Title: Building a Mendelian Randomization Pipeline to find causal estimates between metabolomic exposures and diseases.

Project Description:

The project aims to develop a Mendelian Randomization Pipeline to investigate causal relationships between metabolomic exposures and diseases. Mendelian Randomization is a statistical approach that uses genetic variants as instrumental variables to assess causal effects. In this study, metabolomic data will be analyzed to identify potential causal associations with various diseases. The pipeline will involve data preprocessing, instrumental variable selection, causal estimation, and statistical analysis to provide insights into the causal effects of metabolomic exposures on disease outcomes. The project seeks to contribute to the understanding of metabolic pathways and their influence on the development of diseases, ultimately providing valuable information for precision medicine and targeted interventions.

Duties/Activities:

- Make use of R/ Python for data preprocessing steps
- Run various MR Models such as IVW, MR Egger, WM etc.
- Analyze causal estimates and generate reports on findings.

Required Skills:

- Programming skills in R or Python.
- Problem solving and analytical skills.

Learning Opportunities:
- Work on real projects.
- Elevate bioinformatics knowledge.
- Ability to analyze genetic and metabolomic material.

Expected Team Size: *1-2*

Mentors

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