TIMOTHY JOHNSTONE

Sr. Principal Computational Scientist | AWS-Certified Cloud Solutions Architect

(503) 318-0962 | Seattle, WA | timothy.g.johnstone@gmail.com | timothyjohnstone.com

PROFESSIONAL SUMMARY --

Ph.D. geneticist and computational leader specializing in cloud architecture and NGS bioinformatics. 20+ years of experience analyzing data from novel sequencing assays, developing high-throughput screening modalities, and engineering cloud-native bioinformatics pipelines. Passionate about building and managing secure, scalable cloud systems and developer resources from the ground up to accelerate high-growth biotech organizations and analytical teams.

AREAS OF EXPERTISE --

Infrastructure & Cloud
- Multi-account AWS (Control Tower)
- Scientific Computing (HPC)
- Infrastructure as Code (IaC)
- Cloud Governance & FinOps

Computational Biology
- NGS/HTS Data Analysis
- Data Management
- Pipeline Engineering (Nextflow)
- RNA, Cell, & Gene Therapy

Development & AI
- Python/R
- CI/CD (GitHub Actions, Docker)
- LLM, RAG, MLOps
- Version Control & Documentation

PROFESSIONAL EXPERIENCE --

Senior Principal Computational Scientist; Cloud Architect | Shape Therapeutics | Seattle, WA | 2021 – 2025
Head of Cloud and technical lead for a division of computational biology and ML scientists, managing all aspects of cloud infrastructure and scientific software development. Oversaw computational analysis of complex genomic screens and guided the development, documentation practices, and culture of a successful team.
- **AWS Infrastructure:** Built & managed a multi-account AWS environment for 120+ users and 200TB+ of data from scratch, including cost optimization, networking, security, systems administration, authentication, and user training.
- **AI/MLOps**: Orchestrated the development of an internal LLM+RAG chatbot for researchers and deployed GPU compute, ML experiment tracking, and infrastructure for protein engineering and foundation model training.
- **Bioinformatics:** Designed experiments, wrote Nextflow pipelines, and processed NGS data for novel high-throughput screening assays to improve editing efficiency, assess viral genome integrity, and refine cell line development.
- **Automation & Data Management:** Engineered a fully automated, Python-based solution for synchronizing Illumina and Nanopore NGS data to the cloud, and orchestrated internal and external data sharing for collaborations.
- **CI/CD & DevOps:** Built robust CI/CD pipelines using GitHub Actions and a secure portal (AWS ALB, ECS, S3, VPC, IAM, Route53, CloudFormation, Okta) for internally hosted web-apps, dashboards, static hosting, and Docker images.
- **Software Development:** Developed a Python package for optimized fuzzy matching of DNA/RNA sequences which was integrated into many internal analytical pipelines, reducing development and primary analysis time over 50%.

Principal Scientist | Bristol Myers Squibb (Celgene) | Seattle, WA | 2019 – 2021
Drove the development of novel analytical assays for CAR/TCR constructs, executed multi-omics analyses, developed analytical applications and pipelines, and served as the primary lead for a major cloud migration.
- **Assay Development:** Led the analysis of lentiviral integration site analysis data and CRISPR indels, resulting in non-clinical reports that directly informed multiple successful BLA and IND filings.
- **Pipeline Engineering:** Developed rapid analytical pipelines for Nanopore sequencing data to determine recombination patterns in CAR and eTCR constructs, leading to integrity improvement for multiple clinical candidates.
- **Cloud Strategy:** Planned and executed a major post-acquisition cloud migration to ensure the scalability and integration of 3+ years of NGS analytics data, AI/ML efforts, web applications, and reproducible research tools.
- **Web Applications:** Developed an R Shiny application used to prioritize candidates for preclinical CAR development.

Senior Data Scientist | Juno Therapeutics | Seattle, WA | 2016 – 2019
Leveraged breakthrough single-cell and bulk sequencing technologies to discover novel antigen receptors for cancer immunotherapy. Constructed bioinformatics tools and developed the company's cloud-based computing infrastructure for single-cell and bulk sequencing technologies. Juno was acquired by Celgene during my tenure.

- **NGS Pipelines:** Constructed and optimized pipelines for ATACSeq, RNASeq, and TMISeq to yield actionable biological conclusions, collaborating with molecular biology and translational researchers throughout the company.
- **Clonality Analysis:** Led the development of timecourse T-cell clonality analyses in R, tracking patient samples from product to post-infusion. Refined algorithms to improve signal-to-noise ratios and eliminate false positives.
- **Process Optimization:** Implemented event notifications and automations to improve the efficiency of the NGS sequencing workflow for data scientists, eliminating hours to days of lost communication time with each analysis.
- **Cloud Development & HPC:** Managed the company's NGS analytics cloud infrastructure and optimized Snakemake pipelines on autoscaling clusters (AWS ParallelCluster) with thousands of CPUs.

Graduate Researcher | Yale University School of Medicine | New Haven, CT | 2012-2016
Investigated non-canonical translation and regulatory roles of uORFs in the vertebrate transcriptome.

- **Novel NGS methods:** Utilized ribosome profiling, GRO-seq, microRNA-seq, and others to discover translated regions in RNAs previously deemed non-coding, find novel enhancers in viral response, and elucidate piRNA biogenesis.
- **Data Science:** Leveraged R and Python to systematically characterize novel small ORFs in large genomic datasets.

Undergrad Team Leader | Brown Center for Computational Molecular Biology | Providence RI | 2009-2012
Managed a team of undergraduate lab members as lead annotator for the discovery of DNA cis-regulatory modules and release of a genome browser focused on transcriptional regulation.

Bioinformatics Research Assistant | OHSU Affymetrix Microarray Core | Portland, OR | 2006; 2008
Performed statistical analyses, managed large scale blood sample study data, developed protocols for nanogram-level RNA handling, and acted as a biological advisor for PSU physics labs, resulting in authorship on multiple publications.

EDUCATION ---

Ph.D. in Genetics, Yale University, *New Haven, CT* | 2012-2016
B.S. with Honors in Computational Biology, Brown University, *Providence, RI* | 2008-2012

For publications, patents, certifications, and additional qualifications, visit **linkedin.com/in/timjohnstone**