

Package ‘BibPlots’

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Title Plot Functions for Use in Bibliometrics

Version 0.0.8

Description Currently, the package provides several functions for plotting and analyzing bibliometric data (JIF, Journal Impact Factor, and paper percentile values), beamplots with citations and percentiles, and three plot functions to visualize the result of a reference publication year spectroscopy (RPYS) analysis performed in the free software ‘CRExplorer’ (see <<http://crexplorer.net>>). Further extension to more plot variants is planned.

Depends R (>= 3.1.2)

License EUPL

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`beampLOT`*Create a beampLOT using raw citations from a WoS download*

Description

Create a beampLOT using raw citations from a WoS download. Use the format "Other File Format -> Tab-delimited (Win, UTF-8)" and provide the downloaded file name. A simple weighting of citation counts is also available for comparison of older with newer publications.

Usage

```
beampLOT(wos_file, do_weight = FALSE, ...)
```

Arguments

| | |
|------------------------|--|
| <code>wos_file</code> | is the file name of the downloaded WoS export in the format Tab-delimited (Win, UTF-8). |
| <code>do_weight</code> | is a boolean to specify if citation counts should be weighted with their age. The older the publication, the smaller the weight. The weight depends on the difference between the year until that citations are counted (i.e., the current calendar year in the case of WoS downloads) and the publication year. A weighting factor of 1 is used for a difference of 0, 1/2 for a difference of 1, ..., and 1/11 for differences of ten or more. |
| <code>...</code> | further parameters passed to <code>stripchart</code> . |

Details

`beampLOT(wos_file="WoS_savedrecs.txt", do_weight=boolean)` Only the argument `wos_file` is mandatory. The argument `do_weight` is optional and `FALSE` by default.

Literature:

- Haunschild, R., Bornmann, L., & Adams, J. (2019). R package for producing beampLOTS as a preferred alternative to the h index when assessing single researchers (based on downloads from Web of Science), *Scientometrics*, DOI 10.1007/s11192-019-03147-3, preprint: <https://arxiv.org/abs/1905.09095>

Examples

```
## Not run: beampLOT("WoS_savedrecs.txt")
```

| | |
|-----------------|---|
| beampLOT_scopus | <i>Create a beampLOT using raw citations from a Scopus download</i> |
|-----------------|---|

Description

Create a beampLOT using raw citations from a Scopus download. Use the CSV/Excel format and provide the downloaded file name. A simple weighting of citation counts is also available for comparison of older with newer publications.

Usage

```
beampLOT_scopus(scopus_file, do_weight = FALSE, ...)
```

Arguments

| | |
|-------------|---|
| scopus_file | is the file name of the downloaded Scopus export in the format CSV/Excel. |
| do_weight | is a boolean to specify if citation counts should be weighted with their age. The older the publication, the smaller the weight. The weight depends on the difference between the year until that citations are counted (i.e., the current calendar year in the case of Scopus downloads) and the publication year. A weighting factor of 1 is used for a difference of 0, 1/2 for a difference of 1, ..., and 1/11 for differences of ten or more. |
| ... | further parameters passed to stripchart. |

Details

beampLOT_scopus(scopus_file="Scopus.csv", do_weight=boolean) Only the argument scopus_file is mandatory. The argument do_weight is optional and FALSE by default.

Literature:

- Haunschild, R., Bornmann, L., & Adams, J. (2019). R package for producing beampLOTS as a preferred alternative to the h index when assessing single researchers (based on downloads from Web of Science), *Scientometrics*, DOI 10.1007/s11192-019-03147-3, preprint: <https://arxiv.org/abs/1905.09095>

Examples

```
## Not run: beampLOT_scopus("Scopus.csv")
```

| | |
|------------|--|
| DAMBibPlot | <i>Create a difference against mean plot using journal and paper percentile values</i> |
|------------|--|

Description

Provide journal and paper percentile values in a data frame, e.g. `df`, and the function call `DAMBibPlot(df)` creates the difference against mean plot. `DAMBibPlot` takes some optional arguments to modify its behaviour, see arguments and details.

