Michael **Hall**

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Summary

I am currently a senior postdoctoral researcher in the Bacterial Genomics group at the University of Queensland's Centre for Clinical Research (UQCCR). I develop computational methods for analysing microbial genomes to improve detection, surveillance, and control of infectious diseases. My primary expertise is in pangenome graphs, Nanopore sequencing, genome assembly, and variant calling. I am passionate about reproducible, open source, and user-friendly bioinformatics, and I strive to apply these best practices to strengthen Australia's capacity for evidence-based public health response and preparedness.

Experience

Centre for Clinical Research, The University of Queensland

Brisbane, Australia

Postdoctoral Research Fellow (Level B.1) - Bacterial Genomics Group

July 2025 – present

- Led genomic analysis of linezolid-resistant *Enterococcus faecium* and *E. faecalis* isolates from Queensland to investigate resistance emergence and dissemination. Located resistance determinants from genome assemblies and plasmids, and contextualised local strains alongside historical Queensland datasets, national linezolid-resistant collections, and global genomes. Developed scalable workflows to integrate >36,000 assemblies with rich metadata, perform variant calling, and support high-resolution phylogenetic and comparative analyses.

Peter Doherty Institute for Infection and Immunity, The University of Melbourne

Melbourne, Australia

Postdoctoral Research Fellow (Level B.1) - Coin Group

Feb. 2022 - June 2025

- Developed computational methods for predicting drug resistance in *M. tuberculosis*.
- Assessing host removal methods with pangenome databases and extraction of *M. tuberculosis* sequencing reads from metagenomic samples.
- Evaluating Nanopore sequencing-based variant calling methods in bacterial genomes.
- High-performance computing (HPC) representative supporting researchers in how to use the university's HPC resources.
- Developed a software method and algorithm for estimating the genome size of an organism from DNA sequencing experiments.

Child Health Research Centre, University of Queensland

Brisbane, Australia

Senior Scientific Officer

Nov. 2021 - Feb. 2022

- Analysed Nanopore direct RNA sequencing data to distinguish bacterial from viral sepsis by detecting RNA modification signatures. Assembled and processed signal-level data, and benchmarked deep learning models to identify motif-specific signal perturbations indicative of RNA structural variation.

Education

University of Cambridge

Cambridge, United Kingdom

Doctor of Philosophy - PhD, Bioinformatics

Sep. 2017 - Mar. 2022

- Supervisor: Zamin Iqbal.
- Thesis title: *Examining bacterial variation with genome graphs and Nanopore sequencing*.
- Developed a graph-based algorithm and software tool that detects genetic differences across bacterial genomes without relying on a single reference, improving accuracy when working with diverse or messy data.
- Developed a system to predict drug resistance in tuberculosis by analysing genetic patterns across many samples, helping identify mutations linked to treatment failure.
- Created and tested workflows for clustering tuberculosis samples based on their DNA, comparing results from different sequencing technologies to assess reliability.
- Co-led an international study evaluating Nanopore sequencing for tuberculosis in resource-limited settings; analysed 150+ clinical samples, developed the TBpore analysis tool (20,000+ downloads), and enabled clinical adoption by supporting implementation and training with Madagascar's National TB Program.
- Trained a custom machine learning model to improve accuracy of DNA sequence data from tuberculosis samples, showing how tailored models can boost performance.

The University of Queensland

Brisbane, Australia

Master of Bioinformatics - Research Extensive

Feb. 2016 - Aug. 2017

- Research thesis title: *A web-based platform for real-time analysis of multiple data streams for tracking and detection of antimicrobial resistance*.
- Taught courses included software engineering, bioinformatics skills, computational statistics, algorithms and data structures, and database systems.
- GPA: 7.0
- Master of Molecular Biology and Master of Bioinformatics Prize, which is awarded to the student with the highest cumulative GPA in the MMolBiol and MBioinf programs.

