Package 'GeneticMediation'

April 26, 2020

Type Package

Title Genetic Causal Mediation

License GPL-3
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https://github.com/tydarnell/GeneticMediation
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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
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Imports BiocManager, data.table, IRanges, mediation, readr, stats
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R topics documented:
chr_numeric
chr_numeric
clean_data
clean_data data_by_chr data_prep_spc data_prep_spg
clean_data
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clean_data data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all
clean_data data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all match_chr
clean_data . data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all match_chr med.res_spc
clean_data data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all match_chr med.res_spc med.res_spg
clean_data data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all match_chr med.res_spc med_res_spg med_all_spc
clean_data data_by_chr data_prep_spc data_prep_spg GeneticMediation last_to_first lu make_folder match_all match_chr med.res_spc med.res_spg

2 clean_data

med_table_spc .			 														8
med_table_spg .			 														9
sum_zero			 														9
transpose_readcou	ınt																9

Index 10

chr_numeric

Chromosome Numeric

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

Clean Data

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 3

data_by_chr	Data by Chromosome	
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Description

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

Usage

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

Arguments

	chrs	Character vec	ctor of chromo	osomes names
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snps SNP information dataframe peaks Peak information dataframe

data_prep_spc SNP-Peak-Clinical Data Prep Helper

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 SNP-Peak-Gene Data Prep Helper

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

4 lu

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

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

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 5

make_folder

Make Folder

Description

Make a folder only if the folder does not already exist

Usage

```
make_folder(path)
```

Arguments

path

path for new folder

match_all

Match 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_chr

Match Chromosome

Description

Match Peaks and SNPs in a chromosome

Usage

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

Arguments

snp.info SNP information peak.info Peak information

6 med.res_spg

med.res_spc SNP-Peak-Clinical Mediation Data Prep

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	SNP-Peak-Gene Mediation Data Prep

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 7

med_all_spc SNP-Peak-Cli	inical Mediation Table
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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 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

8 med_table_spc

med_chr_spg SNP-

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

med_table_spg 9

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

sum_zero Sum Zero

Description

Get names of columns that have a sum of zero

Usage

sum_zero(df)

Arguments

df dataframe

Description

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

Usage

transpose_readcount(readcount.path)

Arguments

 ${\tt readcount.path} \ \ ChIP\text{-}seq\ readcount\ data frame\ file\ path$

Index

Tania CND	
*Topic SNP	med_chr_spc, 7
match_all, 5	med_chr_spg, 8
match_chr, 5	med_table_spc, 8
*Topic chromosome	med_table_spg, 9 *Topic transpose
chr_numeric, 2	transpose_readcount, 9
*Topic column	*Topic unique
last_to_first, 4	1u, 4
*Topic data	*Topic zero
clean_data, 2	sum_zero, 9
data_by_chr, 3	Suiii_Zei 0, 9
data_prep_spc, 3	chr_numeric, 2
data_prep_spg, 3	clean_data, 2
med.res_spc,6	crean_uata, z
med.res_spg, 6	data_by_chr, 3
*Topic first	data_prep_spc, 3
last_to_first, 4	data_prep_spg, 3
*Topic folder	=1 1 = 1 67
make_folder, 5	GeneticMediation, 4
*Topic last	GeneticMediation-package
<pre>last_to_first, 4</pre>	(GeneticMediation), 4
*Topic length	
lu, 4	last_to_first, 4
*Topic match	lu, 4
match_all, 5	mala Caldan 5
match_chr, 5	make_folder, 5
*Topic mediation	match_all, 5
<pre>med_all_spc, 7</pre>	match_chr, 5
<pre>med_chr_spc, 7</pre>	med.res_spc,6
med_chr_spg,8	med.res_spg, 6
<pre>med_table_spc, 8</pre>	med_all_spc,7
<pre>med_table_spg, 9</pre>	med_chr_spc, 7
*Topic numeric	med_chr_spg, 8
chr_numeric, 2	med_table_spc, 8
*Topic peak	med_table_spg, 9
match_all, 5	sum_zero,9
match_chr, 5	3um_221 0, 7
*Topic prep	transpose_readcount, 9
data_prep_spg, 3	, – ,
med.res_spc, 6	
*Topic readcount	
transpose_readcount, 9	
*Topic table	
med_all_spc, 7	
= = 1 /	