# Package 'MAPITR'

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**Title** MArginal ePIstasis Test for Regions

**Version** 1.1.2

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**Description** A genetic analysis tool and variance component model for identifying marginal epistasis between pathways and the rest of the genome. 'MAPITR' uses as input a matrix of genotypes, a vector of phenotypes, and a list of pathways. 'MAPITR' then iteratively tests each pathway for epistasis between any variants within the pathway versus any variants remaining in the rest of the genome. 'MAPITR' returns results in the form of p-values for every pathway indicating whether the null model of there being no epistatic interactions between a pathway and the rest of the genome can be rejected.

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**URL** https://github.com/mturchin20/MAPITR

**BugReports** https://github.com/mturchin20/MAPITR/issues

**Depends** R (>= 3.3.0)

**Imports** stats, doParallel, Rcpp (>= 1.0.5), CompQuadForm

**Suggests** testthat, knitr, rmarkdown

**Encoding** UTF-8

**LazyData** true

**NeedsCompilation** yes

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**LinkingTo** Rcpp, RcppArmadillo

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MAPITR *MArginal ePIstasis Test for Regions (*MAPITR*)*

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## Description

Run MAPITR for a group of pathways on a single phenotype and a set of genome-wide SNPs

## Usage

```
MAPITR(
  Genotypes,
  Phenotype,
  Pathways,
  Covariates = NULL,
  CenterStandardize = TRUE,
  OpenMP = FALSE,
  cores = NULL,
  ...
)
```

## Arguments

| | |
|---|---|
| Genotypes | A n x p matrix containing the genotypes (0/1/2) for all p SNPs across all n individuals. No default value. |
| Phenotype | A vector containing phenotypic values for all individuals being analyzed. No default value. |

`Pathways` A r x 2 matrix containing the pathway names and then a comma-separated list of the `Genotypes` column indices representing each SNP in the associated pathway. Note, this second column of comma-separated indices are the numeric positions for each SNP in `Genotypes` and not the SNP IDs or column names. No default value.

`Covariates` A n x q matrix containing any q additional covariates that should be included in the M-projection matrix of the model. See Turchin et al. 2020 for details. Note that these are covariates which are applied to both sides of the model, ie the phenotype as well as the genotypes. A y-intercept term is automatically included and does not need to be part of this n x q matrix. No default value.

`CenterStandardize`
A logical `TRUE/FALSE` flag that indicates whether the genotype matrix `Genotypes` should be centered and standardized before analysis. This is a recommended step. Indicate `FALSE` if this is a preprocessing step that has already been done prior to running `MAPITR`. The default value is TRUE.

`OpenMP` A logical `TRUE/FALSE` flag that indicates whether OpenMP versions of `MAPITR` should be implemented. OpenMP versions of the underlying Rcpp code will run more quickly, but requires the user to be operating an R version that has been installed with OpenMP access. The default value is FALSE.

`cores` A numeric value providing the expected number of cores if the OpenMP version of the code is being used. `parallel::detectCores()` is used by default to assign this variable when no value is given. A value generally should only be given when needing finer control of the code or for testing purposes. The default value is NULL.

`...` Additional optional arguments.

## Value

A list containing two entries. First, a dataframe (`Results`) containing in the first column the list of pathways that were analyzed, in the second column the associated `MAPITR` p-values for each pathway, in the third column the associated `MAPITR` variance component estimates for each pathway, and in the fourth column the associated `MAPITR` PVEs for each pathway. Second, a matrix (`Eigenvalues`) containing the n associated `MAPITR` eigenvalues for each pathway per column.

## Examples

```
data(MAPITR_TestData_Genotypes, MAPITR_TestData_Phenotype,
MAPITR_TestData_Pathways)
MAPITROutput <- MAPITR(MAPITR_TestData_Genotypes, MAPITR_TestData_Phenotype,
MAPITR_TestData_Pathways, OpenMP=FALSE)
MAPITROutput$Results
```

MAPITR_SimData_Genotypes *MAPITR SimData Genotypes*

## Description

A simulated dataset of genotypes for use in vignettes

## Format

A data frame with 500 rows (individuals) and 750 variables (SNPs)

## Source

Manually created

MAPITR_SimData_Pathways *MAPITR SimData Pathways*

## Description

A simulated set of pathways for use in vignettes

## Format

A data frame with 5 rows (pathways) and 2 variables (pathway name, comma-separated list of pathway column indices)

## Source

Manually created

MAPITR_SimData_PCs *MAPITR SimData PCs*

## Description

Top 10 principal components from the simulated genotypes for for use in vignettes

## Format

A data frame with 500 rows (individuals) and 10 variables (PCs)

## Source

Manually created

MAPITR_SimData_Phenotype
*MAPITR SimData Phenotype*

## Description

A simulated set of phenotypes for use in vignettes

## Format

A data frame with 500 rows (individuals) and 1 variables (phenotype)

## Source

Manually created

MAPITR_TestData_Genotypes
*MAPITR TestData Genotypes*

## Description

A simulated dataset of genotypes for use in unit tests

## Format

A data frame with 500 rows (individuals) and 750 variables (SNPs)

## Source

Manually created

MAPITR_TestData_Pathways *MAPITR TestData Pathways*

## Description

A simulated set of pathways for use in unit tests

## Format

A data frame with 5 rows (pathways) and 2 variables (pathway name, comma-separated list of pathway column indices)

## Source

Manually created

MAPITR_TestData_PCs *MAPITR TestData PCs*

## Description

Top 10 principal components from the simulated genotypes for for use in unit tests

## Format

A data frame with 500 rows (individuals) and 10 variables (PCs)

## Source

Manually created

MAPITR_TestData_Phenotype *MAPITR TestData Phenotype*

## Description

A simulated set of phenotypes for use in unit tests

## Format

A data frame with 500 rows (individuals) and 1 variables (phenotype)

## Source

Manually created

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