

# Package ‘litReview’

August 7, 2026

**Title** Summarizing Graphs for Literature Reviews

**Version** 1.0.0

**Description** Summarizes and visualizes categorical data extracted during literature reviews and evidence syntheses, starting from a data frame with one row per study. Generates publication-ready bar, stacked bar, histogram, waffle, donut, treemap, alluvial, trend, co-occurrence, 'UpSet', tree, and study-by-criteria matrix figures, together with world maps and formatted summary tables. Plot functions return standard 'ggplot2' objects that can be further customized, and an interactive 'Shiny' application is included for building figures without writing code. Aims to help researchers report study characteristics consistently across many publications.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**URL** <https://github.com/sonsoleslp/litReview>,  
<https://sonsoles.me/litReview/>

**BugReports** <https://github.com/sonsoleslp/litReview/issues>

**Imports** cli, dplyr, ggplot2, ggtext, gt, rlang, tidyr (>= 1.3.0)

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RColorBrewer, treemapify, maps, knitr, readxl, rmarkdown, shiny  
(>= 1.7.0), testthat (>= 3.0.0)

**Config/Needs/website** ggalluvial, ggfittext, ggupset, treemapify, maps

**Config/testthat/edition** 3

**VignetteBuilder** knitr

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|                                            |
|--------------------------------------------|
| import_from_google_drive                   |
| <i>Import Data from a Google Drive URL</i> |

---

**Description**

Downloads an Excel file from a URL and reads a specified sheet.

**Usage**

```
import_from_google_drive(url, sheet)
```

**Arguments**

- url                      Character. The download URL for the Excel file.
- sheet                    Character or integer. The sheet name or index to read.

**Value**

A data frame with the contents of the specified sheet.

**Examples**

```
## Not run:
df <- import_from_google_drive(
  "https://drive.google.com/uc?export=download&id=FILE_ID",
  sheet = 1
)

## End(Not run)
```

---

PALETTE

*Default Color Palette*


---

**Description**

A character vector of 8 hex colors for use in literature review plots.

**Usage**

```
PALETTE
```

**Format**

An object of class character of length 8.

**Details**

Anywhere a colors (or palette-style fill) argument accepts this vector, you may instead pass the **name of an RColorBrewer palette** (e.g. "Set2", "Dark2", "Blues"); it is expanded to the number of categories needed. For the heatmap and map fills, a sequential/diverging ColorBrewer name (e.g. "Blues", "RdYlBu") switches to [ggplot2::scale\\_fill\\_distiller\(\)](#). Using a ColorBrewer name requires the **RColorBrewer** package.

**See Also**

[RColorBrewer::brewer.pal\(\)](#)

**Examples**

```
PALETTE
# A ColorBrewer palette name works wherever `colors` is accepted:
if (requireNamespace("RColorBrewer", quietly = TRUE)) {
  reviewWaffle(studies, Design, colors = "Set2")
}
```

reviewAlluvial

*Create an Alluvial (Sankey) Plot***Description**

Shows co-occurrence and flow between categories across multiple columns. Each study traces a path through the strata. Requires the **ggalluvial** package.

**Usage**

```
reviewAlluvial(
  data,
  cols,
  sep = "\r\n",
  study_id = StudyID,
  colors = PALETTE,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  labels = c("none", "prop", "count", "both"),
  flow_labels = FALSE,
  flow_alpha = 0.25,
  stratum_width = 0.5,
  axis_labels = NULL
)
```

**Arguments**

|                            |                                                                                                                                                                                                    |
|----------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | A data frame.                                                                                                                                                                                      |
| <code>cols</code>          | Character vector of column names to use as axes (left to right).                                                                                                                                   |
| <code>sep</code>           | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> . When a column contains multi-value cells, each combination generates a separate alluvium.                            |
| <code>study_id</code>      | Column containing study identifiers (quoted or unquoted). Defaults to <code>StudyID</code> .                                                                                                       |
| <code>colors</code>        | Character vector. Fill colors for strata, cycled or matched by name. Defaults to <a href="#">PALETTE</a> .                                                                                         |
| <code>base_size</code>     | Numeric. Base font size in points. Defaults to 12.                                                                                                                                                 |
| <code>na.rm</code>         | Logical. Drop rows with missing values? Defaults to <code>TRUE</code> .                                                                                                                            |
| <code>na_label</code>      | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                                                                                    |
| <code>labels</code>        | Character. What to show on each stratum. One of <code>"none"</code> (default), <code>"prop"</code> (proportion within axis), <code>"count"</code> , or <code>"both"</code> (count and proportion). |
| <code>flow_labels</code>   | Logical. If <code>TRUE</code> , show counts on the flows between strata. Defaults to <code>FALSE</code> .                                                                                          |
| <code>flow_alpha</code>    | Numeric. Transparency of flows (0–1). Defaults to 0.25.                                                                                                                                            |
| <code>stratum_width</code> | Numeric. Width of stratum bars. Defaults to 0.5.                                                                                                                                                   |
| <code>axis_labels</code>   | Character vector of custom axis labels (same length as <code>cols</code> ), or <code>NULL</code> to use the column names. Defaults to <code>NULL</code> .                                          |

**Value**

A [ggplot2::ggplot](#) object.

