

MeTime R package

August 12, 2022

| | |
|--------------------------------|---|
| <code>add_col_normality</code> | <i>Function to check normality and add data to col data</i> |
|--------------------------------|---|

Description

A method applied on the s4 object of class "metime_analyser" to check normality of the metabolites and add it to corresponding columns

Usage

```
add_col_normality(object, which_data, type, metab_names)
```

Arguments

| | |
|--------------------------|---|
| <code>object</code> | An object of class metime_analyser |
| <code>which_data</code> | dataset on which the method is to be applied |
| <code>type</code> | type of test, "shapiro" and "kruskal" are available |
| <code>metab_names</code> | column that has the metabolite names in col_data. |

Value

S4 object with shapiro wilk test related data in the col_data

Examples

```
object <- add_col_normality(object=data, which_data=c("lipid_data","nmr_data"), type="shapiro", metab_names=c("m
```

```
add_distribution_vars_to_rows
```

Function to add measurements taken at screening time for samples to be added to all timepoints in row data

Description

A method applied on the s4 object of class "metime_analyser" to add all those datapoints that were measured only during screening to all the respective samples at all timepoints in row_data lists

Usage

```
add_distribution_vars_to_rows(
  object,
  screening_vars,
  distribution_vars,
  which_data
)
```

Arguments

| | |
|------------|---|
| object | An object of class metime_analyser |
| which_data | dataset to which the information is to be added |
| vars | A character naming the vars of interest |

Value

object of class metime_analyser with phenotype data added to row data

Examples

```
# adding APOEGrp, PTGENDER, and diag group to all data points and prepping the object for viz_distribution_plotter()
object <- add_distribution_vars_to_rows(object=data, screening_vars=c("APOEGrp", "DXGrp_longi", "PTGENDER"),
distribution_vars=c("Age", "BMI", "ADNI_MEM", "ADNI_LAN", "ADNI_EF", "APOEGrp", "DXGrp_longi", "PTGENDER"), which_data="row_data")
```

```
add_metabs_as_covariates
```

Function to add metabolites as covariates for network construction

Description

Method applied on metime_analyser object to add other metabolite data to a certain dataset

Usage

```
add_metabs_as_covariates(object, which_data, which_metabs)
```

Arguments

| | |
|--------------|---|
| object | A S4 object of class metime_analyser |
| which_data | Dataset to which the metab data is to be added(please note that this a single character) |
| which_metabs | list of names of metabs and name of the list represents the dataset from which the metabs are to be acquired. eg: which_metabs=list(nmr_data=c("metab1", "metab2"), lipid_data=c("")) |

Value

S4 object with metabs added for GGM to another dataset

add_phenotypes_as_covariates

Function to add covariates to the dataset of interest for GGMs

Description

adds Covariates to data matrices in metime_analyser S4 object

Usage

```
add_phenotypes_as_covariates(
  object,
  which_data,
  covariates,
  class.ind,
  phenotype
)
```

Arguments

| | |
|------------|---|
| object | object of class metime_analyser |
| which_data | Dataset to which the covariates is to be added |
| covariates | character vector names of covariates. |
| class.ind | Logical to convert factor variables into class.ind style or not |
| phenotype | Logical. If True will extract from phenotype dataset else uses row data |

Value

S4 object with covariates added to the dataset

| | |
|--------------------|---|
| add_screening_vars | <i>Function to add measurements taken at screening time for samples to be added to all timepoints</i> |
|--------------------|---|

Description

A method applied on the s4 object of class "metime_analyser" to add all those datapoints that were measured only during screening to all the respective samples at all timepoints

Usage

```
add_screening_vars(object, vars)
```

Arguments

| | |
|--------|---|
| object | An object of class metime_analyser |
| vars | A character naming the vars of interest |

Value

phenotype data which can be replaced into the original object or use it separately with a different object

Examples

```
# adding APOEGrp, PTGENDER to all data points
new_with_apoegrp_sex <- add_screening_vars(object=metime_analyser_object, vars=c("APOEGrp", "PTGENDER"))
```

| | |
|------------------------------|--|
| calc_conservation_metabolite | <i>Function to calculate metabolite conservation index</i> |
|------------------------------|--|

