

Package ‘metagear’

May 8, 2026

Version 0.7

Date 2021-02-15

Title Comprehensive Research Synthesis Tools for Systematic Reviews and Meta-Analysis

Description Functionalities for facilitating systematic reviews, data extractions, and meta-analyses. It includes a GUI (graphical user interface) to help screen the abstracts and titles of bibliographic data; tools to assign screening effort across multiple collaborators/reviewers and to assess inter-reviewer reliability; tools to help automate the download and retrieval of journal PDF articles from online databases; figure and image extractions from PDFs; web scraping of citations; automated and manual data extraction from scatter-plot and bar-plot images; PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flow diagrams; simple imputation tools to fill gaps in incomplete or missing study parameters; generation of random effects sizes for Hedges' d, log response ratio, odds ratio, and correlation coefficients for Monte Carlo experiments; covariance equations for modelling dependencies among multiple effect sizes (e.g., effect sizes with a common control); and finally summaries that replicate analyses and outputs from widely used but no longer updated meta-analysis software (i.e., metawin).

Funding for this package was supported by National Science Foundation (NSF) grants DBI-1262545 and DEB-1451031. CITE: Lajeunesse, M.J. (2016) Facilitating systematic reviews, data extraction and meta-analysis with the metagear package for R. *Methods in Ecology and Evolution* 7, 323-330 <[doi:10.1111/2041-210X.12472](https://doi.org/10.1111/2041-210X.12472)>.

Type Package

Depends R (>= 3.3.2)

Imports Matrix, MASS, metafor (>= 1.9-9), stringr

SystemRequirements Tcl/Tk toolkit (X11 Quarts for Mac)

VignetteBuilder R.rsp

License GPL (>= 2)

URL <http://lajeunesse.myweb.usf.edu/> <https://github.com/mjlajeunesse/>
<https://www.youtube.com/c/LajeunesseLab/>

Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
Suggests EBImage, ape, hexView, RCurl, testthat, R.rsp
NeedsCompilation no
Author Marc J. Lajeunesse [aut, cre] (ORCID:
<https://orcid.org/0000-0002-9678-2080>)
Maintainer Marc J. Lajeunesse <lajeunesse@usf.edu>
Repository CRAN
Date/Publication 2021-02-15 15:40:02 UTC

Contents

metagear-package	3
abstract_screener	4
browse_DOI	6
chachi	7
covariance_commonControl	8
effort_distribute	9
effort_initialize	11
effort_merge	12
effort_redistribute	13
effort_summary	14
example_references_metagear	15
figure_add	16
figure_barPlot	17
figure_detectAllPoints	18
figure_detectAxis	19
figure_display	20
figure_displayDetectedPoints	21
figure_displayDetections	22
figure_extractDetectedPoints	22
figure_read	23
figure_removeOutlyingPoints	24
figure_scatterPlot	24
figure_splitPlot	26
figure_transformByColors	27
figure_transformToBinary	28
figure_write	29
impute_missingness	29
impute_SD	30
isPDF	31
Kam_et_al_2003_Fig2.jpg	31
Kortum_and_Acymyan_2013_Fig4.jpg	32
MA_effectsTable	32

PDFs_collect	33
PDF_download	35
PDF_extractImages	36
plot_PRISMA	36
random_d	38
random_missingness	39
random_N	40
random_OR	40
random_pairedN	41
random_r	42
random_RR	43
replicate_MetaWin2.0	44
replicate_phyloMeta1.3	45
scrape_bibliography	46

Index	47
--------------	-----------

metagear-package	<i>Research synthesis tools to facilitate systematic reviews, data extraction, and meta-analysis.</i>
------------------	---

Description

metagear is a comprehensive, multifunctional toolbox with capabilities aimed to cover much of the research synthesis taxonomy: from applying a systematic review approach to objectively assemble and screen the literature, to extracting data from studies, and to finally summarize and analyze these data with the statistics of meta-analysis. More information about **metagear** can be found at <http://lajeunesse.myweb.usf.edu/>.

Details

What to cite?

Lajeunesse, M.J. (2016) Facilitating systematic reviews, data extraction and meta-analysis with the metagear package for R. *Methods in Ecology and Evolution* 7: 323-330. [download [here](#)]

Installation and Dependencies.

metagear has one external dependency that need to be installed and loaded prior to use in R. This is the EBImage R package (Pau et al. 2010) available only from the Bioconductor repository: <https://www.bioconductor.org/>.

To properly install **metagear**, start with the following R script that loads the Bioconductor resources needed to install the EBImage (also accept all of its dependencies):

```
install.packages("BiocManager");
BiocManager::install("EBImage")
library(metagear)
```

Finally for Mac OS users, installation is sometimes not straightforward as the `abstract_screener()` requires the Tcl/Tk GUI toolkit to be installed. You can get this toolkit by making sure the latest X11 application (xQuartz) is installed from here: <https://www.xquartz.org/>.

Author(s)

Marc J. Lajeunesse (University of South Florida, Tampa USA)

References

Pau, G., Fuchs, F., Sklyar, O., Boutros, M. and Huber, W. (2010) EBImage: an R package for image processing with applications to cellular phenotypes. *Bioinformatics* 26: 979-981.

abstract_screener	<i>A GUI screener to quickly code candidate studies for inclusion/exclusion into a systematic review or meta-analysis.</i>
-------------------	--

Description

A GUI screener to help scan and evaluate the title and abstract of studies to be included in a systematic review or meta-analysis.

Usage

```
abstract_screener(
  file = file.choose(),
  aReviewer = NULL,
  reviewerColumnName = "REVIEWERS",
  unscreenedColumnName = "INCLUDE",
  unscreenedValue = "not vetted",
  abstractColumnName = "ABSTRACT",
  titleColumnName = "TITLE",
  browserSearch = "https://www.google.com/search?q=",
  fontSize = 13,
  windowWidth = 70,
  windowHeight = 16,
  theButtons = c("YES", "maybe", "NO"),
  keyBindingToButtons = c("y", "m", "n"),
  buttonSize = 10,
  highlightColor = "powderblue",
  highlightKeywords = NA
)
```

Arguments

file	The file name and location of a .csv file containing the abstracts and titles. The .csv file should have been initialized with <code>effort_initialize</code> and populated with screeners (reviewers) using <code>effort_distribute</code> .
aReviewer	The name (a string) of the reviewer to screen abstracts. It is used when there are multiple reviewers assigned to screen abstracts. The default column label is "REVIEWERS" as initialized with <code>effort_distribute</code> .
reviewerColumnName	The name of the column heading in the .csv file that contains the reviewer names that will screen abstracts. The default column label is "REVIEWERS".
unscreenedColumnName	The name of the column heading in the .csv file that contains the screening outcomes (i.e. vetting outcomes by a reviewer). Unscreened references are by default labeled as "not vetted". The reviewer then can code to "YES" (is a relevant study), "NO" is not relevant and should be excluded, or "MAYBE" if the title/abstract is missing or does not contains enough information to fully assess inclusivity. The default label of this column is "INCLUDE".
unscreenedValue	Changes the default coding (a string) of "not vetted" that designates whether an abstract remains to be screened or vetted.
abstractColumnName	The name of the column heading in the .csv file that contains the abstracts. The default label of this column is "ABSTRACT".
titleColumnName	The name of the column heading in the .csv file that contains the titles. The default label of this column is "TITLE".
browserSearch	Change the url for the browser title search; the default is Google.
fontSize	Change the font <code>gWidgets::size</code> of the title and abstract text.
windowWidth	Change the default width of the GUI window.
windowHeight	Change the default height of the GUI window.
theButtons	A vector of coding buttons included on the screener. The default is YES, maybe, and NO. Buttons can be removed as added by changing this vector. For example, <code>theButtons = c("YES", "NO")</code> to remove the maybe-button, or <code>theButtons = c("YES", "maybe", "NO", "model")</code> to add a "model" button that tags studies specifically as "model".
keyBindingToButtons	A vector of specific keyboard bindings to buttons. They are keyboard shortcuts to buttons and the default binding is y for YES-button, m for maybe-button, and n for NO-button. If theButtons parameter is modified then these keybindings should also be modified.
buttonSize	Change the default <code>gWidgets::size</code> of buttons.
highlightColor	The color of keywords highlighted in title and abstract. The default is blue, but for classic yellow use "palegoldenrod".
highlightKeywords	A string or list of keywords that will be highlighted in title and abstract.

