# Package 'GeneticMediation'

April 26, 2020

**Type** Package

**Title** Genetic Causal Mediation

**Version** 1.1.0

**License** GPL-3

**URL** https://tydarnell.github.io/GeneticMediation,

https://github.com/tydarnell/GeneticMediation

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

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**Description** Provides methods for conducting causal mediation
analysis on data from the ROSMAP study and for cleaning,
matching, and preparing the data for analysis.

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

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

**Suggests** tidyverse

## R topics documented:

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chr_numeric                           *Chromosome Numeric*

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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                            *Clean Data*

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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 | *Combine Data SNP-Peak-Clinical*

---

#### 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 | *Combine Data SNP-Peak-Gene*

---

#### 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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GeneticMediation | *GeneticMediation: A package for conducting causal mediation analysis on ROSMAP data*

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#### Description

GeneticMediation provides methods for conducting causal mediation analysis on data from the ROSMAP study. It also provides methods for cleaning, matching, and preparing the data for analysis.

#### Author(s)

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

#### See Also

Useful links:

- https://tydarnell.github.io/GeneticMediation
- https://github.com/tydarnell/GeneticMediation

last_to_first *Last to First*

### Description

Make the last column the first column in a dataframe

### Usage

```
last_to_first(df)
```

### Arguments

df          dataframe

lu *Length Unique*

### Description

Get the length of unique values in a vector

### Usage

```
lu(x)
```

### Arguments

x          vector

make_folder *Make Folder*

### 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 *Match SNPs Peaks All Chromosomes*

---

### 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 |

---

match_snp_peak *Match SNPs and Peaks*

---

### 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 *SNP-Peak-Clinical Mediation Data Prep*

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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                    *SNP-Peak-Gene Mediation Data Prep*

---

### 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                    *SNP-Peak-Clinical Mediation Table*

---

### 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                    *SNP-Peak-Clinical Mediation Table Chromosome*

---

### 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                    *SNP-Peak-Gene Mediation Table Chromosome*

---

### 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

---

med_table_spc          *SNP-Peak-Clinical Mediation Table*

---

### 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          *SNP-Peak-Gene Mediation Table*

---

### 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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snp_peak_bychr *SNPs and Peaks by Chromosome*

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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

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