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.
- 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 abberant 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

dyzhang32@gmail.com
Website
GitHub
LinkedIn
Google Scholar

LANGUAGES

Python
R
Rust
Bash

TECHNOLOGIES

Git
Nextflow
Docker
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

A complete list of my publications is available via Google Scholar

2020

Incomplete annotation of disease-associated genes is limiting our understanding of Mendelian and complex neurogenetic disorders

Science advances

• Role: First author, lead analyst.