DR DOUG SPEED

EDUCATION & EMPLOYMENT HISTORY

2020 – present	Professor, Department of Quantitative Genetics and Genomics, **Aarhus University** Head of Human Genetics Section
2017 – 2020	Marie Curie Fellow, **Aarhus University**
2010 – 2017	Postdoc / Medical Research Council Fellow, **University College London**
2006 – 2010	PhD in Statistical Genetics, **University of Cambridge**
2000 – 2004	Honour Degree in Mathematics (First Class), **University of Oxford**

GRANTS (all as sole applicant)

2023	European Research Council Consolidator Grant (2M euros).
2021	AUFF Starting Grant (1.8M Danish kroner)
2019	Lundbeck Foundation Experiment Award (1.9M Danish kroner)
2017	Sapere Aude Grant from Danmarks Frie Forskningsfond (5.6M Danish kroner)
2017	Marie Curie COFUND Fellowship (300,000 euros)
2014	MRC Career Development Fellowship in Biostatistics (450,000 British pounds)

Note that I have also been a co-applicant on successful grants from the Australian Research Council (2018, 275,000 euros) and the BBSRC (2017, 550,000 euros).

AWARDS

2023	Winner of the CAGI 6 Polygenic Risk Score Challenge (www.genomeinterpretation.org)
2021	University Nominee for EliteForsk (EliteResearch) Prize, Ministry of Education, Denmark
2021	Faculty nominee for Victor Albeck Prize, Aarhus University, Denmark
2013	Young Biometrician of the Year (Fisher Memorial Trust & International Biometrics Soc.)

RESEARCH SUMMARY

My research focuses on developing statistical tools to solve genetic problems. In particular, I am a world-expert in creating tools to analyse complex traits and common diseases. Broadly speaking, research in human statistical genetics has three main aims: to identify genetic variants that influence traits, to construct prediction models, and to understand genetic architecture. Remarkably, I have developed tools that perform best for the second and third of these aims.

I make all my tools freely-available within my software package LDAK (www.ldak.org). To date, LDAK has been downloaded over 4000 times and has 200-300 regular users. I originally designed LDAK to enable more precise estimation of "SNP heritability," the total proportion of phenotypic variation explained by SNPs (a basic type of genetic variant). Accurate estimates of SNP heritability are important for knowing the potential of genetic studies and of SNP-based prediction models. Using LDAK I demonstrated that for many common diseases (e.g., Schizophrenia, Type I & II Diabetes) the contribution of SNPs is substantially higher than previously realised (for this work, I was awarded the Young Biometrician of the Year prize by the Fisher Memorial Trust & International Biometrics Society).

Over the years, I have repeatedly added new tools to LDAK. These include tools for single-SNP and gene-based association analysis, for estimating the number of causal loci, finding regions of the genome enriched for heritability, calculating confounding bias, and measuring the impact of selection on genetic architecture. The two most recent additions to LDAK are LDAK-Bolt-Predict and LDAK-BayesR-SS, which are currently the most accurate methods for constructing SNP-based prediction models.

Aside from developing tools, I have taken responsibility for a number of genetic analyses. I performed the first genome-wide association study (GWAS) of drug response in epilepsy, I carried out gene expression analysis as part of the METABRIC study (results which redefined how we classify breast cancer patients), and was the lead analyst for the International League against Epilepsy (ILAE) meta-analysis consortium, which discovered two new epilepsy risk variants.

PUBLICATIONS

As of April 2024, I have had 55 publications (16 as first-author, five as last-author, the rest as middle author). Google Scholar reports that my total number of citations is 10,602 and my h-index is 25. Below is a selection of my publications, with the eight most important underlined. These eight publications were published in the American Journal of Human Genetics, Brain, Genome Research, Nature Communications, Nature Reviews Genetics and Nature Genetics (three times). As of April 2024 they have been cited 2200 times (on average 40 citations per paper, per year).

D. Speed and D. Evans (2024). Estimating disease heritability from complex pedigrees allowing for ascertainment and covariates. **American Journal of Human Genetics**.

L. Balbuena, E. Peters and **D. Speed** (2023). Using polygenic risk scores to investigate the evolution of smoking and mental health outcomes in UK biobank participants. **Acta Psychiatrica Scandinavica.**

T. Berrandou, D. Balding and **D. Speed** (2023). LDAK-GBAT: fast and powerful gene-based association testing using summary statistics. **American Journal of Human Genetics**.

