Gibran Hemani

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Present Appointment

MRC Integrative Epidemiology Unit, University of Bristol — UK
Professor 2023, Associate Professor 2021, Senior Research Fellow 2018, Research Fellow 2014 — Jan-14 to present

Previous Appointments

Queensland Brain Institute, University of Queensland — Australia
Post doctoral statistical geneticist — Jan-12 to Dec-13

Academic Qualifications

University of Bristol — Bristol
Fellow of the Higher Education Academy, UK — Sep-19 to Sep-21

University of Edinburgh — Edinburgh
PhD in Quantitative Genetics — Oct-07 to Aug-11

- Genetics Society 'Best PhD thesis in population and quantitative genetics' 2011

University of Nottingham — Nottingham
BSc (hons) Genetics (2:1) — Sep-03 to Jun-06

Special Awards, Honours and Distinctions

Rising Stars of Science Award — Research.com
Ranked 2nd nationally and 137th internationally for H-index within 12 years of first paper — 2022

Fellow of the Higher Education Academy. — CREATE, UoB
2022

Highly Cited Researcher Award — Clarivate / Web of Science
Top 1% of researchers internationally (assigned 'Cross-field' category) — 2021-2023

Sir Kenneth Mather Memorial prize — The Genetics Society
Best PhD thesis in quantitative and population genetics — 2011

Teaching and related administration

The teaching-research nexus has been central to my career, starting during my PhD when I wrote and delivered a 2-day course on R programming for researchers at the Roslin Institute. Since then I have taught on topics relating to genetics, statistics and programming to undergraduates across disciplines in medicine, biology and psychology. There has been a major shift towards using genetic data in epidemiological research over the last several years and my academic background in statistical genetics has created opportunities and substantial demand for teaching in this field at the post-graduate and life-long learning levels. I am particularly proud of my record of writing and delivering courses on genetic epidemiology to participants who are under-represented in genomic data science. In line with this I am also co-leading the BMS Decolonising the Curriculum group, which is now piloting a curriculum review framework that we developed for Bristol Medical School.

(i) Undergraduate and taught postgraduate (past 3 years)

Evidence Based Medicine unit in MB ChB programme — University of Bristol
Tutor — 2020-

- 15 1st year undergraduate medical students
- 5 hours prep, 10 hours contact time

Genes and behaviour (PSYC30018) — University of Bristol
Lecturer — 2018-2021

- 100 3rd year undergraduate students
- Wrote and delivered three lectures
- 6 hours prep, 4 hours contact time

Genomic Medicine iBSc — University of Bristol
Pastoral tutoring — 2017, 2018

- Two students on the Genomic Medicine iBSc
- 8 hours contact time

Genomic Data Science unit in Genomic Medicine iBSc — University of Bristol
Course lead — 2016-2018, 2020

- Up to 13 intercalating 3rd year medical dentistry and veterinary students
- Led, co-wrote and delivered 4-week module (20 credits)
- Organised material for several lecturers on programming, statistics, genetic analysis
- Set formative and summative coursework assessments
- Designed and wrote exams
- Delivered lectures, tutorials, practicals, assessed debates
- Transitioned to flipped classroom format
- 50 hours prep, 20 hours contact time
- Several students publish papers each year on the subject.

(ii) Major teaching responsibilities in previous years

Statistical genetics unit in Biomedical Capstone Course — University of Queensland
Course lead — 2012, 2013

- 250 3rd year undergraduate biomedical students
- Wrote four lectures and two workshops on GWAS written
- Set and marked coursework assessments
- Delivered lectures and practicals, and coordinated lecturers and tutors
- 25 hours prep, 10 hours contact time

(iii) Innovatory units and teaching methods

Flipped classroom: In the second year of the iBSc Genomic Medicine course I redesigned the R programming training section to be a flipped classroom, using online games for students to learn the basic principles of programming at home and the tutor led sessions as an opportunity to synthesise those skills into applied examples. The students were more adept at programming than in the previous year, and also more enthused about the subject. I transitioned the rest of the module to a flipped classroom in 2020 during the Covid-19 pandemic.

