

Adrià Mitjavila Ventura

Bioinformatician

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

Education

PhD. in Bioinformatics , <i>Universitat Oberta de Catalunya (UAB)</i> , Online	2022 - Present
MSc. Bioinformatics and Biostatistics , <i>Universitat Oberta de Catalunya (UOC)</i> , Online	2018 - 2022
MSc. Molecular Genetics and Biotechnology , <i>Universidad de Sevilla (US)</i> , Seville (Spain)	2017 - 2018
BSc. Biotechnology , <i>Universitat de Girona (UdG)</i> , Girona (Spain)	2012 - 2017

Employment

Institut Josep Carreras (IJC)	Badalona (Spain)
PhD student in Bioinformatics	11/2022 - Present
- Study of the role of transposable elements in the evolution of gene regulation in mammals.	
Bioinformatician	08/2021 - 11/2022
- Study of the variation Piwi-interacting RNAs (piRNAs) across closely-related species.	
- Analysis of small RNA-seq, RNA-seq and genomics data for the study of piRNAs.	
Istituto Europeo di Oncologia (IEO)	Milan (Italy)
Bioinformatician	07/2019 - 08/2021
- Study of different signaling pathways in the development of cancer and stem cell differentiation.	
- Analysis and integration of RNA-, ChIP- and 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)
Research assistant	07/2018 - 10/2018
- 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)
Research internship student	07/2017 - 09/2017
- 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 - 07/2017
- Analysis of the mucosa-associated microbiota from human intestinal biopsies	
- DNA extraction, qPCR, analysis of sequencing data.	
Internship student	09/2016 - 01/2017
- Analysis of pathogens in food and water samples. Food Forensics.	
- DNA extraction, qPCR, molecular cloning, bacterial culture.	

Publications

JOURNAL ARTICLES

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](https://doi.org/10.1080/15476286.2020.1845504).

PRESENTATIONS AND POSTERS

Mitjavila & 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 thesis (UOC, 2022) | Grade: 9.7/10 (*with honours*) | Supervisor: Dr. Tanya Vavouri.

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

- Master thesis (US, 2018). | Grade: 9.2/10. | Supervisors: Dr. Sebastián Chávez de Diego and Dr. Gabriel Gutiérrez Pozo.
- 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 thesis (UdG, 2017). | Grade: 9.4/10. | Supervisor: Prof. Jesús García-Gil.

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

- [p10tMICS](#): visualization of omics and sequencing data in R.
- [ggmitji](#): cool functions to complement ggplots.
- [chromHMMviewR](#): visualize outputs from [ChromHMM](#).

Others.

- [DNAm](#): shinyApp with learning purposes that transforms a name to DNA/RNA sequence.
- [DNApp](#): shinyApp with some DNA-related applications, including [DNAm](#)
- [MYomics](#): shinyApp to visualize several omics data. *Ongoing*

Organizations

Societat Catalana de Biologia (SCB). 2018 - Present

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

Honours & Awards

INPhINIT Incoming PhD Fellowship (LaCaixa, 2022-2025)

Master's thesis **with honours** (UOC, 2022)

Elite athlete (BOE, 2015-2021)

World Rowing Under-23 Champion (FISA, 2016)

References

Available upon request.