

Adrià Mitjavila Ventura

Bioinformatician

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 👤 [amitjavilaventura.github.io](https://github.com/amitjavilaventura) 🔗 [amitjavilaventura](https://www.linkedin.com/company/amitjavilaventura)

Bioinformatician with training in Molecular Genetics and Biotechnology. Interested in omics data analysis to study the mechanisms of gene regulation and their evolution.

Education

PhD in Bioinformatics, *Universitat Autònoma de Barcelona (UAB)*, Online 2022 - Present
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

PhD student in Bioinformatics 11/2022 - Present
Institut Germans Trias i Pujol (IGTP) & Institut Josep Carreras (IJC) Badalona (Spain)

- Study of the role of transposable elements in the evolution of gene regulation in mammals.
- Analysis and integration of small RNA-seq, RNA-seq and other genomics data.
- Mentoring of undergraduate students and colleagues.
- Workshops addressed to high-school students.

Bioinformatician 08/2021 - 11/2022
Institut Josep Carreras (IJC) Badalona (Spain)

- Study of the variation Piwi-interacting RNAs (piRNAs) across closely-related species.
- Analysis and integration of small RNA-seq, RNA-seq and other genomics data.
- Mentoring of BSc and MSc degree students.
- Workshops addressed to high-school 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.

Bioinformatician 07/2019 - 08/2021
Istituto Europeo di Oncologia (IEO) Milan (Italy)

- Study of several signaling pathways in the development of cancer and stem cell differentiation.
- Analysis and integration of RNA-seq, ChIP-seq and ATAC-seq data.
- Comparison of distinct peak callers for ATAC-seq data.
- Comparison of sequencing depths for RNA-seq and their impact on differential expression analysis.

Master's thesis student & Research assistant 09/2017 - 10/2018
Instituto de Biomedicina de Sevilla (IBiS) Seville (Spain)

- Study of Ccr4 and Xrn1 and their influence in nucleosome positioning and transcription 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.

Internship & Bachelor's thesis student 09/2016 - 07/2017
Microbial. Sistemas i aplicacions analítiques, S.L. Girona (Spain)

- Analysis of the mucosa-associated microbiota from human intestinal biopsies
- Analysis of food and water samples for pathogen identification and food forensics.
- DNA extraction, qPCR, molecular cloning, analysis, statistical analysis of NGS (metagenomics) 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.

Publications

JOURNAL ARTICLES

Begley *et al.* **Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration.** *RNA Biology*. 2021. 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).

Mitjavila & Vavouri. **Fast evolution of piRNA cluster expression across three mouse species.** Poster presentation at the annual workshop of the PhD program in Bioinformatics from the *Universitat Autònoma de Barcelona* (February 2023).

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, ENSEMBL Browser (multiple genomes)
- *Other*: Analysis of sequences, ENSEMBL Compara, Biomart, BLAST

Informatics

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

Development

R packages

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

See more on my [Github profile](#)

Organizations

[Catalan Society of Biology \(SCB\)](#). 2018 - Present

[Biotechnologists Association of Catalunya \(ASBTEC\)](#). 2017 - Present (*Board member since 2019*)

Honours & Awards

[INPhINIT Incoming PhD Fellowship](#) (*La Caixa* Foundation, 2022-2025)

[Master's thesis with honours](#) (UOC, 2022)

[SEMM PhD Fellowship](#) (SEMM, 2019, *declined*)

[Elite athlete](#) (BOE, 2015-2021)

[World Rowing Under-23 Champion](#) (FISA, 2016)

References
