DAVID ZHANG

Experienced bioinformatician who has experience developing robust, user-friendly software in python or R to facilitate diagnostics and drug discovery.

💼 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 workflow[1] for running aberrant splicing analyses on an **AWS** instance.

2017 | 2016

Research Technician
University College London 📍 London, UK

· **Goal**: Investigate the impact of genetic variation on the age of onset of dementia and cognition within Down syndrome patients.

🎓 EDUCATION

2022 | 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 | 2015

MSc, Neuroscience
University College London 📍 London, UK

· **Thesis**: The role of mitochondrial dysfunction in Xerodoma pigmentosum

· **Grade**: Merit (68%)

· Awarded post-graduate support scheme bursary (£10,000)

CONTACT

- ✉ dyzhang32@gmail.com
- ⦿ GitHub
- in LinkedIn
- 🪪 Google Scholar

LANGUAGE SKILLS
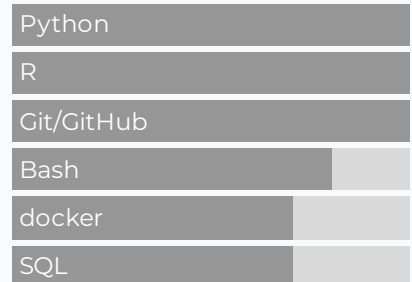
Skill
Python
R
Git/GitHub
Bash
docker
SQL

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%)

H.S.

Queen Elizabeth's School   Barnet, UK

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

📈 SOFTWARE & PROGRAMMING

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**.

R packages

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

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**.

Web scraping

- Applied the python packages **Beautiful Soup** and **Selenium** to web scrape[9] information on all UK biotechnology companies.

Data science blog

- Chess-related blog post[10] 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 analyse[11] chess.com data.

🖥 TEACHING EXPERIENCE

2020

Developing Bioconductor packages
University College London   📍 Virtual Event

· Hosted workshop[12] on best practices for developing Bionconductor
  packages using biocthis[13].

2020

R package development
Rstats club   📍 Virtual Event

· Presentation[14] about unit testing fundamentals, the importance of
  testing and new features released in the R package testthat edition 3.
· Presentation[15] about pre-commit hooks in R.
· Presentation[15] about the best practices of developing R packages.

2020
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2018

R fundamentals
Clinician Coders   📍 London, UK

· Developed materials[17] and lead workshops that aimed to teach R
  fundamentals to clinicians.

2020
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2017

RNA-sequencing for diagnostics
Kings College London   📍 London, UK

· Lectured graduate level students about how transcriptomics can be
  applied in the diagnostic pipeline.

📖 SELECTED PUBLICATIONS

2022

ggtranscript: an R package for the visualization and interpretation of transcript isoforms using ggplot2
bioRxiv

· Gustavsson EK, **Zhang D**, Reynolds RH, Garcia-Ruiz S, Ryten M
· **Role**: Co-first author.
· DOI: https://doi.org/10.1101/2022.03.28.486050

A complete list of publications is available via Google Scholar[18]

2021

Developmental Consequences of Defective ATG7-Mediated Autophagy in Humans
The New England Journal of Medicine

· Collier J, Guissart C, Oláhová M, Sasorith S, Piron-Prunier F, Suom Fi,
  Zhang D, Martinez-Lopez N, Leboucq N, Bahr A, Azzarello-Burri S, Reich
  S, Schöls L, Polvikoski TM, Meyer P, Larrieu L, Schaefer AM, Alsaif HS,
  Alyamani S, Zuchner S, Barbosa IA, Deshpande C, Pyle A, Rauch A,
  Synofzik M, Alkuraya FS, Rivier F, Ryten M, McFarland R, Delahodde A,
  McWilliams TG, Koenig M, and Taylor RW.
· **Role**: Analyst
· DOI: https://doi.org/10.1056/NEJMoa1915722

2021 ● **Megadepth: efficient coverage quantification for BigWigs and BAMs**
Bioinformatics

· Wilks C, Ahmed O, Baker DN, **Zhang D**, Collado-Torres L, Langmead B.
· **Role**: R package developer.
· **DOI**: https://doi.org/10.1093/bioinformatics/btab152

2021 ● **Integration of eQTL and Parkinson's disease GWAS data implicates 11 disease genes**
Jama Neurology

· Kia DA, **Zhang D**, Guelfi S, Manzoni C, Hubbard L, United Kingdom Brain Expression Consortium (UKBEC), International Parkinson's Disease Genomics Consortium (IPDGC), Reynolds RH, Botía JA, Ryten M, Ferrari R, Lewis PA, Williams N, Trabzuni D, Hardy J, Wood NW.
· **Role**: Co-first author.
· **DOI**: https://doi.org/10.1001/jamaneurol.2020.5257

2020 ● **Incomplete annotation of disease-associated genes is limiting our understanding of Mendelian and complex neurogenetic disorders.**
Science advances

· **Zhang D**, Guelfi S, Ruiz SG, Costa B, Reynolds RH, D'Sa K, Liu W, Courtin T, Peterson A, Jaffe AE, Hardy J, Botia JA, Collado-Torres L and Ryten M.
· **Role**: First Author.
· **DOI**: https://doi.org/10.1126/sciadv.aay8299

🔗 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
12: https://dzhang32.github.io/biocthis_workshop/
13: https://bioconductor.org/packages/release/bioc/html/biocthis.html
14: https://youtu.be/ClAin7vTwq0
15: https://github.com/dzhang32/rstats_pres
16: https://github.com/dzhang32/rstats_pres
17: https://github.com/ClinicianCoders/ClinicianCoders
18: https://scholar.google.com/citations?user=PAcm4wUAAAAJ&hl=en