

# Dane Gellerup

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Experienced bioinformatics software engineer with 8+ years of experience building scalable, distributed clinical genomics analysis systems on AWS. Specialized in Python parallelization and Rust for high-performance computing and automation. Proven success reducing system runtimes by over 75% and scaling processing of 100+ GB datasets with AWS-native tools. Passionate about delivering efficient and reliable genetic analysis software, building infrastructure to support engineering teams, and enabling clinicians to make informed care decisions.

## CORE SKILLS

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**Bioinformatics & NGS:** SAM/BAM/VCF · FASTQ/FASTA · Illumina · Clinical Genomics

**Programming:** Python · Rust · SQL · Bash · Git · CI/CD · Unit Testing

**Cloud & DevOps:** AWS (S3, EC2, Lambda, RDS, CloudWatch, SQS, CloudFormation) · Docker · Linux · CircleCI

**Frontend:** Angular · React · TypeScript · HTML/CSS

**Tools & Concepts:** Agile · Jira · ETL · Data Integrity · Parallel Computing

## WORK EXPERIENCE

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### Scisco Genetics Inc.

Senior Full Stack Software Engineer - Bioinformatics

JANUARY 2018 – PRESENT, SEATTLE, WA

- Design, build, and deploy backend systems across AWS, Linux, macOS, and Windows, supporting both internal tools and external partner-facing platforms used by clinics across the U.S. and internationally.
- Develop and maintain APIs and backend logic powering Sciscloud, Scisco Genetics' secure web application, enabling automated ETL pipelines, result registration, and real-time data updates.
- Architect and manage custom AWS ECR Docker images, reducing container build times by 80% and saving dozens of engineering hours monthly.
- Lead and own production-ready software systems, including infrastructure supporting clinical donor matching workflows and longitudinal patient monitoring.
- Implement CI/CD pipelines using Git, Docker, and CircleCI with integrated unit and integration testing across multiple environments.
- Refactor performance-critical modules in Python and Rust, achieving a 75% runtime reduction for core analysis pipelines.
- Built tools to accelerate research and development, including a streaming file splitter for parallel AWS Lambda processing of 100+ GB datasets stored on S3.
- Actively modernize and support internal infrastructure by evaluating emerging technologies and implementing scalable, best-practice solutions.
- Collaborate cross-functionally with the CEO, CTO, and senior stakeholders to align infrastructure development with scientific and business goals.

### LifeSpan BioSciences

Genomics Analyst

SEPTEMBER 2017 – DECEMBER 2017, SEATTLE, WA

- Developed custom pipelines and software for human genome analysis using **GATK Best Practices**, enabling robust variant discovery across large Illumina sequencing datasets.
- Automated preprocessing steps including alignment, deduplication, and base quality recalibration using BBTools, BWA, Picard, and GATK.

## WORK EXPERIENCE (CONTINUED)

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### Fred Hutchinson Cancer Research Center

Graduate Intern

JUNE 2017 - AUGUST 2017, SEATTLE, WA

- Created custom Python scripts to manage viral sequence data, allowing for quicker lookup and access by the research team.
- Created quality analysis workflows to scan sequence data on intake and report reads/files outside of quality threshold.

### AIDS Vaccine Research Laboratory - UW Madison

Associate Research Specialist - NGS

OCTOBER 2013 - AUGUST 2016 · Madison, WI

- Managed end-to-end processing of clinical and research samples for **Illumina Miseq** sequencing, including library prep, QC, and run management.
- Developed custom Python, Bash, and R scripts to streamline demultiplexing, adapter trimming, and downstream QC analysis for **HIV/AIDS research pipelines**.
- Maintained meticulous documentation and adhered to lab protocols supporting regulated academic genomics research.

## EDUCATION

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### Boston University // MS, Bioinformatics

SEPTEMBER 2016 - MAY 2017, BOSTON, MA

### University of Wisconsin - Madison // BS, Genetics; Certificate (Minor), Computer Science

SEPTEMBER 2007 - MAY 2012, MADISON, WI

## TECHNICAL PROJECTS

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### DrySeq – Full-Stack Genomic Analysis Platform

<https://www.dryseq.com>

Currently in development at: <https://github.com/dgellerup/DrySeq>

For access, please email [danegellerup@uwalumni.com](mailto:danegellerup@uwalumni.com) for an invite code

Designed and built a secure web application for uploading, managing, and analyzing genomic and primer sequence data. DrySeq features user authentication, FASTA/FASTQ file uploads, automated backend processing with Python, and result tracking via PostgreSQL. The app uses a modern frontend built in React with a clean sidebar-based UI and integrates with a custom Express.js + Python backend. Engineered for scalability, performance, and long-term maintainability with CI/CD pipelines and AWS deployment in mind.

**Stack:** React · TypeScript · Express.js · Python · PostgreSQL · Prisma