

Preliminary Conference Programme

Wednesday, September 17, 2008

09:30 - 17:50 [Tutorial on Grid Computing](#)

10:00 - 18:00 EMBnet Annual General Meeting

The tutorial is intended for students/conference attendants and will be held in parallel with the EMBnet AGM at the conference site.

Thursday, September 18, 2008

10:00-18:00 **Registration**

PRESENTATIONS

SPEAKERS

10.00-11.00

Opening Cerimony

*D'Elia Domenica
Bongcam-Rudloff Erik
Saccone Cecilia*

EMBnet 20th Anniversary Celebration

Opening remarks: EMBnet yesterday, today,
tomorrow

11:00-11.30

Coffee Break

SESSION 1: BIOINFORMATICS FOR BIODIVERSITY

Chairperson: Saccone Cecilia

11:30-12:10

Keynote lecture

Biodiversity Informatics: Enabling a
Macroscopic View of Biology

*Sarkar Indra Neil
MBL, Massachusetts
(USA)*

Keynote lecture

12:10-12:50

The Barcode of Life: Bringing Genomics to
Biodiversity

*Hajibabaei Mehrdad
Canadian Centre for DNA
Barcoding
University of Guelph (CA)*

12:50-14:30

Lunch

14:30-14:50

Towards barcode markers in Fungi: an intron
map of Ascomycota mitochondria

*Santamaria Monica
ITB-Bari, CNR (IT)*

14:50-15:10	Gains and losses of lineage-specific group II introns in mitochondria of Gymnosperms: molecular evolutionary and phylogenetic implications	<i>Regina Teresa M.R. Università della Calabria (IT)</i>
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SESSION 2: TRAINING AND E-LEARNING

Chairperson: Valverde José R.

15:10-15:50	Keynote lecture	<i>Tan Tin Wee YLL School of Medicine National University of Singapore (SG)</i>
	Policies, Network, Resources, Materials and Curricula for advancing bioinformatics education: 10 years of APBioNet	
15:50-16:10	Metagenome annotation: an opportunity for undergraduate bioinformatics teaching	<i>Hingamp Pascal Mediterranean University (FR)</i>
16:10-16:30	Grid-based business-to-academia collaborations	<i>Kamuzinzi Richard Université Libre de Bruxelles (BE)</i>
16:30-17:00	Coffee Break	
17:00-17:20	Sprints at genesilico - software engineering techniques in a bioinformatics lab	<i>Rother Kristian Int. Inst. of Mol.Cell Biol. (PL)</i>
17:20-17:40	Towards semantic interoperability of bioinformatics tools and biological databases	<i>Pettifer Steve Manchester University (UK)</i>
	Sponsor talk	
17:40-18:10	IMGT®, an ontology and a system that bridge the gap between sequences and 3D structures	<i>Duroux Patrice IMGT®, Institut de Génétique Humaine, CNRS (FR)</i>
	Parallel events (Open Round Table & Poster session)	
	Open Round Table	
18:10	Presentation and discussion on new tools for Bioinformatics teaching	
18:10-20:30	Poster Session	
20:30	Welcome Party	

Friday, September 19, 2008

SESSION 3: 'OMICS', COMPARATIVE STUDIES AND EVOLUTION

Chairperson: Pesole Graziano

09:30-10:10	Keynote lecture Evolution of gene regulatory code	<i>Kel Alexander E. BIOBASE GmbH (DE)</i>
10:10-10:30	A greater diversity of riboswitches identified through the presence of alternative structures and other constraints	<i>Naville Magali Université Paris-Sud (FR)</i>
10:30-10:50	IMGT/LIGMOTIF: a tool for immunoglobulin and T cell receptor gene identification and description in large genomic sequences	<i>Lane Jérôme Université Montpellier 2 (FR)</i>
10:50-11:20	Coffee break & Poster Session	
11:20-11:40	Functional assessment of time course microarray data	<i>Conesa Ana Centro de Investigación Príncipe Felipe (ES)</i>
11:40-12:00	CHIPSTER – user friendly analysis software for dna microarray data	<i>Korpelainen Eija, CSC (FI)</i>
12:00-12:20	Characterization and analysis of the expression pattern of microRNAs in the grapevine <i>Vitis vinifera</i>	<i>Piccolo Viviana, University of Milan (IT)</i>
12:20-12:40	Improving the prediction of protein behaviour in hydrophobic interaction chromatography and aqueous two-phase systems with clustering methods	<i>Salgado J. Cristian University of Chile (CL)</i>
12:40-13:00	Contact coordination patterns and electrostatic potential at alpha carbon atoms: a dossier of protein secondary structure elements	<i>Neshich Goran Embrapa Informatica Agropecuaria (BR)</i>
13:00-14:30	Lunch	
	Chairperson: Bongcam-Rudloff Erik	
14:30-14:50	Deciphering the connectivity structure of biological networks using MIXNET	<i>Miele Vincent, CNRS, Lyon (FR)</i>
14:50-15:10	Automatic inferring drug gene regulatory networks using computational intelligences	<i>Floares Alexandru, SAIA (RO)</i>

