

Saturday, September 27

---

9h30 Registration opens, welcome coffee  
**12h-13h Light buffet**  
 13h15-13h30 Welcoming speeches  
 13h30-14h20 **Invited talk Chair: Shoshana Wodak**  
**Thomas Lengauer** Analyzing resistance phenomena in HIV with bioinformatics methods

**Contributed talks - Genetic networks**

**Chair: David Gilbert**

14h20-14h45 A description of dynamical graphs associated to elementary regulatory circuits. *Elisabeth Rémy, Brigitte Mossé, Claudine Chaouiya, Denis Thieffry*  
 14h45-15h00 Using ChIP data to decipher regulatory logic of MBF and SBF during the Yeast cell cycle. *Feng Gao, Harmen Bussemaker*  
 15h00-15h15 Validation of noisy dynamical system models of gene regulation inferred from time-course gene expression data at arbitrary time intervals. *Michiel de Hoon, Sascha Ott, Seiya Imoto, Satoru Miyano*  
 15h15-15h30 Accuracy of the models for gene regulation - a comparison of two modeling methods. *Kimmo Palin*  
**15h30-16h10 Coffee Break**

**Contributed talks - Genetic networks and gene expression**

**Chair: Stéphane Robin**

16h10-16h35 Extracting active pathways from gene expression data. *Jean-Philippe Vert, Minoru Kanehisa*  
 16h35-17h00 Gene networks inference using dynamic Bayesian networks. *Bruno-Edouard Perrin, Liva Ralaivola, Florence d'Alché-Buc, Samuele Bottani, Aurélien Mazurie*  
 17h00-17h25 Estimating gene networks from gene expression data by combining Bayesian network model with promoter element detection. *Yoshinori Tamada, Sunyong Kim, Hideo Bannai, Seiya Imoto, Kousuke Tashiro, Satoru Kuhara, Satoru Miyano*  
 17h25-17h50 Biclustering microarray data by Gibbs sampling. *Qizheng Sheng, Yves Moreau, Bart De Moor*  
 17h50-18h15 Discover significant rules for classifying cancer Diagnosis Data. *Jinyan Li, Huiqing Liu, See-Kiong Ng, Limsoon Wong*  
**19h-22h Cocktail at "Le Palais de la Découverte"**  
*(Avenue Franklin Roosevelt near the Champs Elysées)*

Sunday, September 28

---

9h-9h50 **Invited talk - Chair: Satoru Miyano**  
**Nir Friedman** Models for identifying regulation networks

**Contributed talks - Gene expression and motifs**

**Chair: Alvis Brazma**

9h50-10h15 The shortest common supersequence problem in a microarray production setting. *Sven Rahmann*  
 10h15-10h40 Exploring potential target genes of signaling pathways by predicting conserved transcription factor binding sites. *Christoph Dieterich, Ralf Herwig, Martin Vingron*

**Flash presentations - Genetic networks, gene expression**

**Chair: Alvis Brazma**

10h40-10h45 Graph theory based methodology for comparing interaction networks between genes across organisms. *Gaëlle Lelandais, Pierre Vincens, Claude Jacq, Stéphane Vialette*  
 10h45-10h50 Spotting effects in cDNA experiments. *T. Mary-Huard, S. Robin, J.-J. Daudin*  
 10h50-10h55 Design of a clinical microarray chip. *Jochen Jäger, Rainer Spang*  
 10h55-11h00 Classification of cancers by gene expression profiles from peripheral blood. *Andrey Loboda, Michael Nebozhyn, Steven W. Johnson, Peter J. O'Dwyer, Calen Nichols, Linda Alila, Louise C. Showe, Michael K. Showe*  
**11h00-11h45 Posters and Coffee Break**

Sunday, September 28

---

**Contributed talks - Gene expression and motifs**

**Chair: Philipp Bucher**

- 11h45-12h00 Modular decision system and information integration for improved disease outcome prediction. *Matthias Futschik, Mi Sullivan, Anthony Reeve, Nikola Kasabov*
- 12h00-12h15 Genomic distribution of short motifs involved in DNA repair in pathogenic and non pathogenic *Escherichia coli*. *Isabelle Bourgain, Hélène Chiapello, Christelle Hennequet-Antier, Stéphane Robin, Sophie Schbath, Alexandra Gruss, Meriem El Karoui*
- 12h15-12h40 Searching for statistically significant regulatory modules. *Timothy Bailey, William Noble*
- 12h40-13h05 Computational detection of cis-regulatory modules. *Stein Aerts, Peter Van Loo, Gert Thijs, Yves Moreau, Bart De Moor*
- 13h05-14h30 Lunch**
- 14h30-15h20 **Invited talk Chair: James McInerney**  
**Hiroshi Akashi** Metabolic economics and microbial proteome evolution

