Home

Preliminary Conference Programme

Wednesday, September 17, 2008

09:00 - 17:30 Tutorial on Grid Computing
09:00 - 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
10.00-11.30	**Opening Cerimony** **EMBnet 20th Anniversary Celebration** Opening remarks: EMBnet yesterday, today, tomorrow	*Domenica D'Elia* *Erik Bongcam-Rudloff* *Cecilia Saccone* *Chris Sander*
11:30-12.00	**Coffee Break**	
	SESSION 1: BIOINFORMATICS FOR BIODIVERSITY Chairperson:	
	Keynote lecture	
12:30-13:00	Biodiversity Informatics: Enabling a Macroscopic View of Biology	*Indra Neil Sarkar* *MBL, Massachusetts (USA)*
13:00-14:30	**Lunch**	
14:30-15:00	**Keynote lecture**	*Mehrdad Hajibabaei* *Canadian Centre for DNA*

	The Barcode of Life: Bringing Genomics to Biodiversity	*Barcoding* *University of Guelph (CA)*
15:00-15:20	Towards barcode markers in Fungi: an intron map of Ascomycota mitochondria	*Monica Santamaria, ITB - CNR (IT)*
15:20-15:40	Gains and losses of lineage-specific group II intron in mitochondria of Gymnosperms: Molecular evolutionary And Phylogenetic Implications	*Regina Teresa M.R.* *Università della Calabria (IT)*
15:40- 16:10	**Coffee Break**	
	SESSION 2: TRAINING AND E-LEARNING Chairperson:	
	Keynote lecture	
16:10-16:40	Policies, Network, Resources, Materials and Curricula for advancing bioinformatics education: 10 years of APBioNet	*Tin WeeTan* *YLL School of Medicine* *National University of Singapore (SG)*
16:40-17:00	Metagenome annotation: an opportunity for undergraduate bioinformatics teaching	*Hingamp Pascal* *Mediterranean University (FR)*
17:00–17:20	Grid-based business-to-academia collaborations	*Kamuzinzi Richard* *Université Libre de Bruxelles (BE)*
17:20-17:40	Sprints at genesilico - software engineering techniques in a bioinformatics lab	*Rother Kristian* *Int. Inst. of Mol.Cell Biol. (PL)*
17:40-18:10	Towards semantic interoperability of bioinformatics tools and biological databases	*Pettifer Steve* *Manchester University(UK)*
18:10-18:30	**Sponsor talk** IMGT®, an ontology and a system that bridge the gap between sequences and 3D structures	Patrice Duroux *IMGT®, Institut de Génétique Humaine,* *CNRS (FR)*
18:30-20:30	**POSTER SESSION**	
20:30	**Welcome Party**	

Friday, September 19, 2008

SESSION 3: 'OMICS', COMPARATIVE STUDIES AND EVOLUTION

Chairperson:

09:30-10:10	**Keynote lecture** Evolution of gene regulatory code	*Alexander E. Kel* *BIOBASE GmbH (DE)*
10:10-10:30	A greater diversity of riboswitches identified through the presence of alternative structures and other constraints	*Naville Magali* *Université Paris-Sud (FR)*
10:30-10:50	IMGT/LIGMOTIF: a tool for immunoglobulin and T cell receptor gene identification and description in large genomic sequences	*Lane Jérôme* *Université Montpellier 2 (FR)*
10:50-11:20	**Coffee break /POSTER SESSION**	
11:20-11:40	Functional assessment of time course microarray data	*Ana Conesa* *Centro de Investigación Principe Felipe (ES)*
11:40-12:00	CHIPSTER – user friendly analysis software for dna microarray data	*Kallio Aleksi, CSC (FI)*
12:00-12:20	Characterization and analysis of the expression pattern of microRNAs in the grapevine V*itis vinifera*	*Piccolo Viviana, University of Milan (IT)*
12:20-12:40	Improving the prediction of protein behaviour in hydrophobic interaction chromatography and aqueous two-phase systems with clustering methods	*Ugarte Jorge E.* *University of Chile (CL)*
12:40-13:00	Contact coordination patterns and electrostatic potential at alpha carbon atoms: a dossier of protein secondary structure elements	*Borro Luiz* *Embrapa Informatica Agropecuaria (BR)*
13:00-14:30	**Lunch**	
14:30-15:10		*Chris Sander*

