Axel Rodríguez-Pérez

BSc in Genomic Sciences

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Education

Bachelors in Science in Genomic Sciences   *Juriquilla, Qro, MX*
NATIONAL AUTONOMOUS UNIVERSITY OF MEXICO (UNAM)   *2021 – 2025*

- Relevant Coursework: *Calculus, Statistics, Linear Algebra, Molecular and Cell Biology, Statistical Models in Human Genetics, Human Genomics in Health and Disease, Cancer Genomics, Evolutionary Genomics, Bioinformatics and Statistics, Machine Learning Applications in Genomics*.

Research Experience

Research Intern   *Leuven, Belgium*
LABORATORY OF MOLECULAR CANCER BIOLOGY, CENTER FOR CANCER BIOLOGY, VIB - KU LEUVEN   *August 2024 – June 2025*

Supervisors: Jean-Christophe Marine, PhD. & Joanna Pozniak, PhD.

- Analyzed the perivascular niche in melanoma using Molecular Cartography spatial transcriptomics data.
- Designed pipelines for transcript assignment, quality assessment, and robust cell-type annotation.
- Built spatial neighbor graphs and co-occurrence models to study cell–cell interactions.
- Contributed to and adapted Python pipelines for processing multiplexed tissue imaging data (NanoNail and CIVO micro-dosing devices)
- Implemented automated image preprocessing and segmentation workflows using Cellpose and Dask for large-scale datasets.
- Performed spatial analyses and clustering to evaluate treatment responses at single-cell resolution.
- Processed and analyzed bulk RNA-seq data from treated melanoma cell lines using HPC workflows.
- Identified treatment-specific gene signatures and enriched pathways through differential expression and functional analysis.
- Quantified volumetric and surface changes in melanoma cell lines under Palbociclib treatment.
- Applied vector-based models to characterize magnitude and direction of cellular responses.

Research Intern   *Juriquilla, Qro, MX*
CANCER GENOMICS AND BIOINFORMATICS LAB, INTERNATIONAL LABORATORY FOR HUMAN GENOME
RESEARCH (LIIGH -UNAM)   *May 2022 – July 2024*

Supervisors: Carla Daniela Robles Espinoza, PhD. & Martha Estefanía Vázquez Cruz, PhD.

- Analyzed spatial proteomics data from acral lentiginous melanoma patient samples using GeoMx Digital Spatial Profiler (35 protein markers).
- Developed and benchmarked machine learning models (Random Forest, Logistic Regression) to predict ulceration status from tumor and TME regions.
- Applied advanced preprocessing and cross-validation strategies, achieving high predictive accuracy (PR-AUC ≈ 0.98 in TME samples).
- Identified immune-related markers (e.g., CD8, PD-1) as key predictors of ulceration, providing potential clinical insights.
- Documented analyses in R and prepared a comprehensive technical report with reproducible workflows.
- Gained hands-on training in molecular biology techniques, including nucleic acid extraction, quantification, and agarose gel electrophoresis.
- Cultured mammalian cell lines (NIH 3T3, A375 melanoma): thawing, passaging, contamination detection, and cryopreservation.
- Performed bacterial transformation, plasmid amplification, and purification with quality control.
- Applied functional assays (foci formation, crystal violet staining, scratch, proliferation) to assess oncogenic potential.

- Conducted mammalian cell transfection and antibiotic selection; prepared buffers, reagents, and sterile culture media.

Publications

1. Vazquez-Cruz, M. E., Basurto-Lozada, P., Molina-Aguilar, C., Orozco-Ruiz, S., Van Haastrecht, B., Simonin-Wilmer, I., Martinez-Said, H., Alvarez-Cano, A., Garcia-Ortega, D. Y., Hidalgo-Miranda, A., Hinojosa-Ugarte, D., Ferreira, I., Tavares-De-La-Paz, L. A., Olguin, J. E., Salinas, I., **Rodriguez-Perez, A.**, Martinez-Gomez, J. M., Van Der Zee, I., Grimes, D. R., . . . Robles-Espinoza, C. D. (2025). The microenvironment of ulcerated acral melanoma is characterised by an inflammatory milieu and an enhanced humoral immune response. *medRxiv (Cold Spring Harbor Laboratory)*. `https://doi.org/10.1101/2025.05.05.25325616`

Presentations & Talks

Machine Learning models for ulceration prediction in mexican melanoma cohort

International Laboratory for Human Genome Research (LIIGH -UNAM)

Mini-Symposium: Acral Melanoma Research in Latin America

May 2024

- Presented research on applying machine learning (Random Forest, Logistic Regression, LASSO) to spatial proteomics data from Mexican acral melanoma patients.
- Discussed methodology (data preprocessing, feature selection, PCA, upsampling) and evaluation metrics (PR-AUC).
- Highlighted potential clinical applications of computational models in melanoma prognosis.

Teaching & Mentorship Experience

Invited Speaker

Remotely

5th Summer School: Introduction to Genomic Sciences, LIIGH-UNAM

July 2025

Talk title: *Genes, code, and decisions: lessons on starting a scientific career*.

- Delivered am interactive talk as part of the "My Science and My Life" series.
- Shared personal trajectory and lessons for early-career students, combining genomics, coding, and career decision-making.

Guest Instructor

Remotely

Undergraduate Program in Genomic Sciences, UNAM

November 2024

- Assisted in teaching "*Introduction to Single-Cell and Spatial Transcriptomics*" lecture for third-semester undergraduate students.
- Clarified core concepts and addressed student questions to facilitate understanding.

Achievements & Funding

- UNAM High Academic Performance Scholarship 2023-2024.
- UNAM High Academic Performance Scholarship 2022-2023.
- UNAM High Academic Performance Scholarship 2021-2022.
- UNAM Financial Support Scholarship 2021.

Courses

Hands-on introduction to targeted spatial transcriptomics data analysis
Leuven, Belgium

VIB Training
December 2024

Machine Learning and Deep Learning Workshop
Ghent, Belgium

VIB Training
November 2024

Nextflow for reproducible and automated data analysis
Leuven, Belgium

VIB Training
November 2024

Introduction to NGS analysis
Leuven, Belgium

VIB Training
October 2024

Docker and Apptainer (Singularity) for reproducible and automated data analysis
Leuven, Belgium

VIB Training
October 2024

Technical Skills & Interests

Programming Languages
R, Python, Bash, SQL, MATLAB, Git

Bioinformatic skills
GitHub, High Performance Computing (HPC), Conda, Docker, Nextflow, RMarkdown, Quarto, Jupyter Notebooks

Data Analysis and Visualization
tidyverse, ggplot2, plotly, seaborn, matplotlib, pandas, numpy

Omics data types
Bulk RNA-seq, Single-cell RNA-seq, Spatial Transcriptomics, Proteomics, Genome Wide Association Studies (GWAS), Next-Generation Sequencing (NGS)

Laboratory skills
DNA/RNA extraction and quantification, Mammalian cell culture, Bacterial transformation, plasmid prep, lipofectamine transfection, Functional assays

Languages
Spanish (native), English (proficient)

Interests
Computational biology and cancer genomics

My research interests lie at the intersection of computational biology and cancer genomics, with a particular focus on spatial and single-cell omics. I aim to develop and apply statistical and machine learning approaches to study cellular heterogeneity, tumor–microenvironment interactions, and therapy response. I am also interested in building scalable, reproducible workflows for multi-omics data analysis in high-performance computing environments.