



Head



Assoc. Prof. Dr. Michael Traugott
Institute of Ecology
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Duration / Credits

24th – 28th September 2018 /
equals 4 ECTS-Credits

Location

Institute of Ecology,
University of Innsbruck, Austria

Course Fee

€ 600,- (including course and bench fees, course materials and documentation)
A reduced fee of € 540,- applies if the MOTI course is booked in combination with the MATI course.

Website

www.uibk.ac.at/projects/mati

Contact

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Enrolment

until 30th June 2018
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METABARCODING OF TROPHIC INTERACTIONS (MOTI)

UNIVERSITY COURSE



Target audience

Graduate students as well as postdoctoral researchers and technicians who wish to use next generation sequencing (NGS) techniques for their studies of trophic interactions and want to understand the bioinformatics tools for the processing of NGS data.

A maximum of 20 participants will be allowed for the course and a first come first served basis applies.

Modules

Lecture Series

The lecture series delivers the methodological background for applications of NGS in trophic interactions research and for investigations of other environmental DNA (eDNA). Current examples of NGS usage in these ecological disciplines, the different sequencing platforms, study design and workflow for NGS are presented. Besides laboratory workflows, computational requirements and software for NGS analysis are addressed.

Practical Course

In the practical part of the course, an example dataset from targeted amplicon sequencing on an Illumina platform will be bioinformatically analysed by each participant with support of the lecturers. Course members learn which software is needed for the different steps of data analysis such as for example the quality check of NGS raw data, which steps are necessary to receive reads out of the raw data and how to identify organisms from the obtained reads with a local BLAST search. The outcome of the dataset will be discussed within the group.

Content and Learning Target

Participants of the MOTI course will be introduced into the field of next generation sequencing (NGS) for trophic interactions research with a special focus on NGS data processing and evaluation. Participants will get an overview on the current NGS technologies, the set up-of NGS-based DNA analyses and practically train the processing of NGS data.

As costs for NGS applications are continuously decreasing, NGS becomes more and more attractive for ecologists to target ecological questions such as food webs and community assessment using eDNA. In contrast to full genome sequencing, this course focuses on targeted amplicon sequencing which allows detecting sequences of many different organisms from an ecosystem within a single sample. In comparison to other molecular methods, such as diagnostic assays employing taxon-specific primers or Sanger sequencing, knowledge in bioinformatics is necessary to process NGS data.

By completing this course participants have learned what to consider when planning their own NGS study and they will obtain the technical background for running NGS and data analysis with bioinformatics tools. The provided information and skills will also be helpful for dealing with NGS providers and for building up your own computational infrastructure for NGS data processing.

Coverage / Duration

The MOTI-Course includes a lecture series and practical data analysis (Σ 4 ECTS-Credits). The course will be held from 24th to 28th September 2018, directly after the two weeks „MATI“ course. Please check our website for more detailed information.

Qualification

Certificate of the University of Innsbruck in Metabarcoding of Trophic Interactions. Participants who wish to obtain the ECTS-Credits have to generate a protocol on the practical coursework and to pass a final exam.