

# Package: miRetrieve (via r-universe)

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**Type** Package

**Title** miRNA Text Mining in Abstracts

**Version** 1.3.4

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**Description** Providing tools for microRNA (miRNA) text mining. miRetrieve summarizes miRNA literature by extracting, counting, and analyzing miRNA names, thus aiming at gaining biological insights into a large amount of text within a short period of time. To do so, miRetrieve uses regular expressions to extract miRNAs and tokenization to identify meaningful miRNA associations. In addition, miRetrieve uses the latest miRTarBase version 8.0 (Hsi-Yuan Huang et al. (2020) ``miRTarBase 2020: updates to the experimentally validated microRNA–target interaction database" <doi:10.1093/nar/gkz896>) to display field-specific miRNA-mRNA interactions. The most important functions are available as a Shiny web application under <<https://miretrieve.shinyapps.io/miRetrieve/>>.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.1.0)

**Imports** dplyr (>= 1.0.7), forcats (>= 0.5.1), ggplot2 (>= 3.3.5), magrittr (>= 2.0.1), openxlsx (>= 4.2.4), plotly (>= 4.9.4.1), purrr (>= 0.3.4), readr (>= 2.0.1), readxl (>= 1.3.1), rlang (>= 0.4.11), scales (>= 1.1.1), stringr (>= 1.4.0), textclean (>= 0.9.3), tidyr (>= 1.1.3), tidytext (>= 0.3.1), topicmodels (>= 0.2.12), wordcloud (>= 2.6), xml2 (>= 1.3.2), zoo (>= 1.8-9)

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add_col_topic	<i>Add topic column to data frame</i>
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### Description

Add topic column to a data frame.

### Usage

```
add_col_topic(df, col.topic = "Topic", topic.name = "Topic1")
```

**Arguments**

<code>df</code>	Data frame which the topic column is added to.
<code>col.topic</code>	String. Name of the topic column to be created.
<code>topic.name</code>	String. Topic name to be contained in <code>col.topic</code> .

**Details**

Add a topic column to a data frame. This topic column is named `col.topic` and contains the string `topic.name`.

**Value**

Data frame with a topic column added.

**See Also**

[assign\\_topic\(\)](#)

---

animal_keywords	<i>Keywords - animals.</i>
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---

**Description**

Keywords to identify abstracts using animal models.

**Usage**

```
animal_keywords
```

**Format**

An object of class character of length 12.

---

assign_topic	<i>Assign topics based on precalculated scores</i>
--------------	--

---

### Description

Assign topics to abstracts based on precalculated scores.

### Usage

```
assign_topic(  
  df,  
  col.topic,  
  threshold,  
  topic.names = NULL,  
  col.topic.name = "Topic",  
  col.pmid = "PMID",  
  discard = FALSE  
)
```

### Arguments

df	Data frame containing precalculated topic scores and PubMed-IDs.
col.topic	Character vector. Vector with column names containing precalculated topic scores.
threshold	Integer vector. Vector containing thresholds for topic columns. Positions in threshold correspond to positions in col.topic.
topic.names	Character vector. Optional. Vector containing names of new topics. Positions in topic.names correspond to positions in col.topic. If topic.names is not provided, col.topic is used to name the new topics.
col.topic.name	String. Name of the new topic column.
col.pmid	String. Column containing PubMed-IDs.
discard	Boolean. If discard = TRUE, only abstracts with a newly assigned topic are kept. Abstracts without a newly assigned topic are discarded.

### Details

Assign topics to abstracts based on precalculated scores. `assign_topic()` compares different precalculated topic scores and assigns the abstract to the topic with the highest score. If there is a tie between topic scores, the abstract is assigned to all topics in question. If an abstract matches no topic, it is assigned to the topic "Unknown".

### Value

Data frame with topics based on precalculated topic scores.

**See Also**

[calculate\\_score\\_topic\(\)](#), [plot\\_score\\_topic\(\)](#), [add\\_col\\_topic\(\)](#)

Other score functions: [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

assign\_topic\_lda      *Assign topics based on LDA model*

---

**Description**

Assign topics to abstracts based on an LDA model.

**Usage**

```
assign_topic_lda(df, lda_model, topic.names, col.pmid = PMID)
```

**Arguments**

df	Data frame to assign topics to. Should be the same data frame that the LDA model was fitted on.
lda_model	LDA-model.
topic.names	Character vector. Vector containing names of the new topics. Must have the same length as the number of topics lda_model was fitted on.
col.pmid	Symbol. Column containing PubMed-IDs.

**Details**

Assign topic to abstracts based on an LDA model. To identify the subject of a topic, use [plot\\_lda\\_term\(\)](#).

**Value**

Data frame with topics assigned to each abstract based on an LDA model.

**See Also**

[fit\\_lda\(\)](#), [plot\\_lda\\_term\(\)](#), [assign\\_topic\(\)](#)

Other LDA functions: [fit\\_lda\(\)](#), [plot\\_lda\\_term\(\)](#), [plot\\_perplexity\(\)](#)

---

biomarker_keywords	<i>Keywords - biomarkers.</i>
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---

**Description**

Keywords to identify abstracts reporting about miRNAs as biomarkers.

**Usage**

```
biomarker_keywords
```

**Format**

An object of class character of length 18.

---

calculate_score_animals	
-------------------------	--

*Calculate animal model scores for abstracts*

---

**Description**

Calculate animal model score for each abstract to indicate possible use of animal models.

