Gibran Hemani

Senior Research Fellow, University of Bristol

8 Picton Mews, Bristol, BS6 5PB, United Kingdom

+44(0)7930951876 | explodecomputer@gmail.com | explodecomputer.com | explodecomputer | explodecomputer

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Academic Qualifications

University of Bristol — *Bristol*

Associate of the Higher Education Academy, UK — *Sep-19 to Mar-20*

University of Edinburgh — *Edinburgh*

PhD in Quantitative Genetics — *Oct-07 to Aug-11*

University of Nottingham — *Nottingham*

BSc (hons) 2:1 — *Sep-03 to Jun-06*

Employment

MRC Integrative Epidemiology Unit, University of Bristol — *UK*

Senior research fellow — *Jan-18 to present*

MRC Integrative Epidemiology Unit, University of Bristol — *UK*

Research fellow — *Jan-14 to Dec-17*

Queensland Brain Institute, University of Queensland — *Australia*

Post doctoral statistical geneticist — *Jan-12 to Dec-13*

Awards

Sir Kenneth Mather Memorial prize — *The Genetics Society*

Best PhD thesis in quantitative and population genetics — *2011*

Publications

Selected publications organised by category are listed below. Full publication list on google scholar.

- H-index: **44**
- i10-index: **87**
- Number of publications: **155**

Academic journal papers (refereed)

1. Griffith, G., T Morris, T., Tudball, M., Herbert, A. & Mancano, G. *et al.* Collider bias undermines our understanding of covid-19 disease risk and severity. *Nature Communications* (2020) Role: senior author. Position: 13/13.

2. John Lawson, D., Martin Davies, N., Haworth, S., Ashraf, B. & Howe, L. *et al.* Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity? *Human Genetics* (2020) Role: senior author. Position: 7/9.

3. T Morris, T., M Davies, N., Hemani, G. & Davey Smith, G. Population phenomena inflate genetic associations of complex social traits. *Science Advances* (2020) Role: senior author.

4. Zheng, J., Haberland, V., Baird, D., Walker, V. & C Haycock, P. *et al.* Phenome-wide mendelian randomization mapping the influence of the plasma proteome on complex diseases. *Nature Genetics* (2020) Role: senior author; International co-authors. Non-academic co-authors. Position: 32/34 (joint last).

5. G Richardson, T., Hemani, G., R Gaunt, T., L Relton, C. & Davey Smith, G. A transcriptome-wide mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. *Nature communications* (2020) Role: main analyst.

6. L Anderson, E., D Howe, L., H Wade, K., Ben-Shlomo, Y. & David Hill, W. *et al.* Education, intelligence and alzheimer's disease: Evidence from a multivariable two-sample mendelian randomization study. *International journal of epidemiology* (2020) Role: senior author. Position: 13/13.

7. Brumpton, B., Sanderson, E., Heilbron, K., Pires Hartwig, F. & Harrison, S. *et al.* Avoiding dynastic, assortative mating, and population stratification biases in mendelian randomization through within-family analyses. *Nature communications* (2020) Role: senior author. Position: 32/33 (joint last).

8. Cho, Y., C Haycock, P., Sanderson, E., R Gaunt, T. & Zheng, J. *et al.* Exploiting horizontal pleiotropy to search for causal pathways within a mendelian randomization framework. *Nature communications* (2020) Role: senior author. Position: 8/8.

9. Emma Russell, A., Ford, T., Gunnell, D., Heron, J. & Joinson, C. *et al.* Investigating evidence for a causal association between inflammation and self-harm: A multivariable mendelian randomisation study. *Brain, behavior, and immunity* (2020) Role: senior author. Position: 9/10 (joint last).

10. G Richardson, T., Harrison, S., Hemani, G. & Davey Smith, G. An atlas of polygenic risk score associations to highlight putative causal relationships across the human phenome. *Elife* (2019) Role: main analyst.

11. P Morris, A., H Le, T., Wu, H., Akbarov, A. & J van der Most, P. *et al.* Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. *Nature communications* (2019) Role: main analyst; International co-authors. Position: 6/72.

