

- Faculté des sciences
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Evolutionary genetics (3BL2215)

Filières concernées	Nombre d'heures	Validation	Crédits ECTS
Master en biologie	Cours: 7 dj	contrôle continu: 1	3

ph=période hebdomadaire, pg=période globale, j=jour, dj=demi-jour, h=heure, min=minute

Période d'enseignement:

- Semestre Printemps

Equipe enseignante:

Christian Parisod, Laboratoire de botanique évolutive, e-mail : christian.parisod@unine.ch
François Felber, Musée et Jardins botaniques cantonaux vaudois, e-mail: francois.felber@vd.ch

Objectifs:

This course offers an advanced overview of microevolutionary processes causing variability within species. It addresses the main concepts and methods of evolutionary genetics, and offers a rich toolbox that is central to the evolutionary ecology and the management of natural populations. Lectures of F. Felber explore important environmental questions having an impact on our society, whereas C. Parisod focuses on interactions between landscape elements, gene flow and adaptation.

Contenu:

- The origin of genetic variation (CP, 2h)
 - Genome organization and evolution
 - Molecular markers
 - High throughput sequencing approaches
- From population genetics to landscape genetics (CP, 4h)
 - Reminder on plant population genetics (genetic drift, gene dispersal, selection)
 - Evaluation of spatial patterns of genetic variability (Fstat, SPAGeDi, STRUCTURE)
 - Putting the landscape in population genetics
 - Handling of environmental datasets (ArcGIS spatial toolkits)
 - Scale issues: phylogeography vs population genomics (synthesis)
- Environmental questions of societal importance (FF, 4h)
 - Plants and climate changes
 - Invasive species
 - Gene flow between crops and wild relatives
 - Analysis of case studies (synthesis)
- Inference of gene flow in real landscapes (CP, 2h)
 - Landscape distance/resistance
 - Overlay techniques
 - Contemporary gene flow and multiple regressions
 - Problems and prospects (synthesis)
- Inference of adaptation in real landscapes (CP, 2h)
 - Methods to detect selection at the molecular level (Sam²ada, BayeScan, BayEnv)
 - Taking population subdivision and demography into account
 - Introduction to Approximate Bayesian Computing
 - Integrating evolutionary and functional approaches to infer loci adaptation
 - Problems and prospects (synthesis)
- Analysis of real datasets with relevant software (CP, 8h)

Forme de l'évaluation:

Short individual report describing analyses done on a real dataset and delivered max. 2 weeks after the course. The report takes the form of a short research article (ca. 2000 words, excluding references, tables and figures).

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Documentation:

An updated bibliography will be given during the first lecture.

Forme de l'enseignement:

Ex Cataedra lectures, reading and discussion of case studies and practical analysis of datasets