

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, *Universitat Oberta de Catalunya (UAB)*, Online 2018 - 2022
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)

PhD student in Bioinformatics 11/2022 - Present

Bioinformatician 08/2021 - 11/2022

- 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.
- Master's thesis (UOC, 2022): *Analysis of the variation in piRNA expression across three Mus species*. Grade: 9.7/10 (**with honours**). Supervisor: Dr. Tanya Vavouri.

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.
- 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)

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.
- Master's thesis (US, 2018): *Influence of Xrn1 in nucleosome positioning across Saccharomyces cerevisiae genome and its effects in transcription*. Grade: 9.2/10. Supervisors: Dr. Sebastián Chávez de Diego and Dr. Gabriel Gutiérrez Pozo.

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.

- Bachelor's thesis (UdG, 2017): *Butyrate-induced changes in the diversity of the intestinal mucosa-associated microbiota in colorectal cancer patients submitted to a lateral ileostomy*. Grade: 9.4/10. Supervisor: Prof. Jesús García-Gil.

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

- Role: Bioinformatician, master student (UOC, 2022), PhD student (UAB) | Supervisor: Dr. Tanya Vavouri.
- Description: *As part of my master's thesis (UOC, 2021-22) and PhD project (UAB, 2022-Present), I am studying Piwi-interacting RNAs (piRNAs), small RNAs that silence transposons in the germline of most animals, and the variation of piRNA-producing loci across closely related species of mouse.*

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

- Role: Master student (US, 2018). | Supervisors: Dr. Sebastián Chávez de Diego and Dr. Gabriel Gutiérrez Pozo.
- Description: *As part of my master's thesis (US, 2018), I participated in a project to study Xrn1, a protein involved in the degradation of mRNA, and its role in the nucleosome localization and transcription of *Saccharomyces cerevisiae*. Analyzing MNase-seq data, we found that Xrn1 knockout induce an increase nucleosome occupancy around TSS, likely explaining a decrease in transcription initiation, whereas in the gene body, the nucleosome occupancy decreases as a consequence of the RNA pol II backtracking. Results were validated using MNase-qPCR for two selected genes in Xrn1 conditional mutants.*
- 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

- Undergraduate student (UdG, 2017). | Supervisor: Prof. Jesús García-Gil.
- Description: *As part of my bachelor's thesis (UdG, 2017).*

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.
- [ggitji](#): 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](#): 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.