



Societat Catalana  
de **BIOLOGIA**

# **X Bioinformatics and Genomics Symposium (BGS-X)**

Organized by:

Cavanilles Institute of Biodiversity and Evolutionary Biology (ICBiBE)  
Institute for Integrative Systems Biology (I2SysBio)  
Bioinformatics and Genomics Section of the SCB  
Bioinformatics Barcelona – BIB

Sponsored by:



*Charles Darwin Hall*

**Campus de Burjassot (UVEG)**

Avinguda Vicent Andrés Estellés, Burjassot

**December 15<sup>th</sup> - 16<sup>th</sup>, 2022**

ORGANIZING COMMITTEE:

Ana Conesa (I2SysBio)  
Ferran Palero (ICBiBE)

SUPPORT:

Mario Cáceres (UAB)  
Roderic Guigó (CRG-UPF)  
Ana Ripoll (UAB, BIB)  
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<https://www.iec.cat/jornades/genomica2022.asp>

## **FOREWORD**

The *Bioinformatics and Genomics Symposium* is a conference held every year since 2013 with the aim of promoting the development of bioinformatics and genomics and their application. The main objective of this meeting is to promote scientific interaction between different groups, presenting the excellent research carried out in bioinformatics and genomics, as well as advances in our understanding of the genome in humans and other organisms, new technological developments, applications, and the impact of genomic data in evolutionary biology, among other areas. Originally designed to bring together world specialists in the subject, this symposium has already been successfully organized on 9 occasions, having fallen the responsibility as hosts of its 10th edition to the researchers Ferran Palero (ICBiBE, UVEG) and Ana Conesa (I2SysBio, CSIC-UVEG). This year we intend to gather in Valencia more than 150 scientists and experts from several countries, who will be able to participate in the form of oral presentations and posters, as well as social events to promote relationships and future collaborations between attendees. We hope you will have a fruitful visit to Valencia and enjoy the meeting!

The organizing Team

# PROGRAM

## *December 15<sup>th</sup>*

12:00 – 13:00 Pick up documentation at the Aulari Interfacultatiu (Campus de Burjassot).

13:00 – 14:00 Welcome lunch/reception and opening of the symposium

### **SESSION I.**

14:00 - 14:45 **Invited Lecture: Mark Blaxter (Sanger).** 500 completed genome sequences from the Tree of Life: New genomes yield new biology.

14:45 - 15:00 **Maria Diaz Ros (UAB).** Long-term inversion recurrence and segmental duplication conservation during mammalian evolution.

15:00 - 15:15 **Carles Galià Camps (UB).** A worldwide invasive pangenome sheds light on multiple molecular evolutionary processes.

15:15 - 15:30 **José Miguel Serradell Noguera (UPF).** North Africa demographic history through an ABC-DL approach.

15:30 - 16:00 Coffee Break

### **SESSION II.**

16:00 - 16:15 **Jorge García Calleja (UPF).** Exploring genetic adaptation in the Iberian peninsula using a genome wide scan of positive selection in the GCAT data.

16:15 - 16:30 **Francesc Ganau Penella (CNAG).** Can GWAS data be used to detect adaptation among human complex phenotypes?

16:30 - 16:45 **Sergio Andreu Sánchez (Groningen U.).** Genetic, environmental and intrinsic determinants of the human antibody epitope repertoire.

16:45 - 17:00 **Winona Oliveros Diez (BSC).** Systematic characterization of regulatory variants of blood pressure genes.

17:00 - 17:15 **Lorena Alonso (BSC).** TIGER: The gene expression regulatory variation landscape of human pancreatic islets.

17:15 - 17:30 **Sponsored talk: Lluc Cabús (Floomics).** Plasma cell-free RNA monitoring for the early detection of complex diseases.

17:30 - 19:00 Cocktail and free poster viewing with authors

20:00 - 22:00 Dinner at the Octubre Centre de Cultura Contemporània (<https://octubre.cat/>)

## *December 16<sup>th</sup>*

### **SESSION III.**

- 9:30 - 10:15 **Invited Lecture: Julio Saez-Rodriguez (Heidelberg U.).** Knowledge-based machine learning to extract disease mechanisms from single-cell multi-omics data.
- 10:15 - 10:30 **Aida Ripoll Cladellas (BSC).** A fast and robust statistical framework for gene-wise single-cell differential expression meta-analysis.
- 10:30 - 10:45 **Paola Corbín Agustí (UV).** Genome-scale metabolic models and the discovery of new metabolic pathways.
- 10:45 - 11:00 **José Camacho Páez (Granada U.).** Improved statistical inference in omics analysis with Variable-selection Anova Simultaneous Component Analysis (VASCA).
- 11:00 - 11:30 Coffee Break

### **SESSION IV.**

- 11:30 - 11:45 **Ferriol Calvet Riera (CRG).** A universal protein-coding gene finder.
- 11:45 - 12:00 **Michal Zasisza Alvarez (UB).** A machine learning approach to RNA-editing.
- 12:00 - 12:15 **Alejandra González Sánchez (Vall Hebron).** Recombinant characterization of circulating non-polio enterovirus in Europe.
- 12:15 - 12:30 **Julia Hillung (I2SysBio).** Accumulation dynamics of DVGS during experimental evolution of betacoronaviruses.
- 12:30 - 12:45 **Miguel Álvarez-Herrera (I2SysBio).** Real-time surveillance of SARS-CoV-2: effects of variation in the spike N-terminal domain of variants of concern
- 12:45 - 13:00 **Sponsored talk: Seqera Labs sponsored talk.**
- 13:00 - 14:30 Lunch and free poster viewing

### **SESSION IV.**

- 14:30 - 15:15 **Invited Lecture: Yolanda Sanz (IATA).** Gut microbes - many ways of speaking to the human host
- 15:15 - 15:30 **Trishla Sinha (Groningen U.).** Lifelines NEXT: temporal development of the gut microbiome in relation to health and environment in 713 mother–infant pairs
- 15:30 - 15:45 **Olfat Khannous (BSC).** Microbiome profiling from fecal immunochemical test reveals microbial signatures with potential for colorectal cancer screening.
- 15:45 - 16:00 **Giuseppe D'auria (FISABIO).** The impact of third generation sequencing on the study of microbial diversity: filling the short-reads gap
- 16:00 - 16:30 Coffee Break

## **SESSION V.**

- 16:30 - 16:45 **Ana Conesa (I2SysBio)**. Benchmarking of Long read transcriptomics methods for transcriptome identification and quantification: the LRGASP project.
- 16:45 - 17:00 **Gazaldeep Kaur (CRG)**. Digging into the hidden layer of the human and mouse transcriptomes
- 17:00 - 17:15 **Francisco J. Silva (UV)**. Tissue specific expression of antimicrobial peptide genes in *Blattella Germanica*
- 17:15 - 17:30 Award to the best oral communication and poster and end of the symposium.