

Package: gwasglue2 (via r-universe)

September 23, 2024

Title GWAS summary data sources connected to analytical tools

Version 0.0.0.9000

Description Description: Many tools exist that use GWAS summary data for colocalisation, fine mapping, Mendelian randomization, visualisation, etc. This package is a conduit that connects R packages that can retrieve GWAS summary data to various tools for analysing those data.

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URL <https://github.com/MRCIEU/gwasglue2>

BugReports <https://github.com/MRCIEU/gwasglue2/issues>

Depends methods, R (>= 4.0.0)

Imports dplyr

Suggests covr, digest, GenomicRanges, graphics, IRanges, knitr, rmarkdown, rtracklayer, stats, testthat (>= 3.0.0), TwoSampleMR, utils

VignetteBuilder knitr

Remotes mrcieu/TwoSampleMR

Config/testthat/edition 3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Collate 'constructors.R' 'dataset.R' 'convertTo.R' 'globals.R'
'harmonise.R' 'harmoniseLD_method.R' 'harmonise_ld.R'
'harmonise_method.R' 'liftover.R' 'meta.R' 'plot.R'
'summaryset.R' 'utils.R' 'wrappers.R'

Repository <https://mrcieu.r-universe.dev>

RemoteUrl <https://github.com/MRCIEU/gwasglue2>

RemoteRef HEAD

RemoteSha c93b3a1fca7d2eae5d40bd62117091b1ad57f0fa

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addToMetadata *Add to metadata in the SummarySet*

Description

Add to metadata in the SummarySet

Usage

```
addToMetadata(
  summary_set,
  id = getMetadata(summary_set)$id,
  sample_size = getMetadata(summary_set)$sample_size,
  nsnp = getMetadata(summary_set)$nsnp,
  trait = getMetadata(summary_set)$trait,
  sd = getMetadata(summary_set)$sd,
  unit = getMetadata(summary_set)$unit,
  ncontrol = getMetadata(summary_set)$ncontrol,
  build = getMetadata(summary_set)$build,
  population = getMetadata(summary_set)$population,
  ncase = getMetadata(summary_set)$ncase
)
```

```
## S4 method for signature 'SummarySet'
addToMetadata(
  summary_set,
  id = getMetadata(summary_set)$id,
  sample_size = getMetadata(summary_set)$sample_size,
  nsnp = getMetadata(summary_set)$nsnp,
  trait = getMetadata(summary_set)$trait,
  sd = getMetadata(summary_set)$sd,
  unit = getMetadata(summary_set)$unit,
  ncontrol = getMetadata(summary_set)$ncontrol,
  build = getMetadata(summary_set)$build,
  population = getMetadata(summary_set)$population,
  ncase = getMetadata(summary_set)$ncase
)
```

Arguments

- `summary_set` A gwasglue2 SummarySet object.
- `id` GWAS study ID.
- `sample_size` Sample size.

n SNP	Number of variants in the study.
trait	Phenotype name corresponding the the variant.
sd	Trait standard deviation.
unit	Unit.
n control	Number of controls in study.
build	genome build version.
population	Study sample population.
n case	Number of cases in study.

Value

gwasglue2 SummarySet object with metadata stored.

add_summaryset	<i>Add a SummarySet to a DataSet</i>
----------------	--------------------------------------

Description

Add a SummarySet to a DataSet

Usage

```
add_summaryset(
  summary_sets,
  dataset,
  harmonise = TRUE,
  tolerance = 0.08,
  action = 1
)
```

Arguments

summary_sets	one or more gwasglue2 Summarysets objects to add to an existent DataSet object. If more than one it should be a list
dataset	The gwasglue2 DataSet object to add to
harmonise	logical (default TRUE). It harmonises the summary sets in the DataSet against each other.
tolerance	Inherited from harmoniseData() (default 0.08)
action	Inherited from harmoniseData() (Default 1) <ul style="list-style-type: none"> • action = 1: Assume all alleles are coded on the forward strand, i.e. do not attempt to flip alleles • action = 2: Try to infer positive strand alleles, using allele frequencies for palindromes (default, conservative); • action = 3: Correct strand for non-palindromic SNPs, and drop all palindromic SNPs from the analysis (more conservative).

Value

A harmonised gwasglue2 DataSet object with input SummarySets added

assertSameShape	<i>Assert if the shapes of SummarySets in the gwasglue2 DataSet are the same</i>
-----------------	--

Description

Assert if the shapes of SummarySets in the gwasglue2 DataSet are the same

Usage

```
assertSameShape(dataset)
```

```
## S4 method for signature 'DataSet'
assertSameShape(dataset)
```

Arguments

dataset A gwasglue2 DataSet object.