(iv) Contribution to Life-long learning and continuing professional development courses

Genetic epidemiology and Mendelian randomisation — MRC/UVRI, Entebba, Uganda

Course co-lead — 2023

- 30 researchers from across Africa
- Co-write and delivered 5 day short course on genetic epidemiology and Mendelian randomisation, plus 1 day hackathon.

Genetic Analysis of Population-based Association Studies short course — Wellcome Genome Campus

Course co-lead — 2018-

- 40+ international post-graduate students and researchers
- Invited to co-lead a course that has been running for 12 years, approx
- Contribute to course design, and recent redesign for online teaching
- Delivering lectures and practicals
- 24 hours prep, 10 hours contact time

MR-Base workshop, MR conference — Bristol

Course lead — 2017, 2019

- 60 International post-graduate students and researchers
- Wrote and delivered lectures and tutorials on how to use the MR-Base database and R packages
- 12 hours prep, 6 hours contact time

Statistical methods for mediation short course — University of Bristol

Lecturer — 2017, 2018

- 40 post-graduate students and researchers
- Wrote and delivered one lecture + practical
- 8 hours prep, 3 hours contact time

Genetic Epidemiology short course at EEPE — Florence, Italy

Course co-lead — 2016-2019,2022-

- 20 international post-graduate students and researchers
- Co-wrote and delivered (with Prof Dave Evans) 5-day course
- Prepared and delivered lectures + practicals
- 40 hours prep, 12 hours contact time

Genomic medicine iBSc — University of Bristol

Lecturer — 2016-2018, 2020

- Up to 13 intercalating 3rd year medical, dentistry and veterinary students
- Wrote and delivered three lectures to other units
- 8 hours prep, 3 hours contact time

Statistical genetics short course University of Bristol

Lecturer 2015-

- 40 post-graduate students and researchers
- Wrote and delivered two lectures + practicals
- 16 hours prep, 6 hours contact time

UNIX and Genetic epidemiology Pelotas, Brazil

Course co-lead 2015

- 30 researchers and post-graduate students
- Co-wrote and delivered 7-day course
- Lectures and practicals
- Setup cloud-based computing system for practical sessions
- 40 hours prep, 15 hours contact time

Mendelian randomisation short course University of Bristol

Lecturer 2014-

- 40 post-graduate students and researchers
- Wrote and delivered two lectures + practicals
- 16 hours prep, 6 hours contact time

Genetic epidemiology, H3Africa project Johannesberg, South Africa

Course co-lead 2014

- 30 researchers and post-graduate students
- Co-wrote and delivered (with Dr Nic Timpson) 5-day course
- Delivered lectures and practicals
- 50 hours prep, 20 hours contact time

18th Summer Institute in Statistical Genetics Seattle USA

Teaching assistant 2013

- 40+ international post-graduate students and researchers
- Teaching assistant for: “Human Complex Traits” and “Animal Genetic Data Analysis”
- 20 hours prep, 10 hours contact time

Introduction to git and programming workflows University of Queensland

Workshop lead 2013

- 15 researchers
- Wrote and delivered one-day workshop
- 12 hours prep, 6 hours contact time

Introduction to Statistics University of Queensland

Lecturer 2012

- 40+ post-graduate students and researchers
- Wrote and delivered one lecture for a professional Development Course
- 3 hours prep, 1 hour contact time

Introduction to R University of Edinburgh

Course co-lead 2009

- 30 researchers and post-graduate students
- Co-wrote and delivered (with Joseph Powell) 2-day short course on R programming
- 15 hours prep, 6 hours contact time

(v) Collaborative teaching projects

Developed external speaker programmes for iBSc medical students, involving Jeff Barrett from OpenTargets and the Sanger Institute; Rob Scott from GlaxoSmithKlein; and Jonathan Ives from the Centre for Ethics in Medicine.

