

Alejandro Ponce

BIOINFORMATICS ANALYST | RNA-SEQ | VIRAL GENOMICS | REPRODUCIBLE HPC

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PROFILE

Bioinformatics analyst and computational researcher specializing in bulk and single-cell RNA-seq, viral genomics, and reproducible analysis on HPC. Builds R/Python/Nextflow workflows, benchmarks defensible reporting thresholds, and translates complex results into publication-ready evidence, SOPs, and public-data submissions.

TECHNICAL FOCUS

Transcriptomics: bulk RNA-seq, scRNA-seq, DESeq2, fgsea/MSigDB, WGCNA, Seurat | Viral genomics: LoFreq, iVar, samtools, bcftools, intrahost SNV analysis

Scientific computing: R, Python, Bash, Nextflow/nf-core, SLURM, Singularity/Apptainer, Git | Delivery: ggplot2, Quarto, SOPs, SRA/GenBank submissions

EXPERIENCE

University of Tennessee Health Science Center | Researcher I, Bioinformatics

May 2024 - Present

- Develop bulk RNA-seq time-course analyses for CNS infection models using DESeq2, fgsea/MSigDB, and WGCNA; connect modules and pathways to viral load and clinical measures.
- Build low-frequency viral variant workflows with LoFreq and iVar, including primer masking, strand-bias, depth, replicate, and reportable-threshold rules.
- Run Seurat single-cell workflows and scale reproducible analyses with SLURM job arrays, containers, reusable job templates, and standardized publication figures.

Onteko Inc. | Co-Founder / Bioinformatics & ML Lead (part-time)

2022 - Present

- Lead R&D spanning Python scientific software, automated LIBS acquisition, spectral QC, instrument integration, and biological seed-classification workflows.
- Apply PLS, SVM, regularized models, and XGBoost; achieved ~0.86 balanced accuracy / 0.94 ROC AUC in a 1,693-seed ploidy study and ~86% target enrichment in a doubled-haploid study.

MLM Medical Labs | Research Associate

Jul 2021 - Oct 2023

- Supported phase 2-3 clinical-trial laboratory programs through flow-cytometry and plate-based assay validation, receptor-occupancy development, SOPs, and GxP study data packages.

SELECTED OPEN-SOURCE WORK

Viral intrahost variant workflow. Virus-agnostic Nextflow DSL2 pipeline combining LoFreq/iVar calls, consequence annotation, coverage QC, selection analysis, haplotype reconstruction, CI, and SLURM/container execution. [GitHub](#)

Virology & genomics analysis templates. Fourteen reusable R/Python workflows for RNA-seq, WGCNA, VCF, selection, coverage, enrichment, and publication-oriented exports with deterministic synthetic data. [Live gallery](#)

ProLIBSpector - public edition. Python/PyQt scientific software for simulated LIBS acquisition, preprocessing, NIST line matching, interactive spectra, and multi-element spatial mapping. [GitHub](#)

EDUCATION

M.S. Bioinformatics | Brandeis University

2024

B.S. Biology, magna cum laude | University of Memphis

2021

SELECTED PUBLICATIONS

- Spruill-Harrell BB, Ponce-Flores A, et al. Purifying selection constrains Jujuitiba virus evolution in wild *Oligoryzomys nigripes* communities. *PLOS Pathogens* (2026). [DOI](#) ↗
- Roach CM, Streblow ZJ, Zhang Y, Ogorek TJ, Ponce-Flores A, et al. Restructuring antiviral quinazolinone frameworks to derive and optimize inhibitors of Chikungunya virus. *ACS Med. Chem. Lett.* 16(11), 2320-2327 (2025). [DOI](#) ↗
- Williams EP, Xue Y, Yang D, Lee J, Ponce-Flores A, et al. Broad-spectrum antiviral BDGR-164 protects against lethal neurotropic alphavirus infection in mice. *Antiviral Research* (2025). [DOI](#) ↗