



I Jornada de Bioinformàtica i Biologia Computacional

Barcelona, 22 de novembre de 2013

Auditori RBA, Diagonal 189

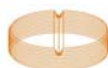
AGENDA

08:30–9:00	Registre
9:00–9:15	Benvinguda i obertura de l'acte A càrrec de: Dr. Joandomènec Ros, President de l'Institut d'Estudis Catalans Dr. Modesto Orozco, Director del Programa en Biologia Computacional IRB-BSC
	Sessió 1. Chair: Patrik Aloy
9:15–9:30	<i>Sequence Classification using Reference Taxonomies.</i> Gabriel Valiente, UPC.
9:30–9:45	<i>Functional Annotation of a Planarian Transcriptome.</i> Josep Abril, UB.
9:45–10:00	<i>Phenotypic characterization of the 8p23 inversion: Accounting for population stratification in inversion calls.</i> Alejandro Cáceres, CREAL, IMIM.
10:00–10:15	<i>Integrating Bioinformatics and Systems Biology.</i> Rui Alves, UdL.
10:15–10:30	<i>Metabolite identification using complex network analysis.</i> Antoni Aguilar-Mogas, URV.
10:30–10:45	<i>Horizontal gene transfer in fungi.</i> Marina Marcet-Houben, CRG.
10:45–11:15	Cafè i sessió de pòsters
	Sessió 2. Chair: Leonardo Pardo
11:15–11:30	<i>A sensitive composite method to detect genomic regions under positive selection in 1000genomes data.</i> Johannes Engelken, UPF.
11:30–11:45	<i>Genomic Recycling: Long Non-Coding RNAs and Transposable Elements.</i> Rory Johnson, CRG.
11:45–12:00	<i>Bioinformatic tools for Molecular Evolution and Comparative Genomics: Implementation of new methods to detect lineage-specific gene family expansions and contractions.</i> Pablo Librado, UB.
12:00–12:15	<i>Identification of recently evolved genes in human and chimpanzee using next generation sequencing technologies.</i> Jorge Ruiz Orera, IMIM.
12:15–12:30	<i>De novo assembly and phellem comparative transcriptomics of two Quercus species differing in cork production ability.</i> Pau Boher, UdG.
12:30–12:45	<i>Surface fitting of 2D diffusion-edited 1H-NMR spectroscopy data for the characterisation of human plasma lipoproteins.</i> Xavier Correig, URV.
12:45–13:45	Presentació de la iniciativa Bioinformatics Barcelona (BIB) A càrrec de: Dra. Ana Ripoll, Presidenta Executiva del BIB Dr. Ferran Sanz, Director Científic del BIB
13:45–15:00	Dinar i sessió de pòsters

	Sessió 3. Chair: Arcadi Navarro
15:00–15:15	<i>Identification of cancer drivers across tumor types.</i> Núria López-Bigas, ICREA-UPF.
15:15–15:30	<i>Interactome3D: adding structural details to protein networks.</i> Roberto Mosca, IRB.
15:30–15:45	<i>Inference with viral diversity indices: Clonal and NGS approaches.</i> Josep Gregori Font, VHIR.
15:45–16.00	<i>Design of aggregation-resistant biotherapeutics.</i> Salvador Ventura, UAB.
16:00-16:15	<i>Pythia: the tool for polypharmacology.</i> Emiliana d'Oria, Intelligent Pharma SL.
16:15-16:30	<i>Metaphenotypes: Identification of the KNG1 Gene as a Major Genetic Determinant of Coagulation Pathway-Related Traits.</i> Helena Brunel, Institut d'Investigació Biomèdica de Sant Pau.
16:30-17:00	Cafè i sessió de pòsters
	Sessió 4. Chair: Jordi Villà-Freixa
17:00-17:15	<i>TCS: a multiple sequence alignment reliability measure suitable for homology and evolutionary modeling.</i> Jia Ming Chang, CRG.
17:15-17:30	<i>Elucidating the network of miRNAs and alternative splicing in breast cancer.</i> Babita Singh, UPF.
17:30-17:45	<i>The GEM mapper: key features and future roadmap.</i> Paolo Ribeca, CNAG.
17:45-18:00	<i>Efficient, multi-thread and reproducible computational pipeline to analyze the effect of 41 inversions on the transcriptomes of 185 individuals</i> Lorena Pantano, IBB-UAB.
18:00-18:15	<i>Using binding free energy changes upon mutation to train empirical contact potentials for protein-protein interactions.</i> Iain Moal, BSC.
18:15-18:30	<i>When 10% seems 100%: value and limits in the prediction of pathological mutations.</i> Xavier de la Cruz, VHIR.
18:30-18:45	Cloenda A càrrec de: Dr. Roderic Guigó, Coordinador de la Secció de Biologia Computacional de la Societat Catalana de Biologia (SCB) Dr. Josep Clotet, Secretari General de la SCB

Institucions col·laboradores:

FUNDACIÓ RBA



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