**Usage**

```
calculate_score_animals(
  df,
  keywords = animal_keywords,
  case = FALSE,
  threshold = NULL,
  indicate = FALSE,
  discard = FALSE,
  col.abstract = Abstract
)
```

**Arguments**

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. The score is calculated based on these keywords. How much weight a keyword in keywords carries is determined by how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score. The predefined keywords can be accessed via <code>miRetrieve::animal_keywords</code> .
case	Boolean. If case = TRUE, terms contained in keywords are case sensitive. If case = FALSE, terms contained in keywords are case insensitive.

threshold	Integer. Optional. Threshold to decide if an abstract is considered to use animal models or not. If indicate = TRUE or discard = TRUE and threshold is not specified, threshold is automatically set to 1.
indicate	Boolean. If indicate = TRUE, an extra column is added. This extra column contains "Yes" or "No", indicating the use of animal models in abstracts.
discard	Boolean. If discard = TRUE, only abstracts are kept where animal models are present.
col.abstract	Symbol. Column containing abstracts.

### Details

Calculate animal model score for each abstract to indicate possible use of animal models. This score is added to the data frame as an additional column `Animal_score`, containing the calculated animal model score. To decide which abstracts are considered to contain animal models, a threshold can be set via the `threshold` argument. Furthermore, an additional column can be added, verbally indicating the use of animal models in an abstract. Choosing the right threshold can be facilitated using `plot_score_animals()`.

### Value

Data frame with calculated animal model scores. If `discard = FALSE`, adds extra columns to the original data frame with the calculated animal model scores. If `discard = TRUE`, only abstracts with animal models are kept.

### See Also

[plot\\_score\\_animals\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

calculate\_score\_biomarker

*Calculate biomarker scores for abstracts*

---

### Description

Calculate biomarker score for each abstract to indicate possible use of miRNAs as biomarker.

### Usage

```
calculate_score_biomarker(
  df,
  keywords = biomarker_keywords,
  case = FALSE,
  threshold = NULL,
```



```

    indicate = FALSE,
    discard = FALSE,
    col.abstract = Abstract
  )

```

### Arguments

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. The score is calculated based on these keywords. How much weight a keyword in keywords carries is determined by how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score. The predefined keywords can be accessed via <code>miRetrieve::biomarker_keywords</code> .
case	Boolean. If <code>case = TRUE</code> , terms contained in keywords are case sensitive. If <code>case = FALSE</code> , terms contained in keywords are case insensitive.
threshold	Integer. Optional. Threshold to decide if use of miRNAs as biomarker are present in an abstract or not. If <code>indicate = TRUE</code> or <code>discard = TRUE</code> and <code>threshold</code> not specified, <code>threshold</code> is automatically set to 1.
indicate	Boolean. If <code>indicate = TRUE</code> , an extra column is added. This extra column contains "Yes" or "No", indicating the use of miRNAs as biomarker in abstracts.
discard	Boolean. If <code>TRUE</code> , only abstracts are kept where miRNAs as biomarker.
col.abstract	Symbol. Column containing abstracts.

### Details

Calculate biomarker score for each abstract to indicate possible use of miRNAs as biomarker. This score is added to the data frame as an additional column `Biomarker_score`, containing the calculated biomarker score. To decide which abstracts are considered to contain use of miRNAs as biomarker, a threshold can be set via the `threshold` argument. Furthermore, an additional column can be added, verbally indicating the general use of miRNAs as biomarker in an abstract. Choosing the right threshold can be facilitated using `plot_score_biomarker()`.

### Value

Data frame with calculated biomarker scores. If `discard = FALSE`, adds extra columns to the original data frame with calculated biomarker scores. If `discard = TRUE`, only abstracts are with miRNAs as biomarker are kept.

### See Also

[plot\\_score\\_biomarker\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

```
calculate_score_patients
```

*Calculate patients scores for abstracts*

---

### Description

Calculate patients score for each abstract to indicate possible use of patient material.

### Usage

```
calculate_score_patients(
  df,
  keywords = patients_keywords,
  case = FALSE,
  threshold = NULL,
  indicate = FALSE,
  discard = FALSE,
  col.abstract = Abstract
)
```

### Arguments

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. The score is calculated based on these keywords. How much weight a keyword in keywords carries is determined by how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score. The predefined keywords can be accessed via <code>miRetrieve::patients_keywords</code> .
case	Boolean. If <code>case = TRUE</code> , terms contained in keywords are case sensitive. If <code>case = FALSE</code> , terms contained in keywords are case insensitive.
threshold	Integer. Optional. Threshold to decide if use of patient tissue is present in an abstract or not. If <code>indicate = TRUE</code> or <code>discard = TRUE</code> and <code>threshold</code> not specified, <code>threshold</code> is automatically set to 1.
indicate	Boolean. If <code>indicate = TRUE</code> , an extra column is added. This extra column contains "Yes" or "No", indicating the use of patient tissue in abstracts.
discard	Boolean. If <code>discard = TRUE</code> , only abstracts are kept where use of patient tissue is present.
col.abstract	Symbol. Column containing abstracts.

### Details

Calculate patient score for each abstract to indicate possible use of patient material. This score is added to the data frame as an additional column `Patient_score`, containing the calculated patients score. To decide which abstracts are considered to contain patient material, a threshold can be set via the `threshold` argument. Furthermore, an additional column can be added, verbally indicating the general use of patient material. Choosing the right threshold can be facilitated using `plot_score_patients()`.

