

DAVID ZHANG

By bridging bioinformatics and engineering, I translate genetic and transcriptomic data into software that delivers real-world impact. I have lead cross-functional projects across the full software development lifecycle from prototyping innovative solutions to implementing and maintaining robust, production-ready pipelines.

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WORK EXPERIENCE

Present
|
2024



Senior bioinformatics engineer

[CoSyne Therapeutics](#)

📍 London, UK (hybrid)

- Lead the optimisation and scaling of machine learning tools for single-cell perturb-seq data comprising millions of cells. Collaborate closely with AI, engineering, and computational biology teams, ensuring key internal stakeholders are consistently informed of progress. Apply these tools to generate actionable insights and inform strategic decisions around company direction.
- Design and deploy a data pipeline to ingest, tidy and version-control data for the CoSyne knowledge graph. Automate the release of the graph to AWS using terraform and CI/CD, improving the efficiency and traceability of data updates.
- Build and maintain infrastructure tooling including docker images, terraform modules, CI/CD workflows and cruft templates to streamline bioinformatics analyses.

2024
|
2022



Senior bioinformatics software engineer

[Congenica](#)

📍 Hinxton, UK (hybrid)

- Developed scalable nextflow pipelines to process solid tumor DNA-sequencing data covering alignment, variant calling, driver mutation annotation, and therapy matching.
- Collaborated with clinical and bioinformatics teams to investigate driver variant misclassifications. Led the design, refinement, and implementation of solutions within an agile scrum team, effectively translating complex scientific concepts for engineers without a bioinformatics background to ensure accurate and aligned development.
- Built python and R packages to improve the efficiency of clinical verification, reducing time taken by 2 weeks per quarterly release.

2021



Bioinformatician internship (2 months)

[Verge Genomics](#)

📍 London, UK (remote)

- Created a reproducible aberrant splicing detection pipeline using docker for drug target discovery in C9orf72 ALS patients.



EDUCATION

2022
|
2017



PhD, Bioinformatics

University College London

📍 London, UK

- Analysed bulk RNA-sequencing data with the aim of improving the diagnosis rate of rare disease patients. Focussed on detection of aberrant splicing events as a strategy to prioritise pathogenic variants.
- Released R/Bioconductor packages that enable bioinformatics analyses and interpretation. Championed best practices for software development through teaching workshops and courses.

CONTACT

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🌐 [Website](#)

🐙 [GitHub](#)

in [LinkedIn](#)

🔗 [Google Scholar](#)

LANGUAGES

🐍 Python

📊 R

🦀 Rust

</> Bash

TECHNOLOGIES

🔗 Git

🔧 Nextflow

🐳 Docker

aws AWS

🐳 Kubernetes

2016
|
2015



MSc, Neuroscience

University College London

📍 London, UK

- Grade: Merit (68%)

2015
|
2012



BSc, Biomedical science

University College London

📍 London, UK

- Grade: 2:1 (69%)



OPEN-SOURCE SOFTWARE

Present
|
2022



Web development

- [Portfolio website](#): Showcases my favourite open-source contributions. Built with Django and deployed using PythonAnywhere.

2024



Rust packages

- [tuni](#): Unify transcript identifiers across different samples.

2023
|
2021



Python packages

- [autogroceries](#): Use Selenium to automate your grocery shop.
- [stravaboard](#): An extendable Streamlit dashboard for tracking Strava runs.

2022
|
2020



R packages

- [ggtranscript](#): Visualising transcript structure and annotation using ggplot2.
- [dasper](#): Detection of aberrant splicing events in RNA-sequencing data.



SELECTED PUBLICATIONS

2022



[ggtranscript: an R package for the visualization and interpretation of transcript isoforms using ggplot2](#)

Bioinformatics

- Role: Co-first author, R package developer.

2021



[Developmental Consequences of Defective ATG7-Mediated Autophagy in Humans](#)

The New England Journal of Medicine

- Role: Analyst

2021



[Megadepth: efficient coverage quantification for BigWigs and BAMs](#)

Bioinformatics

- Role: R package developer

2020



[Incomplete annotation of disease-associated genes is limiting our understanding of Mendelian and complex neurogenetic disorders](#)

Science advances

- Role: First author, lead analyst.

A complete list of my publications is available via [Google Scholar](#)