Usage

```
DAMBibPlot(
  df,
  off_set = 0,
  print_stats = TRUE,
  do_plot = TRUE,
  digits = 1,
  ...
)
```

Arguments

| | |
|--------------------------|--|
| <code>df</code> | data frame with journal and paper percentiles |
| <code>off_set</code> | determines the location of additional plotted information (number of points in each quadrant), values between 0 and 40 might be useful (optional parameter). The default value is 0. |
| <code>print_stats</code> | boolean variable (optional parameter) which determines if the additional statistical values are printed to the R console (T: yes print, F: no do not print). The default value is T. |
| <code>do_plot</code> | boolean variable (optional parameter) which determines if the difference against mean plot is actually produced (T: yes plot, F: no do not plot). The default value is T. |
| <code>digits</code> | integer value to determine the number of desired digits after the decimal point for statistical values (optional parameter). The default value is 1. |
| <code>...</code> | additional arguments to pass to the <code>plot</code> function |

Details

`DAMBibPlot(df=data_frame, off_set=numeric_value, print_stats=boolean, do_plot=boolean)` Only the argument `df` is necessary. All other arguments are optional.

Literature:

- Bland, J. M., & Altman, D. G. (1986). Statistical Methods for Assessing Agreement between Two Methods of Clinical Measurement. *Lancet*, 1(8476), 307-310, <https://www.ncbi.nlm.nih.gov/pubmed/2868172>

Cleveland, W. S. (1985). The elements of graphing data. Monterey, CA: Wadsworth Advanced Books and Software.

- Bornmann, L., & Haunschild, R. (2017). Plots for visualizing paper impact and journal impact of single researchers in a single graph, DOI: 10.1007/s11192-018-2658-1, preprint: <https://arxiv.org/abs/1707.04050>

An example data frame is provided as `example_researcher` in the package. It can be used to create a difference against mean plot using default values.

Examples

```
data(example_researcher)
```

```
DAMBibPlot(example_researcher)
```

| | |
|---------------------------------|--|
| <code>example_researcher</code> | <i>Example data set from publication for scatter plot and difference against mean plot</i> |
|---------------------------------|--|

Description

Contains the data set (`example_researcher`).

| | |
|--------------------------------|---|
| <code>inv_perc_beamplot</code> | <i>Create a beamplot using inverted percentile values</i> |
|--------------------------------|---|

Description

Create a beamplot using inverted percentile values.

Usage

```
inv_perc_beamplot(rd, au_name = "Example Researcher", ...)
```

Arguments

| | |
|----------------------|--|
| <code>rd</code> | is a dataframe with two columns: (i) publication year and (ii) inverted percentile value with one row per paper/dataset. |
| <code>au_name</code> | is the name of the researcher this beamplot belongs to. |
| <code>...</code> | further parameters passed to <code>stripchart</code> . |

Details

`inv_perc_beamplot(rd, au_name='Name of researcher')` Only the `rd` is argument mandatory. It has to be a dataframe with two columns: (i) publication year and (ii) inverted percentile value with one row per paper/dataset.

Literature:

- Haunschild, R., Bornmann, L., & Adams, J. (2019). R package for producing beamplots as a preferred alternative to the h index when assessing single researchers (based on downloads from Web of Science), *Scientometrics*, DOI 10.1007/s11192-019-03147-3, preprint: <https://arxiv.org/abs/1905.09095>
 - Bornmann, L. & Marx, W. (2014a). Distributions instead of single numbers: percentiles and beam plots for the assessment of single researchers. *Journal of the American Society of Information Science and Technology*, 65(1), 206–208 - Bornmann, L. & Marx, W. (2014b). How to evaluate individual researchers working in the natural and life sciences meaningfully? A proposal of methods based on percentiles of citations. *Scientometrics*, 98(1), 487-509. DOI: 10.1007/s11192-013-1161-y. - Bornmann, L., & Haunschild, R. (2018). Plots for visualizing paper impact and journal impact of single researchers in a single graph. *Scientometrics*, 115(1), 385-394. DOI: 10.1007/s11192-018-2658-1.

