



Position Title:	Postdoctoral Researcher, Epigenome Editing Computational Genomics
Classification:	Level A/B
Faculty/Office:	Health and Medical Sciences
School/Division:	Centre for Medical Research
Centre/Section:	Harry Perkins Institute of Medical Research
Supervisor Title:	Professor Ryan Lister

Your work area

This position is based within the the Epigenetics and Genomics Laboratory, led by Ryan Lister and located at the Harry Perkins institute of Medical Research and the UWA Centre for Medical Research (CMR), within the Faculty of Health and Medical Sciences. The [Lister Lab](#) is comprised of molecular, cellular and computational biologists, forming a multi-disciplinary team environment undertaking a diverse range of epigenetics and genomics research. We utilize molecular, cellular, genomic and computational approaches in multiple systems to investigate cellular mechanisms that control the usage of information encoded in the genome, and their roles in cell function and development. We have a particular interest in characterization and manipulation of the epigenome and cell identity using genomic and synthetic approaches.

Reporting Structure

Reports to: Professor Ryan Lister

Your role

A post-doctoral position is available for a computational biologist to undertake research in the area of targeted epigenome editing. The successful applicant will have the opportunity to lead the computational analyses in research projects using sequencing-based high-throughput single cell profiling techniques to develop, optimize and apply new mammalian epigenome editing tools. The appointee will collaborate closely with experimental biologists in the group and will lead the computational analysis and interpretation of genomic datasets, in addition to contributing to experimental design and project direction.

Candidates with a background in computational biology and experience in single cell genomics are encouraged to apply. Candidates should have a PhD in a relevant discipline (Bioinformatics, Computer Science, Molecular Biology, etc). Demonstrated expertise in at least one common programming language (e.g. R, Python, Perl, C++, Java) and software version control (e.g. GitHub) is essential. Previous experience in the analysis of high-throughput sequencing data (e.g. RNA-seq, ChIP-seq, DNA methylation, chromatin accessibility) and statistical modeling of high-dimensional data is highly desirable. An understanding of the experimental techniques underlying such genomics experiments is advantageous. This is a full-time position, initially for a period of two years, with the possibility of further extension.

Key responsibilities

- Lead the computational analyses in research projects using sequencing-based high-throughput single cell profiling techniques to develop, optimize and apply new mammalian epigenome editing tools.
- Collaborate closely with experimental biologists in the group, including contribution to experimental design and project direction.
- Establish computational approaches for single cell genomics data analysis specific to the research project, and where appropriate aid colleagues in the use of such approaches.
- Keep high quality records and use systems for fully reproducible recording of data analysis processes and results, for example using version control systems such as GitHub and reports generated using R Markdown or Python Jupyter Notebook.
- Write research articles for publication in leading international journals.

- Teach and supervise new researchers and students in the use and development of computational research approaches relevant to his/her project.
- Travel for research meetings and for research collaboration visits.
- Other duties as directed.

Your specific work capabilities (selection criteria)

- PhD in Bioinformatics, Computer Science, Molecular Biology or related discipline.
- Demonstrated expertise in at least one common programming language (e.g. R, Python, Perl, C++, Java) and software version control (e.g. GitHub) is essential.
- Previous experience in the analysis of high-throughput sequencing data (e.g. RNA-seq, ChIP-seq, DNA methylation, chromatin accessibility) and statistical modeling of high-dimensional data is highly desirable.
- An understanding of the experimental techniques underlying such genomics experiments is advantageous.
- A demonstrated record of research productivity / publication in relevant areas.

Special Requirements

Nil

Compliance

Workplace Health and Safety: All supervising staff are required to undertake effective measures to ensure compliance with the Occupational Safety and Health Act 1984 and related University requirements (including Safety, Health and Wellbeing Objectives and Targets). All staff must comply with requirements of the Occupational Safety and Health Act and all reasonable directives given in relation to health and safety at work, to ensure compliance with University and Legislative health and safety requirements. Details of the safety obligations can be accessed at <http://www.safety.uwa.edu.au>

Equity and Diversity: All staff members are required to comply with the University's Code of Ethics and Code of Conduct and Equity and Diversity principles. Details of the University policies on these can be accessed at http://www.hr.uwa.edu.au/publications/code_of_ethics, <http://www.equity.uwa.edu.au>