Participants will gain both an understanding of the cutting-edge non-parametric methods for analysis of high-dimensional data and tools for performing such analyses in R. The course is a collaboration between the research schools ClimBEco and GENECO.*

*The course is free of charge for ClimBEco and GENECO PhD students as well as students enrolled at the Faculty of Science at Lund University. Students from outside Lund University, and not within any affiliations mentioned above, are welcome to apply but will be charged, see below. **Credit points:** Hp: 1,5 hp*

Introduction to R (2-4 May: G)

*This course's aim is to provide a basic introduction to R, preparing students for additional R courses within ClimBEco and GENECO. The course will use a combination of brief lectures and tutorials where the students will work on prepared problems. We will cover: basic R commands, basic data manipulation in R (different data structures), import and export of data, plotting commands, functions for data summary and manipulation (e.g. computing means, variances, maxima, minima, and apply-functions) and – time permitting – basic statistics. Course leader is Johan Lindström (MERGE). The course is a collaboration between the research schools ClimBEco and GENECO.*

*The course "Introduction to R" is organised particularly for students registered for the course "High-Dimensional Data Analysis in Ecology and Evolutionary Biology Using R" May 28 – 1 June. For that reason, these students will be given priority. Still, in terms of space, we will fill the course with other students interested in R – mainly students enrolled in ClimBEco and GENECO, and then at the faculty of science at Lund University. Students from outside Lund University, and not within any affiliations mentioned above, are welcome to apply but will be charged, see below. **Credit points:** Hp:  $1,5 * 3/5 = 0.9$  hp*



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## Using Phylogenetic Trees to Study Trait Evolution and Perform Comparative Analyses (9-13 April: G)

### Part 1 (9th – 11th April) Comparative analyses: accounting for phylogenetic relationships when conducting data analyses

Led by Dr Charlie Cornwallis

*This course will entail lectures on the types of datasets where it may be important to control for phylogenetic relatedness between species and the types of considerations when obtaining/selecting a phylogeny. There will be information on different approaches to comparative analyses (incl. the different R packages available for these approaches) and the practical considerations for conducting these analyses. There will also be workshops using toy datasets to run a comparative analysis in the R packages Ape, Geiger, PhyTools, MCMCglmm & Bayes traits. This course will give you 1,5 credit points.*

### Part 2 (12th – 13th April) Using phylogenetic trees to study trait evolution

Led by Niklas Wahlberg

*This course follows on from the Molecular Phylogenetics Course run in October 2017. Although it is not a pre-requisite to have attended the previous course, participants will require the knowledge covered in the Molecular Phylogenetics Course (please contact Prof Niklas Wahlberg if you have any questions about the what skills you need for this course). The course will include lectures on how to use phylogenies to study the dynamics of trait evolution (mainly about diversification rate models). There will also be discussion of the commonly used models and considerations when choosing between such models e.g. continuous versus discrete traits. There will also be workshops using your own, or toy, data (phylogeny & traits) to apply selected diversification rate models. This course will give you 1,0 credit point.*

### Workshop on genomics in Cesky Krumlov (January 7-20; G)

*The Workshop on Genomics was developed in response to the increasing demand for training on how to effectively analyze and manage data generated by modern sequencing technologies. The Workshop curriculum includes extensive coverage of fundamental techniques required of all studies utilizing modern sequence data. This includes management and modification of modern sequence data files, using the Unix command-line and editors to manipulate large data files, assembly and best practices for sequence data generation, management and analysis. The second-half of the Workshop is devoted to specific sub-disciplines within the genomic sciences. While these topics may change from year-to-year, efforts are made to devote significant amounts of time to techniques being used widely in the field (e.g. transcriptomics, genome assembly, metagenomics, population genomics).*



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2017

### Introduction to UNIX for Biologists. (20-22 November: G)

*Introductory course to using the UNIX environment and to using the UNIX-terminal for processing biological data. This course is organized by Geneco and PlantLink.*

