Dave Ting Pong Tang

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Summary

I am currently a post-doctoral researcher at the Telethon Kids Institute, working on the analysis of human whole exome sequencing data sets. One of the main goals of my current research is to develop new methodologies and pipelines that can contextualise genetic variants with respect to various phenotypes of interest. Prior to this position, I was a Marie Curie Early Stage Researcher in the lab of Piero Carninci, primarily working on the analysis of high-throughput transcriptome sequencing data sets. As part of this work, I developed methods to identify sequencing artefacts and studied different classes of non-coding RNAs. My ultimate goal is to further our understanding of how the non-coding aspect of the human (and mammalian) genomes plays a role in governing biological function.

I am passionate about bioinformatics and maintain a blog where I write about bioinformatics and topics associated with bioinformatics, such as biology, statistics, and computer science. I am always on the lookout on new things to learn and I am fully in support of the open science and reproducible research movement.

Personal

DOB	1983 March 31st
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: methods development and data analysis 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

- Investigating the potential role of DNA variants in relation to biological function and disease.
- 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.

Bioinformatic Skills

- Data analysis of high-throughput sequencing data from DNA-Seq, RNA-Seq, CAGE-Seq, sRNA-Seq, and ChIP-Seq.
- Knowledge and the ability to use various bioinformatic databases, APIs, repositories, and tools.
- The application of biostatistics for 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, bash, JavaScript, HTML, SQL, and PHP.
- Open science and reproducible research tools: git, cloud computing (AWS), WordPress, Jekyll, Docker, and R Markdown/Markdown.

Honours and Awards

2010	CSIRO Chairman's Medal
2008	CSIRO Partnership Excellence Award

Workshop and Course Attendances

2015	UQ winter school in mathematical and computational biology
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
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
2012	Session chair for the Patients and Medicines forum
2012	Presenter at the RIKEN OSC bioinformatics course

Hobbies and Interests

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

Academic References

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Publications

[1] G. Baynam, N. Pachter, F. McKenzie, S. Townshend, J. Slee, C. Kiraly-Borri, A. Vasudevan, A. Hawkins, S. Broley, L. Schofield, H. Verhoef, C. E. Walker, C. Molster, J. M. Blackwell, S. Jamieson, **Tang, D.**, T. Lassmann, K. Mina, J. Beilby, M. Davis, N. Laing, L. Murphy, T. Weeramanthri, H. Dawkins, and J. Goldblatt. The rare and undiagnosed diseases diagnostic service - application of massively parallel sequencing in a state-wide clinical service. *Orphanet J Rare Dis*, 11(1):77, 2016. URL: http://www.ncbi.nlm.nih.gov/pubmed/27287197.

[2] **Tang, D.**, D. Anderson, R. W. Francis, G. Syn, S. E. Jamieson, T. Lassmann, and J. M. Blackwell. Reference genotype and exome data from an Australian Aboriginal population for health-based research. *Sci Data*, 3:160023, 2016. URL: http://www.ncbi.nlm.nih.gov/pubmed/27070114.

[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.

[5] A. Saxena, **Tang, D.**, and P. Carninci. piRNAs warrant investigation in Rett Syndrome: an omics perspective. *Dis. Markers*, 33(5):261–275, 2012. URL: http://www.ncbi.nlm.nih.gov/pubmed/22976001.

[6] S. Francia, F. Michelini, A. Saxena, **Tang, D.**, M. de Hoon, V. Anelli, M. Mione, P. Carninci, and F. d'Adda di Fagagna. Site-specific DICER and DROSHA RNA products control the DNA-damage response. *Nature*, 488(7410):231–235, Aug 2012. URL: http://www.ncbi.nlm.nih.gov/pubmed/22722852.

[7] R. D. Thiagarajan, N. Cloonan, B. B. Gardiner, T. R. Mercer, G. Kolle, E. Nourbakhsh, S. Wani, **Tang, D.**, K. Krishnan, K. M. Georgas, B. A. Rumballe, H. S. Chiu, J. A. Steen, J. S. Mattick, M. H. Little, and S. M. Grimmond. Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. *BMC Genomics*, 12:441, 2011. URL: http://www.ncbi.nlm.nih.gov/pubmed/21888672.

[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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[11] K. Georgas, B. Rumballe, M. T. Valerius, H. S. Chiu, R. D. Thiagarajan, E. Lesieur, B. J. Aronow, E. W. Brunskill, A. N. Combes, **Tang, D.**, D. Taylor, S. M. Grimmond, S. S. Potter, A. P. McMahon, and M. H. Little. Analysis of early nephron patterning reveals a role for distal RV proliferation in fusion to the ureteric tip via a cap mesenchyme-derived connecting segment. *Dev. Biol.*, 332(2):273–286, Aug 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19501082.

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