

# 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
- Analysis and integration of RNA-seq, ChIP-seq and ATAC-seq data.
  - Development of a Snakemake pipeline for ATAC-seq.
- 09/2017  
|  
10/2018
- Master's thesis student & Research assistant**  
*Instituto de Biomedicina de Sevilla, Gene expression lab* Seville, Spain
- Analysis of MNase-seq data.
  - Performance and analysis of MNase-qPCR experiments.
- 09/2016  
|  
06/2017
- Internship & Bachelor's thesis student**  
*Microbial. Sistemas i aplicacions analítiques, S.L.* Girona, Spain
- qPCR of intestinal biopsies to detect/quantify bacterial genres.
  - 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 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 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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📱 [biobit.netlify.app](https://biobit.netlify.app)

## SKILLS

### Omics data analysis:

Microarray, RNA-/ChIP-/ATAC-/MNase-seq

### Programming/scripting:

R/Bioconductor, Python, Bash

### Other (informatics):

Snakemake, Conda, Docker, Git

### 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 2021-04-27.