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Wednesday July 6th, 2005

8:00 – 9:30 Registration

9:30 – 10:00 Opening ceremony

Session 1: Comparative genomics and annotations (I) – Chairman: Guy Perrière

10:00 – 11:00 Invited conference: *Comparative analysis of genes, genomes and metagenomes* – **Peer Bork** (European Molecular Biology Laboratory, Heidelberg)

11:00 – 11:30 Coffee break / Poster sessions / Exhibitors

Session 2: Comparative genomics and annotations (II) – Chairman: Laurent Duret

11:30 – 11:50 *Identification of programmed ribosomal -1 frameshifting sites in the genome of Saccharomyces cerevisiae* – **Bekaert M.**, Richard H., Prum B., and Rousset J.P.

11:50 – 12:10 *MOSAIC: An online database for systematic determination of the mosaic structure of bacterial genomes* – **Chiapello H.**, Bourgait I., Sourivong F., Jacquemard A., Petit M.A., and El Karoui M.

12:10 – 12:30 *Directed acyclic coloured multigraphs for expert eukaryotic gene annotation* – **Djebali S.**, Delaplace F., and Roest Crollius H.

12:30 – 12:35 *Boosting BLAST for classifying protein domains* – Capponi C., Fichant G., Denis F., and **Quentin Y.**

12:35 – 12:40 *UMLS-based biomedical annotation of functional genomic data* – **Marquet G.**, Guérin E., Moussouni F., Loréal O., and Burgun A.

12:40 – 12:45 *Analyse du contexte génétique d'un gène* – **Colombo T.**, and Quentin Y.

12:45 – 12:50 *Caractérisation d'introns de plantes par leur représentation spatiale* – **Toffano-Nioche C.**, Gros P.E., Hérisson J., and Gherbi R.

12:50 – 12:55 *Fresh insights into the Musa genome and its comparison with rice* – **Lescot M.**, Ciampi A.Y., Ruiz M., Blanc G., Leebens-Mack J., Glasmieur O., D'Hont A., Rodrigues Da Silva F., Ronning C.M., Cheung F., Haas B.J., Althoff R., Arbogast T., Hine E., Papas G., Souza M., Miller R., Town C.D., and Piffanelli P.

12:55 – 13:00 *Assemblage ciblé: Recherche d'une famille de gènes sur un génome non assemblé* – **Giraud M.**, Quignon P., Retout E., Morin E., Valin A.S., Lavenier D., Rimbault M., Galibert F., and Nicolas J.

13:00 – 14:00 Lunch break

14:00 – 15:00 Even poster/ Exhibitors

Session 3: Gene expression and transcriptome – Chairman: Pierre Vincens

15:00 – 16:00 Invited conference: *Prediction of regulatory elements in non-coding sequences: Evaluation of pattern discovery results in microbes and higher organisms* – **Jacques Van Helden** (Service de Conformation des Macromolécules Biologiques et de Bioinformatique, Université Libre de Bruxelles)

16:00 – 16:20 *Evaluation of the gene-specific dye bias in cDNA microarray experiments* – Martin-Magniette M.L., **Aubert J.**, Cabannes E., and Daudin J.J.

16:20 – 16:40 *Modeling and mining transcriptional regulation from expression data* – **Elati M.**, Radvanyi F., and Rouveirol C.

16:40 – 17:10 Coffee break / Poster sessions / Exhibitors

Session 4: Transcriptome and metabolism – Chairman: Stéphane Robin

- 17:10 – 17:30 *Optimization of Between Group Analysis of gene expression disease class prediction: A new jackknife-based gene selection procedure* – **Baty F.**, Bihl M.P., Perrière G., Culhane A.C., and Brutsche M.
- 17:30 – 17:50 *Évaluation d'une classification hiérarchique par la prise en compte des répétitions expérimentales* – Bréhélin L., and **Martin O.**
- 17:50 – 17:55 *Le Restriction Fragment Differential Display: Méthode d'analyse à grande échelle du transcriptome* – **Naouar N.**, Cléris G., de Laplanche E., Simonnet H., and Perrière G.
- 17:55 – 18:00 *A new pooling strategy for high-throughput screening: The Shuffled Transversal Design* – **Thierry-Mieg N.**
- 18:00 – 18:05 *Modelling epithelium polarization with the ctrl-Dev package* – **Le Garrec J.F.**, Lopez P., and Kerszberg M.
- 18:05 – 18:10 *Fouille de données biomédicales complexes: Extraction de règles et de profils génétiques dans le cadre de l'étude du syndrome métabolique* – **Maumus S.**, Napoli A., Szathmary L., and Visvikis-Siest S.
- 18:10 – 18:15 *SemanticBio: Building conceptual scientific workflows over web services* – **Lacroix Z.**, and Ménager H.
- 18:15 – 18:20 *Apprentissage de règles de réaction biochimique à partir de propriétés en logique temporelle* – Calzone L., **Chabrier-Rivier N.**, Fages F., and Soliman S.
- 18:20 – 20:00 Cocktail**

