

# 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.