





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/





EDUCATION

- Present
|
2017
- **PhD, Bioinformatics**
University College London  London, UK
 - **Thesis:** Using transcriptomics to improve the genetic diagnosis rate of rare disease patients.
- 2016
|
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%)
- 2012
|
2007
- **H.S.**
Queen Elizabeth's School  Barnet, UK
 - **Grades:** Maths (A*), Biology (A*), Chemistry (A*), Sociology (A).

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

 dychang32@gmail.com
 [GitHub](#)
 [LinkedIn](#)
 [ResearchGate](#)

LANGUAGE SKILLS



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 2022-02-11.



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**.

Present
|
2021

● Python packages

- **codino**⁶ 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 scrape⁷ information on all UK biotechnology companies.

2021

● Data science blog

- Chess-related blog post⁸ 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 analyse⁹ 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/codino>
- 7: https://github.com/dzhang32/biotech_web_scrape
- 8: <https://towardsdatascience.com/how-has-the-queens-gambit-impacted-the-popularity-of-online-chess-43594efe5a98>
- 9: <https://github.com/dzhang32/chess>