Note**Installation and troubleshooting**

For Mac OS users, installation is sometimes not straightforward as this screener requires the Tcl/Tk GUI toolkit to be installed. You can get this toolkit by making sure the latest X11 application (xQuartz) is installed, see here: <https://www.xquartz.org/>. More information on installation is found in metagear's vignette.

How to use the screener

The GUI itself will appear as a single window with the first title/abstract listed in the .csv file. If abstracts have already been screened/coded, it will begin at the nearest reference labeled as "not vetted". The SEARCH WEB button opens the default browser and searches Google with the title of the reference. The YES, MAYBE, NO buttons, which also have keyboard shortcuts y and n, are used to code the inclusion/exclusion of the reference. Once clicked/coded the next reference is loaded. The SAVE button is used to save the coding progress of screening tasks. It will save coding progress directly to the loaded .csv file. **Closing the GUI, and not saving, will result in the loss of screening efforts relative to last save.**

There is also an ISSUE FIXES menu bar with quick corrections to screening errors. These include ISSUE FIXES: REFRESH TITLE AND ABSTRACT TEXT which reloads the text of the current abstract in case portions were deleted when copying and pasting sections, ISSUE FIXES: STATUS OF CURRENT ABSTRACT which provides information on whether or not the abstract was previously screened, and ISSUE FIXES: RETURN TO PREVIOUS ABSTRACT that backtracks to the previous abstract if a selection error occurred (note a warning will appear of there is a change to its inclusion/exclusion coding).

Examples

```
## Not run:

data(example_references_metagear)
effort_distribute(example_references_metagear,
                  initialize = TRUE,
                  reviewers = "marc",
                  save_split = TRUE)
abstract_screener("effort_marc.csv",
                  aReviewer = "marc",
                  highlightKeywords = "and")

## End(Not run)
```

Description

Uses the DOI name of a study reference to locate the e-journal website, or reference/citation website in Web of Science, Google Scholar, or CrossRef. Opens in default web-browser.

Usage

```
browse_DOI(theDOI, host = "DOI")
```

Arguments

theDOI	A string that identifies an electronic document on the web.
host	A string that defines the domain link used to open the DOI. The default, "DOI", will open to the web page associated with the DOI (e.g., publisher website). Other options include "WOS" that will open the DOI in Web of Science, "GS" in Google Scholar, and "CRF" in Crossref.

Examples

```
## Not run:  
  
browse_DOI("10.1086/603628")  
  
## End(Not run)
```

chachi

A small tribute to Chachi.

Description

Rest easy little bud, 200?-2016.

Usage

```
chachi()
```

 covariance_commonControl

Generates a sampling variance-covariance matrix for modeling dependencies among effect sizes due to sharing a common control.

Description

Generates K by K sampling variance-covariance (VCV) matrix that models the dependencies that arise due to using the same control group study parameters when estimating multiple effect sizes. This VCV matrix can then be used in meta-analysis. Currently only supports VCV calculation for log response ratios (see Lajeunesse 2011).

Usage

```
covariance_commonControl(
  aDataFrame,
  control_ID,
  X_t,
  SD_t,
  N_t,
  X_c,
  SD_c,
  N_c,
  metric = "RR"
)
```

Arguments

aDataFrame	A data frame containing columns with all study parameters used to estimate effect sizes (e.g., means, SD, N's for treatment and control groups). Must also contain a column that codes which effect sizes share a common control. See example below.
control_ID	Label of the column that codes groups of effect sizes that share the mean, SD, and N of a control group.
X_t	Column label for the means of (t)reatment group used to estimate the effect size.
SD_t	Column label for the standard deviations (SD) of the treatment group used to estimate the effect size.
N_t	Column label for the sample size (N) of the treatment group used to estimate the effect size.
X_c	Column label for the means of (c)ontrol group used to estimate the effect size.
SD_c	Column label for the standard deviations (SD) of the control group used to estimate the effect size.
N_c	Column label for the sample size (N) of the control group used to estimate the effect size.
metric	Option to designate which effect size metric for which the common control VCV matrix is to be estimated. Default is "RR" for log response ratio.

Value

A K by K sampling variance-covariance matrix and a data frame aligned with the block diagonal design of the sampling matrix.

Note**Response Ratio's (RR) with a comon control group**

Following Lajeunesse (2011), when two (or more) reponse ratio (RR) effect sizes share a common control mean (\bar{X}_C), such as $RR_{A,C} = \ln(\bar{X}_A/\bar{X}_C)$ and $RR_{B,C} = \ln(\bar{X}_B/\bar{X}_C)$, then they share a sampling covariance of:

$$\text{cov}(RR_{A,C}, RR_{B,C}) = \frac{(SD_C)^2}{N_C \bar{X}_C^2},$$

where the SD and N are the standard deviation and sample size of \bar{X}_C , respectively.

References

Lajeunesse, M.J. 2011. On the meta-analysis of response ratios for studies with correlated and multi-group designs. *Ecology* 92: 2049-2055.

effort_distribute *Assigns title/abstract screening efforts to a team.*

Description

Randomly distributes screening tasks evenly or unevenly across multiple team members. It populates this effort in a data frame column that includes this screening work (e.g., ABSTRACTS and TITLES).

Usage

```
effort_distribute(
  aDataFrame = NULL,
  dual = FALSE,
  reviewers = NULL,
  column_name = "REVIEWERS",
  effort = NULL,
  initialize = FALSE,
  save_split = FALSE,
  directory = getwd()
)
```

Arguments

aDataFrame	A data.frame containing the titles and abstracts to be screened by a team. The default assumes that the data.frame has already been formatted using <code>effort_initialize</code> . This data.frame will be populated with screening efforts. See example: example_references_metagear
dual	When TRUE, distributes effort using a dual screening design where two members will screen the same random collection of titles/abstracts. Requires the team to have an even number of members.
reviewers	A vector with the names of each team member.
column_name	Changes the default label of the "REVIEWERS" column that contains the screening efforts of each team member.
effort	A vector of percentages used to allocate screening tasks among each team member. When not called explicitly, assumes effort to be distributed evenly among all members. Must be the same length as the number of team members, and also sum to 100.
initialize	When TRUE, initializes the data.frame so that efforts could be distributed, calls: effort_initialize . Default is FALSE.
save_split	Saves the allocated team effort into separate <code>effort_*.csv</code> files for individual screening tasks. These files can be given to each member to screen their random title/abstract subset. All files can be merged once all screening tasks have been completed using effort_merge .
directory	Changes the default location/directory for where the <code>effort_*.csv</code> will be saved. If not explicitly called, it will deposit files in the current working directory.

Value

A data.frame with title/abstract screening efforts randomly distributed across a team.

See Also

[effort_initialize](#), [effort_merge](#), [effort_summary](#)

Examples

```
## Not run:  
  
data(example_references_metagear)  
theTeam <- c("Christina", "Luc")  
effort_distribute(example_references_metagear, initialize = TRUE, reviewers = theTeam)  
  
## End(Not run)
```

effort_initialize *Formats a reference dataset for title/abstract screening efforts.*

Description

Adds columns with standardized labels to a data frame with bibliographic data on journal articles. These columns will be used to assign reviewers, implementation of dual screening design, and the coding of inclusion/exclusions screening decisions.

Usage

```
effort_initialize(  
  aDataFrame,  
  study_ID = TRUE,  
  unscreenedValue = "not vetted",  
  dual = FALSE,  
  front = TRUE  
)
```

Arguments

aDataFrame	A data.frame object that includes the titles and abstracts to be screened. It will be formatted for screening efforts. See example: example_references_metagear
study_ID	When FALSE, does not add a column "STUDY_ID" that includes a unique identification number for each reference (row) in the dataFrame.
unscreenedValue	Changes the default coding (a string) of "not vetted" that designates whether an abstract remains to be screened or vetted as part of the "INCLUDE" column.
dual	When TRUE, formats dataFrame for a dual screening (paired) design. Creates two reviewer teams: REVIEWERS_A and REVIEWERS_B.
front	When FALSE, adds new columns to the back end of the dataframe. When TRUE, adds columns to the front.

