Tyrone **Chen**

PhD Student · Bioinformatics and Computational Biology

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Education

Monash University   *Melbourne, Australia*

PhD student (Bioinformatics)   *2019 - 2022*

- Project title: Identification of biological signals by combining distinct categories of biological data through machine learning.

Australian National University   *Canberra, Australia*

Bachelor of Science (Molecular Biology and Plant Science); Hons. (Bioinformatics)   *2010 - 2013*

Research Experience

Bioinformatics lab, School of Biological Sciences, Faculty of Science, Monash University (Dr Sonika Tyagi)   *Melbourne, Australia*

PhD Student (Bioinformatics)   *2019 - PRESENT*

- Applying machine learning to integrate biological data across multiple modalities.
- Large scale data (1-10 TB) analysis.
- Contributed to writing and data analysis for peer-reviewed academic publications.
- Open source software development for biological data analysis.

Stemformatics Project, Australian Institute for Bioengineering and Nanotechnology, University of Queensland; Centre for Stem Cell Systems, Department of Anatomy and Neuroscience, University of Melbourne (Prof. Christine Wells)   *Brisbane and Melbourne, Australia*

Research Assistant (Bioinformatics)   *2014-2016; 2016 - 2019*

- Curated and ran large quantities of microarray, high throughput sequencing and single cell data through pipelines on high performance compute clusters to contribute to a database of interest for both internal and external collaborators.
- Large scale data (1-10 TB) and metadata standardisation/management as well as retrieving and transmitting these in an accessible format to requesters.
- Contributed to data analysis for peer-reviewed academic publications.
- Open source software development for microarray and high throughput sequencing pipelines.

John Curtin School of Medical Research, Australian National University (Prof. Gavin Huttley)   *Canberra, Australia*

Honours Scholar (Bioinformatics)   *2013*

- Honours project on the development of a computational motif discovery toolkit for identification of signals in biological data.
- Implemented an algorithm in python using information theory and numerical optimisation to discover contiguous and discontigous signals in biological sequence data.

Research School of Biology, Australian National University (Prof. Murray Badger)   *Canberra, Australia*

Summer research student (Plant Biology, Microscopy)   *2012 - 2013*

- Carried out a systematic analysis of physiology of the land plant *Hirschfeldia incana* to identify the principles underlying its relatively high photosynthetic rate compared to closely related plants in its family.
- Performed plant growth under controlled conditions and conducted subsequent physiological measurements including microscopy as well as associated imaging and leaf gas exchange measurements.

Research School of Biology, Australian National University (Dr. Iain Searle)   *Canberra, Australia*

Undergraduate research student (Molecular Biology, Plant Biology)   *2012*

- Investigated the possible effect of mutations in the small RNA silencing mechanism which might contribute to genomic instability.
- Performed sterile plant and bacterial growth, PCR, transformation and gel electrophoresis, antibiotic screens, RNAase digestion, DNA extraction and media preparation.

Teaching Experience

Monash University   *Melbourne, Australia*

Data Fluency Associate Instructor   *2019-PRESENT*

- Running software carpentry sessions in unix shell, github, python, R, high performance computing cluster usage and deep learning.

College of Medicine, Biology & Environment, Australian National University   *Canberra, Australia*

Peer mentor for biology students   *2011*

- Facilitated learning among undergraduate biology students by running tutoring sessions and designing exercises.

Other Experience

TraffixGroup   *Melbourne, Australia*

Supervisor (Tram Surveyor)   *2014*

- Led a team to count and interview passengers across Melbourne's tram routes.

Research School of Biology, Australian National University   *Canberra, Australia*

Laboratory Technician   *2012*

- Maintained a molecular biology laboratory focused on non-coding RNA in plants.

Honours & Awards

Australia

Australian Government Research Training Program Scholarship

2019-2022 Australian Government Research Training Program Scholarship to pursue full-time candidature in the Doctor *Canberra, Australia* of Philosophy (PhD) with the School of Biological Sciences, Monash University.

