Mendelian Randomization: Methods for Using Genetic Variants in Causal Estimation (Chapman Hall/CRC Interdisciplinary Statistics)

Stephen Burgess, Simon G. Thompson
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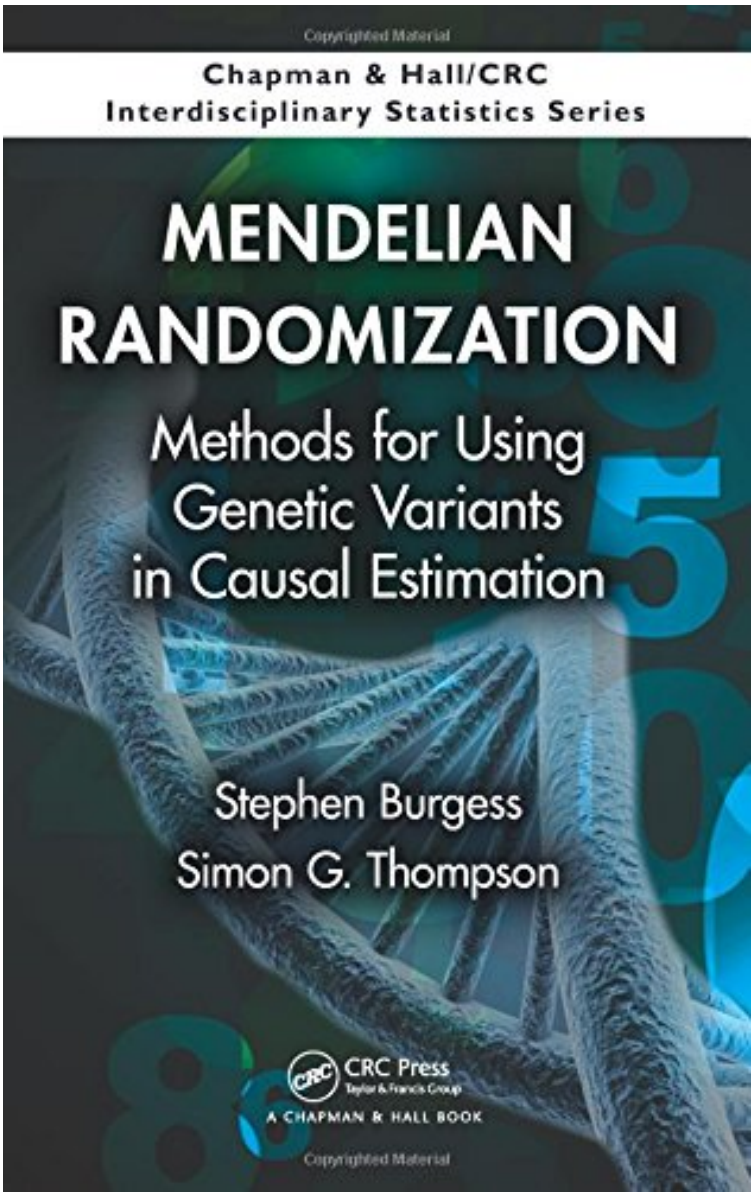

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Stephen Burgess, Simon G. Thompson : Mendelian Randomization: Methods for Using Genetic Variants in Causal Estimation (Chapman Hall/CRC Interdisciplinary Statistics) before purchasing it in order to gage whether or not it would be worth my time, and all praised Mendelian Randomization: Methods for Using Genetic Variants in

Causal Estimation (Chapman Hall/CRC Interdisciplinary Statistics):

Presents the Terminology and Methods of Mendelian Randomization for Epidemiological Studies Mendelian randomization uses genetic instrumental variables to make inferences about causal effects based on observational data. It, therefore, can be a reliable way of assessing the causal nature of risk factors, such as biomarkers, for a wide range of disease outcomes. Mendelian Randomization: Methods for Using Genetic Variants in Causal Estimation provides thorough coverage of the methods and practical elements of Mendelian randomization analysis. It brings together diverse aspects of Mendelian randomization spanning epidemiology, statistics, genetics, and econometrics. Although the book mainly focuses on epidemiology, much of the material can be applied to other areas of research. Through several examples, the first part of the book shows how to perform simple applied Mendelian randomization analyses and interpret their results. The second part addresses specific methodological issues, such as weak instruments, multiple instruments, power calculations, and meta-analysis, relevant to practical applications of Mendelian randomization. In this part, the authors draw on data from the C-reactive protein Coronary heart disease Genetics Collaboration (CCGC) to illustrate the analyses. They present the mathematics in an easy-to-understand way by using nontechnical language and reinforcing key points at the end of each chapter. The last part of the book examines the potential of Mendelian randomization in the future, exploring both methodological and applied developments. This book gives statisticians, epidemiologists, and geneticists the foundation to understand issues concerning the use of genetic variants as instrumental variables. It will get them up to speed in undertaking and interpreting Mendelian randomization analyses. Chapter summaries, paper summaries, web-based applications, and software code for implementing the statistical techniques are available on a supplementary website.