Value

A data.frame formatted for title/abstract screening efforts.

See Also

[effort_distribute](#), [effort_merge](#), [effort_summary](#)

Examples

```
data(example_references_metagear)  
effort_initialize(example_references_metagear)
```

effort_merge	<i>Merges multiple files that had title/abstract screening efforts distributed across a team.</i>
--------------	---

Description

Combines (merges) multiple effort_*.csv files within the same directory that represent the completed screening efforts of multiple team members. These files were originally generated with [effort_distribute](#).

Usage

```
effort_merge(directory = getwd(), reviewers = NULL, dual = FALSE)
```

Arguments

directory	The directory name for the location of multiple .csv files. Assumes the current working directory if none is explicitly called. File names must include the "effort_" string as originally generated by effort_distribute .
reviewers	A vector of reviewer names (strings) used to merge effort from a select group of team members. Must be an even collection (e.g., pairs of reviewers) when a dual design was implemented.
dual	When TRUE, merges files implementing a dual screening design.

Value

A single data.frame merged from multiple files.

See Also

[effort_initialize](#), [effort_distribute](#), [effort_summary](#)

Examples

```
## Not run:  
  
data(example_references_metagear)  
theTeam <- c("Christina", "Luc")  
# warning effort_distribute below, will save two files to working  
# directory: effort_Christina.csv and effort_Luc.csv  
effort_distribute(example_references_metagear, initialize = TRUE,  
                 reviewers = theTeam, save_split = TRUE)  
effort_merge()  
  
## End(Not run)
```

effort_redistribute *Redistributes title/abstract screening efforts among a review team.*

Description

Randomly re-distributes screening tasks from one reviewers to the rest of the reviewing team. Used when screening effort needs to be re-allocated among reviewing team members.

Usage

```
effort_redistribute(
  aDataFrame,
  column_name = "REVIEWERS",
  reviewer = NULL,
  remove_effort = 100,
  reviewers = NULL,
  effort = NULL,
  save_split = FALSE,
  directory = getwd()
)
```

Arguments

aDataFrame	A data.frame containing the titles and abstracts to be screened by a team. The default assumes that the data.frame has already been formatted using <code>effort_initialize</code> and populated with <code>effort_distribute</code> .
column_name	Changes the default label of the "REVIEWERS" column that contains the screening efforts of each team member.
reviewer	The name of the reviewer whose effort is to be redistributed.
remove_effort	The percentage of effort to be redistributed among the team. The default is that 100% of the effort will be re-distributed.
reviewers	A vector of the names of each team member that will take on additional work.
effort	A vector of percentages used to allocate screening tasks among each team member. When not called explicitly, assumes effort to be distributed evenly among all members. Must be the same length as the number of team members, and also sum to 100.
save_split	Saves the allocated team effort into separate "effort_*.csv" files for individual screening tasks. These files can be given to each member to screen their random title/abstract subset. All files can be merged once all screening tasks have been completed using <code>effort_merge</code> .
directory	Changes the default location/directory for where the "effort_*.csv" will be saved. If not explicitly called, it will deposit files in the current working directory.

Value

A single data.frame with effort re-allocated among team members.

effort_summary	<i>Provides a text summary of screening efforts among the reviewing team.</i>
----------------	---

Description

Summarizes the number of studies screened, which were identified to be included/excluded from the project, as well as those with conflicting agreement on their inclusion/exclusion. If a dual (paired) design was implemented to screen references, then it also provides inter-reviewer agreement estimate following Cohen (1960) that describes the agreement (or repeatability) of screening/coding decisions. The magnitudes of inter-reviewer agreement estimates are then interpreted following Landis & Koch (1977).

Usage

```
effort_summary(
  aDataFrame,
  column_reviewers = "REVIEWERS",
  column_effort = "INCLUDE",
  dual = FALSE,
  quiet = FALSE
)
```

Arguments

aDataFrame	A data.frame containing the titles and abstracts that were screened by a team. The default assumes that the data.frame is the merged effort across the team using effort_merge.
column_reviewers	Changes the default label of the "REVIEWERS" column that contains the screening efforts of each team member.
column_effort	Changes the default label of the "INCLUDE" column that contains the screening decisions (coded references) of each team member.
dual	When TRUE, provides a summary of the dual screening effort as well as estimation of inter-reviewer agreements following Cohen's (1960) kappa (K) and Landis and Koch's (1977) interpretation benchmarks.
quiet	When TRUE, does not print to console the summary table.

Value

A data frame with summary information on the screening tasks of a reviewing team.

References

Cohen, J. 1960. A coefficient of agreement for nominal scales. Educational and Psychological Measurement 20: 37-46.

Landis, J.R., and Koch, G.G. 1977. The measurement of observer agreement for categorical data. *Biometrics* 33: 159-174.

See Also

[effort_initialize](#), [effort_distribute](#), [effort_merge](#)

example_references_metagear

A collection of bibliographic references

Description

An example dataset containing 11 journal references. The variables are described below.

Usage

```
data(example_references_metagear)
```

Format

A data frame with 12 rows and 9 variables.

Details

- **AUTHORS.** Authors of the journal article
- **YEAR.** Publication year
- **TITLE.** Article title
- **JOURNAL.** Journal name
- **VOLUME.** Journal volume number
- **LPAGES.** Lower page number
- **UPAGES.** Upper page number
- **DOI.** Digital object identifier (DOI) of journal article
- **ABSTRACT.** Full text of the journal article abstract

figure_add	<i>Manually add/detect points to a scatter plot figure.</i>
------------	---

Description

Allows for the user to manually add an unlimited number of points to a figure image, by left-clicking over a figure's point. Click on the red upper-right box called "EXIT" to end recording the position of manually detected points.

Allows for the user to manually add an unlimited number of points to a figure image, by left-clicking over a figure/image point. Click on the red upper-right box called "EXIT" to end recording the position of manually detected points.

Usage

```
figure_add(file = file.choose(), color = "#009900", size = 0.03)
```

```
figure_add(file = file.choose(), color = "#009900", size = 0.03)
```

Arguments

file	The file name and location of a figure. Prompts for file name if none is explicitly called. Can also be a binary figure image with detected points (an EBImage object). See: figure_detectAllPoints
color	The color to paint the manually detected points; default is green.
size	The radius of the painted points.

Value

A data frame with detected points.

A data frame with detected points.

See Also

[figure_detectAllPoints](#)

[figure_detectAllPoints](#)

figure_barPlot	<i>Detect and display all bar plot objects.</i>
----------------	---

Description

Automated detection of grouped data displayed in a bar-plot/chart figure image. The default returns these detected objects as an EBImage raster image, and as a vector of all the estimated lengths that are proportional to the values presented on each bar (and their error bars, if they are present). Note that the extracted points will be sorted by their positioning on the X-axis (or Y if the plot is a horizontal bar plot). For example, if there were error bars in the figure these will be grouped with the detected bar column. However, within these X-axis positioning they will not be sorted. See vignette for worked several illustrations.

Usage

```
figure_barPlot(  
  file = file.choose(),  
  horizontal = FALSE,  
  binary_threshold = 0.6,  
  axis_thickness = 3,  
  axis_sensitivity = 0.2,  
  axis_length = 0.75,  
  axis_X_color = "#00ABAB",  
  axis_Y_color = "#B0D36A",  
  Y_min = 0,  
  Y_max = 100,  
  bar_width = 9,  
  bar_sensitivity = 0.1,  
  point_color = "#0098B2",  
  point_size = 9,  
  ignore = FALSE  
)
```

Arguments

file	The file name and location of a bar-plot figure. Prompts for file name if none is explicitly called.
horizontal	If TRUE then aims to detect objects from a bar-plot that depicts data horizontally (rather than vertically).
binary_threshold	A proportion from zero to one designating the gray-scale threshold to convert pixels into black or white. Pixel intensities below the proportion will be converted to black, and those above white.
axis_thickness	An integer used to designate the thickness of the axis lines on a figure. Close alignment to the thickness of the axis on a figure will improve axis detection.

axis_sensitivity	A value designating the sensitivity of identifying straight lines on figure. A smaller number results in a higher sensitivity to identify axes.
axis_length	The relative size of the axis to the figure. The default is that axis lengths are 0.75 (75 percent) the size of the figure. This option is necessary since bar lengths may be similar to the axis length. Values should range between zero and one.
axis_X_color	The color to paint the detected X-axis.
axis_Y_color	The color to paint the detected Y-axis.
Y_min	The minimum Y value displayed on the Y-axis (used to scale detected data points).
Y_max	The maximum Y value displayed on the Y-axis (used to scale detected data points).
bar_width	An integer value designating the width of vertical lines on bars. A smaller number should be used when the width of bars are small (as well as the width of error bars).
bar_sensitivity	A value designating the sensitivity of identifying the vertical lines on bars. A smaller number should be used when the thickness of bars are small (as well as the width of error bars).
point_color	The color to paint the circles identifying the detected levels on bar columns and error bars.
point_size	An integer used to designate the size of the points painting the detected bars on a figure.
ignore	When TRUE does not display painted image with detections, only returns the data frame with detected points.