	Keynote lecture Systems biology of cancer pathways	*Memorial Sloan-Kettering Cancer Center* *New York (USA)*
15:10-15:30	Deciphering the connectivity structure of biological networks using MIXNET	*Miele Vincent, CNRS, Lyon (FR)*
15:30-15:50	Automatic inferring drug gene regulatory networks using computational intelligences tools	*Floares Alexandru, SAIA (RO)*
15:50-16:10	Possible role for proximity of genes in their expression in rice and Arabidopsis	*Shahmuradov Ilham A., COMSATS (PK)* *Institute of Botany(AZ)*
16:10-16:40	**Coffee break /POSTER SESSION**	
16:40-17:00	A chemogenomics view of protein-ligand spaces	*Helena Strömbergsson* *Uppsala University (SE)*
17:00-17:20	In silico prediction of escape mutants of the HIV-1 protease	*Agramonte Alina* *University of Informatic Sciences (CU)*
17:20-17:40	The RHNUMTS compilation	*Attimonelli Marcella* *University of Bari (IT)*
17:40-18:00	Homologous gene families databases for comparative genomics	*Perriere Guy, University of Lyon (FR)*
18:00-18:30	**Keynote lecture** Data Challenges in the Worldwide LHC Computing Grid (WLCG)	*Vincent Breton* *CNRS-IN2P3* Université Blaise Pascal (FR)
18:30-18:40	The EMBRACE project	Gisel Andreas, ITB-CNR (IT)
18:40 – 20.00	**POSTER SESSION**	
21:00	**Gala Dinner**	

Saturday, September 20, 2008

SESSION 4: ADVANCED BIOINFORMATICS

	TECHNOLOGIES AND APPLICATIONS Chairperson:	
	Keynote lecture	
09:00-09:30	Data Challenges in the Worldwide LHC Computing Grid (WLCG)	*Jamie Shiers* *CERN Grid Deployment Group, IT Department, Geneva, Swiss*
09:30-09:50	Massive non natural proteins structure prediction using Grid technologies	*Polticelli Fabio* *University Roma Tre (IT)*
09:50-10:10	The Genius Grid portal and the robot certificates: a new tool for e-science	*Giuseppe La Rocca* *INFN, Catania (IT)*
10:10- 10:30	GPU accelerated RNA-RNA interaction algorithm	*Rizk Guillaume* *IRISA-Symbiose (FR)*
10:30 -11:00	**Coffee break /POSTER SESSION**	
11:00-11:20	The interpretation of protein structures based on graph theory	*Habibi Mahnaz* *Shahid Beheshti University, Tehran, Iran*
11:20 – 11:40	ENGINEDB: A repository of functional analogues	*De Sario Giulia* *ITB, CNR, Bari (IT)*
11:40 – 12:00	GOMIR: A stand alone application for human microRNA target analysis and gene ontology clustering	*Roubelakis Maria* *Academy of Athens, BResearch Foundation, Athens (GR)*
12:00 – 12:20	When data integration leads to a new concept: The orphan enzymes	*Lespinet Olivier* *Institut de Génétique et Microbiologie, Université Paris-Sud 11, Orsay (FR)*
12:20 - 12:40	Integrating ERV sequence and structural features with DAS and EBIOX	*Martínez Barrio Álvaro* *The Linnaeus Centre for Bioinformatics, Uppsala University (SE)*
12:40 - 13:10	**Sponsor talk (SGI)**	*Silicon Graphics S.p.A.*
13:10 - 14:10	**Lunch**	

14:10 - 14:30	Computational annotation of UTR cis-regulatory modules through frequent pattern mining	*Turi Antonio* *Department of Computer Science, University of Bari (IT)*
14:30 - 14:50	A bioinformatics knowledge discovery application for Grid computing	*Marcello Castellano* *Politecnico di Bari (IT)*
14:50 - 15:00	**Concluding remarks**	