Value

logical TRUE/FALSE

convertForTwoSampleMR	<i>Convert tool to TwoSampleMR format</i>
-----------------------	---

Description

Converts SummarySets within a Dataset to a format that can be read by TwoSampleMR

Usage

```
convertForTwoSampleMR(dataset)
```

```
## S4 method for signature 'DataSet'
convertForTwoSampleMR(dataset)
```

Arguments

dataset The gwasglue2 DataSet object

Value

The gwasglue2 SummarySet object converted to TwoSampleMR format

create_dataset	<i>Creates a DataSet object using gwasglue2 SummarySet objects, and harmonise data against data</i>
----------------	---

Description

Creates a DataSet object using gwasglue2 SummarySet objects, and harmonise data against data

Usage

```
create_dataset(
  summary_sets = list(),
  harmonise = TRUE,
  tolerance = 0.08,
  action = 1
)
```

Arguments

summary_sets	A list of gwasglue2 SummarySet objects
harmonise	logical (default TRUE). It harmonises the summary sets in the DataSet against each other.
tolerance	Inherited from harmoniseData() (default 0.08)
action	Inherited from harmoniseData() (Default 1) <ul style="list-style-type: none"> • action = 1: Assume all alleles are coded on the forward strand, i.e. do not attempt to flip alleles • action = 2: Try to infer positive strand alleles, using allele frequencies for palindromes (default, conservative); • action = 3: Correct strand for non-palindromic SNPs, and drop all palindromic SNPs from the analysis (more conservative).

Value

A harmonised gwasglue2 DataSet object

create_dataset_from_tibble	<i>Creates a DataSet object using GWAS summary statistics, and harmonise data against data</i>
----------------------------	--

Description

Creates a DataSet object using GWAS summary statistics, and harmonise data against data

Usage

```

create_dataset_from_tibble(
  data = list(),
  metadata = NULL,
  harmonise = TRUE,
  tolerance = 0.08,
  action = 1,
  beta_col = "beta",
  se_col = "se",
  samplesize_col = "n",
  pvalue_col = "p",
  chr_col = "chr",
  position_col = "position",
  rsid_col = "rsid",
  effect_allele_col = "ea",
  other_allele_col = "nea",
  eaf_col = "eaf",
  id_col = "id",
  trait_col = "trait",
  ...
)

```

Arguments

data	A list of GWAS summary data (tibbles)
metadata	A list with metadata information. If NULL, it creates metadata with information retrieved from the dataset.
harmonise	logical (default TRUE). It harmonises the summary sets in the DataSet against each other.
tolerance	Inherited from harmoniseData() (default 0.08)
action	Inherited from harmoniseData() (Default 1) <ul style="list-style-type: none"> • action = 1: Assume all alleles are coded on the forward strand, i.e. do not attempt to flip alleles • action = 2: Try to infer positive strand alleles, using allele frequencies for palindromes (default, conservative); • action = 3: Correct strand for non-palindromic SNPs, and drop all palindromic SNPs from the analysis (more conservative).
beta_col	Name of column with effect sizes. The default is "beta".
se_col	Name of column with standard errors. The default is "se".
samplesize_col	Column name for sample size. The default is "n".
pvalue_col	Name of column with p-value. The default is "p".
chr_col	Column name for chromosome . The default is "chr".
position_col	Column name for the position. Together, with @param chr gives the physical coordinates of the variant. The default is "position".

rsid_col	Required name of column with variants rs IDs. The default is "rsid".
effect_allele_col	Name of column with effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "ea".
other_allele_col	Name of column with non effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "nea".
eaf_col	Name of column with effect allele frequency. The default is "eaf".
id_col	The default is "id".
trait_col	Column name for the column with phenotype name corresponding the the variant. The default is "trait"
...	Other columns

Value

A harmonised gwasglue2 DataSet object

See Also

[create_metadata\(\)](#) to create a metadata object

create_metadata	<i>Metadata object</i>
-----------------	------------------------

Description

Reads metadata and converts it to gwasglue2 format.

