Alán F. Muñoz

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Computational biologist who identifies the bottlenecks of biological discovery at scale and builds compact tools to remove them. As a Research Scientist at Purdue University, I work across drug discovery, data science, engineering and image-based profiling: I define which problems matter, design solutions, and evaluate their impact in our biological understanding.

Work Experience

Research Scientist *Purdue University* (September 2026–Present)
Department of Biological Sciences, College of Science
Visiting Scientist *Broad Institute of MIT and Harvard* (September 2026–Present)
Postdoctoral Associate *Broad Institute of MIT and Harvard*, Boston MA (2023–September 2026)

- **Led a GSK-funded collaboration** on high-content imaging, which involves 8 biologists and data scientists, I defined the project scope and designed an end-to-end automated processing framework built on previous work, streamlining steps from image acquisition through feature extraction and evaluation — a foundational shift toward fully automated profiling
- **Built JUMP-lite** to democratize large-scale Cell Painting data for biological discovery. Processed >40 million images (~100 TB) from using GPU-accelerated infrastructure and showed that 98% lossy compression preserves biological signal, producing a curated 100 GB benchmark usable by groups without specialized compute (accepted at WACV)
- **Engineered cp_measure** to address a key bottleneck in image-based profiling: computational biologists lacked programmatic access to morphological feature extraction, limiting automated processing, I exposed CellProfiler's measurement engine as an open source library, now adopted across the community and integrated into spatial transcriptomics workflows via Squidpy (ICML 2025)
- **Created the JUMP Hub**, bridging the gap between the JUMP dataset's scale and researchers' ability to use it — tutorials, interactive data browsers, notebooks, and programmatic access tools that let biologists explore millions of profiling measurements without specialized infrastructure
- **Led development of deep learning counterfactual methods** to interpret how chemical compounds alter cellular morphology, enabling biologists to identify drug effects from visual phenotypes (mentoring an MSc intern)
- **Accelerated copairs** with a 200× speedup of mean Average Precision computation to evaluate information retrieval, reducing processing time from hours to seconds (Kalinin et al., *Nature Communications* 2025)
- **Designed Nahual**, a framework to systematically benchmark heterogeneous DL models in isolated, reproducible environments, enabling rigorous comparison of representation methods across the JUMP-lite dataset

Education

PhD in Quantitative Biology, Biochemistry and Biotechnology
University of Edinburgh, UK (2018–2023)
Thesis: "Phenotyping single cells of Saccharomyces cerevisiae using an end-to-end analysis of high-content time-lapse microscopy."

- Discovered a link between cytosolic pH oscillation, acidification, and cell division rate in budding yeast, revealing pervasive metabolic oscillations at the single-cell level
- Developed the ALIBY framework (segmentation, tracking, single-cell extraction) that fully automated time series analysis, increasing throughput by 15×, later extended for the Broad's automated profiling pipelines

Bachelor in Genomic Sciences *National Autonomous University of Mexico* (2014–2018)
Modelled and experimentally validated diffusion-driven antibiotic resistance; identified potential phylogenetic markers in *Staphylococcus* genomes.

Research Internships

- **Max Planck Institute for Evolutionary Biology, Germany** (2018): Neutral selection models linking host reproduction to microbial evolution
- **University of Northern British Columbia, Canada** (2017): Clinical target classification from gastric cancer microarrays

Awards & Funding

- **2026** — Chiesi Young Investigator Speaker Award, FASEB Science Research Conference: Organelle Cross-Talk in Cellular Homeostasis (Melbourne, FL, USA).
- **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

Selected Publications (Google Scholar)