*The terminal interface in UNIX, the environment on which the operating systems Linux and Mac are built, is a central tool for processing and managing biological data. It inherently provides a variety of programs and commands for performing text-file manipulation, and is frequently the main platform for more advanced bioinformatic tools. Large processing clusters like UPPMAX are also often based on a UNIX environment. Basic knowledge of how to navigate, manage data and perform data processing in UNIX is a highly useful and versatile skill for anyone working with biological data. It is also a crucial skill to have when working with command-line based bioinformatic software.*

### Understanding Population Genetics. (23-27 October: G)

*Population genetics with its many mathematical formulae provides perhaps the sharpest analytical tool in biological research. Its results are used everywhere, from evolutionary explanations to analyses of inherited diseases and many other applications. To really understand the strength of population genetics it is important to have worked through the most important derivations at least once. This course gives an introduction to the formal side of population genetics with the attempt to keep biological relevance in focus.*

### Making Phylogenetic Trees. (2-4 October: G)

*The Geneco course "Making Phylogenetic Trees" run by Prof Niklas Wahlberg will be at Lund University from the 2nd to 4th of October. This 3 day course will provide an introduction to the fundamental principles of building phylogenies using molecular data, as well as the latest techniques and programmes in this field.*

*The aims of this course are to introduce the theory and practice of phylogenetic inference from molecular data and to provide an introduction to some of the most used methods and computer programs. The emphasis will be on model-based methods using maximum likelihood and Bayesian inference, with a focus on DNA sequences as data. We will introduce programs such as RAxML, MrBayes, as well as BEAST for timing of divergence analyses. The course will consist of lectures, demonstrations of computer programs, and independent projects on fully analysing an example dataset (either your own or given by the lecturer). The course is available to everyone and there is no charge for attendance. The course counts towards ECTS 1,5 points/ 1,5 hp for students.*

### Molecular phylogenetics course for GENECO (October 2nd to 4th)

*The aims of this course are to introduce the theory and practice of phylogenetic inference from molecular data and to provide an introduction to some of the most used methods and computer programs. The emphasis will be on model-based methods using maximum likelihood and Bayesian inference, with a focus on DNA sequences as data. We will introduce programs such as RAxML, MrBayes, as well as BEAST for timing of divergence*



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analyses. The course will consist of lectures, demonstrations of computer programs, and independent projects on fully analysing an example dataset (either your own or given by the lecturer).

### Intro to Bioinformatics using NGS data – (25-29 September: G)

The course will provide an entry-level introduction to a wide range of analytical techniques for massively parallel sequencing, including basic Linux commands. We will pair lectures on the theory of analysis algorithms with practical computational exercises demonstrating the use of common tools for analyzing data from each of several common sequencing study designs.

### Estimating signs of selection in genes and genomes – (June 13-15; G)

Only 2% of our genome encodes proteins but these genes are often of key interest for ecologists and evolutionary biologists when studying adaptation and evolution. In this course, you will learn how to detect signs of positive and negative selection both in single genes and in genomes. Maria Anisimova will be our teacher and she is very experienced working with, for example, selection in a phylogenetic framework and measuring evolutionary rates. At present Maria is Head of Applied Computational Genomics at Zurich University of Applied Sciences.

Cost: Geneco PhD students and students/researchers enrolled at Lund University Faculty of Science free of charge. Others SEK 1000 + VAT.

Credits: ECTS 1,5 points/ 1,5 hp

Two themes over three days

*Modeling molecular evolution and phylogenetics*

- Markov models of substitutions
- Hypothesis testing and model selection
- Data formats and visualisation
- Phylogenetic inference
- ML tree inference: Exercises with PHYML

*Detecting positive selection with codon models*

- Natural selection and codon models
- Exercises with PAML (basics, one ratio model)
- Modeling variability of selection
- Exercises with PAML (branch models)
- Site models, detecting residues under selection
- Exercises with PAML (site models)

### Workshop on genomics in Cesky Krumlov (January 8-21; G)

The Workshop on Genomics was developed in response to the increasing demand for training on how to effectively analyze and manage data generated by modern sequencing technologies. The Workshop curriculum includes extensive coverage of fundamental techniques required of all studies utilizing modern sequence data. This includes management and modification of modern sequence data files, using the Unix command-line and editors to manipulate large data files, assembly and best practices for sequence data generation, management and analysis. The second-half of the Workshop is devoted to specific sub-disciplines within the genomic sciences. While these topics may change from year-to-year, efforts are made to devote significant amounts of time to techniques being used widely in the field (e.g. transcriptomics, genome assembly, metagenomics, population genomics).