(iv) Postgraduate advising

Daniel Searby
Wellcome Trust, PhD student 2024-2028

- Primary supervisor
- Primary supervisor

Aaron Mitchell
Wellcome Trust, PhD student 2023-2027

- Secondary supervisor

Tim Larson
Wellcome Trust, PhD student 2023-2027

- Secondary supervisor

Liza Darrous
University of Lausanne, PhD student 2022-2023

- Visiting PhD student

Lily Andrews
CRUK, PhD student 2020-2024

- Secondary supervisor

Amanda Forde
Science Foundation Ireland, PhD student 2020-2024

- Secondary supervisor
- Co-supervising with international colleague (John Ferguson), Republic of Ireland

Giulio Centorame
NHMRC, PhD student 2020-2024

- Secondary supervisor
- Co-supervising with international colleague (Dave Evans), Australia

Huiling Zhao
Wellcome Trust, PhD student 2020-2024

- Secondary supervisor

Chris Moreno-Stokoe
BBSRC, PhD student 2018-2022

- Secondary supervisor

Hannah Wilson
BBSRC and GSK, PhD student 2017-2021

- Primary supervisor

Thomas Battram
Wellcome Trust, PhD student 2016-2020

- Primary supervisor
- Passed viva with distinction

Laurence Howe
Wellcome Trust, PhD student 2014-2018

- Secondary supervisor
- Passed viva with distinction
- Awarded best doctoral research prize 2018/2019 in Faculty of Health Sciences

(vii) Major achievements in teaching administration

International short courses on statistical genetics: I have organised, developed and delivered short courses (typically week-long, in collaboration with internal and/or external colleagues) to researchers at institutes in South Africa, Italy, Brazil and at the Wellcome Genome Centre in Cambridge.

Genomic Data Science module: I designed, organised and delivered a 20 credit module for medical students that involves teaching them programming and genomic data analysis from scratch. This has run for 4 years, and consistently gets very positive feedback, and the students achieve a high standard.

Decolonising the curriculum: I lead the Medical Anti-Racism Taskforce Special Interest Group on decolonising the curriculum in the Bristol Medical School (11 members). We are developing a curriculum review framework that is now being piloted in five modules across the school (http://decolbms.org.uk). I also liaise with numerous related groups across the university.

MR-Base software course: I developed a course to teach researchers how to use my own software (MR-Base), with the course being heavily over-subscribed and gaining very positive feedback and increased usage of the software.

Research and related administration

During my PhD I developed statistical and computational methods to detect genetic interactions influencing complex traits. This work led to my first post-doctoral position that expanded my work into determining genetic architectures of complex disease, and developing expertise in handling high dimensional genomic data. My fellowship work lies at the interface between statistical genetics, causal inference and high performance computing. A major output that integrates these fields has been the development of the MR-Base and OpenGWAS causal inference analytical platform. These software platforms are used by researchers globally and has led directly to funding for five post-doctoral positions from three private companies (GSK, Biogen, CHDI). I currently lead or co-lead three major international collaborations. These activities will continue and expand in 2023 as co-lead of the Mendelian randomisation programme in MRC IEU 3.0.

(i) Publications

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

- H-index: **71**
- i10-index: **152**
- Number of publications: **236**

Chapters in Edited Books

1. Hemani, G. Meta-analysis in genetic association studies. Systematic Reviews in Health Research: Meta-Analysis in Context (2022) Contrib.: 100% (main author).

Academic journal papers (refereed)

1. Howe, L., Nivard, M., Morris, T., Hansen, A., Rasheed, H., et al. Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature genetics (2022) Contrib.: 20% (senior author). International co-authors. Position: 100/101 (joint last).