Queensland University of Technology

Brisbane, Australia

Bachelor of Biomedical Science

Feb. 2013 - Dec. 2015

- GPA: 7.0

Skills

Research	Bioinformatics, Microbial genomics, Genome graphs, Variant calling, Genome assembly, Nanopore data analysis, Metagenomics, Pipeline creation
Languages	Python, Rust, Bash, SQL (basic), C++
Data Science	Hypothesis testing, model evaluation, variant calling, experimental design
Data Engineering	Reproducible pipelines, workflow automation, Snakemake, HPC/SLURM, Docker
Tools	Git, GitHub, Conda, Jupyter, Pandas, NumPy, Matplotlib, SciPy, scikit-learn

Honours & Awards

2025	**Best lightning talk**, ABACBS conference	*Adelaide, AUS*
2024	**Best lightning talk**, MicroSeq conference	*Virtual, AUS*
2022	**Best lightning talk**, ABACBS conference	*Melbourne, AUS*
2018	**The Master of Molecular Biology and Master of Bioinformatics Prize**, University of Queensland	*Brisbane, AUS*
2016	**Westpac Future Leaders Scholarship**, Westpac Scholar Trust	*Australia*

Presentations

MicroSeq — *Virtual, Australia*

Accepted talk — *Sept. 2024*

- Evaluating nanopore-base variant calling in bacterial genomes

Australian Society for Microbiology Hour — *Virtual, Australia*

Invited talk — *Jul. 2024*

- Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data

Australian Society for Microbiology annual conference — *Brisbane, Australia*

Selected talk — *Jul. 2024*

- Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data

International Congress of Genetics — *Melbourne, Australia*

Selected talk — *Jul. 2023*

- Drug resistance prediction for *Mycobacterium tuberculosis* with reference graphs

Australia Genomics Technology Association (AGTA) Conference — *Sunshine Coast, Australia*

Selected talk — *Nov. 2022*

- Drug resistance prediction for *Mycobacterium tuberculosis* with reference graphs

Leadership, Committees, and Events

Committees

2025	**Co-convenor**, Centre for Clinical Research Multiomic Subcommittee Oxford Nanopore Technologies Working group	*The University of Queensland*

Events

2025	**Session Chair and Panel Organisation**, UQ Centre for Clinical Research Infectious Disease Symposium	*Brisbane, Australia*
2023	**Workshop Coordinator**, Australian Bioinformatics and Computational Biology Society (ABACBS) Conference	*Brisbane, Australia*
2023	**Co-organiser**, Clinical Informatics Symposium (ABACBS Satellite Event)	*Brisbane, Australia*

Supervision

2024-present	**Masters Student**, Detection of novel antimicrobial resistance-conferring mutations in *Mycobacterium tuberculosis*	*The University of Melbourne*
2025-present	**Masters Student**, Exploring the scale of human DNA leakage into public metagenomic data	*The University of Queensland*
2025-present	**MPhil Student**, Investigating plasmid evolution and transmission and analysing the long-term dynamics of OXA-181 resistance plasmids in Brisbane to inform improved genomic surveillance	*The University of Queensland*
2024-present	**PhD Student**, Member of advisory committee	*The University of Melbourne*

Publications

Summary

To date, I have 20 peer-reviewed articles, with eight as first author. Collectively, these works have received 3,252 citations (Google Scholar). My Field-Weighted Citation Index (FWCI) is 6.36 (SciVal), representing a citation rate 536% above the field average. I have contributed to open-source bioinformatics software, with programs I've developed or contributed to amassing over 1.6 million downloads.

Select Publications

[1] **Michael B. Hall**, Yiyang Xue, Tricia S. E. Lee, Ella Herring, et al. "Novel transposon Tn*8026* acts as a global driver of transmissible linezolid resistance in *Enterococcus* via a linear plasmid". In: *medRxiv* (2026). DOI: 10.64898/2026.03.04.26347163.

[2] Aleix Canalda-Baltrons, Matthew Silcocks, **Michael B. Hall**, et al. "Genome graphs reveal the importance of structural variation in Mycobacterium tuberculosis evolution and drug resistance". In: *Nature Communications* 16.1 (2025). DOI: 10.1038/s41467-025-65779-9.

[3] Sophie Gagnon, Emmanuelle Ametepe, Floriane Point, William Cloutier Charette, Arpita Chakravarti, Paul Rivest, Pierre-Marie Akochy, Hafid Soualhine, Zamin Iqbal, **Michael B. Hall**, and Simon Grandjean Lapierre. "TBpore cluster: A novel phylogenetic pipeline for tuberculosis transmission studies using nanopore next-generation sequencing data". In: *PLOS ONE* 20.6 (2025). DOI: 10.1371/journal.pone.0325914. **1 citation**.