**Examples**

```
df <- data.frame(
  StudyID = paste0("S", 1:6),
  Design = c("RCT", "Cohort", "RCT", "RCT", "Cohort", "RCT"),
  Quality = c("High", "Low", "High", "Low", "Low", "High"),
  Outcome = c("Positive", "Negative", "Positive", "Negative",
              "Positive", "Positive"),
  stringsAsFactors = FALSE
)
if (requireNamespace("ggalluvial", quietly = TRUE)) {
  reviewAlluvial(df, c("Design", "Quality", "Outcome"))
}
```

---

reviewBar

---

*Create a Summary Bar Chart*


---

**Description**

Summarizes a column from literature review data and produces a horizontal bar chart with frequency and percentage labels. Returns a standard [ggplot2::ggplot](#) object that can be customized with `+`.

**Usage**

```
reviewBar(
  data,
  col,
  fill = "#7BB0D1",
  width = 0.6,
  sep = "\r\n",
  studlabs = FALSE,
  study_id = StudyID,
  label_space = 1.6,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  na_in_percent = TRUE,
  na_last = FALSE
)
```

**Arguments**

|                            |                                                                                                                    |
|----------------------------|--------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | A data frame with at least a study ID column and the column named by <code>col</code> .                            |
| <code>col</code>           | Column to visualize (quoted or unquoted).                                                                          |
| <code>fill</code>          | Character. Bar fill color. Defaults to "#7BB0D1".                                                                  |
| <code>width</code>         | Numeric. Bar width (0–1). Defaults to 0.5.                                                                         |
| <code>sep</code>           | Character. Separator for multi-value cells. Defaults to "\r\n".                                                    |
| <code>studlabs</code>      | Logical. If TRUE, draws study ID labels on bars using <code>ggfittext::geom_bar_text()</code> . Defaults to FALSE. |
| <code>study_id</code>      | Column containing study identifiers (quoted or unquoted). Defaults to <code>StudyID</code> .                       |
| <code>label_space</code>   | Numeric. Multiplier for x-axis headroom to fit labels. Defaults to 1.6.                                            |
| <code>base_size</code>     | Numeric. Base font size in points; controls proportional scaling of all text and elements. Defaults to 12.         |
| <code>na.rm</code>         | Logical. Drop missing values? Defaults to TRUE.                                                                    |
| <code>na_label</code>      | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to "Not reported".                  |
| <code>na_in_percent</code> | Logical. Include missing rows in the percentage denominator? Defaults to TRUE.                                     |
| <code>na_last</code>       | Logical. If TRUE, place the missing-value category last regardless of its frequency. Defaults to FALSE.            |

**Value**

A `ggplot2::ggplot` object.

**Examples**

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  stringsAsFactors = FALSE
)
reviewBar(df, Design)
reviewBar(df, Design, fill = "#59a14f") + ggplot2::labs(title = "Designs")
```

---

reviewHistogram

---

*Create a Numeric Histogram*


---

**Description**

Bins the values of a numeric column and plots the frequency of each bin. Optionally stacks bars by a second categorical column. Returns a `ggplot2::ggplot` object that can be customized with `+`.

**Usage**

```
reviewHistogram(
  data,
  col,
  fill_by = NULL,
  bins = 30,
  binwidth = NULL,
  fill = "#7BB0D1",
  colors = PALETTE,
  sep = "\r\n",
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported"
)
```

**Arguments**

|           |                                                                                                                             |
|-----------|-----------------------------------------------------------------------------------------------------------------------------|
| data      | A data frame containing at least the column named by col.                                                                   |
| col       | Numeric column to bin (quoted or unquoted).                                                                                 |
| fill_by   | Optional categorical column to stack the bars by (quoted or unquoted). If NULL (default), bars are drawn in a single color. |
| bins      | Integer. Number of bins. Passed to <code>ggplot2::geom_histogram()</code> . Ignored when binwidth is set. Defaults to 30.   |
| binwidth  | Numeric. Optional bin width. Overrides bins when set. Defaults to NULL.                                                     |
| fill      | Character. Bar fill color when fill_by is NULL. Defaults to "#7BB0D1".                                                      |
| colors    | Character vector. Fill colors cycled across categories when fill_by is set. Defaults to <a href="#">PALETTE</a> .           |
| sep       | Character. Separator for multi-value cells in fill_by. Defaults to "\r\n".                                                  |
| base_size | Numeric. Base font size in points; controls proportional scaling of all text and elements. Defaults to 12.                  |
| na.rm     | Logical. Drop rows with missing values in col (and, when set, in fill_by)? Defaults to TRUE.                                |
| na_label  | Character. Label for missing values in fill_by when na.rm = FALSE. Defaults to "Not reported".                              |

**Value**

A [ggplot2::ggplot](#) object.

**Examples**

```
df <- data.frame(
  StudyID = paste0("S", 1:20),
  SampleSize = c(30, 45, 60, 22, 88, 120, 35, 51, 74, 66,
                 40, 95, 110, 28, 72, 58, 41, 33, 80, 105),
  Design = rep(c("RCT", "Cohort", "Case-control", "Other"), 5)
```

```
)
reviewHistogram(df, SampleSize, bins = 8)
reviewHistogram(df, SampleSize, fill_by = Design, bins = 8)
```

---

reviewMap

---

*Create a World Map of Study Counts*


---

## Description

Counts the number of studies per country and shades a world map accordingly. Country values may be English names, common aliases (e.g. "United States", "United Kingdom"), or ISO 2- or 3-letter codes (e.g. "US"/"USA", "GB"/"GBR"), all resolved automatically. Any value that cannot be matched to a map region triggers a warning listing it, so it is easy to correct. Returns a [ggplot2::ggplot](#) object.

## Usage

