BLAKE BOWEN

blakebowen97@gmail.com | linkedin.com/in/blake-bowen | github.com/blakebowen

Education

Graduate Certificate of Data Engineering   Jul. 2021 – Present
Australian National University   *Canberra, ACT*
Coursework: Relational Databases, Programming for Data Scientists, Data Wrangling, Data Mining

Bachelor of Biomedicine in Clinical Pathology (Honours)   Feb. 2020 – Nov. 2020
The University of Melbourne   *Parkville, VIC*
Thesis: Understanding the role of somatic *TERT* alterations in phaeochromocytoma using single-nuclei ATAC sequencing

Bachelor of Science in Genetics   Feb. 2016 – Feb. 2020
The University of Melbourne   *Parkville, VIC*
Coursework: Genetics, genomics, developmental and stem cell biology, biochemistry, pharmacology, physiology, ecology, creative writing

Technical Skills

Programming languages and libraries: R (tidvyerse, ggplot2, Renv), Python (Pandas, matplotlib, plotly, jupyter), Bash, SQL, Git/Github/Gitlab and Conda.
High-performance computing: Proficient using the command-line-only interface of high-performance computing clusters for analysis of very large datasets (terabytes), including use of job schedulers (SLURM, PBS)
Data visualisation: Skilled at creating high-quality figures for peer-reviewed publications and presentations using R (ggplot2), Adobe Illustrator, Biorender and Microsoft Excel.
Genomic data analysis: Experienced in analysis of genomic data, from various technologies including bulk and single cell RNA-seq, bulk and single cell ATAC-seq, ChIP-seq as well as clinical patient metadata using various tools including Bioconductor, Seurat, Signac, limma and EdgeR.

Experience and Projects

Research Assistant   Nov. 2020 – Present
University of Melbourne Centre for Cancer Research (UMCCR)   *Parkville, VIC*
Rare Disease Oncogenomics (RADIO) Laboratory
- Member of a cross-functional cancer research team (Genomics, Histology and Analytical), responsible for performing statistical analyses and visualisation of large genomics datasets using R, command line tools and high-performance computing
- Used a Spearman correlation-based method to classify phaeochromocytoma single nuclei RNA-seq data, confirming chromaffin cells as the cell of origin of phaeochromocytoma and highlighting oncofoetal characteristics of pheochromocytoma subtypes

Honours Research Project   Feb. 2020 – Nov. 2020
University of Melbourne Centre for Cancer Research (UMCCR)   *Parkville, VIC*
Rare Disease Oncogenomics (RADIO) Laboratory
- Established a bioinformatic framework for analysing phaeochromocytoma single nuclei ATAC-seq data, enabling quality control, identification of accessible DNA regions and cell type classification of 10 samples
- Discovered 17 transcriptomic and 2719 epigenetic alterations specific to an aggressive subset of phaeochromotyoma, providing new insight to the biology of these tumours
- Awarded the J. E. Taylor Honours Award ($2000), awarded to the top student who has completed a cancer-related Honours project with the Department of Clinical Pathology

Manuscripts in Preparation

- Zethoven M*, Martelotto L*, Pattison A*, **Bowen B*** et al., A phaeochromocytoma and paraganglioma single cell and whole tissue gene-expression atlas for subtype and theranostic discovery. *Under review.* *Equal contribution
- Multi-omics analysis of metastatic *SDHB*-associated phaeochromocytoma and paraganglioma. *In preparation*.

Presentations

- **A single nuclei RNA-seq comparison of phaeochromocytoma and paraganglioma with the foetal adrenal medulla**, University of Melbourne Centre for Cancer research Seminar (Oct. 2021)
- Presented data and research findings both internally at the UMCCR and to international collaborators