

# Package ‘GeneticMediation’

April 30, 2020

**Type** Package

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

**Version** 1.1.0.9000

**License** GPL-3

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

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**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)

**biocViews**

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

**Suggests** testthat,  
spelling,  
covr,  
knitr,  
rmarkdown

**Language** en-US

**VignetteBuilder** knitr

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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> |
|------------|-------------------|

---

**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 |

---

|                  |                                       |
|------------------|---------------------------------------|
| combine_data_spc | <i>Combine Data SNP-Peak-Clinical</i> |
|------------------|---------------------------------------|

---

**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 |
|-----|-----------------|

---

|                  |                                   |
|------------------|-----------------------------------|
| combine_data_spg | <i>Combine Data SNP-Peak-Gene</i> |
|------------------|-----------------------------------|

---

**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 |
|-----|-----------------|

---

|               |                      |
|---------------|----------------------|
| last_to_first | <i>Last to First</i> |
|---------------|----------------------|

---

**Description**

Make the last column the first column in a dataframe

**Usage**

```
last_to_first(df)
```

**Arguments**

|    |           |
|----|-----------|
| df | dataframe |
|----|-----------|

---

|    |                      |
|----|----------------------|
| lu | <i>Length Unique</i> |
|----|----------------------|

---

**Description**

Get the length of unique values in a vector

**Usage**

```
lu(x)
```

**Arguments**

|   |        |
|---|--------|
| x | vector |
|---|--------|

---

|             |                    |
|-------------|--------------------|
| make_folder | <i>Make Folder</i> |
|-------------|--------------------|

---

**Description**

Make a folder only if the folder does not already exist

**Usage**

```
make_folder(path)
```

**Arguments**

|      |             |
|------|-------------|
| path | folder path |
|------|-------------|

---

|           |   |
|-----------|---|
| match_all | <i>Match SNPs Peaks All Chromosomes</i> |
|-----------|---|

---

**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 | <i>Match SNPs and Peaks</i> |
|----------------|-----------------------------|

---

**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    |

---

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

---

**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 |

---

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

---

**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 |

---

|               |                                |
|---------------|--------------------------------|
| mediation_spg | <i>Mediation SNP-Peak-Gene</i> |
|---------------|--------------------------------|

---

**Description**

Mediation analysis one SNP-Peak-Gene match

**Usage**

```
mediation_spg(med.res.data, match_row, simulations = 1000)
```

**Arguments**

|              |  |
|--------------|--|
| med.res.data | gene mediation data                                    |
| match_row    | row in match dataframe: col1 SNP, col2 Peak, col3 Gene |
| simulations  | number of simulations, 1000 by default                 |

---

|             |  |
|-------------|--|
| med_all_spc | <i>SNP-Peak-Clinical Mediation Table</i> |
|-------------|--|

---

**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> |
|-------------|---|

---

**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> |
|-------------|---|

---

**Description**

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

**Usage**

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

**Arguments**

|              |   |
|--------------|---|
| chr          | chromosome name                               |
| gene_matches | list of peak-SNP matches for each gene        |
| covar        | covariates string, separate covariates with + |
| simulations  | number of simulations to run                  |

---

|               |  |
|---------------|--|
| med_table_spc | <i>SNP-Peak-Clinical Mediation Table</i> |
|---------------|--|

---

**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> |
|---------------|--------------------------------------|

---

**Description**

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

**Usage**

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

**Arguments**

|              |   |
|--------------|---|
| med.res.data | gene mediation data                                       |
| match_row    | row in match dataframe: col1 SNP, col2 Peak, col3 Gene    |
| covar        | covariates character variable, separate covariates with + |
| simulations  | number of simulations to run                              |

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|           |                  |
|-----------|------------------|
| merge_csv | <i>Merge CSV</i> |
|-----------|------------------|

---

**Description**

merge multiple csv files into a single dataframe

**Usage**

```
merge_csv(path)
```

**Arguments**

|      |                                     |
|------|-------------------------------------|
| path | path to folder containing csv files |
|------|-------------------------------------|



---

|               |                      |
|---------------|----------------------|
| setup_folders | <i>Setup Folders</i> |
|---------------|----------------------|

---

**Description**

Creates data, data/mediator, results folders

**Usage**

```
setup_folders()
```

---

|                |                                     |
|----------------|-------------------------------------|
| snp_peak_bychr | <i>SNPs and Peaks by Chromosome</i> |
|----------------|-------------------------------------|

---

**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            |

---

|          |                 |
|----------|-----------------|
| sum_zero | <i>Sum Zero</i> |
|----------|-----------------|

---

**Description**

Get names of columns that have a sum of zero

**Usage**

```
sum_zero(df)
```

**Arguments**

|    |           |
|----|-----------|
| df | dataframe |
|----|-----------|

---

|                     |                            |
|---------------------|----------------------------|
| transpose_readcount | <i>Transpose Readcount</i> |
|---------------------|----------------------------|

---

**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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