- **Muñoz, A.F.**, Fredin Haslum, J., Shen, R., Carpenter, A.E., and Singh, S. "JUMP-lite: Compact, reproducible benchmarking of cell representations." Accepted at the *IEEE/CVF Winter Conference on Applications of Computer Vision (WACV 2027)*.
  Led the project from conception through design, implementation, and analysis.
- **Muñoz, A.F.**, et al. "cp_measure: API-First Feature Extraction for Image-Based Profiling Workflows." *ICML CODEML Workshop*, 2025.
  Led development. Modular library extracting CellProfiler's measurement engine for programmatic, scalable feature extraction across imaging modalities including spatial transcriptomics.
- Kalinin, A.A., ..., **Muñoz, A.F.**, et al. "A Versatile Information Retrieval Framework for Evaluating Profile Strength and Similarity." *Nature Communications* 16, 5181 (2025).
  Key contributor. Built the 200× faster mAP implementation enabling evaluation at JUMP scale.
- Wongprommoon, A., **Muñoz, A.F.**, et al. "Single-Cell Metabolic Oscillations Are Pervasive and May Alleviate a Proteome Constraint." *bioRxiv*, 2024.
  Key contributor. Developed the image processing framework to identify single-cell metabolic oscillations.
- Pietsch, J.M.J., **Muñoz, A.F.**, et al. "Determining Growth Rates from Bright-Field Images of Budding Cells through Identifying Overlaps." *eLife* 12: e79812 (2023).
  Key contributor. Built an ML tracking system for growth rate estimation from bright-field time-lapse microscopy.
- Chandrasekaran, S.N., Eric Alix, John Arevalo, Adriana Borowa, Patrick J. Byrne, William G. Charles, Zitong S. Chen, Beth A. Cimini, Boxiong Deng, **Muñoz et A.F.**, et al. "Morphological map of under-and overexpression of genes in human cells." *Nature Methods* 22, no. 8 (2025): 1742–1752.
- Sivagurunathan, S., Patrick Byrne, **Muñoz, A.F.**, John Arevalo, Anne E. Carpenter, Shantanu Singh, Maria Kost-Alimova, and Beth A. Cimini. "Alternate dyes for image-based profiling assays." *SLAS Discovery* (2025): 100268.
- Fuentes-Hernández, A., Anastasia Hernández-Koutoucheva, **Muñoz, A.F.**, 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, L., César Arreguín-Pérez, Gamaliel López-Leal, **Muñoz, A.F.**, et al. "Phylogenomics Picks out the Par Excellence Markers for Species Phylogeny in the Genus Staphylococcus." *PeerJ* 6 (2018): e5839.

Skills

- **Systems & reproducibility:** Nix/NixOS, containers (Docker, Podman), monorepo design, cloud (AWS, GCP), CI/CD
- **Scientific computing:** GPU programming (JAX, CuPy), Dask, high-performance statistical testing, Nextflow
- **Languages (10+ years):** Python (scientific stack), Bash, Julia, SQL/DuckDB, R, Rust, Nix
- **Data & analysis:** signal processing, batch correction methods
- **Deep learning:** PyTorch, TensorFlow, scikit-learn/scikit-image, ML devops
- **Wet lab:** Fluorescence microscopy, high-content time-lapse imaging, microfluidic device design, yeast experimental protocols

Mentorship

- **2024** — MSc supervisor, Broad Institute: DL methods for biological interpretability of high-content imaging; weekly check-in and design of decisions for training data and training of models. Resulted in a retreat poster at the Broad Institute.
- **2021** — MSc supervisor, U. of Edinburgh: Mathematical modelling of resource allocation in cells; weekly check-ins and discussions on math models, models, resulted in an *MSc Thesis*.
- **2021** — MSc supervisor, U. of Edinburgh: Analysis of fluorescence signals and colocalisation in budding yeast; weekly check-ins, resulted in an *MSc Thesis*.

Selected Talks

- **2026/11/02** — Learning cellular representations that matter: deep learning for morphological profiling, SBI2 13th Annual Conference (Boston, MA, USA)
- **2026/10/21** — Invited talk: Uncovering biological relationships through morphological profiling: The JUMP-Cell Painting dataset and tools, FASEB Science Research Conference: Organelle Cross-Talk in Cellular Homeostasis (Melbourne, FL, USA)

- **2024/10** — Flash Talk: JUMP-Hub, I2K 2024: From Images to Knowledge (Human Technopole, Milan, Italy)
- **2024/05** — Cell Circuits and Epigenomics Seminar Series (Broad Institute, Boston, US)
- **2022/10** — NextGenBUG (University of Edinburgh, Edinburgh, UK)

Selected Posters

- **2026/11** — JUMP-lite: Compact, reproducible benchmarking of cell representations, SBI2 13th Annual Conference (Boston, MA, USA)