

Doctoral Programs  
CUSO Ecology & Evolution and Interuniversity in Organismal Biology

**Phylogeography, macroecology and biogeography**

<b>Place</b>	:	University of Neuchâtel, Faculty of Sciences, Emile-Argand 11, UniMail, Aula Louis-Guillaume ALG, 2nd floor main building F	Map: <a href="http://www2.unine.ch/files/content/sites/dp-biol/files/shared/DPbiol/forms/Site_unimail.gif">http://www2.unine.ch/files/content/sites/dp-biol/files/shared/DPbiol/forms/Site_unimail.gif</a>
<b>Tuesday 9, Session Biogeography</b>			
<b>Lectures</b>			
09:30	:	Welcome by <b>Edward Mitchell</b>	
09:35	:	<b>Enrique Lara</b> The impact of protist taxonomy on biogeographical inferences	
10:40	:	Coffee break	
11:00	:	<b>Maria Aguilar</b> Microorganisms are not randomly distributed in space: myxomycetes and protostelids	
12:30	:	Lunch in the Restaurant "Le Romarin"	
<b>Practical part</b>			
14:30-17:30	:	<b>Maria Aguilar</b> Using MAXENT software for species habitat modelling	
<b>Wednesday 10, Session Macroecology</b>			
09:00	:	<b>Joaquin Hortal</b> Introduction to macroecology and measuring biodiversity	
10:00	:	Coffee break	
10:20	:	<b>Joaquin Hortal</b> Describing ignorance: shortfalls in our knowledge about biodiversity	
11:20	:	<b>Diego Fontaneto</b> DNA taxonomy in macroecology	
12:30	:	Lunch in the Restaurant "Le Romarin"	
<b>Practical part</b>			
14:30-15:30	:	<b>Diego Fontaneto</b> DNA-based species delimitation methods	
15:30-17:30	:	<b>Joaquin Hortal</b> Discussion about the concepts on each student's research to identify which aspect (or aspects) of biodiversity (and predictors) they need to measure and how can these be measured ( <u>Bring your own data and questions to get the most out of Joaquin!</u> )	

Thursday 11, Session Phylogeography	
09:00	: <b>Thierry Heger</b> Soil protist distribution at a local and global scale
09:15	: Coffee break
10:00	: <b>Nadir Alvarez</b> Identifying within- and among-species genetic variation using RAD sequencing: implications for ecology, evolution and systematics
11:00	: <b>Sylvain Dubey</b> Conservation genetics in threatened reptile species
12:00	: <b>Students' talks</b> (2 presentations of 15 minutes)
12:30	: Lunch in the Restaurant "Le Romarin"
	<b>Practical part</b>
14:30-17:30	: Students will be divided in 3 groups of 8-9 people and will assist to three practicals (rotation every one hour) <ul style="list-style-type: none"> <li>• <b>Thierry Heger:</b> High-throughput sequencing data: taxonomy assignment of microeukaryote sequences with QIIME</li> <li>• <b>Nadir Alvarez:</b> RADseq-based phylogenies: a case study investigating the causes of mitonuclear discordance</li> <li>• <b>Sylvain Dubey:</b> Intraspecific molecular dating in conservation</li> </ul>
<b>Disclosure for practicals</b> (Please, note that you should bring <b>your own laptop</b> )	
	<ul style="list-style-type: none"> <li>• <b>For the workshop on Tuesday</b> (MAXENT): more information will be given on that day</li> <li>• <b>For the practical on Wednesday</b> (DNA-based species delimitation methods), bring a laptop with the following softwares: <ol style="list-style-type: none"> <li>1. R (<a href="http://www.r-project.org/">http://www.r-project.org/</a>) with the packages ape, MASS and paran</li> <li>2. A web browser, such as Chrome, Safari, Explorer, etc., and a working wireless connection</li> <li>3. A text editor (e.g. NotePad, WordPad, TextWrangler, Word, etc.)</li> <li>4. An alignment editor (I suggest Mesquite (<a href="http://mesquiteproject.org/">http://mesquiteproject.org/</a>), but any other one will work)</li> <li>5. A tree viewer (I suggest FigTree (<a href="http://tree.bio.ed.ac.uk/software/figtree">http://tree.bio.ed.ac.uk/software/figtree</a>), but any other one will work)</li> <li>6. The data for this practical part will be delivered on that day</li> <li>7.</li> </ol> </li> <li>• <u>Also remember to bring your own data and questions on biogeography and macroecology for the second part of the practical:</u> Joaquin Hortal will be available for two hours to give you some advice!</li> </ul>
	<ul style="list-style-type: none"> <li>• <b>For the practical on Thursday</b>(mixed methods), bring a laptop with the following softwares: <ol style="list-style-type: none"> <li>1. BEAST 1.8 (<a href="http://beast.bio.ed.ac.uk/">http://beast.bio.ed.ac.uk/</a>)</li> <li>2. Tracer 1.6 (<a href="http://tree.bio.ed.ac.uk/software/tracer/">http://tree.bio.ed.ac.uk/software/tracer/</a>)</li> <li>3. Figtree 1.4 (<a href="http://tree.bio.ed.ac.uk/software/figtree/">http://tree.bio.ed.ac.uk/software/figtree/</a>)</li> <li>4. Arlequin 3.5 (<a href="http://cmpg.unibe.ch/software/arlequin35/">http://cmpg.unibe.ch/software/arlequin35/</a>)</li> <li>5. pyRAD 3.0 (<a href="https://github.com/dereneaton/pyrad/releases">https://github.com/dereneaton/pyrad/releases</a>)</li> <li>6. faststructure 1.0 + dependencies (<a href="http://rajanil.github.io/fastStructure/">http://rajanil.github.io/fastStructure/</a>)</li> <li>7. phyML 3.1 (<a href="http://www.atgc-montpellier.fr/phyml/binaries.php">http://www.atgc-montpellier.fr/phyml/binaries.php</a>)</li> </ol> </li> </ul>