Shaun Jackman

PhD Student Bioinformatics, BASc (First Class Hons.) Computer Engineering

Background

I am a PhD student 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 amateur chef. I have twelve years of industry and academic experience developing software in C++ and a variety of scripting languages, including six 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 GNU/Linux and Mac OS X. When developing performance-critical software, I understand the hardware from the transistor up.

Education

2012–present PhD Student Bioinformatics, 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 (First Class Hons.) Computer Engineering, Simon Fraser University

Scholarship 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 Agency 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 including DMX512, analog, PWM and contact closure. Modernized the lighting control industry in developing a device, the Pathport, to adapt legacy lighting control equipment to Ethernet. This industry-changing product won an award for best new product at the industry trade show, Lighting Dimensions International.

2002 May–Aug — 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 the Mac OS package manager, Homebrew-science, and the Debian distribution of GNU/Linux.

Selected Publications

8 of 19 peer-reviewed publications, h-index 14, over 2000 citations

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 TVCG*

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 (ABySS), sequence alignment (BWA, gmap, exonerate, BLAT, BLAST), variant calling (samtools), genome annotation (MAKER) and visualization and inspection of genome assemblies and rearrangements (IGV)

Programming languages

C++, C, R, Python, Ruby, Matlab, Haskell and assembly

Parallel processing

OpenMP, MPI and POSIX threads

Operating systems

Mac OS X, Debian, Ubuntu and other GNU/Linux distributions

Awards

University of British Columbia

2013–present   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