Robert A. Petit III, PhD

Senior Bioinformatics Scientist

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OBJECTIVE

Bioinformatician focused on bacterial pathogen genomics and reproducible workflow development, including AI-assisted engineering. Over 15+ years I have built open-source tools used by thousands of users worldwide, and I contribute regularly to community projects such as Bioconda and nf-core.

PROFESSIONAL EXPERIENCE

Bioinformatics Consultant

Simple Bioinformatics, LLC, Cheyenne, WY, 2026–Present

Part-time consulting on sequencing and data analysis, including AI-driven strategies.

- Deployed local inference of open-weight models (DeepSeek, Qwen, GLM) with vLLM, llama.cpp, and SGLang on NVIDIA and AMD GPUs
- Implemented LLM-assisted development, prompt, and review workflows

Senior Bioinformatics Scientist

Wyoming Public Health Laboratory, Cheyenne, WY, 2021–Present

In-house bioinformatician where I develop tools and facilitate trainings.

- Expanded Bactopia and released tools including camlhmp, genome-dl, and gigatyper
- Built and maintain genomic surveillance on Microsoft Azure

Adjunct Professor

University of Wyoming, Laramie, WY, 2022–Present

Adjunct professor in the Department of Mathematics and Statistics where I mentor graduate students and serve on thesis committees.

Senior Data Analyst

Emory University, Atlanta, GA, 2018–2021

Bioinformatician in Tim Read's lab and the Georgia Emerging Infections Program where I developed Bactopia and maintained their Linux servers.

Information Analyst III

Emory University, Atlanta, GA, 2011–2013

Developed sequencing analysis protocols locally on Linux servers I maintained as well as on AWS.

EDUCATION

2018, Doctor of Philosophy in Population Biology, Ecology, and Evolution
Emory University, Atlanta, GA
2011, Master of Science in Bioinformatics
Georgia Institute of Technology, Atlanta, GA
2010, Bachelor of Science in Biology
Valdosta State University, Valdosta, GA

HIGHLIGHTS

Developed Bactopia (bactopia.io) workflow for large scale bacterial genomics

Involved in **40+ Peer-Reviewed Academic Publications**

Grants: CZI $150,000; AWS Cloud Credits and Education, $37,500; Cancer Genomics Cloud, $15,000

Talk: How we avoided AI slop in Bactopia, Nextflow Summit Boston 2026

SKILLS

Domains: Microbial genomics, Nextflow, high-throughput analysis

Platforms: Nextflow, Microsoft Azure (AZ-900), AWS, GitHub

SELECT PUBLICATIONS

camlhmp: reproducible microbial typing tools. MRA 2026

Bactopia: flexible bacterial genome pipeline. mSystems, 2020

S. aureus viewed from 40,000+ genomes. PeerJ, 2018

B. anthracis detection in metagenomes. PeerJ, 2018