James Boocock

Curriculum Vitae

Education

2014–2016 (expected)	**Masters**, *The University of Otago*, Dunedin, NZ. Genetics	
2012–2013	**Diploma for Graduates**, *The University of Otago*, Dunedin, NZ. Genetics and Statistics	
2008–2012	**Bachelor of Science**, *The University of Otago*, Dunedin, NZ. Computer Science	

Computer Skills

Basic	SQL, Amazon API Tools, Circos
Intermediate	Java, C, C++, Linux System Administration, Parallelisation, IBM Load Leveler, Git, visualisation packages (ggplot2, circos, Gvis, Inkscape, Base R)
Advanced	Python, Unix Command-line, R, RStudio, Bioinformatics software (samtools, bcftools, pseq, XHMM, bedtools, …)

Background

I utilise my knowledge of computer science, statistics, and genetics to investigate questions related to the genetics of complex disease and agriculture. My masters project focuses on the impact that copy number variation has on gout and the apple genome.

Employment

2015–Present	**Associate Research Fellow**, *Anatomy Department*, University of Otago.
Summary	Responsible for the processing and analysis of sequenced ancient and modern DNA samples in the Matisoo-smith laboratory at the University of Otago.
Outputs	Creation of a pipeline for processing modern and ancient DNA samples https://github.com/smilefreak/ancient_dna_pipeline.
2013–Present	**Assosciate Research Fellow**, *Biochemistry Department*, University of Otago.
Summary	

- Rare and common variant analysis of captured sequence data from 427 hyperuricaemic cases and 455 controls.
- Causal variant analysis of a published Uric acid GWAS dataset using fine mapping software.
- Rare and common variant analyses of the mitochondrial genomes from people of Polynesian ancestry.

Outputs	○ Development of Shiny app for performing SNP variant QC https://github.com/smilefreak/siteQCresequencing
	○ Creation of a Python package for performing finemapping analysis https://github.com/smilefreak/fine_mapping_pipeline
2012–2013	**Summer Studentship**, *Summer Of eResearch*, University of Otago and NZ eScience Infrastructure (NESI).
Summary	Worked on an interface between Galaxy and Galaxy using Python. Other work from the project involved developing a bioinformatics pipeline for analyses of selection signatures in genomic data. The pipeline has been published in Frontiers in genetics https://github.com/smilefreak/selectionTools.
2012–2013	**Summer Studentship**, *Summer Of eResearch*, University of Otago and NZ eScience Infrastructure (NeSI).
Summary	The project focused on maintaining a local Galaxy bioinformatics instance. Added a large amount of tools to the local Galaxy instance (Galaxy is a web interface for bioinformatics software) requiring scripting in Bash and Python https://github.com/smilefreak/OtagoGalaxy.

Teaching

2015–Present	**Mozilla Study Group Coordinator**, University of Otago.
	Coordinator and founding member of the University of Otago Mozilla Study Group http://smilefreak.github.io/studyGroup/.
2015–Present	**Instructor**, *Software carpentry*.
	Trained software carpentry instructor capable of teaching the Python, Shell, R, Bash, Git, or Database modules. To date, have been involved in organising and instructing at one workshop locally.
2015 April	**Guest Lecturer**, *Statistics Department*, University of Otago.
	Delivered a lecture to a 4th year statistical bioinformatics paper (STAT435). Content was focused on Next-Generation sequencing (NGS) technologies and core computing skills, such as the Shell and R programming.
2014–2015	**Lego robot tutor**, *Computer Science*, University of Otago.
	Taught 8-12 year old children basic programming and problem solving using Lego Mindstorms robots
2011–2013	**Laboratory teaching assistant**, *Computer Science*, University Of Otago.
	Demonstrated for first and second year CS courses that had course content involving algorithms, datastructures, and programming. Knowledge of C, Java, and python was required
2011–2013	**Private Tutoring**, *Computer Science*, University of Otago.
	Privately tutored 2nd and 3rd year computer science students. Knowledge of Java, C, and SQL was required.

Awards

2014   Departmental stipend ($13,000) for Masters degree

Academic Outputs

2015   *Elzabeth A. Matisoo-Smith, Anna Gosling, James Boocock et al.* A European mitochondrial haplotype identified in ancient Phoenician remains from Carthage, North Africa (Submitted to the Journal of Archaelogical science)

2015   *J Boocock, D Chagné, TR Merriman, M Black*, The distribution and impact of common copy-number variation in the genome of the domesticated apple, Malus x domestica Borkh (in review at BMC Genomics).

2015   *Karen Greig, James Boocock, Stefan Prost, et al*, Complete Mitochondrial Genomes of New Zealand's First Dogs (PLoS ONE)

2015   *S Sawaya, J Boocock, MA Black, NJ Gemmell*, Exploring possible DNA structures in real-time polymerase kinetics using Pacific Biosciences sequencer data (BMC bioinformatics).

2014   *M Cadzow, J Boocock, HT Nguyen, P Wilcox, TR Merriman and MA Black*. A bioinformatics workflow for detecting signatures of selection in genomic data (Frontiers in genetics), joint first author

2013   *J Boocock, TR Merriman, MA Black and D Chagne*. Copy number variation in Malus x domestica (apple). Mapnet NZ Conference (Lincoln October 2013).

2013   *J Boocock, D Eyers, P Wilcox, TR Merriman and MA Black*. Connecting Genetics Researchers to NeSI, eResearchNZ Conference (Christchurch July 2013).

Interests

- Guitar
- Open source Software
- Crowd sourcing
- Weight lifting
- Reading
- Data re-use

References

Avaliable on request