



Societat Catalana
de **BIOLOGIA**



BIOINFORMATICS
BARCELONA

VI 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 Bioinformatics Barcelona - BIB

Patrocinada per:

Hi col·labora:



genes



Atos



PROGRAMA

Auditori CaixaForum

Av. Francesc Ferrer i Guàrdia, 6-8.

Barcelona

20 de desembre de 2018

COMITÈ ORGANITZADOR:

Patrick Aloy (ICREA, IRB Barcelona)
Miquel Àngel Pujana (IDIBELL)
Ricard Gavalrà (UPC)
Mario Cáceres (ICREA, UAB)
Roderic Guigó (CRG-UPF)
Ana Ripoll (UAB, BIB)

SUPPORT:

Mariàngels Gallego (SCB)
Maite Sánchez (SCB)
Begoña Duran (BIB)

8:30 - 9:15 Registration

9:15 - 9:30 Wellcome and opening of the symposium
Representant (Obra Social “La Caixa”)
Dra Ana Ripoll (Bioinformatics Barcelona)
Dr Montserrat Coromines (Societat Catalana de Biologia)

SESSION I. Chair Marc Martí-Renom (ICREA, CRG-CNAG).

9:30 - 10:15 **Invited Lecture: Henk Stunnenberg** (RIMLS, Netherlands).
Epigenetic (de)regulation in health and disease.

10:15 - 10:30 **Pablo Baeza (CRG)**. Combinatorial genetics reveals a scaling law for the effects of mutations on splicing.

10:30 - 10:45 **Pablo Latorre Doménech (IRB Barcelona)**. Sensitive, high-throughput single-cell RNA-Seq reveals within-clonal transcript-correlations in yeast populations.

10:45 - 11:00 **Marta Puig Font (UAB)**. Determining the impact of uncharacterized inversions in the human genome by droplet digital PCR (ddPCR).

11:00 - 11:30 Coffee Break

SESSION II. Chair Baldo Oliva (UPF).

11:30 - 11:45 **Lidia Mateo (IRB Barcelona)**. Exploring the OncoGenomic Landscape of cancer.

11:45 - 12:00 **Bernhard Knapp (UIC)**. Predicting T-cell receptor binding using hierarchical natural Monte Carlo simulations.

12:00 - 12:15 **Janet Piñero (UPF)**. Network, transcriptomic and genomic characterization of genes relevant for drug response.

12:15 - 13:00 **Invited Lecture: Júlio Sáez-Rodríguez** (BioQuant, Germany).
Dynamic logic models complement machine learning to improve cancer treatment.

13:00 - 14:30 Lunch and free poster viewing

SESSION III. Chair Xavier Daura (ICREA, UAB).

- 14:30 - 14:45 **Oriol Pich (IRB Barcelona)**. Somatic and germline mutation rates in nucleosome-occupied DNA.
- 14:45 - 15:00 **Maria Pilar Francino (FISABIO)**. Metabolic adaptation in the human gut microbiota during pregnancy and the first year of life.
- 15:00 - 15:15 **Sergio Picart-Armada (UPC)**. A tissue-specific network-based pathway test and application to GWAS data.
- 15:15 - 15:30 **Alejandro Caceres (ISGlobal)**. Extreme downregulation of chromosome Y and male disease.
- 15:30 - 15:45 **Marina Ruiz Romero (CRG)**. Time and tissue contribution to gene expression during tissue differentiation and development.
- 15:45 - 16:00 **Giovanni Iacono (CRG-CNAG)**. Single-cell transcriptomics unveils gene regulatory network plasticity.

16:00 - 16:30 Coffee Break

SESSION IV. Chair Patrick Aloy (ICREA, IRB Barcelona).

- 16:30 - 16:45 **Davide Cirillo (BSC)**. Training IBM Watson with MelanomaMine.
- 16:45 - 17:00 **Renée Beekman (IDIBAPS)**. Integration of genomic and epigenomic data, including the three-dimensional chromatin structure, refines regulatory mechanisms at chronic lymphocytic leukemia risk loci.
- 17:00 - 17:15 **Josu Aguirre Gómez (VHIR)**. The clinical costs of in silico tools: a novel approach to choose the best pathogenicity predictor for healthcare applications.
- 17:15 - 18:00 **Invited Lecture: Lars Juhl Jensen (Uni of Copenhagen, Denmark)**. Population-wide data and text mining of electronic health records.
- 18:00 - 19:00 Poster viewing with authors and cocktail
- 19:00 - 19:15 *Genes* award to the best oral communication and poster and end of the symposium.
- 19:15 Guided visit to the CaixaForum (requires registration).