Y. Zhou, Z. Zhang, ..., **D. Speed (penultimate author)** and S. Huang (2022). Graph pangenome captures missing heritability and empowers tomato breeding. **Nature.**

Q. Zhang, F. Prive, B. Vilhjalmsson and **D. Speed** (2021). Improved genetic prediction of complex traits from individual-level data or summary statistics. **Nature Communications.**

D. Speed, J. Holmes and D. Balding (2020). Evaluating and improving heritability models using summary statistics. **Nature Genetics.**

D. Speed and D. Balding (2019). SumHer better estimates the SNP heritability of complex traits from summary statistics. **Nature Genetics.**

D. Speed, N. Cai, the UCLEB Consortium, M. Johnson, S. Nejentsev and D. Balding (2017). Reevaluation of SNP heritability in complex human traits. **Nature Genetics**.

D. Speed and D. Balding (2015). Relatedness in the post-genomic era: is it still useful? **Nature Reviews Genetics.**

D. Speed and D. Balding (2014). MultiBLUP: improved SNP-based prediction for complex traits. **Genome Research.**

D. Speed, D. Balding, M. Johnson, et al. (2014). Describing the genetic architecture of epilepsy using heritability analysis. **Brain.**

The International League Against Epilepsy Consortium on Complex Epilepsies (2014). Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. **Lancet Neurology**. *I was the lead analyst for the consortium, writing the protocols, and performing the analysis for 6 of the 12 contributing sites.*

D. Speed, C. Hoggart, S. Petrovski, M. Johnson, et al. (2014). Genome-wide association study and biological pathway analysis of epilepsy prognosis in a prospective cohort of newly treated epilepsy. **Human Molecular Genetics.**

D. Speed, G. Hemani, M. Johnson and D. Balding (2013). SNP-based heritability analysis with dense data. **American J. Human Genetics.**

D. Speed, G. Hemani, M. Johnson and D. Balding (2012). Improved Heritability Estimation from Genome-Wide SNPs. **American J. Human Genetics.**

C. Curtis, ..., **D. Speed (Author 7),** et al. (2012). The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. **Nature.**

INVITED CONFERENCE PRESENTATIONS (last five years)

2024 Human Genome Meeting (Rome, Italy)
2024 European Mathematical Genetics Meeting (Vienna, Austria)
2023 Critical Assessment of Genome Interpretation 6 (Berkeley, USA).
2022 31st International Biometric Conference (Riga, Latvia)
2020 European Society for Human Genetics (Berlin, Germany)

Additionally, I have also been invited to talk at over 25 universities, including Cambridge, Oxford, Bristol, Imperial, Kings, Leiden and Melbourne.

SUPERVISION AND THESIS EXAMINATION

As main supervisor: Postdoc Takiy Berrandou (2021-), Postdoc Xuan Zhou (2021-2023), PhD Kenneth Enevoldsen (2020-2024), Postdoc Qianqian Zhang (2019-2020). As co-supervisor: PhD Jasper Hof (2020-2024), PhD Anubhav Kaphle (2018-2021), PhD Denis Kia (2014-2018), PhD Cian Murphy (2011-2015). Additionally, I have supervised 12 masters project students (ranging from 4-9 months), and have examined 3 PhD theses and 3 PhD upgrades.

TEACHING AND WORKSHOPS

At Aarhus university, I teach a one-month PhD-level course on GWAS analysis (5 ECTS), and a half-term MSC-level course on Statistical Genetics (also 5 ECTS). While at UCL, I contributed towards the MSC-level course "Statistics for Interpreting Genetic Data" (initially, as a teaching assistant, then lecturer, before becoming course organizer in 2016).

I regularly run one-day workshops on methods for analyzing GWAS data (e.g., in UK, Denmark and Estonia); the six courses so far have attracted over 200 participants. I have provided half-day practical sessions on heritability analysis for seven summer schools. In February 2016 I ran (with David Balding) the 14th Armidale Genetics Summer Course (New South Wales), a one-week summer course on statistical genetics with approximately 50 participants (mainly PhD and postdocs).

JOURNAL EDITING and REVIEWING

I am an editor for Annals of Human Genetics and a guest editor for PLOS Genetics.
I have reviewed for over 20 journals, including at least three times for each of Nature Genetics, Science, AJHG, PLOS Genetics, EJHG, Bioinformatics and Genetic Epidemiology.

INSTITUTIONAL RESPONSIBILITIES

I am currently a member of my department's management team, its research strategy group and also its PhD committee. I held similar positions in my final years at UCL.

ORGANIZATION OF SCIENTIFIC MEETINGS

I currently co-organize the annual meetings of the Aarhus University Personalized Medicine Network (approximately 200 attendees). From 2014-2017, I was a committee member for the International Biometrics Society, co-organizing six half-day meetings (between 30 and 120 attendees).

REFEREES

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