Nhi Hin

✉ hello@nhihin.com   📞 +61 424 875 797   🔗 nhihin   🐦 nhihin   ⌨ nhihin

Experience

Bioinformatician
South Australian Genomics Centre (SAGC)

📅 August 2020 – Ongoing   📍 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).
- <u>Hin N</u> , 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.
- <u>Hin N*</u> , 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.

Objective

Australian Bioinformatician with 4+ years of experience in transcriptomics and solid background in Alzheimer's disease research. Seeking to bring expertise in single-cell and spatial transcriptomics to Alkahest Inc. Highly skilled in statistics, data visualization, and creative thinking.

Awards

- **2021 - Recipient of 10X-Millenium 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.

Education (cont.)

Bachelor of Science (Advanced)

The University of Adelaide

📅 2014 – 2016 | **GPA:** 6.8 / 7

- **Majors:** Genetics and Chemistry

Publications

* indicates shared first-authorship

- <u>Hin N</u> , 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.
- <u>Hin N*</u> , 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*, <u>Hin N*</u> , 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, <u>Hin, N</u> , 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, <u>Hin N</u> , 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, <u>Hin N</u> , 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.

Conference Presentations

Talks

- RNA-seq analysis of a zebrafish model of Alzheimer's disease reveals the importance of iron homeostasis. Presented at *COMBINE Symposium* and *Joint GIW-ABACBS International Conference*. December 2019. Sydney, Australia. (**Oral Presentation Prize / 1st place**, out of 15 speakers)
- Computational Analysis Reveals an Early Brain Iron Deficiency Response in a Zebrafish Mutation Model of Familial Alzheimer's Disease. Presented at the *Back to Basics: Understanding the Molecular Basis of Alzheimer's Disease workshop*. September 2019. Sydney, Australia.
- Bioinformatics analysis of familial Alzheimer's disease-like zebrafish. Presented at the *AustraliaJapan Neurodegenerative Disease Symposium*. June 2019. Adelaide, Australia. (**Best Presentation Award**, out of 50 speakers)
- Diving into Alzheimer's Disease with Transcriptome Analysis of a Zebrafish Model. Presented at *COMBINE Symposium*. October 2017. Adelaide, Australia. (**Oral Presentation Prize / 3rd place**, out of 15 speakers)

Posters

- Iron Enriched. Presented at *AMSI BioInfoSummer,* December 2019. Sydney, Australia. (**Best Poster Prize**, out of 35 entrants)
- RNA-seq analysis of aging and Alzheimer's disease in a zebrafish model. Presented at the *Model Organisms for Human Health Australia (MOHHA) Conference*, June 2017. Melbourne, Victoria. (**Best Poster Prize**, out of 36 entrants)

Teaching Experience

Tutor for South Australian Genomics Centre Workshop Series

📅 August 2021

- Developed and taught workshop material for class of 100+ attendees.
- **Topics:** Bulk RNA-seq Analysis, Single-cell RNA-seq Analysis

Tutor for Spring Into Bioinformatics Workshop

📅 September 2019

- Developed and taught workshop material for class of 50+ students, as part of the University of Adelaide's Bioinformatics Hub Workshop Series.
- **Topics:** Introduction to R and RStudio for Biological Research; Gene Expression Analysis for RNA-seq Data; QC and Alignment for Next-Generation Sequencing Data

Scientific and Technical Expertise

Programming Languages

- R, including use of tidyverse, Bioconductor, shiny, and workflowR
- Python, including use of NumPy, pandas, and scikit-learn
- Shell scripting

Bioinformatics Data Processing and Analysis

- Single-cell RNA-seq
- Spatial transcriptomics
- Bulk RNA-seq
- Microarrays
- CRISPR screens
- LS-MS/MS proteomics
- Metagenomics
- Whole genome bisulfite sequencing
- Whole genome sequencing
- 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

- Use of high performance computing (HPC) resources via SLURM
- Development of pipelines/workflows using Snakemake, Nextflow, and workflowR
- Use of Git and version control
- Use of 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
- Deployment of applications on Google Cloud Platform
- Use of SQL databases

Other Technical Skills

- Adobe Photoshop and InDesign for scientific illustration and poster design
- HTML/CSS and website management

Referees

Dr. Jimmy Breen

- @ Former Head of Bioinformatics, South Australian Genomics Centre
- ✉ jimmy.breen@adelaide.edu.au
- ☎ +61 477 830 366

A/Prof. Michael Lardelli

- @ The University of Adelaide
- ✉ michael.lardelli@adelaide.edu.au
- ☎ (08) 8313 3212