Package 'PanViz'

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Type Package

Title Integrating Multi-Omic Network Data With Summay-Level GWAS Data

Version 1.6.0

Description
This pacakge integrates data from the Kyoto Encyclopedia of Genes and Genomes (KEGG) with summary-level genome-wide association (GWAS) data, such as that provided by the GWAS Catalog or GWAS Central databases, or a user's own study or dataset, in order to produce biological networks, termed IMONs (Integrated Multi-Omic Networks). IMONs can be used to analyse trait-specific polymorphic data within the context of biochemical and metabolic reaction networks, providing greater biological interpretability for GWAS data.

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Encoding UTF-8

LazyData false

RoxygenNote 7.1.2

BugReports https://github.com/LucaAnholt/PanViz/issues

URL https://github.com/LucaAnholt/PanViz

Imports tidyr, stringr, dplyr, tibble, magrittr, futile.logger, utils, easycsv, rentrez, igraph, RColorBrewer, data.table, colorspace, grDevices, rlang, methods

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Contents

`adjl_to_G` *adj_to_G*

Description

Internal function that constructs an IMON (Integrated Multi-Omic Network) for an inputted adjacency list containing adjacency information between KEGG genes and queried SNPs.

Usage

```
adjl_to_G(adjl_G_S)
```

Arguments

adjl_G_S	- adjacency list containing relevant adjacencies between inputted SNPs and genes from KEGG

Value

igraph object representing total IMON for inputted SNPs

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adjl_to_G_grouped *adjl_to_G_grouped*

Description

Internal function that constructs either a variable-coloured or uncoloured IMON (Integrated Multi-Omic Network) for an inputted adjacency list containing adjacency information between KEGG genes and queried SNPs.

Usage

```
adjl_to_G_grouped(
  adjl_G_S,
  unique_group_names,
  unique_group_cols,
  group_snps,
  colour_groups,
  ego,
  progress_bar
)
```

Arguments

adjl_G_S	- adjacency list containing relevant adjacencies between inputted SNPs and genes from KEGG
unique_group_names	- a list of the unique group/variable names in the provided GWAS Catalog association file
unique_group_cols	- a list of unique colours for each unique group/variable in the provided GWAS Catalog association file
group_snps	- a recursive list containing the lists of SNPs belonging to each unique group/variable in the provided GWAS Catalog association file
colour_groups	- boolean: whether or not user has chosen to colour the network by the unique group/variables in the provided GWAS Catalog association file
ego	- the egocentric order (centred around the SNPs in the network) in which to build the network i.e. pathlength from SNPs downwards towards the metabolome
progress_bar	- boolean: whether or not user has decided to have a progress bar print to the console

Value

- an igraph object containing the IMON

`adj_list_to_igraph` *adj_list_to_igraph*

Description

internal function that assembles all the KEGG data into a network/graph

Usage

```
adj_list_to_igraph(adjl_G_S)
```

Arguments

`adjl_G_S`	adjacency list containing relevant adjacent SNPs/KEGG genes

Value

an igraph object, containing a network representing all the KEGG data

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`colour_IMON` *colour network by categorical group levels*

Description

colour network by categorical group levels

Usage

```
colour_IMON(G, progress_bar)
```

Arguments

`G`	- igraph object containing uncoloured IMON
`progress_bar`	Boolean (default = TRUE) argument that controls whether or not a progress bar for calculations/KEGGREST API GET requests should be printed to the console

Value

- igraph object containing coloured IMON

dbSNP_query_check *dbSNP_query_check*

Description

dbSNP_query_check

Usage

```
dbSNP_query_check(query)
```

Arguments

query	- raw query data from NCBI dbSNP API

Value

- vector containing either 0 (denoting successful query) or NA (unsuccessful query)

dbSNP_query_clean *dbSNP query clean up function*

Description

Internal function clean up raw SNP data queried from NCBI dbSNP via Entrez API depending on whether or not it could be successfully queried

Usage

```
dbSNP_query_clean(query)
```

Arguments

query	- raw dbSNP query object

Value

- dataframe of separate chromosome number, position and ID

decompose_IMON *decompose_IMON*

Description

This function returns a list of fully connected IMONs from a single parent unconnected IMON.