**Value**

Data frame with calculated patient scores. If `discard = FALSE`, adds extra columns to the original data frame with the calculated patient tissue scores. If `discard = TRUE`, only abstracts with use of patient tissue are kept.

**See Also**

[plot\\_score\\_patients\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

`calculate_score_topic` *Calculate scores of a self-chosen topic*

---

**Description**

Calculate score of a self-chosen topic for each abstract to identify abstracts possibly corresponding to the topic of interest.

**Usage**

```
calculate_score_topic(
  df,
  keywords,
  case = FALSE,
  col.score = "topic_score",
  col.indicate = NULL,
  threshold = NULL,
  discard = FALSE,
  col.abstract = Abstract
)
```

**Arguments**

<code>df</code>	Data frame containing abstracts.
<code>keywords</code>	Character vector. Vector containing keywords. The score is calculated based on these keywords. How much weight a keyword in keywords carries is determined by how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score.
<code>case</code>	Boolean. If <code>case = TRUE</code> , terms contained in keywords are case sensitive. If <code>case = FALSE</code> , terms contained in keywords are case insensitive.
<code>col.score</code>	String. Name of <code>topic_score</code> column.

col.indicate	String. Optional. Name of indicating column. If a string is provided, an extra column is added to df, indicating if the abstract corresponds to the topic of interest by "Yes" or "No".
threshold	Integer. Optional. Threshold to decide if abstract corresponds to topic of interest. If col.topic is specified or discard = TRUE without threshold being specified, threshold is automatically set to 1.
discard	Boolean. If discard = TRUE, only abstracts are kept that correspond to the topic of interest.
col.abstract	Symbol. Column containing abstracts.

### Details

Calculate score of a self-chosen topic for each abstract to identify abstracts possibly corresponding to the topic of interest. This score is added to the data frame as an additional column, usually called `topic_score`, containing the calculated topic score. If there is more than one topic of interest, the column `topic_score` should be appropriately renamed. To decide which abstracts are considered to correspond to the topic of interest, a threshold can be set via the `threshold` argument. Furthermore, an additional column can be added, verbally indicating if the abstract corresponds to the topic. Choosing the right threshold can be facilitated using `plot_score_topic()`.

### Value

Data frame with calculated topic scores. If `discard = FALSE`, adds extra columns to the original data frame with the calculated topic scores. If `discard = TRUE`, only abstracts corresponding to the topic of interest are kept.

### See Also

[assign\\_topic\(\)](#), [plot\\_score\\_topic\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

combine\_df

*Combine data frames into one data frame*

---

### Description

Combine data frames into one data frame.

### Usage

```
combine_df(...)
```

### Arguments

... Data frames to combine into one data frame. Data frames must have the same number of columns and the same column names.

**Details**

Combine data frames into one data frame. `combine_df()` accepts several data frames that are combined into one data frame. Data frames to be combined must have the same number of columns and the same column names.

**Value**

Combined data frame.

**See Also**

Other combine functions: [combine\\_mir\(\)](#)

---

`combine_mir`*Combine miRNA vectors into one*

---

**Description**

Combine miRNA vectors into one.

**Usage**

```
combine_mir(...)
```

**Arguments**

`...` Character vectors. Character vectors containing miRNA names.

**Details**

Combine miRNA vectors into one. miRNA names occurring more than once are reduced to one instance.

**Value**

Combined character vector containing miRNA names.

**See Also**

[get\\_mir\(\)](#)

Other combine functions: [combine\\_df\(\)](#)

---

combine_stopwords	<i>Combine data frames containing stop words</i>
-------------------	--

---

**Description**

Combine data frames containing stop words into one data frame.

**Usage**

```
combine_stopwords(...)
```

**Arguments**

... Data frames with stop words. Data frames must have two columns named "word" and "lexicon".

**Details**

Combine data frames containing stop words into one data frame. Provided data frames must have two columns named "word" and "lexicon".

**Value**

Combined data frame with stop words.

**See Also**

[generate\\_stopwords\(\)](#), [stopwords\\_miretrieve](#), [tidytext::stop\\_words](#)

Other stopword functions: [generate\\_stopwords\(\)](#)

---

compare_mir_count	<i>Compare count of miRNA names between different topics</i>
-------------------	--

---

**Description**

Compare count of miRNA names between different topics.

**Usage**

```
compare_mir_count(  
  df,  
  mir,  
  topic = NULL,  
  normalize = TRUE,  
  col.topic = Topic,  
  col.mir = miRNA,  
  col.pmid = PMID,  
  title = NULL  
)
```

**Arguments**

<code>df</code>	Data frame containing columns for miRNA names, topics, and PubMed-IDs.
<code>mir</code>	Character vector. Vector specifying which miRNA names to compare.
<code>topic</code>	Character vector. Optional. Vector specifying which topics to compare.
<code>normalize</code>	Boolean. If <code>normalize = TRUE</code> , plot the proportion of abstracts mentioning a miRNA name compared to all abstracts in a topic. If <code>normalize = FALSE</code> , plot the absolute number of abstracts mentioning a miRNA in a topic.
<code>col.topic</code>	Symbol. Column containing topic names.
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.
<code>title</code>	String. Plot title.

