

# Shaun Jackman

PhD Bioinformatics, BAsC Computer Engineering

[sjackman@gmail.com](mailto:sjackman@gmail.com) • +1-778-235-0342 • <https://sjackman.ca>

I am a PhD graduate in bioinformatics, a first class honours graduate in computer engineering, an open-source software developer, an avid traveller, a singer, and an enthusiastic cook. I have sixteen years of industry and academic experience developing software in C++, Python, and R, including ten years developing high-performance parallel algorithms for genome sequence assembly, and six years developing embedded and real-time control systems. I developed ABySS 1.0, the first software tool to assemble a human genome from Illumina sequencing, as well as ABySS 2.0, the first assembler to reconstruct a twenty-gigabase conifer genome, seven times the size of the human genome. I enjoy camping, cycling, swing dancing, theatre, and cooking and sharing good food with friends, and I sing tenor with the internationally recognized Chor Leoni Men's Choir.

## Education and Employment

### **2019–present—Senior Computational Biologist—10x Genomics**

Developed algorithms for the flagship single-cell gene expression software tool, Cell Ranger, which is implemented in Rust and Python.

### **2012–2019—PhD Bioinformatics—University of British Columbia**

NSERC Canada Graduate Scholarship (CGS) student in bioinformatics. Published five papers as the first author. The memory-efficient genome sequence assembly tool ABySS 2.0 (2017) has received over 100 citations. Coursework in bioinformatics, statistics, machine learning, and genetics. GPA 4.26 (93%)

### **2008–2012—Computational Biologist—BC Cancer Genome Sciences Centre**

Developed the genome sequence assembly software package, ABySS, implemented in C++. This heavily parallel and distributed software system, which uses both MPI and OpenMP for parallel computation, was the first system to assemble a human genome using short-read sequencing technology.

### **2004–2007—Embedded Firmware Developer—Pathway Connectivity**

Developed the firmware for Pathway's product line of lighting control devices. These devices, which use Atmel's AVR and ARM microcontrollers, convert between a variety of lighting-control protocols. Modernized the lighting control industry in developing a device, the Pathport, to adapt legacy serial equipment to an Ethernet network. This device won an award for best new product at the industry trade show, Lighting Dimensions International.

### **1998–2004—BAsC Computer Engineering—Simon Fraser University**

First class honours scholarship student in computer engineering. Completed an honours undergraduate thesis and two years of co-op work experience at three companies. GPA 3.85

## **Expertise**

### **Bioinformatics and Genomics**

Analysis of DNA and RNA sequencing, including genome sequence assembly, sequence alignment, variant calling, genome annotation, visualization, and inspection of genome assemblies, variants, and rearrangements. Developed ABySS 2.0 to assemble twenty gigabase conifer genomes, seven times the size of human.

### **Data Analysis Pipelines**

Extensive experience in constructing data analysis workflows, visualization, reporting, and communicating results effectively with aesthetic appeal.

### **Problem Solving and Leadership**

A practiced talent to decompose complex problems into well-defined components, enabling concurrent development by a team. Daily involvement in reviewing code to provide constructive criticism with empathy, to improve both the developer's skills as well as code quality. Use of automated testing to ensure correctness and provide timely automated feedback on code quality to developers.

### **Open-source Developer**

Developer and member of the project leadership committee of Homebrew, the package manager for macOS and Linux. Created Homebrew for Linux, and grew its community of fifty thousand users.

### **Sequencing Technologies and Genomic Assays**

10x Genomics Chromium, Illumina HiSeq, Oxford Nanopore, Bionano Genomics

### **Programming Languages**

Rust, C++, C, Python, R, Ruby, shell, and assembly

### **Programming Methodologies**

Functional, generic, and object-oriented programming

### **Parallel Processing**

OpenMP, POSIX threads, C++ threads, and MPI

### **Continuous Integration**

CircleCI, Travis CI, Azure Pipelines, and GitHub Actions

### **Cloud and Containerization**

AWS, Docker, and Singularity

### **Version Control**

Git and GitHub wizard. Proven ability to solve any git calamity.

## Selected Publications

A selection from over 30 peer-reviewed publications, h-index of 21, and over 8,000 citations  
**ORCA: A Comprehensive Bioinformatics Container Environment for Education and Research**

SD Jackman, T Mozgacheva, S Chen, *et al.* (2019) *Bioinformatics*  
**Tigmint: Correcting assembly errors using linked reads from large molecules**

SD Jackman, L Coombe, J Chu, *et al.* (2018) *BMC Bioinformatics*  
**ABBySS 2.0: Resource-efficient assembly of large genomes using a Bloom filter**

SD Jackman, BP Vandervalk, H Mohamadi, *et al.* (2017) *Genome Research*  
**Organellar Genomes of White Spruce (*Picea glauca*): Assembly and Annotation**

SD Jackman, RL Warren, EA Gibb, *et al.* (2015) *Genome Biology and Evolution*  
**UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation**

SD Jackman, J Bohlmann, I Birol. (2015) *PLOS ONE*  
**Assembling the 20 Gb white spruce (*Picea glauca*) genome from WGSS data**

I Birol, A Raymond, SD Jackman, *et al.* (2013) *Bioinformatics*  
**Draft genome of the mountain pine beetle, *Dendroctonus ponderosae* Hopkins**

CI Keeling, MM Yuen, . . . , SD Jackman, *et al.* (2013) *Genome Biology*  
**De novo assembly and analysis of RNA-seq data**

G Robertson, J Schein, . . . , SD Jackman, *et al.* (2010) *Nature Methods*  
**Assembling genomes using short-read sequencing technology**

SD Jackman, I Birol (2010) *Genome Biology*  
**De novo transcriptome assembly with ABySS**

I Birol, SD Jackman, CB Nielsen, *et al.* (2009) *Bioinformatics*  
**ABySS-Explorer: visualizing genome sequence assemblies**

CB Nielsen, SD Jackman, I Birol, *et al.* (2009) *IEEE Transactions on Visualization and Computer Graphics*  
**ABySS: a parallel assembler for short read sequence data**

JT Simpson, K Wong, SD Jackman, *et al.* (2009) *Genome Research*