Usage

```
create_metadata(
  metadata = NULL,
  id = NA,
  sample_size = NA,
  nsnp = NA,
  trait = NA,
  sd = NA,
  unit = NA,
  ncontrol = NA,
  build = NA,
  population = NA,
  ncase = NA,
  ...
)
```


Arguments

metadata	A dataframe with metadata information. Not required.
id	GWAS study ID.
sample_size	Sample size.
nsnp	Number of variants in the study.
trait	Phenotype name corresponding the the variant.
sd	Trait standard deviation.
unit	Unit
ncontrol	Nb of controls in study
build	genome build version.
population	Study sample population.
ncase	Number of cases in study.
...	Other metadata information

Value

A metadata list.

create_summaryset	<i>A function to create a gwasglue2 SummarySet object from different sources and formats</i>
-------------------	--

Description

A function to create a gwasglue2 SummarySet object from different sources and formats

Usage

```
create_summaryset(
  data,
  metadata = NULL,
  type = "tibble",
  qc = FALSE,
  beta_col = NULL,
  se_col = NULL,
  samplesize_col = NULL,
  pvalue_col = NULL,
  logpvalue_col = NULL,
  chr_col = NULL,
  position_col = NULL,
  rsid_col = NULL,
  effect_allele_col = NULL,
  other_allele_col = NULL,
```

```

    eaf_col = NULL,
    id_col = NULL,
    trait_col = NULL,
    build = NULL
  )

```

Arguments

data	GWAS summary statistics.
metadata	A list with metadata information. If NULL, it creates metadata with information retrieved from the dataset
type	Input @param data type. Default is "tibble". Other options: "vcf"
qc	Quality control. It checks the @param data and look for problems that can stop gwasglue2 from running. If TRUE gwasglue will try to solve the problems. Default is FALSE
beta_col	Name of column with effect sizes. The default is "beta" for @param type "tibble" and "ES" for @param type "vcf" ..
se_col	Name of column with standard errors. The default is "se" for @param type "tibble" and "SE" for @param type "vcf".
samplesize_col	Column name for sample size. The default is "n" for @param type "tibble" and "SS" for @param type "vcf".
pvalue_col	Name of column with p-value. The default is "p".
logpvalue_col	Name of column with log(p-value). The default is "LP" for @param type "vcf".
chr_col	Column name for chromosome . The default is "chr" for @param type "tibble" and "seqnames" for @param type "vcf".
position_col	Column name for the position. Together, with @param chr gives the physical coordinates of the variant. The default is "position" for @param type "tibble" and "start" for @param type "vcf".
rsid_col	Required name of column with variants rs IDs. The default is "rsid" for @param type "tibble" and "ID" for @param type "vcf".
effect_allele_col	Name of column with effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "ea" for @param type "tibble" and "ALT" for @param type "vcf".
other_allele_col	Name of column with non effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "nea" for @param type "tibble" and "REF" for @param type "vcf".
eaf_col	Name of column with effect allele frequency. The default is "eaf" for @param type "tibble" and "AF" for @param type "vcf".
id_col	GWAS study ID column. The default is "id".
trait_col	Column name for the column with phenotype name corresponding the the variant. The default is "trait"
build	Reference genome assembly to generate the genomic data. Default is NULL. <ul style="list-style-type: none"> Options are "NCBI34", "NCBI35", "NCBI36", "GRCh37" or "GRCh38".

Value

A gwasglue2 SummarySet object

See Also

[create_metadata\(\)](#) to create a metadata object

create_summaryset_from_gwasvcf

A function to create a gwasglue2 SummarySet object from a vcf file

Description

A function to create a gwasglue2 SummarySet object from a vcf file

Usage

```
create_summaryset_from_gwasvcf(
  data,
  metadata = NULL,
  qc = FALSE,
  beta_col = "ES",
  se_col = "SE",
  samplesize_col = "SS",
  logpvalue_col = "LP",
  pvalue_col = "p",
  chr_col = "seqnames",
  position_col = "start",
  rsid_col = "ID",
  effect_allele_col = "ALT",
  other_allele_col = "REF",
  eaf_col = "AF",
  id_col = "id",
  build = NULL
)
```

Arguments

data	GWAS summary statistics. In the GWAS vcf dataframe format
metadata	A list with metadata information. If NULL, it creates metadata with information retrieved from the dataset
qc	Quality control. It checks the @param data and look for problems that can stop gwasglue2 from running. If TRUE gwasglue will try to solve the problems. Default is FALSE
beta_col	Name of column with effect sizes. The default is "ES".
se_col	Name of column with standard errors. The default is "SE".

