

## Rencontres Interdisciplinaires de l'Évolution Moléculaire Alphy/AIEM 23-25th of January 2023, Amphithéâtre Boucherle, Bâtiment Boucherle, Campus Santé de la Tronche, U. Grenoble Alpes

Final program

Monday, January 23 <sup>rd</sup> 2023		Tuesday, January 24 <sup>th</sup> 2023		Wednesday, January 25 <sup>th</sup> 2023	
		8h30	Opening	8h30	Opening
		9h00	Invited speaker - Anne-Florence Bitbol - Optimization and historical contingency in protein sequences	9h00	Jean-Baptiste Grodwohl - Opening Motor Kimura's archives: on the history of molecular evolution and the neutralist scho
		9h45	Ignacio Bravo - Transcriptomic, proteomic and functional cis- and trans-acting effects in human cells of gene expression with varying codon usage preferences, in a long-term selection experiment	9h20	Leonardo Trujillo - Adaptive walks don't do walks on hypercubes
		10h05	Luca Nesterenko - Phyloformer: Towards fast and accurate phylogeny reconstruction with self-attention networks	9h40	Thibaut Capblancq - In search of islands speciation in the genomes of two Coenonympha butterfly sister species
		10h25	Coffee break	10h00	Elise Gay - Mitonuclear discordance in the great white shark (Carcharodon carcharias sex biased dispersal, mitonuclear incompatibility, or both?
		10h55	Florian Bénitière - Investigating the impact of random genetic drift on synonymous codon usage in metazoans	10h20	Coffee break
		11h15	Margaux Jullien – COCOATree: benchmarking coevolution methods for sector identification	10h50	Alia Abbara - Spatially structured populations on graphs beyond update rule
13h00	Welcome coffee and registration	11h35	Romain Feron - Reproducible workflows to study conservation of genomic sequence using multispecies whole genome alignments	11h10	Thomas Forest - Birds demography inference based on genomic data
13h30	Introduction	11h55	Rémi-Vinh Coudert - MPS-Sampling (Multi Proteins Similarity Sampling) to select evolutionary significant representative genomes from large databases	11h30	Riccardo Poloni - Genetics and genomics help understanding the colour polymorphis in the invasive Box Tree Moth
13h45	Invited speaker - François Parcy - Evolution of the floral regulator LEAFY	12h05	Lea Bou Dagher - Evolutionary signal captured from topological properties of proteins via persistent homology	11h50	Matthieu Joron - Subtle signals of adaptive introgression in the late stages of the speciation continuum
14h30	Paul Zaharias - Robustness of Felsenstein's versus Transfer Bootstrap Supports with respect to Taxon Sampling	12h25	Lunch break	12h20	Conclusion
14h50	Nisha Dwivedi - Resolving the evolutionary history of Nesoenas picturata in the Mascarenes	14h00	Invited speaker - Mathieu Groussin - Evolution of host-gut microbiome interactions in the context of industrialization	12h30	Lunch (to go)
15h10	Clément Gain - A quantitative theory for genomic offset statistics	14h45	Flora Gaudillière - Understanding the evolutionary dynamics of insertion sequences in prokaryotic genomes		
15h30	Cofffee break	15h05	Fanny Mazzamurro - Evolution of natural transformation in bacteria		
16h00	Marie Raynaud - Population genomics reveal PRDM9-dependent recombination landscapes in salmonids	15h25	Sophie-Carole Chobert - Unraveling the relative emergence of quinones biosynthetic pathways		
16h20	Thibault Latrille - Up to 25% of beneficial mutations in protein sequences are not adaptive innovations in mammals	15h45	Coffee break		
16h40	Julien Joseph - Recombination and selection efficiency in humans	16h15	Guillaume Louvel - Causes of discord in eukaryotic protein domains inherited from Archaea		
17h00	Antoine Taupenot - Social polymorphism and supergene in the ant Myrmecina graminicola: insights from population genomics	16h35	Anton Crombach - Cell type diversification across paleo- and neocortex revealed by single cell multiomics analysis		
17h20	Poster session & beers	16h55	Jasmine Gamblin - Beyond one-gain models for pangenome evolution		
19h00	End of first day	17h15	Charles Coluzzi - Epistatic interactions between genetic background and antibiotic resistances genes (and vice versa)		
		17h35	Mélodie Bastian - Bridging the gap between population genomic and phylogenetic approaches by the study of the effective population size		
		20h00	Gala dinner @Bouillon A		