

# Package ‘GeneticMediation’

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**Type** Package

**Title** An R Package for Causal Mediation Analysis of ROSMAP Data

**Version** 1.1.0

**License** GPL-3

**URL** <https://github.com/tydarnell/GeneticMediation>,  
<https://tydarnell.github.io/GeneticMediation>

**Author** Ty Darnell [aut, cre]

**Maintainer** Ty Darnell <tydarnell@gmail.com>

**Description** Provides methods for cleaning and processing data from the ROSMAP study  
and preparing it for causal mediation analysis

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Depends** R (>= 3.6.0)

**Imports** BiocManager, data.table, IRanges, mediation, readr, stats

## R topics documented:

check_data . . . . .	2
chr_numeric . . . . .	2
clean_data . . . . .	2
combine_data_spc . . . . .	3
combine_data_spg . . . . .	3
last_to_first . . . . .	3
lu . . . . .	4
make_folder . . . . .	4
match_all . . . . .	4
match_snp_peak . . . . .	5
med.res_spc . . . . .	5
med.res_spg . . . . .	5
med_all_spc . . . . .	6
med_chr_spc . . . . .	6
med_chr_spg . . . . .	7
med_table_spc . . . . .	7
med_table_spg . . . . .	8

setup_folders . . . . .	8
snp_peak_bychr . . . . .	8
sum_zero . . . . .	9
transpose_readcount . . . . .	9

## Index 10

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check_data	<i>Check Data</i>
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### Description

Checks if the data is in the data folder

### Usage

```
check_data()
```

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chr_numeric	<i>Chromosome Numeric</i>
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### Description

Convert chromosome names from character to numeric. Useful when sorting a dataframe by chromosome number.

### Usage

```
chr_numeric(Chr)
```

### Arguments

Chr	a character column or vector of chromosome names
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clean_data	<i>Clean Data</i>
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### Description

Clean snp.info, peak.info data and save as data/chipseq.RData

### Usage

```
clean_data(snp.path, peak.path)
```

### Arguments

snp.path	path to SNP information dataframe
peak.path	path to Peak annotation dataframe

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combine_data_spc	<i>Combine Data SNP-Peak-Clinical</i>
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**Description**

SNP-Peak-Clinical data: combine projid, SNPs, PCs, membership, age, gender, peaks, and outcome data for a chromosome

**Usage**

```
combine_data_spc(chr)
```

**Arguments**

chr	chromosome name
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combine_data_spg	<i>Combine Data SNP-Peak-Gene</i>
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**Description**

SNP-Peak-Gene Data: combine projid, SNPs, PCs, membership, age, gender, peaks, gene and outcome data for a chromosome.

**Usage**

```
combine_data_spg(chr)
```

**Arguments**

chr	chromosome name
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last_to_first	<i>Last to First</i>
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**Description**

Make the last column the first column in a dataframe

**Usage**

```
last_to_first(df)
```

**Arguments**

df	dataframe
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lu	<i>Length Unique</i>
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**Description**

Get the length of unique values in a vector

**Usage**

```
lu(x)
```

**Arguments**

x	vector
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make_folder	<i>Make Folder</i>
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**Description**

Make a folder only if the folder does not already exist

**Usage**

```
make_folder(path)
```

**Arguments**

path	folder path
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match_all	<i>Match SNPs Peaks All Chromosomes</i>
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**Description**

Match SNPs and Peaks in all chromosomes and return dataframe of matches

**Usage**

```
match_all(snp.info, peak.info, chrs)
```

**Arguments**

snp.info	SNP information
peak.info	Peak information
chrs	character vector of chromosome names

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match_snp_peak	<i>Match SNPs and Peaks</i>
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**Description**

Match SNPs and Peaks in a chromosome

**Usage**

```
match_snp_peak(snp.info, peak.info)
```

**Arguments**

snp.info	SNP information for chr
peak.info	Peak information chr

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med.res_spc	<i>SNP-Peak-Clinical Mediation Data Prep</i>
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**Description**

Prepare a chromosome of SNP-Peak-Clinical data for mediation analysis and save as "data/spc.res/res\_chr.RData"

**Usage**

```
med.res_spc(chr, all_matches)
```

**Arguments**

chr	chromosome name
all_matches	dataframe of SNP-Peak matches for all chromosomes

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med.res_spg	<i>SNP-Peak-Gene Mediation Data Prep</i>
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**Description**

Prepare a chromosome SNP-Peak-Gene data for mediation analysis data and save as "data/spg.res/res\_chr.RData"

**Usage**

```
med.res_spg(chr, med.data, matches, mediator.path)
```

**Arguments**

chr	chromosome name
med.data	gene mediation data
matches	SNP-Peak-Gene matches dataframe

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med_all_spc	<i>SNP-Peak-Clinical Mediation Table</i>
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**Description**

Create a table of SNP-Peak-Clinical mediation results for all chromosomes

**Usage**

```
med_all_spc(chrs, covar, simulations)
```

**Arguments**

chrs	character vector of chromosome names
covar	covariates string, each covariate separated by +
simulations	number of simulations to run

---

med_chr_spc	<i>SNP-Peak-Clinical Mediation Table Chromosome</i>
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**Description**

Create SNP-Peak-Clinical mediation table for SNP-Peak matches in a chromosome

**Usage**

```
med_chr_spc(matches, med.res.data, covar, simulations)
```

**Arguments**

matches	SNP-Peak matches dataframe for a chromosome
med.res.data	mediation data
covar	covariates string, separate covariates with +
simulations	number of simulations to run

