

JASON GILLILAND

Computational Biologist & Software Engineer

11 Monadnock Lane
Merrimack, NH 03054
📞 (508) 517 9413
✉️ jdagilliland@gmail.com
🌐 jdagilliland.com
in [jason-gilliland](#)
🐙 [jdagilliland](#)

Technical Skills

Data	ggplot2, Plotly, R-Shiny, Matplotlib,	Data Analysis	NumPyro, JAX, Tidyverse,
Visualization	seaborn		data.table, NumPy, SciPy, Pandas
SQL	PostgreSQL, MSSQL, SQLite	Platforms	Linux/UNIX, MacOS, Windows, Sun Grid Engine (SGE)
Languages	Python, Haskell, R, JavaScript, Matlab, C/C++, Perl	DevOps	Git, Docker, Jenkins, Mercurial, NixOS, Nixpkgs
AWS	EC2, EBS, S3, RDS, IAM, Code-Commit, Batch	Office	LibreOffice, L ^A T _E X, MS Office, Tibco Spotfire

Professional Experience

Pillar Biosciences

Senior Computational Biologist

Natick, MA

November 2021–March 2024

- Optimized hyperparameters for machine learning algorithms to suit different panels, using a random search of the parameter space and custom loss functions.
- Adapted machine learning based CNV caller from proof of concept code to fully operational pipeline component, which reduced false positive calls by ten fold.
- Refactored code bases which had diverged for years of independent development into a coherent whole which met the needs of both. Integrated the git history to reflect the development of both repositories.
- Streamlined the flow of application data between microservices to enforce loose coupling. This helped enable more flexible application execution and faster run times.
- Implemented a BWA based NGS contamination filter to remove known contaminating sequences before they could confound important results.
- Developed an NGS QC application which enabled the production team to spot reagent contamination before it caused costly errors.
- Created a binary parser for raw Illumina outputs to provide data for NGS QC.

Merck Research Laboratories, IT**Boston, MA***Senior Specialist, Scientific Solutions Engineering**April 2020–October 2021*

- Drove product discovery for a data visualization tool for gene expression analysis.
- Led an international engineering team in implementing an R-Shiny data visualization application from the ground up.
- Instituted a Scrum based workflow to maintain feature delivery.
- Architected a data model for storing and displaying complex scientific data across several experimental domains: single cell RNA sequencing (scRNA-Seq), CRISPR, bulk RNA-Seq, microarray.
- Constructed efficient data queries for a database including tables hundreds of millions of rows in length.
- Integrated R-Shiny with a highly specialized scientific Python library (ScanPy) using containerization (Singularity).
- Deployed R-Shiny application to multiple environments automatically using Jenkins.
- Designed informative and attractive scientific visualizations and user interfaces used by dozens of biologists to facilitate drug discovery.

Merck Research Laboratories**Boston, MA***Senior Scientist, Computational Biology**February 2016–March 2020*

- Provisioned and managed AWS resources for computationally intensive bioinformatics applications.
- Developed and maintained QC analysis pipeline for next generation sequencing (NGS) datasets on a high performance computing cluster (HPC).
- Ported bioinformatics processing pipelines from on-prem HPC infrastructure to proprietary cloud computational biology platforms Seven Bridges and DNAnexus, as well as to AWS resources using the Cromwell and Nextflow pipeline DSLs.
- Productized a single-cell RNA-Seq pipeline using Sun Grid Engine.
- Facilitated the transfer and storage of hundreds of TBs of NGS data using Aspera, AWS, Seven Bridges, DNAnexus, and even one time a bunch of hard drives through the mail.

Merck Research Laboratories**West Point, PA***Genetics Intern**June 2015–August 2015*

- Created visualization workflows and SQL queries to aid drug candidate safety evaluation.
- Analyzed and integrated data from next generation sequencing, microarray, nanostring and qPCR experiments.
- Developed statistical power analyses to inform genomics experimental design.

University of Pennsylvania School of Medicine**Philadelphia, PA***Technical Consultant**June 2015–September 2015*

- Instructed PhD level researchers in laser capture microdissection.

Merck Research Laboratories**West Point, PA***Genetics Intern**June 2014–August 2014*

- Organized data sets from heterogeneous sources into a cohesive database to increase clarity, and statistical power.
- Designed workflow to integrate several Matlab data sources into SQL Server database.
- Created statistical data visualizations of gene expression data in Tibco Spotfire, and Matlab.
- Analyzed and integrated data from next generation sequencing, microarray, and qPCR experiments.

Drexel University
Research Technician

Philadelphia, PA
February 2014–June 2014

- Designed flexible command line interfaces for custom tools, accommodating a variety of workflows and standards.
- Deployed self-contained Python packages for easy distribution and installation on high-performance computing platforms.
- Programmed Python application software to analyze and visualize phylogenetic trees of sequencing data.

University of Pennsylvania School of Medicine
Research Specialist

Philadelphia, PA
May 2009–June 2013

- Managed dozens of data sets and thousands of measurements from hundreds of samples.
- Coordinated and performed data processing and analysis for high-throughput next-generation sequencing experiments (RNA-Seq).
- Designed a high throughput qPCR experiment which required 3 technicians, handled data from dozens of patients, and used hundreds of samples.
- Engineered computational image analysis techniques based on OpenCV for characterization of histology image data, used to automatically quantify hundreds of photomicrographs.
- Overhauled gene expression quantitation (qPCR) procedures in laboratory, as well as accompanying data management and statistical analysis strategy.
- Programmed custom data acquisition software for a 3rd party sensor with no published interface.
- Devised a technique for manual single cell sorting for qPCR experiments with which I was able to collect high quality RNA from as few as 100 cells. I then instructed graduate level researchers in its execution.
- Learned flow cytometry, and conducted flow cytometry experiments.
- Engineered techniques for extracting high quality RNA from hard to isolate tissue samples.
- Performed gel electrophoresis, and instructed fellow technicians in the nuances of that technique.
- Conducted RNA isolation and purification.
- Performed RNA to cDNA synthesis for qPCR experiments.
- Performed and instructed PhD researchers in laser capture microdissection.
- Performed and instructed PhD researchers in robot-assisted liquids handling.

Education

Drexel University
Master of Science in Biomedical Engineering
Concentration in Bioinformatics, GPA 3.96

Philadelphia, PA
December 2015

University of Pennsylvania
Bachelor of Arts in Biology
Concentration in Neurobiology

Philadelphia, PA
August 2012