









- 12h15 - 12h20  Long-term needs for evolvability and robustness shape genome structure: A simulation study.
C. Knibbe, G. Beslon and J-M. Fayard.

12h20 - 14h00 Déjeuner 

Session 4 : Structures Macromoléculaires
Président : Gilbert Deléage

- 14h00 - 15h00 **Conférence Invitée : François Major**
Modelling RNA Sequence and Structure.
- 15h00 - 15h30 Pause Café 
- 15h30 - 16h30 ● Session Poster
● Séminaire technologique
« Apple : Cluster de calcul et solution de stockage pour les laboratoires »
Bruno Vercelli (Apple France)
- 16h30 - 16h50 Identification of non random motifs in protein loops using a structural alphabet.
L. Regad, J. Martin and A-C. Camproux.
- 16h50 - 17h10 Semantic map of services for structural bioinformatics.
P. Tufféry, Z. Lacroix, H. Ménager.
- 17h10 - 17h30 Learning automata on protein sequences.
F. Coste, Goulven Kerbellec.
- 17h30 - 17h35  MiGaL: An efficient tool for RNA secondary structures comparison.
J. Allali, Y. d'Aubenton-Carafa, C. Thermes, M-F. Sagot.

- 17h35 - 17h40  MAGOS: Multiple Alignment and mOdelling Server.
N. Garnier, A. Friedrich, H. Nguyen, E. Bettler, L. Moulinier, C. Geourjon, G. Deleage, O. Poch.
- 17h40 - 17h45  A flexible model for protein fold recognition.
G. Collet, N. Yanev, A. Marin, R. Andonov, J-F. Gibrat.
- 17h45 - 17h50  Structural study of outer membrane proteins using structural alphabet.
J. Martin, A. G. de Brevern, A-C. Camproux.
- 17h50 - 17h55  Generating Random Genomic Sequences and Structures with GenRGenS*
Yann Ponty, Michel Termier and Alain Denise.
- 17h55 - 18h00  MS2PH-db: A new database to analyse proteins implicated in human genetic diseases.
A. Friedrich, N. Garnier, H. Nguyen, E.I Bettler, G. Deléage, O. Poch, L. Moulinier.

En soirée

Gala JOBIM
Bordeaux 5-7 juillet 2006



Hangar 14
(173 Quais des
Chartrons)


Vendredi 7 Juillet 2006

Session 5 : Phylogénie
Président : Guy Perrière

- 9h00 - 10h00 **Conférence Invitée : Olivier Gascuel**
Neighbor-Joining Revealed
- 10h00 - 10h30 Pause Café 

- 10h30 - 10h50 Adaptation des algorithmes agglomérés NJ, UNJ, BioNJ et MVR pour l'inférence très rapide de superarbres.
A. Criscuolo.
- 10h50 - 11h10 Hybrid evolutionary algorithm for reconstructing phylogenetic trees.
A. Goëffon, J-M. Richer, J-K. Hao.
- 11h10 - 11h30 Votez veto pour l'Arbre de la Vie : la méthode PhysIC pour reconstruire des superarbres.
V. Berry, V. Ranwez, P-H. Fabre, E. J.P. Douzery.
- 11h30 - 11h50 Des milliers d'arbres de gènes pour reconstruire l'histoire du vivant.
S. Abby, M. Gouy, V. Daubin.
- 11h50 - 11h55  SCISSORS - A new approach for building orthologous families in closely related genomes.
N. Pons, J-M. Batto, S. Dusko Ehrlich, P. Renault.
- 11h55 - 12h00  Bio++: A set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics.
J. Duthail, S. Gaillard, E. Bazin, S. Glémin, V. Ranwez, N. Galtier1, K. Belkhir.
- 12h00 - 12h05  Posterior inference on the stem cell population of the human colon crypt through analysis of methylation patterns.
P. Nicolas, D. Shibata and S. Tavaré.
- 12h05 - 12h10  Tracking the evolutionary and functional shifts connection: The lipase-esterase example.
A. Levasseur, P. Gouret, M. Asther, P. Pontarotti.

