

Victorian Centre for Biostatistics

Seminar

Thursday 21st February

10.30am to 11.30am

Danks Room, Level 5

Murdoch Childrens Research Institute

Royal Childrens Hospital, Flemington Road, Parkville

“Investigation of pleiotropy in Mendelian randomisation studies using aggregate genetic data”

Dr Fabiola Del Greco

Mendelian randomisation (MR) allows estimation of the casual effect of a modifiable phenotype on a disease outcome using genes as instrumental variables. If the phenotype causally affects the disease, genes altering the phenotype level will be associated with disease, and the effect of the phenotype can be estimated from the gene-phenotype and gene-disease associations. MR estimates are unconfounded provided that some assumptions are met. The main assumption is the absence of pleiotropy, that is the gene influences the outcome only through the given phenotype. Excluding pleiotropy may be difficult even for well-studied genes, and the use of multiple instruments can indirectly address the issue: if all genes represent valid instruments, their MR estimates will vary only by chance. Formal testing of pleiotropy can be performed by the Hausman test, but the test requires individual data on both gene-phenotype and gene-disease associations for each gene. An alternative approach to test for the possible presence of pleiotropy, based on the use of between-instrument heterogeneity in a meta-analysis of MR estimates from multiple instruments, is presented. This approach can be used with aggregate data, that is estimates and standard errors of both gene-phenotype and gene-disease associations for each instrument.

Fabiola Del Greco completed a PhD in Statistics at the university G. d'Annunzio of Pescara (Italy) in 2007. Since 2009, she has worked at the Center for Biomedicine, EURAC research, in Bolzano (Italy). Her main fields of activity are: Genetic epidemiology; Statistical genetics; Stochastic processes.

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