```
reviewMap(
  data,
  country_col = Country,
  sep = "\r\n",
  fill = "#7BB0D1",
  base_size = 12,
  na.rm = TRUE
)
```

## Arguments

|             |                                                                    |
|-------------|--------------------------------------------------------------------|
| data        | A data frame with at least the column named by country_col.        |
| country_col | Country column (quoted or unquoted). Defaults to Country.          |
| sep         | Character. Separator for multi-value cells. Defaults to "\r\n".    |
| fill        | Character. High-end color for the gradient. Defaults to "#7BB0D1". |
| base_size   | Numeric. Base font size in points. Defaults to 12.                 |
| na.rm       | Logical. Drop missing values? Defaults to TRUE.                    |

## Details

Unlike the categorical plots, reviewMap() takes only na.rm: a choropleth has no missing-value category to label (na\_label) and shows a colour scale rather than a percentage (na\_in\_percent), so those arguments do not apply. Countries with no data are shaded with a neutral na.value.

## Value

A [ggplot2::ggplot](#) object.



## Examples

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3"),
  Country = c("Spain", "Spain", "Germany"),
  stringsAsFactors = FALSE
)
if (requireNamespace("maps", quietly = TRUE)) {
  reviewMap(df)
}
```

---

reviewMatrix

---

*Create a Study-by-Criteria Coding Matrix*


---

## Description

Draws an evidence / coding matrix: one row per study, one column per criterion, and a tile wherever a study addresses a criterion. The tile **fill** encodes an optional per-study attribute (e.g. document type) and the **letter** inside each tile is the cell's own value (e.g. a coding level such as O/D/M). Column headers can carry the number of studies addressing each criterion. Returns a standard [ggplot2::ggplot](#) object.

## Usage

```
reviewMatrix(
  data,
  cols,
  color_by = NULL,
  study_id = StudyID,
  levels = NULL,
  colors = PALETTE,
  show_counts = TRUE,
  base_size = 12,
  label_wrap = 20,
  empty_fill = "#FCFCE6",
  tile_color = "white",
  na.rm = TRUE,
  na_label = "Not reported"
)
```

## Arguments

|          |                                                                                                                                                                   |
|----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data     | A data frame with one row per study.                                                                                                                              |
| cols     | Character vector of criterion column names, in the order they should appear on the x-axis. Each cell holds the code shown in the tile, or NA/"" for no tile.      |
| color_by | Optional column name (character) giving each study's category, mapped to the tile fill (e.g. "DocumentType"). NULL (default) fills all tiles with a single color. |

|             |                                                                                                                                                                                                                                                       |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| study_id    | Column with the study labels for the y-axis (quoted or unquoted). Defaults to StudyID.                                                                                                                                                                |
| levels      | Optional named character vector mapping cell codes to descriptions for the "Level" legend, e.g. c(0 = "Operationalized", D = "Discussed", M = "Mention"). The names fix the legend order. NULL (default) labels the legend with the codes themselves. |
| colors      | Character vector of fill colors for the color_by categories. Defaults to <a href="#">PALETTE</a> .                                                                                                                                                    |
| show_counts | Logical. Append " (N=k)" to each column header, where k is the number of studies addressing that criterion. Defaults to TRUE.                                                                                                                         |
| base_size   | Numeric. Base font size in points. Defaults to 12.                                                                                                                                                                                                    |
| label_wrap  | Integer. Wrap axis labels longer than this many characters. NULL/Inf disables. Defaults to 20.                                                                                                                                                        |
| empty_fill  | Character. Fill for the background grid behind empty cells. Defaults to "#FCFCE6".                                                                                                                                                                    |
| tile_color  | Character. Border color between tiles. Defaults to "white".                                                                                                                                                                                           |
| na.rm       | Logical. If TRUE (default), cells with a missing/empty value are left blank (the study did not address that criterion). If FALSE, they are drawn as an explicit tile labelled with na_label.                                                          |
| na_label    | Character. Code shown in unaddressed cells when na.rm = FALSE. Defaults to "Not reported".                                                                                                                                                            |

## Details

The input is one row per study (wide format): a study-id column, an optional grouping column for the fill, and one column per criterion holding the cell code (or NA/empty where the study does not address that criterion).

## Value

A [ggplot2::ggplot](#) object.

## Examples

```
studies_wide <- data.frame(
  StudyID = c("Tam 2024", "Schiff 2021", "Reddy 2023", "Yu 2023"),
  Type    = c("Journal", "Journal", "Journal", "Conference"),
  Accuracy = c("O", "D", "D", "M"),
  Equity   = c(NA, "D", "D", "O"),
  Ethics   = c("O", "D", "D", "O"),
  stringsAsFactors = FALSE
)
reviewMatrix(studies_wide, c("Accuracy", "Equity", "Ethics"),
  color_by = "Type",
  levels = c(0 = "Operationalized", D = "Discussed", M = "Mention"))
```

---

|               |                                       |
|---------------|---------------------------------------|
| reviewOverlap | <i>Create a Co-occurrence Heatmap</i> |
|---------------|---------------------------------------|

---

## Description

Counts how many studies share each combination of values in two columns and displays the result as a tile heatmap. Returns a [ggplot2::ggplot](#) object.

