

Monday 23rd, 2012

Student Symposium Program

9:00AM	Student Symposium Registration	Student Symposium Poster Session	
10:00AM	Student Symposium Keynote (Chair: Salvador Capella) • Ben Lehner (CRG, Barcelona) Predicting the phenotypes of individuals: why would a mutation kill me, but not you?		
11:00AM	Coffee break	Student Symposium Poster Session	
11:30AM	Student Symposium Session 1 (Chair: Lorena Pantano) Eneritz Agirre (UPF, Barcelona) The role of epigenetics and small RNAs in the regulation of pre-mRNA splicing. Inna Povolotskaya (CRG, Barcelona) Stop codons in bacteria are not selectively equivalent. João Curado (CRG, Barcelona & GABBA/UP, Porto) Deep sequencing of RNA from distinct sub-cellular fractions shows that splicing in the human genome occurs predominantly during transcription.		
1:00PM	Lunch Student Symposium Poster Session		
2:15AM	Student Symposium Session 2 (Chair: Ana Fernandes Oliveira) Núria Radó-Trilla (FIMIM, Barcelona) Low-complexity regions as a mechanism of protein diversification. Yassine Souilmi (MVU, Rabat) SNP4Forensic Project. Hiren Karathia (UdLL, Lleida) Homol-MetReS: A web application for integration between molecular systems biology and evolutionary biology.		
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	JBI2012 Welcome	INB Meeting	

Monday 23rd, 2012

JB12012 Program

2:00AM to 3:30PM	JBI2012 Registration	
3:45PM	JBI2012 Welcome	
4:00PM	JBI2012 Keynote #1. Chair: Ferran Sanz • Søren Brunak (CBS, Denmark) Interfacing sequencing and network biology data to personal healthcare sector information.	
5:00PM	INB Session. Chair: Christian Blaschke Current challenges and limitations for bioinformatics researchers. In this session a group of expert bioinformaticians will discuss their views on where the current challenges and limitations lie that researchers in this field experience. In continuation the attendees of the session will have the possibility to address questions to the invited experts and offer their own take on the subject. This will be a very interactive and lively session that we hope will serve both newcomers and veterans in bioinformatics to enrich their views around these interesting questions.	

Tuesday 24th, 2012

	JBI2012 Keynote #2 (Chair: Marc A. Marti-Renom) • Leonid Mirny (MIT, Boston) Higher-order chromatin architecture: bridging physics and biology.		
10:00AM	Coffee break	Poster Session I (odd posters)	
	Simon C. Heath (CNAG, Barcelona) Joint estimation of methylation probability and genotype from whole genome bisulfite sequence data. Juan Ramón Gonzalez (CREAL, Cerdanyola) Gene-specific count data distributions are required in RNA-seq experiments with extensive replication. Eva Maria Novoa (IRB, Barcelona) A Role for tRNA Modifications in Genome Structure and Codon Usage. Ignacio Medina (CIPF, Valencia) The first HPC pipeline for Next Generation Sequencing data analysis. Tomas Marques-Bonet (ICREA-IBE, Barcelona) Structural variation from next generation sequencing. Limits of the technology and lessons from the Great Ape Genome Project.		
12:30PM	Lunch	Poster Session I (odd posters)	
	JBI2012 Session 2. Highlights 2011 (I) (Chairs: Modesto Orozco & Alfonso Valencia) Davide Baù (CIPF, Valencia) The three-dimensional folding of the α-globin gene domain reveals formation of chromatin globules. Tanya Vavouri (CRG, Barcelona) Chromatin organization in sperm may be the major functional consequence of base composition variation in the human genome. Javier Macia (UPF, Barcelona) Distributed biological computation with multicellular engineered networks.		
4:00PM	Coffee break	Poster Session I (odd posters)	
	JBI2012 Session 3. Structural Bioinformatics (Chairs: Patrick Aloy & Cláudio Soares) Toni Giorgino (GRIB-IMIM, Barcelona) Molecular recognition of SH2-phosphopeptide by molecular dynamics. Pablo Minguez (EMBL, Heidelberg) A global network of crosstalking post-translational modifications. Joan Planas-Iglesias (GRIB-IMIM, Barcelona) To Bind or not To Bind: Predicting protein-protein interactions from favouring and disfavouring local structural features. Antonio Morreale (CBM-CSIC, Madrid) A reverse combination of structure-based and ligand-based strategies for virtual screening.		
	Antonio Morreale (CBM-CSIC, Madrid)	and-based strategies for virtual screening.	

Wednesday 25th, 2012

9:00AM	JBI2012 Keynote #3 (Chair: Baldomero Oliva)		
0.007 111	Luís Serrano (CRG, Barcelona)		
	A quantitative systems biology study on a model bacterium.		
10:00AM	Coffee break	Poster Session II (even posters)	
10:30AM	JBI2012 Session 4. Genome Annotation (Chairs: Ana Teresa Freitas & Roderic Guigó) • Antonio M. Mérida (UM, Málaga) Sma3s: a 3 stages software for sequences make sense. • Paolo Ribeca (CNAG, Barcelona) The GEM toolkit: world-class short read mapping, 100% made-in-Spain. • M. Gonzalo Claros (UM, Málaga) Highly efficient pre-processing of NGS reads and identification of full-length genes. • Beatriz García-Jiménez (UCIII, Madrid) Relational Learning-based Extension for Reactome Pathways with Sequence Features and Interactions.		
12:30PM	Lunch	Poster Session II (even posters)	
2:30PM	JBI2012 Session 5. Highlights 2011 (II) (Chairs: Modesto Orozco & Alfonso Valencia) Patrick Aloy (IRB, Barcelona) Interactome mapping suggests new mechanistic details underlying Alzheimer's disease. Ana M. Rojas (IMMPC, Badalona) The RAS Superfamily of signaling proteins: a 2011 update. Mar Gonzàlez-Porta (EBI, Cambridge) Estimation of alternative splicing variability in human populations.		
4:00PM	Coffee break	Poster Session II (even posters)	
4:30PM	Bl2012 Session 6. Phylogenetics and evolution (Chairs: José Pereira Leal & Arcadi Navarro) Alberto Pascual-García (CBM-CSIC, Madrid) Detecting bacterial interactions from environmental samples: Ecological aggregations favor bacterial cosmopolitanism. Hernán Dopazo (CIPF, Valencia) Does Nature Play Dice with Genomes? Jaime Huerta-Cepas (CRG, Barcelona) Nested Phylogenetic Reconstruction: scalable resolution in large phylogenies. Urko M. Marigorta (IBE-CSIC, Barcelona) Recent human evolution, continental differences in genes for complex disease and the common gene/common variant hypothesis. Antonio Barbadilla (IBB-UAB, Cerdanyola) Population genomics of 158 genomes of Drosophila melanogaster.		
6:00PM	Communication Awards and Concluding Remarks		
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