Usage

```
decompose_IMON(G)
```

Arguments

G	- igraph object containing non-fully connected IMON

Value

- list of igraph objects, where each index contains a fully connected IMON

Examples

```
data("er_snp_vector")
G <- PanViz::get_IMON(snp_list = er_snp_vector, ego = 5, save_file = FALSE)
G_list <- decompose_IMON(G)
```

ego_IMON *ego_IMON*

Description

Internal function for trimming IMON to ego-centred (centred around SNPs) to specified order (pathway length from SNPs)

Usage

```
ego_IMON(G, ego)
```

Arguments

G	- igraph object representing IMON
ego	- the selected ego-centred path length

Value

- ego-centred IMON set at desired path length

er_snp_vector *Summary-level GWAS data vector for estrogen-receptor positive breast cancer (EFO_1000649)*

Description

A dataset containing a vector of SNPs (summary-level GWAS data) associated with estrogen-receptor positive breast cancer (EFO_1000649), collated by the GWAS Catalog.

Usage

```
data(er_snp_vector)
```

Format

A vector with 110 elements

get_grouped_IMON *get IMON with SNP and or all network vertices coloured by group variables (either studies or phenotypes)*

Description

This function constructs an IMON (Integrated Multi-Omic Network) with SNPs/or whole network coloured by selected categorical levels (either studies or phenotypes)

Usage

```
get_grouped_IMON(
  dataframe,
  groupby = c("studies", "traits"),
  ego = 5,
  save_file = c(FALSE, TRUE),
  export_type = c("igraph", "edge_list", "graphml", "gml"),
  directory = c("wd", "choose"),
  colour_groups = c(FALSE, TRUE),
  progress_bar = c(TRUE, FALSE)
)
```

Arguments

dataframe	A dataframe including 3 columns in the following order and with the following names: snps, studies, traits (all character vectors)
groupby	Choose whether to group SNP and or network colouring by either studies or traits

ego	This dictates what length order ego-centred network should be constructed. If set to 5 (default and recommended), an IMON with the first layer of the connected metabolome will be returned. If set above 5, the corresponding extra layer of the metabolome will be returned. If set to 0 (not recommended) the fully connected metabolome will be returned. Note, this cannot be set between 0 and 5.
save_file	Boolean (default = FALSE) argument that indicates whether or not the user wants to save the graph as an exported file in their current working directory
export_type	This dictates the network data structure saved in your working directory. By default this outputs an igraph object, however, you can choose to export and save an edge list, graphml or GML file.
directory	If set to "choose" this argument allows the user to interactively select the directory of their choice in which they wish to save the constructed IMON, else the file will be saved to the working directory "wd" by default
colour_groups	Boolean (default = FALSE) chooses whether or not to colour the whole network by grouping variables
progress_bar	Boolean (default = TRUE) argument that controls whether or not a progress bar for calculations/KEGGREST API GET requests should be printed to the console

Value

An igraph object containing the constructed IMON with coloured SNPs/and or whole network by selected grouping variable

Examples

```
##getting GWAS Catalog association tsv file and cleaning up using
##GWAS_catalog_tsv_to_dataframe function:
path <- system.file("extdata",
  "gwas-association-downloaded_2021-09-13-EFO_1000649.tsv",
   package="PanViz")
df <- PanViz::GWAS_data_reader(file = path,
  snp_col = "SNPS",
  study_col = "STUDY",
  trait_col = "DISEASE/TRAIT")
##creating uncoloured IMON:
G <- PanViz::get_grouped_IMON(dataframe = df,
  groupby = "studies",
  ego = 5,
  save_file = FALSE,
  colour_groups = FALSE)
##creating IMON where vertices/edges are coloured by the variable study:
G <- PanViz::get_grouped_IMON(dataframe = df,
  groupby = "studies",
  ego = 5,
  save_file = FALSE,
  colour_groups = TRUE)
```

get_IMON *get_IMON*

Description

Internal function that constructs an IMON (Integrated Multi-Omic Network) for an inputted vector of SNPs and exports an igraph file.

