Shaun Jackman

BASc (First Class Hons.) Computer Eng.

Background

I am a first class honours graduate in computer engineering, a masters student in bioinformatics, a computer and electronics enthusiast, an open-source software advocate, an avid traveller, a climber, a singer and an experimental amateur chef. I have ten years of industry experience developing software in C++, C and assembly, including four 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.

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 MPI, pthread 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 DIN-rail-mounted devices, which use Atmel's AVR microcontroller, convert between a variety of lighting-control protocols including DMX512, analog, PWM and contact closure. Modernized the lighting control industry by developing a novel piece of equipment, 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 — Debian developer

Maintain open-source software packages for the Debian distribution of GNU/Linux. Member of the Debian Med team, which maintains a menagerie of bioinformatics software.

Selected publications

De novo assembly and analysis of RNA-seq data
G Robertson, J Schein, R Chiu, R Corbett, M Field, **SD Jackman** et al.
Nature Methods 2010

Assembling genomes using short-read sequencing technology
SD Jackman and I Birol *Genome Biology* 2010

De novo transcriptome assembly with ABySS
I Birol, **SD Jackman**, CB Nielsen et al. *Bioinformatics* 2009

ABySS-Explorer: visualizing genome sequence assemblies
CB Nielsen, **SD Jackman**, I Birol et al.
IEEE Transactions on Visualization and Computer Graphics 2009

ABySS: a parallel assembler for short read sequence data
JT Simpson, K Wong, **SD Jackman** et al. *Genome Research* 2009

Education

2012–present MSc Bioinformatics, University of British Columbia
Scholarship student in bioinformatics.

1998–2004 BASc (First Class Hons.) Computer Eng., 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.

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), visualization and inspection of genomic re-arrangements (IGV) and analysis of tumour-normal pairs to identify somatic mutations

Programming languages
C++, C, assembly language, Python, Matlab, Java, Perl and Haskell

Parallel processing
POSIX threads, OpenMP and MPI

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

Awards

University of British Columbia
2012–present CIHR/MSFHR Strategic Training Program in Bioinformatics

Simon Fraser University
1999–2004 Open Undergraduate Scholarship
1998–1999 Tadeusz Specht Memorial Entrance Scholarship in Science