Description

Method applied on the object metime_analyser to calculate the metabotype conservation index

Usage

```
calc_conservation_metabolite(object, which_data, verbose)
```

Arguments

| | |
|------------|---|
| object | An object of class metime_analyser |
| which_data | Name of the dataset to be used |
| verbose | Information provided on steps being processed |

Value

List of conservation index results

Examples

```
#calculating metabolite_conservation_index  
out <- calc_metabolite_conservation(object=metime_analyser_object, which_data="Name of the dataset")
```

calc_conservation_metabotype

Function to calculate metabotype conservation index

Description

Method applied on the object metime_analyser to calculate the metabotype conservation index

Usage

```
calc_conservation_metabotype(object, which_data, verbose)
```

Arguments

| | |
|------------|---|
| object | An object of class metime_analyser |
| which_data | Name of the dataset to be used |
| verbose | Information provided on steps being processed |

Value

List of conservation index results

Examples

```
#calculating metabotype_conservation_index  
out <- calc_metabotype_conservation(object=metime_analyser_object, which_data="Name of the dataset")
```

calc_correlation_pairwise

Function to calculate correlation

Description

calculate pairwise correlations This function creates a dataframe for plotting from a dataset.

Usage

```
calc_correlation_pairwise(object, which_data, method)
```

Arguments

| | |
|------------|---|
| object | S4 Object of class metime_analyser |
| which_data | specify datasets to calculate on. One or more possible |
| method | default setting: method="pearson", Alternative "spearman" also possible |

Value

data.frame with pairwise results

Examples

```
# Example to calculate correlations
dist <- calc_correlation(object=metime_analyser_object, which_data="name of the dataset",
  method="pearson")
```

calc_dimensionality_reduction

Function to calculate dimensionality reduction methods such as tsne, umap and pca.

Description

A method to apply on s4 object of class metime_analyse in order to obtain information after dimensionality reduction on a dataset/s

Usage

```
calc_dimensionality_reduction(object, which_data, type)
```

Arguments

| | |
|------------|--|
| object | An object of class metime_analyser |
| which_data | a character vector - Names of the dataset from which the samples will be extracted |
| type | type of the dimensionality reduction method to be applied. Accepted inputs are "UMAP", "tSNE", "PCA" |

Value

a list with two dataframes containing the dimensionality reduction information 1) samples - data of the individuals(".\$samples") 2) metabs - data of the metabolites(".\$metabs")

Examples

```
#calculate PCA
pca <- calc_dimensionality_reduction(object=metime_analyser_object, which_data="name/s of the dataset/s", type="PCA")
#calculate UMAP
pca <- calc_dimensionality_reduction(object=metime_analyser_object, which_data="name/s of the dataset/s", type="UMAP")
#calculate tSNE
pca <- calc_dimensionality_reduction(object=metime_analyser_object, which_data="name/s of the dataset/s", type="tSNE")
```

calc_distance_pairwise

Function to calculate dissimilarity using distance measures

Description

calculate pairwise distances This function creates a dataframe for plotting from a dataset.

Usage

```
calc_distance_pairwise(object, which_data, method)
```

Arguments

| | |
|------------|---|
| object | S4 Object of class metime_analyser |
| which_data | specify datasets to calculate on. One or more possible |
| method | default setting: method="euclidean", Alternative "maximum", "minimum", "manhattan", "canberra", "minkowski" are also possible |

Value

data.frame with pairwise results

Examples

```
# Example to calculate pairwise distances
dist <- calc_pairwise_distance(object=metime_analyser_object, which_data="name of the dataset",
                              method="euclidean")
```

calc_featuresselection_boruta

Function to calculate dependent variables

Description

An S4 method to be applied on the metime_analyser object so as to calculate dependent variables

Usage

```
calc_featuresselection_boruta(
  object,
  which_x,
  which_y,
  verbose,
  output_loc,
  file_name
)
```

Arguments

| | |
|------------|---|
| object | An object of class metime_analyser |
| which_x | Name of the dataset to be used for training |
| which_y | Name of the dataset to be used for testing |
| verbose | Information provided on steps being processed |
| output_loc | path to the parent directory where in the out file will be stored |
| file_name | name of the out file |