samplesize_col	Column name for sample size. The default is "SS".
logpvalue_col	Name of column with log(p-value). The default is "LP".
pvalue_col	Name of column with p-value. The default is "p".
chr_col	Column name for chromosome . The default is "seqnames".
position_col	Column name for the position. Together, with @param chr gives the physical coordinates of the variant. The default is "start".
rsid_col	Required name of column with variants rs IDs. The default is "ID".
effect_allele_col	Name of column with effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "ALT".
other_allele_col	Name of column with non effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "REF".
eaf_col	Name of column with effect allele frequency. The default is "AF".
id_col	GWAS study ID column. The default is "id".
build	Reference genome assembly to generate the vcf file. Default is NULL. <ul style="list-style-type: none"> Options are "NCBI34", "NCBI35", "NCBI36", "GRCh37" or "GRCh38".

Value

A gwasglue2 SummarySet object

See Also

[create_metadata\(\)](#) to create a metadata object

create_summaryset_from_tibble

A function to create a gwasglue2 SummarySet object from a tibble

Description

A function to create a gwasglue2 SummarySet object from a tibble

Usage

```
create_summaryset_from_tibble(
  data = tibble(),
  metadata = NULL,
  qc = FALSE,
  beta_col = "beta",
  se_col = "se",
  samplesize_col = "n",
  pvalue_col = "p",
```

```

chr_col = "chr",
position_col = "position",
rsid_col = "rsid",
effect_allele_col = "ea",
other_allele_col = "nea",
eaf_col = "eaf",
id_col = "id",
trait_col = "trait",
build = NULL
)

```

Arguments

data	GWAS summary statistics. A tibble
metadata	A list with metadata information. If NULL, it creates metadata with information retrieved from the dataset
qc	Quality control. It checks the @param data and look for problems that can stop gwasglue2 from runing. If TRUE gwasglue will try to solve the problems. Default is FALSE
beta_col	Name of column with effect sizes. The default is "beta" for @param type "tibble" and "ES"for @param type "vcf"..
se_col	Name of column with standard errors. The default is "se" for @param type "tibble" and "SE"for @param type "vcf".
samplesize_col	Column name for sample size. The default is "n" for @param type "tibble" and "SS"for @param type "vcf".
pvalue_col	Name of column with p-value. The default is "p".
chr_col	Column name for chromosome . The default is "chr" for @param type "tibble" and "seqnames"for @param type "vcf".
position_col	Column name for the position. Together, with @param chr gives the physical coordinates of the variant. The default is "position" for @param type "tibble" and "start"for @param type "vcf".
rsid_col	Required name of column with variants rs IDs. The default is "rsid" for @param type "tibble" and "ID"for @param type "vcf".
effect_allele_col	Name of column with effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "ea" for @param type "tibble" and "ALT"for @param type "vcf".
other_allele_col	Name of column with non effect allele. Must contain only the characters "A", "C", "T" or "G". The default is "nea for @param type "tibble" and "REF"for @param type "vcf".
eaf_col	Name of column with effect allele frequency. The default is "eaf" for @param type "tibble" and "AF"for @param type "vcf".
id_col	GWAS study ID column. The default is "id".

trait_col	Column name for the column with phenotype name corresponding the the variant. The default is "trait"
build	Reference genome assembly to generate the genomic data. Default is NULL. <ul style="list-style-type: none"> Options are "NCBI34", "NCBI35", "NCBI36", "GRCh37" or "GRCh38".

Value

A gwasglue2 SummarySet object

See Also

[create_metadata\(\)](#) to create a metadata object

create_summary_set_from_lbf

Create SummarySet from log Bayes Factor

Description

Create SummarySet from log Bayes Factor

Usage

```
create_summary_set_from_lbf(summaryset, lbf, L)
```

Arguments

summaryset	gwasglue2 SummarySet object
lbf	p-vector of log Bayes Factors for each SNP
L	credible set index number

Value

marginalised summaryset (beta, se and trait id)

DataSet-class	<i>An S4 class to represent the Data Set</i>
---------------	--

Description

An S4 class to represent the Data Set

DataSet function

Usage

DataSet(...)

Arguments

... Array of gwasglue2 SummarySet object names.

