Quantitative Evolutionary Genetics

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Dear participants,

Below you will find a schedule of the upcoming Quantitative Evolutionary Genetics course. The course will start on Monday, December 6th at 9:30 and will finish Friday, December 17th at noon. 10 students will attend the course (see list below), with two being M2 master students from the ENS Imalis program and the rest PhD students from several French and non-French institutions. Besides the faculty, we will also be joined remotely by 2 established researchers. Lectures, and some of the computer tutorials, will be in room 313 or 316 on the 3rd floor, and most will be broadcasted at the BBB site: https://bbb.bio.ens.psl.eu/b/hen-z44-2ee (please keep this link and access to the lectures private; there will be no recording).

During the afternoons of the first week several computer tutorials on data analysis will take place. During the afternoons of the second week students will work in pairs on projects simulating the evolution of quantitative traits (check the list below for the student groups). All students will present their computer project on Friday, 17th in the morning. Imalis students will be evaluated by attendance to the lectures and an oral presentation of the simulation project, all other students will have a certificate of attendance.

Lecture slides and other relevant information will be uploaded to the Moodle site during the course (https://moodle.bio.ens.psl.eu/), and also to the Owncloud site (https://cloud.biologie.ens.fr/index.php/s/Ns2d6G6FLcOpSlw), to which all students and faculty should have access to. Again, you should not share this link or contents with anybody outside the course.

We are still in the middle of the COVID pandemic and thus we all must follow common sense rules such as wearing a mask while inside the building and keeping some physical distance between each other. Most, if not all, participants are vaccinated but precautions still need to be taken.

Schedule

<u>Monday, 6</u>
9:30   "Sources of variation in quantitative traits" – H. Teotónio, room 313
14:00   "Mixed models and matrix algebra – computer tutorial" – C. Dillmann, room 313

<u>Tuesday, 7</u>
9:30   "Estimating quantitative genetic parameters" – P. de Villemereuil, room 316

14:00 "Va and heritability – computer tutorial" – P. de Villemereuil, room 313

Wednesday, 8
9:30   "Natural selection and adaptation" – P. de Villemereuil, room 316
14:00 "Estimating natural selection – computer tutorial" – P. de Villemereuil, room 313

Thursday, 9
9:30   "QTL and genome-wide association mapping" – S. Nicolas and T. Mary-Huard, room 313
14:00 "QTL and GWAS mapping – computer tutorial" – S. Nicolas and T. Mary-Huard, room 313/316

Friday, 10
9:30   "Artificial selection and genomic prediction" – T. Flutre and L. Moreau, room 316
14:00 "Genome prediction for artificial selection – computer tutorial" – T. Flutre and L. Moreau, room 313/316

Monday, 13
9:30   "The genetics of multivariate phenotypes" – A. LeRouzic, room 313
14:00 "Simulation projects" – M. Tenaillon and A. Le Rouzic, room 313

Tuesday, 14
9:30   "Experiments on adaptive landscapes" – H. Teotónio, room 316
14:00 "Simulation projects" – M. Tenaillon, D. Abu-Awad and A. Le Rouzic room 313

Wednesday, 15
9:30   "The infinitesimal model" – A. Véber, room 316
11:00 "The functional basis of dominance and epistasis" – C. Dillmann, room 316
14:00 "Simulation projects" – M. Tenaillon and D. Abu-Awad, room 313

Thursday, 16
9:30   "Evolution of quantitative traits in natural populations" – C. Teplitsky, room 316
14:00 independent student group work

Friday, 17
9:30   20-25 min group presentations of simulation projects in order (see below), room 316

Faculty

Name	position	from	email
Diala Abu-Awad	professor	Paris-Saclay Gif-sur-Yvette	diala.abu-awad@universite-paris-saclay.fr
Pierre de Villemereuil	professor	EPHE Paris	pierre.devillemereuil@ephe.psl.eu
Christine Dillmann	professor	Paris-Saclay Gif-sur-Yvette	christine.dillmann@inrae.fr
Timothée Flutre	researcher	INRAE Gif-sur-Yvette	timothee.flutre@inrae.fr
Arnaud Le Rouzic	researcher	CNRS Gif-sur-Yvette	lerouzic@egce.cnrs-gif.fr

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Céline Teplitsky	researcher	CNRS Montpellier	Celine.teplitsky@cefe.cnrs.fr
Amendine Véber	researcher	CNRS Paris	amandine.veber@cmap.polytechnique.fr

Students

Name	position	from	email
Jordan Dijoux	PhD	ERCANE Reunion	jordan.dijoux@ercane.re
Léa Fieschi-Méric	PhD	Univ Liege	leafieschimeric@gmail.com
Elizabeth Gibson	PhD	Brown University	elizabeth_gibson@brown.edu
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Tiphaine Vidal	researcher	INRAE Bioger	tiphaine.vidal@inrae.fr
Nina Vittorelli	M2	ENS Paris	vittorel@edu.bio.ens.psl.eu

Computer tutorials

During the afternoons of the first week, teachers will introduce students to a few datasets and how to analyze them to estimate basic quantitative genetic parameters. Although we will have common computers it would be good if you bring own. Most demonstrations will be done using R/RStudio, GitHub and Bioconductor, which you can download and install in your computer beforehand (https://www.rstudio.com/, https://github.com/, https://www.bioconductor.org/). Several packages within these will then be installed during the course.

Simulation Projects

Students will work in groups of two during the second week of the course, and will both present their simulation project in the last day. There are five projects, each about understanding the role of different factors in the evolution of quantitative traits. Although you will have access to common computers it is better if you work with own computer to do the simulations. The projects are assigned as follows (though you can change if you really want to work on a particular topic; let's us know during the first week):

project	topic	group	
1	mutation	Jordan Dijoux	Léa Fieschi-Méric
2	dominance	Lukas Metzger	Tom Parée
3	recombination	Nina Vittorelli	Laura-Li Jeannot
4	selfing	Elizabeth Gibson	Claire Lescoat
5	fitness	Michel Turbet-Delof	Apolline Petit