Team

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Duration / Credits

23rd – 27th September 2019 /
equals 4 ECTS-Credits

Location

Department 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 31st July 2019
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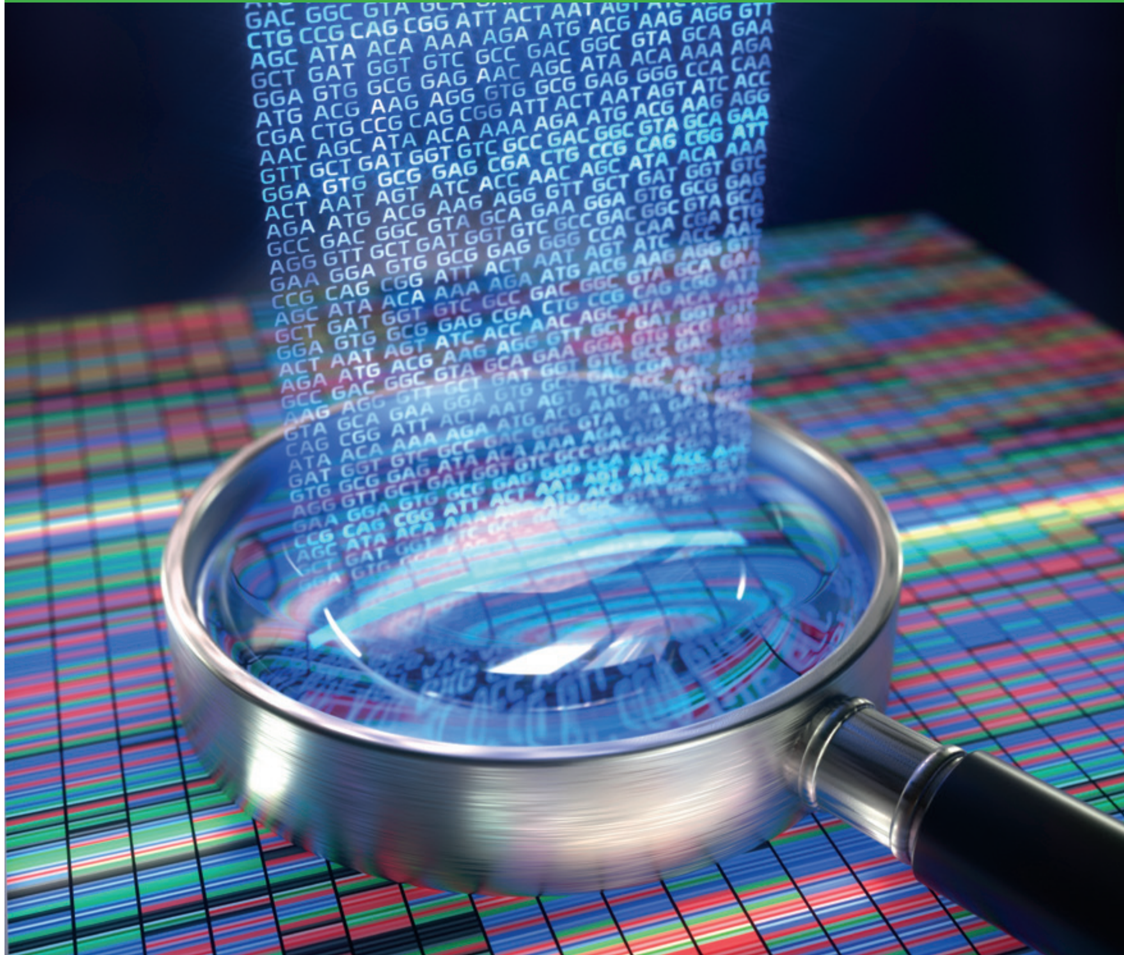
Koordinationsstelle für
universitäre Weiterbildung

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 and metabarcoding for studies on trophic interactions and who want to understand and be able to apply the bioinformatic tools for the processing of NGS data.

The course provides a methodological introduction and a hands-on training in bioinformatic analyses for beginners in the field of targeted amplicon sequencing. It aims at providing you with a basic understanding of the bioinformatic steps needed to process metabarcoding data.

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

Modules

Lecture series

The lecture series delivers the methodological background for metabarcoding trophic interactions and for investigations of other environmental DNA (eDNA) using NGS techniques. 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 metabarcoding 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.
Please note that this course does not include the assessment of different bioinformatics pipelines and of the statistical analyses of metabarcoding data. It rather aims at providing you with a basic understanding of the bioinformatic steps needed to process metabarcoding data which will allow you to work with and modify existing bioinformatic protocols.

Content and Learning Target

Participants of the MOTI course will be introduced into the field of metabarcoding of 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 sets.

As costs for NGS applications are continuously decreasing, metabarcoding 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 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 key to process NGS data.

By completing this course participants have learned what to consider when planning their own metabarcoding study and they will obtain the technical background for running NGS and data analysis with bioinformatic 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 bioinformatic data analysis (equals Σ 4 ECTS-Credits). The course will be held from 23rd to 27th September 2019, 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.