

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.



EXPERIENCE

- 07/2019
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Present
- 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.
 - Development of a Snakemake pipeline for ATAC-seq.
- 09/2017
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10/2018
- Master's thesis student & Research assistant**
Instituto de Biomedicina de Sevilla, Gene expression lab 📍 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. Sistemes 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.
 - qPCR of intestinal biopsies to detect/quantify bacterial genders.
 - Statistical analysis of high-throughput sequencing data to quantify bacteria species.

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.*
- 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.*

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, 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)

DEVELOPMENT

[chromHMMviewR](#)

[DPomics](#) (ongoing)

[ATAC-seq snakemake](#) (ongoing)

More on [my GitHub profile](#)

References available upon request.
Build with [pagedown](#), code [here](#).
Last updated on 2021-05-22.