Value

List of conservation index results

calc_ggm_genenet_crosssectional

An automated fuction to calculate GGM from genenet crosssectional version

Description

automated fuction that can be applied on metime_analyser object to obtain geneNet network along with threshold used

Usage

```
calc_ggm_genenet_crosssectional(object, which_data, threshold, timepoint)
```


Arguments

| | |
|------------|---|
| object | S4 object of class metime_analyser |
| which_data | a character or a character vector naming the datasets of interest |
| threshold | type of threshold to be used for extracting significant edges. allowed inputs are "li", "FDR", "bonferroni" |
| timepoints | timepoints of interest that are to be used to build networks(as per timepoints in rows) |

Value

Network data with edgelist, partial correlation values and associated p-values and corrected p-values

calc_ggm_genenet_longitudnal

An automated fuction to calculate GGM from genenet longitudinal version

Description

automated funtion that can be applied on metime_analyser object to obtain geneNet network along with threshold used

Usage

```
calc_ggm_genenet_longitudnal(object, which_data, threshold, timepoints)
```

Arguments

| | |
|------------|---|
| object | S4 object of class metime_analyser |
| which_data | a character or a character vector naming the datasets of interest |
| threshold | type of threshold to be used for extracting significant edges |
| timepoints | timepoints of interest that are to be used to build networks(as per timepoints in rows) |

Value

Network data with edgelist, partial correlation values and associated p-values and corrected p-values

`calc_ggm_multibipartite_lasso`

An automated function to calculate GGM from multibipartite lasso approach

Description

automated function that can be applied on s4 object of class metime_analyser to calculate a network using multibipartite lasso

Usage

```
calc_ggm_multibipartite_lasso(object, which_data, alpha, nfolds, timepoints)
```

Arguments

| | |
|-------------------------|---|
| <code>object</code> | S4 object of class metime_analyser |
| <code>which_data</code> | a character or a character vector naming the datasets of interest |
| <code>alpha</code> | tuning parameter for lasso + ridge regression in glmnet |
| <code>nfolds</code> | nfolds for cv.glmnet |
| <code>timepoints</code> | timepoints of interest that are to be used to build networks(as per timepoints in rows) |

Value

Network data with edges and their respective betas

`calc_temporal_ggm`

An automated function to calculate temporal network with lagged model

Description

calculates temporal networks for each dataset with a lagged model as used in graphical VAR

Usage

```
calc_temporal_ggm(object, which_data, lag, timepoints, alpha, nfolds)
```

Arguments

| | |
|------------|---|
| object | S4 object of class metab_analyser |
| which_data | dataset or datasets to be used |
| lag | which lagged model to use. 1 means one-lagged model, similiary 2,3,..etc |
| timepoints | timepoints of interest that are to be used to build networks(in the order of measurement) |
| alpha | parameter for regression coefficient |
| nfolds | nfolds parameter for glmnet style of regression |

Value

temporal network data with edgelist and regression values

| | |
|------------|--|
| calc_ttest | <i>Function to calculate students t-test</i> |
|------------|--|

Description

Method for S4 object of class metime_analyser for performing t-test

Usage

```
calc_ttest(object, which_data, timepoints, split_var)
```

Arguments

| | |
|------------|---|
| object | S4 object of class metime_analyser |
| which_data | dataset or datasets to be used for the analysis |
| timepoints | two timepoints of interest to perform the test on |
| split_var | split variable for testing such as diagnostic group etc |

Value

t-test result as a list or a list of t-test results

check_col_normality *Function to check for col_normality data whether it is added or not.*

Description

function to check whether col_normality data is added to the object or not

Usage

```
check_col_normality(object, which_data)
```

Arguments

| | |
|------------|---------------------------------------|
| object | S4 object of class of metime_analyser |
| which_data | dataset/s to check |

Value

NULL if it passes all the sanity checks

check_ids_and_classes *Function to check the ids in the data and data format*

Description

sanity check to check for ids and order of the data

Usage

```
check_ids_and_classes(object)
```

Arguments

| | |
|--------|---------------------------------------|
| object | S4 object of class of metime_analyser |
|--------|---------------------------------------|

Value

NULL if it passes all the sanity checks

check_rownames_and_colnames

Function to check the format of rownames and colnames and if they are same or not

Description

sanity check to check for rownames of the data

Usage

```
check_rownames_and_colnames(object)
```

Arguments

object S4 object of class of metime_analyser

Value

NULL if it passes all the sanity checks

get_append_analyser_object

This function appends an object of class metime_analyser with a new dataset.

