Shaun Jackman, Bioinformatics PhD Candidate

I am a PhD candidate in bioinformatics, a first class honours graduate in computer engineering, a computer and electronics enthusiast, an open-source software developer and advocate, an avid traveller, a hiker, a singer, and an experimental cook. I have fifteen years of industry and academic experience developing software in C++ and a variety of scripting languages, including nine years developing high-performance distributed and parallel algorithms for genome sequence assembly, and six years developing embedded and real-time control systems. I have extensive experience developing portable software for POSIX systems such as Linux and macOS. When developing performance-critical software, I understand the hardware from the transistor up.

Education

2012–present—Bioinformatics PhD Candidate—University of British Columbia

NSERC CGS-M and CGS-D scholarship student in bioinformatics. Coursework in bioinformatics, statistics, machine learning, and genetics. GPA 4.26 (93%)

1998–2004—BASc Computer Engineering—Simon Fraser University

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

Work Experience

2008–2012—Computational biologist—BC Cancer Genome Sciences Centre

Developed the genome sequence assembly software package, ABySS. 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 Inc.

Developed the firmware for Pathway's product line of small, low-cost lighting control devices. These small 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 to adapt legacy lighting control equipment to Ethernet. This industry-changing product, the Pathport, won an

award for best new product at the industry trade show, Lighting Dimensions International.

2002 May—Co-op work experience—Vortek Industries Ltd.

Worked on the rapid thermal processing tool used in the manufacturing of semiconductor devices. Developed the temperature sensor and lamp power control system using the QNX real-time operating system.

Volunteer Experience

2002–present—Open-source developer

Maintain open-source bioinformatics software packages for Homebrew and Linuxbrew. Lead developer of Linuxbrew, the Homebrew package manager for Linux.

Selected Publications

A selection of 12 of 29 peer-reviewed publications, h-index of 20, and over 7,000 citations

ABySS 2.0: Resource-efficient assembly of large genomes using a Bloom filter

Jackman SD, Vandervalk BP, Mohamadi H, Chu J, Yeo S, Hammond SA, Jahesh G, Khan H, Coombe L, Warren RL, et al. (2017) **Genome Research**

Organellar Genomes of White Spruce (*Picea glauca*): Assembly and Annotation

Jackman SD, Warren RL, Gibb EA, Vandervalk BP, Mohamadi H, Chu J, Raymond A, Pleasance S, Coope R, Wildung MR, et al. (2015) *Genome Biology and Evolution*

Improved white spruce (*Picea glauca*) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism

Warren RL, Keeling CI, Yuen MMS, Raymond A, Taylor GA, Vandervalk BP, Mohamadi H, Paulino D, Chiu R, **Jackman SD**, et al. (2015) *The Plant Journal*

UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation

Jackman SD, Bohlmann J, Birol İ. (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, NY Liao, TR Docking, SK Chan, GA Taylor, DL Palmquist, **SD Jackman**, et al. (2013) *Genome Biology*

The genome and transcriptome of the pine saprophyte Ophiostoma piceae

S Haridas, Y Wang, L Lim, SM Alamouti, **SD Jackman**, et al. (2013) *BMC Genomics*

De novo assembly and analysis of RNA-seq data

G Robertson, J Schein, R Chiu, R Corbett, M Field, **SD Jackman** et al. (2010) *Nature Methods*

Assembling genomes using short-read sequencing technology

SD Jackman and 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*

Knowledge

Bioinformatics

Techniques for analysis of whole-genome shotgun sequencing and RNA-seq, including *de novo* sequence assembly, sequence alignment, variant calling, genome annotation, and visualization and inspection of genome assemblies, variants, and rearrangements.

Programming languages

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

Parallel processing

OpenMP, MPI, and POSIX threads.

Operating systems

macOS, Debian, Ubuntu, and other GNU/Linux distributions.

Awards

University of British Columbia

- 2013-2018 Natural Sciences and Engineering Research Council of Canada (NSERC) Canada Graduate Scholarship (CGS-M and CGS-D)
- 2012–2013 CIHR/MSFHR Strategic Training Program in Bioinformatics

Simon Fraser University

- 1999–2004 Open Undergraduate Scholarship
- 1998–1999 Tadeusz Specht Memorial Entrance Scholarship in Science