**Details**

Compare count of miRNA names between different topics by plotting the number of abstracts mentioning the miRNA in a topic. This count can either be normalized, thus plotting the proportion of abstracts mentioning a miRNA name compared to all abstracts of a topic, or it can be not normalized, thus plotting the absolute number of abstracts mentioning a miRNA per topic.

**Value**

Bar plot comparing the count of miRNA names between different topics.

**See Also**

[compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\\_unique\(\)](#), [compare\\_mir\\_terms\(\)](#)

---

`compare_mir_count_log2`*Compare log2-frequency count of miRNA names between two topics*

---

### Description

Compare log2-frequency count of miRNA names between two topics

### Usage

```
compare_mir_count_log2(  
  df,  
  mir,  
  topic = NULL,  
  normalize = TRUE,  
  col.topic = Topic,  
  col.mir = miRNA,  
  col.pmid = PMID,  
  title = NULL  
)
```

### Arguments

<code>df</code>	Data frame containing miRNA names, topics, and PubMed-IDs.
<code>mir</code>	Character vector. Vector specifying which miRNA names to compare.
<code>topic</code>	Character vector. Optional. Vector specifying which topics to compare. If <code>topic = NULL</code> , all topics in <code>df</code> are used.
<code>normalize</code>	Boolean. If <code>normalize = TRUE</code> , proportion of abstracts mentioning a miRNA name compared to all abstracts of a topic are used. If <code>normalize = FALSE</code> , the absolute number of abstracts mentioning a miRNA name is used.
<code>col.topic</code>	Symbol. Column containing topics.
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.
<code>title</code>	String. Plot title.

### Details

Compare log2-frequency count of miRNA names between two topics by plotting the log2-ratio of the miRNA count in two topics. The miRNA count per topic can either be normalized, thus taking the proportion of abstracts mentioning a miRNA name compared to all abstracts in a topic, or not normalized, thus taking the absolute number of abstracts mentioning a miRNA in a topic. The log2-plot is greatly inspired by the book “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” by Silge and Robinson.



**Value**

List containing bar plot comparing the log2-frequency count of miRNA names between two topics and its corresponding data frame.

**References**

Silge, Julia, and David Robinson. 2016. “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” JOSS 1 (3). The Open Journal. <https://doi.org/10.21105/joss.00037>.

**See Also**

[compare\\_mir\\_count\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_unique\(\)](#), [compare\\_mir\\_count\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\\_unique\(\)](#), [compare\\_mir\\_terms\(\)](#)

---

compare\_mir\_count\_unique

*Compare top count of unique miRNA names per topic*

---

**Description**

Compare top count of unique miRNA names per topic

**Usage**

```
compare_mir_count_unique(
  df,
  top = 5,
  topic = NULL,
  normalize = TRUE,
  colour = "steelblue3",
  col.topic = Topic,
  col.mir = miRNA,
  col.pmid = PMID,
  title = NULL
)
```

**Arguments**

df	Data frame containing miRNA names, topics, and PubMed-IDs.
top	Integer. Specifies number of top unique miRNAs to plot.
topic	Character vector. Optional. Vector specifying which topics to compare. If topic = NULL, all topics in df are used.
normalize	Boolean. If normalize = TRUE, proportion of abstracts mentioning a miRNA name compared to all abstracts of a topic are used. If normalize = FALSE, the absolute number of abstracts mentioning a miRNA name is used.

colour	String. Colour of bar plot.
col.topic	Symbol. Column containing topics.
col.mir	Symbol. Column containing miRNA names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

### Details

Compare top count of unique miRNA names per topic by plotting the the miRNA count of unique miRNAs per topic. Per topic, the unique miRNAs are identified and their count is plotted. The miRNA count can either be normalized, thus taking the proportion of abstracts mentioning a miRNA name compared to all abstracts in a topic, or not normalized, thus taking the absolute number of abstracts mentioning a miRNA in a topic.

### Value

Bar plot comparing frequency of unique miRNA count per topic.

### See Also

[compare\\_mir\\_count\(\)](#), [compare\\_mir\\_count\\_log2\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\\_unique\(\)](#), [compare\\_mir\\_terms\(\)](#)

---

compare_mir_terms	<i>Compare count of terms associated with a miRNA name over various topics</i>
-------------------	--

---

### Description

Compare count of top terms associated with a miRNA name over various topics.

### Usage

```
compare_mir_terms(
  df,
  mir,
  top = 20,
  token = "words",
  ...,
  topic = NULL,
  shared = TRUE,
  normalize = TRUE,
  stopwords = stopwords_miretrieve,
  stopwords_ngram = TRUE,
  position = "dodge",
```

```

col.mir = miRNA,
col.abstract = Abstract,
col.topic = Topic,
col.pmid = PMID,
title = NULL
)

```

## Arguments

df	Data frame containing miRNA names, abstracts, topics, and PubMed-IDs.
mir	String. miRNA name of interest.
top	Integer. Number of top terms to plot.
token	String. Specifies how abstracts shall be split up. Taken from <code>unnest_tokens()</code> in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."
...	Additional arguments for tokenization, if necessary.
topic	Character vector. Optional. Specifies topics to plot. If <code>topic = NULL</code> , all topics in <code>df</code> are plotted.
shared	Boolean. If <code>shared = TRUE</code> , only terms that are shared between all topics are plotted.
normalize	Boolean. If <code>normalize = TRUE</code> , normalizes the number of abstracts to the total number of abstracts with a miRNA name in a topic.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when <code>token = 'ngrams'</code> .
position	Character vector. Vector containing either "dodge" or "facet". Determines if bar plots are on top of or next to each other.
col.mir	Symbol. Column containing miRNA names.
col.abstract	Symbol. Column containing abstracts.
col.topic	Symbol. Column containing topic names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