Value

A vector of scaled lengths for detected column and error bars.

figure_detectAllPoints

Automated detection of plotted points from a scatter-plot figure image.

Description

Attempts to detect all points of a certain shape and size from a scatter-plot figure image (even those lying outside of the axis range).

Usage

```
figure_detectAllPoints(
  aBinaryPlot,
  sensitivity = 0.2,
  point_shape = "circle",
  point_size = 5
)
```

Arguments

aBinaryPlot	A binary figure image (an EBImage object). See: figure_transformToBinary
sensitivity	A value designating the sensitivity of identifying unique points that overlap. A smaller number results in a higher sensitivity to split overlapping points; a larger number will extract only a single point from a cluster of overlapping points.
point_shape	The shape of points on figure: can be "circle", "square", or "diamond". If these options do not fit the shape found in a figure, use the option that best approximates that shape.
point_size	An integer used to designate the size of the points on the figure. Close alignment to the size of the points on a figure will improve point detection. See EBImage to help determine which size to use.

Value

An EBImage object with detected scatter-plot points.

See Also

[figure_detectAxis](#)

figure_detectAxis	<i>Detect an axis from a figure image.</i>
-------------------	--

Description

Attempts to detect either the X (horizontal) or Y (vertical) axis from a plotted figure.

Attempts to detect either the X (horizontal) or Y (vertical) axis from a plotted figure.

Usage

```
figure_detectAxis(
  aBinaryPlot,
  axis_type = "X",
  axis_thickness = 5,
  sensitivity = 0.2
)
```

```
figure_detectAxis(
  aBinaryPlot,
  axis_type = "X",
  axis_thickness = 5,
  sensitivity = 0.2
)
```

Arguments

aBinaryPlot	A binary figure image (an EBIImage object). See: figure_transformToBinary
axis_type	The axis to be detected from a figure: can be X or Y.
axis_thickness	An integer used to designate the thickness of the axis lines on a figure. Close alignment to the thickness of the axis on a figure will improve axis detection.
sensitivity	A value designating the sensitivity of identifying straight lines on a figure. A smaller number results in a higher sensitivity to identify axes.

Value

An EBIImage object with detected points.

An EBIImage object with detected points.

See Also

[figure_detectAllPoints](#)

[figure_detectAllPoints](#)

figure_display	<i>Displays an image plot.</i>
----------------	--------------------------------

Description

Displays a .jpg, .jpeg, .png, or .tiff image file containing a plotted figure, or plots an EBIImage object.

Usage

```
figure_display(file = file.choose(), browser = FALSE)
```

Arguments

file	The file name and location of a plot figure or EBIImage object. Prompts for file name if nothing is explicitly called. Preferably in .jpg format.
browser	When "TRUE", displays the figure image in the default web browser.

Value

An EBIImage object figure.

See Also

[figure_read](#)

`figure_displayDetectedPoints`*Displays detected points on figure.*

Description

Generates a raster image of a figure with the detected points painted on a background/reference figure.

Usage

```
figure_displayDetectedPoints(  
    aDetectedPlot,  
    background = NULL,  
    color = "red",  
    size = 2,  
    ignore = FALSE  
)
```

Arguments

<code>aDetectedPlot</code>	A binary figure image with detected points (an EBIImage object). See: figure_detectAllPoints
<code>background</code>	An EBIImage figure of same size to be used as background (e.g., the original (RGB/color) figure image).
<code>color</code>	The color to paint the detected points.
<code>size</code>	The radius of the painted points.
<code>ignore</code>	When TRUE does not display painted image, only returns painted image EBIImage object.

Value

A RGB EBIImage painted with detected points.

See Also

[figure_displayDetections](#)

figure_displayDetections

Displays the detected figure objects.

Description

Generates a raster image of a figure with the detected objects painted on a background/reference figure.

Usage

```
figure_displayDetections(
  aDetectedPlot,
  background = NULL,
  color = "red",
  ignore = FALSE
)
```

Arguments

aDetectedPlot	A binary figure image with detected objects (an EImage object).
background	An EImage figure of same size to be used as background (e.g., the original [RGB/color] figure image).
color	The color to paint the detected objects.
ignore	When TRUE does not display painted image, only returns painted image EImage object.

Value

A RGB EImage painted with detected figure objects.

figure_extractDetectedPoints

Extracts data points from a detected image.

Description

Extracts raw X and Y data from the points detected in a scatter-plot figure.

Usage

```
figure_extractDetectedPoints(
  aDetectedPlot,
  xAxis = NULL,
  yAxis = NULL,
  X_min = NULL,
  X_max = NULL,
  Y_min = NULL,
  Y_max = NULL,
  summarize = TRUE
)
```

Arguments

aDetectedPlot	A binary figure image with detected points (an EBImage object). See: figure_detectAllPoints
xAxis	A binary figure image with detected X-axis (an EBImage object). See: figure_detectAxis .
yAxis	A binary figure image with detected Y-axis (an EBImage object). See: figure_detectAxis .
X_min	The minimum value of X reported on the figure X-axis.
X_max	The maximum value of X reported on the figure X-axis.
Y_min	The minimum value of Y reported on the figure Y-axis.
Y_max	The maximum value of Y reported on the figure Y-axis.
summarize	When TRUE returns a summary of the regression parameters (intercept + slope * X), R-squared, Pearson's product moment correlation coefficient (r), and its variance (var_r) and sample size (N).

Value

A data frame with the extracted X and Y values.

figure_read	<i>Reads/loads a figure image from file.</i>
-------------	--

Description

Reads a .jpg, .jpeg, .png, or .tiff image file containing a plotted figure.

Usage

```
figure_read(file = file.choose(), display = FALSE)
```

Arguments

file	The file name and location of a plot figure. Prompts for file name if none is explicitly called. Preferably in .jpg format.
display	When "TRUE", displays the figure as a raster image.

Value

An EImage object figure.

See Also

[figure_write](#)

figure_removeOutlyingPoints

Remove outlier points from a figure.

Description

Removes all detected points outside of axis range. Requires three detected images: one based on [figure_detectAllPoints](#), and two others based on detected X- and Y-axes (i.e. [figure_detectAxis](#))

Usage

```
figure_removeOutlyingPoints(aDetectedPlot, xAxis = NULL, yAxis = NULL)
```

Arguments

`aDetectedPlot` A binary figure image with detected points (an EImage object). See: [figure_detectAllPoints](#)
`xAxis` A binary figure image with detected X-axis (an EImage object). See: [figure_detectAxis](#)
`yAxis` A binary figure image with detected Y-axis (an EImage object). See: [figure_detectAxis](#)

Value

An EImage object with detected points within the specified X- and Y-axis ranges.

figure_scatterPlot *Detect and display all scatter plot objects.*

Description

Automated detection of the X-axis, Y-axis, and points on a scatter-plot figure image. The default returns these detected objects as an EImage raster image, as well as the estimated effect size (correlation coefficient or r) of the data within the scatter-plot.