2. Min, J., Hemani, G., Hannon, E., Dekkers, K., Castillo-Fernandez, J., et al. Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature genetics (2021) Contrib.: 30% (main author). International co-authors. Position: 2/150 (joint first).
3. Lyon, M., Andrews, S., Elsworth, B., Gaunt, T., Hemani, G. & Marcora, E. The variant call format provides efficient and robust storage of GWAS summary statistics. Genome biology (2021) Contrib.: 30% (senior author). International co-authors. Position: 5/6 (joint last).
4. Hemani, G., Powell, J., Wang, H., Shakhbazov, K., Westra, H.-J., et al. Phantom epistasis between unlinked loci. Nature (2021) Contrib.: 40% (main author). International co-authors. Position: 1/16.
5. Griffith, G., 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) Contrib.: 40% (senior author). Position: 14/14.
6. Zheng, J., Haberland, V., Baird, D., Walker, V., Haycock, P., et al. Phenome-wide mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature genetics (2020) Contrib.: 20% (senior author). Non-academic co-authors. Position: 32/34 (joint last).
7. Brumpton, B., Sanderson, E., Heilbron, K., Hartwig, F., Harrison, S., et al. Avoiding dynastic, assortative mating, and population stratification biases in mendelian randomization through within-family analyses. Nature communications (2020) Contrib.: 30% (senior author). Position: 32/33 (joint last).
8. Anderson, E., Howe, L., Wade, K., Ben-Shlomo, Y., Hill, W., et al. Education, intelligence and alzheimer's disease: Evidence from a multivariable two-sample mendelian randomization study. International journal of epidemiology (2020) Contrib.: 30% (senior author). Position: 13/13 (last author).
9. Cho, Y., Haycock, P., Sanderson, E., Gaunt, T., Zheng, J., et al. Exploiting horizontal pleiotropy to search for causal pathways within a mendelian randomization framework. Nature communications (2020) Contrib.: 40% (senior author). Position: 8/8 (last author).
10. Hemani, G., Zheng, J., Elsworth, B., Wade, K., Haberland, V., et al. The MR-base platform supports systematic causal inference across the human phenome. elife (2018) Contrib.: 30% (main author). International co-authors. Position: 1/20.
11. Richardson, T., Haycock, P., Zheng, J., Timpson, N., 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) Contrib.: 30% (senior author). Position: 8/8.
12. Hemani, G., Tilling, K. & Smith, G. Orienting the causal relationship between imprecisely measured traits using GWAS summary data. PLoS genetics (2017) Contrib.: 70% (main author).
13. Richardson, T., Zheng, J., Smith, G., Timpson, N., Gaunt, T., 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) Contrib.: 30% (senior author). Position: 7/7.
14. Gaunt, T., Shihab, H., Hemani, G., Min, J., Woodward, G., et al. Systematic identification of genetic influences on methylation across the human life course. Genome biology (2016) Contrib.: 20% (main author). Position: 3/14 (joint first).
15. Hemani, G., Knott, S. & Haley, C. An evolutionary perspective on epistasis and the missing heritability. PLoS genetics (2013) Contrib.: 80% (main author).
16. Hemani, G., Yang, J., Vinkhuyzen, A., 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) Contrib.: 40% (main author). International co-authors. Position: 1/23.
17. Hemani, G., Theocharidis, A., Wei, W. & Haley, C. EpiGPU: Exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. Bioinformatics (2011) Contrib.: 80% (main author).

Review articles

1. Smith, G. & Hemani, G. Mendelian randomization: Genetic anchors for causal inference in epidemiological studies. Human molecular genetics (2014) Contrib.: 50% (main author).
2. Wei, W.-H., Hemani, G. & Haley, C. Detecting epistasis in human complex traits. Nature Reviews Genetics (2014) Contrib.: 40% (main author). International co-authors.