Value

A gwasglue2 DataSet object

Slots

summary_sets A list of SummarySet objects (default NA).

overlap_variants among all SummarySets

is_resized logical (default FALSE).

is_harmonised logical (default FALSE).

overall_dropped_SNPs A vector of RSIDs that were removed from the summary_sets.

dropped_SNPs A list of pairwise harmonising output (SNPs removed from the summary_sets)

palindromic_SNPs A list of pairwise harmonising output.

ambiguous_SNPs A list of pairwise harmonising output.

incompatible_alleles_SNPs A list of pairwise harmonising output.

ld_matrix LD matrix from reference population

is_harmonisedLD logical (default FALSE).

zscores vector of calculated z-scores

susie_marginalised logical (default FALSE).

susieR susieR::susie_rss() output

is_converted logical (default FALSE).

describe A description of the DataSet (default NA).

trait_organisation A list with the trait organization within the DataSet (default NA).

dataset_to_hyprcoloc *DataSet to hyprcoloc*

Description

dataset_to_hyprcoloc is a wrapper function used inside ritarasteiro/hyprcoloc::hyprcoloc() to read DataSet objects

Usage

```
dataset_to_hyprcoloc(dataset)
```

Arguments

dataset gwasglue2 DataSet object

Value

parameters needed to run hyprcoloc

dimData *Dimensions of the GWAS Summary Statistics data*

Description

Dimensions of the GWAS Summary Statistics data

Usage

```
dimData(summary_set)
```

```
## S4 method for signature 'SummarySet'  
dimData(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object

Value

The dimensions of the GWAS Summary Statistics data

download_chainfile *Chain files downloader*

Description

Human genome chain files are download from UCSC

Usage

```
download_chainfile(from = "GRCh37", to = "GRCh38")
```

Arguments

from	genome assembly to which GWAS summary data is currently mapped. Default "GRCh37".
	<ul style="list-style-type: none"> • Other options: "NCBI34", "NCBI35", "NCBI36" and "GRCh38"
to	genome assembly to which should be mapped. Default "GRCh38"
	<ul style="list-style-type: none"> • Other options: "NCBI34", "NCBI35", "NCBI36" and "GRCh37"

Value

A chain file

getAttributes *Get Method to retrieve the attributes linked to the SummarySet*

Description

Get Method to retrieve the attributes linked to the SummarySet

Usage

```
getAttributes(summary_set)

## S4 method for signature 'SummarySet'
getAttributes(summary_set)
```

Arguments

summary_set	A gwasglue2 SummarySet object
-------------	-------------------------------

Value

The attributes associated with the SummarySet

getData	<i>Get Method to retrieve the GWAS Summary Statistics</i>
---------	---

Description

Get Method to retrieve the GWAS Summary Statistics

Usage

```
getData(dataset, index)

## S4 method for signature 'DataSet'
getData(dataset, index)
```

Arguments

dataset	A gwasglue2 DataSet object
index	Index of gwasglue2 SummarySet objects within DataSet

Value

A tibble with GWAS summary statistics

See Also

Similar to [getSummaryData\(\)](#)

getLDMatrix	<i>Get Method to retrieve the Linkage Disequilibrium matrix</i>
-------------	---

Description

Get Method to retrieve the Linkage Disequilibrium matrix

Usage

```
getLDMatrix(dataset)

## S4 method for signature 'DataSet'
getLDMatrix(dataset)
```

Arguments

dataset	A gwasglue2 DataSet object
---------	----------------------------

Value

The LD matrix

getLength	<i>Size of the DataSet</i>
-----------	----------------------------

Description

Size of the DataSet

Usage

```
getLength(dataset)
```

```
## S4 method for signature 'DataSet'  
getLength(dataset)
```

Arguments

dataset A gwasglue2 DataSet objec

Value

Number of gwasglue2 SummarySet objects within the DataSet

getMetadata	<i>Get Method to retrieve the metadata stored in the SummarySet</i>
-------------	---

Description

Get Method to retrieve the metadata stored in the SummarySet

Usage

```
getMetadata(summary_set)
```

```
## S4 method for signature 'SummarySet'  
getMetadata(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object.