Faculty of Science Dean's Postgraduate Research Scholarship

2019-2022 Faculty of Science Dean's Postgraduate Research Scholarship to pursue full-time candidature in the Doctor of Philosophy (PhD) with the School of Biological Sciences, Monash University.   *Melbourne, Australia*

Data Fluency Digital Toolkit Poster Competition 2019 prize

2019 Awarded a prize for an oral presentation and associated poster presented as part of the Data Fluency Digital Toolkit Poster Competition 2019 held in Monash University.   *Melbourne, Australia*

USA

2013-2015 **Sponsored Membership**   *Washington, DC, USA*
American Association for the Advancement of Science (Science Program for Excellence in Science)

Skills

Computational

- Machine learning: pytorch and tensorflow
- Languages and markup: python, R, bash, pSQL, LaTeX, restructured text
- Version control: git, mercurial
- Virtual environment management: conda, virtualenv, pip
- Usage of high performance compute clusters and associated job submissions: PBS, SGE, slurm
- Efficient management, organisation, archival, retrieval and standardisation of large quantities of data and metadata (1-10TB) per dataset
- Reproducible research practices and documentation: jupyter notebooks, Rmarkdown
- Workflow languages: Snakemake and Nextflow
- Graphic design for posters and scientific articles: Adobe inDesign, Adobe Illustrator example poster available online

Bioinformatics, Mathematics and Statistics

- Data integration: sPLSDA
- Data visualisation: PCA, interactive plots, genome browsers
- Differential gene expression analyses
- Information theory: mutual information, relative entropy
- Signal processing: Fourier transform, autocorrelation
- Numerical optimisation: simulated annealing
- Motif enrichment analyses
- Batch effect correction
- Specialised software: data analysis (ComBAT, deseq, edgeR, fastqc, ISMARA, limma, MEME suite, mixOmics, multiqc, pandas, pytorch, supervised normalisation, tensorflow, variance partitioning, voom), data visualisation (ggplot, glimma, matplotlib, Rcircos, seaborn)

Biology

- Microscopy: light microscopy and associated sample preparation
- Plant physiology: Leaf gas exchange measurements, Membrane inlet mass spectrometry, fieldwork, plant growth
- Molecular biology: PCR, Molecular cloning, bacterial transformation, antibiotic screens, gel electrophoresis, RNAase digestion, DNA extraction, sterile plant growth, media preparation

- Teaching and training: usage of microarray and high throughput sequencing pipelines, introduction to programming (python, R, unix shell, HPC), github, deep learning, peer mentoring for undergraduate biology students
- Project management and task organisation
- Awareness of cultural and professional diversity and clear communication
- Social media editor [Stemformatics Project twitter], [Monash Computational Biology lab twitter]

Professional Development

SOCIETY MEMBERSHIPS

- Software carpentries instructor - 2020-present.
- Professional membership with the Australasian Genomic Technologies Association (AGTA) - 2014-2015.
- Professional membership with the Australian Bioinformatics And Computational Biology Society (ABACBS) - 2014-present.
- Sponsored membership with the American Association for the Advancement of Science (Science Program for Excellence in Science) - 2013-2015.
- Professional membership with the Institute of Electrical and Electronics Engineers (IEEE) - 2013-present.

VOLUNTEER EXPERIENCE

- Workshop assistance at the Introduction to Python workshop, 28th March, 2019, Monash University, Clayton, Australia.
- Community outreach with visiting students at the University of Melbourne (2016), University of Queensland (2014) and Australian National University (2013)

CONTRIBUTIONS TO OPEN SOURCE SOFTWARE LIBRARIES

- MONET multi-omics clustering algorithm. git repository
- Modules for use with the s4m shell framework used in the Stemformatics project. git repository
- The extra tools needed to run the Stemformatics project and add datasets into it. git repository
- Software carpentries lesson material. git repository

CONFERENCE AND WORKSHOP ATTENDANCE

- Conference presentation at the 28th International Conference on Intelligent Systems for Molecular Biology (ISMB), 13-16th July, 2020*
- Conference presentation at the Bioinformatics Open Source Conference (BOSC 2020), 20-23rd July, 2020*
- Conference presentation at the Australian Bioinformatics and Computational Biology Conference, 9-11th December, 2019, University of Sydney, Sydney, Australia.
- Conference presentation at the Australian Bioinformatics and Computational Biology Conference, 26-29th November, 2018, University of Melbourne, Melbourne, Australia.
- Conference presentation at the Single Cell Genomics Conference, 14-16th September, 2016, Wellcome Genome Campus Conference Centre, Cambridge, United Kingdom.
- Workshop attendance at the QFAB RNA-Sequencing workshop, 19-20th November, 2014, Queensland Biosciences Precinct, University of Queensland, Australia.
- Conference presentation at the Australasian Genomic Technologies Association 14th Annual Conference (AGTA), 13-15th October, 2014, Crown Promenade Hotel, Melbourne, Australia.
- * *virtual participation due to the COVID-19 pandemic of 2020*

Publications

http://orcid.org/0000-0002-9207-0385

Journal Articles

2020 — Paul W Angel, Nadia Rajab, Yidi Deng, Chris M Pacheco, **Tyrone Chen**, Kim-Anh Lê Cao, Jarny Choi, Christine A Wells. A simple, scalable approach to building a cross-platform transcriptome atlas *PLOS Computational Biology. doi: 10.1101/2020.03.09.984468* — *Link*

