

Shaun Jackman

PhD Bioinformatics, BAsc Computer Engineering
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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.

Education and Employment

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 over fifteen thousand users.

Sequencing Technologies and Genomic Assays

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

Programming Languages

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*

ABYSS 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*