Usage

```
get_IMON(
  snp_list,
  ego = 5,
  save_file = c(FALSE, TRUE),
  export_type = c("igraph", "edge_list", "graphml", "gml"),
  directory = c("wd", "choose"),
  progress_bar = c(TRUE, FALSE)
)
```

Arguments

snp_list	A vector of SNPs (strings/characters) using standard NCBI dbSNP accession number naming convention (e.g. "rs185345278")
ego	This dictates what length order ego-centred network should be constructed. If set to 5 (default and recommended), an IMON with the first layer of the connected metabolome will be returned. If set above 5, the corresponding extra layer of the metabolome will be returned. If set to 0 (not recommended) the fully connected metabolome will be returned. Note, this cannot be set between 0 and 5.
save_file	Boolean (default = FALSE) argument that indicates whether or not the user wants to save the graph as an exported file in their current working directory
export_type	This dictates the network data structure saved in the chosen directory. By default this outputs an igraph object, however, you can choose to export and save an edge list, graphml or GML file.
directory	If set to "choose" this argument allows the user to interactively select the directory of their choice in which they wish to save the constructed IMON, else the file will be saved to the working directory "wd" by default
progress_bar	Boolean (default = TRUE) argument that controls whether or not a progress bar for calculations/KEGGREST API GET requests should be printed to the console

Value

An igraph object containing the constructed IMON

Examples

```
##getting vector of SNPs to query:
data("er_snp_vector")
##build IMON using vector:
G <- PanViz::get_IMON(snp_list = er_snp_vector, ego = 5, save_file = FALSE)
```

GWAS_data_reader *GWAS_data_reader*

Description

GWAS_data_reader

Usage

```
GWAS_data_reader(file, snp_col, study_col, trait_col)
```

Arguments

file	- Character (string) containing the directory path to a .tsv or .csv file containing summary level GWAS data, typically this can be sourced from major GWAS databases such as the GWAS Catalog or GWAS Central.
snp_col	- Character (string) reflecting the column name containing the SNP (standard dbSNP accession number, e.g. rs992531) data. In data sourced from the GWAS Catalog, this column will typically be named "SNPS" and in GWAS Central this will typically be "Source Marker Accession".
study_col	- Character (string) reflecting the column name containing the study names associated with each SNP. In data sourced from the GWAS Catalog, this column will typically be named "STUDY" and in GWAS Central this will typically be "Study Name".
trait_col	- Character (string) reflecting the column name containing the trait/phenotype names associated with each SNP. In data sourced from the GWAS Catalog, this column will typically be named "DISEASE/TRAIT" and in GWAS Central this will typically be "Annotation Name".

Value

A processed dataframe containing only the columns including GWAS studies, traits/phenotypes and relevant SNPs in NCBI standard accession number naming convention

Examples

```
##getting directory path to GWAS Catalog association .tsv file:
path = system.file("extdata",
  "gwas-association-downloaded_2021-09-13-EFO_1000649.tsv",
  package="PanViz")
##opening/cleaning data:
df <- PanViz::GWAS_data_reader(file = path,
  snp_col = "SNPS",
  study_col = "STUDY",
  trait_col = "DISEASE/TRAIT")
##getting directory path to GWAS Central association .tsv file:
path = system.file("extdata", "GWASCentralMart_ERplusBC.tsv",
  package="PanViz")
##opening/cleaning data:
df <- PanViz::GWAS_data_reader(file = path,
  snp_col = "Source Marker Accession",
  study_col = "Study Name",
  trait_col = "Annotation Name")
```