- 12h10 - 12h15  "Mutability" of gene functions in Homo sapiens.
E. Loire, P.Netter, F. Praz, D. Higuët, G. Achaz.
- 12h15 - 12h20  C.A.S.S.I.O.P.E Clever Agent System for Synteny Inheritance and Other Phenomena in Evolution.
V. Lopez Rascol, P. Gouret, S. Grusea, E. Danchin, P. Pontarotti.

12h20 - 14h00 Déjeuner 

Session 6 : Protéomique
Président : David Sherman

- 14h00 - 15h00 **Conférence Invitée : Henning Hermjacob**
IntAct and PSI - Standards and data bases for molecular interactions.
- 15h00 - 16h00 ● Pause Café 
● Session Poster
- 16h00 - 16h15 Présentation de JOBIM2007 Marseille.
Alain Guénoche
- 16h15 - 16h30 Communication de la SFBI.
Guy Perrière
- 16h30 - 16h45 Conclusions.
Remise des prix :
« Meilleure communication orale »
« Meilleur poster ».
- 16h45 Fin de JOBIM2006
Rendez-vous à Marseille en 2007.



Programme

Mercredi 5 Juillet 2006

- 8h30 - 10h00 Accueil des participants
- 10h00 - 10h30 Cérémonie d'ouverture
B. Bégau - Président de l'Université
Victor Segalen Bordeaux 2.
G. Perrière - Président de la Société
Française de Bioinformatique (SFB).
A. de Daruvar, A. Groppi -
Présidents du Comité d'OrganisationJOBIM2006.

Session 1 : Séquences / Motifs

Président : Alain Denise

- 10h30 - 11h30 **Conférence Invitée : Jens Stoye**
Index Structures in Biological
Sequence Analysis: From Simplicity
to Complexity and Back.
- 11h30 - 12h00 Pause Café ☕
- 12h00 - 12h20 Using bioinformatics to get new
insights into *E. coli* DNA maintenance.
P. Brézellec, M. Hoebeke, M-S. Hiet, S. Pasek,
J-L. Ferat.
- 12h20 - 12h40 Sélection de motifs candidats pour
la régulation des gènes chez
Arabidopsis thaliana sur des critères
topologiques.
V. Bernard, V. Brunaud, C. Serizet, M-L.
Martin-Magniette, M. Caboche, S. Aubourg,
A. Lecharny.
- 12h40 - 12h45 CaPSuLo, an integrative web tool for
predicting subcellular location of
proteins.
D. Perret, A. Bairoch, A-L. Veuthey.

- 12h45 - 12h50 Ed'Nimbus: A lossless filter for long
multiple repetitions with edit distance.
P. Peterlongo, N. Pisanti, A. Pereira do Lago, M-F.
Sagot.
- 12h50 - 12h55 Database and comparison of non
ribosomal peptides.
S. Caboche, V. Leclère, P. Jacques, M. Pupin,
G. Kucherov.
- 12h55 - 13h00 Hidden Markov Models hierarchical
classification for *ab initio* - Prediction
of protein subcellular localization.
H. Richard, M-H. Mucchielli, B. Prum, F. Képès.
- 13h00 - 13h05 *In silico* prediction and experimental
validation of alternative splicing in
the yeast *Yarrowia lipolytica*.
I. Blanc-Lenfle, C. Gaillardin, S. Casaregola,
C. Neuvéglise.
- 13h05 - 13h10 Characterisation and *ab initio* prediction
of Human RNA polymerase II promoters.
C. Hébert, H. Roest Crolius.

Session 2 : Génomique

Président : Pascal Durrens

- 14h30 - 15h30 **Conférence Invitée : Antoine Danchin**
From symplectic to synthetic biology:
Universals in bacterial genomes.
- 15h30 - 16h30 ● Pause Café ☕
● Session Poster
- 16h30 - 16h45 Décrypton : Accélérer la recherche
en génomique et protéomique
grâce au grid computing.
J. Delplancq (IBM).