## Usage

```
reviewOverlap(
  data,
  col1,
  col2,
  sep = "\r\n",
  fill = "#7BB0D1",
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  studlabs = FALSE,
  study_id = StudyID,
  label_wrap = 15
)
```

## Arguments

|                         |                                                                                                                                                               |
|-------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>       | A data frame with at least the columns named by <code>col1</code> and <code>col2</code> .                                                                     |
| <code>col1</code>       | First column (quoted or unquoted), mapped to the x-axis.                                                                                                      |
| <code>col2</code>       | Second column (quoted or unquoted), mapped to the y-axis.                                                                                                     |
| <code>sep</code>        | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> .                                                                                 |
| <code>fill</code>       | Character. High-end color for the gradient. Defaults to <code>"#7BB0D1"</code> .                                                                              |
| <code>base_size</code>  | Numeric. Base font size in points. Defaults to 12.                                                                                                            |
| <code>na.rm</code>      | Logical. Drop missing values? Defaults to <code>TRUE</code> .                                                                                                 |
| <code>na_label</code>   | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                                               |
| <code>studlabs</code>   | Logical. If <code>TRUE</code> , show comma-separated study IDs inside each tile instead of (or below) the count. Defaults to <code>FALSE</code> .             |
| <code>study_id</code>   | Column containing study identifiers (quoted or unquoted). Used when <code>studlabs = TRUE</code> . Defaults to <code>StudyID</code> .                         |
| <code>label_wrap</code> | Integer. Wrap axis tick labels longer than this many characters onto multiple lines. Set to <code>NULL</code> or <code>Inf</code> to disable. Defaults to 15. |

## Value

A [ggplot2::ggplot](#) object.

## Examples

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  Country = c("UK", "UK", "Spain", "Spain"),
  stringsAsFactors = FALSE
)
reviewOverlap(df, Design, Country)
reviewOverlap(df, Design, Country, studlabs = TRUE)
```

---

reviewPie

---

*Create a Donut or Pie Chart*


---

## Description

Summarizes a column and displays frequencies as a donut (default) or pie chart with count and percentage labels. Returns a [ggplot2::ggplot](#) object.

## Usage

```
reviewPie(
  data,
  col,
  sep = "\r\n",
  colors = PALETTE,
  donut = TRUE,
  study_id = StudyID,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  na_in_percent = TRUE,
  na_last = FALSE
)
```

## Arguments

|           |                                                                                               |
|-----------|-----------------------------------------------------------------------------------------------|
| data      | A data frame with at least a study ID column and the column named by col.                     |
| col       | Column to visualize (quoted or unquoted).                                                     |
| sep       | Character. Separator for multi-value cells. Defaults to "\r\n".                               |
| colors    | Character vector. Fill colors cycled across categories. Defaults to <a href="#">PALETTE</a> . |
| donut     | Logical. If TRUE (default), renders a donut chart. If FALSE, renders a filled pie chart.      |
| study_id  | Column containing study identifiers (quoted or unquoted). Defaults to StudyID.                |
| base_size | Numeric. Base font size in points. Defaults to 12.                                            |

|               |                                                                                                         |
|---------------|---------------------------------------------------------------------------------------------------------|
| na.rm         | Logical. Drop missing values? Defaults to TRUE.                                                         |
| na_label      | Character. Label for missing values when na.rm = FALSE. Defaults to "Not reported".                     |
| na_in_percent | Logical. Include missing rows in the percentage denominator? Defaults to TRUE.                          |
| na_last       | Logical. If TRUE, place the missing-value category last regardless of its frequency. Defaults to FALSE. |

## Value

A `ggplot2::ggplot` object.

## Examples

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  stringsAsFactors = FALSE
)
reviewPie(df, Design)
reviewPie(df, Design, donut = FALSE)
```

---

reviewStackedBar

---

*Create a Stacked / Grouped Bar Chart*


---

## Description

Cross-tabulates a primary category (`col`) against a grouping variable (`group`) and displays the result as horizontal stacked bars. Use `position = "fill"` for within-category proportions (each bar sums to 100%) or `position = "stack"` for raw counts. Both columns may contain multi-value cells, which are split before counting. Returns a standard `ggplot2::ggplot` object.

## Usage

```
reviewStackedBar(
  data,
  col,
  group,
  position = c("fill", "stack"),
  fill = PALETTE,
  width = 0.7,
  sep = "\r\n",
  study_id = StudyID,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  na_last = FALSE,
  labels = TRUE
)
```

Arguments

|           |                                                                                                                                                      |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| data      | A data frame with at least the columns named by col and group.                                                                                       |
| col       | Primary category (quoted or unquoted); one horizontal bar per value.                                                                                 |
| group     | Grouping/splitting column (quoted or unquoted); mapped to the bar fill.                                                                              |
| position  | Character. "fill" (default) scales each bar to 100% to compare proportions; "stack" shows raw counts.                                                |
| fill      | Character vector of fill colors for the groups. Defaults to <a href="#">PALETTE</a> .                                                                |
| width     | Numeric. Bar width (0–1). Defaults to 0.7.                                                                                                           |
| sep       | Character. Separator for multi-value cells. Defaults to "\r\n".                                                                                      |
| study_id  | Column containing study identifiers (quoted or unquoted). Defaults to StudyID. Present for API consistency; not currently used.                      |
| base_size | Numeric. Base font size in points. Defaults to 12.                                                                                                   |
| na.rm     | Logical. Drop missing values? Defaults to TRUE.                                                                                                      |
| na_label  | Character. Label for missing values when na.rm = FALSE. Defaults to "Not reported".                                                                  |
| na_last   | Logical. If TRUE (and na.rm = FALSE), place the missing category last — at the bottom of the axis and the end of each bar/legend. Defaults to FALSE. |
| labels    | Logical. Draw the count (or percentage) inside each segment? Defaults to TRUE.                                                                       |

Value

A [ggplot2::ggplot](#) object.