Thursday July 7th, 2005

Session 5: Evolution and phylogeny (I) – Chairman: Eduardo Rocha

- 9:00 – 10:00 Invited conference: *The evolution of gene order* – **Laurence Hurst** (Department of Biology and Biochemistry, Bath University)
- 10:00 – 10:20 *Replication-associated strand asymmetries in mammalian genomes: Towards detection of replication origins* – **Touchon M.**, Nicolay S., Audit B., Brodie of Brodie E.B., d'Aubenton-Carafa Y., Arneodo A., and Thermes C.
- 10:20 – 10:40 *Évolution des architectures multidomaines chez les bactéries* – **Pasek S.**, Brézellec P., and Risler J.L.
- 10:40 – 11:00 *Extensive phylogenetic analyses reveal that hyperthermophilic bacteria have been subject to massive horizontal gene transfers from archaea* – **Calteau A.**, Gouy M., and Perrière G.
- 11:00 – 11:30 [Coffee break / Poster sessions / Exhibitors](#)

Session 6: Evolution and phylogeny (II) – Chairman: Alain Guénoche

- 11:30 – 11:50 *New approaches to improve the soundness of the deep evolutionary relationships in genomic trees of microorganisms* – **Sculo Q.**, Lespinet O., and Labedan B.
- 11:50 – 12:10 *SDM: Une méthode de distance rapide pour les études de phylogénomique* – **Crisuolo A.**, Berry V., Douzery E.J.P., and Gascuel O.
- 12h10 – 12h30 *Voisinage d'arbre évolutif appliqué au problème Maximum Parcimonie* – **Goëffon A.**, Richer J.M., and Hao J.K.
- 12:30 – 12:35 *Do orthologous gene phylogenies really support tree-thinking ?* – **Baptiste E.**, Susko E., Leigh J., McLeod D., Charlebois R.L., and Doolittle W.F.
- 12:35 – 12:40 *Phylogenomics of the Archaea: The impact of taxonomic sampling and heterogeneity of evolutionary rates* – **Gribaldo S.**, and Brochier C.
- 12:40 – 12:45 *Génération et visualisation de la phylogénie des Bacteria pour l'étude des incohérences taxinomie-phylogénie* – Flandrois J.P., Mignard S., **Dantony E.**, Gouy M., and Devulder G.
- 12:45 – 12:50 *Algorithmes incrémentaux pour l'alignement et la phylogénie de grandes familles de séquences homologues* – **Dufayard J.F.**, **Perrière G.**, and **Gouy M.**
- 12:50 – 12:55 *Bioinformatic sequence identification from sequence family databases* – **Arigon A.M.**, Perrière G., and Gouy M.
- 12:55 – 13:00 *Formation of the Arabidopsis pentatricopeptide repeat (PPR) family* – Bruyère C., Rivals E., and **Lecharny A.**

13:00 – 14:00 Lunch break

14:00 – 15:00 Uneven posters / Exhibitors

Session 7: Macromolecular structure (I) – Chairwoman: Christine Gaspin

- 15:00 – 16:00 Invited conference: *Finding the right address: An analysis of protein-DNA recognition* – **Richard Lavery** (Laboratoire de Biochimie Théorique, Université Paris VII)
- 16:00 – 16:20 *Prediction of in-plane amphipathic membrane segment based on an SVM method* – **Sapay N.**, Guermeur Y., and Deléage G.
- 16:20 – 16:40 *The European Hepatitis C Virus database* – Charavay C., Crisan D., Grando D., Geourjon C., Penin F., Deléage G., and **Combet C.**