2020 — **Tyrone Chen**, Sonika Tyagi. Integrative computational epigenomics to build data-driven gene regulation hypotheses *GigaScience. doi: 10.1093/gigascience/giaa064* — *Link*

2020 — Ali Motazedian, Freya F. Bruveris, Santhosh V. Kumar, Jacqueline V. Schiesser, **Tyrone Chen**, Elizabeth S. Ng, Ann P. Chidgey, Christine A. Wells, Andrew G. Elefanty, Edouard G. Stanley. Multipotent RAG1+ progenitors emerge directly from haemogenic endothelium in human pluripotent stem cell-derived haematopoietic organoids. *Nature Cell Biology. doi: 10.1038/s41556-019-0445-8* — *Link*

2019 — *[Acknowledged]* Nadia Rajab, Paul W Angel, Mariola Kurowska-Stolarska, Simon Milling, Chris M Pacheco, Matt Rutar, Jarny Choi, Christine A Wells. iMAC: An interactive atlas to explore phenotypic differences between in vivo, ex vivo and in vitro-derived myeloid cells in the Stemformatics platform. *bioRxiv. doi: 10.1101/719237* — *Link*

2018 — *[Acknowledged]* Shahzya Chaudhury, Caitríona O'Connor, Ana Cañete, Joana Bittencourt-Silvestre, Evgenia Sarrou, Áine Prendergast, Jarny Choi, Pamela Johnston, Christine A. Wells, Brenda Gibson, Karen Keeshan. Age-specific biological and molecular profiling distinguishes paediatric from adult acute myeloid leukaemias. *Nature communications. doi: 10.1038/s41467-018-07584-1* — *Link*

2018 — Jarny Choi, Chris M. Pacheco, Rowland Mosbergen, Othmar Korn, **Tyrone Chen**, Isha Nagpal, Steve Englart, Paul W. Angel, Christine A. Wells. Stemformatics: visualise and download curated stem cell data. *Nucleic Acids Research. doi: 10.1093/nar/gky1064* — *Link*

2018 — *[Acknowledged]* Suzanne K. Butcher, Christine E. O'Carroll, Christine A. Wells, Ruaidhrí J. Carmody. Toll-like receptors drive specific patterns of tolerance and training on restimulation of macrophages. *Frontiers in immunology. 2018;9.* — *Link*

2016 — Florian Rohart, Elizabeth A. Mason, Nicholas Matigian, Rowland Mosbergen, Othmar Korn, **Tyrone Chen**, Suzanne Butcher, Jatin Patel, Kerry Atkinson, Kiarash Khosrotehrani, Nicholas M. Fisk, Kim-Anh Lê Cao, Christine A. Wells (2016). A molecular classification of human mesenchymal stromal cells. *PeerJ, 4, e1845.* — *Link*

2016 — Kenneth Sinclair, Stephanie Yerkovich, **Tyrone Chen**, Jonathan McQualter, Peter Hopkins, Christine Wells, Daniel Chambers (2016). Mesenchymal stromal cells are readily recoverable from lung tissue, but not the alveolar space, in healthy humans. *Stem Cells. doi: 10.1002/stem.2419.* — *Link*

Conference Proceedings and Poster presentations

2020 — **Tyrone Chen**, Kim-Anh Le Cao, Sonika Tyagi. Multi-omics data integration for the discovery of COVID-19 drug targets *[version 1; not peer reviewed]. F1000Research 2020, 9 (ISCB Comm J):698 (poster) (https://doi.org/10.7490/f1000research.1118023.1).* Presentation at the International Society for Computational Biology Conference 2020, Montreal, Canada (virtual due to COVID-19), Bioinformatics Community Conference 2020, Toronto, Canada (virtual due to COVID-19) — *Link*

2019 — **Tyrone Chen**, Jason D. Rigby, Matthew D. McGee, Sonika Tyagi. Deep learning has potential for harmonising multi-omics data to discover weak regulatory features *[version 1; not peer reviewed]. F1000Research 2019, 8:2068 (poster) (https://doi.org/10.7490/f1000research.1117749.1).* Presentation at the Australian Bioinformatics and Computational Biology Society Annual Conference 2019, Sydney, New South Wales, Australia. — *Link*

2019 — Paul W Angel, Matthew Rutar, Nadia Rajab, **Tyrone Chen**, Isha Nagpal, Jarny Choi, Christine A Wells. Mapping the blood cell landscape in stemformatics *[version 1; not peer reviewed]. F1000Research 2019, 8:206 (poster) (https://doi.org/10.7490/f1000research.1116449.1).* Presentation at the 40th Annual Lorne Genome Conference 2019, Lorne, Victoria, Australia. — *Link*