Examples

```
df <- data.frame(
  StudyID = paste0("S", 1:6),
  Design = c("RCT", "Cohort", "RCT", "Cohort", "RCT", "Cohort"),
  Risk = c("Low", "High", "Low", "Moderate", "High", "Low"),
  stringsAsFactors = FALSE
)
reviewStackedBar(df, Design, Risk)
reviewStackedBar(df, Design, Risk, position = "stack")
```

---

|             |                        |
|-------------|------------------------|
| reviewTable | Create a Summary Table |
|-------------|------------------------|

---

Description

Summarizes a column from literature review data and returns a formatted [gt::gt\(\)](#) table showing each category, its associated study IDs, frequency, and percentage.

**Usage**

```
reviewTable(
  data,
  col,
  sep = "\r\n",
  study_id = StudyID,
  latex = FALSE,
  cite = FALSE,
  na.rm = TRUE,
  na_label = "Not reported",
  na_in_percent = TRUE,
  na_last = FALSE
)
```

**Arguments**

|                            |                                                                                                                                                                                                |
|----------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | A data frame with at least a study ID column and the column named by <code>col</code> .                                                                                                        |
| <code>col</code>           | Column to summarize (quoted or unquoted).                                                                                                                                                      |
| <code>sep</code>           | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> .                                                                                                                  |
| <code>study_id</code>      | Column containing study identifiers (quoted or unquoted). Defaults to <code>StudyID</code> .                                                                                                   |
| <code>latex</code>         | Logical. If <code>TRUE</code> , returns the table as LaTeX code via <code>gt::as_latex()</code> instead of a <code>gt::gt()</code> object. Defaults to <code>FALSE</code> .                    |
| <code>cite</code>          | Logical. If <code>TRUE</code> , treats values in <code>study_id</code> as BibTeX reference keys and wraps the per-row study list in <code>\cite{...}</code> . Defaults to <code>FALSE</code> . |
| <code>na.rm</code>         | Logical. Drop missing values? Defaults to <code>TRUE</code> .                                                                                                                                  |
| <code>na_label</code>      | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                                                                                |
| <code>na_in_percent</code> | Logical. Include missing rows in the percentage denominator? Defaults to <code>TRUE</code> .                                                                                                   |
| <code>na_last</code>       | Logical. If <code>TRUE</code> , place the missing-value category last regardless of its frequency. Defaults to <code>FALSE</code> .                                                            |

**Value**

A `gt::gt()` table, or a LaTeX character string if `latex = TRUE`. The LaTeX output prints cleanly in the console, and renders automatically in knitr/R Markdown chunks with `results = "asis"`.

**Examples**

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  stringsAsFactors = FALSE
)
reviewTable(df, Design)
reviewTable(df, Design, latex = TRUE, cite = TRUE)
```

reviewTree

*Create a Hierarchical Tree Diagram***Description**

Draws a left-to-right node-link tree from a set of columns given **in order**. The first column forms the top-level branches, the next column their children, and so on; multi-value cells are split so a study can sit in several branches. Each level-1 branch gets its own colour, inherited by its descendants, and the leaves can attach a wrapped list of the studies that reach them. Returns a standard [ggplot2::ggplot](#) object.

**Usage**

```
reviewTree(
  data,
  cols,
  study_id = StudyID,
  sep = "\r\n",
  show_members = TRUE,
  member_wrap = 36,
  label_wrap = 18,
  counts = c("none", "count", "percent", "both"),
  root_label = "All studies",
  colors = PALETTE,
  root_fill = "#F4F4C8",
  base_size = 11,
  na.rm = TRUE,
  na_label = "Not reported",
  na_last = FALSE
)
```

**Arguments**

|              |                                                                                                                                    |
|--------------|------------------------------------------------------------------------------------------------------------------------------------|
| data         | A data frame with one row per study.                                                                                               |
| cols         | Character vector of columns defining the hierarchy, from root (first) to leaf (last). Each level branches by that column's values. |
| study_id     | Column with the study labels collected at the leaves (quoted or unquoted). Defaults to StudyID.                                    |
| sep          | Character. Separator for multi-value cells. Defaults to "\r\n".                                                                    |
| show_members | Logical. Attach a box listing the contributing studies at each leaf. Defaults to TRUE.                                             |
| member_wrap  | Integer. Wrap the member list at this many characters. Defaults to 36.                                                             |
| label_wrap   | Integer. Wrap node labels at this many characters. Defaults to 18.                                                                 |



|            |                                                                                                                                                                                                                                                                                 |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| counts     | Character. Annotate each node with the number and/or percentage of studies it covers: "none" (default), "count", "percent", or "both". Counts are distinct studies; percentages are relative to all studies, so sibling branches may sum past 100% when cells are multi-valued. |
| root_label | Character. Text for the root node. Defaults to "All studies".                                                                                                                                                                                                                   |
| colors     | Character vector of branch colours (one per level-1 value). Defaults to <a href="#">PALETTE</a> .                                                                                                                                                                               |
| root_fill  | Character. Fill for the root node. Defaults to "#F4F4C8".                                                                                                                                                                                                                       |
| base_size  | Numeric. Base font size in points. Defaults to 11.                                                                                                                                                                                                                              |
| na.rm      | Logical. Drop missing values? Defaults to TRUE.                                                                                                                                                                                                                                 |
| na_label   | Character. Label for missing values when na.rm = FALSE. Defaults to "Not reported".                                                                                                                                                                                             |
| na_last    | Logical. If TRUE (and na.rm = FALSE), order the missing branch last (at the bottom) at every level. Defaults to FALSE.                                                                                                                                                          |

**Value**

A [ggplot2::ggplot](#) object.

**Examples**