2016

### Workshop on genomics in Cesky Krumlov (January, 2 weeks; G)

See above.



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### Introduction to UNIX for biologists (November 9-11; G)

*Introductory course to using the UNIX environment and to using the UNIX-terminal for processing biological data.*

### PYTHON bioinformatics programming (November 21-25; G)

*A need for basic programming skills is often identified in research projects where huge amounts of data is produced. This "crash course" will provide students with no programming experience with these skills.*

### DNA amplification technology (week 41; LS)

*The course covers real-time quantitative PCR (qPCR) analysis from sampling to evaluation of results. The aim of the course is to improve the understanding of the biochemical and physical principles behind PCR, thus giving the students the tools for designing, optimising and using PCR/qPCR assays.*

### Quantitative PCR (week 48; LS)

*A hands-on course in quantitative PCR. You will learn about the quantitative nature of the PCR reaction, qPCR chemistries, potential side reactions and how to avoid them, specificity and efficiency of the reaction, primer design, sample preparation, relative and absolute quantifications, standardization and verification, and trouble shooting! The course will introduce you to quantification of DNA (for genomic variations and species determinations) and RNA (for gene expression analyses).*

## 2015

### Workshop on genomics in Cesky Krumlov (January 11-24; G)

*See above.*

### Understanding population genetics (April 20-24; G)

*Population genetics with its many mathematical formulae provides perhaps the sharpest analytical tool in biological research. Its results are used everywhere, from evolutionary explanations to analyses of inherited diseases and many other applications. To really understand the strength of population genetics it is important to have worked through the most important derivations at least once. This course gives an introduction to the formal side of population genetics with the attempt to keep biological relevance in focus.*

### Analysing RAD-tags using Stacks (October 5-9; G)

*Reduced representation sequencing using Restriction Associated Digestion (RAD-tags) of genomic DNA and subsequent high throughput sequencing has proven an effective approach for studying both model (with a sequenced genome) and non-model organisms. It can be used for studying population structure of wild populations by identifying large numbers of SNPs. During the course we will cover the theory behind RADSeq and best laboratory practises as well as in depth analysis of RADSeq data using the Stacks software, Structure as well as identifying signatures of selection.*

### PYTHON bioinformatics programming (week 39; LS)

*See above.*

### DNA amplification technology (October 19-23; LS)

*See above.*

### Transcriptome analysis (November 16-20; LS)

*Information pending.*

### Introduction to bioinformatics using NGS data (November 16-20; SLL)

*Information pending.*

### Quantitative PCR (November 23-27; G)

*See above.*



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2014

Workshop on genomics in Cesky Krumlov (January, 2 weeks; G)

*See above.*

Introduction to molecular Ecology (March, 2 weeks; G)

*A practically oriented course providing the basics for DNA analyses in any kind of free-living organism. It gives a broad introduction to commonly used techniques in molecular ecology from microsatellites to next-generation sequencing. In parallel with the practical parts, there will be lectures giving the theoretical background to the exercises.*

Phylogenomics (May 5-9; G)

*The course comprises lectures, discussions, and group activities focused on design of phylogenomic studies. Expected learning outcomes are that participants should be able to recognize, articulate, differentiate, explain, compare and apply core concepts of phylogenomics, recall relevant literature, and design studies to solve relevant phylogenetic problems using genomic data (broadly defined).*

Evolutionary ecology of host-pathogen interactions (October-November; G)

*The course will give you an overview of the theoretical foundation for research on evolutionary aspects of host-pathogen interactions, and the state of the art of empirical research in this field.*

Next generation data and data bases (November 3-7; G)

*Information pending.*

DNA amplification technology (October 20-24; LS)

*See above.*

PERL bioinformatics programming (September 22-26; LS)

*Information pending.*

PYTHON bioinformatics programming (October 13-17; LS)

*See above.*

Transcriptome analysis (November 17-21; LS)

*Information pending.*

Quantitative PCR (November 24-28; LS)

*See above.*