Usage

```

figure_scatterPlot(
  file = file.choose(),
  binary_threshold = 0.6,
  binary_point_fill = FALSE,
  binary_point_tolerance = 2,
  axis_thickness = 5,
  axis_sensitivity = 0.2,
  axis_X_color = "#00ABAB",
  X_min = 40,
  X_max = 140,
  axis_Y_color = "#B0D36A",
  Y_min = 40,
  Y_max = 140,
  point_sensitivity = 0.2,
  point_shape = "circle",
  point_size = 3,
  point_color = "#0098B2",
  ignore = FALSE
)

```

Arguments

<code>file</code>	The file name and location of a scatter plot figure. Prompts for file name if none is explicitly called.
<code>binary_threshold</code>	A proportion from zero to one designating the gray-scale threshold to convert pixels into black or white. Pixel intensities below the proportion will be converted to black, and those above white.
<code>binary_point_fill</code>	If TRUE then fills empty points/symbols in figure.
<code>binary_point_tolerance</code>	An integer used to designate the size of the points to the fill. Increase value to better fill empty points.
<code>axis_thickness</code>	An integer used to designate the thickness of the axis lines on a figure. Close alignment to the thickness of the axis on a figure will improve axis detection.
<code>axis_sensitivity</code>	A value designating the sensitivity of identifying straight lines on figure. A smaller number results in a higher sensitivity to identify axes.
<code>axis_X_color</code>	The color to paint the detected X-axis.
<code>X_min</code>	The minimum X value displayed on the X-axis (used to scale detected data points).
<code>X_max</code>	The maximum X value displayed on the X-axis (used to scale detected data points).
<code>axis_Y_color</code>	The color to paint the detected Y-axis.

Y_min	The minimum Y value displayed on the Y-axis (used to scale detected data points).
Y_max	The maximum Y value displayed on the Y-axis (used to scale detected data points).
point_sensitivity	A value designating the sensitivity of identifying unique points that overlap. A smaller number results in a higher sensitivity to split overlapping points; a larger number will extract only a single point from a cluster of overlapping points.
point_shape	The shape of points on figure: can be "circle", "square", or "diamond". If these options do not fit the shape found in a figure, use the option that best approximates that shape.
point_size	An integer used to designate the size of the points on the figure. Close alignment to the size of the points on a figure will improve point detection. See EBImage package to help determine which size to use.
point_color	The color to paint the detected scatter plot points.
ignore	When TRUE does not display painted image, only returns painted image EBImage object.

Value

A data frame with detected points.

figure_splitPlot	<i>Splits a composite figure that contains multiple plots.</i>
------------------	--

Description

Automatically detects divisions among multiple plots found within a single figure image file. It then uses these divisions to split the image into multiple image files; each containing only a single X-Y plot. Currently only works on composite figures that have a matrix-style presentation where each sub-plot has the same size.

Usage

```
figure_splitPlot(
  file = file.choose(),
  binary_threshold = 0.6,
  space_sensitivity_X = 0.4,
  space_sensitivity_Y = 0.6,
  border_buffer = 5,
  guess_limit = 10,
  ignoreX = FALSE,
  ignoreY = FALSE,
  quiet = FALSE
)
```

Arguments

file	The file name and location of a composite figure. Prompts for file name if none is explicitly called.
binary_threshold	A proportion from zero to one designating the gray-scale threshold to convert pixels into black or white. Pixel intensities below the proportion will be converted to black, and those above white.
space_sensitivity_X	A proportion ranging from zero to one that designates the size of the separation among sub-plots along the X-axis relative to the largest empty space detected in the figure image. As space_sensitivity_X approaches 1, finer empty spaces (e.g., empty spaces found in between plot captions and the axis line) will be treated as plot divisions.
space_sensitivity_Y	A proportion ranging from zero to one that designates the size of the separation among sub-plots along the Y-axis relative to the largest empty space detected in the figure image. As space_sensitivity_Y approaches 1, finer empty spaces (e.g., empty spaces found in between plot captions and the axis line) will be treated as plot divisions.
border_buffer	An integer value designating the amount of empty space around the figure image that should be ignored. As the number increases, more blank space near the image's edge will be ignored.
guess_limit	An integer value designating the number of guesses for within a figure image. The default value designates the top 10 guesses of divisions. Increase this number if there are more than 6 subplots per axis.
ignoreX	When TRUE, ignores detection of sub-plots along the X-axis.
ignoreY	When TRUE, ignores detection of sub-plots along the Y-axis.
quiet	When TRUE, does not print to console the saved file names.

Value

The number of sub-plots saved to file.

figure_transformByColors

Transforms RGB figure into list of binary images.

Description

Generates a list of binary images relative to the number of colors in an RGB figure. Useful to do when there are multiple objects in a figure presented with different colors.

Usage

```
figure_transformByColors(aFigure, colorsToSplit = 2)
```

Arguments

aFigure	The original (RBG/color) figure image (an EImage object).
colorsToSplit	An integer designating the number of colors in the figure. The number indicates the number of color intensities to divide into separate binary figures.

Value

A colorsToSplit + 1 list of EImage black and white objects. The final item in this list will be an inverse binary of the original figure.

See Also

[figure_transformToBinary](#)

figure_transformToBinary

Transforms figure to binary image.

Description

Transforms a figure into a black and white image. This pre-processing of the image is necessary to help identify objects within the figure (e.g., axes, plotted points).

Usage

```
figure_transformToBinary(
  aFigure,
  threshold = 0.6,
  point_fill = FALSE,
  point_tolerance = 2
)
```

Arguments

aFigure	The original figure image (an EImage object).
threshold	A proportion from zero to one designating the gray-scale threshold to convert pixels into black or white. Pixel intensities below the proportion will be converted to black, and those above white. Helps remove noise and increase contrast among candidate objects to detect.
point_fill	If TRUE then fills empty points/symbols in figure.
point_tolerance	An integer used to designate the size of the points to fill. Increase value to better fill empty points.

Value

An EImage black and white object ready for object detection.

figure_write	<i>Saves/writes a figure image.</i>
--------------	-------------------------------------

Description

Writes a figure image to file and returns the file name.

Usage

```
figure_write(aFigure, file = NULL)
```

Arguments

aFigure	The EBIImage figure.
file	Name and location of file to save. Supports .jpg, .png, and .tiff image formats.

Value

Vector of file names.

See Also

[figure_read](#)

impute_missingness	<i>Provides a summary of missingness in a dataset.</i>
--------------------	--

Description

Generates a summary of the percentage of missing data in a dataset. Provides insight on the appropriateness of imputation methods. For example, if 30% of data is missing, then perhaps this is too much to impute.

Usage

```
impute_missingness(aDataFrame)
```

Arguments

aDataFrame	A data.frame containing columns that will be assessed for missingness.
------------	--

Value

A data frame that summarizes percent missingness for each column of a dataset.

Examples

```
data(example_references_metagear)
impute_missingness(example_references_metagear)
```

impute_SD	<i>Imputes missing standard deviations in a dataset.</i>
-----------	--

Description

Imputes (fills gaps) of missing standard deviations (SD) using simple imputation methods following Bracken (1992) and Rubin and Schenker's (1991) "hot deck" approach.

Usage

```
impute_SD(
  aDataFrame,
  columnSDnames,
  columnXnames,
  method = "Bracken1992",
  range = 3,
  M = 1
)
```

Arguments

aDataFrame	A data frame containing columns with missing SD's (coded as NA) and their complete means (used only for nearest-neighbor method).
columnSDnames	Label of the column(s) with missing SD. Can be a string or list of strings.
columnXnames	Label of the column(s) with means (X) for each SD. Can be a string or list of strings. Must be complete with no missing data.
method	The method used to impute the missing SD's. The default is "Bracken1992" which applies Bracken's (1992) approach to impute SD using the coefficient of variation from all complete cases. Other options include: "HotDeck" which applies Rubin and Schenker's (1991) resampling approach to fill gaps of missing SD from the SD's with complete information, and "HotDeck_NN" which resamples from complete cases with means that are similar to missing SD's.
range	A positive number on the range of neighbours to sample from for imputing SD's. Used in combination with "HotDeck_NN". The default is 3; which indicates that the 3 means that are most similar in rank order to the mean with the missing SD will be resampled.
M	The number of imputed datasets to return. Currently only works for "HotDeck" method.

Value

An imputed (complete) dataset.

