

# BLAKE BOWEN

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## Education

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### Graduate Certificate of Data Engineering

*Australian National University*

Jul. 2021 – Present

*Canberra, ACT*

Coursework: Relational Databases, Programming for Data Scientists, Data Wrangling, Data Mining

### Bachelor of Biomedicine in Clinical Pathology (Honours)

*The University of Melbourne*

Feb. 2020 – Nov. 2020

*Parkville, VIC*

Thesis: Understanding the role of somatic *TERT* alterations in pheochromocytoma using single-nuclei ATAC sequencing

### Bachelor of Science in Genetics

*The University of Melbourne*

Feb. 2016 – Feb. 2020

*Parkville, VIC*

Coursework: Genetics, genomics, developmental and stem cell biology, biochemistry, pharmacology, physiology, ecology, creative writing

## Technical Skills

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**Programming languages and libraries:** R (tidyverse, 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

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### Research Assistant

*University of Melbourne Centre for Cancer Research (UMCCR)*

Nov. 2020 – Present

*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 pheochromocytoma single nuclei RNA-seq data, confirming chromaffin cells as the cell of origin of pheochromocytoma and highlighting oncofetal characteristics of pheochromocytoma subtypes

### Honours Research Project

*University of Melbourne Centre for Cancer Research (UMCCR)*

Feb. 2020 – Nov. 2020

*Parkville, VIC*

Rare Disease Oncogenomics (RADIO) Laboratory

- Established a bioinformatic framework for analysing pheochromocytoma 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 pheochromocytoma, 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

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- Zethoven M\*, Martelotto L\*, Pattison A\*, **Bowen B\*** et al., A pheochromocytoma 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 pheochromocytoma and paraganglioma. *In preparation*.

## Presentations

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- **A single nuclei RNA-seq comparison of pheochromocytoma 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