



Societat Catalana
de **BIOLOGIA**



BIOINFORMATICS
BARCELONA

VII 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
Spanish National Bioinformatics Institute (INB)

Amb el suport de:

Atos



GCAT TACG GCAT *genes*
an Open Access Journal by MDPI



PROGRAMA

Auditori edifici Vèrtex

Campus Nord UPC

Plaça Eusebi Güell 6, Barcelona

17 de desembre de 2019

COMITÈ ORGANITZADOR:

Gabriel Valiente (UPC)
Mònica Bayés (CNAG-CRG)
Julio Rozas (UB)
Mario Cáceres (ICREA, UAB)
Roderic Guigó (CRG-UPF)
Ana Ripoll (UAB, BIB)

SUPORT:

Mariàngels Gallego (SCB)
Maite Sánchez (SCB)
Simón Perera (BIB)

- 8:30 - 9:15 Registration
- 9:15 - 9:30 Wellcome and opening of the symposium

SESSION I. Chair: Julio Rozas (UB)

- 9:30 - 10:15 **Invited Lecture: David Posada** (University of Vigo). Understanding tumor evolution within patients.
- 10:15 - 10:30 **Jon Lerga-Jaso** (UAB). Comprehensive analysis of the influence of human inversions on gene expression, epigenetic changes and phenotypic variation.
- 10:30 - 10:45 **Marta Coronado-Zamora** (UAB). Mapping natural selection through the *Drosophila melanogaster* life-cycle.
- 10:45 - 11:00 **Alejandro Sánchez-Gracia** (UB). Comparative genomics and transcriptomics in onychophorans and tardigrades shed light on the origin and evolution of arthropod chemosensory gene families.
- 11:00 - 11:30 Coffee Break

SESSION II. Chair: Mònica Bayés (CNAG-CRG)

- 11:30 - 11:45 **Virginia Díez-Obrero** (ICO-IDIBELL). Gene expression and splicing regulation in the colon helps to explain the genetic heritability of many complex traits and diseases.
- 11:45 - 12:00 **Jara Cárcel Márquez** (IR Sant Pau). Genomics and epigenomics. An integromic approach in stroke omics.
- 12:00 - 12:15 **Manuel Solís-Moruno** (UPF). Genetic load of somatic variants in primary immunodeficiency diseases.
- 12:15 - 13:00 **Invited Lecture: Mihaela Zavolan** (University of Basel). The role of RNA 3' end processing in defining mammalian cell types.
- 13:00 - 14:30 Lunch and free poster viewing

SESSION III. Chair: Ana Vivancos (VHIO)

- 14:30 - 14:45 **Miranda D. Stobbe** (CNAG-CRG). Recurrent somatic mutations reveal new insights into consequences of mutagenic processes in cancer.
- 14:45 - 15:00 **Claudia Arnedo-Pac** (IRB Barcelona). OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers.
- 15:00 - 15:15 **Anna Pedrola Gómez** (IDIBAPS). PCIG: a web-based application to infer immunological and genomic determinants across cancer types.
- 15:15 - 15:30 **Juan A. Subirana** (UPC). Non-coding satellites in bacteria. Their eventual role in nucleoid stabilization.

15:30 - 15:45 **Silvia Galan** (CNAG-CRG). Definition of “structural alphabets” for determining the relationship between structural patterns and genomic features.

15:45 - 16:00 **Mar González-Ramírez** (CRG). Histone modifications at enhancers are good predictors of gene expression.

16:00 - 16:30 Coffee Break

SESSION IV. Chair: Gabriel Valiente (UPC)

16:30 - 16:45 **Julien Lagarde** (CRG). An assessment of methods for third-generation long-read transcriptome sequencing.

16:45 - 17:00 **Carlos Ruiz Arenas** (ISGlobal). Historical recombination variability contributes to deciphering the genetic basis of phenotypic traits.

17:00 - 17:15 **Jordi Leno-Colorado** (CRAG). GSAW: A graphical interface package for population genomic analyses using high-throughput sequence data.

17:15 - 18:00 **Invited Lecture: Giorgio Valentini** (University of Milan). Machine Learning for Computational Biology and Precision Medicine.

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.