Examples

```
## Not run: inv_perc_beamplot(rd, au_name='Name of researcher')
```

jpscatter

Create a scatter plot using journal and paper percentile values

Description

Provide journal and paper percentile values in a data frame, e.g. `df`, and the function call `jpscatter(df)` creates the scatter plot. The function `jpscatter` takes some optional arguments to modify its behaviour, see arguments and details.

Usage

```
jpscatter(df, off_set = 0, print_stats = TRUE, do_plot = TRUE, digits = 1, ...)
```

Arguments

| | |
|--------------------------|--|
| <code>df</code> | data frame with journal and paper percentiles |
| <code>off_set</code> | determines the location of additional plotted information (number of points in each quadrant), values between 0 and 40 might be useful (optional parameter). The default value is 0. |
| <code>print_stats</code> | boolean variable (optional parameter) which determines if the additional statistical values are printed to the R console (T: yes print, F: no do not print). The default value is T. |
| <code>do_plot</code> | boolean variable (optional parameter) which determines if the scatter plot is actually produced (T: yes plot, F: no do not plot). The default value is T. |

`digits` integer value to determine the number of desired digits after the decimal point for statistical values (optional parameter). The default value is 1.

`...` additional arguments to pass to the [plot](#) function

Details

`jpscatter(df=data_frame, off_set=numeric_value, print_stats=boolean, do_plot=boolean, digits=integer)`
 Only the argument `df` is necessary. All other arguments are optional.

Literature:

- Bornmann, L., & Haunschild, R. (2017). Plots for visualizing paper impact and journal impact of single researchers in a single graph, DOI: 10.1007/s11192-018-2658-1, preprint: <https://arxiv.org/abs/1707.04050>

An example data frame is provided as `example_researcher` in the package. It can be used to create a scatter plot using default values.

Examples

```
data(example_researcher)

jpscatter(example_researcher)
```

ncr_comp

Create a spectrogram using data from the free software CRExplorer

Description

Provide the contents of CSV files from the 'CRExplorer' in data frames, e.g. `df1` and `df2`, and the function call `ncr_comp(df1, df2, py1, py2)` creates a plot with both sets of NCR values. Here, `py1` and `py2` are the lowest and highest publication year to be used in the plot. The function `ncr_comp` takes some optional arguments to modify its behaviour, see arguments and details.

Usage

```
ncr_comp(
  df1,
  df2,
  py1,
  py2,
  col_cr = "red",
  smoothing = TRUE,
  par_pch = 20,
  ...
)
```

Arguments

| | |
|-----------|---|
| df1 | data frame 1 with reference publication year and number of cited references, e. g., as exported from the CRExplorer (File > Export > CSV (Graph)). |
| df2 | data frame 2 with reference publication year and number of cited references, e. g., as exported from the CRExplorer (File > Export > CSV (Graph)). |
| py1 | determines lowest reference publication year which should be shown in the graph. |
| py2 | determines highest reference publication year which should be shown in the graph. |
| col_cr | character color name value to determine color of the line and points of the number of cited references (optional parameter). The default value is "red". |
| smoothing | boolean variable (optional parameter) which determines if the lines of the spectrogram are smoothed or not. (T: yes apply smoothing, F: no do not apply smoothing). The default value is T. |
| par_pch | integer value to set the point type (optional parameter). The default value is 20. |
| ... | additional arguments to pass to the <code>plot</code> , <code>points</code> , and <code>lines</code> functions. |

Details

`ncr_comp <- function(df1, df2, py1, py2, col_cr = "red", smoothing = TRUE, par_pch = 20, ...)`
 Only the arguments `df1`, `df2`, `py1`, and `py2` are necessary. All other arguments are optional. Please use the function `legend` to add a user-defined legend. The solid curve represents the data from `df1` and the dotted curve represents the data from `df2`.

