Mendelian Randomisation for Causal Inference in Epidemiology

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In epidemiology, we are often faced with the problem that we can neither randomise exposure nor rule out unobserved confounding between the exposure and outcome of interest, e.g. alcohol consumption and coronary heart disease. Without any further information it is then impossible to draw credible conclusions about the causal effect of exposure. However, if one is a lucky, instances of Nature's radmisation can be exploited. For example, people with a certain variant of the ALDH2 gene consume as good as no alcohol and can be regarded as a random sample of the population. As genes are randomly passed on from parents to offspring according to Mendel's laws, we call this Mendelian randomisation and can statistically exploit such genetic data to draw causal conclusions. In economics the principle behind this approach is known as instrumental variable inference, the genetic variant(s) being the instrument(s) for the desired effect of exposure on outcome.
In this presentation I will give an overview of Mendelian randomization methods, the underlying assumptions and some successful applications. I will address some recent challenges which are concerned with multiple instruments, i.e. the simultaneous use of more than one genetic variant, weak instruments, i.e. genetic variants that only weakly predict the exposure, and non-linear models as one would typically want to use for binary outcomes.

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