Selected published open source software

CAMERA 2022

- Cross-Ancestry Mendelian Randomisation R package
- https://github.com/yoonsucho/CAMERA

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/

babytime 2018

- R package to calculate costs and scheduling for people going on shared parental leave
- https://github.com/explodecomputer/shared-parental-leave

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

(ii) Forthcoming publications

1. Sadreev, I., Elsworth, B., Mitchell, R., Paternoster, L., Sanderson, E., et al. Navigating sample overlap, winner's curse and weak instrument bias in mendelian randomization studies using the UK biobank. MedRxiv (2021) Contrib.: 40% (senior author). Position: 12/12 (last author).
2. Elsworth, B., Lyon, M., Alexander, T., Liu, Y., Matthews, P., et al. The MRC IEU OpenGWAS data infrastructure. BioRxiv (2020) Contrib.: 30% (senior author). Non-academic co-authors. Position: 14/14 (joint last).

(iii) Research grants

Total income as PI, from 5 grant(s): **3,548,749 GBP**

Total income as CI, from 7 grant(s): **4,021,252 GBP**

Current income as PI, from 1 grant(s): **1,971,091 GBP**

Current income as CI, from 2 grant(s): **2,540,580 GBP**

Building the OpenGWAS platform towards a sustainable model for scientific discovery and translation
Wellcome Trust 2023
- Amount: 100,000 GBP ; Role: Co-PI ; Dates: 2023-07-18 to 2024-07-18 ; Proportion: 0%

IEU3 - Programme 1 Mendelian randomisation
MRC 2022
- Amount: 1,971,091 GBP ; Role: PI ; Dates: 2023-04-01 to 2028-03-31 ; Proportion: 100%

BRC2 - Translational Population Science Theme
NIHR 2022
- Amount: 1,912,067 GBP ; Role: Co-I ; Dates: 2022-12-01 to 2027-11-30 ; Proportion: 0%

Causes and consequences of mental disorders: The environmental and genetic influences of parents on offspring.
NIH 2022
- Amount: 766,480 USD ; Role: Co-I ; Dates: 2022-07-15 to 2027-05-31 ; Proportion: 5%

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
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%

(iv) Indications of external recognition

Editorships

PLoS Computational Biology
Invited guest editor 2017

Appointment to national or international bodies

PLoS Computational Biology
Expert evaluation panel for the Our Future Health study 2021

Invited member of the Genotype Chip Design Committee for the Our Future Health Study, that will be used to genotype up to 5 million people in the UK 2019 - 2021

Invitations for degree examinations

Richard Packer University of Leicester
PhD thesis external examiner 2022

Jisu Shin University of South Australia
Dissertation of Master of precision medicine external examiner 2020

Edward Steere Witswatersrand University, SA
Dissertation of Master of Science in Engineering external examiner 2016

Invited lectures (last 3 years)

NIH/NIDA Genetics and Epigenetics meeting, Maryland USA *Primer in Mendelian randomisatio*	Invited talk 2024
ECNP Network workshop, University of Muenster, Germany *Mendelian randomisation for causal inference of molecular phenotypes on complex traits*	Invited talk 2024
American Society of Human Genetics *The importance of families in future biobanks*	Invited talk 2023
University of Galway *The future of genetic biobanks*	Invited talk 2023
University of Edinburgh *Recent developments in Mendelian randomisation*	Invited talk 2023
Epigenomics of Common Disease 2023, Cambridge *Challenges and future directions for causal inference of molecular traits*	Invited talk 2023
Centre for Health Sciences Education conference, Bristol *Workshop: Decolonising the Medicul School Curriculums*	Invited workshop 2023
BenevolentAI seminar series *The MR-Base and OpenGWAS projects*	Invited talk 2022
Cure Huntington's Disease Initiative seminar series *Exploring the assumptions in Mendelian randomisation*	Invited talk 2022
BILT Compassionate Conference *Decolonising the Bristol medical school curriculum*	Conference plenary 2022
Mendel @ 200 conference, Bristol *Contemporary genome-wide association studies in the light of Mendelian inheritance*	Conference plenary 2022
Broad Institute (Harvard and MIT) methods seminar *Within-sibship GWAS for Mendelian randomisation*	Invited talk 2022
DECOLWEEK, Bristol *Decolonising your discipline*	Invited panel member 2021
Mendelian Randomization conference, Bristol *Results from large scale consortia*	Invited session chair 2021
GSK seminar series *Mendelian randomisation for molecular exposures*	Invited talk 2021
Channing Network seminar series, Harvard University *Using Mendelian randomisation to detect causal influences of molecular features on complex traits*	Invited talk 2021