Description

function to apply on metime_analyse object to append a new dataset into the existing object

Usage

```
get_append_analyser_object(object, data, col_data, row_data, name)
```

Arguments

| | |
|----------|---|
| object | S4 object of class metime_analyser |
| data | data.frame containing data |
| col_data | data.frame containing col_data: id column of col data has to match colnames of data |
| row_data | data.frame containing row_data: id column of row data has to match rownames of data |
| name | Name of the new dataset |

Value

An object of class metime_analyser

Examples

```
# append data frames into the metime_analyser object
appended_object <- get_append_metab_object(object=metime_analyser_object, data=data, row_data=data, col_data=col_data)
```

```
get_betas_for_multibipartite_lasso
```

Function to perform multibipartite style regression on a list of matrices

Description

Performs multibipartite lasso in cv.glmnet style on a list of matrices that have metabolite information from different platforms

Usage

```
get_betas_for_multibipartite_lasso(list_of_mats, alpha, nfolds)
```

Arguments

| | |
|--------------|---|
| list_of_mats | a list with matrices and samples ordered similarly |
| alpha | alpha for cv.glmnet regression. Defines style of penalty. |
| nfolds | nfolds for cv.glmnet |

Value

returns a list with information of the combinations in context

```
get_files_and_names
```

Function to pack all the data into a single object of class "metime_analyser"

Description

This function loads all the files from the parent directory. It assumes a certain naming pattern as follows: "datatype_Nonelcollrow_data.rds" Any other naming pattern is not allowed. The function first writes all files into a list and each type of data is packed into its respective class i.e. col_data, row_data or data

Usage

```
get_files_and_names(path, annotations_index)
```

Arguments

`path` Path to the parent directory

`annotations_index` a list to be filled as follows = `list(phenotype="Name or index of the files", medication="Name or index of the files")`

Value

An object of class `metime_analyser`

Examples

```
# Input in the parent directory from which the data files are to be extracted along with annotations_index to specify
get_files_and_names(path=/path/to/parent/directory, annotations_index=list(phenotype="Name of phenotype file", m
```

| | |
|------------------------------|--|
| <code>get_ggm_genenet</code> | <i>Function to calculate a dynamic GeneNet GGM from a longitudinal data matrix</i> |
|------------------------------|--|

Description

calculates GGM on longitudinal data matrix and returns a dataframe with edges, partial correlation and associated p-values

Usage

```
get_ggm_genenet(data, threshold = c("bonferroni", "FDR", "li"))
```

Arguments

`data` data matrix in a longitudinal format

`threshold` type of multiple hypothesis correction. Available are Bonferroni("bonferroni"), Benjamini-Hochberg("FDR") and independent tests method("li", also see Li et al)

Value

a dataframe with edges, partial correlation and associated p-values

```
get_make_analyser_object
```

Function to pack all the data into a single object of class "metime_analyser"

Description

This function creates an object of class metime_analyser from a dataset.

