







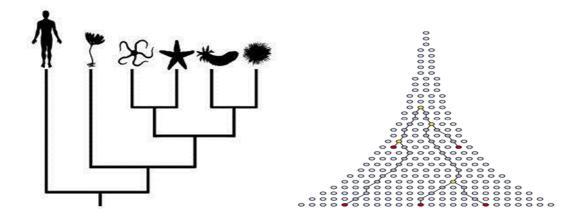


Bridging Phylogeny and Population genetics: Inferring divergence and selection at both interspecies and intraspecies level

Dates: 27 August-1 September 2019.

Venue: The Campus at Fondazione Edmund Mach in San Michele all'Adige (Trento, Italy between mountains and vineyards, http://www.fmach.it/eng), and The Botanical Garden of University of Padua (the world oldest botanical garden, http://www.ortobotanicopd.it/en).

Scientific content: Phylogeny studies inter-specific variations and typically describes the macroveolutionary changes of organisms over long time scales; population genetics instead typically focuses on the intra-species variability and describes microevolutionary changes occurred during the relatively recent history of a population. The two disciplines are characterised by different tools and methods, and too often phylogeneticists do not understand what population geneticists do, and vice versa. With this course we aim at stimulating a dialogue and a constructive discussion between students and teachers with phylogenetics, population genetics, but also ecological backgrounds, in such a way that we can appreciate the complementary nature of these disciplines. All students should be united by the will to understand better each other's methodological processes. The aim is to form students that are capable of understanding both approaches and filling the gap between the two disciplines. We will do this by providing the theoretical and practical bases of both phylogenetics and population genetics. The course will cover some important applications such as detection of positive selection using PAML, site frequency spectrum analysis using Sweepfinder, inference of divergence time using BEAST, inference of population past demography using Fastsimcoal. Every day we will alternate topics on PHYLOgenetics, POPulation genetics, and a MIXture of them.



Teachers:

Lino Ometto (evolutionary zoologist, University of Pavia)

Emiliano Trucchi (population geneticist, Marche Polytechnic University and University of Oslo)

Omar Rota-Stabelli (molecular phylogeneticist, Fondazione Edmund Mach)

Francesca Cagnacci (Movement Ecologist, Fondazione Edmund Mach)

Daniele Silvestro (molecular phylogeneticist, University of Gothenburg)

Erlend Nilsen (population ecologist, NINA- Norway)

Participation: This course is aimed at PhD students, but participation of post-docs, researchers, managers and motivated MSc is also encouraged. There will be room for a maximum of 25 participants, with priority given to students from the IRSAE network and the SIBE society.

Fees and costs: The course is supported by the International Research School in Applied Ecology (IRSAE www.irsae.no), and co-organized by Fondazione Edmund Mach, NINA, and the Italian Society for Evolutionary Biology. Fees and costs vary according to affiliations. IRSAE participants: Fees, board and lodging are covered by the IRSAE network; they may also obtain reimbursement for travel costs through IRSAE and their institution. SIBE members pay no fees. Otherwise, students: 130€; Researchers/Seniors: 250€. In all cases food (lunch+dinner) plus lodging in the campus can be booked at 80 €/day. Alternative lodging possibilities are available in the area.

5 ECTS credits will be assigned, after positive grades in a final exam.

Format: This 5 days course consists of a meet and greet evening + three full days with technical seminars and practical labs + one day of excursion to nearby hut with symposium and lectures + a trip to Padua (2h bus drive, organised and paid by the school) with final lectures. For those interested is possible to extend the staying in Padova to attend the congress of the Italian Society for Evolutionary Biology https://sibe2019.sibe-iseb.it/; the first day of the congress is free for students; to attend full meeting registration is required.

Registration: Please send an Email (with subject: Phylo-PopSchool2019), containing a brief description of your PhD project and a description of the relevance of the course to your research, along with your CV, to Omar Rota Stabelli (omar.rota@fmach.it), cced to Henriette Gelink (henriette.gelink@inn.no). Deadline: 25th June, 2019. Notification of acceptance: 28th June, 2019. More and upcoming info/material on: http://irsae.no/courses-conferences-and-workshops/upcoming-courses

Organizers: Omar Rota-Stabelli & Francesca Cagnacci, Research and Innovation Centre, Fondazione Edmund Mach; Erlend B. Nilsen, NINA, Norway



The Fondazione Edmund Mach in San Michele all' Adige.

COURSE SCHEDULE:

Tue 27 th August Welcome	6 pm	Arrival & Meet and Greed
	Evening: MIX	Why merging phylogeneticists and population geneticists? (all teachers)
Wed 28 th August Lectures + practical	am: PHYLO	Introduction to Phylogeny for population geneticists (Rota-Stabelli) Hands-on lab for begenniers (Rota-Stabelli);
	pm: POP	Introduction to Population genetics for phylogeneticists (Ometto and Trucchi) Hands-on lab for beginners (Ometto and Trucchi).
	Evening: MIX	Students flash presentations of their work
Thur 29 th August Lectures + practical	am: PHYLO	Phylogenomics and the harvest of orthologs (Ometto, Rota-Stabelli) Hands on with reciprocal blast (Ometto)
	pm: POP	Inferring demographic parameters from population genomic data (Trucchi) Hands-on on Fastsimcoal2 / Stairway plot (Trucchi)
	Evening: MIX	Learning some Evolutionary principles using the hystory of human beverages (Ometto and Rota-Stabelli)
Fri 30 th August Excursion + lectures	Am: EXCURSION	Trip to a nearby mountain hut (Malga Kraun)
	Pm: MIX	Population and Movement Ecology what could be the interactions with phylo/pop genetics? (Cagnacci) Biogeography concerns studying population ecology and genetics (Nielsen)
	Evening: MIX	"The coalescence: when population meets phylogeny (all teachers)"
Sat 31 st August Lectures + practical	Am: PHYLO	Inferring patterns and selection from phylogenomic data (Ometto) Hands-on on dN-dS using PAML (Ometto)
	Am_MIX	Validating (or breaking) the principles of phylogenetic comparative methods in the light of microevolution (Silvestro)
	Pm: POP	Inference of selection from population genomic data (Trucchi) Hands-on on Sweepfinder2 (Trucchi)
	Evening: MIXING	Bayesian joint estimation of molecular co-evolution and phylogenetic relationships (Silvestro)
Sun 1 st September Trip to Padova + lectures	am PHYLO	7:00 BUS to Orto Botanico, Padova 10:00 Inferring divergence from molecular data using BEAST (Rota-Stabelli)
	Pm PHYLO+	14:30 SIBE Congress starts (first day free to course students) 15:00 Inferring macroevolutionary processes from phylogenies and fossils (Silvestro) as part of the Sympoisum Phylogenetics, Phylogenomics & Phylogeography
	evening	7:00 Cocktail in Orto Botanico 7:30 Music event (SIBE'S GOT TALENT) at SIBE congress. Open to everybody.



The Botanical Garden of the University of Padua