12. Leland Taylor, D., U Jackson, A., Narisu, N., Hemani, G. & R Erdos, M. *et al.* Integrative analysis of gene expression, dna methylation, physiological traits, and genetic variation in human skeletal muscle. *Proceedings of the National Academy of Sciences* (2019) Role: main analyst; International co-authors. Position: 4/22.

13. J Howe, L., G Richardson, T., Arathimos, R., Alvizi, L. & R Passos-Bueno, M. *et al.* Evidence for dna methylation mediating genetic liability to non-syndromic cleft lip/palate. *Epigenomics* (2019) Role: senior author. Position: 17/18.

14. J Howe, L., J Lawson, D., M Davies, N., St Pourcain, B., J Lewis, S., Davey Smith, G. & Hemani, G. Genetic evidence for assortative mating on alcohol consumption in the uk biobank. *Nature communications* (2019) Role: senior author. Position: 7/7.

15. Hemani, G., Zheng, J., Elsworth, B., H Wade, K. & Haberland, V. *et al.* The mr-base platform supports systematic causal inference across the human phenome. *Elife* (2018) Role: main author; International co-authors. Position: 1/20.

16. L Min, J., Hemani, G., Davey Smith, G., Relton, C. & Suderman, M. Meffil: Efficient normalization and analysis of very large dna methylation datasets. *Bioinformatics* (2018) Role: main analyst.

17. E Haas, M., G Aragam, K., A Emdin, C., G Bick, A. & Hemani, G. *et al.* Genetic association of albuminuria with cardiometabolic disease and blood pressure. *The American Journal of Human Genetics* (2018) Role: main analyst; International co-authors. Position: 5/8.

18. G Richardson, T., C Haycock, P., Zheng, J., J Timpson, N. & R Gaunt, T. *et al.* Systematic mendelian randomization framework elucidates hundreds of cpg sites which may mediate the influence of genetic variants on disease. *Human molecular genetics* (2018) Role: senior author. Position: 8/8.

19. J Howe, L., Keun Lee, M., C Sharp, G., Davey Smith, G. & St Pourcain, B. *et al.* Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. *PLoS genetics* (2018) Role: senior author. Position: 16/17.

20. Ye, J., G Richardson, T., L McArdle, W., L Relton, C., M Gillespie, K., Suderman, M. & Hemani, G. Identification of loci where dna methylation potentially mediates genetic risk of type 1 diabetes. *Journal of autoimmunity* (2018) Role: senior author. Position: 7/7.

21. Hemani, G., Tilling, K. & Davey Smith, G. Orienting the causal relationship between imprecisely measured traits using gwas summary data. *PLoS genetics* (2017) Role: main author.

22. J Noyce, A., A Kia, D., Hemani, G., Nicolas, A. & Ryan Price, T. *et al.* Estimating the causal influence of body mass index on risk of parkinson disease: A mendelian randomisation study. *PLoS medicine* (2017) Role: main analyst. Position: 3/19.

23. G Richardson, T., Zheng, J., Davey Smith, G., J Timpson, N., R Gaunt, T., L Relton, C. & Hemani, G. Mendelian randomization analysis identifies cpg sites as putative mediators for genetic influences on cardiovascular disease risk. *The American Journal of Human Genetics* (2017) Role: senior author. Position: 7/7.

24. R Gaunt, T., A Shihab, H., Hemani, G., L Min, J. & Woodward, G. *et al.* Systematic identification of genetic influences on methylation across the human life course. *Genome biology* (2016) Role: main author. Position: 3/14 (joint first).

25. White, J., Sofat, R., Hemani, G., Shah, T. & Engmann, J. *et al.* Plasma urate concentration and risk of coronary heart disease: A mendelian randomisation analysis. *The lancet Diabetes & endocrinology* (2016) Role: main analyst. Position: 3/52.

26. Yang, J., Bakshi, A., Zhu, Z., Hemani, G. & AE Vinkhuyzen, A. *et al.* Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature genetics* (2015) Role: main analyst; International co-authors. Position: 4/25.