tools

15:10-15:30	A chemogenomics view of protein-ligand spaces	<i>Strömbergsson Helena</i> <i>Uppsala University (SE)</i>
15:30-15:50	In silico prediction of escape mutants of the HIV-1 protease	<i>Agramonte Alina</i> <i>University of Informatic Sciences (CU)</i>
15:50-16:10	The RHNUMTS compilation	<i>Attimonelli Marcella</i> <i>University of Bari (IT)</i>
16:10-16:40	Coffee break & Poster Session	
16:40-17:00	Homologous gene families databases for comparative genomics	<i>Perriere Guy</i> <i>University of Lyon (FR)</i>

SESSION 4: ADVANCED BIOINFORMATICS TECHNOLOGIES AND APPLICATIONS

Chairperson: Andreas Gisel

17:00-17:40	Keynote lecture	<i>Breton Vincent</i> <i>CNRS-IN2P3</i>
	Grids for Life Sciences: status and perspectives	<i>Université Blaise Pascal (FR)</i>
17:40-18:20	Keynote lecture	<i>Shiers Jamie</i> <i>CERN Grid Deployment Group, IT Department(CH)</i>
	Data Challenges in the Worldwide LHC Computing Grid (WLCG)	
18:20- 20.00	Poster Session	
21:00	Gala Dinner	

Saturday, September 20, 2008

SESSION 4: ADVANCED BIOINFORMATICS TECHNOLOGIES AND APPLICATIONS

Chairperson: George Magklaras

09:00- 09:20	Massive non natural proteins structure prediction using Grid technologies	<i>Polticelli Fabio</i> <i>University Roma Tre (IT)</i>
09:20-09:40	The Genius Grid portal and the robot certificates: a new tool for e-science	<i>La Rocca Giuseppe</i> <i>INFN, Catania (IT)</i>
09:40- 10:00	GPU accelerated RNA-RNA interaction algorithm	<i>Rizk Guillaume</i> <i>IRISA-Symbiose (FR)</i>

10:00-10:10	The EMBRACE Project	<i>Gisel Andreas ITB-Bari, CNR (IT)</i>
10:10 - 10:40	Coffee break & Poster Session	
10:40 – 11:00	HTC for ASPIC: a distributed web resource for alternative splicing prediction and transcript isoform characterization	<i>Picardi Ernesto Dep. of Biochem. and Mol. Biol., University of Bari (IT)</i>
11:00 – 11:20	ENGINEADB: A repository of functional analogues	<i>Gisel Andreas ITB-Bari, CNR (IT)</i>
11:20 – 11:40	GOMIR: A stand alone application for human microRNA target analysis and gene ontology clustering	<i>Roubelakis Maria Academy of Athens, BRF(GR)</i>
11:40 – 12:00	When data integration leads to a new concept: the orphan enzymes	<i>Lespinet Olivier Institut de Génétique et Microbiologie, Université Paris-Sud 11 (FR)</i>
12:00- 12:20	Integrating ERV sequence and structural features with DAS and EBIOX	<i>Martinez Barrio Alvaro and Lagercrantz Erik The Linnaeus Centre for Bioinformatics, Uppsala University (SE)</i>
12:20-12:40	Computational annotation of UTR cis-regulatory modules through frequent pattern mining	<i>D'Elia Domenica ITB-Bari, CNR (IT)</i>
12:40-13:00	A bioinformatics knowledge discovery application for Grid computing	<i>Castellano Marcello Politecnico di Bari (IT)</i>
13:00-13:15	Concluding remarks	
13:15- 15:00	Lunch	