

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 organisations that act ethically and with integrity to deliver tangible benefits to its customers.

Employment

- 2022– **Research Assistant** Population Health and Immunity Division, WEHI, VIC.
Software development of Linkdatagen (Perl) and exSTRa (R). Updated annotation to hg38 using UCSC tools.
- 2017–2020 **Research Associate** Mathematics and Statistics, Murdoch University, WA.
Analysed array data for use in a consortium led meta-analyses. Presented four oral symposium presentations. Set up a pipeline in Snakemake to process over 600 next-generation sequencing samples on the Pawsey high-performance computing (HPC) infrastructure. Constructed an epigenetic ageing clock from methylation data and compared it to existing clocks. Tutored first year statistics subject. Also received science journalism interview training from Dr Chris Smith of the *Naked Scientists*. Published two peer-reviewed articles and two preprints.
- 2010–2017 **Research Technician** Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research (WEHI), VIC.
Developed a pipeline to process next-generation sequencing data that the entire lab could use. 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 the computer systems were set up.
- 2009–2010 **Summer Vacation Scholarship** Bioinformatics Division, WEHI
- 2007–2008 **Vacation Scholarship** Uni. of Melbourne Mathematics and Statistics Department

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. This was compared to other methods developed at the same time. These methods can speed up the diagnosis of 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

Skills with work experience

- R, R Studio, package development, unit testing and Rmarkdown (11 years)
- Statistical models and testing, including elastic net regression
- Probability calculations
- Teaching statistics and R programming
- 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)
- Version control with git and GitHub/GitLab (6 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

Activities and affiliations

- 2018– Member of *Statistical Society of Australia*
Held **Secretary** position for WA branch in 2019 and 2020.
Held **Treasurer** position for VIC branch in 2020.
- 2013– *Australian Bioinformatics and Computational Biology Society Inc (ABACBS)* member
2020 **Organiser** for the *WA Young Statisticians Workshop 2020* (Statistical Society of Australia event), including preparing the website <https://ysw2020.netlify.app/>
- 2019 Participated in a 2-day workshop on Nextflow with leading developer Paolo Di Tommaso at Pawsey Supercomputing Centre.
- 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.
- 2019 R two-day workshop **helper** at UWA.
- 2018 *Resbaz Perth 2018* R workshop **helper**, including bash and git teaching.
- 2013 *EMBL Australia PhD Course* **helper** in workshop on next-generation sequencing
- 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

Full list at <https://tinyurl.com/RickMTankard-Scholar>

Conference presentations

- 2019 Oral: Women in STEMM: Murdoch University Research Symposium (Armstrong group)
- 2018 Poster: ABACBS conference
- 2018 Oral: Pawsey Bioinformatics Symposium 2018
- 2018 Oral: Data Science Week Symposium held at Murdoch University
- 2017 Oral: Murdoch Annual Research Symposium
- 2015 Poster: *Genemappers*, Perth WA Australia
- 2015 Poster: *Lorne Genome Conference*, Lorne VIC Australia
- 2014 Oral (Three Minute Thesis format): *Australian Neurogenics Conference*, Brisbane QLD

2014	Oral: <i>Walter and Eliza Hall Institute of Medical Research Student Symposium</i> .
2014	Poster: <i>Australasian Genomic Technologies Association</i> , Melbourne VIC Australia
2014	Poster: <i>Australian Bioinformatics Conference</i> , Melbourne VIC Australia
2014	Poster: <i>International Conference on Systems Biology</i> , Melbourne VIC Australia
2014	Poster: <i>Genemappers</i> , Barossa Valley SA
2014	Poster: <i>Lorne Genome Conference</i> , Lorne VIC Australia
2013	Oral: <i>Workshop on Fragile-X and Other Early Onset Disorders</i> , Barossa Valley SA
2012	Digital poster: <i>Human Genome Meeting (HGM)</i> , Sydney NSW Australia
2011	Poster: <i>Genemappers</i> , Hobart SA Australia

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	\$4000 per year plus HECS 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>

Nextflow pipelines for GangSTR and ExpansionHunter Denovo.

<https://gitlab.com/trickytank/GangSTR-nf>

<https://gitlab.com/trickytank/expansionhunterdenovo-nf>

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/>

Bio::SNP::TOPBOT

Perl module to determine strand of SNPs using Illumina's TOP/BOT designation
<https://github.com/trickytank/Bio-SNP-TOPBOT>

Hobbies

- Minor editing of English Wikipedia articles <https://en.wikipedia.org/wiki/User:TrickyTank>
- Learning about basic cryptography and computer security principles