27. R Robinson, M., Hemani, G., Medina-Gomez, C., Mezzavilla, M. & Esko, T. *et al.* Population genetic differentiation of height and body mass index across europe. *Nature genetics* (2015) Role: main analyst; International co-authors. Position: 2/43.

28. M Visscher, P., Hemani, G., AE Vinkhuyzen, A., Chen, G.-B. & Hong Lee, S. *et al.* Statistical power to detect genetic (co) variance of complex traits using snp data in unrelated samples. *PLoS Genet* (2014) Role: main analyst; International co-authors. Position: 2/8.

29. Hemani, G., Shakhbazov, K., Westra, H.-J., Esko, T. & K Henders, A. *et al.* Detection and replication of epistasis influencing transcription in humans. *Nature* (2014) Role: main author; International co-authors. Position: 1/14.

30. F McRae, A., E Powell, J., K Henders, A., Bowdler, L. & Hemani, G. *et al.* Contribution of genetic variation to transgenerational inheritance of dna methylation. *Genome biology* (2014) Role: main analyst; International co-authors. Position: 5/10.

31. Hemani, G., Knott, S. & Haley, C. An evolutionary perspective on epistasis and the missing heritability. *PLoS Genet* (2013) Role: main author.

32. Hemani, G., Yang, J., Vinkhuyzen, A., E Powell, J. & Willemsen, G. *et al.* Inference of the genetic architecture underlying bmi and height with the use of 20,240 sibling pairs. *The American Journal of Human Genetics* (2013) Role: main author; International co-authors. Position: 1/23.

33. Speed, D., Hemani, G., R Johnson, M. & J Balding, D. Improved heritability estimation from genome-wide snps. *The American Journal of Human Genetics* (2012) Role: main analyst; International co-authors.

34. Hemani, G., Theocharidis, A., Wei, W. & Haley, C. EpiGPU: Exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. *Bioinformatics* (2011) Role: main author.

Review articles

1. Hemani, G., Bowden, J. & Davey Smith, G. Evaluating the potential role of pleiotropy in mendelian randomization studies. *Human molecular genetics* (2018) Role: main author.

2. Richmond, R., Hemani, G., Tilling, K., Davey Smith, G. & Relton, C. Challenges and novel approaches for investigating molecular mediation. *Human molecular genetics* (2016) Role: main author.

3. Davey Smith, G. & Hemani, G. Mendelian randomization: Genetic anchors for causal inference in epidemiological studies. *Human molecular genetics* (2014) Role: main author.

4. Wei, W.-H., Hemani, G. & S Haley, C. Detecting epistasis in human complex traits. *Nature Reviews Genetics* (2014) Role: main author; International co-authors.

Selected published open source software

AscRtain *2020*

- Sensitivity analysis for collider bias in observational data
- https://github.com/explodecomputer/epigpu

GoDMC *2019*

- Website and API for querying genetic assocations with DNA methylation
- http://mqtldb.godmc.org.uk/

MR-TRYX *2019*

- Exploiting horizontal pleiotropy in Mendelian randomization
- https://explodecomputer.github.io/tryx/

OpenGWAS *2019*

- The OpenGWAS data infrastructure
- https://gwas.mrcieu.ac.uk/

USS pension model *2018*

- Web-app for projected pensions across different valuations
- http://www.uss-pension-model.com/

ALSPAC data dictionary *2017*

- R package and web-app for searching for ALSPAC variables
- http://variables.alspac.bris.ac.uk/

MR-Base *2016*

- Automated Mendelian randomization
- https://www.mrbase.org/

simulateGP *2016*

- Simulation methods for genotype-phenotype associations
- https://explodecomputer.github.io/simulateGP/

gctaPower *2013*

- Power calculations for genomic REML analysis
- https://shiny.cnsgenomics.com/gctaPower/

epiGPU *2012*

- Exhaustive searches for genetic interactions parallelised across graphics cards
- https://github.com/explodecomputer/epigpu

Forthcoming publications

1. L Min, J., Hemani, G., Hannon, E., F Dekkers, K. & Castillo-Fernandez, J. *et al.* Genomic and phenomic insights from an atlas of genetic effects on dna methylation. *medRxiv* (2020) Role: main author; Accepted in Nature Genetics. Position: 2/150 (joint first).