## Details

Compare count of top terms associated with a miRNA name over various topics. miRNA names and topics must be in a data frame `df`, while terms are taken from abstracts contained in `df`. Number of top terms to plot is regulated by `top`. Terms can either be evaluated as their raw count, e.g. in how many abstracts they are mentioned in conjunction with the miRNA name, or as their relative count, e.g. in how many abstracts containing the miRNA they are mentioned compared to all abstracts containing the miRNA. `compare_mir_terms()` is based on the tools available in the **tidytext** package.

**Value**

Bar plot comparing the count of terms associated with a miRNA name over two topics.

**See Also**

[compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#), [compare\\_mir\\_count\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\\_unique\(\)](#)

---

compare\_mir\_terms\_log2

*Compare log2-frequency count of terms associated with a miRNA name*

---

**Description**

Compare log2-frequency count of terms associated with a miRNA name over two topics.

**Usage**

```
compare_mir_terms_log2(  
  df,  
  mir,  
  top = 20,  
  token = "words",  
  ...,  
  topic = NULL,  
  shared = TRUE,  
  normalize = TRUE,  
  stopwords = stopwords_miretrieve,  
  stopwords_ngram = TRUE,  
  col.mir = miRNA,  
  col.abstract = Abstract,  
  col.topic = Topic,  
  col.pmid = PMID,  
  title = NULL  
)
```

**Arguments**

df	Data frame containing miRNA names, abstracts, topics, and PubMed-IDs.
mir	String. miRNA name of interest.
top	Integer. Number of top terms to plot.

token	String. Specifies how abstracts shall be split up. Taken from <code>unnest_tokens()</code> in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."
...	Additional arguments for tokenization, if necessary.
topic	Character vector. Optional. Specifies which topics to plot. Must have length two. If <code>topic = NULL</code> , all topics in <code>df</code> are plotted.
shared	Boolean. If <code>shared = TRUE</code> , only terms that are shared between the two topics are plotted.
normalize	Boolean. If <code>normalize = TRUE</code> , normalizes the number of abstracts to the total number of abstracts in a topic.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when <code>token = 'ngrams'</code> .
col.mir	Symbol. Column containing miRNA names.
col.abstract	Symbol. Column containing abstracts.
col.topic	Symbol. Column containing topic names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

## Details

Compare log<sub>2</sub>-frequency count of terms associated with a miRNA name over two topics by plotting the log<sub>2</sub>-ratio of the term count associated with a miRNA name over two topics. miRNA names and topics must be in a data frame `df`, while terms are taken from abstracts contained in `df`. Number of top terms to plot is regulated by `top`. Terms can either be evaluated as their raw count, e.g. in how many abstracts they are mentioned in conjunction with the miRNA name, or as their relative count, e.g. in how many abstracts containing the miRNA they are mentioned compared to all abstracts containing the miRNA. `compare_mir_terms_log2()` is based on the tools available in the **tidytext** package. The log<sub>2</sub>-plot is greatly inspired by the book “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” by Silge and Robinson.

## Value

List containing bar plot comparing the log<sub>2</sub>-frequency of terms associated with a miRNA over two topics and its corresponding data frame.

## References

Silge, Julia, and David Robinson. 2016. “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” *JOSS* 1 (3). The Open Journal. <https://doi.org/10.21105/joss.00037>.

**See Also**

[compare\\_mir\\_terms\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#), [compare\\_mir\\_count\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\\_unique\(\)](#), [compare\\_mir\\_terms\(\)](#)

---

compare\_mir\_terms\_scatter

*Compare shared terms associated with a miRNA name*

---

**Description**

Compare shared terms associated with a miRNA name over two topics.

**Usage**

```
compare_mir_terms_scatter(
  df,
  mir,
  top = 1000,
  token = "words",
  ...,
  topic = NULL,
  stopwords = stopwords_miretrieve,
  stopwords_ngram = TRUE,
  html = TRUE,
  colour.point = "red",
  colour.term = "black",
  col.mir = miRNA,
  col.abstract = Abstract,
  col.topic = Topic,
  col.pmid = PMID,
  title = NULL
)
```

**Arguments**

df	Data frame containing miRNA names, abstracts, topics, and PubMed-IDs.
mir	String. miRNA name of interest.
top	Integer. Number of top terms to plot.
token	String. Specifies how abstracts shall be split up. Taken from <code>unnest_tokens()</code> in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."

...	Additional arguments for tokenization, if necessary.
topic	Character vector. Optional. Specifies which topics to plot. Must have length two. If topic = NULL, all topics in df are plotted.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when token = 'ngrams'.
html	Boolean. Specifies if plot is returned as an HTML-widget or static.
colour.point	String. Colour of points for scatter plot.
colour.term	String. Colour of terms for scatter plot.
col.mir	Symbol. Column containing miRNAs.
col.abstract	Symbol. Column containing abstracts.
col.topic	Symbol. Column containing topics names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

## Details

Compare shared terms associated with a miRNA name over two topics. These terms are displayed as a scatter plot, which is either interactive as an HTML-widget, or static. This is regulated via the `html` argument. miRNA names and topics must be in a data frame `df`, while terms are taken from abstracts contained in `df`. Number of top terms to choose is regulated by `top`. Terms are evaluated as their raw count and plotted on a log10-scale. `compare_mir_terms_scatter()` is based on the tools available in the **tidytext** package. The term-plot is greatly inspired by “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” by Silge and Robinson.

