

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 dzhang32.github.io/cv/



WORK EXPERIENCE

present
|
2022

Machine learning engineer

[Ladder therapeutics](#)

📍 London, UK (remote)

- **Goal:** Implementing and engineering production-ready software leveraging RNA biology and chemistry to accelerate drug discovery.

2021

Bioinformatician internship (2 months)

[Verge Genomics](#)

📍 London, UK (remote)

- **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.



EDUCATION

2022
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2017

PhD, Bioinformatics

University College London

📍 London, UK

- **Thesis:** Using transcriptomics to improve the genetic diagnosis rate of rare disease patients.
- Developed and released software that facilitate transcriptomic analyses with a focus on diagnostics.

2016
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2015

MSc, Neuroscience

University College London

📍 London, UK

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

2015
|
2012

BSc, Biomedical science

University College London

📍 London, UK

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

CONTACT

✉ dychang32@gmail.com

🐙 [GitHub](#)

in [LinkedIn](#)

📖 [ResearchGate](#)

LANGUAGE SKILLS

Python

R

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 [datadrivencv](#) and [pagedown](#).

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

Last updated on 2022-04-15.

2012
|
2007



H.S.

Queen Elizabeth's School

📍 Barnet, UK

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



SOFTWARE & PROGRAMMING

Present
|
2020



Bioconductor packages

- **dasper**²: Detection of aberrant splicing events in RNA-sequencing. **Author** and **maintainer**.
- **megadePTH**³: BigWig and BAM related utilities. An R wrapper for the megadePTH software developed by Chris Wilks. **Co-author** and **maintainer**.
- **ODER**⁴: Optimising the definition of Expressed Regions. Submitted to Bioconductor. **Co-author** and **maintainer**.

Present
|
2022



R packages

- **ggtranscript**⁵: Visualising transcript structure and annotation using ggplot2. **Author** and **maintainer**.
- **autorecipes**⁶: Automate your recipe planning. **Author** and **maintainer**.

Present
|
2021



Python packages

- **autogroceries**⁷: Automate your grocery shop. **Author** and **maintainer**.
- **codino**⁸ converts a codon design to the expected amino acid frequencies, and vice versa. **Author** and **maintainer**.

2021



Web scraping

- Applied the python packages **Beautiful Soup** and **Selenium** to web scrape⁹ information on all UK biotechnology companies.

2021



Data science blog

- Chess-related blog post¹⁰ was selected for the hand-on-tutorials column in Towards Data Science, which displays pieces that highlight best practices of data science.
- Applied popular data science packages in **python** to analyse¹¹ chess.com data.



LINKS

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>