

ADRIÀ MITJAVILA VENTURA

Bioinformatician at *Istituto Europeo di Oncologia* | MSc

Biotechnologist living around computers, interested in data analysis to support experimental research as well as in pure (bio)computational experiments and in software/pipeline development. More on [my website](#).



EXPERIENCE

- 08/2021
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Present
- Bioinformatician**
Institut Josep Carreras, Vavouri's lab 📍 Badalona, Spain
- 07/2019
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07/2021
- Bioinformatician**
Istituto Europeo di Oncologia, Pasini's lab 📍 Milan, Italy
- Study of Wnt/ β catenin signaling pathway -and others- in the context of colorectal cancer and stem cell development. | Analysis and integration of RNA-seq, ChIP-seq and ATAC-seq data.
- 09/2017
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10/2018
- Master's thesis student & Research assistant**
Instituto de Biomedicina de Sevilla, Gene expression 📍 Seville, Spain
- Study of Xrn1 and Ccr4 roles in yeast nucleosome architecture and gene transcription. | Analysis of MNase-seq data. | Performance and analysis of MNase-qPCR experiments.
- 09/2016
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06/2017
- Internship & Bachelor's thesis student**
Microbial. Sistemas i aplicacions analítiques, S.L. 📍 Girona, Spain
- Microbiological and molecular analyses for pathogen detection and food forensics. | Study of butyrate effects on the ileal microbiota of colectomized colorectal cancer patients.



EDUCATION

- 2018
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Present
- MSc in Bioinformatics and Biostatistics**
Universitat Oberta de Catalunya 📍 Online
- 2017
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2018
- MSc in Molecular Genetics and Biotechnology**
Universidad de Sevilla - Grade: 9.33/10 📍 Seville, Spain
- Master's thesis: *Influence of Xrn1 in nucleosome positioning across Saccharomyces cerevisiae genome and its effects in transcription*. Grade: 9.2/10
- 2012
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2017
- BSc in Biotechnology**
Universitat de Girona - Grade: 8.12/10 📍 Girona, Spain
- Bachelor's thesis: *Butyrate-induced changes in the diversity of intestinal mucosa-associated microbiota in colorectal cancer patients submitted to a lateral ileostomy*. Grade: 9.4/10



PUBLICATIONS

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

CONTACT

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SKILLS

Omics data analysis:

Microarray,
(small)RNA-/ChIP-/ATAC-/MNase-seq

Programming/scripting:

R/Bioconductor, Python, Bash

Other (informatics):

R Markdown, Snakemake, Git, HPC,
Conda, Docker

Experimental:

(RT-)(q)PCR, primer design,
electrophoresis, WB, MNase-
digestion, bacterial culture

Languages:

Catalan (Native), Spanish (Native),
English (C1 - IELTS 7.5), Italian (Basic)

CODE

[chromHMMviewR](#)
[plotmics](#)
[DPomics](#) (ongoing)
[ATAC-seq snakemake](#) (ongoing)
More on [my GitHub profile](#)

References available upon request.
Build with [pagedown](#), code [here](#).
Last updated on 2021-09-22.