## Value

Scatter plot comparing shared terms of a miRNA between two topics.

## References

Silge, Julia, and David Robinson. 2016. “tidytext: Text Mining and Analysis Using Tidy Data Principles in R.” *JOSS* 1 (3). The Open Journal. <https://doi.org/10.21105/joss.00037>.

## See Also

`compare_mir_terms()`, `compare_mir_terms_log2()`

Other compare functions: `compare_mir_count_log2()`, `compare_mir_count_unique()`, `compare_mir_count()`, `compare_mir_terms_log2()`, `compare_mir_terms_unique()`, `compare_mir_terms()`

---

 compare\_mir\_terms\_unique

*Compare terms uniquely associated with a miRNA name*


---

## Description

Compare terms uniquely associated with a miRNA name over topics.

## Usage

```
compare_mir_terms_unique(
  df,
  mir,
  top = 20,
  token = "words",
  ...,
  topic = NULL,
  stopwords = stopwords_miretrieve,
  stopwords_ngram = TRUE,
  normalize = TRUE,
  colour = "steelblue3",
  col.mir = miRNA,
  col.abstract = Abstract,
  col.topic = Topic,
  col.pmid = PMID,
  title = NULL
)
```

## Arguments

df	Data frame containing miRNA names, abstracts, topics, and PubMed-IDs.
mir	String. miRNA name of interest.
top	Integer. Number of top terms to plot.
token	String. Specifies how abstracts shall be split up. Taken from <code>unnest_tokens()</code> in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."
...	Additional arguments for tokenization, if necessary.
topic	Character vector. Optional. Specifies which topics to plot. If <code>topic = NULL</code> , all topics in <code>df</code> are plotted.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when <code>token = 'ngrams'</code> .



normalize	Boolean. If normalize = TRUE, relative term frequency is plotted, denoting the relative number of papers with mir mentioning the term compared to all papers with mir mentioning the term. If normalize = FALSE, absolute term frequency is plotted, denoting the number of papers with mir the term is mentioned in.
colour	String. Colour of bar plot.
col.mir	Symbol. Column containing miRNAs.
col.abstract	Symbol. Column containing abstracts.
col.topic	Symbol. Column containing topics names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

### Details

Compare terms uniquely associated with a miRNA name over topics. miRNA names and topics must be in a data frame `df`, while terms are taken from abstracts contained in `df`. Number of top terms to choose is regulated by `top`. Terms are evaluated either as the number of times they are mentioned in all abstracts with the miRNA name of interest, or the number of times they are relatively mentioned compared to all abstracts with the miRNA name of interest. `compare_mir_terms_unique()` is based on the tools available in the **tidytext** package.

### Value

Bar plot containing unique miRNA-terms associations per topic.

### See Also

[compare\\_mir\\_terms\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#)

Other compare functions: [compare\\_mir\\_count\\_log2\(\)](#), [compare\\_mir\\_count\\_unique\(\)](#), [compare\\_mir\\_count\(\)](#), [compare\\_mir\\_terms\\_log2\(\)](#), [compare\\_mir\\_terms\\_scatter\(\)](#), [compare\\_mir\\_terms\(\)](#)

---

count_mir	<i>Count miRNA names in a data frame</i>
-----------	--

---

### Description

Count occurrence of miRNA names in a data frame.

### Usage

```
count_mir(df, col.mir = miRNA)
```

### Arguments

df	Data frame containing miRNA names.
col.mir	Symbol. Column containing miRNA names.

**Details**

Count occurrence of miRNA names in a data frame. The count of miRNA names is returned as a separate data frame, only listing the miRNA names and their respective frequency.

**Value**

Data frame. Data frame containing miRNA names and their respective frequency.

**See Also**

[plot\\_mir\\_count\(\)](#), [count\\_mir\\_threshold\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#)

Other count functions: [count\\_mir\\_threshold\(\)](#), [count\\_snp\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#), [plot\\_mir\\_count\(\)](#)

---

count\_mir\_threshold     *Count occurrence of miRNA names above threshold*

---

**Description**

Count occurrence of miRNA names above a threshold.

**Usage**

```
count_mir_threshold(df, threshold = 1, col.mir = miRNA, col.pmid = PMID)
```

**Arguments**

df	Data frame containing miRNA names and PubMed-IDs.
threshold	Integer or float. If threshold $\geq 1$ , counts number of miRNA names in at least threshold abstracts. If threshold is between 0 and 1, counts number of miRNA names mentioned in at least threshold abstracts of all abstracts in df.
col.mir	Symbol. Column containing miRNA names.
col.pmid	Symbol. Column containing PubMed-IDs.

**Details**

Count occurrence of miRNA names above a threshold. This threshold can either be an absolute value, e.g. 3, or a float between 0 and 1, e.g. 0.2. If threshold is an absolute value, number of distinct miRNA names mentioned in at least threshold abstracts is returned. If threshold is a float between 0 and 1, number of distinct miRNA names mentioned in at least threshold abstracts of all abstracts in df is returned.

