Mendelian Randomization: Harnessing the power of population diversity and family relatedness

*All times are in BST.

Wednesday 7th July, 2021

9:30	Opening address
9:40	**Methods for family-based studies** **Chair: Neil Davies, University of Bristol** 9:40 Alex Havdahl*, University of Oslo. Separating direct and indirect genetic effects using trio designs in the Norwegian Mother, Father and Child Cohort Study (MoBa) 10:00 Gunn-Helen Moen, University of Oslo. Methods for enabling and improving the power of Mendelian randomization studies of parental environmental exposures and offspring outcomes 10:10 Liang-Dar (Daniel) Hwang, University of Queensland. Using adopted singletons to partition maternal genetic effects into pre- and post-natal effects on offspring phenotype 10:20 Matthew Tudball, University of Bristol. Almost exact Mendelian randomization
10:30-11:00	**Q&A, Methods for family-based studies**
11:00	Break
11:30	**Applications in family-based studies** **Chair: TBC** Laurence Howe*, Within-sibship GWAS and Mendelian randomization Geng Wang, Investigating a potential causal relationship between maternal blood pressure during pregnancy and future offspring cardiometabolic health. Amanda Hughes, The causal effects of child and parental BMI on neurodevelopment: a within family Mendelian randomization study using MoBa
12:10	**STROBE-MR guidelines** Veronika Skrivankova, STROBE-MR guidelines
12:30-13:00	**Q&A, Applications in family-based studies and STROBE-MR guidelines**
13:00	Lunch break
14:00	**Poster 1 session**
15:00	Break
15:30	**Poster 2 session**
16:30	Close of day 1

Thursday 8th July, 2021

9:30	**Methods for large-scale consortia** **Chair: David Evans, University of Queensland** 9:30 Sonjia Swanson*, Erasmus Medical Centre. What do we learn with instrumental variables? 9:50 Richard Howey*, Newcastle University. Bayesian network analysis incorporating genetic anchors complements conventional Mendelian randomization approaches for exploratory analysis of causal relationships in complex data 10:10 Amy Mason, University of Cambridge. Non-linear Mendelian Randomisation on Summarised Data: A comparative performance of semiparametric methods with and without individual-level data 10:20 Vasilios Karageorgi, University of Exeter. Sparse Dimensionality Reductions for highly correlated exposures in Mendelian Randomization
10:30-11:00	**Q&A, Methods for large-scale consortia**
11:00	Break
11:30	**Poster 3 session**
12:30	Lunch break
13:30	**Results from large scale consortia – parallel session 1** **Chair: Jie Zheng, University of Bristol** 13:30 Wei Zhou*, Massachusetts General Hospital and the Broad Institute. Global Biobank meta-analysis initiative 13:50 Fernanda Morales-Berstein, University of Bristol. Assessing the impact of maternal blood pressure on perinatal health: A systematic Mendelian randomization study 14:05 Si Fang, University of Bristol. Jackknife resampling Mendelian randomization enables investigation into sex-specific effects within a multivariate setting 14:20 James Yarmolinsky, University of Bristol. Association between genetically-proxied therapeutic inhibition of antihypertensive drug targets and risk of common cancers 14:35 Alvaro Hernaez, Norwegian Institute of Public Health. A Mendelian randomisation analysis of body mass index and subfertility: the Norwegian Mother, Father and Child Cohort Study
13:30	**General methods – parallel session 2** **Chair: Steve Burgess, University of Cambridge** 13:30 Ninon Mounier, University of Lausanne. Two-sample Mendelian Randomization: correction for winner's curse and weak instruments bias for unknown degree of sample overlap 13:45 Ashish Patel, University of Cambridge. Using many invalid instruments to improve Mendelian randomization estimates 14:00 Apostolos Gkatzionis, University of Bristol. Using instruments for selection to adjust for selection bias in Mendelian randomization

	14:15 Jonathan Sulc, University of Lausanne. PolyMR provides reliable inference of non-linear causal effects and shows the high prevalence of these in the UK Biobank 14:30 Wes Spiller, University of Bristol. Estimating and visualising multivariable Mendelian randomization analyses within a radial framework.
14:45	Break
15:30	**General applications & methods – parallel session 3** **Chair: Luisa Zuccolo, University of Bristol** 15:30 Linda Zollner, University of Heidelberg. Genetic admixture as the exposure of interest: Mapuche Native American ancestry and gallbladder cancer risk 15:45 Andrew Grant, University of Cambridge. Noise-augmented directional clustering of genetic association data identifies distinct mechanisms underlying obesity 16:00 Tim Morris, University of Bristol. Mendelian randomization with time-varying exposures 16:15 Eleanor Sanderson, University of Bristol. The use of negative control outcomes to detect population stratification in Mendelian randomization with application to population and within family GWAS results.
15:30	**Results from large scale consortia – parallel session 4** **Chair: Gibran Hemani, University of Bristol** 15:30 Neil Goulding, University of Bristol. The relationship between BMI and Covid-19: methods for exploring selection bias in a two-sample Mendelian randomisation study. Findings from the BHF-NIHR COVIDITY Flagship project. 15:45 Brandon Lim, University of Exeter. Using genetics to test whether maternal thyroid hormone levels (TSH and FT4) are causally related to offspring birthweight 16:00 Qian Yang, University of Bristol. Evaluating causal effects of chronotype preference on pregnancy and perinatal outcomes: a Mendelian randomization study in up to 232521 women of European descent 16:15 Emma Hazelwood, University of Bristol. Identifying molecular mediators of the relationship between body mass index and endometrial cancer risk: a Mendelian randomization analysis
16:30	Close of day 2

Friday 9th July, 2021

9:00	**Applications of MR in diverse populations** **Chair: Emma Anderson, University of Bristol** 9:00 Justo Lorenzo*, University of Heidelberg. MR in admixed Latin Americans: Challenges and recommendations?

	9:20 Nora Franceshini*, Gillings School of Global Public Health. Leveraging GWAS in diverse populations to enhance understanding of kidney disease 9:40 John Muriuki, KEMRI. Malaria is a cause of iron deficiency in African children 9:50 Robert Clarke, University of Oxford. Mendelian randomization study of the shape and strength and age-specific associations of systolic blood pressure with risk of vascular diseases in Chinese adults
10:00	Break
10:30	**Methods for incorporating population diversity** **Chair: Venexia Walker, University of Bristol** 10:30 Yukinori Okado*, Osaka University. Cross-population Mendelian randomization analysis and application for novel drug discovery 10:50 Humaira Rasheed*, Norwegian University of Science and Technology. Trans-ethnic Mendelian randomization study reveals causal relationships between cardio-metabolic factors and chronic kidney disease 11:10 Yoonsu Cho, University of Bristol. Jointly modelling multiple ancestral populations using GWAS summary data improves causal inference 11:20 Patrick Turley, University of Southern California. Multi-Ancestry Meta-Analysis yields novel genetic discoveries and ancestry-specific associations
11:30-12:30	**Q&A, Applications of MR in diverse populations and Methods for incorporating population diversity**
12:30	**Closing address** George Davey Smith
13:00	**Close of conference**