---

med_chr_spg	<i>SNP-Peak-Gene Mediation Table Chromosome</i>
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**Description**

Create a SNP-Peak-Gene mediation table for a chromosome

**Usage**

```
med_chr_spg(chr, gene_matches, simulations)
```

**Arguments**

chr	chromosome name
gene_matches	list of peak-SNP matches for each gene
simulations	number of simulations to run

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med_table_spc	<i>SNP-Peak-Clinical Mediation Table</i>
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**Description**

Create SNP-Peak-Clinical mediation table for a SNP-Peak match

**Usage**

```
med_table_spc(med.res.data, match_row, covar, simulations)
```

**Arguments**

med.res.data	mediation data
match_row	row in match dataframe, should have 2 columns
covar	covariates character variable, separate covariates with +
simulations	number of simulations to run

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med_table_spg	<i>SNP-Peak-Gene Mediation Table</i>
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**Description**

Create a mediation table for one SNP-Peak-Gene match

**Usage**

```
med_table_spg(med_dat, match_row, simulations)
```

**Arguments**

med_dat	gene mediation data
match_row	row in match dataframe: col1 SNP, col2 Peak, col3 Gene
simulations	number of simulations to run

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setup_folders	<i>Setup Folders</i>
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**Description**

Creates data, data/mediator, results folders

**Usage**

```
setup_folders()
```

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snp_peak_bychr	<i>SNPs and Peaks by Chromosome</i>
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**Description**

save snp.info, peak.info for each chromosome as "data/chipseq/chipseq\_chr.RData"

**Usage**

```
snp_peak_bychr(chrs, snps, peaks)
```

**Arguments**

chrs	Character vector of chromosomes names
snps	SNP information dataframe
peaks	Peak information dataframe



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`sum_zero`*Sum Zero*

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**Description**

Get names of columns that have a sum of zero

**Usage**

```
sum_zero(df)
```

**Arguments**

`df`                      dataframe

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`transpose_readcount`*Transpose Readcount*

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**Description**

Read in and transpose ChIP-seq Readcount dataframe and match project id

**Usage**

```
transpose_readcount(readcount.path)
```

**Arguments**

`readcount.path` ChIP-seq readcount dataframe file path

# Index

- \*Topic **SNP**
    - match\_all, [4](#)
    - match\_snp\_peak, [5](#)
  - \*Topic **check**
    - check\_data, [2](#)
  - \*Topic **chromosome**
    - chr\_numeric, [2](#)
  - \*Topic **clinical**
  - combine\_data\_spc, [3](#)
  - \*Topic **column**
    - last\_to\_first, [3](#)
  - \*Topic **combine**
    - combine\_data\_spc, [3](#)
    - combine\_data\_spg, [3](#)
  - \*Topic **data**
    - check\_data, [2](#)
    - clean\_data, [2](#)
    - combine\_data\_spc, [3](#)
    - combine\_data\_spg, [3](#)
    - med.res\_spc, [5](#)
    - med.res\_spg, [5](#)
    - snp\_peak\_bychr, [8](#)
  - \*Topic **first**
    - last\_to\_first, [3](#)
  - \*Topic **folder**
    - make\_folder, [4](#)
    - setup\_folders, [8](#)
  - \*Topic **gene**
    - combine\_data\_spg, [3](#)
  - \*Topic **last**
    - last\_to\_first, [3](#)
  - \*Topic **length**
    - lu, [4](#)
  - \*Topic **match**
    - match\_all, [4](#)
    - match\_snp\_peak, [5](#)
  - \*Topic **mediation**
    - med\_all\_spc, [6](#)
    - med\_chr\_spc, [6](#)
    - med\_chr\_spg, [7](#)
    - med\_table\_spc, [7](#)
    - med\_table\_spg, [8](#)
  - \*Topic **numeric**
    - chr\_numeric, [2](#)
  - \*Topic **peak**
    - clean\_data, [2](#)
    - match\_all, [4](#)
    - match\_snp\_peak, [5](#)
  - \*Topic **prep**
    - med.res\_spc, [5](#)
  - \*Topic **readcount**
    - transpose\_readcount, [9](#)
  - \*Topic **setup**
    - setup\_folders, [8](#)
  - \*Topic **snp**
    - clean\_data, [2](#)
  - \*Topic **table**
    - med\_all\_spc, [6](#)
    - med\_chr\_spc, [6](#)
    - med\_chr\_spg, [7](#)
    - med\_table\_spc, [7](#)
    - med\_table\_spg, [8](#)
  - \*Topic **transpose**
    - transpose\_readcount, [9](#)
  - \*Topic **unique**
    - lu, [4](#)
  - \*Topic **zero**
    - sum\_zero, [9](#)
- 
- check\_data, [2](#)
  - chr\_numeric, [2](#)
  - clean\_data, [2](#)
  - combine\_data\_spc, [3](#)
  - combine\_data\_spg, [3](#)
- 
- last\_to\_first, [3](#)
  - lu, [4](#)
- 
- make\_folder, [4](#)
  - match\_all, [4](#)
  - match\_snp\_peak, [5](#)
  - med.res\_spc, [5](#)
  - med.res\_spg, [5](#)
  - med\_all\_spc, [6](#)
  - med\_chr\_spc, [6](#)
  - med\_chr\_spg, [7](#)
  - med\_table\_spc, [7](#)

med\_table\_spg, [8](#)  
setup\_folders, [8](#)  
snp\_peak\_bychr, [8](#)  
sum\_zero, [9](#)  
transpose\_readcount, [9](#)