```
data(studies)
reviewTree(studies, c("InterventionType", "Intervention"), study_id = Author)
```

---

reviewTreemap

*Create a Treemap*


---

**Description**

Displays category frequencies as nested rectangles whose area is proportional to the count. Optionally color by a second column for a hierarchical view. Requires the **treemapify** package.

**Usage**

```
reviewTreemap(
  data,
  col,
  color_by = NULL,
  sep = "\r\n",
  colors = PALETTE,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  study_id = StudyID,
  studlabs = FALSE,
  border_col = "white"
)
```

**Arguments**

|            |                                                                                                                                                                                                                              |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data       | A data frame.                                                                                                                                                                                                                |
| col        | Column whose values define the rectangles (quoted or unquoted).                                                                                                                                                              |
| color_by   | Optional second column (quoted or unquoted) used to fill the rectangles. When supplied the treemap is grouped hierarchically by color_by, with col nested inside. When NULL (default), rectangles are colored by col itself. |
| sep        | Character. Separator for multi-value cells. Defaults to "\r\n".                                                                                                                                                              |
| colors     | Character vector. Fill colors, cycled or matched by name. Defaults to <a href="#">PALETTE</a> .                                                                                                                              |
| base_size  | Numeric. Base font size in points. Defaults to 12.                                                                                                                                                                           |
| na.rm      | Logical. Drop missing values? Defaults to TRUE.                                                                                                                                                                              |
| na_label   | Character. Label for missing values when na.rm = FALSE. Defaults to "Not reported".                                                                                                                                          |
| study_id   | Column containing study identifiers (quoted or unquoted). Defaults to StudyID.                                                                                                                                               |
| studlabs   | Logical. If TRUE, show study IDs inside each rectangle. Defaults to FALSE.                                                                                                                                                   |
| border_col | Character. Color of rectangle borders. Defaults to "white".                                                                                                                                                                  |

**Value**

A [ggplot2::ggplot](#) object.

**Examples**

```
df <- data.frame(
  StudyID = paste0("S", 1:8),
  Design = c("RCT", "Cohort", "RCT", "RCT", "Cohort", "RCT", "Cohort", "RCT"),
  Quality = c("High", "Low", "High", "Low", "Low", "High", "Low", "High"),
  stringsAsFactors = FALSE
)
if (requireNamespace("treemapify", quietly = TRUE)) {
  reviewTreemap(df, Design)
  reviewTreemap(df, Design, color_by = Quality)
}
```

---

reviewTrend

---

*Create a Year-Trend Bar Chart*


---

**Description**

Shows how the values in a column distribute across publication years as a stacked bar chart. Returns a [ggplot2::ggplot](#) object.

**Usage**

```
reviewTrend(
  data,
  col,
  year_col = Year,
  sep = "\r\n",
  colors = PALETTE,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  na_last = FALSE,
  labels = c("none", "count", "percent", "both", "studies"),
  study_id = StudyID
)
```

**Arguments**

|                        |                                                                                                                                                                                                                                                    |
|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>      | A data frame with at least <code>StudyID</code> (or the column set by <code>study_id</code> ), the column named by <code>col</code> , and a year column.                                                                                           |
| <code>col</code>       | Column to visualize (quoted or unquoted).                                                                                                                                                                                                          |
| <code>year_col</code>  | Year column (quoted or unquoted). Defaults to <code>Year</code> .                                                                                                                                                                                  |
| <code>sep</code>       | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> .                                                                                                                                                                      |
| <code>colors</code>    | Character vector. Fill colors cycled across categories. Defaults to <a href="#">PALETTE</a> .                                                                                                                                                      |
| <code>base_size</code> | Numeric. Base font size in points. Defaults to 12.                                                                                                                                                                                                 |
| <code>na.rm</code>     | Logical. Drop missing values? Defaults to <code>TRUE</code> .                                                                                                                                                                                      |
| <code>na_label</code>  | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                                                                                                                                    |
| <code>na_last</code>   | Logical. If <code>TRUE</code> (and <code>na.rm = FALSE</code> ), place the missing category last in the stack and legend. Defaults to <code>FALSE</code> .                                                                                         |
| <code>labels</code>    | Character. What to display on each bar segment. One of <code>"none"</code> (default), <code>"count"</code> , <code>"percent"</code> (within-year), <code>"both"</code> (count and percent), or <code>"studies"</code> (comma-separated study IDs). |
| <code>study_id</code>  | Column containing study identifiers (quoted or unquoted). Used when <code>labels = "studies"</code> . Defaults to <code>StudyID</code> .                                                                                                           |

**Value**

A [ggplot2::ggplot](#) object.

**Examples**

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Year = c(2020, 2021, 2021, 2022),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  stringsAsFactors = FALSE
)
```

```

)
reviewTrend(df, Design)
reviewTrend(df, Design, labels = "count")
reviewTrend(df, Design, labels = "percent")
reviewTrend(df, Design, labels = "studies")

```

---

**reviewUpset**
*Create an UpSet Plot of Value Combinations*


---

**Description**

Visualizes how the values of a multi-value column co-occur across studies. Each study contributes the *set* of distinct values it reports; the plot shows the size of each observed combination (intersection) as a bar, with a dot matrix beneath indicating which values make up that combination. This scales past the pairwise [reviewOverlap\(\)](#) when three or more values can co-occur. Returns a standard [ggplot2::ggplot](#) object.