Value

The gwasglue2 SummarySet metadata.

getRSID	<i>Get Method to retrieve RSID/variants stored in the SummarySet</i>
---------	--

Description

Get Method to retrieve RSID/variants stored in the SummarySet

Usage

```
getRSID(summary_set)
```

```
## S4 method for signature 'SummarySet'  
getRSID(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object

Value

The RSID/variants

See Also

Similar to [getVariants\(\)](#)

getShape	<i>Get the Shape of the gwasglue2 objects</i>
----------	---

Description

Get the Shape of the gwasglue2 objects

Usage

```
getShape(object)
```

```
## S4 method for signature 'SummarySet'  
getShape(object)
```

Arguments

object A gwasglue2 SummarySet or DataSet object.

Value

The shape of the gwasglue2 object

getSummaryData	<i>Get Method to retrieve the GWAS Summary Statistics from the SummarySet</i>
----------------	---

Description

Get Method to retrieve the GWAS Summary Statistics from the SummarySet

Usage

```
getSummaryData(summary_set)

## S4 method for signature 'SummarySet'
getSummaryData(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object.

Value

A tibble with GWAS summary statistics

getSummarySet	<i>Get Method to retrieve the gwasglue2 SummarySet object</i>
---------------	---

Description

Get Method to retrieve the gwasglue2 SummarySet object

Usage

```
getSummarySet(dataset, index)

## S4 method for signature 'DataSet'
getSummarySet(dataset, index)
```

Arguments

dataset A gwasglue2 DataSet object
index Index of gwasglue2 SummarySet objects within DataSet

Value

summarySet gwasglue2 SummarySet object

getTraitOrg	<i>Get the trait organisation of the gwasglue2 DataSet</i>
-------------	--

Description

Get the trait organisation of the gwasglue2 DataSet

Usage

```
getTraitOrg(dataset)
```

```
## S4 method for signature 'DataSet'  
getTraitOrg(dataset)
```

Arguments

dataset A gwasglue2 DataSet object.

Value

The trait organisation of the gwasglue2 object

getVariants	<i>Get Method to retrieve RSID/variants stored in the SummarySet</i>
-------------	--

Description

Get Method to retrieve RSID/variants stored in the SummarySet

Usage

```
getVariants(summary_set)
```

```
## S4 method for signature 'SummarySet'  
getVariants(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object

Value

The RSID/variants

See Also

Similar to [getRSID\(\)](#)

harmoniseData	<i>Harmonise the alleles and effects between two summary sets</i>
---------------	---

Description

Harmonise the alleles and effects between two summary sets

Usage

```
harmoniseData(dataset, tolerance, action)

## S4 method for signature 'DataSet'
harmoniseData(dataset, tolerance, action)
```

Arguments

dataset	The gwasglue2 DataSet object
tolerance	Tolerance value.
action	Level of strictness in dealing with SNPs. <ul style="list-style-type: none">• action = 1: Assume all alleles are coded on the forward strand, i.e. do not attempt to flip alleles• action = 2: Try to infer positive strand alleles, using allele frequencies for palindromes (default, conservative);• action = 3: Correct strand for non-palindromic SNPs, and drop all palindromic SNPs from the analysis (more conservative).

Value

The gwasglue2 DataSet object harmonised

harmonise_ld	<i>Harmonise data against LD matrix</i>
--------------	---

Description

Function to create a LDmatrix gwasglue2 object and set the @slot ld_matrix u

Usage

```
harmonise_ld(dataset, bfile = NULL, plink_bin = NULL)
```

Arguments

dataset	The DataSet gwasglue2 object
bfile	It corresponds to the path and prefix of the plink files used to build the LD correlation matrix.
plink_bin	Path to the plink executable

Value

The DataSet gwasglue2 object harmonised

harmonise_ld_dat	<i>Harmonise LD matrix against summary data (now it just looks for overlaped variants. The harmonisation is done in ld_matrix_local) harmonise_ld_dat() is based TwoSampleMR::harmonise_ld_dat()</i>
------------------	--

Description

Harmonise LD matrix against summary data (now it just looks for overlaped variants. The harmonisation is done in ld_matrix_local) harmonise_ld_dat() is based TwoSampleMR::harmonise_ld_dat()

Usage

```
harmonise_ld_dat(x, ld)
```

Arguments

x	harmonised dataset
ld	Output from ld_matrix

Value

List of dataset and harmonised LD matrix

isHarmonised	<i>Check if the DataSet is harmonised</i>
--------------	---

Description

Check if the DataSet is harmonised

Usage

```
isHarmonised(dataset)
```

```
## S4 method for signature 'DataSet'
isHarmonised(dataset)
```


Arguments

dataset A gwasglue2 DataSet object

Value

TRUE/FALSE

isHarmonisedLD *Check if the DataSet is harmonised against LD matrix*

Description

Check if the DataSet is harmonised against LD matrix

Usage

```
isHarmonisedLD(dataset)

## S4 method for signature 'DataSet'
isHarmonisedLD(dataset)
```

Arguments

dataset A gwasglue2 DataSet object

Value

TRUE/FALSE

lbf_to_z_cont *Convert log Bayes Factor to summary stats*

Description

Convert log Bayes Factor to summary stats

Usage

