### README

The code used for this study is openly available on GitHub, accompanied by instructions for use and required tools (https://github.com/EulaLouse/250221MR-analyses).

This repository contains the code needed to reproduce all results and plots in the paper "Causal Effects of Parkinson’s Disease on Cortical Structure: A Multi-Ancestry Mendelian Randomization Study". Code snippets are separated into files mirroring the organization of figures in the manuscript. All code can be run in R (version 4.3.2).

**Figure S1-S28.R**: Code required to generate MR results. Use GWAS data from different populations as input exposure factor data and cortical structure GWAS data as input outcome factor data. Run the code to perform Mendelian randomization analysis and generate scatter plots, forest plots, funnel plots, and leave-one-out plots.

**Figure 2.R**: Code required to generate results for genetic colocalization analysis. Perform genetic colocalization analysis using data from different populations and cortical structure data to obtain post-validation probabilities and visualize the colocalization results.

**Figures 3 and 4.R**: Code required to visualize a data frame containing subgroup information using forest plots. The original data for forest plots is organized and summarized based on MR results.

**Figure 6.R**: Code required to generate Figure 6, which takes the summarized IVW results as input data and creates a heatmap without row or column clustering.

**Figures 7-8 and Figures S29-S30.R**: Code required for gene enrichment analysis. Use the organized gene IDs as the input file and analyze the enrichment pathways in the GO database, KEGG database, and Wiki database using the code, generating bubble plots and bar charts.

**Figure 9.R**: Code required to generate a Sankey diagram. Organize and summarize the pathways and related genes obtained from the enrichment analysis into an input file, then run the code to create the Sankey diagram.