James Boocock

Curriculum Vitae

▬▬ Education

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

▬▬ Programming Skills

Basic SQL,Amazon API Tools

Intermediate JAVA,C,C++,R,Linux System Administration, Parralel Programming,IBM Load Leveler,Statistics,GIT,Bioinformatics Tools

Advanced Python, Unix Command-line

▬▬ Work Experience

2013–Present **Assosciate Research Fellow**, *Biochemistry Department*, University of Otago.
Investigating Copy-number variation in plant and human DNA sequence.

Current Work
- Developed a custom XML-RPC server using python for processing data from the 1000 Genomes Project on Amazon EC2 for further processing on local HPC instances.
- Used the R programming language to analyse copy number variation in apple DNA sequence data.
- Processing large genomic data sets using Unix command-line tools.

2012–2013 **Summer Studentship**, *Summer Of eResearch*, University of Otago and NZ eScience Infrastructure (NESI).
Worked on an interface between galaxy and Globus using Python. Other work from the project involved developing a bioinformatics pipeline for analyses of selection signatures in genomic data. The pipeline is currently in preparation for publication and can be found at the url https://github.com/smilefreak/MerrimanSelectionPipeline

Outputs
- Developed a prototype version of a Galaxy Globus interface using grython a jython version of Grisu which is an open source Java framework designed to sit on top of grid middleware.
- Parralelisation of genomic selection tools for standard use, and development of scripts to take advantage of the NeSI IBM load leveler cluster.
- Python program to run genomic selection tools and process the intermediate data files.

2012–2013 **Summer Studentship**, *Summer Of eResearch*, University of Otago and NZ eScience Infrastructure (NeSI).

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. The github repo for that project can be found at the url https://github.com/smilefreak/OtagoGalaxy, this project remained a common fixture throughout all subsequent employment. Also helped members of the Merriman Lab with statistical and programming based questions writing scripts and adding tools to the galaxy instance as required.

Outputs
- Wrapped or created tools at the request of lab members and some faculty to the galaxy instance. The main languages used were bash and python with some C and Java.
- Server setup and administration of the galaxy server, requiring extensive unix command-line usage.

2011-2013 **Laboratory teaching assistant**, *Computer Science Department*, University Of Otago.

Assisted with laboratories for first and second year over three years focusing on algorithms, datastructures and Object-orientated programming. C and Java were the languages used for these papers.

2011-2013 **Private Tutoring**, *Computer Science*, University of Otago.

Tutored two students through many computer science papers in the second and third year of their computer science degree. Java, C and SQL languages were required.

Academic Outputs

2013 In preparation for publication: A*M Cadzow, J Boocock, HT Nguyen, P Wilcox, TR Merriman and Michael A Black* bioinformatics workflow for detecting signatures of selection in genomic data (manuscript in preparation)

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
- Opensource Software
- Crowd Sourcing
- Weight Lifting
- Reading
- Data re-use