



Tuesday, May 27th

08:00 Participants welcoming

08:45 Workshop opening – **Dominique Joly and Guy Perrière**

Session 1 – Phylogeny (chair: G. Perrière)

09:00 Spotlight on the Thaumarchaeota – **Céline Brochier-Armanet** (Laboratoire de Biométrie et Biologie Evolutive, Lyon), invited talk

09:30 Depicting the microbial diversity from high-throughput sequencing amplicons: a phylogenetic approach – **Najwa Taib** (Laboratoire Microorganismes : Génome et Environnement, Aubière)

09:50 RADseq, phylogenies and estimation of genetic diversity – **Marie Cariou** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)

10:10 Empirical assessment of RAD sequencing for interspecific phylogeny – **Astrid Cruaud** (Centre de Biologie pour la Gestion des Populations, Montferrier-sur-Lez)

10:30 **Coffee break and posters**

Session 2 – Phylogeny and taxonomic assignation (chair: L. Le Gall)

11:00 Robust estimation of phylogenetic diversity: steer clear of rare species – **Thibault Latrille** (Ecole Normale Supérieure de Lyon)

11:20 Co-phylogeny reconstruction via an Approximate Bayesian Computation – **Christian Baudet** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)

11:40 Examining the bacterial diversity of oligotrophic soil environments using metagenomic approaches – **Michael DuBow** (Laboratoire de Génomique et Biodiversité Microbienne des Biofilms, Orsay)

12:00 Bioenergetic use of arsenic in haloarchaea revealed by metagenomic analysis – **Nicolas Rascovan** (Institute of Agrobiotechnology of Rosario)

12:20 SortMeRNA2: ribosomal RNA classification for taxonomic assignation – **Hélène Touzet** (Laboratoire d'Informatique Fondamentale de Lille)

12:40 **Lunch and posters**

Session 3 – Diversity analysis (chair: D. Joly)

14:00 The use of metabarcoding in monitoring of biological diversity: some notes on complementarity and validation – **Nigel Gilles Yoccoz** (The Arctic University of Norway, Tromsø), invited talk

14:30 GnS-PIPE: an optimized bioinformatic pipeline to efficiently assess microbial taxonomic diversity of complex environments using high throughput sequencing technologies – **Sébastien Terrat** (Plateforme GenoSol, Dijon)

14:50 High-throughput molecular ecology of carabid beetles: trophic interactions and pest control – **Stefaniya Kamenova** (Centre d'Etudes Biologiques de Chizé)

15:10 Protist community structure in coastal arctic environments: does ocean acidification affect marine microbes? – **Lucie Bittner** (Institut de Biologie Paris Seine)

15:30 Evidence for a core bacterial microbiota among geographically and genetically different populations of the tiger mosquito *Aedes albopictus* – **Guillaume Minard** (Laboratoire d'Ecologie Microbienne, Lyon)

15:50 Toward solving the mystery of “chameleon” cyanobacteria – **Laurence Garczarek** (Station Biologique de Roscoff)

16:10 **Coffee break and posters**

Session 4 – Metagenomics (chair: E. Pelletier)

16:40 Non invasive identification of past oral microbial flora – **Olivier Gorgé** (Institut Jacques Monod, Paris)

17:00 The Arctic snowpack microbial community highlighted by metagenomics and metatranscriptomics – **Lorrie Maccario** (Laboratoire Ampère, Lyon)

17:20 Rhizosphere heterogeneity shapes abundance and activity of sulfur-oxidizing bacteria in vegetated salt marsh sediments – **François Thomas** (Laboratoire Interdisciplinaire des Environnements Continentaux, Nancy)

17:40 Poster session and RTP-GE scientific committee meeting

19:30 **Buffet dinner**



Wednesday, May 28th

Session 5 – Barcoding and population genomics (chair: J.Y. Rasplus)

09:00 High-throughput molecular barcoding as a tool for assessment and monitoring the environmental impact associated with aquaculture – **Jan Pawlowski** (Department of Genetics and Evolution, Geneva), invited talk

09:30 Speciation, hybridization, and introgression among three closely-related butterfly species in the Alps – **Thibaut Capblancq** (Laboratoire d'Ecologie Alpine, Grenoble)

09:50 Comparative Pop(pool)ation genomics of two chronotypes of the metazoan parasite *Schistosoma mansoni*: insights into adaptation to a new host – **Eve Toulza** (Laboratoire Ecologie et Evolution des Interactions, Perpignan)

10:10 Genome analyses of symbiont-bearing trypanosomatids indicate that the bacterium is essential for amino acid and vitamin production – **Cecilia Coimbra Klein** (Laboratório Nacional de Computação Científica, Petrópolis)

10:30 Coffee break and posters

Session 6 – Sequence analysis (chair: M. DuBow)

11:00 RecStat: a set of R utilities for Coding DNA Sequences prediction in metagenomes – **Guy Perrière** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)

11:20 UrQt: unsupervised quality trimming for NGS data – **Laurent Modolo** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)

11:40 MacSyFinder: mining genomes for molecular systems – **Sophie Abby** (Laboratoire de Génomique Evolutive des Microbes, Paris)

12:00 *De novo* transcriptome assembly for a non model species, the blood-sucking bug *Triatoma brasiliensis*, a vector of Chagas disease – **Axelle Marchant** (Laboratoire Evolution, Génomes et Spéciation, Gif-sur-Yvette)

12:20 A framework for identifying sex-linked genes using RNAseq data – **Aline Muyle** (Laboratoire de Biométrie et Biologie Evolutive, Lyon)

12:40 Lunch and posters

Session 7 – Genomics and metabolism (chair: D. Faure)

14:00 *Wolbachia* through time: palaeosymbiology – **Mark Blaxter** (Institute of Evolutionary Biology, Edinburgh), invited talk

14:30 Metabolic response of a planktonic ecosystem to environmental perturbation – **Amos Kirilovsky** (Génoscope-Centre National de Séquençage, Evry)

14:50 What are the most abundant genes in marine plankton? – **Magali Lescot** (Laboratoire Information Génomique et Structurale, Marseille)

15:10 Use of single cell amplified genome and metatranscriptomics to survey *Pelagomonas calceolata* metabolism – **Bonora Mario Neou** (Génoscope-Centre National de Séquençage, Evry)

15:30 End of the workshop