

# MICHAEL J. MARTINEZ

(203) 224-0107 | [Mike.j.martinez99@gmail.com](mailto:Mike.j.martinez99@gmail.com) | [LinkedIn](#) | [Github](#)

## EDUCATION

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### M.Sc. | University of Connecticut | Microbial Systems Analysis

Advisors: Dr. Joerg Graf, Dr. Jonathan Klassen, Dr. Sarah Hird

Graduation Date: May 2023

### B.S. | University of Connecticut | Molecular and Cell Biology

Minor: Psychological Sciences

Graduation Date: May 2021

## PROFESSIONAL / RESEARCH EXPERIENCE

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### Geisel School of Medicine – Center for Quantitative Biology

Research Scientist, Genomic Data Science Core

Lebanon, NH

Oct 2024 - Current

- Created an open-source R package (RGenEDA) geared toward bulk RNA-Seq exploratory data analysis, facilitating frameworks for reproducible and unified analysis within a bioinformatics core.
- Developed reproducible Snakemake workflows for WXS, bulk ATAC-Seq, and miRNA-Seq reducing data-preprocessing time and allowing for increased scalability.
- Converted the core's repertoire of Conda environments to Pixi Workspaces, developing robust SOPs for their use for both core staff and the larger Dartmouth community.
- Support Dartmouth researchers through development of boutique-analysis pipelines for tRNA-Seq and other proprietary sequencing strategies for nuclear receptors.
- Analyze a wide range of projects for core clientele spanning eukaryotic and prokaryotic genomics including scRNA, scATAC, 10x visium/Xenium, MGX, WXS, and bulk sequencing.

### UConn Health Center – Department of Molecular Oncology

Clinical Research Technician I, Rosenberg Lab

Farmington, CT

Jun 2023 – Sept 2024

- Spearheaded the design and application of computational methods in R for multi-omics studies including bulk RNASeq, 16S, and targeted metabolomics across multiple projects
- Utilized bash scripting to automate the processing of raw fastq files for bulk RNASeq on an HPC
- Completed a full DEG/GSEA analysis of Pirc rats in R through multiple Bioconductor packages to highlight the combinatorial effect of naproxen and EPA in colorectal cancer chemoprevention
- Examined the spatial immune architecture of clinical CRC tumor samples through multiplex imaging mass cytometry
- Generated effective and publication quality figures through R to easily communicate findings

### Intus Biosciences

Computational Intern, R&D

Farmington, CT

Jun 2022 – Sept 2022

- Leveraged synthetic PacBio and Oxford Nanopore long reads as a standardized ground-truth input to validate proprietary microbiome clustering software to resolve sequences down to strain resolution
- Aided in pipeline development through a series of custom R scripts to process taxonomy call files

### UConn Molecular and Cell Biology

Student, Klassen Lab

Storrs, CT

Sept 2021 – May 2023

- Managed LIMs database and deposition of raw sequencing reads to NCBI's SRA service
- Assembled and annotated bacterial genomes from Illumina MiSeq reads using SPAdes and Prokka
- Investigated fungal communities of *T. septentrionalis* fungus gardens using R (DADA2 and Phyloseq)

## SKILLS

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**Comp bio:** R, Bash, Python, Snakemake, High-performance cluster computing, Conda environments, R package development, read QC/mapping/alignment

**Omics:** Bulk RNASeq (DESeq2, clusterProfiler), 16S (Phyloseq), MGX (MetaPhlan, Humann3), 10X Multiome, scRNASeq, scATAC (Seurat, Signac), Imaging mass cytometry (imcRtools, cytometer), metabolomics, miRNA-Seq, tRNA-Seq.