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.



Bioinformatician 07/2019

Istituto Europeo di Oncologia, Pasini's lab

Milan, Italy

Present

- 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 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.



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 Present

MSc in Bioinformatics and Biostatistics Universitat Oberta de Catalunya

Online

2017

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 2017

BSc in Biotechnology

Universitat de Girona - Grade: 8.12/10

Girona, Spain

• Bachelor's thesis: Butyrate-induced changes in the diversity of intestinal mucosaassociated microbiota in colorectal cancer patients submitted to a lateral ileostomy. Grade: 9.4/10



PUBLICATIONS (D)



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.



CONTACT

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SKILLS

Omics data analysis:

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

Programming/scripting:

R/Bioconductor, Python, Bash

Other (informatics):

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

Experimental:

(RT-)(q)PCR, primer design. electrophoresis, WB, MNasedigestion, 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