Alan F. Muñoz

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Computational biologist with a data analysis and AI/ML skillset. I use computational tools to solve the scientific and technical challenges that arise from knowledge biological databases and high throughput assays, from -omics to imaging, as well as knowledge databases. I balance biological expertise and technical proficiency on cutting-edge AI/ML/Stats methods to accelerate drug discovery through mechanistic biological insights.

WORK EXPERIENCE

Postdoctoral associate

Broad Institute of MIT and Harvard, Boston MA (2023 – Present)

Interpreting biological impact of drugs in high content imaging

Used deep learning via counterfactuals to quantify the effects of chemical compounds on cellular phenotypes.
Designed, implemented and evaluated automated pipelines for label-free microscopy in collaboration with GSK.
Identified novel genetic links using statistical (mAP, Deep Learning) methods on images form the JUMP dataset (~100TB).

JUMP-Cell Painting analyses

Implemented GPU statistical analyses to process data from **>20 million images** of drug-affected cell fingerprints.
Developed web and programmatic interfaces to explore high-throughput data and microscopy images, and link to databases.

Scientific software engineering

>200x Speed-up of information retrieval statistical metrics based on mean Average Precision.
Identified the need of a library for interpretable object featurization, created it and it became widely used in the field.
Pioneered a monorepo-based approach at the Broad Institute for scientific software development.
Created WebAssembly tools for users to query to complement their data with knowledge from imaging.
Integrated LLMs and RAGs into development workflows and internal databases, developed a personal knowledge management system.

EDUCATION

PhD in Quantitative Biology, Biochemistry and Biotechnology

University of Edinburgh, UK (2018–2022).

Thesis: *"Phenotyping single cells of Saccharomyces cerevisiae using an end-to-end analysis of high-content time-lapse microscopy."*

High throughput microscopy acquisition and analysis

Discovered link betweek cytosolic pH oscillation, acidification and cell division rate in budding yeast
15x increase in analysis throughput of microfluidic time lapse experiments, by developing a Deep Learning framework to segment, track and extract single cell information.
Designed and performed high throughput microfluidic experiments.
Developed a mathematical models for resource allocation upon energy constraints and tested them using microscopy and metabolomics data.

Bachelor in Genomic Sciences

National Autonomous University of Mexico, Mexico (2014–2018)

Diffusion-driven antibiotic resistance: Modelled and tested experimentally the impact of spatial heterogeneity on antibiotic resistance.
Phylogenomics: Identified potential phylogenetic markers on Staphylococcus genomes.

Max Planck Institute for Evolutionary Biology, Germany 2018

Host-microbiome neutral model: Developed and implemented neutral selection models to link host reproduction and death effect on microbial evolution.

University of Northern British Columbia, Canada 2017

ML biomarker prediction: Classified clinical targets from gastric cancer microarrays using multiple ML classifiers.

SKILLS

High-performance implementation of statistical testing frameworks
Best practices for programming, documentation and technical computing
Statistical methods for high throughput analyses: average precision frameworks, signal processing, data integration (Seurat, Harmony, Sphering, COMBAT)
10+ years of scientific Python experience: scipy, statsmodels, polars/pandas, duckdb, numpy
High performance computing: Deep Learning/GPU (JAX, Cupy), Dask
AI,ML and Deep Learning and Deep Learning: PyTorch, Tensorflow, scikit-learn/scikit-image/scikit-time, RAG methods
Languages (7+ years of experience): Bash, Julia, SQL, Lisp, R, UNIX tools (e.g., Awk, Sed), Rust(1), Nix(2)
Additional tech: git, Cloud compute (AWS, GCP), RDKit, REST APIs, Containers (Docker, Podman)

AWARDS/FUNDING

2025 Funding from GSK for deep learning methods for imaging
2023 Funding from GSK for a joint collaboration on high throughput imaging
2018 Marie Curie Early Stage Researcher (Europe's Horizon 2020) fellowship
2018 National Council of Science and Technology (Mexico), PhD fellowship
2017 Max Planck Institute for Evolutionary Biology scholarship
2017 National Autonomous University of Mexico, International scholarship
2016 Mitacs Globalink Research (Canada), scholarship

EXPERIMENTAL EXPERIENCE

Fluorescence microscopy and high-content time-lapse imaging.
Design of microfluidic experiments, pressure and flow control automation.
Programatic design of bespoke microfluidic devices.
Development of bespoke tools via 3D programmatic modelling and printing.
Automation of plate readers for fluorescence readings.
Culture and yeast transformation.

