

# Axel Rodríguez-Pérez

BSC IN GENOMIC SCIENCES

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## Education

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### Bachelors in Science in Genomic Sciences

NATIONAL AUTONOMOUS UNIVERSITY OF MEXICO (UNAM)

Juriquilla, Qro, MX

2021 – 2025

- GPA: 3.52/4.0
- 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

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### Research Intern

LABORATORY OF MOLECULAR CANCER BIOLOGY, CENTER FOR CANCER BIOLOGY, VIB - KU LEUVEN

Leuven, Belgium

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

CANCER GENOMICS AND BIOINFORMATICS LAB, INTERNATIONAL LABORATORY FOR HUMAN GENOME RESEARCH (LIIGH -UNAM)

Juriquilla, Qro, MX

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

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- 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., Olgun, 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 milieus and an enhanced humoral immune response. *medRxiv (Cold Spring Harbor Laboratory)*. <https://doi.org/10.1101/2025.05.05.25325616>

## Presentations & Talks

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### Machine Learning models for ulceration prediction in mexican melanoma cohort

MINI-SYMPOSIUM: ACRAL MELANOMA RESEARCH IN LATIN AMERICA

International Laboratory for Human Genome Research (LIIGH -UNAM)

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

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### Invited Speaker

5TH SUMMER SCHOOL: INTRODUCTION TO GENOMIC SCIENCES, LIIGH-UNAM

Remotely

July 2025

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

- Delivered an 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

UNDERGRADUATE PROGRAM IN GENOMIC SCIENCES, UNAM

Remotely

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

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- 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

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### Hands-on introduction to targeted spatial transcriptomics data analysis

Leuven, Belgium

VIB TRAINING

December 2024

### Machine Learning and Deep Learning Workshop

VIB TRAINING

Ghent, Belgium

November 2024

### Nextflow for reproducible and automated data analysis

VIB TRAINING

Leuven, Belgium

November 2024

### Introduction to NGS analysis

VIB TRAINING

Leuven, Belgium

October 2024

### Docker and Apptainer (Singularity) for reproducible and automated data analysis

Leuven, Belgium

VIB TRAINING

October 2024

## Technical Skills & Interests

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### 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.