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

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.

Istituto Europeo di Oncologia (IEO)

Milan (Italy)

Bioinformatician

- 07/2019 07/2021

- 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)

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.

07/2017 - 09/2017

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.

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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.

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: shinyApp to visualize several omics data. Ongoing

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Organizations
Societat Catalana de Biologia (SCB). 2018 - Present
Associació de Biotecnòlegs de Catalunya (ASBTEC). 2017 - Present
Honours & Awards
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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