

TUESDAY, JULY 10

- 8:30-9:45 Welcoming of the attendees
9:45-10:00 Introduction

Session 1- Evolution, Phylogeny and Comparative Genomics

Chairman: Etienne Pardoux

- 10:00-11:00 **Invited Speaker: Manolo Gouy:** Apports de la génomique comparative à l'étude de l'évolution des mitochondries chez les protistes
- 11:00-11:20 Phylogeny of nitrogen fixation in Bacteria and Archaea, Nicolas Blavet and **Guy Perrière**
- 11:20-11:50 Coffee Break-Posters
- 11:50-12:10 A new phylogeny-based method to detect sites under evolutionary constraint in proteins, **Julien Dutheil**
- 12:10-12:30 Représentation Matricielle sans Parcimonie, Alexis Criscuolo and Vincent Ranwez
- 12:30-12:35 Assessing the utility of single-copy genes present as orthologs in most fungal genomes for building robust phylogenies, **Gabriela Aguilera**, Sylvain Marthey, Hélène Chiapello, Elisabeth Fournier and François Rodolphe, Annie Gendrault-Jacquemard, Marc-Henri Lebrun and Tatiana Giraud
- 12:35-12:40 Des gènes viraux dans les génomes des Archaea et Bactéries et l'hypothèse du réservoir viral pour l'origine des ORFans, **Diego Cortez**, Simonetta Gribaldo and Patrick Forterre
- 12:40-12:45 Horizontal gene transfer detection in mollicute bacteria, Aurélien Barre, Pascal Sirand Pugnet, Alain Blanchard and Christine Citti
- 12:45-12:50 Genome evolution: 'en bloc' duplication and positive selection, **Elodie Darbo** and Pierre Pontarotti
- 12:50-12:55 Génomique comparative des *Borrelia* et évolution adaptative de *Borrelia recurrentis*, **Magali Lescot**, Stéphane Audic, Catherine Robert, Guillaume Blanc, Sally J. Cutler, Didier Raoult, Jean-Michel Claverie et Michel Drancourt
- 12:55-13:00 GENOMICRO: comparative genomics at small evolutionary scale, **Vincent Lombard** and Laurent Duret
- 13:00-13:05 DrosOCB: a high resolution map of conserved non coding sequences in Drosophila, **Loredana Martignetti**, Michele Caselle, Bernard Jacq and Carl Herrmann

13:05 Lunch

Session 2- Algorithms and Statistics for Sequence Analysis and Genomics

Chairman: Bernard Prum

- 14:30-15:30 **Invited Speaker- Robert Giegerich:** Dynamic Programming -- the Cool Way
- 15:30-15:50 DARN! A soft constraint solver for RNA motif localization, **Matthias Zytnicki**, Christine Gaspin and Thomas Schiex
- 15:50-16:50 Coffee Break-Posters

- 16:50-17:10 Statistical tests to compare motif count exceptionalities, Stéphane Robin, **Sophie Schbath** and V. Vandewalle
- 17:10-17:30 Estimating genetic richness in EST libraries, **Hugues Richard** and Martin Vingron
- 17:30-17:35 Local similarities and clustering of biological sequences: new insights from N-local decoding, Eduardo Corel, Ramzi El Feghali, Fanny Gerardin, Mark Hoebeke, Marc Nadal, Alexandra Louis, Ivan Laprevotte, Alexandre Grossmann and Claudine Devauchelle
- 17:35-17:40 Composition Shifting Site Analyser (ComSSA): Interactive compositional, functional and structural interpretation of multiple sequence alignments, Thomas Bernard, Philippe Lieutaud, Etienne Danchin, Stephen G Withers, Bernard Henrissat and Pedro Coutinho
- 17:40-17:45 Statistical test for conserved genomic regions, **Simona Grusea**, Etienne Pardoux, Virginie Lopez-Rascal and Pierre Pontarotti

Session 3- Text Mining and Ontologies

Chairman: Bernard Jacq

- 17:45-18:05 Analyse des formes prédicatives dans des textes biomédicaux, pour l'identification d'interactions géniques, Elisabeth Godbert, M. Madhi Malik and Jean Royaute
- 18:05-18:10 Extraction d'Information pour le ciblage des gènes impliqués dans les maladies génétiques, **Mouna Kamel** and Eric Perret
- 18:10-18:15 Using knowledge about pathways as an organizing principle for disease ontologies, **Julie Chabali**, Olivier Dameron and Anita Burgun