**Value**

Integer with the number of distinct miRNA names in df.

**See Also**

[plot\\_mir\\_count\\_threshold\(\)](#), [count\\_mir\(\)](#), [plot\\_mir\\_count\(\)](#)

Other count functions: [count\\_mir\(\)](#), [count\\_snp\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#), [plot\\_mir\\_count\(\)](#)

---

count\_snp

*Count SNPs in a data frame*

---

**Description**

Count occurrence of SNPs in a data frame.

**Usage**

```
count_snp(df, col.snp = SNPs, col.pmid = PMID)
```

**Arguments**

df	Data frame containing SNPs and PubMed IDs.
col.snp	Symbol. Column containing SNPs.
col.pmid	Symbol. Column containing PubMed IDs.

**Details**

Count occurrence of SNPs in a data frame. The count of SNPs is returned as a separate data frame, only listing the SNPs and their respective frequency.

**Value**

Data frame. Data frame containing SNPs and their respective frequency.

**See Also**

[extract\\_snp\(\)](#), [get\\_snp\(\)](#), [subset\\_snp\(\)](#)

Other count functions: [count\\_mir\\_threshold\(\)](#), [count\\_mir\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#), [plot\\_mir\\_count\(\)](#)

---

count_target	<i>Count targets in data frame</i>
--------------	------------------------------------

---

**Description**

Count occurrence of targets in a data frame.

**Usage**

```
count_target(df, col.target = Target, add.df = TRUE)
```

**Arguments**

df	Data frame containing a column with targets.
col.target	Symbol. Column containing targets.
add.df	Boolean. If add.df = TRUE, adds column Target_count to df containing the count of targets. If add.df = FALSE, returns a new data frame with the count of targets.

**Details**

Count occurrence of targets in a data frame. The count of targets can either be returned as a separate data frame, only listing the targets and their respective frequency, or it can be added to the data frame provided as an extra column.

**Value**

Data frame, either with the targets and their frequency as a new data frame, or with the frequency of targets added as a new column to the input data frame df.

**See Also**

[join\\_targets\(\)](#), [plot\\_target\\_count\(\)](#)

Other target functions: [join\\_mirtarbase\(\)](#), [join\\_targets\(\)](#), [plot\\_target\\_count\(\)](#), [plot\\_target\\_mir\\_scatter\(\)](#)

---

df_crc	<i>Dataset of PubMed data of miRNAs in Colorectal Cancer</i>
--------	--

---

**Description**

A dataset PubMed abstracts of miRNAs in Colorectal Cancer.

**Usage**

```
df_crc
```

**Format**

A data frame.

**Source**

<https://pubmed.ncbi.nlm.nih.gov/>

---

df_mirtarbase	<i>miRTarBase version 8.0</i>
---------------	-------------------------------

---

**Description**

The most recent miRTarBase version 8.0, containing miRNA stem, capitalized targets, and PMIDs.

**Usage**

df\_mirtarbase

**Format**

A data frame with the columns "miRNA\_tarbase", "Target", and "PMID".

**Details**

miRTarBase was published in

Hsi-Yuan Huang, Yang-Chi-Dung Lin, Jing Li, et al., miRTarBase 2020: updates to the experimentally validated microRNA–target interaction database, *Nucleic Acids Research*, Volume 48, Issue D1, 08 January 2020, Pages D148–D154, <https://doi.org/10.1093/nar/gkz896>

**Source**

<https://miRTarBase.cuhk.edu.cn:443/>

---

df_panc	<i>Dataset of PubMed data of miRNAs in Pancreatic Cancer</i>
---------	--

---

**Description**

A dataset PubMed abstracts of miRNAs in Pancreatic Cancer.

**Usage**

df\_panc

**Format**

A data frame.

**Source**

<https://pubmed.ncbi.nlm.nih.gov/>

---

df_test	<i>Test dataset of PubMed abstracts</i>
---------	---

---

**Description**

Test dataset of 20 PubMed abstracts.

**Usage**

```
df_test
```

**Format**

A data frame.

**Source**

<https://pubmed.ncbi.nlm.nih.gov/>

---

extract_mir_df	<i>Extract miRNA names from abstracts in data frame</i>
----------------	---

---

**Description**

Extract miRNA names from abstracts in a data frame.

**Usage**

```
extract_mir_df(  
  df,  
  threshold = 1,  
  col.abstract = Abstract,  
  extract_letters = FALSE  
)
```

### Arguments

df	Data frame containing abstracts.
threshold	Integer. Specifies how often a miRNA must be mentioned in an abstract to be extracted.
col.abstract	Symbol. Column containing abstracts.
extract_letters	Boolean. If <code>extract_letters = FALSE</code> , only the miRNA stem is extracted (e.g. <i>miR-23</i> ). If <code>extract_letters = TRUE</code> , the miRNA stem with trailing letter (e.g. <i>miR-23a</i> ) is extracted.

### Details

Extract miRNA names from abstracts in a data frame. miRNA names can either be extracted with their stem only, e.g. *miR-23*, or with their trailing letter, e.g. *miR-23a*. miRNA names are adapted to the most recent miRBase version (e.g. miR-97, miR-102, miR-180(a/b) become miR-30a, miR-29a, and miR-172(a/b), respectively). Additionally, how often a miRNA must be mentioned in an abstract to be extracted can be regulated via the `threshold` argument. Ultimately, abstracts not containing any miRNA names are silently dropped. As many abstracts do not adhere to the miRNA nomenclature, it is recommended to extract only the miRNA stem with `extract_letters = FALSE`.

