

Package ‘amanida’

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Title Meta-Analysis for Non-Integral Data

Version 0.1.0

Description Combination of results for meta-analysis using significance and effect size only. P-values and fold-change are combined to obtain a global significance on each metabolite. Produces a volcano plot summarising the relevant results from meta-analysis. Vote-counting reports for metabolites. And explore plot to detect discrepancies between studies at a first glance.

URL <https://github.com/mariallr/amanida>

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R topics documented:

amanida	2
amanida_palette	3
amanida_read	3
amanida_report	4
amanida_vote	5
compute_amanida	6
explore_plot	7
getsampleDB	8
METATables-class	8
sample_data	8
volcano_plot	9
vote_plot	9

Index	11
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amanida	<i>amanida</i>
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Description

amanida: A package for Meta-Analysis with non-integral data

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Results combination for meta-analysis using only significance and effect size.

- P-values and fold-change are combined to obtain a global significance on each metabolite.
- Produces a volcano plot summarizing the relevant results from meta-analysis.
- Qualitative meta-analysis for metabolites
- Graphical representation of qualitative analysis by bar plot
- Trend explore plot to detect discrepancies between studies at a first glance

amanida_palette	<i>Get nice colour-blind colours</i>
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Description

Get nice colour-blind colours

Usage

```
amanida_palette()
```

Value

vector of colours

amanida_read	<i>Import data</i>
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Description

amanida_read imports the data and formats for compute_amanida or amanida_vote functions

Usage

```
amanida_read(file, mode, coln, separator = NULL)
```

Arguments

file	path to file
mode	indicate if data will be quantitative or qualitative. Options are: <ul style="list-style-type: none">• "quan" for quantitative meta-analysis using p-value and fold-change• "qual" for qualitative meta-analysis using trend label
coln	columns names to use. It has to be in order identification, p-values, fold-changes, sample size and reference.
separator	the separator used on file

Details

Note that amanida_read skips rows with missing values or NA. Negatives values for fold-change are transformed to positive (1/value).

Formats compatible are csv, xlsx, xls or txt.

Value

tibble table with data imported

Examples

```
coln <- c("Compound Name", "P-value", "Fold-change", "N total", "References")
input_file <- getsampleDB()
datafile <- amanida_read(input_file, mode = "quan", coln, separator=";")
```

amanida_report	<i>Report</i>
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Description

amanida_report creates a report from the data using amanida functions

Usage

```
amanida_report(
  input_file,
  separator = NULL,
  analysis_type = NULL,
  column_id,
  pvalue_cutoff = NULL,
  fc_cutoff = NULL,
  votecount_lim
)
```

Arguments

input_file	path to the original dataset in xlsx, xls, csv or txt format
separator	indicate the separator used in the input_file parameter
analysis_type	indicate if data will be quantitative, qualitative or both. Options are: <ul style="list-style-type: none"> • "quan-qual" for quantitative and qualitative meta-analysis • "quan" for quantitative meta-analysis using p-value and fold-change • "qual" for qualitative meta-analysis using trend label
column_id	vector containing columns names to use. It has to be in order identification, p-values, fold-changes, sample size and reference.
pvalue_cutoff	numeric value to consider statistical significance
fc_cutoff	numeric value to consider significance for effect size
votecount_lim	minimum numeric value for vote-counting visualization

Details

This function uses directly the dataset to create a report with the meta-analysis results. In case of quantitative analysis amanida_report uses the functions amanida_read and compute_amanida for analyse the input data. Then the results are showed using volcano_plot, explore_plot and vote_plot.

Value

an html document saved in the working directory

Examples

```
## Not run:
column_id = c("Compound Name", "P-value", "Fold-change", "N total", "References")
input_file <- getsampleDB()

amanida_report(input_file, separator = ";", column_id, analysis_type = "quan",
               pvalue_cutoff = 0.05, fc_cutoff = 4, votecount_lim = 2)

## End(Not run)
```

amanida_vote

Qualitative meta-analysis

Description

amanida_vote performs vote-counting on qualitative data.

Usage

```
amanida_vote(data)
```

Arguments

data data imported using amanida_read function

Details

Vote-counting is computed without trend division. Punctuation of entries is based on trend, up-regulation gives 1, down-regulation give -1 and equal behavior gives 0. Total sum is divided then by the total number of entries on each compound.

Note that amanida_vote skips rows with missing values or NA.

Formats compatible are csv, xlsx, xls or txt.

