

Experience

Computational Biologist

Alkahest Inc.

📅 June 2021 - Ongoing

📍 San Carlos, US (Remote)

- Developed best-practices, reproducible, FAIR workflows for analysis of single-cell RNA-seq datasets.
- Identified opportunities for integrating external databases (e.g. GWAS Catalog, DrugBank) to improve understanding and interpretation of current analyses and workflows.
- Developed Connectivity Map (CMap) framework for integrated analysis of plasma proteomic, single-cell RNA-seq, and bulk RNA-seq datasets.
- Prepared and presented educational talks to improve statistical knowledge across the company.
- Performed statistical and bioinformatics review of posters and manuscripts.
- Conceptualised and conducted investigations comparing different approaches (e.g. 10X and SmartSeq platforms; different differential expression approaches) to determine best-practices across company.

Bioinformatician

South Australian Genomics Centre (SAGC)

📅 August 2020 – April 2021

📍 Adelaide, Australia

- Developed custom workflows and pipelines to enable reproducible processing and analysis of single-cell, spatial, and bulk transcriptomic data.
- Integrated single-cell datasets from multiple tissues (skin and heart) by applying appropriate statistical and machine learning techniques in R and Python.
- Applied trajectory and velocity analysis techniques to identify and characterise novel progenitor cell types during tissue development and wounding.
- Deployed web applications for visualising large-scale single-cell datasets using R/Shiny and Google Cloud Platform.
- Consulted with remote clients and collaborators on diverse multi-omics problems, and quoted for, implemented and delivered 8+ tailored bioinformatics solutions within time and budgetary constraints.

Education

Doctor of Philosophy (Bioinformatics)

The University of Adelaide

📅 2017 – 2020

- **Thesis Title:** Transcriptome analysis of zebrafish genetic models to reveal early molecular drivers of Alzheimer's disease

Key Projects

Iron Responsive Element (IRE)-Mediated Responses to Iron Dyshomeostasis in Alzheimer's Disease

📅 Jun 2019 – Aug 2020 | 🛠 R, shell scripting, Snakemake, High Performance Computing, R/Bioconductor, limma and edgeR, GSEA, workflowR

- Developed workflow for exploring iron homeostasis at the transcriptional level and applied this to analyze zebrafish, mouse, and human datasets.
- Presented findings at International Joint GIW-ABACBS Conference (Sydney, Dec 2019), winning Best Student Presentation Award (1st Prize).

Summary

Data scientist with 3+ years of experience in industry bioinformatics. Strong interest and background in neurodegenerative disease and brain aging research.

Awards

- **2021 - Recipient of 10X-Millennium Science Spatial Pioneers Fellowship Scheme** . Australia.
- **2021 - Semi-Finalist in Channel 7 7NEWS Young Achiever Awards** . Adelaide, Australia.
- **2020 - Doctoral Research Medal (top 4% of theses submitted in 2020)** . The University of Adelaide. Adelaide, Australia.
- **2020 - Best Student Presentation Award (1st Place), out of 15 speakers** , Joint GIW-ABACBS International Conference. Sydney, Australia.
- **2019 - Best Poster Presentation Award, out of 35 entrants** , AMSI BioInfoSummer. Sydney, Australia.
- **2019 - Best Presentation Award, out of 50 speakers** , Australia-Japan Joint Neurodegenerative Disease Symposium. Adelaide, Australia.
- **2019 - CHOOSEMaths Travel Grant Winner, one of 20 winners selected nationally** , Australian Mathematical Sciences Institute (AMSI). Sydney, Australia.
- **2017 - Oral Presentation Award (3rd Place), out of 15 speakers** , COMBINE Symposium. Adelaide, Australia.
- **2017 - Best Conference Poster Award, out of 36 entrants** , Model Organisms in Human Health Australia (MOHHA). Yarra Valley, Victoria.

References

References provided upon request.

- **Hin N** , Newman M, Pederson S, Lardelli M. Iron Responsive Element Mediated Responses to Iron Dyshomeostasis in Alzheimer's Disease. *J. Alzheimer's Dis.* 2021;84(4):1597-630.