18:15 Cocktail-Aperitif

WEDNESDAY, JULY 11

Session 4- Gene, Genome and Protein Organization

Chairman: Jean-Michel Claverie

- 9:30-10:30 **Invited Speaker: Jean-Philippe Vert:** Supervised reconstruction of biological networks
- 10:30-10:50 A new type of Hidden Markov Models to predict complex domain architecture in protein sequences, **Raluca Uricaru**, Laurent Brehelin and Eric Rivals
- 10:50-11:20 Coffee Break-Posters
- 11:20-11:40 Swelfe : analyse de la dynamique de répétition chez les gènes, les protéines et leurs structures, **Anne-Laure Abraham**, Joel Pothier and Eduardo Rocha
- 11:40-12:00 Certains gènes (ou parties de gènes) transférés horizontalement participent rapidement à l'évolution modulaire des protéines d'un hôte, **Sophie Pasek**, Jean-Luc Ferat, Mark Hoebeke, and Pierre Brezellec
- 12:00-12:20 Microsatellites et mutabilité des fonctions cellulaires chez l'homme, **Etienne Loire**, Françoise Praz, Dominique Higué, Pierre Netter and Guillaume Achaz

- 12:20-12:25 Genome-wide identification of splicing variants in the human genome, **Fabien Rouet**, Diego Pallares, Cyril Soucaille, Seth Jonhson, Richard Einstein, Laurent Bracco and Mike Brenner
- 12:25-12:30 Analysis of four polymorphic minisatellites suggests frequent genetic exchanges among House Mouse subspecies, **Eric Rivals**, François Bonhomme, Annie Orth, Gemma Grant, Alec Jeffreys and Philippe Bois
- 12:30-12:35 When repeats meet chromatin: Relationship between repeats and heterochromatin dynamics, Anna-Sophie Fiston-Lavier, Charles Vejnar and Hadi Quesneville
- 12:35-12:40 Looking for bladder cancer progression pathways in Comparative Genomic Hybridization data, **Eric Letouzé**, France Loirat, Yves Allory, Emmanuel Barillot, François Radvanyi and Frédéric Guyon
- 12:40-12:45 Microarray based exploration of pri-MiR transcripts, Karine Robbe, Bruno Cardinaud, Kevin Lebrigand and Pascal Barbry
- 12:45-12:50 GINCOS: a method to normalize Affymetrix GeneChip Human Mapping 50K Set, **Guillem Rigail**, Philippe Hupe, Jean-Philippe Meyniel, Charles Decraene and Emmanuel Barillot
- 12:50-12:55 Microarray reporter quality control and design with miQC, **Samuel Granjeaud**, Emmanuel Beaudoin, Julien Textoris, Fabrice Lopez and Pascal Hingamp
- 12:55-13:00 DBF-MCL a new algorithm for rapidly and accurately extracting cluster of co-regulated genes from microarray data, **Julien Textoris**, Fabrice Lopez, Elisabeth Remy, Samuel Granjeaud, Cathy Nguyen and Denis Puthier

13:00 Lunch

Session 4- Gene, Genome and Protein Organization (end)

Chairman: Alain Viari

- 14:30-14:35 Mapping of *cis*-regulatory regions in T cell-specific genes using genome-wide location analysis, **Touati Benoukraf**, Sebastien Jaeger, Salvatore Spicuglia and Pierre Ferrier
- 14:35-14:40 Discovery of Novel *Cis*-regulatory Elements in the IL2RA Gene and IL-2 Co-expressed Genes, Pierre Cauchy, Frederic Rosa, Marielle Bedotto, Denis Thieffry, and Jean Imbert
- 14:40-14:45 InSide4D : A cross species expression pattern database, Yannick Haudry and Thorsten Henrich
- 14:45-14:50 Digital representation of embryonic development : the NISEED system and its application to ascidians, Olivier Tassy, Fabien Daian, **Delphine Dauga** and Patrick Lemaire

Session 5- Structural Biology and Proteomics

Chairman: Jean-François Gibrat

- 14:50-15:50 **Invited Speaker: David Jones:** Predicting the functions of intrinsically unfolded proteins
- 15:50-16:50 Coffee Break-Posters
- 16:50-17:10 Inter-residue contacts analysis using local structure descriptors, **Juliette Martin**,