Usage

```
get_make_analyser_object(
  data,
  col_data,
  row_data,
  annotations_index,
  name = NULL
)
```

Arguments

| | |
|-------------------|---|
| data | data.frame containing data |
| col_data | data.frame containing col_data: id column of col data has to match colnames of data |
| row_data | data.frame containing row_data: id column of row data has to match rownames of data |
| annotations_index | a list to be filled as follows = list(phenotype="Name or index of the file/list", medication="Name or index of the files/list") |
| name | character. Name you want to assign to the new dataset that is being added on |

Value

An object of class metime_analyser

Examples

```
# new_metime_analyser_object <- get_make_metab_object(data=data_frame, col_data=col_data_frame, row_data=row_data,
  annotations_index=list(phenotype="name of phenotype", medication="name of medication"))
```

get_make_plotter_object

Function to make a plottable object for viz functions

Description

function to generate metime_plotter object from plot data and metadata

Usage

```
get_make_plotter_object(data, metadata, calc_type, calc_info, plot_type, style)
```

Arguments

| | |
|-----------|---|
| data | dataframe of plotable data obtained from any calc object |
| metadata | dataframe with the metadata for the plot table mentioned above. To obtain these see get_metadata_for_rows() and get_metadata_for_columns() |
| calc_type | A character to specify type of calculation - will be used for comp_ functions For networks the accepted notations are "genenet_ggm", "multibipartite_ggm", and "temporal_network" |
| calc_info | A string to define the information about calculation |
| plot_type | type of the plot you want to build. eg: "box", "dot" etc. Its a character vector |
| style | Style of plot, accepted inputs are "ggplot", "circos" and "visNetwork". Is a singular option. |

get_metadata_for_columns

Get metadata for columns(in most cases for metabolites)

Description

function to generate a metadata list for building the MeTime plotter object

Usage

```
get_metadata_for_columns(object, which_data, columns, names, index_of_names)
```

Arguments

| | |
|----------------|--|
| object | S4 object of class MeTime Analyser |
| which_data | Names of dataset/s to be used |
| columns | A list of character vectors for the columns of interest. Length of the list should be same as length of which_data |
| names | A Character vector with the new names for the columns mentioned above |
| index_of_names | character vector to define the name of the column in which names of the variables are stored |

Value

data.frame with metadata information

get_metadata_for_rows *Get metadata for rows(in most cases for samples)*

Description

function to generate a metadata list for building the MeTime plotter object

Usage

```
get_metadata_for_rows(object, which_data, columns)
```

Arguments

| | |
|------------|--|
| object | S4 object of class MeTime Analyser |
| which_data | Names of dataset/s to be used |
| columns | A list of character vectors for the columns of interest. Length of the list should be same as length of which_data |

Value

data.frame with metadata information for rows

get_palette *Get a palette of "n" distinct colorblind friendly colors*

Description

Function to get a palette of distinct colorblind friendly colors, the distinctiveness is determined by the difference in their hue values.

Usage

```
get_palette(n)
```

Arguments

| | |
|---|--|
| n | number of colors wanted in the palette |
|---|--|

Value

a color palette vector with colors in the form of hex codes

Examples

```
# colors=get_palette(n=10)
```

get_samples_and_timepoints

Function to know the number of timepoints and the total number of samples available at that point

Description

A method applied onto s4 object of class "metime_analyser" so as to obtain the number of unique samples available at each timepoint.

Usage

```
get_samples_and_timepoints(object, which_data)
```

Arguments

| | |
|------------|------------------------------------|
| object | An object of class metime_analyser |
| which_data | Name of the dataset in context |

Value

A data table with timepoints and number of samples at each timepoint

Examples

```
# newdata <- get_samples_and_timepoints(object=metime_analyser_object, which_data="Name of dataset of interest")
```

get_text_for_plot

Function to Obtain textual information for visualization in interactive plots

Description

a standard function to be applied on data matrices or dataframes with the colnames of interest such that the information from columns is visualized in the interactive plot

Usage

```
get_text_for_plot(data, colnames)
```

Arguments

| | |
|----------|---|
| data | a dataframe with plotting data along with other variables for visualization |
| colnames | a character vector with the names of the variables that you want to see on the plot |

Value

a vector with strings that can be parsed into plot_ly text.

Examples

```
# text = get_text(data=data.frame, colnames=c("names", "of", "columns", "of", "interest"))
```

metime_analyser-class *Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.*

Description

Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.

Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.

Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.

Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.

Constructor to generate an object of class metime_analyser. contains slots - list_of_data: For the list of all data matrices. - list_of_col_data: list of all the col data files in the same order. - list_of_row_data: list of all the row data files in the same order. - annotations: list with phenotype and medication. Each of which is character that represents the name of the aforementioned dataset types.

