



Education

Monash University

Melbourne, Australia

PHD STUDENT (BIOINFORMATICS)

2019 - PRESENT

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

Australian National University

Canberra, Australia

BACHELOR OF SCIENCE (HONS. 1ST CLASS) (BIOINFORMATICS)

2010 - 2013

- Honours thesis title: A novel motif discovery algorithm for discovering shared motifs in non-homologous sequences.
- Undergraduate research project: An investigation of the potential role of small RNA in maintaining genomic stability of plants.
- Summer research project: A systematic analysis of the photosynthetic properties of the land plant *Hirschfeldia incana*

Academic Experience

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

Melbourne, Australia

PHD STUDENT (COMPUTATIONAL BIOLOGY)

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, Centre for Stem Cell Systems, Department of Anatomy and Neuroscience, University of Melbourne (Prof. Christine Wells)

Melbourne, Australia

RESEARCH ASSISTANT (BIOINFORMATICS)

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.

Stemformatics Project, Australian Institute for Bioengineering and Nanotechnology, University of Queensland (Prof. Christine Wells)

Brisbane, Australia

RESEARCH ASSISTANT (BIOINFORMATICS)

2014 - 2016

- Duties and achievements are the same as previously listed role Research Assistant (Bioinformatics).

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 discontiguous 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.

Non-academic Experience

Monash University

DATA FLUENCY ASSOCIATE INSTRUCTOR

Melbourne, Australia

2019-PRESENT

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

TraffixGroup

SUPERVISOR (TRAM SURVEYOR)

Melbourne, Australia

2014

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

Research School of Biology, Australian National University

LABORATORY TECHNICIAN

Canberra, Australia

2012

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

College of Medicine, Biology & Environment, Australian National University

PEER MENTOR FOR BIOLOGY STUDENTS

Canberra, Australia

2011

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

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 of Philosophy (PhD) with the School of Biological Sciences, Monash University. Canberra, Australia

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

Sponsored Membership

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

Skills

COMPUTATIONAL

- Machine learning: keras and tensorflow
- Languages: python (pandas, matplotlib), R (Bioconductor), bash, pSQL, LaTeX/overleaf, 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
- Workflow languages: Snakemake and Nextflow
- Graphic design for posters and scientific articles: Adobe InDesign, [example poster available online](#)

MATHEMATICS

- Information theory: mutual information, relative entropy
- Signal processing: Fourier transform, autocorrelation
- Numerical optimisation: simulated annealing

BIOINFORMATICS AND STATISTICS

- Data visualisation: PCA, interactive plots, genome browsers
- Differential gene expression analyses: ANOVA, pairwise t-tests
- Motif enrichment analyses: ISMARA, MEME suite
- Batch effect correction: limma, ComBAT, supervised normalisation

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

OTHER

- Teaching and training: usage of microarray and high throughput sequencing pipelines, introduction to programming (python, R, unix shell, HPC), peer mentoring for undergraduate biology students
- Time management and task organisation
- Liaising with external collaborators across disciplines to obtain experimental data and relevant metadata
- Clear communication with individuals across diverse cultural and professional backgrounds
- Contributing to an organisation's social media on a specific topic [[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, 14 July 2016.
- Community outreach with visiting students at the University of Queensland, 14 September 2014.
- Community outreach with visiting students at the Australian National University, 2013.

CONTRIBUTIONS TO OPEN SOURCE SOFTWARE LIBRARIES

- 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.
- Software carpentries instructor training, 10-11th November, 2019, Monash University, Melbourne, Australia.
- Workshop attendance at the [Introduction to Tensor Flow and Machine Learning workshop](#), 22nd March, 2019, Monash University, Melbourne, Australia.
- Workshop attendance at the Machine Learning workshop, 29th November, 2018, University of Melbourne, Melbourne, Australia.
- Workshop attendance at the BioIT workshop, 26th November, 2018, University of Melbourne, Melbourne, 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 attendance at the Australian Bioinformatics Conference, 11-12th October, 2014, Royal Children's Hospital, Melbourne, Australia.
- Conference presentation at the Australasian Genomic Technologies Association 14th Annual Conference (AGTA), 13-15th October, 2014, Crown Promenade Hotel, Melbourne, Australia.
- Seminar and discussion group attendance for relevant topics in the University of Queensland, University of Melbourne, the Walter and Eliza Hall Institute of Medical Research, Monash University, Royal Melbourne Institute of Technology.
- * virtual participation due to the COVID-19 pandemic of 2020

Publications

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](#)