16:40 – 17:10 Coffee break / Poster sessions / Exhibitors

Session 8: Macromolecular structures and genomics – Chairman: Joël Pothier

- 17:10 – 17:30 *Méthodes de filtrage des résultats des recherches BLAST pour l'obtention d'alignements multiples dédiés à l'analyse structurale* – **Friedrich A.**, Moulinier L., Ripp R., Garnier N., Bettler E., Deléage G., and Poch O.
- 17:30 – 17:50 *Modélisation de cystéines oxydées à l'aide de la programmation logique inductive* – **Jacquemain I.**, and Nicolas J.
- 17:50 – 17:55 *Core's extraction based neural network model for proteins fold recognition* – **Benabdeslem K.**, Deléage G., and Geourjon C.
- 17:55 – 18:00 *Choice of the optimal Hidden Markov Model for secondary structure prediction* – **Martin J.**, Gibrat J.F., and Rodolphe F.
- 18:00 – 18:05 *Statistical analysis of protein-protein interactions: Organization and contribution of interfacial residues* – Luo S.W., Ray N., Cavin X., and Maigret B.
- 18:05 – 18:10 *Définition de mesures décrivant l'environnement local des acides aminés pour une application à l'évaluation des modèles structuraux* – **Taly J.F.**, Martin J., Marin A., and Gibrat J.F.
- 18:10 – 18:15 *AGMIAL: A distributed genome annotation system based on cooperative Web services* – **Bossy R.**, Loux V., Bryson K., Nicolas P., Bessières P., and Gibrat J.F.
- 18:15 – 18:20 *Champs de Markov cachés et fusion de données individuelles et paires pour l'identification de groupes de gènes* – Forbes F., and **Vignes M.**

20:00 – 23:00 Official reception dinner

Friday July 8th, 2005

Session 9: Interactions and predictions (I) – Chairman: Gilbert Deléage

- 9:00 – 10:00 Invited conference: *Evolution of the mitochondrial proteome and its applications for protein function prediction* – **Martijn Huynen** (Center for Molecular and Biomolecular Informatics, Radboud University)
- 10:00 – 10:20 *DbW: Automatic update of a functional family-specific multiple alignment* – **Prigent V.**, Thierry J.C., Poch O., and Plewniak F.
- 10:20 – 10:40 *Prédire l'interaction des protéines de la superfamille du MHC avec la β 2-microglobuline en combinant classifieur Bayésien «naïf» et alignement multiple IMGT* – **Duprat E.**, Lefranc M.P., and Gascuel O.
- 10:40 – 11:00 *SIGffRid: Programme de recherche des sites de fixation des facteurs de transcription par approche comparative* – **Touzain F.**, Schbath S., Debled-Renneson I., Aigle B., Leblond P., and Kucherov G.

11:00 – 11:30 Coffee break / Poster sessions / Exhibitors

Session 10: Interactions and predictions (II) – Chairman: Claude Thermes

- 11:30 – 11:50 *Prediction of human isochores using a hidden Markov model* – **Melo de Lima C.**, Guéguen L., Piau D., and Gautier C.

- 11:50 – 12:10 *A taxonomy-traversing approach to discover cis-acting elements in prokaryotes* – **Janky R.**, et van Helden J.
- 12:10 – 12:30 *ClusterInspector: A tool to visualize ontology-based relationships between biological entities* – Bérard S., Tichit L., and **Herrmann C.**
- 12:30 – 12:50 *A docking analysis of the statistical physics of protein-protein recognition* – **Bernauer J.**, Poupon A., Azé J., and Janin J.

12:50 – 14:20 Lunch break

Session 11: Regulatory networks – Chairman: Denis Thieffry

- 14:20 – 15:20 Invited conference: *Chemical genomics and chemical bioinformatics* – **Minoru Kanehisa** (Bioinformatics Center, Institute for Chemical Research, Kyoto University)
- 15:20 – 15:40 *Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in Escherichia coli* – **Batt G.**, Ropers D., de Jong H., Geiselman J., Mateescu R., Page M., and Schneider D.
- 15:40 – 16:00 Special: Homage to **Serge Hazout**
- 16:00 – 17:00 Presentation of the **French Bioinformatics Society**

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