`metime_plotter-class` *creating metime_plotter class that converts calculations and meta-data as a plotable object to parse into viz_plotter Contains slots - plot_data: list of Dataframe(s) with plotting data and metadata for visualization. Dataframes is an option only for visNetwork() plots. Need a list of two dataframes: Nodes dataframe and edge dataframe named as .\$.node and .\$.edge - plot: ggplot(), circos() or visNetwork() object - calc_type: A vector to specify type of calculation - will be used for comp_functions - calc_info: string to define the information about calculation - plot_type: A character vector to define the type of plots that are needed. - style: Character that defines the style of plot i.e. a ggplot(), circos() or visNetwork() plot. Is always a singular input. Cannot have two styles in one object.*

Description

creating metime_plotter class that converts calculations and metadata as a plotable object to parse into viz_plotter Contains slots - plot_data: list of Dataframe(s) with plotting data and metadata for visualization. Dataframes is an option only for visNetwork() plots. Need a list of two dataframes: Nodes dataframe and edge dataframe named as .\$.node and .\$.edge - plot: ggplot(), circos() or visNetwork() object - calc_type: A vector to specify type of calculation - will be used for comp_functions - calc_info: string to define the information about calculation - plot_type: A character vector to define the type of plots that are needed. - style: Character that defines the style of plot i.e. a ggplot(), circos() or visNetwork() plot. Is always a singular input. Cannot have two styles in one object.

creating metime_plotter class that converts calculations and metadata as a plotable object to parse into viz_plotter Contains slots - plot_data: Dataframe with plotting data and metadata for visualization - plot: ggplot(), circos() or visNetwork() object with predefined aesthetics - calc_type: A vector to specify type of calculation - will be used for comp_functions - calc_info: string to define the information about calculation - plot_type: A character vector to define the type of plots that are needed.

`mod_convert_s4_to_s3` *Function to Convert S4 object of class metime_analyser to an S3 object with same architecture*

Description

converter function to be applied onto metime_analyse object to convert into a standard list of S3 type.

Usage

```
mod_convert_s4_to_s3(object)
```

Arguments

object An object of class metime_analyser

Value

An S3 object of the same data as metime_analyser in other words all slots are now converted into nested lists

Examples

```
# convert S4 object to a list
s3_list <- mod_convert_s4_to_s3(object=metime_analyser_object)
```

```
mod_extract_common_samples
```

Function to get only common samples from the dataframes in list_of_data

Description

A method applied on object of class metime_analyse to extract common samples across datasets. Also has an option to split the data according timepoints(mod_split_acc_time()).

Usage

```
mod_extract_common_samples(object, time_splitter = FALSE)
```

Arguments

object An object of class metime_analyser

time_splitter A boolean input: True leads to splitting of the data wrt time, False returns all the dataframes as they are with common rows

Value

list_of_data with common samples across all time points

Examples

```
# extracting common samples across all datasets
new_list_of_data <- mod_common_sample_extractor(object=metime_analyser_object)
```

| | |
|---------------|--|
| mod_filter_tp | <i>Functions for selecting time points</i> |
|---------------|--|

Description

a method applied onto class metime_analyser in order to extract timepoints of interest from a dataset

Usage

```
mod_filter_tp(object, timepoints, full, which_data)
```

Arguments

| | |
|------------|--|
| object | An object of class metime_analyser |
| timepoints | time points to be selected |
| full | if TRUE subjects are only selected if measured in all selected time points |
| which_data | Name of the dataset to be used |

Value

An object of class metime_analyser with processed data

Examples

```
#example to use this function
object <- mod_filter_tp(object, timepoints=c(0,12,24), full=TRUE, which_data="Name of the dataset")
```

| | |
|----------------------------|--|
| mod_merge_metime_analysers | <i>Function to merge one or more metime_analyser objects</i> |
|----------------------------|--|

Description

function to merge multiple metime_analyser objects

Usage

```
mod_merge_metime_analysers(list_of_objects, annotations_index)
```

Arguments

| | |
|-------------------|---|
| list_of_objects | list of metime analyser objects that are to be merged |
| annotations_index | new list with annotations_index. Can also set to be NULL. |