**Usage**

```

reviewUpset(
  data,
  col,
  sep = "\r\n",
  study_id = StudyID,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
  n_intersections = 15,
  sort_by = c("freq", "degree"),
  fill = "#7BB0D1"
)

```

**Arguments**

|                        |                                                                                                                                   |
|------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>      | A data frame with at least the columns named by <code>col</code> and <code>study_id</code> .                                      |
| <code>col</code>       | Multi-value column to analyze (quoted or unquoted).                                                                               |
| <code>sep</code>       | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> .                                                     |
| <code>study_id</code>  | Column containing study identifiers (quoted or unquoted). One combination is formed per study. Defaults to <code>StudyID</code> . |
| <code>base_size</code> | Numeric. Base font size in points. Defaults to 12.                                                                                |
| <code>na.rm</code>     | Logical. Drop missing values? Defaults to <code>TRUE</code> .                                                                     |
| <code>na_label</code>  | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                   |

|                 |                                                                                                                 |
|-----------------|-----------------------------------------------------------------------------------------------------------------|
| n_intersections | Integer. Maximum number of combinations (bars) to display, keeping the largest. Defaults to 15.                 |
| sort_by         | Character. Order bars by "freq" (intersection size, default) or "degree" (number of values in the combination). |
| fill            | Character. Bar and matrix-dot color. Defaults to "#7BB0D1".                                                     |

## Details

Requires the **ggupset** package.

## Value

A [ggplot2::ggplot](#) object.

## Examples

```
df <- data.frame(
  StudyID = paste0("S", 1:5),
  Outcome = c("Pain", "Pain\nFunction", "Function",
              "Pain\nFunction\nQoL", "QoL"),
  stringsAsFactors = FALSE
)
if (requireNamespace("ggupset", quietly = TRUE)) {
  reviewUpset(df, Outcome, sep = "\n")
}
```

---

reviewWaffle

---

*Create a Waffle Chart*


---

## Description

Summarizes a column and displays frequencies as a grid of colored squares. Each square represents one occurrence. Returns a [ggplot2::ggplot](#) object.

## Usage

```
reviewWaffle(
  data,
  col,
  sep = "\r\n",
  colors = PALETTE,
  ncol = 5,
  study_id = StudyID,
  base_size = 12,
  na.rm = TRUE,
  na_label = "Not reported",
```

```

    na_in_percent = TRUE,
    na_last = FALSE
  )

```

### Arguments

|                            |                                                                                                                                     |
|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | A data frame with at least a study ID column and the column named by <code>col</code> .                                             |
| <code>col</code>           | Column to visualize (quoted or unquoted).                                                                                           |
| <code>sep</code>           | Character. Separator for multi-value cells. Defaults to <code>"\r\n"</code> .                                                       |
| <code>colors</code>        | Character vector. Fill colors cycled across categories. Defaults to <a href="#">PALETTE</a> .                                       |
| <code>ncol</code>          | Integer. Number of columns in the grid. Defaults to 5.                                                                              |
| <code>study_id</code>      | Column containing study identifiers (quoted or unquoted). Defaults to <code>StudyID</code> .                                        |
| <code>base_size</code>     | Numeric. Base font size in points. Defaults to 12.                                                                                  |
| <code>na.rm</code>         | Logical. Drop missing values? Defaults to <code>TRUE</code> .                                                                       |
| <code>na_label</code>      | Character. Label for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                     |
| <code>na_in_percent</code> | Logical. Include missing rows in the percentage denominator? Defaults to <code>TRUE</code> .                                        |
| <code>na_last</code>       | Logical. If <code>TRUE</code> , place the missing-value category last regardless of its frequency. Defaults to <code>FALSE</code> . |

### Value

A [ggplot2::ggplot](#) object.

### Examples

```

df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", "RCT", "Case-control"),
  stringsAsFactors = FALSE
)
reviewWaffle(df, Design)

```

---

run\_app

*Launch the litReview Shiny App*

---

### Description

Opens an interactive Shiny application for uploading literature review data and creating summary plots. The app provides a notebook-style interface where plots are added as cards that can be individually downloaded or exported together as a ZIP file.

### Usage

```
run_app(...)
```

**Arguments**

... Arguments passed to `shiny::runApp()`, such as `port` or `launch.browser`.

**Value**

Called for its side-effect (launches the app). Returns the value of `shiny::runApp()` invisibly.

**Examples**

```
if (interactive()) {
  run_app()
}
```

---

studies

*Example Literature Review Dataset*


---

**Description**

A synthetic dataset of 50 fictional studies for demonstrating the plotting functions in **litReview**. Contains 27 columns covering common fields extracted during a literature review, including a block of methodological reporting criteria suitable for `reviewMatrix()`.

