

JASON GILLILAND

Computational Biologist & Software Engineer

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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, Mat- lab, 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*