Value

A merged metime_analyser object

| | |
|----------------|---|
| mod_remove_nas | <i>Function to remove NA's from data matrices</i> |
|----------------|---|

Description

A method applied on S4 object to remove NA's and change data accordingly

Usage

```
mod_remove_nas(object)
```

Arguments

| | |
|------------|---|
| object | S4 object of class metime_analyser |
| which_data | dataset/s for which the method is to be applied |

Value

S4 object with NA's removed and data manipulated accordingly

| | |
|-----------------------|---|
| mod_split_acc_to_time | <i>Function to split data according to time</i> |
|-----------------------|---|

Description

Function to split the list of dataframes into a nested list with each dataframe being split into into dataframes of different timepoints

Usage

```
mod_split_acc_to_time(object)
```

Arguments

| | |
|--------|------------------------------------|
| object | An object of class metime_analyser |
|--------|------------------------------------|

Value

list_of_data with each dataframe being broken into a list of dataframes with respect to the timepoint they belong to

Examples

```
#splitting data according to time
new_data <- mod_split_acc_to_time(object=metime_analyser_object)
```

| | |
|---------------|---|
| mod_trans_log | <i>Function to apply log transformation</i> |
|---------------|---|

Description

Function to log transform data

Usage

```
mod_trans_log(object, which_data, base)
```

Arguments

| | |
|------------|------------------------------------|
| object | An object of class metime_analyser |
| which_data | Name of the dataset to be used |
| base | base of log to be used |

Value

An object of class metime_analyser with processed data

Examples

```
# example to apply log transformation
object <- mod_logtrans(object, which_data="name of the dataset", base=2)
```

| | |
|------------------|-----------------------------------|
| mod_trans_zscore | <i>Function to scale the data</i> |
|------------------|-----------------------------------|

Description

Functions for scaling

Usage

```
mod_trans_zscore(object, which_data)
```

Arguments

| | |
|------------|------------------------------------|
| object | An object of class metime_analyser |
| which_data | Name of the dataset to be used |

Value

An object of class metime_analyser with processed data

Examples

```
# example to apply scaling
object <- mod_zscore(object, which_data="name of the dataset")
```

save_analyser_object *Function to extract analyser object data into a csv*

Description

extracts information from analyser object and saves it as a csv

Usage

```
save_analyser_object(object, which_data)
```

Arguments

| | |
|------------|-----------------------------------|
| object | An object of class metime_plotter |
| which_data | Character to specify the dataset |

Value

saves the data in the working directory as a csv and returns nothing

Examples

```
see examples here
save_analyser_object(object, which_data="dataset")
```

save_plot_from_plotter
 Function to save interactive plots

Description

extracts plot from plotter object and saves it as a widget

Usage

```
save_plot_from_plotter(object, out)
```

Arguments

| | |
|--------|--|
| object | An object of class metime_plotter |
| out | Character to specify path of the output file to save the widget in |

Value

saves the plot and returns nothing

Examples

```
save_plot_from_plotter(object)
```

| | |
|---------------------|---|
| save_plotter_object | <i>Function to extract plot data into a csv</i> |
|---------------------|---|

Description

extracts information from plotter object and saves it as a csv

Usage

```
save_plotter_object(object, out)
```

Arguments

| | |
|--------|--|
| object | An object of class metime_plotter |
| out | Character to specify path of the output file or character vector in case of visNetwork |

Value

saves the data into a csv and returns nothing

Examples

```
see examples here
Network : save_plotter_object(object, out=c("edge.csv", "node.csv", "meta.csv"))
Others : save_plotter_object(object, out="outfile.csv")
```

| | |
|--------------------|----------------------------------|
| set_parallel_cores | <i>register parallel backend</i> |
|--------------------|----------------------------------|

Description

function to run in order to perform the analysis parallely thereby saving time

Usage

```
set_parallel_cores(n_cores = NULL)
```

Arguments

n_cores A number of specified cores.

