

# 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:

```
“r # 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” )
```