Adrià Mitjavila Ventura

Bioinformatician

☆ Girona (Spain) adria.mitjavila94@gmail.com amitjavilaventura.github.io 🖸 amitjavilaventura

Biotechnologist with training in Molecular Genetics and Bioinformatics. Interested in omics data analysis to study the mechanisms of gene regulation in mammals.

Education _

MSc. Bioinformatics and Biostatistics, Universitat Oberta de Catalunya (UOC), Online 2018 - 2022 **MSc. Molecular Genetics and Biotechnology**, *Universidad de Sevilla (US)*, Seville (Spain) 2017 - 2018 BSc. Biotechnology, Universitat de Girona (UdG), Girona (Spain) 2012 - 2017

Employment _

Institut Josep Carreras (IJC)

Badalona (Spain)

Bioinformatician

08/2021 - Present

- Study of the Piwi-interacting RNAs (piRNAs) and their variation across closely-related species.
 Analysis of small RNA-seq data for the study of piRNAs.
 Approach to reduce gene length differences for differential expression analysis with multiple species.
- Mentoring of bachelor's and master's thesis students.

Istituto Europeo di Oncologia (IEO)

Milan (Italy) 07/2019 - 07/2021

Bioinformatician

- Study of differnt signaling pathways in the development of cancer and stem cell differentiation.
 Analysis and integration of RNA-, ChIP- and ATAC-seq data.
 Development of a pipeline to process and analyze ATAC-seq data.

 - Comparison of different software for ATAC-seq peak calling.
 Comparison of sequencing depths for RNA-seq and their impact on differential expression analysis.

Instituto de Biomedicina de Sevilla (IBiS)

Seville (Spain) 07/2018 - 10/2018

Research assistant

- Study of protein Ccr4 and its influence in nucleosome positioning and transcriptional regulation in yeast.
- Computational analysis of MNase-seq data.

Master's thesis student

09/2017 - 07/2018

- Study of protein Xrn1 and its influence in nucleosome positioning and transcriptional regulation in yeast.
- Computational analysis of MNase-seq data. MNase-qPCR experiments: DNA digestion, primer design, qPCR.

Institut d'Investigació Biomèdica de Girona

Girona (Spain) 07/2017 - 09/2017

Research internship student

- Identification of new factors (genetic and bacterial) related to adipose tissue physiology and obesity.

- DNA and RNA extraction from animal and human biopsies/feces.

Microbial. Sistemes i aplicacions analítiques, S.L.

Girona (Spain)

Bachelor's thesis student

01/2017 - 06/2017

- Analysis of the mucosa-associated microbiota from human intestinal biopsies
- DNA extraction, qPCR, analysis of sequencing data.

Internship student

09/2016 - 06/2017

- Analysis of pathogens in food and water samples. Food Forensics.
- DNA extraction, qPCR, molecular clonning, bacterial culture.

Updated: Jun. 9, 2022 1/3

Publications _

JOURNAL ARTICLES

V. Begley et al. 2020 Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. RNA Biology. DOI: 10.1080/15476286.2020.1845504.

Presentations and posters

A. Mitjavila & T. Vavouri. Analysis of piRNA variation across three Mus species (in Catalan). Oral presentation at the Jornades de Biologia de la Reproducció from the Catalan Society of Biology (March 2022).

Projects _

ACADEMIC PROJECTS

Analysis of the variation in piRNA expression across three Mus species

- Master's tesis (UOC, 2022). | Supervisor: Dr. Tanya Vavouri. | Grade: 9.7/10, with honours.

Influence of Xrn1 in nucleosome positioning across Saccharomyces cerevisiae genome and its effects in transcription

- Master's tesis (US, 2018). | Supervisors: Dr. Sebastián Chávez de Diego and Dr. Gabriel Gutiérrez Pozo. | Grade: 9.2/10.
- Related publications: Begley et al., RNA Biology, 2020

Butyrate-induced changes in the diversity of the intestinal mucosa-associated microbiota in colorectal cancer patients submitted to a lateral ileostomy

- Bachelor's tesis (UdG, 2017). | Supervisor: Prof. Jesús García-Gil. | Grade: 9.4/10.

Skills _

Languages

- Catalan (native)
- Spanish (bilingual)
- English (IELTS 7.5 C1)
- Italian (basic)

Bioinformatics

- Omics data analysis: Microarray, (small) RNA-seq, ChIP-seq, ATAC-seq, MNase-seq Genomic Browsers: IGV, UCSC Genome Browser
- Other: Analysis of sequences, ENSEMBL Compara, Biomart

Informatics

- Languages: R/Bioconductor, Bash, Python (basic)
- Other: R Markdown, Snakemake, Conda, Docker, Singularity, Git, HPC, LaTeX

Development _

R packages

- plotMICS: visualization of omics and sequencing data in R.
- ggmitji: cool functions to complement ggplots.
- chromHMMviewR: visualize outputs from ChromHMM.

Others.

- DNAme: shinyApp with learning purposes that transforms a name to DNA/RNA sequence.
- DNApp: shinyApp with some DNA-related applications, including DNAme
- MYomics: shiny App to visualize several omics data. Ongoing

Updated: Jun. 9, 2022 2/3

Organizations _____

Societat Catalana de Biologia (SCB). 2018 - Present

Associació de Biotecnòlegs de Catalunya (ASBTEC). 2017 - Present (Board member. 2019 - Present)

Honours & Awards _____

LaCaixa INPhINIT Incoming PhD Fellowsip (2022-2025)

Master's thesis with honours (UOC, 2022)

Elite athlete (2015-2021)

World Rowing Under-23 Champion (2016)

References _

Available upon request.

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