Value

METAtable S4 object with vote-counting for each compound on @slot vote

Examples

```
coln = c("Compound Name", "Behaviour", "References")
input_file <- system.file("extdata", "dataset2.csv", package = "amanida")
data_votes <- amanida_read(input_file, mode = "qual", coln, separator = ";")

vote_result <- amanida_vote(data_votes)
```

compute_amanida	<i>Combine statistical results and compute vote-counting</i>
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Description

compute_amanida Combines for the same entry or metabolite the statistical values of p-value and fold-change. Also is computed a vote-counting for each compound.

Usage

```
compute_amanida(datafile)
```

Arguments

datafile data imported using amanida_read function

Details

Entries corresponding to metabolites are combined as follows:

- P-values are combined using Fisher method weighted by N and gamma distribution
- Fold-change are combined by weighted mean. Transformation works with fold-change transformed to log scale with base 2.

Vote-counting is computed based on votes. Punctuation of entries is based on trend, up-regulation gives 1, down-regulation give -1 and equal behavior gives 0. Total sum is divided then by the total number of entries on each compound.

Value

METAtable S4 object with p-value combined, fold-change combined and vote-counting for each compound

Examples

```
data("sample_data")

compute_amanida(sample_data)
```

`explore_plot`*Plot for compounds divergence in reports*

Description

`explore_plot` creates a bar-plot showing the votes divided in up-regulated and down-regulated and the global result for each compound.

Usage

```
explore_plot(data, type = "all", counts = NULL)
```

Arguments

<code>data</code>	an tibble obtained by <code>amanida_read</code>
<code>type</code>	select the subset of data to plot. Options are: <ul style="list-style-type: none">• "all": all data will be displayed• "sub": only data over counts value will be displayed. Need counts value.• "mix": will display data over count value and elements with reports in both trends. Need counts value.
<code>counts</code>	value of vote-counting cut-off. Will be only displayed data over the cut-off.

Details

Sum of votes divided by trend are plotted, then is obtained the total result by compound summing both trends.

Value

a ggplot bar-plot showing the sum of votes for each compound divided by the trend

Examples

```
data("sample_data")  
  
explore_plot(sample_data, type = "mix", counts = 1)
```

getsampleDB	<i>Function to sample data path</i>
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Description

Function to sample data path

Usage

```
getsampleDB()
```

METAtables-class	<i>An S4 class to return results from compute_amanida or amanida_vote function</i>
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Description

An S4 class to return results from compute_amanida or amanida_vote function

Slots

stat results for statistics combining p-values and fold-changes

vote vote-counting for metabolites

sample_data	<i>Example input data for the amanida function</i>
-------------	--

Description

A dataset containing results from meta-analysis of metabolomic studies

Usage

```
sample_data
```

Format

A data frame with 143 rows and 6 variables:

id Name of the compound under study

pvalue P-value

foldchange Fold-change

N Number of samples of the compound

ref References

trend Trend: 1 (up), -1 (down) or 0 (none)

volcano_plot	<i>Volcano plot of combined results</i>
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Description

volcano_plot returns a volcano plot of the combined results on each metabolite obtained by compute_amanida function

Usage

```
volcano_plot(mets, cutoff = NULL)
```

Arguments

mets	an S4 METAtables object
cutoff	values for p-value and fold-change significance

Details

Results are presented as $-\log_{10}$ for p-value and \log_2 for fold-change. Values over the cut off are labeled. If not cutoff is provided will be used alpha 0.05 for p-value and 1.5 for logarithmic fold-change.

Value

plot of results

Examples

```
data("sample_data")  
  
amanida_result <- compute_amanida(sample_data)  
volcano_plot(amanida_result)
```

vote_plot	<i>Bar-plot for compounds vote-counting</i>
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Description

vote_plot creates a bar-plot showing the vote-count for each compound.

Usage

```
vote_plot(mets, counts = NULL)
```

Arguments

`mets` an S4 METAtables object obtained by `compute_amanida` or `amanida_vote`.
`counts` value of vote-counting cut-off. Will be only displayed data over the cut-off.

Details

Vote-counting is the sum of number of reports up-regulated and the subtraction of reports down-regulated.

Value

a ggplot bar-plot showing the vote-count per compound

Examples

```
data("sample_data")  
  
result <- compute_amanida(sample_data)  
vote_plot(result)
```

Index

* datasets

sample_data, 8

amanida, 2

amanida_palette, 3

amanida_read, 3

amanida_report, 4

amanida_vote, 5

compute_amanida, 6

explore_plot, 7

getsampleDB, 8

METAtables (METAtables-class), 8

METAtables-class, 8

sample_data, 8

volcano_plot, 9

vote_plot, 9