

James Boocock

Curriculum Vitae

Education

- 2014–2016 **Masters of Science**, *The University of Otago*, Dunedin, NZ.
(expected) 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

Computational 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

Background

I utilise my knowledge of computer science, statistics, and genetics to investigate problems in biology. My masters project has focused around the impact that copy number variation has on gout and the apple genome.

Research Experience

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

- Development of a Shiny app for performing variant QC
<https://github.com/smilefreak/siteQCsequencing>
 - 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).
Worked on an interface between Galaxy and NeSI using Python. Developed a bioinformatics pipeline for analyses of selection signatures in genomic data, which has now 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).
Maintained a local Galaxy server, and added a number of tools to this instance. This project required extensive knowledge of Bash and Python
<https://github.com/smilefreak/OtagoGalaxy>.

Teaching Experience

- 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 in 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 **Robocup Tutor**, *Computer Science*, University of Otago.
Taught 8-12 year old school children basic programming and problem solving using the Lego Mindstorms robots.
- 2011–2013 **Laboratory Demonstrator**, *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 + course fees) for Masters degree

Publications

- 2015 *Elizabeth A. Matisoo-Smith, Anna Gosling, J Boocock et al.* A European mitochondrial haplotype identified in ancient Phoenician remains from Carthage, North Africa (Submitted to the Journal of Archaeological science)
- 2015 *J Boocock, D Chagné, TR Merriman, MA Black*, The distribution and impact of common copy-number variation in the genome of the domesticated apple, *Malus x domestica* Borkh (BMC Genomics).
- 2015 *Karen Greig, J 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

Posters

- 2015 *J Boocock*, My Research Toolkit, ResBaz (Melbourne, Australia February 2015)
- 2014 *J Boocock, M Cadzow, HT Nguyen, David Chagné, P Wilcox, TR Merriman, MA Black*, selectionTools: A pipeline for the detection of genome-wide signatures of selection, applied to *Arabidopsis Thaliana*, QMB 2014 (Queenstown August 2014)

Presentations

- 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 Eysers, P Wilcox, TR Merriman and MA Black*. Connecting Genetics Researchers to NeSI, eResearchNZ Conference (Christchurch July 2013).
- 2013 *J Boocock, E Hills, TR Merriman and MA Black*. Incorporating tools for detecting signatures of selection into Galaxy, eResearch summer studentship presentation (Wellington Feb 2013)
- 2012 *J Boocock, E Hills, TR Merriman and MA Black*. Galaxy and 1000 Genomes, eResearch summer studentship presentation (Auckland Feb 2012)

Professional Reviewing

2015–Present BMC Developmental Biology