CURSO

COURSE

INTRODUCTION TO MENDELIAN RANDOMIZATION

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Mendelian randomization (MR) is an analytical method used to assess the causal effect of particular modifiable risk factors (exposures) on specific phenotypes (outcomes). MR tests and estimates the causal effects of the investigated exposures using genetic variants as instrumental variables, which are rarely affected by confounding or reverse causality, therefore overcoming major limitations of traditional observational studies. Prior experience in MR is not required to attend this course, but some knowledge of epidemiology, genetic epidemiology, genetic association studies, biostatistics (multiple regression analysis) and the R software for statistical computing is beneficial. The objective of the course "Introduction to Mendelian Randomization" is to provide participants with the skills needed to perform basic MR analyses, as well as to understand the strengths and limitations of the methodology. The course will begin with a general introduction to causal inference in epidemiology, including the principles and instrumental variable assumptions of MR. Then, one-sample and two-sample MR will be introduced, followed by power calculation and data harmonization in MR. Further topics of the course will include typical sensitivity analyses to detect potential biases, two-step MR and mediation analysis, the potential of MR for molecular epidemiological studies that investigate omics data, and recent developments in MR methodology. The course is a combination of lectures and practical assignments, where participants will perform MR analyses using publicly available software, for example MR-Base, and gain experience in interpreting MR results.