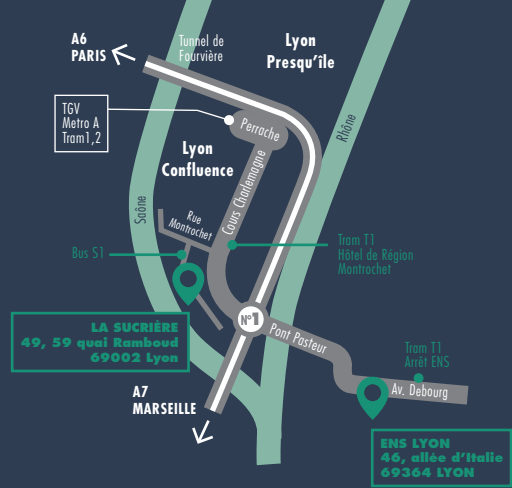


Plan



Sponsors



Jeudi 30 juin

SESSION PLÉNIÈRE 6 - Amphi Mérieux BIOLOGIE DES SYSTÈMES ET RÉSEAUX D'INTERACTIONS (D. Kahn)

09h00 - 10h00 ■ Conférencier invité : S. Aerts
Decoding regulatory landscapes in cancer

10h00 - 10h20 ■ Studying microRNAs
with a system biology approach (L. Guyon)

10h20 - 10h50 ■ Pause café

10h50 - 11h10 ■ The PADMet toolbox :
handling the heterogeneity of data (M. Chevallier)

11h10 - 11h30 ■ Comparative transcriptomic of rodent molars
reveals developmental system drift. (C. Petit)

11h30 - 11h50 ■ Single-cell-based analysis of differentiation (A. Richard)

11h50 - 12h00 ■ Présentation JEBIF (J. Fumey)

12h00 - 13h30 ■ Pause déjeuner

SESSION PLÉNIÈRE 7 - Amphi Mérieux BIOINFORMATIQUE STRUCTURALE (G. Déléage)

13h30 - 14h30 ■ Conférencière invitée : I. Callebaut
Exploring the dark matter proteomes using fold signatures

SESSIONS PARALLÈLES 4

BIOINFORMATIQUE STRUCTURALE (G. Déléage) - Amphi Mérieux

- 14h40 ■ ORION: hybrid profiles for fold recognition (J.-C. Gelly)
- 15h00 ■ Homology-modeling of complex structural RNAs (W. Wang)
- 15h20 ■ ThreaDNA: DNA deformation energy in regulatory protein sequence selectivity (S. Meyer)
- 15h40 ■ Modeling Ebola UTR Structures using SHAPE (A. Saaidi)

DONNÉES CELLULES UNIQUES (A. Siegel) - Salle place de l'école

- 14h40 ■ Modelling gene regulatory networks at single-cell level (U. Herbach)
- 15h00 ■ Count Matrix Factorization and Single Cell Data Analysis (G. Durif)
- 15h20 ■ Stochasticity and Differentiation (A. Guillemin)
- 15h40 ■ TSS-RNAseq study of the NMD targets (C. Malabat)

BIOINFORMATIQUE POUR LA SANTÉ (Y. Vandenbrouck) - Salle des thèses

- 14h40 ■ Vidjil, a platform for interactive analysis of immune repertoires (M. Salson)
- 15h00 ■ Identification of integrin beta-8 regulatory elements by ATAC-Seq (M.-L. Endale Ahanda)
- 15h20 ■ U-BIOPRED focused blood handprint (R. Tching Chi Yen)

16h00 - 16h30 ■ Pause café

SESSION PLÉNIÈRE 8 - Amphi Mérieux

- 16h00 - 16h10 ■ Remise des prix SFBI (M. Thomas-Chollier)
- 16h10 - 16h20 ■ Remise des prix concours Biolnfuse (J. Fumey)
- 16h20 - 16h30 ■ Annonce JOBIM 2017 (G. Marot J.-S. Varré)

CLÔTURE

JOURNÉES OUVERTES
DE BIOLOGIE
INFORMATIQUE
& MATHÉMATIQUES

28 > 30
JUIN
ENS LYON



Mardi 28 juin

DISCOURS D'ACCUEIL - Amphi Mérieux

- 09h00 - 09h10 | Discours de bienvenue (F. Picard)
- 09h10 - 09h20 | Discours de la direction de la recherche, ENS de Lyon (Y. Ricard)
- 09h20 - 09h30 | Discours du vice président recherche, Université Lyon 1 (F. Vallée)

SESSION PLÉNIÈRE 1 - Amphi Mérieux STATISTIQUE DES DONNÉES À HAUT DÉBIT (F. Picard)

09h30 - 10h30 | Conférencier invité : R. Gentleman
Adventures in mRNA splicing

10h30 - 11h00 | Pause café

- 11h00 - 11h20 | Multivariate feature selection with mixOmics (F. Rohart)
- 11h20 - 11h40 | Eigen-Epistasis for detecting Gene-Gene interactions in GWAS (V. Stanislas)
- 11h40 - 12h00 | Identification of 3D Chromatin Organization Features (R. Mourad)

12h00 - 13h30 | Pause déjeuner

SESSION PLÉNIÈRE 2 - Amphi Mérieux PHYLOGÉNIE, EVOLUTION (G. Perrière)

13h30 - 14h30 | Conférencier invité : Alexandros Stamatakis
Challenges and problems in phylogenetic inference and bioinformatics