References

Bracken, M.B. 1992. Statistical methods for analysis of effects of treatment in overviews of randomized trials. *Effective care of the newborn infant* (eds J.C. Sinclair and M.B. Bracken), pp. 13-20. Oxford University Press, Oxford.

Rubin, D.B. and Schenker, N. 1991. Multiple imputation in health-care databases: an overview and some applications. *Statistics in Medicine* 10: 585-598.

 isPDF

Evaluates whether a file is a PDF document.

Description

Checks if provided file is in Portable Document Format (PDF).

Usage

```
isPDF(aFileName, verbose = TRUE)
```

Arguments

aFileName	A string that identifies a file name (and directory path) of the PDF candidate.
verbose	Provides more elaborate description of why the file could not be evaluated as a PDF (e.g., when validating a PDF online). When "quiet", an error message is not generated.

Value

A logical value indicating whether the file is a PDF document.

 Kam_et_al_2003_Fig2.jpg

An example image of a scatterplot figure

Description

A jpg image of a scatterplot from Figure 2 of Kam, M., Cohen-Gross, S., Khokhlova, I.S., Degen, A.A. and Geffen, E. 2003. Average daily metabolic rate, reproduction and energy allocation during lactation in the Sundeval Jird *Meriones crassus*. *Functional Ecology* 17:496-503.

Format

A raw jpg-formated image

Note**How to use**

```
readImage(system.file("images", "Kam_et_al_2003_Fig2.jpg", package = "metagear"))
```

Kortum_and_Acymyan_2013_Fig4.jpg

An example image of a bar plot figure

Description

A jpg image of a bar plot from Figure 4 of Kortum, P., and Acymyan, C.Z. 2013. How low can you go? Is the System Usability Scale range restricted? Journal of Usability Studies 9:14-24.

Format

A raw jpg-formated image

Note**How to use**

```
readImage(system.file("images", "Kortum_and_Acymyan_2013_Fig4.jpg", package = "metagear"))
```

MA_effectsTable

Generate an ANOVA-like effects table for a meta-analysis.

Description

Generates an ANOVA-like effects table that summarizes the within and between-study homogeneity tests (Q-tests), as well as moderator level Q-tests as originally described by Hedges and Olkin (1985; p. 156).

Usage

```
MA_effectsTable(model, weights, data, effects_model = "random")
```

Arguments

model	A two-sided linear formula object describing the model, with the response (effect sizes) on the left of a ~ operator and the moderator variables, separated by +, :, * operators, on the right.
weights	A column label from data.frame of variances to be used as weights.
data	An optional data frame containing the variables named in the model.
effects_model	The default is "random", which specifies a random-effects meta-analysis (DerSimonian and Laird method). Other options include "fixed" which presents fixed-effect analyses.

Value

An lm object of main effects.

References

- DerSimonian, R., and N. Laird. 1986. Meta-analysis in clinical trials. *Controlled Clinical Trials*, 7, 177-188.
- Hedges, L.V., and I. Olkin. 1985. *Statistical methods for meta-analysis*. Academic Press, New York, USA.

PDFs_collect

Attempts to download PDFs from multiple DOI links.

Description

Tries to download a collection of PDF files using multiple digital object identifier (DOI) links. Updates a data frame with the success of these downloads. The function is a wrapper for [PDF_download](#). NOTE: A single DOI may generate multiple PDF files. **If running downloader in Windows, having "WindowsProxy = TRUE" will significantly improve download success.**

Usage

```
PDFs_collect(
  aDataFrame,
  DOIcolumn,
  FileNamecolumn,
  directory = getwd(),
  randomize = FALSE,
  seed = NULL,
  buffer = FALSE,
  validatePDF = TRUE,
  quiet = FALSE,
  showSummary = TRUE,
  WindowsProxy = FALSE
)
```

Arguments

aDataFrame	A data frame containing a column of DOIs and a column of individual file names for each downloaded PDF.
DOIcolumn	The label of the column containing all the DOI links.
FileNamecolumn	The label of the column containing all the strings that will be used to rename the downloaded files.
directory	A string of the location (directory) where downloaded PDF files are to be saved. NOTE: helps to have this directory created before initializing the PDFs_collect function.
randomize	When TRUE will attempt to download PDFs in a random order. This may be necessary to ensure that host websites do not have their HTML and files repeatedly accessed.
seed	An integer used to enforce repeatability when randomly downloading PDFs.
buffer	When TRUE will randomly delay the downloads by a few seconds (with a mean 4 seconds and a range of 1 to 20 seconds). Another strategy to avoid quickly and repeatedly accessing host websites.
validatePDF	When TRUE will only save to files that are valid PDF documents. When FALSE will save all candidate files, even if they are not valid PDF formats.
quiet	When FALSE does not print to console individual download progress and summary.
showSummary	When FALSE does not print overall summary of download successes and failures.
WindowsProxy	When TRUE significantly improves download success for computers running Windows; when FALSE on a Windows based computer, you may only be able to download 30 to 50 PDFs at a time before a connection error occurs and halts all downloads (e.g., InternetOpenUrl failed error).

Value

The data frame with new column containing download-outcome successes.

See Also

[PDF_download](#)

Examples

```
## Not run:

data(example_references_metagear)
someRefs <- effort_initialize(example_references_metagear)
dir.create("metagear_downloads")
PDFs_collect(aDataFrame = someRefs, DOIcolumn = "DOI",
             FileNamecolumn = "STUDY_ID", directory = "metagear_downloads",
             WindowsProxy = TRUE)

## End(Not run)
```

PDF_download

Attempts to download a PDF using a DOI link.

Description

Tries to download a PDF file using the digital objected identifier (DOI) link. Uses ad hoc searches of journal HTML pages to detect candidate PDFs for download. Downloads all candidate pdfs. **If running downloader in Windows, having "WindowsProxy = TRUE" will significantly improve download success.**

Usage

```
PDF_download(  
  DOI,  
  directory = getwd(),  
  theFileName = "temp",  
  validatePDF = TRUE,  
  quiet = FALSE,  
  WindowsProxy = FALSE  
)
```

Arguments

DOI	A string of the DOI (digital object identifier) used to identify the source of a journal article PDF file(s).
directory	A string of the location (directory) were downloaded PDF files are to be saved. Directory name must end with "\\".
theFileName	Used to rename the downloaded file. No need to include extension ".pdf".
validatePDF	When "TRUE" will only save to files that are valid PDF documents. When "FALSE" will save all candidate files, even if they are not valid PDF formats.
quiet	When "FALSE" does not print to console download progress and summary.
WindowsProxy	When TRUE significantly improves download success for computers running Windows; when FALSE on a Windows based computer, you may only be able to download 30 to 50 PDFs at a time before a connection error occurs and halts all downloads (e.g., InternetOpenUr1 failed error).

Value

A string describing the download success. If unsuccessful, returns the type of error during the download attempt.

See Also

[PDFs_collect](#)

PDF_extractImages	<i>Attempts to extract all images from a PDF</i>
-------------------	--

Description

Tries to extract images within a PDF file. Currently does not support decoding of images in CCITT compression formats. However, will still save these images to file; as a record of the number of images detected in the PDF.

Usage

```
PDF_extractImages(file = file.choose())
```

Arguments

file	The file name and location of a PDF file. Prompts for file name if none is explicitly called.
------	---

Value

A vector of file names saved as images.

plot_PRISMA	<i>Plots and creates a PRISMA flow diagram.</i>
-------------	---

Description

Creates a PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flow diagram depicting the 'flow' of study inclusions and exclusions during various systematic review phases. It is meant to describe the number of studies identified, included, excluded, reasons for inclusion/exclusions, and final number of studies used in the meta-analysis. NOTE: currently only supports two start phases, and final phase must not have an exclude branch.

Usage

```
plot_PRISMA(  
  aPhaseVector,  
  colWidth = 30,  
  excludeDistance = 0.8,  
  design = "classic",  
  hide = FALSE  
)
```

Arguments

aPhaseVector	A vector of ordered labels (strings) for each phase of the PRISMA diagram. Labels designating the beginning of the diagram are commented with "START_PHASE:" and those designating exclusion phases "EXCLUDE_PHASE:". These comments will be removed from the diagram.
colWidth	An optional value (integer) designating the width of the text box of each phase.
excludeDistance	An optional value designating the the distance of exclude phase box from the main flow diagram. Larger values (> 0.8) increase this distance.
design	Designates the colorscheme and design of the the flow diagram. The default is classic (as in versions of metagear prior to v. 0.4). Others schemes are also available with color and more flat designs, and these can be further customized; see NOTE below for these details.
hide	When FALSE, the PRISMA flow diagram is not plotted.