```
lbf_to_z_cont(lbf, n, af, prior_v = 50)
```

Arguments

lbf p-vector of log Bayes Factors for each SNP
n Overall sample size
af p-vector of allele frequencies for each SNP
prior_v Variance of prior distribution. SuSiE uses 50

Value

tibble with lbf, af, beta, se, z

ld_matrix_local	<i>modified from ieugwasr::ld_matrix_local () Get LD matrix using local plink binary and reference dataset</i>
-----------------	--

Description

modified from ieugwasr::ld_matrix_local () Get LD matrix using local plink binary and reference dataset

Usage

```
ld_matrix_local(variants, bfile, plink_bin)
```

Arguments

variants	List of variants (in plink 'set range' format).
bfile	Path to bed/bim/fam ld reference panel
plink_bin	Specify path to plink binary. Default = NULL.

Value

data frame

liftover	<i>Remap genomic coordinates to a different genome assembly</i>
----------	---

Description

Converts SummarySet GWAS summary data to a different genome assembly. Human genome chain files are download from ENSEMBL

Usage

```
liftover(summaryset, chainfile = NULL, to = "GRCh38")
```

Arguments

summaryset	A gwasglue2 SummarySet object
chainfile	The chainfile used to remap the genomic coordinates. If NULL a chainfile is downloaded using the to and the summarysetmetadata to check the genome assembly to which GWAS summary data is currently mapped.
to	genome assembly to which should be mapped. Default "GRCh38" <ul style="list-style-type: none"> • Other options: "NCBI34", "NCBI35", "NCBI36", GRCh37" and "GRCh38"

Value

A gwasglue2 SummarySet object with GWAS summary data genomic coordinates remapped.

See Also

[create_metadata\(\)](#) and [addToMetadata\(\)](#) on how to create or add to metadata. Note that if using `chainfile` the analyses are not restricted to Human GWAS.

merge_datasets	<i>Merge Datasets</i>
----------------	-----------------------

Description

Merge Datasets

Usage

```
merge_datasets(datasets)
```

Arguments

datasets A list of gwasglue2 DataSet objects

Value

A gwasglue2 DataSet object with input DataSets merged

meta_analysis	<i>Meta analysis</i>
---------------	----------------------

Description

Statistical combination of the results from two or more separate studies. It uses the fixed-effect model assuming that one true effect size underlies all the studies in the meta-analysis.

Usage

```
meta_analysis(dataset, method = "fixed")
```

Arguments

dataset gwasglue2 DataSet object
method Uses fixed-effect model. Default ("fixed")

Value

gwasglue2 SummarySet object

See Also

[create_metadata\(\)](#) and [addToMetadata\(\)](#) on how to create or add to metadata.

overlapVariants	<i>Look for overlapped variants between SummarySets in the DataSet and Resize</i>
-----------------	---

Description

Look for overlapped variants between SummarySets in the DataSet and Resize

Usage

```
overlapVariants(dataset, action)
```

```
## S4 method for signature 'DataSet'
overlapVariants(dataset, action)
```

Arguments

- | | |
|---------|--|
| dataset | The gwasglue2 DataSet object |
| action | Level of strictness in dealing with SNPs during harmonisation. <ul style="list-style-type: none"> • action = 1: Assume all alleles are coded on the forward strand, i.e. do not attempt to flip alleles • action = 2: Try to infer positive strand alleles, using allele frequencies for palindromes (default, conservative); • action = 3: Correct strand for non-palindromic SNPs, and drop all palindromic SNPs from the analysis (more conservative). |

Value

The gwasglue2 DataSet object resized

plot_gwasglue	<i>Plot</i>
---------------	-------------

Description

Plot

Usage

```
plot_gwasglue(dataset, type, title)
```

Arguments

dataset	gwasglue2 DataSet object
type	Type of plot (Only available "manhattan" plots at the moment)
title	Main title for the plot

Value

A plot

setAttributes	<i>Set Method to store the attributes of the SummarySet</i>
---------------	---

Description

Set Method to store the attributes of the SummarySet

Usage

```
setAttributes(summary_set, mr_label = NULL, ...)
```

```
## S4 method for signature 'SummarySet'
setAttributes(summary_set, mr_label = NULL, ...)
```

Arguments

summary_set	A gwasglue2 SummarySet object
mr_label	It can be either "exposure" or "outcome". Default NULL.
...	Other attributes information

Value

The gwasglue2 SummarySet object with the attributes stored

setMetadata	<i>Set Method to add metadata to the SummarySet</i>
-------------	---

Description

Set Method to add metadata to the SummarySet

Usage

