EE COURSE 2023
EXPERIMENTAL EVOLUTION VIENNA

Experimental Evolution: Exploring Evolutionary Forces in Controlled Environments

University of Veterinary Medicine, Nov 27 - Dec 1, 2023

	time/location	Monday (27.11.23)	Tuesday (28.11.23)	Wednesday (29.11.23)	Thursday (30.11.23)	Friday (1.12.23)
Lectures		**Lecture Hall D (Building GA)**				
	09:00-10:30	**Henrique Teotónio:** Introduction to Experimental Evolution and a few case studies	**Elina Immonen:** Genomic signatures of sex-specific selection	**Michael Desai:** Inferring the structure of genotype-phenotype maps	**Christian Schlötterer:** Experimental evolution in Drosophila	**Elina Immonen:** Experimental evolution of sexual dimorphism
	10:30-11.00	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break - Group picture
	11:00-12:30	**Christian Schlötterer:** Experimental design of E&R studies	**Adam Chippindale:** The Evolutionary Theory of Ageing: What we know (and don't know) from four decades of selection experiments	**Henrique Teotónio:** Adaptation and selection on a recombination modifier	**Michael Desai:** Binding affinity landscapes for immune-viral coevolution	**Adam Chippindale:** Sexual Conflict: Arms race or tug-of-war?
	12:30-14:00	Lunch break	Lunch break	Lunch break	Lunch break	Lunch break

	time/location					
Practicals*		**Computer Room, Institute of Population Genetics, 4th floor (Building HA)**				
	14:00-16:00	*Simulations of E&R under neutrality and selection - SLIM* (**Changyi Xiao, Diogo Ribeiro**)	*Testing for selection with and without time series data - R* (**Sara Duarri Redondo, Changyi Xiao**)	*Haplotype reconstruction - R* (**Sara Duarri Redondo, Yiwen Chen**)	*Microbiome analysis in EE - R* (**Juan Bosco Gracia Alvira**)	*Detecting selection from transcriptomic data - R* (**Dagný Ásta Thorhölludottir, Tejashwini Hegde**)
	16:00-16.30	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break
	16:30-18:30	*Simulations of E&R under neutrality and selection - SLIM* (**Changyi Xiao, Diogo Ribeiro**)	*Testing for selection with and without time series data - R* (**Sara Duarri Redondo, Changyi Xiao**)	*Haplotype reconstruction - R* (**Sara Duarri Redondo, Yiwen Chen**)	*TE analysis* (**Matt Beaumont, Riccardo Pianezza**)	*Detecting selection from transcriptomic data - R* (**Dagný Ásta Thorhölludottir, Tejashwini Hegde**)

*only workshop participants