

LORENA PANTANO

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SUMMARY

Visionary leader in computational biology, excelling in genomic and data visualization for decision-making processes, with a proven track record in Biotech for enhancing target discovery through innovative bioinformatics methods. Leveraged genomics methods expertise to pioneer research at Harvard. Led cross-functional teams towards groundbreaking insights in fibrosis, oncology and neurodegeneration. Proficient in project coordination and mentoring scientists.

EXPERIENCE

Biotech Consultant/Advisor

SEPT 2020 – PRESENT

- Advise on technology, computational biology and bioinformatics strategy for emerging BioTechs building data lakes and novel AI methods to accelerate the process of target discovery, gene editing and drug development pipelines

Head of Computational Biology, Director | NextRNA

MAY 2021- MARCH 2024

Associate Director 2021 - 2022

- Led the computational biology team and strategy by being the interface between Biology, Technology and Drug Discovery teams
- Led the in-Silico Target discovery/validation team integrating NGS technology and innovative visualization methods
- Managed Illumina and Nanopore sequencing technology with internal FTEs and CROs
- Built the RNA structure and RNA-Protein interaction AI engine from SHAPE-Seq and eCLIP-Seq derived data
- Managed the cloud computational infrastructure to ensure reproducibility and scalability

Principal Computational Biologist | Axcella

SEPT 2020 – MAY 2021

- Led R&D pipelines with computational strategies
- Led visualization platform with multi-omics data to understand gene regulation
- Applied machine learning methods to understand population stratification in pre-clinical studies
- Developed bioinformatics cloud infrastructure to ensure reproducibility and scalability

Senior Computational Biologist | eGenesis

SEPT 2019 – SEPT 2020

- Managed the internal NGS team with Oxford Nanopore and Illumina technologies
- Led the research of epigenetics marks to enforce expression of transgenes with machine learning
- Built the technical QA/QC genomic platform
- Developed multi-Omics pipelines in a community environment
- Managed the computational cloud infrastructure

Research Scientist | Harvard T.H. Chan School

MAY 2014 – MAY 2019

Research Associate 2014 - 2017

- Lead the bioinformatic activities in the cross-organ fibrosis project collaboration between Harvard University and Boehringer Ingelheim
- Developed and contributed to the computational platform maintaining the system scalable and reproducible
- Develop tools for NGS data analysis: small RNAseq, (Single Cell and bulk) RNA-seq, CHIP-seq, WholeGenome-seq as part of the bcbio-nextgen python framework and Bioconductor platform
- Developed the visualization and integration of multi-omics NGS data inside the bcbio-nextgen python framework

Co-founder and CTO (part-time) | Ascidea, Barcelona, Spain

SEPT 2011 – MAY 2014

- Led a group of 2 bioinformaticians to manage multi-omics genomics projects
- Developed the cloud computing architect in AWS
- Designed computational pipelines

Post-doctoral fellow (part-time) | Institute of Predictive and Personalized Medicine of Cancer, Barcelona, Spain

SEPT 2011 – MAY 2013

- Determined epigenetic regulation in human germinal cells

LEADERSHIP

13 years of experience mentoring scientists and leading teams in Academia and Biotech environments.

Led cross-functional teams in BigPharma/Academia collaborations and biotech.

Experience in communication cross-teams and with business partners. Managed budget and timelines. Collaborate with business development team.

COMMUNITY

In 2016, I founded the Women in Bioinformatics meet-up to foster women's collaboration in the field and empower this community in the Boston area. In 2010, I founded the ISCB Student Group in Spain to foster Bioinformatics in the student community. I have participated in academic conferences as an organizer such as, Bioconductor Conference and ISCB Student Council.

EDUCATION

PHD BIOMEDICINE | CENTER FOR GENOMIC REGULATION | BARCELONA, SPAIN

2008-2011

M.S IN BIOINFORMATICS FOR HEALTH SCIENCE | UNIVERSITY OF POMPEU FABRA | BARCELONA, SPAIN

2006-2008

B.S BIOCHEMISTRY | UNIVERSITY OF GRANADA | BARCELONA, SPAIN

2000-2005

COMPUTATIONAL PLATFORM

AWS VPC, S3, eNFS, EC2, BATCH, ERC and HPC

GitHub, Docker

Posit Software (Rstudio, Rconnect, Package Manager)

Nextflow, Seqera platform

Python and R, Bioconductor

TECHNOLOGY PLATFORM

Illumina | Nanopore | PacBio

Genetic Manipulation:

(CRISPR, OE with Plasmid, KD with shRNA|ASO)

RNA-Seq, Single Cell, small RNA-Seq

Methylation, CHIP-Seq, ATAC-Seq, eCLIP-Seq