Einladung zum Biometrischen Kolloquium

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'RECENT ADVANCES IN TWO-SAMPLE SUMMARY DATA MENDELIAN RANDOMIZATION'

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ABSTRACT:

The explosion in publicly available data from genome-wide association studies is accelerating the use of Mendelian randomization in epidemiology. Summary data estimates of genetic association from large numbers of variants are now being synthesised to yield causal estimates within the framework of a meta-analysis. In a short time, the field has seen a dramatic rise in the power for testing causal hypotheses. There is a justified concern that when large numbers of genetic variants are included in a Mendelian randomization analyses, with many lacking a firm biological basis for their association with the exposure, a sizeable proportion of these variants are likely to be invalid instrumental variables. Specifically, there is a real danger that many variants will exert pleiotropic effects on the outcome not through the exposure of interest, thus biasing the analysis and leading to incorrect inferences. In this talk I will start by giving a whistle-stop tour of methodological approaches to address the issue of pleiotropy in Mendelian randomization. If there is time, I will finish by discussing recent work on simultaneously adjusting for weak and pleiotropic instruments within MR.