- 16h45 - 17h05 DNA sequence drives nucleosome
occupancy of yeast promoters.
V. Miele, C. Vaillant, Y. d'Aubenton-Carafa,
D. Robelin, B. Prum, C. Thermes.
- 17h05 - 17h25 Bias and benefit induced by
intra-species homologies in guilt by
association methods to predict protein
function.
L. Bréhélin, O. Gascuel.
- 17h25 - 17h45 A comparative genome approach to
marker ordering.
T. Faraut, S. de Givry, P. Chabrier, T. Derrien,
F. Galibert, C. Hitte, T. Schiex.
- 17h45 - 18h05 The clustering of polymorphism
along a DNA sequence and its appli-
cation to the detection of recombi-
nation and selection.
E. Della-Chiesa, C. Dillmann, B. Jung-Muller,
P-H. Gouyon, F. Austerlitz.

- 18h05 - 18h10 Dynamics of microsatellite birth:
Analysis of genomic distribution in
honey bee.
F. Mougél-Imbert, M. Solignac.
- 18h10 - 18h15 Testing for neutrality in samples with
sequencing errors.
G. Achaz, J. Wakeley.
- 18h15 - 18h20 A model of segmental duplication
formation in *Drosophila melanogaster*
genome: The role of transposable
elements.
A. S. Fiston, D. Anxolabéhère, H. Quesneville.
- 18h20 - 18h25 LeARN: The Legume ncRNA data-

Jeudi 6 Juillet 2006

Session 2 : Génomique (suite et fin)

- 9h00 - 9h20 The role of "domain redundancy" in
genetic robustness against null
mutations.
S. Pasek, J-L. Risler, P. Brézellec.
- 9h20 - 9h25 Exploring genome rearrangements
using virtual hybridization.
M. Belcaid, A. Bergeron, A. Chateau,
C. Chauve, Y. Gingras, G. Poisson.
- 9h25 - 9h30 A new method for computing subha-
plotypes.
C. Coulonges, O. Delaneau, J-F. Zagury.

- base: a platform for detecting, clus-
tering and annotating non coding RNA.
C. Noiroi, C. Gaspin, T. Schiex, J. Guouzy.
- 18h25 - 18h30 Analysis of horizontal transfers in the
Mycobacterium tuberculosis complex
in relation with pathogenicity emer-
gence.
J. Becq, V. Rosas-Magallanes, B. Gicquel,
O. Neyrolles, P. Deschavanne.
- 18h30 - 18h35 In search of the terminus of replication
in archaeal genomes.
D. Cortez, P. Forterre, S. Gribaldo.
- 18h35 - 18h40 EPA: integrated system for EST collection
Processing and semi-automatic
Annotation.
J-M. Frigerio, V. Garcia, A. Barré,
N. Mohellibi, D. Jacob, P. Chaumeil,
C. Plomion, A. de Daruvar.

Session 3 : Réseaux / Systems Biology

Président : Vincent Schachter

- 9h30 - 10h30 **Conférence Invitée : Bèla Novak**
Exit from mitosis in budding yeast:
models and experiments.
- 10h30 - 11h00 Pause Café ☕
- 11h00 - 11h20 Dynamical analysis of a generic boolean
model for the control of the mammalian
cell cycle.
A. Fauré, A. Naldi, C. Chaouiya, D. Thieffry.
- 11h20 - 11h40 Uncovering structure in biological
networks.
J-J. Daudin, V. Lacroix, F. Picard, S. Robin, M-
F. Sagot.
- 11h40 - 12h00 Analysis with respect to instrumental
variables for the exploration of
microarray data structures.
F. Baty, M. Facompré, J. Wiegand, J. Schwager,
M. H. Brutsche.
- 12h00 - 12h05 Interactome analysis of *Drosophila*
signalling networks reveals their
modular architecture and a high level
of functional cross-talks.
Anaïs Baudot, Bernard Jacq, Christine Brun.
- 12h05 - 12h10 Correlating gene expression data with
genomic imbalances.
N. Delhomme, G. Toedt, N. Becker, F. Engel,
F. Blond, P. Lichter.
- 12h10 - 12h15 GnpMap the mapping database
update: « The cytogenetic map view ».
M. Alaux, F. Chetouani, D. Steinbach-Samson,
P. Leroy, M. Falque, A-F. Adam-Blondon,