Literature:

- Thor, A., Bornmann, L., Marx, W., Haunschild, R., Leydesdorff, L., & Mutz, Ruediger (2017). Website of the free software 'CRExplorer', <http://www.crexplorer.net>

perc_beamplot *Create a beamplot using percentile values*

Description

Create a beamplot using percentile values.

Usage

```
perc_beamplot(rd, au_name = "Example Researcher", ...)
```

Arguments

| | |
|---------|---|
| rd | is a dataframe with two columns: (i) publication year and (ii) percentile value with one row per paper/dataset. |
| au_name | is the name of the researcher this beamplot belongs to. |
| ... | further parameters passed to <code>stripchart</code> . |

Details

`perc_beamplot(rd, au_name='Name of researcher')` Only the `rd` is argument mandatory. It has to be a dataframe with two columns: (i) publication year and (ii) percentile value with one row per paper/dataset.

Literature:

- Haunschild, R., Bornmann, L., & Adams, J. (2019). R package for producing beamplots as a preferred alternative to the h index when assessing single researchers (based on downloads from Web of Science), *Scientometrics*, DOI 10.1007/s11192-019-03147-3, preprint: <https://arxiv.org/abs/1905.09095>
- Bornmann, L. & Marx, W. (2014a). Distributions instead of single numbers: percentiles and beam plots for the assessment of single researchers. *Journal of the American Society of Information Science and Technology*, 65(1), 206–208
- Bornmann, L. & Marx, W. (2014b). How to evaluate individual researchers working in the natural and life sciences meaningfully? A proposal of methods based on percentiles of citations. *Scientometrics*, 98(1), 487-509. DOI: 10.1007/s11192-013-1161-y.
- Bornmann, L., & Haunschild, R. (2018). Plots for visualizing paper impact and journal impact of single researchers in a single graph. *Scientometrics*, 115(1), 385-394. DOI: 10.1007/s11192-018-2658-1.

Examples

```
## Not run: perc_beamplot(rd, au_name='Name of researcher')
```

rpys

Create a spectrogram using data from the free software CRExplorer

Description

Provide the contents of the CSV (Graph) file from the 'CRExplorer' in a data frame, e.g. `df`, and the function call `rpys(df, py1, py2)` creates the spectrogram. Here, `py1` and `py2` are the lowest and highest publication year to be used in the plot. The function `rpys` takes some optional arguments to modify its behaviour, see arguments and details.

Usage

```
rpys(
  df,
  py1 = min(df$Year),
  py2 = max(df$Year),
  col_cr = "red",
  col_med = "blue",
  smoothing = TRUE,
  par_pch = 20,
  plot_NCR = TRUE,
  plot_Med = TRUE,
  ...
)
```

Arguments

| | |
|------------------------|---|
| <code>df</code> | data frame with reference publication year, number of cited references, and median deviation as exported from the CRExplorer (File > Export > CSV (Graph)). |
| <code>py1</code> | determines lowest reference publication year which should be shown in the graph (optional parameter). |
| <code>py2</code> | determines highest reference publication year which should be shown in the graph (optional parameter). |
| <code>col_cr</code> | character color name value to determine color of the line and points of the number of cited references (optional parameter). The default value is "red". |
| <code>col_med</code> | character color name value to determine color of the line and points of the median deviation (optional parameter). The default value is "blue". |
| <code>smoothing</code> | boolean variable (optional parameter) which determines if the lines of the spectrogram are smoothed or not. (T: yes apply smoothing, F: no do not apply smoothing). The default value is T. |
| <code>par_pch</code> | integer value to set the point type (optional parameter). The default value is 20. |
| <code>plot_NCR</code> | boolean variable (optional parameter) which determines the NCR curve should be plotted. |
| <code>plot_Med</code> | boolean variable (optional parameter) which determines the median deviation curve should be plotted. |
| <code>...</code> | additional arguments to pass to the plot , points , and lines functions. |

Details

`rpys(df=data_frame, py1=integer_value, py2=integer_value, smoothing=boolean, col_cr=character_color_name, col_med=character_color_name, par_pch=integer, plot_NCR=boolean, plot_Med=boolean, ...)` Only the argument `df` is necessary. All other arguments are optional.