**Contributed talks - Gene expression and motifs**

**Chair: Michal Linial**

- 15h20-15h45 Finding subtle motifs by branching from sample strings. *Alkes Price, Sriram Ramabhadran, Pavel Pevzner*
- 15h45-16h10 Finding optimal degenerate patterns in DNA sequences. *Daisuke Shinozaki, Tatsuya Akutsu, Osamu Maruyama*

**Flash presentations - Motifs, protein-protein interactions and proteomics**

**Chair: Michal Linial**

- 16h10-16h15 Automatic procedures for compilation of promoter sequences and their evaluation based on signal content and positional distributions. *Christoph S. Schmid, Viviane Praz, Mauro Delorenzi, Rouaida Perier, Philipp Bucher*
- 16h15-16h20 Modeling the Rho dependent transcription termination sites in the bacterium *Helicobacter pylori*. *Lisa Petersen, Anders Krogh*
- 16h20-16h25 GENOFRAG: A software to design primers optimized for whole genome scanning by long-range PCR amplification. Application to the study of *Staphylococcus aureus* genome plasticity. *Nouri Ben Zakour, Michel Gautier, Rumén Andonov, Dominique Lavenier, Philippe Veber, Alexei Sorokin, Yves Le Loir*
- 16h25-16h30 ISYMOD: A Knowledge Base for integrated system modelling. *Julie Chaballier, Yves Quentin, Cécile Capponi, Gwennaele Fichant*
- 16h30-16h35 PARIS: a system for 2-DE based proteomic data management. *Juhui Wang, Christophe Caron, Michel-Yves Mistou, Christophe Gitton, Alain Trubuil*
- 16h35-17h15 Posters and Coffee Break**

**Contributed talks - Proteomics and repeats**

**Chair: Graziano Pesole**

- 17h15-17h40 A Suffix Tree approach to the interpretation of tandem mass spectra: Applications to peptides of nonspecific digestion and post-translational modifications. *Bingwen Lu, Ting Chen*
- 17h40-18h05 Inferring strengths of protein-protein interactions from experimental data using linear programming. *Morihiro Hayashida, Nobuhisa Ueda, Tatsuya Akutsu*
- 18h05-18h20 Overview of a software pipeline dedicated to automatic MS/MS data analysis. *Erwan Reguer, Estelle Nugues, Romain Cahuzac*
- 18h20-18h35 Resources for bacterial strain identification Using polymorphic tandem repeats. *France Denoeud, Gilles Vergnaud*
- 18h35-18h50 Detecting short inverted segments in a biological sequence. *David Robelin, Bernard Prum*
- 19h30- Gala Diner**

**Monday, September 29**

---

9h-9h50 **Invited talk Chair: Anna tramontano**  
**Janet Thornton** The proteome and the metabolome

**Contributed talks - Metabolic networks and RNAs**  
**Chair: Martin Vingron**

9h50-10h15 Ab initio reconstruction of metabolic pathways. *Frédéric Boyer, Alain Viari*  
 10h15-10h40 A rapid method for detection of putative RNAi target genes in genomic data *Yair Horesh, Amihood Amir, Shulamit Michaeli, Ron Unger*

**Flash presentations - Systems biology and RNAs**  
**Chair: Martin Vingron**

10h40-10h45 The Biochemical Abstract Machine BIOCHAM. *Nathalie Chabrier, François Fages*  
 10h45-10h50 Relevance of the secondary structure of messenger RNA: a statistical study. *Fabrice Thalmann, Hervé Isambert*  
 10h50-10h55 Searching for ncRNAs in protist genomes. *Lesley J. Collins, Thomas J. Macke, David Penny*  
 10h55-11h00 Computational detection of MicroRNAs in animal genomes *Matthieu Legendre, Daniel Gautheret*  
 11h-11h45 **Posters and Coffee Break**

**Contributed talks - RNAs and gene finding**  
**Chair: Søren Brunak**

11h45-12h00 Annotating animal mitochondrial tRNAs: an experimental evaluation of four methods. *Stacia Wyman, Jeffrey Boore*  
 12h00-12h15 Searching the *Saccharomyces cerevisiae* genome for -1 frameshifting sites. *Michaël Bekaert, Jean-Paul Forest, Laure Bidou, Alain Denise, Guillemette Duchateau-Nguyen, Céline Fabret, Christine Froidevaux, Isabelle Hatin, Jean-Pierre Rousset, Michel Termier*  
 12h15-12h40 Fast feature selection using a simple Estimation of Distribution Algorithm : A case study on splice site prediction. *Yvan Saeys, Sven Degroeve, Dirk Aeyels, Yves Van de Peer, Pierre Rouzé*  
 12h40-13h05 HMM sampling and applications to gene finding and alternative splicing. *Simon Cawley, Lior Pachter*  
 13h05-14h30 **Lunch**

14h30-15h20 **Invited talk Chair: Daniel Gautheret**  
**Jürgen Brosius** How significant is 98.5% "junk" in mammalian genomes ?