SESSIONS PARALLÈLES 1

PHYLOGÉNIE (G. Perrière) - Amphi Mérieux

- 14h40 | Detection of molecular convergent evolution signatures (O. Chabrol)
- 15h00 | Lifemap: exploring the entire tree of life (D. de Vienne)
- 15h20 | Joining different levels of molecular evolution (W. Duchemin)
- 15h40 | Robustness of the Parsimonious Reconciliation Method in Cophylogeny (L. Urbini)

STATISTIQUE (C. Matias) - Salle place de l'école

- 14h40 | Statistical Significance for sequence analysis including local score length (S. Mercier)
- 15h00 | Machine learning and the genetic basis of host-pathogen interactions (M. Vignes)
- 15h20 | Latent Block Model for Metagenomic data (J. Aubert)
- 15h40 | Statistical modelling of expression patterns in hybrid species (M. Vignes)

SÉQUENCES PROTÉIQUES (J. Martin) - Salle des thèses

- 14h40 | Large scale analysis of amyloidogenic proteins from 93 proteomes (E. Villain)
- 15h00 | Identification and large scale analysis of tandem repeats in proteomes (F. Richard)
- 15h20 | De novo protein domain discovery from Blast and co-occurrence (C. Menichelli)

16h00 - 16h30 | Pause café

SESSIONS PARALLÈLES 2

PHYLOGÉNIE (G. Perrière) - Amphi Mérieux

- 16h30 | BAT finder: alternative transcript selection in multiple sequence alignments (H. Philippon)
- 16h50 | Change-point detection on a tree to study evolutionary adaptation (P. Bastide)
- 17h10 | Dating with Transfers (A. Davin)

DÉMOS (G. Beslon) - Salle place de l'école

- 16h30 | Web portal for type IV effectors prediction and effectomes comparison (C. Noroy)
- 16h50 | DockNmine, a web portal for ligand binding annotations (S. Téletchéa)
- 17h10 | RiboDB : A dedicated database of prokaryotic ribosomal proteins (F. Jauffrit)

SÉQUENCES NUCLÉIQUES (L. Brinza) - Salle des thèses

- 16h30 | Indexing annotated DNA sequences (T. Rocher)
- 16h50 | Detection of mutated primers and impact on targeted metagenomics results (A. Antoine-Lorquin)
- 17h10 | Sequencing a large plant Y chromosome using the MinION (C. Fruchard)

SESSION POSTER

17h30 - 18h30 | Session posters (Atrium, Salle place de l'école)

18h30 - 20h00 | Apéritif dinatoire à l'Atrium

Mercredi 29 juin

SESSION PLÉNIÈRE 3 - Amphi Mérieux GÉNOMIQUE DES POPULATIONS (L. Duret)

09h00 - 10h00 | Conférencier invité : Louis Lambrecht
Integrative population genomics of mosquito-arbovirus interactions

10h00 - 10h20 | tess3r: a R package for estimating spatial population structure (K. Caye)

10h20 - 10h50 | Pause café

- 10h50 - 11h10 | Prediction and characterization of ciliary proteins by comparative genomics (Y. Nevers)
- 11h10 - 11h30 | Comparative genomics on artificial life (C. Knibbe)
- 11h30 - 11h50 | Joint scaffolding of extant and ancestral genomes (Y. Anselmetti)

11h50 - 13h30 | Pause déjeuner

SESSION PLÉNIÈRE 4 - Amphi Mérieux MÉTAGÉNOMIQUE ET MÉTABARCODING (M. Mariadassou)

13h30 - 14h30 | Conférencier invité : J. Raes
Population level analysis of the human microbiome

SESSIONS PARALLÈLES 3

ÉVOLUTION MOLÉCULAIRE (H. Chiapello) - Amphi Mérieux

- 14h40 | FTAG Finder: determining gene families and TAGs with Galaxy (B. Bouillon)
- 15h00 | Evolution of gene regulation in 20 mammals (C. Berthelot)
- 15h20 | Evolution of internal eliminated sequences in Paramecium (D. Sellis)
- 15h40 | IntegronFinder reveals unexpected patterns of integron evolution (J. Cury)

DÉMOS (B. Audit) - Salle place de l'école

- 14h40 | Meta-analysis of transcriptomic data with Galaxy (S. Blanck)
- 15h00 | SHAMAN : a shiny application for quantitative metagenomic analysis (A. Ghozlane)
- 15h20 | Quick comparison of NGS experiments with Heat-seq. (G. Devailly)
- 15h40 | Customized molecular evolution with bio++ (L. Guéguen)

ÉTUDES D'ASSOCIATION (V. Lacroix) - Salle des thèses

- 14h40 | Encoding genomic variation using De Bruijn Graphs in Bacterial GWAS (M. Jaillard)
- 15h00 | Detecting low frequency somatic mutations with needlstack (T. Delhomme)
- 15h20 | De novo identification of SNPs from RNAseq data for non model species (H. Lopez-Maestre)
- 15h40 | Bacterial ionizing radiation resistance prediction (Z. Manel)

16h00 - 16h30 | Pause café

SESSION PLÉNIÈRE 5 - Amphi Mérieux ASSEMBLÉES GÉNÉRALES

- 16h30 - 17h00 | AG du GDR Bioinformatique Moléculaire (BIM) (H. Touzet)
- 17h00 - 17h30 | IFB (J.-F. Gibrat)
- 17h30 - 18h30 | AG membres SFBI (S. Schbath)

SESSION POSTER

17h30 - 19h30 | Session posters (Atrium, Salle place de l'école)

20h00 - 01h00 | Repas de Gala à La Sucrière