Value

set a parallel backend

show,metime_analyser-method

Setting new print definition for the metime_analyser object

Description

function to see the structure of metime_analyser object

Usage

```
## S4 method for signature 'metime_analyser'  
show(object)
```

Arguments

object S4 object of class metime_analyser

Value

structure of the S4 object

Examples

```
structure(object)
```

show,metime_plotter-method

Setting new print definition for the metime_plotter object

Description

function to see the structure of metime_plotter object

Usage

```
## S4 method for signature 'metime_plotter'  
show(object)
```

Arguments

object S4 object of class metime_plotter

Value

structure of the S4 object

Examples

```
structure(object)
```

structure,metime_plotter-method

Setting new structure definition for the metime_plotter object

Description

function to see the structure of metime_plotter object

Usage

```
## S4 method for signature 'metime_plotter'  
structure(object)
```

Arguments

object S4 object of class metime_plotter

Value

structure of the S4 object

Examples

```
structure(object)
```

| | |
|-----------|--|
| structure | <i>Setting new structure definition for the metime_analyser object</i> |
|-----------|--|

Description

function to see the structure of metime_analyser object

Usage

```
structure(object)
```

Arguments

| | |
|--------|------------------------------------|
| object | S4 object of class metime_analyser |
|--------|------------------------------------|

Value

structure of the S4 object

Examples

```
structure(object)
```

| | |
|--------------------------|--|
| viz_distribution_plotter | <i>Function for Plotting distributions of phenotypic variables</i> |
|--------------------------|--|

Description

A method to be applied onto s4 object so as to obtain distributions of various phenotypic variables

Usage

```
viz_distribution_plotter(object, colname, which_data, strats, phenotype)
```

Arguments

| | |
|------------|---|
| object | An object of class metime_analyser |
| colname | Name of the variable whose distribution is of interest |
| which_data | Name of the dataset from which the samples will be extracted |
| strats | Character vector with colnames that are to be used for stratification |
| phenotype | Logical. If true data will be collected from phenotype_data matrix else from row data |

Value

a list with either 1) density plot, mean table acc to timepoint and variable type or 2) bar plot, line plot, and variable type

Examples

```
# extracting distribuion of Age from dataset1
plot <- viz_distribution_plotter(object, colname="Age", which_data="dataset1", strats="additional columns for fac
```

| | |
|--------------------|--|
| viz_plotter_circos | <i>Setting up standard wrapper for all circos plots for a metime_plotter object.</i> |
|--------------------|--|

Description

plot function for metime_plotter object with different inputs to specialize plots. Used for all calc outputs.

Usage

```
viz_plotter_circos(object, aesthetics, outfile)
```

Arguments

| | |
|------------|--|
| object | S4 object of class metime_plotter |
| aesthetics | list for aesthetics. eg: list(list(x="colname",y="colname",color="colname", shape="colname"), list(...)) for "dot" plot and "heatmap" plot, for heatmap: list(x="colname", y="colname", fill="colname"). Additionally two other character vectors are allowed namely .vis and .strats for text and for facet wrapping. |

| | |
|--------------------|--|
| viz_plotter_ggplot | <i>Setting up standard wrapper for all ggplot plots for a metime_plotter object.</i> |
|--------------------|--|

Description

plot function for metime_plotter object with different inputs to specialize plots. Used for all calc outputs.

Usage

```
viz_plotter_ggplot(object, aesthetics)
```

Arguments

| | |
|------------|--|
| object | S4 object of class metime_plotter |
| aesthetics | list for aesthetics. eg: list(list(x="colname",y="colname",color="colname", shape="colname"), list(...)) for "dot" plot and "heatmap" plot, for heatmap: list(x="colname", y="colname", fill="colname"). Additionally two other character vectors are allowed namely .vis and .strats for text and for facet wrapping. |

Value

metime_plotter object with updated plot

viz_plotter_visNetwork

Setting up standard wrapper for network plots from visNetwork for a metime_plotter object.

Description

plot function for metime_plotter object with different inputs to specialize plots. Used for all calc outputs.

Usage

```
viz_plotter_visNetwork(object, title)
```

Arguments

| | |
|--------|--|
| object | S4 object of class metime_plotter |
| title | character/string that is the title of the graph output |

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