

Bioinformatics@Valencia

The meeting of bioinformatics people in Valencia. 12th of July 2018, CIPF conference room.

Workshop Program

08:30-09:00 *Registration*

09:00-09:15 **Meeting welcome**

Ana Conesa. Genomics of Gene Expression Group. Centro de Investigación Príncipe Felipe.

Session 1: *Bioinformatics for Health*

09:15-09:30 **Joaquín Panadero.** Unidad de Genómica. Instituto de Investigación Sanitaria La Fe.
Introduction to Bioinformatics group at Genomics Unit (IISLaFe).

09:30-09:45 **Miguel Herreros.** INCLIVA.
Presentación Unidad de Bioinformática INCLIVA.

09:45-10:00 **Jorge Jiménez Almazán.** Igenomix.
Igenomix: bioinformatics applications in reproductive medicine.

10:00-10:15 **Iñaki Comas.** Instituto de Biomedicina de Valencia (IBV- CSIC)
Next generation sequencing applied to infectious diseases: from population genomics to functional studies.

10:15-10:30 **Alfonso Benítez.** Instituto de Agroquímica y Tecnología de Alimentos (IATA)
Metagenome assessment to unveil shifts in gut microbiome in response to dietary strategies towards improving the host health.

10:30-10:45 **María de la Iglesia.** Unidad Mixta FISABIO – Centro de Investigación Príncipe Felipe.
BIMCV - Medical Imaging Data Bank - Population Imaging Node Valencia.

10:45-11:00 **Juan M. García Gómez.** BDSlab – Universitat Politècnica de València (UPV).
Towards the Big Data Platform of the Valencia region for Personalized Health.

11:00-11:30 Coffee break (by courtesy of Atos)

Session 2: *Bioinformatics methods*

11:30-11:45 **Ana Conesa.** Genomics of Gene Expression Group. Centro de Investigación Príncipe Felipe.
Methods for multiomics data integration and third generation sequencing data analysis.

11:45-12:00 **Francisco García.** Bioinformatics & Biostatistics Unit. Centro de Investigación Príncipe Felipe.
Gender Differences in Health: Big Data Approaches.

12:00-12:15 **José M. Sempere.** DSIC. Universitat Politècnica de València (UPV).
Computación natural y su aplicación a la bioinformática.

12:15-12:30 **Juan Manuel Orduña.** Universitat de València. Departamento de Informática.
Software tools for DNA methylation analysis.

12:30-12:45 **Vicente Arnau.** Universitat de València - I2SysBio.
Theory, Bioinformatics and Computation in I2SysBio.

- 12:45-13:00 **Alberto Ferrer.** Grupo Ingeniería Estadística Multivariante. UPV.
Modelos estadísticos multivariantes basados en variables latentes. Aplicaciones a la Bioinformática.
- 13:00-13:15 **María Téllez Plaza.** Institute for Biomedical Research. Hospital Clínic de València.
MLML2R: efficient simultaneous maximum likelihood estimation of DNA methylation and hydroxymethylation proportions.
- 13:15-13:30 **Jordi Durban.** IBV - CSIC.
Reconstructing a complex snake venom protein gene locus with nanopore sequencer.

13:30-14:30 Lunch (by courtesy of Atos)

Session 3: *Bioinformatics for Biotechnology*

- 14:30-14:45 **Javier Terol Alcayde.** Centro de Genómica. Instituto Valenciano de Investigaciones Agrarias.
Genomics of the origin and evolution of Citrus.
- 14:45-15:00 **Alejandro Sanz Carbonell.** IBMCP - I2SysBio (CSIC).
Inferring the regulatory network of the miRNA-mediated response to biotic and abiotic stress in melon.
- 15:00-15:15 **José Blanca.** Centro de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV)
A genomic analysis of the tomato diversity using Python and HDF5 files.
- 15:15-15:30 **Mariana Reyes Prieto.** Institute for Integrative Systems Biology (I2SysBio).
Large scale analysis of metabolic networks of endosymbiotic bacteria of insects.
- 15:30-15:45 **Laura G. Macías.** Universitat de València. Departamento de Genética.
Bioinformatic pipelines for studying genomes of yeasts of biotechnological interest.
- 15:45-16:15 **DISCUSSION.** Follow up: value proposal, community forming and future meetings.
- 16:15-18:00 Poster session, Networking & Snacks** (by courtesy of Biobam)

Participants's affiliations

INCLIVA | VLC
Instituto de Investigación Sanitaria



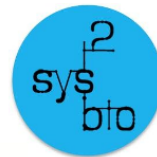
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Fundación para el Fomento de la
Investigación Sanitaria y Biomédica
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Posters

Understanding gender differences in non-alcoholic fatty liver disease from an omics approach. José Francisco Català Senent (Bioinformatics and Biostatistics Unit, CIPF).

