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 (École 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 Microbiennne 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 bionformatic 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’Écologie 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)ulation 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 (Laboratorio 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)