DAVID ZHANG

Experienced bioinformatician who enjoys learning and applying the best practices for method development. I focus on developing robust, user-friendly tools that harness transcriptomic data to improve the rate of genetic diagnosis.

View this CV online with links at dzhana32.aithub.io/cv/

EDUCATION

Present 2017

PhD, Bioinformatics

University College London

O London, UK

 \cdot Thesis: Using transcriptomics to improve the genetic diagnosis rate of rare disease patients.

2016 2015

MSc, Neuroscience

University College London

OLONDON, UK

- · Thesis: The role of mitochondrial dysfunction in Xerodoma pigmentosum
- · Grade: Merit (68%)
- · Awarded post-graduate support scheme bursary (£10,000)

2015 2012

BSc, Biomedical science

University College London

Q London, UK

- · Thesis: Investigating the function of CYFIP1 in the development of rat hippocampal neurons.
- · Grade: 2:1 (69%)

2012 2007

H.S.

Queen Elizabeth's School

Parnet. UK

· Grades: Maths (A*), Biology (A*), Chemistry (A*), Sociology (A).



III WORK EXPERIENCE

2021

Bioinformatician internship (2 months)

Verge Genomics

Remote. US

- · Goal: Set up an aberrant splicing detection pipeline for drug target discovery in C9orf72 ALS patients.
- · Used docker to setup a reproducible workflow¹ for running aberrant splicing analyses on an AWS instance.

CONTACT

☑ dyzhang32@gmail.com

G GitHub

in LinkedIn

ResearchGate

LANGUAGE SKILLS

R	
Python	
Git/GitHub	
Bash	
docker	

The long-form version of my CV with a list of selected publications is available here.

Made with the R package datadrivency and pagedown.

The source code is available at github.com/dzhang32/cv.

Last updated on 2022-03-24.

SOFTWARE & PROGRAMMING

Present | 2020

Bioconductor packages

- dasper²: Detection of aberrant splicing events in RNA-sequencing.
 Author and maintainer.
- megadepth³: BigWig and BAM related utilities. An R wrapper for the megadepth software developed by Chris Wilks. **Co-author** and **maintainer**.
- ODER⁴: Optimising the definition of Expressed Regions. Submitted to Bioconductor. **Co-author** and **maintainer**.

Present | 2022

R packages

- ggtranscript⁵: Visualising transcript structure and annotation using ggplot2. **Author** and **maintainer**.
- autorecipes⁶: Automate your recipe planning. **Author** and **maintainer**.

Present | 2021

Python packages

- autogroceries⁷. Automate your grocery shop. **Author** and **maintainer**.
- · codino⁸ converts a codon design to the expected amino acid frequencies, and vice versa. **Author** and **maintainer**.

2021

Web scraping

 \cdot Applied the python packages $\bf Beautiful~Soup$ and $\bf Selenium~to~web~scrape^9$ information on all UK biotechnology companies.

2021

Data science blog

- Chess-related blog post⁷⁰ was selected for the hand-on-tutorials column in Towards Data Science, which displays pieces that highlight best practices of data science.
- \cdot Applied popular data science packages in python to analyse $^{\text{11}}$ chess.com data.



- 1: https://github.com/dzhang32/auto_splice
- 2: https://bioconductor.org/packages/release/bioc/html/dasper.html
- 3: https://bioconductor.org/packages/release/bioc/html/megadepth.html
- 4: https://github.com/eolagbaju/ODER
- 5: https://github.com/dzhang32/ggtranscript
- 6: https://github.com/dzhang32/autorecipes
- 7: https://github.com/dzhang32/autogroceries
- 8: https://github.com/dzhang32/codino

- 9: https://github.com/dzhang32/biotech_web_scrape
- 10: https://towardsdatascience.com/how-has-the-queens-gambit-impacted-the-popularity-of-online-chess-43594efe5a98
- 11: https://github.com/dzhang32/chess