```
setMetadata(summary_set, metadata)
```

```
## S4 method for signature 'SummarySet'  
setMetadata(summary_set, metadata)
```

Arguments

summary_set	A gwasglue2 SummarySet object.
metadata	A list with metadata information.

Value

gwasglue2 SummarySet object with metadata stored.

setRSID	<i>Set Method to store RSID/variants in the SummarySet</i>
---------	--

Description

Set Method to store RSID/variants in the SummarySet

Usage

```
setRSID(summary_set, variants)
```

```
## S4 method for signature 'SummarySet'  
setRSID(summary_set, variants)
```

Arguments

summary_set	A gwasglue2 SummarySet object
variants	The RSID/variants associated with the GWAS summary statistics

Value

The gwasglue2 SummarySet object with RSID/variants stored

See Also

Similar to [setVariants\(\)](#)

setShape	<i>Set the Shape of the gwasglue2 objects</i>
----------	---

Description

Set the Shape of the gwasglue2 objects

Usage

```
setShape(object, shape)
```

```
## S4 method for signature 'SummarySet'
setShape(object, shape)
```

Arguments

object	A gwasglue2 SummarySet or DataSet object
shape	The shape of the GWAS data

Value

The gwasglue2 object with the shape stored

setTraitOrg	<i>Set the trait organisation of the gwasglue2 DataSet</i>
-------------	--

Description

Set the trait organisation of the gwasglue2 DataSet

Usage

```
setTraitOrg(dataset, ...)
```

```
## S4 method for signature 'DataSet'
setTraitOrg(dataset, ...)
```

Arguments

dataset	A gwasglue2 DataSet object
...	The organisation of the DataSet

Value

The gwasglue2 object with the trait organisation stored

setVariantid	<i>Set Method to create an internal Variant ID for the SummarySet</i>
--------------	---

Description

Set Method to create an internal Variant ID for the SummarySet

Usage

```
setVariantid(summary_set)

## S4 method for signature 'SummarySet'
setVariantid(summary_set)
```

Arguments

summary_set A gwasglue2 SummarySet object

Value

A extra "variantid" column in the GWAS summary statistics tibble. The [getSummaryData\(\)](#) can be used to retrieve it.

setVariants	<i>Set Method to store RSID/variants in the SummarySet</i>
-------------	--

Description

Set Method to store RSID/variants in the SummarySet

Usage

```
setVariants(summary_set, variants)

## S4 method for signature 'SummarySet'
setVariants(summary_set, variants)
```

Arguments

summary_set A gwasglue2 SummarySet object
 variants The RSID/variants associated with the GWAS summary statistics

Value

The gwasglue2 SummarySet object with RSID/variants stored

See Also

Similar to [setRSID\(\)](#)

setZscores	<i>Calculating Z-scores</i>
------------	-----------------------------

Description

Calculating Z-scores

Usage

```
setZscores(dataset)

## S4 method for signature 'DataSet'
setZscores(dataset)
```

Arguments

dataset A gwasglue2 DataSet object

Value

An extra "zscores" column in the GWAS summary statistics tibble.

SummarySet-class	<i>An S4 class to represent the Summary Set</i>
------------------	---

Description

An S4 class to represent the Summary Set

Slots

ss A tibble with the GWAS summary statistics (default NA).
 metadata A list with the metadata associated to ss (default NA).
 variants The RSID/variants associated with ss (default NA).
 attributes Attributes of the SummarySet. Eg. MR label Exposure/Outcome (default NA).
 shape The shape of the SummarySet (default NA).
 shape The shape of the SummarySet (default NA).

- "single": single region
- "multiple": multiple regions
- "independent": independent/scattered variants
- "pruned": genome wide - pruned
- "full": genome wide - full

susie_to_dataset *SusieR to DataSet*

Description

#' susie_to_dataset is a wrapper function used inside ritarseiro/susieR::susie_rss() to create a marginalised DataSet object Converts ABFs to summary statistics and creates a new SummarySet for each credible set. Returns object is a gwasglue2 DataSet class object.

Usage

```
susie_to_dataset(summaryset, s, R)
```

Arguments

summaryset	gwasglue2 SummarySet object
s	susieR object
R	ID matrix

Value

DataSet object

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