`multi_hex_col_mix` *multi_hex_col_mix*

Description

This is a helper function that merges any vector of hex colours

Usage

```
multi_hex_col_mix(col_vector)
```

Arguments

`col_vector` - vector of hex colours

Value

- a single mixed hex color from inputted hex codes

NCBI_clean *NCBI_clean*

Description

NCBI_clean

Usage

```
NCBI_clean(queried_data)
```

Arguments

queried_data	- input queried NCBI gene data

Value

remove genes with no genomic information from NCBI query

NCBI_clean_2 *NCBI_clean_2*

Description

NCBI_clean_2

Usage

```
NCBI_clean_2(queried_data)
```

Arguments

queried_data	- rentrez object queried from NCBI

Value

return chromosome location, start and end position of gene from NCBI query

NCBI_dbSNP_query *NCBI_dbSNP_query*

Description

NCBI_dbSNP_query

Usage

```
NCBI_dbSNP_query(snp_list, progress_bar)
```

Arguments

snp_list	- list of SNPs to be queried via NCBI dbSNP API
progress_bar	Boolean (default = TRUE) argument that controls whether or not a progress bar for calculations/KEGGREST API GET requests should be printed to the console

Value

- raw output from NCBI dbSNP API

reaction_cleanup *reaction_cleanup*

Description

This function helps to cleans up queried KEGG reaction recursive lists + separates compound/metabolite and reaction pair data into new sections

Usage

```
reaction_cleanup(queried_data)
```

Arguments

queried_data	- input queried KEGG reaction data

Value

Trimmed recursive lists containing queried KEGG reaction data

retry *Retry function*

Description

Internal function for handling errors when accessing APIs

Usage

```
retry(
  expr,
  isError = function(x) "try-error" %in% class(x),
  maxErrors = 5,
  sleep = 0
)
```

Arguments

expr	This is the function you want to catch and handle errors from
isError	Function for evaluating if provided expression is throwing an error
maxErrors	The maximum number of errrors it should handle from the function
sleep	The amount of sleep between a caught error and the next attempt

Value

The expression that has been either successfully ran or retried maximum number of times

set_base_graph_attributes *set_base_graph_attributes*

Description

set_base_graph_attributes

Usage

```
set_base_graph_attributes(G, colour_groups)
```

Arguments

G	igraph object containing KEGG network
colour_groups	logical - whether or not user has indicated on colouring the network by categorical variable i.e. study or trait/phenotype (only available via PanViz::get_grouped_IMON())

Value

igraph object with node attributes set

`set_snp_grouping` *snp grouping by chosen categorical variable*

Description

snp grouping by chosen categorical variable

Usage

```
set_snp_grouping(G, unique_group_names, unique_group_cols, group_snps)
```

Arguments

`G`	- igraph object containing IMON
`unique_group_names`	- vector containing unique grouping variable names
`unique_group_cols`	- vector containing unique grouping colours for each variable
`group_snps`	- snps split by each variable/group

Value

- igraph object containing IMON with labelled and coloured snps by grouping variable

---

`snp_gene_chr_match` *snp_gene_chr_match*

Description

snp_gene_chr_match

Usage

```
snp_gene_chr_match(snp_loc, gene_loc)
```

Arguments

`snp_loc`	- snp locations
`gene_loc`	- dataframe of genes and their chromosome numbers and start/stop positions

Value

- a recursive list of gene with their relative snps that have the same chromosome number

snp_gene_map *Fast vectorised SNP to gene chromosome number and genomic location mapping*

Description

Fast vectorised SNP to gene chromosome number and genomic location mapping

Usage

```
snp_gene_map(gene_loc, snp_loc)
```

Arguments

gene_loc	dataframe containing KEGG genes and relevant chromosome number and positions
snp_loc	dataframe containing queried SNPs and relevant chromosome number and positions

Value

an adjacency list of SNPs with their relevant mapped genes to their genomic location

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