2018	Jarny Choi, **Tyrone Chen**, Chris M. Pacheco, Rowland Mosbergen, Othmar Korn, Isha Nagpal, Steve Englart, Paul W. Angel, Christine A. Wells. Stemformatics – visualise and download curated stem cell data *[version 1; not peer reviewed]*. *F1000Research 2018, 7:1843 (poster) (https://doi.org/10.7490/f1000research.1116311.1).* Presentation at the Australian Bioinformatics and Computational Biology Society Annual Conference 2018, Melbourne, Victoria, Australia. *Joint presentation between the first two authors*	*Link*
2018	Paul W Angel, **Tyrone Chen**, Jarny Choi, Kim-Anh Le Cao, Elizabeth Mason, Christine A Wells. Mapping the blood cell landscape in stemformatics *[version 1; not peer reviewed]*. *F1000Research 2018, 7:1872 (poster) (https://doi.org/10.7490/f1000research.1116323.1).* Presentation at the Australian Bioinformatics and Computational Biology Society Annual Conference 2018, Melbourne, Victoria, Australia.	*Link*
2018	Paul W Angel, **Tyrone Chen**, Jarny Choi, Othmar Korn, Rowland Mosbergen, Isha Nagpal, Chris Pacheco Rivera, Christine A. Wells. Stemformatics: Easy visualisation platform for well-curated stem cell data *[version 1; not peer reviewed]*. *F1000Research 2018, 7:1007 (poster) (doi: 10.7490/f1000research.1115766.1). Presentation at the 16th International Society for Stem Cell Research Annual Meeting 2018, Melbourne, Victoria, Australia.*	*Link*
2017	Chris Pacheco Rivera, Rowland Mosbergen, Othmar Korn, **Tyrone Chen**, Isha Nagpal, Christine A. Wells. Ontology challenges for the stem cell community: towards integrative data mining in the Stemformatics atlas. *ICBO 2017, 2137(1), 1 (Conference paper). Proceedings of the 8th International Conference on Biomedical Ontology 2017, Newcastle-upon-Tyne, United Kingdom.*	*Link*
2016	**Tyrone Chen**, Rowland Mosbergen, Othmar Korn and Christine Wells. Stemformatics: a visualisation platform for well-curated biological sequence data *[version 1; not peer reviewed]*. *F1000Research 2016, 5:2352 (poster) (doi: 10.7490/f1000research.1113160.1). Presentation at the Single Cell Genomics Conference 2016, Cambridge, United Kingdom.*	*Link*
2016	Jackson, L., Hopcroft, L.E.M., Rogers, S., Jorgensen, H., Pellicano, F., Wells, C., Mosbergen, R., **Chen, T.**, Vetrie, D. and Holyoake, T.L., 2016, January. Identifying genes and pathways deregulated in chronic myeloid leukaemia stem cells through meta-analysis of transcriptomic data. *In British Journal of Haematology (Vol. 173, pp. 122-122). Wiley-Blackwell.*	*Link not available*
2016	L Jackson, LEM Hopcroft, R Mosbergen, **T Chen**, S Kelly, O Khan, S Rogers, HG Jorgensen, D Vetrie, M Copland, CA Wells, TL Holyoake (2016). LEUKomics: Bringing high throughput stem cell data to the leukaemia research community. *Presentation at the 18th Annual John Goldman Conference on Chronic Myeloid Leukemia: Biology and Therapy 2016, Houston, USA.*	*Link not available*
2015	Suzanne Butcher, Edward Huang, Ashley Waardenberg, Othmar Korn, Rowland Mosbergen, **Tyrone Chen**, Kelly Hitchens, Dipti Vijayan, Anthony Beckhouse, Mark Walker, Tim Barnett, James Frazer, Antje Blumenthal, Matt Sweet, The FANTOM5 consortium, Christine Wells (2015). Diversification of innate immune responses by transcriptional mechanisms. *Presentation at the Lorne Infection and Immunity Conference 2015, Lorne, Australia.*	*Link not available*
2014	**Tyrone Chen**, Rowland Mosbergen, Othmar Korn, Christine A Wells (2014). Stemformatics: a user-friendly database of well-curated biological data. *Presentation at the 14th Annual Conference of the Australasian Genomic Technologies Association (AGTA), Melbourne, Victoria, Australia.*	*Link*
2013	**Tyrone Chen**, Yicheng Zhu, Gavin A Huttley (2013). Do DNA sequences influence recruitment of histone variants? ASMR New Investigator's Conference, Canberra. Australian Capital Territory, Australia.	*Link not available*