

Running a Meta-Analysis with MetaSAIGE

Introduction

This vignette provides a comprehensive guide to using the **MetaSAIGE** package for conducting a meta-analysis on summary statistics from multiple cohorts. Specifically, we'll walk through the process of using the `Run_MetaSAIGE` function, detailing each step required to perform the analysis.

Prerequisites

Before you begin the meta-analysis, ensure you have the following resources available:

- **GWAS Summary Statistics Files:** Generated by SAIGE.
- **SNP Information Files:** Corresponding to the GWAS summary statistics.
- **Gene Files:** Created by the SAIGE-GENE+ `step3_LD_mat.R` script.

Running the `Run_MetaSAIGE` Function

The `Run_MetaSAIGE` function is central to performing the meta-analysis. It requires several key inputs, including the number of cohorts, chromosome number, and paths to the necessary GWAS summary statistics and SNP information files.

Example Usage

Here is an example of how to run the `Run_MetaSAIGE` function:

```
# Load the MetaSAIGE package
library(MetaSAIGE)

# Example of running Run_MetaSAIGE
Run_MetaSAIGE(
  n.cohorts = 2,
  chr = 1,
  gwas_path = c("gwas1.txt", "gwas2.txt"),
  info_path = c("info1.txt", "info2.txt"),
  gene_file_prefix = c("gene1_", "gene2_"),
  col_co = 10,
  output_path = "output.txt",
  ancestry = c(1, 2),
  verbose = TRUE,
  trait_type = "binary"
)
```