**Contributed talks - Sequence analysis and gene finding**  
**Chair: Roderic Guigó**

15h20-15h45 Modelling sequencing errors by combining Hidden Markov Models. *Claudio Lottaz, Christian Iseli, C. Victor Jongeneel, Philipp Bucher*  
 15h45-16h10 Gene prediction with a Hidden Markov Model and new intron submodel. *Mario Stanke, Stephan Waack*

**Flash presentations - Functional genomics**  
**Chair: Roderic Guigó**

16h10-16h15 Compositional analysis of non-coding regions in eukaryotic genomes. *Emanuele Bultrini, Paolo Del Giudice, Elisabetta Pizzi*  
 16h15-16h20 Inferring site-specific evolutionary rates: Bayesian methods are superior. *Itay Mayrose, Dan Graur, Tal Pupko*  
 16h20-16h25 TIGERSearch attacks Proteins. *Jasmin Saric, Uwe Reyle*  
 16h25-16h30 Protein function prediction: Application of a propositional rules learning system to a set of human protein sequences *Manuel J. Gómez, Francisco Javier Guijarro, Ramón P. Otero, Lars J. Jensen, Søren Brunak, Alfonso Valencia*  
 16h30-17h15 **Posters and Coffee Break**

17h15-18h05 **Invited talk Chair: Esko Ukkonen**  
**Pedro Mendes** Simulation meets data analysis: the development of objective tests for functional genomics data analysis algorithms

## Program ECCB'2003

### Contributed talks - Functional genomics and evolution

#### Chair: Alfonso Valencia

- 18h05-18h30 Predicting gene function in *Saccharomyces cerevisiae*. *Amanda Clare, Ross King*  
18h30-18h45 Rules extraction in linkage disequilibrium mapping with an adaptive genetic algorithm *Laetitia Jourdan, Clarisse Dhaenens, El-Ghazali Talb*  
18h50-19h50 **Business meeting at the Parc de la Villette and Poster session for those not wishing to attend the Business meeting**

## Tuesday, September 30

---

9h-9h50

### Invited talk Chair: Mike Hendy

**Andy Waters** Comparative genomics of malaria parasites and its exploitation in a rodent malaria model

### Contributed talks - Protein structure

#### Chair: Jerzy Tiuryn

- 9h50-10h15 A novel approach to fold recognition using sequence-derived properties from sets of structurally similar local fragments of proteins. *Torgeir R. Hvidsten, Andriy Kryshchak, Jan Komorowski, Krzysztof Fidelis*  
10h15-10h40 Flexible structure alignment by chaining aligned fragment pairs allowing twists *Yuzhen Ye, Adam Godzik*  
**Flash presentations - Protein structure**  
**Chair: Jerzy Tiuryn**  
10h40-10h45 Structural similarity search in databases: YAKUSA. *Mathilde Carpentier, Sophie Brouillet, Joël Pothier*  
10h45-10h50 A new 3D statistical potential to predict protein-ligand interactions based on atomic interaction patterns in PDB. *Ernesto Moreno, Luis A. Diego*  
10h50-10h55 An automatic procedure for the search and identification of new unbounded docking examples *Frank Steinacker, Oliver Martin, Philipp Heuser, Dietmar Schomburg*  
10h55-11h00 Classification of Fourier spectra of short protein sequences compared to their corresponding structural classification. *Manoj Tyagi, Henri Ralambondranny, Frédéric Cadet, Philippe Charton, Bernard Offmann*  
11h-11h45 **Posters and Coffee Break**

### Contributed talks - Multiple alignment and phylogeny

#### Chair: Daniel Huson

- 11h45-12h10 Divide-and-Conquer multiple alignment with segment-Based constraints *Michael Sammeth Burkhard Morgenstern, Jens Stoye*  
12h10-12h35 Upper bounds on maximum likelihood for phylogenetic trees  
*Michael Hendy, Barbara Holland*  
12h35-12h50 A Randomized Linear-time Majority Tree Algorithm *Nina Amenta, Fredericke Clarke, Katherine St. John*  
12h50-13h05 Whole genome-based prokaryotic phylogeny . *Stefan Henz, Alexander Auch, Daniel Huson, Kay Nieselt-Struwe, Stephan Schuster*  
13h05-14h30 **Lunch**  
14h30-15h20 **Invited talk Chair: Eduardo Rocha**  
**François Taddei** Sources of genetic and phenotypic variability

### Contributed talks - Comparative genomics

#### Chair: Bernard Prum

- 15h20-15h45 Genome rearrangements in tumor cells: Reconstructing tumor genome architecture. *Pavel Pevzner, Ben Raphael*  
15h45-16h10 MCMC genome rearrangement. *István Miklós*  
16h10-16h25 Single step reconciliation algorithm for duplication, loss and horizontal gene transfer model. *Pawel Gorecki*  
16h25-16h40 Data retrieval and handling tools for the PBIL gene family databases. *Guy Perrière, Jean-François Dufayard, Simon Penel, Julien Grassot, Laurent Duret, Manolo Gouy*  
16h45-17h **Closing remarks**  
17h-18h **Final posters session for those not needing to catch an early train or flight**