(vi) Related administration

Leading group on Covid-19 epidemiology

MRC IEU 2020-2021

- Initiated project, and recruited group of 12 researchers
- Provided analysis of ZOE symptom tracker app for external collaborators
- Culminated in four publications, numerous presentations including to SAGE and HDRUK

Member of the UoB Covid modelling subgroup

University of Bristol 2020-2021

Initiating the OpenGWAS consortium

MRC IEU 2020 to present

- The OpenGWAS data infrastructure receives 2 million queries per week
- The consortium brings together researchers who develop software for GWAS summary data
- Plans to expand the invitation to international collaborators

SEGEG conference organiser

South of England Genetic Epidemiology Group 2019

- Organised the long-running SEGEG conference to be held in Bristol for the first time

Leading work package on MR method development (programme 1)

MRC IEU 2018-2023

- Line managing one post doctoral scientist

Leading statistics and informatics theme in epigenetics programme 4

MRC IEU 2018-2022

Leading Hemani research group

MRC IEU 2018 to present

- Four post-docs and four PhD students
- Weekly group meetings including pastoral and career support

ALSPAC Board of Directors

ALSPAC 2017 to present

Leading genetics work package

ALSPAC 2017 to present

- Line managing one post doctoral scientist

Academic leadership and citizenship

(i) Academic leadership in the discipline

I orchestrate the collection and harmonisation of summary data from genome-wide association studies (GWAS) across hundreds of international research groups through the OpenGWAS project. GWAS summary data is vitally important to a wide range of genetic and epidemiological research activities, and the OpenGWAS infrastructure is the largest of its kind comprising approximately 125 billion genetic associations. It has more than 1000 unique users a month and receives more than 2 million queries per week from all over the world.

I design analytical pipelines by unifying and developing statistical methods with researchers from multiple international groups. For example I developed the MR-Base software platform, which has now been cited over 2200 times since being published in 2018.

I co-lead three international collaborative research efforts: the GoDMC consortium comprising 56 cohorts analysing the genetics of DNA methylation; the OpenGWAS consortium that combines the resources of over 100 groups and consortia; and the Within-Families consortium which brings together 21 family cohorts with genetic and phenotypic

data for improved genetic association meta-analyses

I contributed to the design of the Our Future Health Project, which will genotype 5 million individuals in the UK, as a member of the chip design committee and as an expert reviewer in the procurement stage of the project.

(ii) Academic leadership in the University

MRC Integrative Epidemiology Unit 3.0 — University of Bristol
Programme Leader Track — 2023-2028

- Co-leading (with George Davey Smith) Programme 1 of seven programmes within the unit

Medical Anti-Racism Taskforce — University of Bristol
Group member — 2020 to present

- Leading Special interest group on decolonising the curriculum

UoB Covid-19 Situation Report — University of Bristol
Software developer — 2020 to present

- Web app developed for internal use that provides daily updates and case mapping
- Used daily by the Incident Management Team in targeting Covid-19 actions

Decolonising the medical school curriculum — University of Bristol
Co-lead — 2020 to present

- Co-leading (with Jo Hartland) a group of 10 volunteers to develop, pilot and deploy a curriculum review framework for the medical school (http://decolbms.org.uk)