Deep sequencing and miRNAs profiles in alcoholic's mice cerebral cortex. Carlos Manuel Cuesta Díaz (Centro de Investigación Príncipe Felipe).

Proteomic study of brain-derived exosomes induced by binge ethanol treatment in adolescent mice. Francesc Ibáñez Cabanes (Centro de Investigación Príncipe Felipe).

Hipathia: a new Bioconductor R package for the analysis of signaling pathway and function activity. Marta Hidalgo García (Centro de Investigación Príncipe Felipe).

Characterization of neuronal molecular mechanisms underlying CMT2Z neuropathy. Paula Sancho (Centro de Investigación Príncipe Felipe).

Functional meta-analysis of breast cancer methylation studies. Antonio Manuel Trasierras Fresco (CIPF-Unidad de Bioinformática y Bioestadística; UCO).

FISABIO Sequencing and Bioinformatics Service. Giuseppe D'Auria (FISABIO Sequencing and Bioinformatics Service).

Assembling high-quality Mycobacterium tuberculosis complex genomes from short- and long-read technologies. Miguel Blanco Fuertes (IBV - CSIC).

Integrative meta-analysis of transcriptomic and metabolomic data from oncological studies. Ayelén Rojas-Benedicto (IIS La Fe).

Statistical Modelling of omic data. David Hervás Marín (IIS La Fe).

Comparison of computational tools for prioritizing candidate genes in Usher Syndrome studies. Sandra Alandes Esteve (IIS LaFe / CIPF).

Igh gene characterization by NGS for the study of B-cell receptor repertoire in patients with chronic lymphocytic leukemia. Azahara Fuentes (INCLIVA).

Study of hereditary variants and altered methylation patterns in imprinting disorders. Carolina Monzó (INCLIVA).

Validating low-frequency mutations from deep-sequencing serial samples to infer bacterial population dynamics. Miguel Ángel Moreno Molina (Instituto de Biomedicina de Valencia - CSIC).

Next Generation Sequencing data analysis pipeline design from FFPE samples to detect very low frequency allelic variants. Jorge Martín Arana (Instituto de Investigación Sanitaria INCLIVA).

Clasificación del conjunto de genes de Drosophila melanogaster atendiendo al nivel de expresión en los distintos tejidos, para la comprensión de los mecanismos moleculares. Paula Navarrete López (UBB- CIPF).

Comparison analysis of pipelines for type 2 diabetes mellitus exome studies. Verónica Lendínez Tortajada (UGDG-INCLIVA).

samtools/bcftools: an alternative variant calling protocol to GATK standards. Luz María González García (Unidad de Genómica, Instituto de Investigación La Fe).

A subset of chromatin factors mediate the coordinated expression of genes transcribed by the three nuclear RNA polymerases in yeast. Jose E Pérez-Ortín (Universitat de València).

*Recombination in the evolution of the syphilis-causing bacteria *Treponema pallidum*.* Marta Pla Díaz (Universitat de València).

PhyloRecomb, a new pipeline to characterise recombination in HIV. Beatriz Beamud Aranguren (Universitat de Valencia-I2SysBio).

Caracterización de nuevas especies bacterianas mediante secuenciación masiva. Neris García-González (Universitat de Valencia-I2SysBio).

Oncología traslacional: identificación de dianas accionables en FFPE y biopsia líquida. Sheila Zúñiga (Fundación INCLIVA).

The challenge of integrating multi-omic multi-factorial data to infer regulatory networks. Sonia Tarazona (Genomics of Gene Expression group, CIPF).

Combining databases and text-mining for biological pathway reconstruction. Salva Casaní (Biobam Bioinformatics, S.L.).

TappAS: Tool for the functional analysis of alternative isoform usage. Lorena de la Fuente (Genomics of Gene Expression group, CIPF).

Integrative visualization of multi-omics data: The PaintOmics 3 Platform. Carlos Martínez (Genomics of Gene Expression group, CIPF).

Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. Sonia Tarazona (Genomics of Gene Expression group, CIPF).

Strategy to remove batch effect between different omic data types. Manuel Ugidos (Genomics of Gene Expression group, CIPF).

Single-cell RNA-seq for the study of isoforms: how is that possible? Ángeles Arzalluz-Luque (Genomics of Gene Expression group, CIPF).

Multi-omics integration to elucidate Minimal Hepatic Encephalopathy's etiology. Héctor Carmona (Genomics of Gene Expression group, CIPF).