- Leslie Regad, Catherine Etchebest and Anne-Claude Camproux
- 17:10-17:30 Candidate Fragments Prediction and their Assembly with a Greedy Algorithm and a Coarse-Grained Force Field to solve Protein Folding, Julien Maupetit, Frederic Guyon, Anne-Claude Camproux, Philippe Derreumaux and Pierre Tuffery
- 17:30-17:35 Biological features of over-represented structural motifs in protein loops, Leslie Regad, Juliette Martin, Gaëlle Debret, Gregory Nuel and Anne-Claude Camproux
- 17:35-17:40 Complex assembly and protective function of sHSPs: prediction of critical sites and properties, **Elodie Duprat**, Stephanie Finet, Ferial Skouri-Panet and Annette Tardieu
- 17:40-17:45 Exploration of Pairing Constraints Identifies a 9 Base Pair Core within Box C/D snoRNA-rRNA Duplexes, **Chun-Long Chen**, Roland Perasso, Liang-Hu Qu and Laurence Amar
- 17:45-17:50 Identification et analyse d'ARN non codant : choix et extension d'Apollo, Marie-Josée Cros, **Erika Sallet**, Annick Moisan, Christine Cierco-Ayrolles and Christine Gaspin
- 17:50-17:55 Modeome3D: un système distribue de création et de gestion de modèles 3D de protéines, **Nicolas Garnier**, Christophe Combet, Christophe Gourgeon, Gilbert Deleage and Emmanuel Bettler
- 17:55-18:00 Tools for DIGE, Samuel Granjeaud, Matthieu Hainaut, Fabrice Labiste and Matthieu Prophyllat
- 18:00-18:05 The PROTICdb database for 2D proteomics, Olivier Langella, Helène Denos, Michel Zivy and Johann Joets
- 18:05-18:10 CAZY: A database and annotation tool for Glycogenomics, Corinne Rancurel, Thomas Bernard, Etienne Danchin, Pedro Coutinho and Bernard Henrissat
- 18:10-19:10 AG SFBI

20:00 Gala Dinner

<http://www.cercle-mixte-garnison-marseille.com/fort-ganteaume.htm#>
http://marseille.envues.free.fr/patrimonu/fort_stnicolas/fond.jpg

THURSDAY, JULY 12

Session 6- Systems Biology

Chairwoman: Anne Siegel

- 9:30-10:30 **Invited Speaker: Nicolas Le Novère**: Kinetic models (in Neurobiology): What, why and how.
- 10:30-10:35 Logical modelling of regulatory networks with GINsim 2.2., Aurelien Naldi, Adrien Fauré, Denis Thieffry and **Claudine Chaouiya**
- 10:35-10:40 Validation of the Autoclass clustering algorithm for the reconstruction of regulation networks from gene expression data, Fiona Achcar, Jean-Michel Camadro and **Denis Mestivier**
- 10:40-10:45 SBMLEditor: effective creation of models in the Systems Biology Markup Language (SBML), **Nicolas Rodriguez**, Marco Donizelli and Nicolas Le Novère
- 10:45-10:50 Heterogeneous data integration: application to detection of metabolic functions involved in stress response in yeast, **Claire Gaugain**, Jean-Marc Schwartz, Jose

- Nacher, Minoru Kanehisa and Antoine de Daruvar
- 10:50-10:55 IntAct an open resource project working on interactions, **Catherine Leroy**, Samuel Kerrien, Yasmin Alam-Faruque, Bruno Aranda, A. Bridge, Cathy Derow, Emily Dimmer, M. Feuermann, Rachael Huntley, Jyoti Khadake, Luisa Montecchi-Palazzi, Sandra Orchard, B. Roechert, Dave Thorneycroft, Yue Zhang, Rolf Apweiler and Henning Hermjakob
- 10:55-11:00 An extracellular matrix interaction map, **Emilie Chautard**, Nicolas Thierry-Mieg, Eric Fanchon and Sylvie Ricard-Blum
- 11:00- 12:00 Coffee Break-Posters
- 12:00-12:20 Decision Diagrams for the Representation and Analysis of Logical Models of Genetic Networks, **Aurelien Naldi**, Denis Thieffry and Claudine Chaouiya
- 12:20-12:40 On the link between oscillations and negative circuits in discrete genetic regulatory networks, Adrien Richard
- 12:40-13:00 Robustness Analysis and Tuning of Synthetic Gene Networks, Gregory Batt, Boyan Yordanov, Ron Weiss and Calin Belta

13:00 Lunch

Session 7- Protein-Protein Interactions

Chairwoman: Christine Brun

- 14:30-15:30 **Invited Speaker: Alfonso Valencia**
- 15:30-16:00 Coffee Break
- 16:00-16:20 Inference and validation of *Synechocystis* protein interaction network using orthology, **Magali Michaut**, Samuel Kerrien, Luisa Montecchi-Palazzi, Franck Chauvat, Corinne Cassier-Chauvat, Jean-Christophe Aude, Pierre Legrain and Henning Hermjakob
- 16:20-16:40 Assessing the exceptionality of network motifs, Franck Picard, Jean-Jacques Daudin, Michel Koskas, Sophie Schbath and Stéphane Robin
- 16:40-17:00 Présentation de Jobim 2008, du GdR de Bioinformatique Moléculaire ...
- 17:00-17:15 Conclusions