BRMS Equality Diversity Inclusion group — University of Bristol
Group member — 2018 to present

- Working in career progression subgroup

USS pension calculator — University of Bristol
Software developer — 2018 to present

- Developed a web-app that allows members of the USS pension scheme to calculate changes to the pension under proposed valuation changes
- Used widely by universities across the country
- http://www.uss-pension-model.com/

Teaching peer review — University of Bristol
Reviewer — 2018

- Causal inference short course, University of Bristol

(iii) Professional activities outside the University

2021 -	Expert evaluation panel for the Our Future Health study
2019 -	Invited member of the Genotype Chip Design Committee for the Our Future Health Study, that will be used to genotype up to 5 million people in the UK
2017 -	Regular peer review for various grant bodies including the MRC, Wellcome Trust, Cancer Research UK
2012 -	Regular contributor to open source software projects (e.g. see https://github.com/explodecomputer/random-metal and https://github.com/explodecomputer/ldsc/)
2011 -	Regular peer review for 20+ academic journals

(iv) Contributions to society

2017 -	Hosting asylum seekers and refugees, working with Bristol City Council and the *Refugees at Home* charity
2015 -	Contributing member to the charity *Statisticians Without Borders*
2014 -	Provide web and software support to local vegan organisations

(v) Entrepreneurship, enterprise and partnerships

2015 -	I have formal partnerships with GlaxoSmithKlein, Biogen, Pfizer and CHDI that arose through developing the MR-Base platform. This has led to five post-doctoral positions and one PhD position being funded by these organisations, and the development of a standardised contract system to enable future such collaborations to occur.

(vi) Good citizenship

2023	Bristol Medical School representative of the University Research Institute task and finish group
2022 -	Member of the University of Bristol Senate (class 4 - Academic Staff)
2020 -	Leading a Special Interest Group on Decolonising the Curriculum, which will bring in a framework for all courses across the medical school for dealing with implicit bias within their learning materials
2020 -	Member of the Bristol Clear mentoring scheme (currently mentoring two early career researchers)
2020	Developed software for the University's Incident Management Team which maps new Covid-19 cases amongst students across the region in real time. This software is used in daily team management meetings
2016 -	Participated in numerous mock interview panels for research fellowships
2015 -	Extensive software development for the MRC IEU research community, most notably the MR-Base and OpenGWAS software platforms which I created and maintain for others to use. I am pleased that this has grown to be a platform for numerous research papers, and contributed substantially to research grants, many of which I am not named on
2014 -	Voluntary curation and documentation of shared data resources
2014 -	Web and software development for the ALSPAC project (e.g. see http://variables.alspac.bris.ac.uk/ and https://github.com/explodecomputer/alspac)
2014 -	Throughout my time in Bristol I have made it a priority to provide informal training to early career researchers, particularly in genetics, software development and reproducible research.

Future plans

I am committed to grow as an academic by understanding, refining and improving the impact of my work.

Teaching: I plan to develop a new professional development course that guides junior researchers and post-graduate students through best practices in code and data management and reproducible digital research. This reflects an important direction for me, of building a teaching-research nexus which I will continue to explore in my decoloni-

sation activities and contributions to life-long learning courses.

Administration: Team science is key to how I work, and though I have had a number of opportunities to lead teams thus far, I will seek opportunities to build my skills in this area, in terms of best serving the projects and people involved.

Research: I co-developed an extensive research plan for the next 5 years of the IEU relating to method development for causal inference and application to the ever changing landscape of genetic and genomic data. However, the structure of MRC units will change after this period, towards one which appears to be more goal oriented around applied research, and on a much longer time horizon than my work has previously worked towards. I will spend this time building ideas and plans for this next phase. I am interested in integrating my decolonisation work, for example by understanding how public and patient involvement may operate with the new wave of deep learning approaches that are yet to make a large impact in participatory genetic epidemiology.