Value

a grid object (grob) list

Note**Using canned or custom PRISMA design layouts**

There are several color schemes and design layouts (e.g. curved or flat) available. These designs include: cinnamonMint, sunSplash, pomegranate, vintage, grey, and greyMono. Custom schemes can also be developed by modifying each aspect of the design. These are:

S color of start phases (default: white)

P color of the main phases (default: white)

E color of the exclusion phases (default: white)

F color of the final phase (default: white)

fontSize the size of the font (default: 12)

fontColor the font color (default: black)

fontFace either plain, bold, italic, or bold.italic (default: plain)

flatArrow arrows curved when FALSE (default); arrows square when TRUE

flatBox boxes curved when FALSE (default); Boxes square when TRUE

For example, changing the defaults to have red rather than white exclusion phases, and square boxes, would be: `design = c(E = "red", flatBox = TRUE)`.

References

Moher, D., Liberati, A., Tetzlaff, J. and Altman, D.G., PRISMA Group. (2009) Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement. *BMJ* 339, b2535.

Examples

```

phases <- c("START_PHASE: # of studies identified through database searching",
           "START_PHASE: # of additional studies identified through other sources",
           "# of studies after duplicates removed",
           "# of studies with title and abstract screened",
           "EXCLUDE_PHASE: # of studies excluded",
           "# of full-text articles assessed for eligibility",
           "EXCLUDE_PHASE: # of full-text excluded, not fitting eligibility criteria",
           "# of studies included in qualitative synthesis",
           "EXCLUDE_PHASE: # studies excluded, incomplete data reported",
           "final # of studies included in quantitative synthesis (meta-analysis)")
plot_PRISMA(phases, design = "cinnamonMint")

```

random_d

Random generation of Hedges' d effect sizes.

Description

Generates random Hedges' d (1981, 1982) effect sizes and their variances.

Usage

```
random_d(K, X_t, var_t, N_t, X_c, var_c, N_c, bias_correction = TRUE)
```

Arguments

K	Number of effect sizes to generate.
X_t	The population mean (μ) of the (t)reatment group.
var_t	The population variance of the treatment group mean.
N_t	The number of samples of the treatment mean. When a non-negative integer, all treatment means will be estimated using the same N. A vector of unequal N's can also be taken; if so, K will be ignored and the number of randomly generated means will equal the length of that vector, and each mean will be based on each N within the vector.
X_c	The population mean (μ) of the (c)ontrol group.
var_c	The population variance of the control group mean.
N_c	The number of samples of the control mean. When a non-negative integer, all control means will be estimated using the same N. A vector of unequal N's can also be taken; if so, K will be ignored and the number of randomly generated means will equal the length of that vector, and each mean will be based on each N within the vector.
bias_correction	When "FALSE", returns Cohen's g effect sizes that are not adjusted using a small-sample correction (J).

Value

A data table with columns of random effect sizes (d) and their variances (var_d).

References

Hedges, L.V. 1981. Distribution theory for Glass's estimator of effect size and related estimators. *Journal of Educational Statistics* 6: 107-128.

Hedges, L.V. 1982. Estimation of effect size from a series of independent experiments. *Psychological Bulletin* 92: 490-499.

Examples

```
random_d(K = 5, X_t = 25, var_t = 1, N_t = 15, X_c = 10, var_c = 1, N_c = 15)
```

random_missingness *Random generation of missingness in a data frame.*

Description

Generates random NA's in in a column or groups of columns of a data frame. Used in imputation simulations based on complete datasets.

Usage

```
random_missingness(aDataFrame, columnNames, percentMissing = 10)
```

Arguments

aDataFrame	A data.frame where missingness will be simulated.
columnNames	A string or a vector of strings that describe the column names (labels) where missingness will be simulated.
percentMissing	The percentage of missingness within specified columns. "Percent missing" uses a binomial distribution to simulate missing data. Default is 10 (i.e. 10% missing). Use impute_missingness for a summary of these randomly generated missing data.

Value

A data table with columns of missing data (specified as NA's).

random_N *Random generation of sample sizes (N) for study outcomes.*

Description

Generates random sample sizes (N) by either sampling from a Negative Binomial or Poisson distribution.

Usage

```
random_N(K, method = "NegativeBinomial", mean = 15, min = 3, NB_size = 15)
```

Arguments

K	Number of sample sizes to generate.
method	A string that defines what sampling distribution to generate random N. The default is "NegativeBinomial" but a "Poisson" distribution can also be used.
mean	The population mean (μ) if "NegativeBinomial", or the lambda (dispersion parameter) if "Poisson". The default is 15, which will generate sample sizes that on average will center around $N = 15$.
min	A non-negative integer that specifies the minimum sample size that can be generated. Default is $N = 3$.
NB_size	Dispersion parameter for the "Negative Binomial" distribution that must be strictly positive, but need not be integer. Default is 15, which creates a long tail for random N's ranging to about $N = 60$. Increase value to create a longer tail of random sample sizes.

Value

A vector of random sample sizes (N).

random_OR *Random generation of odds ratio (OR) effect sizes.*

Description

Generates random odds ratios, logged odds ratios, and their variances (Cornfield 1951).

Usage

```
random_OR(K, p_A, N_A, p_B, N_B, continuity = 0.5, logged = TRUE)
```

Arguments

K	Number of effect sizes to generate.
p_A	The odds of the event of interest for Group A. A probability ranging from zero to one.
N_A	The total number of samples of Group A.
p_B	The odds of the event of interest for Group B. A probability ranging from zero to one.
N_B	The total number of samples of Group B.
continuity	Odds ratios with zero events cannot be computed. Following, Cox (1970), a continuity correction can be added to each cell of the 2 by 2 table to help improve this problem of zero events within the table. The default value added is 0.5.
logged	When "FALSE", returns non-logged transformed odds ratios and appropriate variances. Default is TRUE.

Value

A data table with columns of random effect sizes (OR) and their variances.

References

Cornfield, J. 1951. A method for estimating comparative rates from Clinical Data. Applications to cancer of the lung, breast, and cervix. *Journal of the National Cancer Institute* 11: 1269-1275.

Cox, D.R. 1970. The continuity correction. *Biometrika* 57: 217-219.

Examples

```
random_OR(K = 5, p_A = 0.3, N_A = 100, p_B = 0.1, N_B = 60)
```

random_pairedN

Random generation of paired sample sizes (N) for study outcomes.

Description

Generates random paired sample sizes (N). For example, sample sizes for a treatment group and samples sizes for a control group. These paired N are often correlated within studies.

Usage

```
random_pairedN(K, mean = 15, min = 3, correlation = 0.95)
```

Arguments

K	Number of paired sample sizes to generate.
mean	The lambda (dispersion parameter) of a Poisson distribution. The default is 15, which will generate sample sizes that on average will center around $N = 15$.
min	A non-negative integer that specifies the minimum sample size that can be generated. Default is $N = 3$.
correlation	A correlation ranging from zero to one that specifies how 'similar' the paired sample sizes will be to one another. Default is 0.95 (i.e. the paired sample sizes will be highly correlated).

Value

A data table of paired random sample sizes (N).

random_r	<i>Random generation of correlation coefficients.</i>
----------	---

Description

Generates random correlation coefficients (r or Pearson product-moment correlation coefficients) and their variances (Pearson 1895). Also provides Fisher z -transformed correlation coefficients (Fisher 1915).

Usage

```
random_r(K = 100, correlation = 0.5, N = 10, Fisher_Z = FALSE)
```

Arguments

K	Number of effect sizes to generate.
correlation	The mean population correlation coefficient (ρ) to simulate. Must range between -1 to 1.
N	The number of samples used to estimate each correlation coefficient. When a non-negative integer, all r will be estimated using the same N . A vector of unequal N 's can also be taken; if so, K will be ignored and the number of randomly generated r will equal the length of that vector.
Fisher_Z	When TRUE, also returns the Fisher z -transformed correlation coefficients and their variances (Fisher 1915).