[4] **Michael B Hall**, Chenxi Zhou, and Lachlan J M Coin. "Genome size estimation from long read overlaps". In: *Bioinformatics* 41.11 (2025). DOI: 10.1093/bioinformatics/btaf593. **8,000 software downloads**.

[5] Martin Hunt, Leandro Lima, Daniel Anderson, George Bouras, **Michael Hall**, et al. *AllTheBacteria – all bacterial genomes assembled, available, and searchable*. 2025. DOI: 10.1101/2024.03.08.584059. **53 citations**.

[6] **Michael B Hall** and Lachlan J M Coin. "Pangenome databases improve host removal and mycobacteria classification from clinical metagenomic data". In: *GigaScience* 13 (2024). DOI: 10.1093/gigascience/giae010. **14 citations, 8,000 software downloads**.

[7] **Michael B Hall**, Ryan R Wick, Louise M Judd, An N Nguyen, et al. "Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data". In: *eLife* 13 (2024). DOI: 10.7554/eLife.98300. **45 citations, 3,900 dataset downloads**.

[8] **Michael B. Hall**, Leandro Lima, Lachlan J. M. Coin, and Zamin Iqbal. "Drug resistance prediction for Mycobacterium tuberculosis with reference graphs". In: *Microbial Genomics* 9.8 (2023). DOI: 10.1099/mgen.0.001081. **6 citations**.

[9] Kayzad Nilgiriwala*, Marie-Sylvianne Rabodoarivelo*, **Michael B. Hall***, et al. "Genomic Sequencing from Sputum for Tuberculosis Disease Diagnosis, Lineage Determination, and Drug Susceptibility Prediction". In: *Journal of Clinical Microbiology* 61.3 (2023). DOI: 10.1128/jcm.01578-22. **29 citations**.

[10] **Michael B Hall** and Lachlan J M Coin. "Assessment of the 2021 WHO Mycobacterium tuberculosis drug resistance mutation catalogue on an independent dataset". In: *The Lancet Microbe* (2022). DOI: 10.1016/s2666-5247(22)00151-3. **8 citations**.

[11] **Michael B. Hall**. "Rasusa: Randomly subsample sequencing reads to a specified coverage". In: *Journal of Open Source Software* 7.69 (2022). DOI: 10.21105/joss.03941. **134 citations, 70,000 software downloads**.

[12] **Michael B. Hall**, Marie Sylvianne Rabodoarivelo, Anastasia Koch, Anzaan Dippenaar, et al. "Evaluation of Nanopore sequencing for Mycobacterium tuberculosis drug susceptibility testing and outbreak investigation: a genomic analysis". In: *The Lancet Microbe* (2022). DOI: 10.1016/S2666-5247(22)00301-9. **86 citations, FWCI 8.11, 20,000 software downloads**.

[13] Rachel M. Colquhoun, **Michael B. Hall**, et al. "Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs". In: *Genome Biology* 22.1 (2021). DOI: 10.1186/s13059-021-02473-1. **80 citations, FWCI 2.11, 4,000 software downloads**.

[14] Felix Mölder, Kim Philipp Jablonski, Brice Letcher, **Michael B. Hall**, et al. "Sustainable data analysis with Snakemake". In: *F1000Research* 10 (2021). DOI: 10.12688/f1000research.29032.2. **1,803 citations, FWCI 59.02, 1.5M software downloads**.

[15] Lara Urban, Andre Holzer, J Jotautas Baronas, **Michael B Hall**, et al. "Freshwater monitoring by nanopore sequencing". In: *eLife* 10 (2021). DOI: 10.7554/elife.61504. **136 citations**.

[16] Martin Hunt, Phelim Bradley, Simon Grandjean Lapierre, Simon Heys, Mark Thomsit, **Michael B. Hall**, et al. "Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe". In: *Wellcome Open Research* 4 (2019). DOI: 10.12688/wellcomeopenres.15603.1. **195 citations**.

[17] Haotian Teng, Minh Duc Cao, **Michael B Hall**, et al. "Chiron: Translating nanopore raw signal directly into nucleotide sequence using deep learning". In: *GigaScience* 7.5 (2018). DOI: 10.1093/gigascience/giy037. **211 citations, FWCI 7.27**.