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Summary

I entered the field of bioinformatics in 2005 when I started my honours project investigating the extent of lateral gene transfer in *Staphylococcus*. It was then I was introduced to sequence alignment, phylogenetics, and Unix and Perl. Upon completion of my honours degree, I was unsatisfied with my computational skills and invested five months as a work experience trainee in the lab of Brian Dalrymple. I worked closely with Wes Barris, a systems administrator at that time, who was instrumental in helping me improve my Unix and Perl skills. After my work experience I was hired in the same lab to provide bioinformatic assistance to the International Sheep Genomics Consortium and to assist in the annotation of non-coding RNAs for the Bovine Genome Consortium. I next joined the lab of Sean Grimmond as a Laboratory Information Management System developer for the GUDMAP project. I developed various tools and maintained all the data generated by the University of Queensland GUDMAP team.

In 2010, I decided to pursue a PhD degree as a Marie Curie Early Stage Researcher in the lab of Piero Carninci. I worked on analysing high-throughput sequencing data and received training in various aspects of genomics and transcriptomics. I was active as a PhD student and organised the Student Journal Club, the Chat With Guest sessions, and was involved in organising a conference and workshop. I'm passionate about bioinformatics and maintain a blog where I write about my bioinformatic and research experiences, and provide technical posts to assist people with their bioinformatic analyses.

Personal

DOB	1983 March 31$^{\text{st}}$
Birth place	Hong Kong
Nationality	Australian and British National (Overseas)

Education

2010–2015	PhD Candidate, Vrije University, the Netherlands. PhD thesis: High-throughput sequencing and transcriptomics: data analysis and methods development of large expression data sets.
2001–2005	BSc (Honours) in biochemistry and microbiology, University of Queensland, Australia. Honours thesis: Using a supertree approach to detect laterally transferred genes within *Staphylococcus*.

Past Scientific Positions

2010–2015	Research Associate in the lab of Piero Carninci at RIKEN Yokohama, Japan
2008–2010	Research Assistant in the lab of Sean Grimmond at The University of Queensland, Australia
2006–2008	Research Assistant in the lab of Brian Dalrymple at the Commonwealth Scientific and Industrial Research Organisation, Australia
2005–2006	Research Assistant in the lab of Mark Ragan at the University of Queensland, Australia

Research Interests

- Genomics and transcriptomics; in particular the study of non-coding RNAs and transposable elements expression.
- The application of bioinformatics, in particular machine learning and data mining methods, to biological problems.
- Open science and reproducible research.

Bioinformatic Skills

- Data analysis of high-throughput sequencing data from various *Seq protocols.
- Knowledge and the ability to use various bioinformatic databases, repositories, and tools.
- The application of biostatistics to the analysis of high-throughput sequencing data.

Computer Skills

- Operating systems: Linux/Unix (RHEL/CentOS and Ubuntu), OS X, and Windows.
- Programming/scripting languages: Perl, R, SQL, bash, PHP, JavaScript, Python, and C.
- Pre Web 2.0: CGI, PHP, HTML, MySQL, Apache2, and JavaScript.
- Open science and reproducible research tools: git, GitHub, WordPress, Jekyll, and R Markdown/Markdown.

Honours and Awards

2010	CSIRO Chairman's Medal
2008	CSIRO Partnership Excellence Award

Workshop and Course Attendances

2014	RIKEN/KI doctoral course: Employing Genome-wide Technologies for Functional Regulation in Development and Disease
2013	AMATA conference ECR workshop
2013	Coursera data analysis course from Johns Hopkins University
2013	BrainTrain courses and workshops
2013	RIKEN/KI doctoral course: Epigenomics: Methods and Applications to Disease and Development
2012	SISSA summer school on dopaminergic neurons
2012	RIKEN/KI doctoral course: Functional Regulation in Development and Disease
2011	UQ winter school in mathematical and computational biology
2011	RIKEN/EBI bioinformatics roadshow

Academic and Administrative Experience

2015	MODHEP workshop presenter on analysing CAGE data using R
2013–2014	Organiser of the Chat with Guest sessions at RIKEN CLST DGT
2013–2014	Organiser of the Student Journal Club at RIKEN CLST DGT
2013	Organising committee for the BrainTrain conference
2013	Organiser of the BrainTrain workshop: Identifying regulatory elements in the genome

Hobbies and Interests

Sports (especially basketball), cycling, bioinformatics blogging, self study, and computer games.

Academic References

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RIKEN Yokohama Campus
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Publications

[1] **Tang, Dave** and Piero Carninci. The regulated expression of repetitive elements across human cell types and tissues. *In preparation*, 2015.

[2] **Tang, Dave**, Ana Maria Suzuki, Raffaella Calligaris, Stefano Gustincich, and Piero Carninci. Deep transcriptome sequencing of whole blood samples from Parkinson's disease patients. *In preparation*, 2015.

[3] Y. Hasegawa, **Tang, D.**, N. Takahashi, Y. Hayashizaki, A. R. Forrest, et al. CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. *Sci Rep*, 4:5228, 2014. URL: http://www.ncbi.nlm.nih.gov/pubmed/24957798.

[4] **Tang, D. T.**, C. Plessy, M. Salimullah, A. M. Suzuki, R. Calligaris, S. Gustincich, and P. Carninci. Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. *Nucleic Acids Res.*, 41(3):e44, Feb 2013. URL: http://www.ncbi.nlm.nih.gov/pubmed/23180801.

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[8] R. D. Thiagarajan, K. M. Georgas, B. A. Rumballe, E. Lesieur, H. S. Chiu, D. Taylor, **Tang, D. T.**, S. M. Grimmond, and M. H. Little. Identification of anchor genes during

kidney development defines ontological relationships, molecular subcompartments and regulatory pathways. *PLoS ONE*, 6(2):e17286, 2011. URL: http://www.ncbi.nlm.nih.gov/pubmed/21386911.

[9] H. S. Chiu, J. C. Szucsik, K. M. Georgas, J. L. Jones, B. A. Rumballe, **Tang, D.**, S. M. Grimmond, A. G. Lewis, B. J. Aronow, J. L. Lessard, and M. H. Little. Comparative gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. *Dev. Biol.*, 344(2):1071–1087, Aug 2010. URL: http://www.ncbi.nlm.nih.gov/pubmed/20510229.

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This C.V. was prepared in LATEX and is available at https://github.com/davetang/cv.