DAVID ZHANG

TBA

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

EDUCATION

Present | 2017

Research assistant, part-time PhD, Bioinformatics

University College London — London, UK

- **Thesis**: Using transcriptomics to improve the diagnosis rate of rare disease patients.
- Ultimately, the goal of my PhD is to develop and apply statisical methods and software that improve the genetic diagnosis rate using RNA-sequencing. This involves detection of aberrant RNA-level events when complemented with, DNA sequencing help to resolve variants of unknown significance.

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)

2015 | 2012

BSc, Biomedical science

University College London — London, UK

- **Thesis**:
- **Grade**: 2:1 (69%)

2012 | 2007

H.S.

Queen Elizabeth's School — Barnet, UK

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

RESEARCH EXPERIENCE

2020

Honorary Researcher (2 months)

Johns Hopkins Bloomberg School of Public Health — Remote

- In collaboration with Leonardo Collado-Torres[1], we used the recount3[2] dataset and LIBD samples to study the effect of complex splicing in individuals with neurological disease.

CONTACT

- dyzhang32@gmail.com
- dyzhang32
- dzhang32
- david-zhang32

LANGUAGE SKILLS

- R
- Bash
- Git/GitHub
- Python

*Made with the R package **pagedown**.*

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

Last updated on 2021-03-06.

2017 | 2016

Research Technician

University College London — London, UK

- Used R and bash to investigate the effect of genetic variation on the age of onset of dementia and cognition within Down syndrome patients.

INDUSTRY EXPERIENCE

2020

Bioinformatician internship (3 months)

Verge Genomics — Remote

- Detection of aberrant splicing events in complex disease patients.
- Using AWS infrastructure

SOFTWARE & PROGRAMMING

Present | 2020

Bioconductor packages

- dasper[3]: detection of aberrant splicing events in RNA-sequencing. Author and maintainer. XXX downloads.
- megadepth[4]: BigWig and BAM related utilities. An R wrapper for the megadepth[5] software developed. Co-author and maintainer. XXXX downloads.

2021

Data science blog posts

- Published chess-related blogposts on Medium[6]. Posts were curated by Towards Data Science and selected to for the hands-on-tutorials column, which displays the best pieces for highlight data science principles.
- Applying python through the analysis[7] of chess.com data.

2021 | 2020

Advanced R

- Notes and answers to the advanced R[8] book in the form of a bookdown[9].

2020

Kaggle town

- Organised club to study python and machine learning through kaggle[10] problems.

2018 | 2016

Data wrangling

Neuroimmunology & CSF Laboratory, NHS — London, UK

- Developer and maintainer of data wrangling pipelines that improved the efficiency and standardisation of monthly financial reports.

TEACHING EXPERIENCE

2020

Developing Bioconductor Packages

University College London — Virtual Event

- Hosted workshop[11] on best practices for developing Bionconductor using biocthis[12]

2020

Unit testing using testthat edition 3

rstats club — Virtual Event

- Talk[13] regarding unit testing fundamentals, the importance of testing and new features released in the R package testthat edition 3.

2020 | 2018

R fundamentals

Clinician Coders — London, UK

- Developed materials[14] and lead facilitator for teaching R to clinicians.

2020 | 2017

RNA-sequencing for diagnostics

Kings College London — London, UK

- Invited lecturer to graduate level students on how transcriptomics can be applied in the diagnostic pipeline.

SELECTED PUBLICATIONS

2021

Megadepth: efficient coverage quantification for BigWigs and BAMs

Bioinformatics

- Wilks C, Ahmed O, Baker DN, **Zhang D**, Collado-Torres L, Langmead B. **2021**. *Megadepth: efficient coverage quantification for BigWigs and BAMs*. Bioinformatics.
- **Role**: R package developer.
- DOI: https://doi.org/10.1101/2020.12.17.423317

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. **2021.** *Integration of eQTL and Parkinson's disease GWAS data implicates 11 disease genes.* Jama Neurology.
- **Role**: Co-first author.
- DOI: https://doi.org/10.1001/jamaneurol.2020.5257

2021

Human-lineage-specific genomic elements: relevance to neurodegenerative disease and APOE transcript usage.

Nature Communications

- Chen Z, **Zhang D**, Reynolds RH, Gustavsson EK, Garcia-Ruiz S, D'Sa K, Fairbrother-Brown A, Vandrovcova J, International Parkinson's Disease Genomics Consortium (IPDGC), Hardy J, Houlden H, Gagliano SA, Botiá J, Ryten M. **Human-lineage-specific genomic elements: relevance to neurodegenerative disease and APOE transcript usage.** Nature Communications.
- **Role**: Analyst.
- DOI: TBA

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

- Guelfi 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. **2020.** *Regulatory sites for known and novel splicing in human basal ganglia are enriched for disease-relevant information.* Nature Communications.
- **Role**: Analyst.
- DOI: https://doi.org/10.1038/s41467-020-14483-x

2019

Genetic variability in response to Aβ deposition influences Alzheimer's risk.

Brain Communications

- Salih DA, Bayram S, Guelfi 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. **2019**. *Genetic variability in response to Aβ deposition influences Alzheimer's risk.* Brain Communications.
- **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. **2019.** *Duplication of 10q24 locus: broadening the clinical and radiological spectrum.* Eur J Hum Genet.
- **Role**: Analyst.
- DOI: https://doi.org/10.1038/s41431-018-0326-9

2019

Genetic variation within genes associated with mitochondrial function is significantly associated with later age of onset of Parkinson disease and contributes to disease risk.

NPJ Parkinson's Disease

- Billingsley KJ, Barbosa IA, Bandrés-Ciga S, Quinn JP, Bubb VJ, Deshpande C, Botía JA, Reynolds RH, **Zhang D**, Simpson MA, Blauwendraat C, Nalls MA, Singleton A, International Parkinson's Disease Genomics Consortium (IPDGC), Ryten M, Koks S. **2019.** *Genetic variation within genes associated with mitochondrial function is significantly associated with later age of onset of Parkinson disease and contributes to disease risk.* NPJ Parkinson's Disease.
- **Role**: Data provider.
- DOI: https://doi.org/10.1038/s41531-019-0080-x

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. **2018.** *Variation at the TRIM11 locus modifies Progressive Supranuclear Palsy phenotype.* Annals of Neurology.
- **Role**: Analyst.
- DOI: https://doi.org/10.1002/ana.25308

LINKS

1. http://lcolladotor.github.io/cv/
2. http://bioconductor.org/packages/release/bioc/html/recount3.html
3. https://bioconductor.org/packages/release/bioc/html/dasper.html
4. https://bioconductor.org/packages/release/bioc/html/megadepth.html
5. https://github.com/ChristopherWilks/megadepth
6. https://medium.com/@dzhang32

7. https://github.com/dzhang32/chess
8. https://adv-r.hadley.nz
9. https://dzhang32.github.io/advanced_R/
10. https://github.com/dzhang32/kaggling
11. https://dzhang32.github.io/biocthis_workshop/
12. https://bioconductor.org/packages/release/bioc/html/biocthis.html
13. https://youtu.be/ClAin7vTwq0
14. https://github.com/ClinicianCoders/ClinicianCoders