SELECTED PUBLICATIONS

Muñoz, Alán F., Tim Treis, Alexandr A. Kalinin, Shatavisha Dasgupta, Fabian Theis, Anne E. Carpenter, and Shantanu Singh. 'cp_measure: API-First Feature Extraction for Image-Based Profiling Workflows'. ICML CODEML Workshop, 2025.
Pietsch, Julian M. J., **Alán F. Muñoz**, Diane-Yayra A. Adjavon, Iseabail Farquhar, Ivan B. N. Clark, and Peter S. Swain. 'Determining Growth Rates from Bright-Field Images of Budding Cells through Identifying Overlaps'. Elife 12 (2023): e79812.
Wongprommoon, Arin, **Alán F. Muñoz**, Diego A. Oyarzún, and Peter S. Swain. 'Single-Cell Metabolic Oscillations Are Pervasive and May Alleviate a Proteome Constraint'. bioRxiv, 2024, 2024–2011.
Kalinin, Alexandr A., John Arevalo, Erik Serrano, Loan Vulliard, Hillary Tsang, Michael Bornholdt, **Alán F. Muñoz**, et al. 'A Versatile Information Retrieval Framework for Evaluating Profile Strength and Similarity'. Nature Communications 16, no. 1 (2025): 5181.
Fuentes-Hernández, Ayari, Anastasia Hernández-Koutoucheva, **Alán F. Muñoz**, Raul Dominguez Palestino, and Rafael Peña-Miller. 'Diffusion-Driven Enhancement of the Antibiotic Resistance Selection Window'. Journal of the Royal Society Interface 16, no. 158 (2019): 20190363.
Graña-Miraglia, Lucia, César Arreguín-Pérez, Gamaliel López-Leal, **Alan Muñoz**, Angeles Pérez-Oseguera, Estefan Miranda-Miranda, Raquel Cossío-Bayúgar, and Santiago Castillo-Ramírez. 'Phylogenomics Picks out the Par Excellence Markers for Species Phylogeny in the Genus Staphylococcus'. PeerJ 6 (2018): e5839.

MENTORSHIP

2024 MSc, Broad Institute, On Deep learning methods for biological interpretability of High Content Imaging.
2021 MSc student, University of Edinburgh, On mathematical modelling of resource allocation in cells.
2021 MSc student, University of Edinburgh. On analysis of fluorescence signals and colocalisation in budding yeast.

EVENTS

Talks

2024/10 I2K 2024: From Images to Knowledge (Human Technopole, Milan, Italy)
2024/09 Society of Biomolecular Imaging and Informatics (Broad Institute, Boston, US)
2024/05 Cell Circuits and Epigenomics Seminar Series (Broad Institute, Boston, US)
2022/10/31 NextGenBUG (University of Edinburgh, Edinburgh, UK)
2021/04 Second-year symposium, School of Biological Sciences, University of Edinburgh (virtual)
2018-2022 6 meetings: Marie Curie International Training Network (MCTN) meetings (as part of the MCTN - Syncrop)

Organiser/Panelist

2024/09 **Organiser**: Broad Institute + Cyotadata JUMP Hackathon (Broad Institute, Boston, US)
2024/07 **Panelist**: Hackathon for Multimodal Data Integration (Broad Institute, Boston, US)
2024/06 **Panelist**: BroadHacks Data Integration Panel (Broad Institute, Boston, US)

Posters

2025/07 ICML 2025, CODEML Workshop (Vancouver, Canada)
2025/04 Software Engineering retreat, Broad Institute (Boston, US)
2024/02 Society for Laboratory Automation and Screening (SLAS) 2024 (Boston, US)
2023/12 American Society of Cell Biology (ASCB) 2023 (Boston, US)
2019/11 EMBO Science communication meeting (Heidelberg, Germany)
2019/04 EMBO Whole-cell Modelling School (Centre for Genomic Regulation, Barcelona, Spain)
2017/05 1st Latin American Workshop and Conference in Systems Biology (CINVESTAV, Mexico City, Mexico)

Other events

2023/10 Society of Biomolecular Imaging and Informatics (SBI2) 2023. (Boston)
2016/10 Mathematical Biology Autumn School (Centre for Mathematics UNAM, Morelia, Mexico)
2016/08 International Summer Symposium on Systems Biology (National Institute of Genomic Medicine, Mexico City, Mexico).
2017/08 Sex, Genes and Behaviour Workshop (Center for Genomic Sciences UNAM)
2017/01 Bioathematics: A Multidisciplinary Endeavor Congress (Mathematics Institute of Juriquilla Campus UNAM, Queretaro, Mexico).
2015/11: Evolution and Genomics Symposium (Centre for Genomic Sciences UNAM, Morelos, Mexico).
2015/06 “From Cells to Stars”: Image Analysis Workshop (National Institute of Astronomy UNAM, Puebla, Mexico).

TEACHING

Introduction to Genomics (Teaching assistant, Undergraduate Program in Genomic Sciences, UNAM, 2016).
Linear Algebra (Teaching assistant, Undergraduate Program in Genomic Sciences, UNAM, 2017).
Systems Biology (Teaching assistant, Undergraduate Program in Genomic Sciences, UNAM, 2017).
Introduction to Genomics (Teaching assistant, Undergraduate Program in Genomic Sciences, UNAM, 2017).

PRIZES

Best Poster (1st Latin American Workshop and Conference in Systems Biology, 2017)
Bronze Medal in the International Genetically Engineered Machine Competition 2016 (Boston, 2016)

LANGUAGES

Spanish: Native Speaker
English: C1 (IELTS)
French: 3 years experience.