



Societat Catalana
de **BIOLOGIA**



BIOINFORMATICS
BARCELONA

IV Jornada de Bioinformàtica i Genòmica

Organitzada per:

Secció de Bioinformàtica i Biologia Computacional de la SCB
Secció de Genòmica i Proteòmica de la SCB
Associació Bioinformàtics Barcelona - BIB

Patrocinada per:

Atos **Damm**

PROGRAMA I RESUMS DE LES COMUNICACIONS

PARC DE RECERCA BIOMÈDICA DE BARCELONA (PRBB)

Auditori PRBB

Carrer Aiguader 88

Barcelona

20 de desembre de 2016

COMITÈ ORGANITZADOR:

Núria López-Bigas (ICREA, IRB)
Mario Cáceres (ICREA, UAB)
Roderic Guigó (CRG-UPF)
Ana Ripoll (UAB, BIB)

SUPPORT:

Mariàngels Gallego (SCB)
Maite Sánchez (SCB)
Eva Alloza (BIB)

- 8:30 - 9:15 Registration
- 9:15 - 9:30 Wellcome and opening of the symposium
Dr. Arcadi Navarro (Secretari d'Universitats i Recerca, Generalitat de Catalunya)
Dr. Marc Martí-Renom (Board of Directors of the Societat Catalana de Biologia)
Dra. Ana Ripoll (President of the Bioinformatics Barcelona Association - BIB)

SESSION I. Chair: Núria López-Bigas (ICREA, IRB)

- 9:30 - 10:15 **Morning's Keynote Lecture: Peter Campbell** (Wellcome Trust Sanger Institute, UK). Interrogating the architecture of cancer genomes.
- 10:15 - 10:30 **Ferran Nadeu** (IDIBAPS). Clinical impact of the quantitative subclonal architecture in chronic lymphocytic leukemia.
- 10:30 - 10:45 **Marcos Díaz-Gay** (IDIBAPS). Integrated analysis of germline and tumor DNA for the identification of new genes involved in familial colorectal cancer.
- 10:45 - 11:00 **Natàlia Padilla** (VHIR). Identification of causative mutations in breast and ovarian inherited cancers.
- 11:00 - 11:30 Coffee Break (PRBB terrace)

SESSION II. Chair: Cedric Notredame (CRG)

- 11:30 - 11:45 **Lidia Mateo** (IRB). A PanorOmic view of personal cancer genomes.
- 11:45 - 12:00 **Eduardo Eyra**s (ICREA, UPF). Alternative splicing remodels the protein interaction network of cancer gene drivers.
- 12:00 - 12:15 **Fran Supek** (CRG). The rules and impact of nonsense-mediated mRNA decay in human cancers.
- 12:15 - 12:30 **Marta Guindo** (BSC-CNS). GUIDANCE: An Integrated framework for large scale genome and phenome-wide association studies on parallel computing platforms.
- 12:30 - 12:45 **Jordi Pujols** (UAB). AGGREGSCAN3D (A3D): server for prediction of aggregation properties of protein structures.
- 12:45 - 13:00 **Oriol Senan** (URV). AddClique: A network based model for adduct identification in LC/MS metabolomics.
- 13:00 - 13:15 **Albert Trill** (AtoS). Adapting HPC architectures to the bioinformatics specific needs.
- 13:15 - 14:30 Lunch (PRBB terrace) and free poster viewing

SESSION III. Chair: Jaume Bertranpetit (IBE-UPF)

- 14:30 - 14:45 **Sanja Zivanovic** (IRB). Multi-level strategy for analysis of bioactive drug conformations.
- 14:45 - 15:00 **Julien Lagarde** (CRG). High-throughput manual-quality annotation of full-length long noncoding RNAs with capture long-read sequencing (CLS).
- 15:00 - 15:15 **Juan M. Vaquerizas** (Max Planck Institute for Molecular Biomedicine, Germany). Transcriptional nucleation of topological domains during early embryogenesis.
- 15:15 - 15:30 **Jordi Moreno-Romero** (Swedish University of Agricultural Sciences, Sweden). Parental-specific epigenomics in Arabidopsis.
- 15:30 - 15:45 **Cristina Frías-López** (UB). Evolutionary genomics and transcriptomics of arthropod chemosensory systems: software development and experimental approaches.
- 15:45 - 16:00 **Mayukh Mondal** (IBE-UPF). Unraveling extinct genomes in present day human genomes.

16:00 - 16:30 Coffee Break (PRBB terrace)

SESSION IV. Chair: Mario Cáceres (ICREA, UAB)

- 16:30 - 16:45 **Roger Pique-Regi** (Wayne State University, USA). Functional Genomic analysis of Gene-by-environment interactions across 250 environments.
- 16:45 - 17:00 **Maria Maqueda** (UPC). Independent components of gene expression in endurance runners.
- 17:00 - 17:15 **Ricard Argelaguet** (European Bioinformatics Institute (EMBL-EBI), UK). Disentangling the common and specific sources of variation between different biological layers in multi-view single-cell sequencing.
- 17:15 - 18:00 **Afternoon's Keynote Lecture: John Marioni** (European Bioinformatics Institute (EMBL-EBI), UK). Using single-cell approaches to understand cell fate decisions in early mammalian development.
- 18:00 - 19:00 Poster viewing with authors and beer session organized jointly with the bioinformatics student group RSG-Spain
- 19:00 BIB award to the best oral communication and poster and end of the symposium.