Literature:

- Thor, A., Bornmann, L., & Haunschild, R. (2021). Website of the free software 'CRExplorer', <http://www.crexplorer.net> - Thor, A., Bornmann, L., & Haunschild, R. (2018). CitedReferencesExplorer (CRExplorer) manual. Retrieved December 19, 2019, from <https://andreas-thor.github.io/cre/manual.pdf>

An example data frame is provided as `rpys_example_data` in the package. It can be used to create an example spectrogram.

Examples

```
data(rpys_example_data)

rpys(rpys_example_data, 1935, 2010)
```

| | |
|---------|--|
| rpys_bl | <i>Create a spectrogram with bars and lines using data from the free software CRExplorer</i> |
|---------|--|

Description

Provide the contents of the CSV (Graph) file from the 'CRExplorer' in a data frame, e.g. `df`, and the function call `rpys_bl(df)` creates a spectrogram. Previously, you should use the function `rpys` for a plain line graph to determine the proper parameters, e.g., `x_offset` and `x_range`. Determination of the proper `x_offset` and `x_range` is a bit tricky. Usage of a wrong value of `x_range` will cause an error. Usage of a wrong value of `x_offset` will produce a plot. However, the line for the median deviation and the bars might not be at the proper location. First, adjust `x_range` if necessary, and second, adjust `x_offset` so that the x axis is properly aligned with the line and bars. Compare the plot from `rpys_bl` with your data and the plot from the function `rpys`. The function `rpys_bl` takes some optional arguments to modify its behaviour, see arguments and details.

Usage

```
rpys_bl(  
  df,  
  py1 = min(df$Year),  
  py2 = max(df$Year),  
  x_range = py2 - py1 + 1,  
  col_cr = "grey",  
  col_med = "blue",  
  col_ol = "red",  
  smoothing = TRUE,  
  par_mar = c(5, 5, 1, 5),  
  x_offset = 0,  
  x_min = py1,  
  x_max = py2,  
  x_step1 = 10,  
  x_step2 = 5,  
  y1_min = 0,  
  y1_max = max(df$NCR),  
  y1_step = (max(df$NCR) - min(df$NCR))/5,  
  y2_min = min(df$Median.5),  
  y2_max = max(df$Median.5),  
  y2_step = (max(df$Median.5) - min(df$Median.5))/5,  
  lx = median(df$Year),  
  ly = median(df$Median.5),  
  pl_offset = (max(df$NCR) - min(df$NCR))/50,  
  bar_border = "white",  
  outliers = 2,  
  lpos = 3,  
  pl_cex = 0.9,  
  TFmin = py1,  
)
```

```

    TFmax = py2,
    plot_NCR = TRUE,
    plot_Med = TRUE,
    ...
)

```

Arguments

| | |
|-----------|---|
| df | data frame with reference publication year, number of cited references, and median deviation as exported from the CRExplorer (File > Export > CSV (Graph)). |
| py1 | determines lowest reference publication year which should be shown on the x axis (optional parameter). The default is the minimum RPY. |
| py2 | determines highest reference publication year which should be shown on the x axis (optional parameter). The default is the maximum RPY. |
| x_range | is the range of the x axis (optional parameter). The default is py2-py1+1. |
| col_cr | is a character color name value to determine color of the bars of the number of cited references (optional parameter). The default value is "grey". |
| col_med | is a character color name value to determine color of the line of the median deviation (optional parameter). The default value is "blue". |
| col_ol | is a character color name value to determine color of the outlier labels (optional parameter). The default value is "red". |
| smoothing | boolean variable (optional parameter) which determines if the lines of the spectrogram are smoothed or not. (T: yes apply smoothing, F: no do not apply smoothing). The default value is T. |
| par_mar | integer vector to set the margins (optional parameter). The default value is c(5, 5, 1, 5). |
| x_offset | determines the x axis offset to adjust the median deviation curve properly (optional parameter). The default is 0. |
| x_min | determines lowest reference publication year which should be shown on the x axis (optional parameter). The default is the minimum RPY. |
| x_max | determines highest reference publication year which should be shown on the x axis (optional parameter). The default is the maximum RPY. |
| x_step1 | is the interval of major x tics (optional parameter). |
| x_step2 | is the interval of minor x tics (optional parameter). |
| y1_min | is the minimum left y axis value (optional parameter). |
| y1_max | is the maximum left y axis value (optional parameter). |
| y1_step | is the interval left y axis (optional parameter). |
| y2_min | is the minimum right y axis value (optional parameter). |
| y2_max | is the maximum right y axis value (optional parameter). |
| y2_step | is the interval right y axis (optional parameter). |
| lx | is the x position of the legend (optional parameter). |
| ly | is the y position of the legend according to the right y axis (optional parameter). |