Value

A data table with columns of random effect sizes (r), their variances and sample sizes.

References

Pearson, K. 1895. Notes on regression and inheritance in the case of two parents. Proceedings of the Royal Society of London 58: 240-242.

Fisher, R.A. 1915. Frequency distribution of the values of the correlation coefficient in samples of an indefinitely large population. Biometrika 10: 507-521.

Examples

```
random_r(K = 5, correlation = 0.5, N = 50)
```

random_RR

Random generation of log response ratio (RR) effect sizes.

Description

Generates random log response ratios and their variances (Hedges et al. 1999). NOTE: samples from a log-normal distribution to generate non-negative control and treatment means (following Lajeunesse 2015).

Usage

```
random_RR(K, X_t, var_t, N_t, X_c, var_c, N_c)
```

Arguments

K	Number of effect sizes to generate.
X_t	The population mean (μ) of the (t)reatment group (numerator of ratio).
var_t	The population variance of the treatment group mean.
N_t	The number of samples of the treatment mean. When a non-negative integer, all treatment means will be estimated using the same N. A vector of unequal N's can also be taken; if so, K will be ignored and the number of randomly generated means will equal the length of that vector, and each mean will be based on each N within the vector.
X_c	The population mean (μ) of the (c)ontrol group (denominator of ratio).
var_c	The population variance of the control group mean.
N_c	The number of samples of the control mean. When a non-negative integer, all control means will be estimated using the same N. A vector of unequal N's can also be taken; if so, K will be ignored and the number of randomly generated means will equal the length of that vector, and each mean will be based on each N within the vector.

Value

A data table with columns of random effect sizes (RR) and their variances.

References

- Hedges, L.V., J. Gurevitch, and P.S. Curtis. 1999. The meta-analysis of response ratios in experimental ecology. *Ecology* 80: 1150-1156.
- Lajeunesse, M.J. 2015. Bias and correction for the log response ratio used in ecological meta-analysis. *Ecology*.

Examples

```
random_RR(K = 5, X_t = 25, var_t = 1, N_t = 15, X_c = 10, var_c = 1, N_c = 15)
```

replicate_MetaWin2.0 *Replicate meta-analysis results and summaries from MetaWin 2.0.*

Description

Replicate meta-analysis results and summaries from Rosenberg's et al. (2000) software 'MetaWin' 2.0. Currently only replicates moderator analyses and not meta-regressions.

Usage

```
replicate_MetaWin2.0(
  model,
  weights,
  effects_model = "random",
  data,
  bootstraps = 999
)
```

Arguments

- | | |
|---------------|---|
| model | A two-sided linear formula object describing the model, with the response (effect sizes) on the left of a ~ operator and the moderator variables, separated by +, :, * operators, on the right. NOTE: MetaWin was limited to analyses with a single moderator variable. This function currently supports only categorical moderators. |
| weights | A vector of effect size variances that will be used as weights for the meta-analysis. |
| effects_model | The default is "random", which specifies a random-effects meta-analysis. Other options include "fixed" which presents fixed-effect analyses. |
| data | An optional data frame containing the variables named in model and weights. |
| bootstraps | The number of bootstraps used to estimate confidence intervals. As with 'MetaWin' 2.0, the default is 999. |

References

Rosenberg, M.S., Adams, D.C., and Gurevitch, J. 2000. MetaWin: Statistical Software for Meta-Analysis. Sinauer Associates Sunderland, Massachusetts.

replicate_phyloMeta1.3

Replicate phylogenetic meta-analysis results and summaries from phyloMeta 1.3.

Description

Replicate phylogenetic meta-analysis results and summaries from Lajeunesse (2011) software 'phyloMeta' 1.3. Currently does not fully replicate all functionality.

Usage

```
replicate_phyloMeta1.3(model, weights, data, phylogenyFile)
```

Arguments

model	A two-sided linear formula object describing the model, with the response (effect sizes) on the left of a ~ operator and the moderator variables, separated by +, :, * operators, on the right. NOTE: phyloMeta was limited to analyses with a single moderator variable. This function currently supports only numerical categorical moderators.
weights	A vector of effect size variances that will be used as weights for the meta-analysis.
data	A data frame containing the variables named in model and weights and species names (names must be exact as specified in phylogeny).
phylogenyFile	A text file containing a NEWICK phylogeny. The number of species must be same as (k) number of effect sizes in data.

References

Lajeunesse, M.J. (2011) phyloMeta: a program for phylogenetic comparative analyses with meta-analysis. *Bioinformatics* 27, 2603-2604.

scrape_bibliography *Attempts to scrape/extract bibliographic data from Web of Science.*

Description

A not so elegant way to extract bibliographic data of a research article by scraping the contents of Web of Science (WOS). Requires the DOI (digital object identifier) of an article, as well as web access with an institutional subscription to WOS. Note: This function is not suited to extract data for book chapters available on WOS. Current extractions include: a vector of authors (author), publication year (year), article title (title), journal title (journal), journal volume (volume), page numbers (pages), abstract (abstract), number of references (N_references), number of citations (N_citations), journal impact factor (journal_IF), and the year the journal impact factor was released (journal_IF_year). Finally the date of the scrape is also provided (date_scraped). Bulleted abstracts or those with subheadings or subparagraphs will not be extracted properly.

Usage

```
scrape_bibliography(DOI, quiet = FALSE)
```

Arguments

DOI	A string as the DOI (digital object identifier) of a research article.
quiet	When TRUE, does not print an MLA-style reference of the extracted article.

Value

A list of bibliographic extractions and a timestamp of the scrape.

Examples

```
## Not run:

# use DOI to scrape number of WOS citations of a research article
data(example_references_metagear)
someRefs <- effort_initialize(example_references_metagear)
theWOSRef <- scrape_bibliography(someRefs$DOI[1])
print(paste("citations = ", theWOSRef$N_citations))

## End(Not run)
```

Index

* datasets

example_references_metagear, [15](#)
Kam_et_al_2003_Fig2.jpg, [31](#)
Kortum_and_Acymyan_2013_Fig4.jpg,
[32](#)

abstract_screener, [4](#)

browse_DOI, [6](#)

chachi, [7](#)

covariance_commonControl, [8](#)

effort_distribute, [9](#), [11](#), [12](#), [15](#)
effort_initialize, [10](#), [11](#), [12](#), [15](#)
effort_merge, [10](#), [11](#), [12](#), [15](#)
effort_redistribute, [13](#)
effort_summary, [10–12](#), [14](#)
example_references_metagear, [10](#), [11](#), [15](#)

figure_add, [16](#)

figure_barPlot, [17](#)

figure_detectAllPoints, [16](#), [18](#), [20](#), [21](#), [23](#),
[24](#)

figure_detectAxis, [19](#), [19](#), [23](#), [24](#)

figure_display, [20](#)

figure_displayDetectedPoints, [21](#)

figure_displayDetections, [21](#), [22](#)

figure_extractDetectedPoints, [22](#)

figure_read, [20](#), [23](#), [29](#)

figure_removeOutlyingPoints, [24](#)

figure_scatterPlot, [24](#)

figure_splitPlot, [26](#)

figure_transformByColors, [27](#)

figure_transformToBinary, [20](#), [28](#), [28](#)

figure_write, [24](#), [29](#)

impute_missingness, [29](#), [39](#)

impute_SD, [30](#)

isPDF, [31](#)

Kam_et_al_2003_Fig2.jpg, [31](#)

Kortum_and_Acymyan_2013_Fig4.jpg, [32](#)

MA_effectsTable, [32](#)

metagear-package, [3](#)

PDF_download, [33](#), [34](#), [35](#)

PDF_extractImages, [36](#)

PDFs_collect, [33](#), [35](#)

plot_PRISMA, [36](#)

random_d, [38](#)

random_missingness, [39](#)

random_N, [40](#)

random_OR, [40](#)

random_pairedN, [41](#)

random_r, [42](#)

random_RR, [43](#)

replicate_MetaWin2.0, [44](#)

replicate_phyloMeta1.3, [45](#)

scrape_bibliography, [46](#)