RICK M. TANKARD PhD

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A statistician and bioinformatician who is interested in work that can benefit humanity and the environment. Enjoys programming, automation, and reproducibility. Has a keen interest in science, scientific scepticism, human biology, and disease. Wants to work in projects across a wide variety of topics in team environments and improve machine learning skills.

Employment

Career break – health February 2023 – present

The Walter and Eliza Hall Institute of Medical Research (WEHI) **Victoria, Australia**
Bioinformatics Analyst 18 July 2022 – 17 January 2023

- Collaborated with stakeholders to maximise outcomes from biological data.
- Worked on open-source software in R and Perl with git repositories.
- Wrote documentation in Quarto.

Career break – Health January 2021 – July 2022

Murdoch University **Western Australia, Australia**
Research Associate 12 June 2017 – 20 December 2020

- Analysed array data for use in a consortium led meta-analyses.
- Supervised a summer student, resulting in expansion of open-source projects.
- Presented four oral symposium presentations.
- Set up a pipeline in Snakemake to process over 600 next-generation sequencing samples (60TB) on Pawsey high-performance computing (HPC) infrastructure.
- Constructed an epigenetic ageing clock from methylation data and compared it to existing clocks in R with Elastic-Net in the glmnet package.
- Tutored first year statistics subject.
- Published two peer-reviewed articles and two preprints.

The Walter and Eliza Hall Institute of Medical Research (WEHI) **Victoria, Australia**
Research Technician 2 December 2010 – 10 June 2017

- Developed a pipeline to process genetic sequencing data used across our team.
- For two years, organised the Bioinformatics seminar series, including scheduling, finding external speakers, and introducing each seminar weekly.
- Published twelve peer-reviewed journal articles, three oral conference presentations, ten conference posters and nine public seminars at WEHI.
- Helped onboard new members to the lab, teaching them relevant techniques and how to use server resources.

Education

2013–2018 **Doctor of Philosophy (PhD)** in bioinformatics/medical research
The University of Melbourne / The Walter and Eliza Hall Institute of Medical Research (WEHI), VIC
Thesis title: *Identifying disease-causing short tandem repeat expansions in massively parallel sequencing data, focusing on ataxias.*
http://hdl.handle.net/11343/197796
Developed an algorithm (exSTRa (R and Perl), see software list below) to detect repeat expansions from next-generation sequencing data. These methods can speed up the diagnosis of genetic repeat expansion disorders when whole-genome sequencing is performed.

2006–2010 **Bachelor of Science (Honours)** (Mathematics and Statistics)
The University of Melbourne / WEHI, VIC

2007–2009 **Diploma of Arts** (History and Philosophy of Science)
The University of Melbourne, VIC

Technical Skills

- R, R Studio, package development, unit testing and Rmarkdown (11 years)
- Statistical models and hypothesis testing, such as general linear models, elastic net regression, power calculations, ANOVA
- Machine learning: XGBoost, model validation, deep learning
- Basic SQL and Python
- Teaching statistics and R programming to first-year students and other academics
- Version control with git and GitHub/GitLab (6 years)
- Programming in bash and Perl (11 years)
- Linux (command line), macOS (work/PhD) and Windows (hobby computer)
- High-performance computing (SLURM, Torque PBS) (4 years)
- Continuous Integration (Travis CI) (2 years)
- Containers (Docker and Singularity) (2 years)
- Scientific workflows with Nextflow and Snakemake (1.5 years)
- Adobe Illustrator and Indesign for figures and posters
- Microsoft Office and LibreOffice, including oral presentations with PowerPoint

Volunteering

2018– Member of *Statistical Society of Australia*
Held **Treasurer** position for VIC branch in 2022 and 2023.
Held **Secretary** position for WA branch in 2019 and 2020.

2020 **Organiser** for the *WA Young Statisticians Workshop 2020* (Statistical Society of Australia event), including preparing the website https://ysw2020.netlify.app/

2019 *EMBL ABR Australian BioCommons Hands-on Workshop: Implementing Scalable Bioinformatic Workshops in Snakemake & Nextflow*. **Perth hub facilitator**: helped researchers with their problems as they came up during the workshop. Participate in training during the weeks before in Adelaide.

2019 *Resbaz Perth 2019* **committee member**. Helped organise Docker stream. Taught git stream as a last-minute replacement.

2008–2011 *Melbourne University Dancesport Club* **committee member**, responsible for the website, e-mail lists, class supervision and cash handling.

2007 & 2009 *Professor Harry Messel International Science School* **Staff**
Assisted in recording and publishing lectures and took responsibility for groups of high school students.

Publications and presentations

7 oral presentations and 10 poster presentations at conferences. 21 peer-reviewed publications.

Scholarships

2013–17	Australian postgraduate award (APA)	$24,653 per year
2010	Alan W Harris Honours Scholarship	$5,000
2010	Maurice Belz Scholarship	$7,000
2006–09	Melbourne Access Scholarship	$4,161 per year and BSc course fee waiver

Open-source software

exSTRa R and Perl libraries to detect repeat expansions in next-generation sequencing data. Primary software output from PhD thesis at WEHI. Performed profiling post-PhD to drastically optimise the package. https://github.com/bahlolab/exSTRa

Linkdatagen and VCF2linkdatagen (software updates)
Performed bug fixes, updated to support more platforms, improved Illumina TOP/BOT interpretation to make more SNPs available for linkage analysis and updated documentation. http://bioinf.wehi.edu.au/software/linkdatagen/

rwarrior Game designed to teach the R language in an interactive way. https://github.com/trickytank/Rwarrior