

Trent Newman, PhD

Address: [REDACTED] Street, Melbourne VIC 3000

Mobile: +61 [REDACTED]

Email: [REDACTED]@gmail.com

LinkedIn: <https://www.linkedin.com/in/tacnewman>

ORCID: <https://orcid.org/0000-0002-6767-1429>

Professional Summary

Computational biologist with a strong foundation in molecular genetics, motivated by a fascination with DNA and a passion for solving complex technical problems. I develop bespoke bioinformatic solutions for sequencing and imaging data to understand genetic change across developmental and evolutionary timescales. I'm now seeking to apply my expertise in multi-omics data analysis in a collaborative translational research environment focused on cancer and biomedical discovery.

Skills & Expertise

- **Genomic data analysis:** Experience with DNA methylation, RNA-seq, histone modification and chromatin structure datasets.
- **Computational operations:** Proficient in Python, R, and Bash; experienced with genomic data handling in Unix-based HPC environments using SLURM.
- **Image analysis & microscopy:** Familiar with multi-channel fluorescent labelling of biological molecules and programmatic analysis of microscopy data.
- **Communication & collaboration:** Skilled in mentoring, scientific writing, presenting research and cross-disciplinary collaboration.

Academic Record

PhD in Pathology

University of Otago | 2011 – 2015

BSc (Hons, First Class) in Biotechnology

Victoria University of Wellington | 2007 – 2010

Current Position

Research Fellow – Genomic Imprinting

The University of Melbourne | Apr 2021 – Present

- Analysed allele-specific gene expression using Sanger sequencing, transcriptomic and epigenetic data to identify novel imprinted genes.
- Prepared sequencing libraries (Nanopore long-read and Illumina short-read) and performed sequencing on MinION and PromethION.
- Developed a custom HPC bioinformatic pipeline using parallel job submission with Slurm to identify marsupial imprinted genes from WGBS data (<https://github.com/trentnewman/dmrcan>).
- Contributed to diapause wallaby embryo sample collection for a collaborative single-cell RNA sequencing (scRNA-seq) experiment.

Previous Experience

Postdoctoral Scholar – Molecular and Cellular Biology

University of California, Davis | Jan 2016 – Nov 2019

- Developed code to analyse 3D chromosome dynamics from spinning-disk confocal imaging (1.4M images).
- Performed data QC; collaborated with biophysicists on polymer modelling.
- Maintained a well-documented GitHub repository to support reproducibility (<https://github.com/ucdavis/SeeSpotRun>).
- Ran a workshop on GitHub for laboratory members.

Hatchery Operator – Freshwater

New Zealand King Salmon | Feb 2020 – Apr 2021

- Gained experience in production-focused biological operations outside academia.

Assistant Research Fellow – Pathology

University of Otago | Apr – Dec 2015

- Arranged animal ethics approval, used statistics to predict effective sample size.
- Used RNA-seq to study the effects of maternal diet on oocytes (SRA: SRP074244).

Awards

- Promoted to Grade 2 Research Fellow, University of Melbourne. 2024.
- ECA Travel Grant (\$1.3 k AUD), BioSciences, University of Melbourne. 2024
- Poster Prize Finalist, Society for Reproductive Biology Annual Meeting, 2023.
- Agilent TapeStation (\$51k AUD), Faculty Grant, University of Melbourne. 2021.

Teaching, Training & Memberships

- Honours and Masters student supervision, University of Melbourne (2023–2025).
- Undergraduate research supervision, University of California, Davis (2016–2018).
- Laboratory demonstrator roles, University of Otago (2013–2014).
- Member, Soc. for Repro. Biology and Genetics Soc. of Australasia (since 2021).
- Genomics for Oncologists Course and Molecular Tumour Board meetings, Peter Mac. 2024.
- Advanced Linux & High-Performance Computing – University of Melbourne. 2021.

Conferences

- Genomic Imprinting – from Biology to Disease. Cambridge, UK. 2025.
- Australasian Epigenetics Alliance Meeting. Dunedin, NZ. 2024.
- Society of Reproductive Biology Meeting. Adelaide, AU. 2024.
- International Congress of Genetics. Melbourne, AU. 2023.

Selected Publications

- Newman, T., Ishihara, T., Rizzoli, P., Xiao, L., Gouil, Q., Bond, D.M., Hore, T.A., Shaw, G., & Renfree, M.B. (2024). The *PRKACB* gene is imprinted in marsupials. *Epigenetics & Chromatin*, 17(1), 29.
- Newman, T., Ishihara, T., Shaw, G., & Renfree M.B. (2024). The structure of the *TH/INS* locus and the parental allele expressed are not conserved between mammals. *Heredity*, 133, 21-32.
- Newman, T., Beltran, B., *et al.* (2022). Diffusion and distal linkages govern interchromosomal dynamics during meiotic prophase. *Proceedings of the National Academy of Sciences*, 119(12), e2115883119.
- Newman, T., Jhinku, N., Meier, M., & Horsfield, J. (2016). Dietary intake influences adult fertility and offspring fitness in zebrafish. *PLoS One*, 11(11), e0166394.