| | |
|------------|--|
| pl_offset | is the offset of the year label (optional parameter). |
| bar_border | is the color around the bars (optional parameter). |
| outliers | is an integer that indicates if outliers should be detected (optional parameter): (0: no outlier detection, 1: outliers are detected and marked, 2: only extreme outliers are detected and marked) |
| lpos | is an integer that determines the position of the outlier year label around the point (optional parameter). Values of 1, 2, 3, and 4, respectively indicate positions below, to the left of, above, and to the right of the specified coordinates. |
| pl_cex | is the cex value of the year labels (optional parameter). |
| TFmin | is the first year that should be used for outlier detection according to Tukey's fences. |
| TFmax | is the last year that should be used for outlier detection according to Tukey's fences. |
| plot_NCR | boolean variable (optional parameter) which determines the NCR curve should be plotted. |
| plot_Med | boolean variable (optional parameter) which determines the median deviation curve should be plotted. |
| ... | additional arguments to pass to the <code>plot</code> function. |

Details

`rpys_bl(df=data_frame, pyl=integer_value, py2=integer_value, x_range=integer_value, smoothing=boolean, col_cr=character_color_name, col_med=character_color_name, col_ol=character_color_name, par_mar=integer_vector, plot_NCR=boolean, plot_Med=boolean, x_offset=integer_value, x_min=integer_value, x_max=integer_value, x_step1=integer_value, x_step2=integer_value, y1_min=integer_value, y1_max=integer_value, y1_step=integer_value, y2_min=integer_value, y2_max=integer_value, y2_step=integer_value, lx=integer_value, ly=integer_value, pl_offset=integer_value, bar_border=string_value, outliers=integer_value, lpos=integer_value, pl_cex=floating_point_value, TFmin=integer_value, TFmax=integer_value, ...)` Only the argument `df` is necessary. All other arguments are optional, but many should be provided to produce nice plots.

Literature:

- Thor, A., Bornmann, L., & Haunschild, R. (2021). Website of the free software 'CRExplorer', <http://www.crexplorer.net> - Thor, A., Bornmann, L., & Haunschild, R. (2018). CitedReferencesExplorer (CRExplorer) manual. Retrieved December 19, 2019, from <https://andreas-thor.github.io/cre/manual.pdf>
- Tukey, J. W. (1977). Exploratory data analysis. Boston, MA, USA: Addison-Wesley Publishing Company.

An example data frame is provided as `rpys_example_data` in the package. It can be used to create an example spectrogram.

Examples

```
data(rpys_example_data)
```

```
rpys_bl(rpys_example_data)
```

```
rpys_bl(rpys_example_data, x_min=1930, x_max=2020, x_range=91, x_offset=1, lx=1926, ly=135, y1max=300, y1_step=50, y2_min=-150, y2_max=150, y2_step=25, lpos=1)
```

```
rpys_bl(rpys_example_data, py1=1930, py2=2020, x_offset=1, lx=1926, ly=135, y1max=300,  
y1_step=50, y2_min=-150, y2_max=150, y2_step=25, lpos=1)
```

| | |
|--------------------------------|---|
| <code>rpys_example_data</code> | <i>Example data set for the rpys function</i> |
|--------------------------------|---|

Description

Contains the data sets (`rpys_example_data`).

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