

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]

Maintainer Ty Darnell <tydarnell@gmail.com>

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:

chr_numeric	2
clean_data	2
data_by_chr	3
data_prep_spc	3
data_prep_spg	3
GeneticMediation	4
last_to_first	4
lu	4
make_folder	5
match_all	5
match_chr	5
med.res_spc	6
med.res_spg	6
med_all_spc	7
med_chr_spc	7
med_chr_spg	8

med_table_spc	8
med_table_spg	9
sum_zero	9
transpose_readcount	9

Index	10
--------------	-----------

chr_numeric	<i>Chromosome Numeric</i>
-------------	---------------------------

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

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

data_by_chr	<i>Data by Chromosome</i>
-------------	---------------------------

Description

save snp.info, peak.info for each chromosome as "data/chipseq_chr.RData"

Usage

```
data_by_chr(chrs, snps, peaks)
```

Arguments

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

data_prep_spc	<i>SNP-Peak-Clinical Data Prep Helper</i>
---------------	---

Description

Helper function for SNP-Peak-Clinical mediation data. Combine projid, SNPs, PCs, membership, age, gender, peaks, and outcome data for a chromosome

Usage

```
data_prep_spc(chr)
```

Arguments

chr	chromosome name
-----	-----------------

data_prep_spg	<i>SNP-Peak-Gene Data Prep Helper</i>
---------------	---------------------------------------

Description

Helper function for SNP-Peak-Gene data prep. Combine projid, SNPs, PCs, membership, age, gender, peaks, gene and outcome data for a chromosome.

Usage

```
data_prep_spg(chr, mediator.path)
```

Arguments

chr	chromosome name
mediator.path	path to mediator folder with mediation_chr#_new.RData files

GeneticMediation	<i>GeneticMediation: A package for conducting causal mediation analysis on ROSMAP data</i>
------------------	--

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	<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	path for new folder
------	---------------------

match_all	<i>Match 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_chr	<i>Match Chromosome</i>
-----------	-------------------------

Description

Match Peaks and SNPs in a chromosome

Usage

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

Arguments

snp.info	SNP information
peak.info	Peak information

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/med.res/res_chr.RData"

Usage

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

Arguments

chr	chromosome name
all_matches	dataframe of SNP-Peak matches for all chromosomes
mediator.path	path to mediator folder with mediation_chr#_new.RData files

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/gene.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
mediator.path	path to mediator folder with mediation_chr#_new.RData files

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, simulations)
```

Arguments

chr	chromosome name
gene_matches	list of peak-SNP matches for each gene
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

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_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

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
----------------	--

Index

- *Topic **SNP**
 - match_all, [5](#)
 - match_chr, [5](#)
 - *Topic **chromosome**
 - chr_numeric, [2](#)
 - *Topic **column**
 - last_to_first, [4](#)
 - *Topic **data**
 - clean_data, [2](#)
 - data_by_chr, [3](#)
 - data_prep_spc, [3](#)
 - data_prep_spg, [3](#)
 - med.res_spc, [6](#)
 - med.res_spg, [6](#)
 - *Topic **first**
 - last_to_first, [4](#)
 - *Topic **folder**
 - make_folder, [5](#)
 - *Topic **last**
 - last_to_first, [4](#)
 - *Topic **length**
 - lu, [4](#)
 - *Topic **match**
 - match_all, [5](#)
 - match_chr, [5](#)
 - *Topic **mediation**
 - med_all_spc, [7](#)
 - med_chr_spc, [7](#)
 - med_chr_spg, [8](#)
 - med_table_spc, [8](#)
 - med_table_spg, [9](#)
 - *Topic **numeric**
 - chr_numeric, [2](#)
 - *Topic **peak**
 - match_all, [5](#)
 - match_chr, [5](#)
 - *Topic **prep**
 - data_prep_spg, [3](#)
 - med.res_spc, [6](#)
 - *Topic **readcount**
 - transpose_readcount, [9](#)
 - *Topic **table**
 - med_all_spc, [7](#)
 - med_chr_spc, [7](#)
 - med_chr_spg, [8](#)
 - med_table_spc, [8](#)
 - med_table_spg, [9](#)
 - *Topic **transpose**
 - transpose_readcount, [9](#)
 - *Topic **unique**
 - lu, [4](#)
 - *Topic **zero**
 - sum_zero, [9](#)
- chr_numeric, [2](#)
- clean_data, [2](#)
- data_by_chr, [3](#)
- data_prep_spc, [3](#)
- data_prep_spg, [3](#)
- GeneticMediation, [4](#)
- GeneticMediation-package
(GeneticMediation), [4](#)
- last_to_first, [4](#)
- lu, [4](#)
- make_folder, [5](#)
- match_all, [5](#)
- match_chr, [5](#)
- med.res_spc, [6](#)
- med.res_spg, [6](#)
- med_all_spc, [7](#)
- med_chr_spc, [7](#)
- med_chr_spg, [8](#)
- med_table_spc, [8](#)
- med_table_spg, [9](#)
- sum_zero, [9](#)
- transpose_readcount, [9](#)