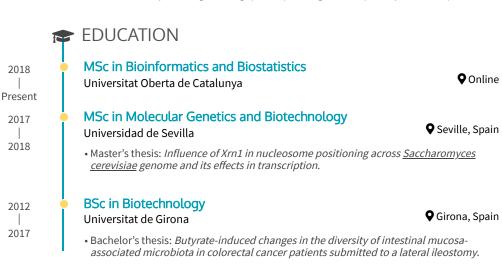
ADRIÀ MITJAVILA VENTURA

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 Bioinformatician 07/2019 Istituto Europeo di Oncologia, Pasini's lab Present • Analysis and integration of RNA-seq, ChIP-seq and ATAC-seq data. • Development of a Snakemake pipeline for ATAC-seq. Master's thesis student & Research assistant 09/2017 Seville, Spain Instituto de Biomedicina de Sevilla, Gene expression lab 10/2018 · Analysis of MNase-seq data. • Performance and analysis of MNase-qPCR experiments. Internship & Bachelor's thesis student 09/2016 Girona, Spain Microbial. Sistemes i aplicacions analítiques, S.L. 06/2017 • qPCR of intestinal biopsies to detect/quantify bacterial genres. • Statistical analysis of high-throughput sequencing data to quantify bacteria species.





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.



CONTACT

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SKILLS

Omics data analysis:

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

Programming/scripting:

R/Bioconductor, Python, Bash

Other (informatics):

Snakemake, Conda, Docker, Git

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