

# 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, Parallelisation, IBM Load Leveler, Statistics, Git, Bioinformatics Tools  
Advanced Python, Unix Command-line

---

### Background

My work to date has utilised my knowledge of computer science and Unix systems to implement HPC solutions for problems in genomic data analysis and human health applications. This work involved close collaboration with biologists, statisticians and other computer scientists.

---

### Work Experience

2013–Present **Associate Research Fellow**, *Biochemistry Department*, University of Otago.  
Summary 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).

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 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 Galaxy interface using grython a jython version of Grisu which is an open source Java framework designed to sit on top of grid middleware.
  - Parallelisation 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).
- 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. 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.
- Outputs
- Wrapped or created tools at the request of lab members and 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*, University Of Otago.
- Summary 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.
- Summary Tutored two students through many computer science papers in the second and third year of their computer science degree. Knowledge of Java, C and SQL was required.

## Academic Outputs

- 2013 *M Cadzow, J Boock, HT Nguyen, P Wilcox, TR Merriman and MA Black*. A bioinformatics workflow for detecting signatures of selection in genomic data (manuscript in preparation)
- 2013 *J Boock, TR Merriman, MA Black and D Chagne*. Copy number variation in *Malus x domestica* (apple). Mapnet NZ Conference (Lincoln October 2013).
- 2013 *J Boock, D Eysers, 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

Available on request