

Rodolfo Padilla

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Computational biologist with 3+ years of wet lab experience (BSL-2, GMP-aligned environments) and expertise in bioinformatics pipeline development. Specialized in translating experimental questions into automated, reproducible workflows using Python, R, and machine learning for research and diagnostics.

Professional Experience

University of Oregon: Laboratory Technician (10/23 - 1/25) (Eugene, OR)

- Performed molecular biology workflows including sample preparation, microscopy, and aseptic technique in BSL-2 certified laboratory following GMP-aligned protocols
- Developed R and Python pipelines for ecological and biological data analysis, improving reproducibility
- Maintained data integrity and documentation standards consistent with GLP expectations

New Frontier Data: Software Developer (6/17 - 1/19) (Washington D.C)

- Developed and optimized machine learning models using TensorFlow and PyTorch, improving inference performance and deployment stability
- Integrated models into production pipelines, collaborating cross-functionally within agile development teams
- Focused on scalability, usability, and maintainability of ML-driven systems

Potomac Holistics: Internet Marketing Manager (8/21 - 8/22) (Rockville, MD)

- Oversaw website architecture, POS integration, and database management; optimized uptime/performance and implemented automated marketing workflows with data-driven processes

Retail Data LLC: Data Collector (3/19 - 2/20) (Germantown, MD)

- Performed in-store audits with accuracy validation; developed QC processes and data verification workflows

Technical Projects & Portfolio

Projects & Portfolio - [Portfolio site: <https://portfolio-site-pi-vert.vercel.app/>]

Marker Finder - Python/Flask bioinformatics tool automating biomarker discovery and primer design (NCBI API + Primer3), with PDF reporting, containerized deployment.

GBM Drug Sensitivity Visualization (GDSC2 Dataset) - Analyzed mutation-specific drug response in glioblastoma using GDSC2 data. Joined pharmacological and genomic datasets in R to explore relationships between gene mutations and drug sensitivity

TickID Hub - Developed ML pipeline for tick image classification (PyTorch → ONNX) deployed via R Shiny and Docker and implemented batch inference and model monitoring for reproducibility.

Education

University of Oregon - Eugene, OR (2022-2025)

Bachelor of Science in Biology, Minor in Chemistry

Relevant Coursework: Biochemistry, Cell Biology, Bacterial-Host Interactions, Microbiology, Data Analysis/Visualization

Montgomery College - Rockville, MD (2020-2021)

Associate of Science in Biology

Technical Skills

Laboratory & Molecular Biology: Aseptic techniques (BSL-2), PCR/qPCR/ddPCR, DNA/RNA extraction, gel electrophoresis, HPLC/FPLC, microscopy, GMP/CLIA compliance, LIMS

Programming & Software: Python, R, JavaScript; Flask, Django, Node.js, Next.js, React, Shiny; SQLAlchemy, MySQL; Docker, Kubernetes, CI/CD; Git

Scientific Computing & ML: NumPy, Pandas, Matplotlib, SciPy, Biopython, PyTorch, NLP, ONNX, scikit-learn; bioinformatics pipelines, sequence analysis.

Data & Visualization: Statistical analysis, experimental design, reproducible pipelines, dashboards, publication-ready figures.

Professional Strengths: Bilingual (English/Spanish), technical writing, problem-solving, team collaboration, GLP/cGMP compliance.