Accelerated brain aging towards transcriptional inversion in a zebrafish model of the K115fs mutation of human *PSEN2*

📅 Jun 2017 – May 2019 | 🛠️ R, shell scripting, High Performance Computing, WGCNA, Cytoscape, R/Bioconductor, limma

- Performed co-expression network analysis to compare brain transcriptomes in a familial Alzheimer's disease animal model with sporadic Alzheimer's disease in humans.
- Applied multivariate statistics and modelling to analyse bulk RNA-seq and microarray datasets.
- Designed and created visualisation-rich presentations that won 4 awards from multiple nationally-recognised conferences and symposiums.
- **Hin N*** , Newman M*, Kaslin J, Douek AM, Lumsden A, Nik SHM, Dong Y, Zhou XF, Mañucat-Tan NB, Ludington, A, Adelson DL, Pederson S, Lardelli M. Accelerated brain aging towards transcriptional inversion in a zebrafish model of the K115fs mutation of human *PSEN2*. *PLoS One* 2020;15(1):p.e0227258.

Bachelor of Science (Advanced)

The University of Adelaide

📅 2014 – 2016 | GPA: 6.8 / 7

- **Majors:** Genetics and Chemistry
- Thesis on the role of sirtuins in aging

Publications

* indicates shared first-authorship

- Lardelli M, Baer L, **Hin N** , Allen A, Pederson SM, Barthelson K. The Use of Zebrafish in Transcriptome Analysis of the Early Effects of Mutations Causing Early Onset Familial Alzheimer's Disease and Other Inherited Neurodegenerative Conditions. *J. Alzheimer's Dis.* 2023;1:15 (pre-print)
- Okada T, McIlfratrick S, **Hin N** , Aryamanesh N, Breen J, St John JC. Mitochondrial supplementation of *Sus scrofa* metaphase II oocytes alters DNA methylation and gene expression profiles of blastocysts. *Epigenetics Chromatin* 2022;15(1):1-20.
- **Hin N** , Newman M, Pederson S, Lardelli M. Iron Responsive Element Mediated Responses to Iron Dyshomeostasis in Alzheimer's Disease. *J. Alzheimer's Dis.* 2021;84(4):1597-630.
- **Hin N*** , Newman M*, Kaslin J, Douek AM, Lumsden A, Nik SHM, Dong Y, Zhou XF, Mañucat-Tan NB, Ludington, A, Adelson DL, Pederson S, Lardelli M. Accelerated brain aging towards transcriptional inversion in a zebrafish model of the K115fs mutation of human *PSEN2*. *PLoS One* 2020;15(1):p.e0227258.
- Newman M*, **Hin N*** , Pederson S, Lardelli M. Brain transcriptome analysis of a familial Alzheimer's disease-like mutation in the zebrafish presenilin 1 gene implies effects on energy production. *Mol. Brain* 2019;12(1):1-5.
- Dong Y, Newman M, Pederson S, Barthelson K, **Hin, N** , Lardelli, M. Transcriptome analyses of 7-day-old zebrafish larvae possessing a familial Alzheimer's disease-like mutation in *psen1* indicate effects on oxidative phosphorylation, ECM and MCM functions, and iron homeostasis. *BMC Genom.* 2021;22(1):1-16.
- Breen J, McAninch D, Jankovic-Karasoulos T, McCullough D, Smith MD, Bogias KJ, Wan Q, Choudhry, A, **Hin N** , Pederson SM, Bianco-Miotto T. Temporal placental genome wide expression profiles reflect three phases of utero-placental blood flow during early to mid human gestation. *medRxiv* 2020 (Pre-Print).
- Newman M, Nik HM, Sutherland GT, **Hin N** , Kim WS, Halliday, GM, Jayadev S, Smith C, Laird AS, Lucas CW, Kittipassorn T. Accelerated loss of hypoxia response in zebrafish with familial Alzheimer's disease-like mutation of presenilin 1. *Hum. Mol. Genet.* 2020;29(14):2379-94.

Skills

General

- Peer review
- Literature review
- Statistics

Programming

- R, Python, shell scripting

Bioinformatics

- Transcriptomics (bulk, single-cell, spatial)
- Plasma proteomics
- Microarrays
- CRISPR screens
- Analysis of gene co-expression networks
- Accessing and integrating data from biological databases
- Multi-omics analysis and data integration
- Experimental design and power calculations

Software Engineering and Data Management

- High performance computing (HPC)
- Development of pipelines/workflows using Snakemake, workflowR
- Git and version control
- Docker containers and Conda environments
- Development of unit tests

Machine Learning and Data Science

- Data cleaning and pre-processing
- Dealing with missing or censored values and technical batch effects
- Feature selection and engineering
- Supervised analysis problems, including classification and regression
- Unsupervised analysis problems, including clustering, matrix factorisation, and dimension reduction
- Network analysis and graph visualisation
- Web app development using R/Shiny
- Use of SQL databases