2. S Lyon, M., J Andrews, S., L Elsworth, B., R Gaunt, T., Hemani, G. & Marcora, E. The variant call format provides efficient and robust storage of gwas summary statistics. *BioRxiv* (2020) Role: senior author; International co-authors. Accepted in Genome Biology. Position: 5/6 (joint last).

3. Sanderson, E., Richardson, T., Hemani, G. & Davey Smith, G. The use of negative control outcomes in mendelian randomisation to detect potential population stratification or selection bias. *BioRxiv* (2020) Role: senior author; Accepted in International Journal of Epidemiology.

Research grants

Genetic architecture of Huntington's disease progression (Contracts pending)

Cure Huntington's Disease Initiative *2020*

- Amount: 598,881 GBP ; Role: PI ; Dates: 2021-01-01 to 2022-12-31 ; Proportion: 10%

Aetiological Epidemiology

Biogen *2020*

- Amount: 284,525 GBP ; Role: Co-I ; Dates: 2020-09-01 to 2022-08-31 ; Proportion: 5%

The causal map of the human phenome

Wellcome Trust and Royal Society, Sir Henry Dale Fellowship *2017*

- Amount: 1,356,578 GBP ; Role: PI ; Dates: 2018-01-04 to 2023-06-30 ; Proportion: 100%

Classifying mechanisms of pleiotropy to improve causal modelling

BBSRC and GlaxoSmithKline, CASE studentship *2017*

- Amount: 100,000 GBP ; Role: PI ; Dates: 2017-10-01 to 2021-09-30 ; Proportion: 5%

Pathways to self-harm: Biological mechanisms and genetic contribution

Medical Research Councal and Medical Research Foundation *2017*

- Amount: 372,334 GBP ; Role: Co-I ; Dates: 2017-10-01 to 2019-10-01 ; Proportion: 5%

Identification of Traits and Biomarkers for Prediction of Huntington's Disease Phenotypes using Novel causal analysis Methodologies

Cure Huntington's Disease Initiative *2017*

- Amount: 117,059 GBP ; Role: Co-I ; Dates: 2017-04-01 to 2019-03-31 ; Proportion: 10%

Translation of MR for drug target identification; De- tails

GlaxoSmithKline *2017*

- Amount: 349,099 GBP ; Role: Co-I ; Dates: 2017-01-01 to 2020-01-01 ; Proportion: 5%

Translation of MR for drug target identification

Biogen *2017*

- Amount: 436,165 USD ; Role: Co-I ; Dates: 2017-01-01 to 2020-01-01 ; Proportion: 5%

Dissecting genetic interactions in gene expression

University of Queensland, Early Career Research Grant *2013*

- Amount: 34,000 AUD ; Role: PI ; Dates: 2013-01-01 to 2013-12-31 ; Proportion: 2%

Dissecting genetic interactions in complex traits

CASE Studentship, BBSRC and Monsanto *2007*

- Amount: 100,000 GBP ; Role: PI ; Dates: 2007-09-01 to 2011-08-30 ; Proportion: 100%

Invited talks (last 3 years)

The Trøndelag Health Study, Norway *Invited workshop lead*

Multi-omics in longitudinal cohorts *2020*

International Agency for Research on Cancer, France *Invited talk*

Collider bias in Covid-19 research *2020*

Elizabeth Blackwell Institute data week keynote *Invited talk*

New data on Covid-19 is undermined by old statistical problems *2020*

GRC Quantitative Genetics conference, Italy *Invited session chair*

Genetic architecture of complex traits *2019*

Mendelian Randomization conference, Bristol *Conference plenary*

Genetics of DNA methylation *2019*

SEGEG, University of Oxford *Invited talk*

Automating Mendelian randomization *2018*

Edinburgh Alliance in Quantitative Genetics *Invited talk*

Machine learning in Mendelian randomization *2018*

University College London *Invited talk*

Causal graph of the human phenome] *2018*