**Usage**

```
studies
```

**Format**

A data frame with 50 rows and 27 variables:

**StudyID** Unique study identifier (S01–S50).

**bibKey** BibTeX citation key.

**Author** Author list (e.g. "Garcia et al.").

**Year** Publication year (2018–2024).

**Reference** Full reference string.

**Country** Country or countries where the study was conducted. Multi-value cells are separated by newlines.

**Design** Study design (e.g. RCT, Cohort, Cross-sectional).

**SampleSize** Number of participants.

**FollowUpWeeks** Follow-up duration in weeks, or NA.

**AgeGroup** Target age group. May contain multiple values.

**Setting** Study setting (e.g. Hospital, Community, Online).

**Intervention** Intervention type (e.g. CBT, Exercise). May contain multiple values.

**Outcome** Reported outcome (e.g. Pain, Function). May contain multiple values.

**AnalysisApproach** Statistical or analytical approach used.

**RiskOfBias** Risk of bias rating (Low, Moderate, High, or NA).

**FundingSource** Funding source, or NA.

**OpenAccess** Whether the study is open access (Yes, No, or NA).

**InterventionType** Higher-order grouping of Intervention (Behavioral, Educational, Physical, Medical, Multimodal).

**PubType** Publication type (Journal, Conference, Preprint, Report).

**Randomization** Reporting of randomization. Coded "F" (full), "P" (partial), "M" (mentioned), or NA (not addressed). Trial-only item: NA for non-RCT designs.

**Blinding** Reporting of blinding, coded as Randomization. Trial-only item: NA for non-RCT designs.

**SampleJustification** Reporting of sample-size justification, coded "F"/"P"/"M"/NA.

**AttritionReported** Reporting of attrition/dropout, coded as above.

**EthicsApproval** Reporting of ethics approval, coded as above.

**Preregistration** Reporting of preregistration, coded as above.

**EffectSize** Reporting of effect sizes, coded as above.

**LimitationsDiscussed** Reporting of study limitations, coded as above.

## Details

The reporting-criteria columns (Randomization through LimitationsDiscussed) are coded for how fully each study reports the item — "F" full, "P" partial, "M" only mentioned, or NA not addressed — and are designed for the study-by-criteria `reviewMatrix()` plot.

## Examples

```
data(studies)
reviewBar(studies, Design)

# Reporting-criteria matrix
criteria <- c("Randomization", "Blinding", "SampleJustification",
             "AttritionReported", "EthicsApproval", "Preregistration",
             "EffectSize", "LimitationsDiscussed")
reviewMatrix(studies, criteria, color_by = "PubType",
             levels = c(F = "Full", P = "Partial", M = "Mention"))
```



---

|                |                                                  |
|----------------|--------------------------------------------------|
| summarize_data | <i>Summarize Frequency of Values in a Column</i> |
|----------------|--------------------------------------------------|

---

## Description

Splits multi-value cells, counts frequencies, and computes percentages.

## Usage

```
summarize_data(
  data,
  col,
  sep = "\r\n",
  study_id = StudyID,
  na.rm = TRUE,
  na_label = "Not reported",
  na_in_percent = TRUE,
  na_last = FALSE
)
```

## Arguments

|                            |                                                                                                                                                                                                                                         |
|----------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | A data frame containing at least the columns specified by <code>col</code> and <code>study_id</code> .                                                                                                                                  |
| <code>col</code>           | Column to summarize (quoted or unquoted).                                                                                                                                                                                               |
| <code>sep</code>           | Character. The separator used to split multi-value cells. Defaults to <code>"\r\n"</code> .                                                                                                                                             |
| <code>study_id</code>      | Column containing study identifiers (quoted or unquoted). Defaults to <code>StudyID</code> .                                                                                                                                            |
| <code>na.rm</code>         | Logical. If <code>TRUE</code> (default), rows with missing values (NA or empty strings) in <code>col</code> are dropped. If <code>FALSE</code> , they are kept and labelled with <code>na_label</code> .                                |
| <code>na_label</code>      | Character. Label used for missing values when <code>na.rm = FALSE</code> . Defaults to <code>"Not reported"</code> .                                                                                                                    |
| <code>na_in_percent</code> | Logical. If <code>TRUE</code> (default), the denominator for percentages is the total number of rows (including missing). If <code>FALSE</code> , only non-missing rows are counted, so non-missing categories sum to $\approx 100\%$ . |
| <code>na_last</code>       | Logical. If <code>TRUE</code> , the missing-value row (when <code>na.rm = FALSE</code> ) is placed at the bottom of the result regardless of its frequency. Defaults to <code>FALSE</code> (sorted by frequency like all other rows).   |

## Value

A data frame with columns for the grouping variable, Studies (comma-separated study IDs), Frequency, and Percent (numeric, 0–100).

**Examples**

```
df <- data.frame(
  StudyID = c("S1", "S2", "S3", "S4"),
  Design = c("RCT", "Cohort", NA, "RCT"),
  stringsAsFactors = FALSE
)

# Drop NAs (default)
summarize_data(df, Design)

# Keep NAs with a custom label
summarize_data(df, Design, na.rm = FALSE, na_label = "Missing")

# Percentages of non-missing only
summarize_data(df, Design, na_in_percent = FALSE)
```

---

 theme\_litreview

*Literature Review ggplot Theme*


---

**Description**

A clean, manuscript-ready ggplot2 theme with white background, bold axis titles, and bottom legend. All litReview plot functions use this theme by default. The single `base_size` parameter controls the proportional scaling of all text and spacing — increase for posters/slides, decrease for multi-panel figures.

**Usage**

```
theme_litreview(base_size = 12)
```

**Arguments**

`base_size`      Numeric. Base font size in points. Defaults to 12.

**Value**

A `ggplot2::theme` object.

**Examples**

```
library(ggplot2)
ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  theme_litreview()

# Larger for presentations
ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
```

```
theme_litreview(base_size = 18)
```

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