☑ james.kn.dao@gmail.com | 🎢 jmsdao.github.io | 🖸 jmsdao

Skills

Programming Python (numpy/pandas, PyTorch, matplotlib, scikit-learn), R (tidyverse, ggplot2, Bioconductor), Markdown/HTML/CSS **Tools/Services** Linux (WSL2, conda, git), Docker, Jupyter, AWS (EC2, Lambda, S3)

Work Experience _____

Longaevus Technologies

Remote

BIOINFORMATICIAN (PART-TIME)

Mar 2022 - Present

- · Exploratory analysis of public datasets.
- Building web-based tools in R Shiny for analysts.

Tibra Capital Sydney, Australia

JUNIOR QUANT TRADER

Feb 2019 - Feb 2020

- First junior trader of the cohort to be greenlit to trade solo.
- Managed market making operations of equity and index derivatives on the ASX and HKEX.
- Collaborated with quant researchers, software devs and key stakeholders to develop trading strategies, and improve efficiency of operations.

University of New South Wales

- LAB DEMONSTRATOR Jul 2016 - Jun 2018 • Taught 1st to 3rd year laboratory sessions for electrical engineering students.
- · Engaged in project management for student capstone projects.

Publications

· Ilieva, M.; Dao, J.; Miller, H.E.; Madsen, J.H.; Bishop, A.J.R.; Kauppinen, S.; Uchida, S. Systematic Analysis of Long Non-Coding RNA Genes in Nonalcoholic Fatty Liver Disease. Non-coding RNA 2022, 8, x. https://doi.org/10.3390/xxxxx

Relevant Projects _____

Lipidomics Aging Clock (Ongoing)

IN COLLABORATION WITH THE BARSHOP INSTITUTE

- Tools used: Jupyter, Python (numpy/pandas, sklearn, statsmodels, matplotlib)
- Concepts covered: data wrangling/visualzation, PCA/dimensionality reduction, regularized linear models, tree-based learning, ensemble learning, cross-validation, feature importance analysis

Data Processing and RShiny Web App for LiverDB 1

IN COLLABORATION WITH THE LAB OF CARDIOVASCULAR BIOINFORMATICS

- · Tools used: Nextflow, Linux, R (shiny, edgeR, enrichR), Docker, HTML
- Concepts covered: parallelizing bioinformatics pipelines, DGE anaylsis, pathway enrichment analysis, interactive data visualization

Top 12 Ranking in Australia on Rosalind (Bioinformatics Programming Platform)

HTTP://ROSALIND.INFO/STATISTICS/COUNTRIES/AU/

- Tools used: Jupyter, Python (numpy, biopython, networkx, scipy).
- · Concepts covered: algorithmic complexity (big 0), dynamic programming, combinatorics, alignment and assembly

Feedforward Neural Network on the MNIST Dataset Without Deep Learning Libraries

HTTPS://COLAB.RESEARCH.GOOGLE.COM/DRIVE/1FNRZCUNTFT53NKYN5XAXDXSZGDD8V__H

- Tools used: Google Colab, Python (numpy)
- · Concepts covered: deep learning, multi-layer perceptron, backpropagation, stochastic gradient descent
- Trains at <1 sec per epoch on standard Colab CPU, and achieves approx. 93% accuracy on the MNIST test set

Education_

University of New South Wales