Integrative Mendelian randomization for detecting exposure-by-group interactions using group-specific and combined summary statistics

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Introduction

This vignette provides an introduction to the int2MR package. The R package int2MR implements the int2MR method for detecting both direct exposure-outcome effect within comparison group and reference group and exposure-group interaction effect.

Before installing int2MR, ensure that you have the devtools package installed. The package also requires rstan for Bayesian modeling. To install the development version of int2MR, run:

```
# Load devtools package
library(devtools)

## Loading required package: usethis

# Install the int2MR package from GitHub
install_github("Likeli-Ke/int2MR")

## Skipping install of 'int2MR' from a github remote, the SHA1 (7b3157b7) has not changed since last in
## Use 'force = TRUE' to force installation

# Load the int2MR package
library(int2MR)
```

Input Data Format

The int2MR package supports two types of GWAS summary statistics:

- Three-sample data: Utilizes three separate IV-to-outcome GWAS statistics.
- Two-sample data: Utilizes two IV-to-outcome GWAS summary statistics.

To detect the exposure-group interaction effect, it is essential that the proportion of the comparison group (denoted as rho) varies among the provided GWAS summary statistics.

Data Requirements

Your input data should include:

- Number of IVs (instrumental variables)
- Point estimates and squared standard errors for:
 - IV-to-outcome effects
 - IV-to-exposure effects
- Proportion of the comparison group (rho) in each IV-to-outcome GWAS summary statistic.

Load the example datasets provided with the package as follows:

```
data(example_3sample_data)
data(example_2sample_data)
```

For further details on the example data formats included with the package, consult the help pages.

```
help(example_3sample_data)
help(example_2sample_data)
```

Running Examples

This section demonstrates how to run int2MR using simulated data. Two examples are provided: one for three-sample data and one for two-sample data.

Example 1: Three-Sample Data

In this example, we perform an analysis on simulated three-sample data. The parameters include:

- model_type: "3sample"
- Prior distributions: Inverse gamma priors with a shape and scale of 0.1
- MCMC Settings: 2 chains, 10000 iterations with a warm-up period of 2500 iterations, and an adapt_delta of 0.95.

```
## Loading required package: rstan
## Loading required package: StanHeaders
##
## rstan version 2.32.7 (Stan version 2.32.2)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
## For within-chain threading using 'reduce_sum()' or 'map_rect()' Stan functions,
## change 'threads_per_chain' option:
## rstan_options(threads_per_chain = 1)
## Trying to compile a simple C file
## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## using C compiler: 'Apple clang version 16.0.0 (clang-1600.0.26.6)'
## using SDK: ''
## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG
                                                                                      -I"/Library/Frame
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/StanHeade
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen
## /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen/include/Eigen/src/Cor
    679 | #include <cmath>
##
         1
## 1 error generated.
## make: *** [foo.o] Error 1
# Display the results for the three-sample analysis
result_3sample$result_3sample
##
                  se beta
                             pval_beta est_beta_int se_beta_int pval_beta_int
      est beta
## 1 0.1987148 0.03203627 5.546514e-10
                                        -0.1413816 0.05635274
                                                                    0.0121119
```

Example 2: Two-Sample Data

total_effect pval_total

0.05733322 0.1157396

1

This example demonstrates an analysis using simulated two-sample data. The configuration is similar to the three-sample analysis, with model_type set to "2sample".

```
## Trying to compile a simple C file

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c

## using C compiler: 'Apple clang version 16.0.0 (clang-1600.0.26.6)'

## using SDK: ''

## clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library/Frame

## In file included from <built-in>:1:
```

```
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/StanHeade
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen
## In file included from /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen
## /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/library/RcppEigen/include/Eigen/src/Cor
   679 | #include <cmath>
##
         1
## 1 error generated.
## make: *** [foo.o] Error 1
# Display the results for the two-sample analysis
result_2sample$result_2sample
##
                            pval_beta est_beta_int se_beta_int pval_beta_int
      est beta
                 se_beta
## 1 0.1914894 0.03606245 1.096614e-07 -0.1441186 0.05694519
     total_effect pval_total
## 1 0.04737085 0.2823505
```