

DAVID ZHANG

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

View this CV online with links at dzhang32.github.io/cv/



WORK EXPERIENCE

- present
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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.
 - **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.
 - **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.



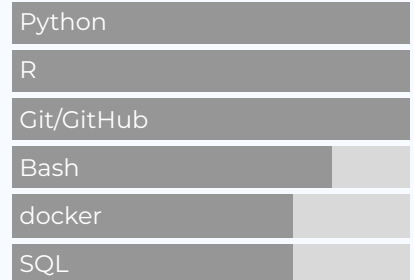
EDUCATION

- 2022
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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.
 - **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)

CONTACT

✉ dzhang32@gmail.com
🐙 [GitHub](#)
in [LinkedIn](#)
🔖 [Google Scholar](#)

LANGUAGES SKILLS



Made with the R packages [datadrivencv](#) and [pagedown](#).

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

Last updated on 2022-05-25.

2015
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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).



SOFTWARE & PROGRAMMING

Present
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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 post⁷⁰ 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 analyse⁷⁷ chess.com data.



TEACHING EXPERIENCE

2020

● Developing Bioconductor packages

University College London

📍 Virtual Event

- Hosted workshop⁷² on best practices for developing Bioconductor packages using biothis⁷³.

2020

● R package development

Rstats club

📍 Virtual Event

- Presentation⁷⁴ about unit testing fundamentals, the importance of testing and new features released in the R package testthat edition 3.
- Presentation⁷⁵ about pre-commit hooks in R.
- Presentation⁷⁵ about the best practices of developing R packages.

2020

● R fundamentals

Clinician Coders

📍 London, UK

- Developed materials⁷⁷ and lead workshops that aimed to teach R fundamentals to clinicians.

2020

● 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>

- 2022 ● **Leveraging omic features with F3UTER enables identification of unannotated 3'UTRs for synaptic genes**
Nature Communications
- Sethi S, Zhang D, Guelfi S, Chen Z, Garcia-Ruiz S, Olagbaju EO, Ryten M, Saini H, Botia JA
 - Role: Adviser.
 - DOI: <https://doi.org/10.1038/s41467-022-30017-z>
- 2021 ● **recount3: summaries and queries for large-scale RNA-seq expression and splicing**
Genome Biology
- Wilks C, Zheng SC, Chen FY, Charles R, Solomon B, Ling JP, Imada EL, Zhang D, Joseph L, Leek JT, Jaffe AE, Nellore A, Collado-Torres L, Hansen KD, Langmead B
 - Role: Adviser.
 - DOI: <https://doi.org/10.1186/s13059-021-02533-6>
- 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, Gueffi 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>
- 2020 ● **Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information.**
Nature Communications
- Gueffi S, D'Sa K, Botía J, Vandrovcova J, Reynolds RH, Zhang D, Trabzuni D, Collado-Torres L, Thomason A, Leyton PQ, Gagliano SA, Nalls MA, UK Brain Expression Consortium, Small KS, Smith C, Ramasamy A, Hardy J, Weale ME & Ryten M.
 - Role: Analyst.
 - DOI: <https://doi.org/10.1038/s41467-020-14483-x>
- 2019 ● **Genetic variability in response to A β deposition influences Alzheimer's risk.**
Brain Communications
- Salih DA, Bayram S, Gueffi S, Reynolds RH, Shuai M, Ryten M, Brenton JW, Zhang D, Matarin M, Botia JA, Shah R, Brookes KJ, Guetta-Baranes T, Morgan K, Bellou E, Cummings DM, Escott-Price V, Hardy J.
 - Role: Analyst.
 - DOI: <https://doi.org/10.1093/braincomms/fcz022>
- 2019 ● **Duplication of 10q24 locus: broadening the clinical and radiological spectrum.**
Eur J Hum Genet
- Holder-Espinasse M, Jamsheer A, Escande F, Andrieux J, Petit F, Sowinska-Seidler A, Socha M, Jakubiuk-Tomaszuk A, Gerard M, Mathieu-Dramard M, Cormier-Daire V, Verloes A, Toutain A, Plessis G, Jonveaux P, Baumann C, David A, Farra C, Colin E, Jacquemont S, Rossi A, Mansour S, Ghali N, Moncla A, Lahiri N, Hurst J, Pollina E, Patch C, Ahn JW, Valat AS, Mezel A, Bourgeot P, Zhang D, Manouvrier-Hanu S.
 - Role: Analyst.
 - DOI: <https://doi.org/10.1038/s41431-018-0326-9>

- 2018 ● **Variation at the TRIM11 locus modifies Progressive Supranuclear Palsy phenotype.**
Annals of Neurology
- Jabbari E, John W, Tan MMX, Maryam S, Pittman A, Ferrari R, Mok KY, **Zhang D**, Reynolds RH, de Silva R, Grimm MJ, Respondek G, Muller U, Al-Sarraj S, Gentleman SM, Lees AJ, Warner TT, Hardy J, Revesz T, Hoglinger GU, Holton JL, Ryten M and Morris HR.
 - Role: Analyst.
 - DOI: <https://doi.org/10.1002/ana.25308>



CONFERENCES

- 2021 ● **The British Society for Genetic Medicine (BSGM)**  Virtual Event
- Talk: dasper: detecting aberrant splicing events in RNA-sequencing data
- 2020 ● **EuroBioc**  Virtual Event
- Talk: dasper: detecting aberrant splicing events in RNA-sequencing data
- 2019 ● **Genomics England Research Conference**  London, UK
- Poster: Predicting disease-causing genes using machine learning
- 2019 ● **Genomics of Rare Disease**  Cambridge, UK
- Poster: The use of transcriptomics to improve gene annotation
 - Poster: Using machine learning to understand and predict genes causing rare neurological disorders
 - Awarded prize for the best poster (£100)
- 2019 ● **International Parkinson's Disease Genomics Consortium (IPDGC)**  Lisbon, Portugal
- Talk: Incomplete annotation of disease-associated genes is limiting our understanding of Mendelian and complex neurogenetic disorders
- 2018 ● **European Society of human genetics (ESHG)**  Milan, Italy
- Poster: Incomplete annotation of OMIM genes is likely to be limiting the diagnostics yield from genetic tests.
- 2018 ● **International Parkinson's Disease Genomics Consortium (IPDGC)**  Reykjavik, Iceland
- Poster: Incomplete annotation of OMIM genes is limiting the diagnostic yield from genetic tests.

2015

● World Science Conference Israel (WSCl)

📍 Jerusalem, Israel

• 1 of 11 UK participants chosen to attend.

🔗 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/CIain7vTwq0>
- 15: https://github.com/dzhang32/rstats_pres
- 16: https://github.com/dzhang32/rstats_pres
- 17: <https://github.com/ClinicianCoders/ClinicianCoders>