





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
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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.
- 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
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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
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2007
- **H.S.**
Queen Elizabeth's School  Barnet, UK
 - **Grades:** Maths (A*), Biology (A*), Chemistry (A*), Sociology (A).

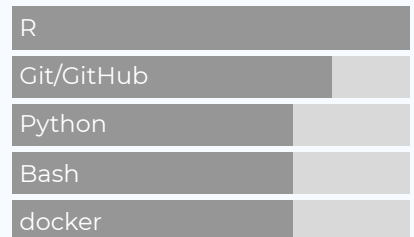
WORK EXPERIENCE

- 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

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🐙 [dzhang32](#)
in [david-zhang32](#)

LANGUAGES SKILLS



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

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

Last updated on 2021-09-27.

2017
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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.



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**.

Present
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2021



Python packages

- **codino**⁵ 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 scrape⁶ information on all UK biotechnology companies.

2021



Data science blog

- Chess-related blog post⁷ 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 analyse⁸ chess.com data.



TEACHING EXPERIENCE

2020



Developing Bioconductor packages

University College London

📍 Virtual Event

- Hosted workshop⁹ on best practices for developing Bioconductor packages using **biocthis**¹⁰.

- 2020 ● **Unit testing using testthat edition 3** 📍 Virtual Event
 rstats club
 • Talk⁷⁷ regarding unit testing fundamentals, the importance of testing and new features released in the R package testthat edition 3.
- 2020 | 2018 ● **R fundamentals** 📍 London, UK
 Clinician Coders
 • Developed materials⁷² and lead workshops that aimed to teach R fundamentals to clinicians.
- 2020 | 2017 ● **RNA-sequencing for diagnostics** 📍 London, UK
 Kings College London
 • Lectured graduate level students about how transcriptomics can be applied in the diagnostic pipeline.







SELECTED PUBLICATIONS

- 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, Shoai 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 (WSCI)**  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/codino>
- 6: https://github.com/dzhang32/biotech_web_scrape
- 7: <https://towardsdatascience.com/how-has-the-queens-gambit-impacted-the-popularity-of-online-chess-43594efe5a98>
- 8: <https://github.com/dzhang32/chess>
- 9: https://dzhang32.github.io/biocthis_workshop/
- 10: <https://bioconductor.org/packages/release/bioc/html/biocthis.html>
- 11: <https://youtu.be/CIain7vTwq0>
- 12: <https://github.com/ClinicianCoders/ClinicianCoders>