### Value

Data frame with miRNA names extracted from abstracts.

### See Also

[extract\\_mir\\_string\(\)](#)

Other extract functions: [extract\\_mir\\_string\(\)](#), [extract\\_snp\(\)](#)

---

extract\_mir\_string      *Extract miRNA names from string*

---

### Description

Extract miRNA names from a string.

### Usage

```
extract_mir_string(string, threshold = 1, extract_letters = FALSE)
```

**Arguments**

string	String. String to search for miRNA names.
threshold	Integer. Specifies how often a miRNA must be mentioned in string to be extracted.
extract_letters	Boolean. If <code>extract_letters = FALSE</code> , only the miRNA stem is extracted (e.g. <i>miR-23</i> ). If <code>extract_letters = TRUE</code> , the miRNA stem with trailing letter (e.g. <i>miR-23a</i> ) is extracted.

**Details**

Extract miRNA names from a string. miRNA names can either be extracted with their stem only, e.g. *miR-23*, or with their trailing letter, e.g. *miR-23a*. Furthermore, miRNA names are adapted to the most recent miRBase version (e.g. miR-97, miR-102, miR-180(a/b) become miR-30a, miR-29a, and miR-172(a/b), respectively).

**Value**

Character vector containing miRNA names, if miRNA names are present in the string. If no miRNA names are present in the string, a message is returned saying "*No miRNA found.*".

**See Also**

[extract\\_mir\\_df\(\)](#)

Other extract functions: [extract\\_mir\\_df\(\)](#), [extract\\_snp\(\)](#)

---

extract_snp	<i>Extract SNPs from abstracts in data frame</i>
-------------	--

---

**Description**

Extract SNPs from abstracts in a data frame.

**Usage**

```
extract_snp(
  df,
  pattern = snp_pattern,
  col.abstract = Abstract,
  indicate = FALSE,
  discard = FALSE
)
```



**Arguments**

df	Data frame containing abstracts.
pattern	String. Regex pattern to identify SNPs.
col.abstract	Symbol. Column containing abstracts.
indicate	Boolean. If indicate = TRUE, add another column called "SNP_present", verbally indicating if a SNP is present in an abstract.
discard	Boolean. If discard = TRUE, only abstracts containing a SNP are kept.

**Details**

Extract SNPs from abstracts in a data frame. SNPs are added to the data frame in a separate column. Furthermore, an optional column can indicate if SNPs are generally present in an abstract.

**Value**

Data frame. If discard = FALSE, return the data frame with an additional column for SNPs. If discard = TRUE, return only abstracts containing SNPs.

**See Also**

[count\\_snp\(\)](#), [get\\_snp\(\)](#), [subset\\_snp\(\)](#)

Other extract functions: [extract\\_mir\\_df\(\)](#), [extract\\_mir\\_string\(\)](#)

---

fit\_lda

*Fit LDA-model*

---

**Description**

Fit LDA-model with k topics.

**Usage**

```
fit_lda(  
  df,  
  k,  
  stopwords = stopwords_miretrieve,  
  method = "gibbs",  
  control = NULL,  
  seed = 42,  
  col.abstract = Abstract,  
  col.pmid = PMID  
)
```

**Arguments**

df	Data frame containing abstracts and PubMed-IDs.
k	Integer. Number of topics to fit. Must be $\geq 2$ .
stopwords	Data frame containing stop words.
method	String. Either "gibbs" or "VEM".
control	Control parameters for LDA modeling. For more information, see the documentation of the <code>LDAcontrol</code> class in the <b>topicmodels</b> package.
seed	Integer. Seed for reproducibility.
col.abstract	Column containing abstracts.
col.pmid	Column containing PubMed-ID.

**Details**

Fit LDA-model with k topics from a data frame. `fit_lda()` is based on `LDA()` from the package **topicmodels**.

**Value**

LDA-model.

**See Also**

[plot\\_perplexity\(\)](#)

Other LDA functions: [assign\\_topic\\_lda\(\)](#), [plot\\_lda\\_term\(\)](#), [plot\\_perplexity\(\)](#)

---

generate\_stopwords      *Generate data frame containing stop words*

---

**Description**

Generate a data frame containing stop words.

**Usage**

```
generate_stopwords(stopwords, combine_with = NULL)
```

**Arguments**

stopwords	Character vector. Vector containing stop words.
combine_with	Data frame containing stop words. Optional. Data frame provided here must have only two columns, namely <code>word</code> and <code>lexicon</code> . This data frame is combined with the data frame created from <code>stopwords</code> . Exemplary data frames are <ul style="list-style-type: none"> <li>• <code>tidytext::stop_words</code> from the <b>tidytext</b> package, or</li> <li>• <code>stopwords_miretrieve</code> from this package.</li> </ul>

**Details**

Generate data frame containing stop words from a character vector. This data frame consists of two columns, namely word, containing the stop words, and lexicon, containing the string "self-defined". Additionally, the created data frame can be combined with other stop words containing data frames, e.g. tidytext::stop\_words or stopwords\_miretrieve.

**Value**

Data frame containing stop words.

**References**

Silge, Julia, and David Robinson. 2016. "tidytext: Text Mining and Analysis Using Tidy Data Principles in R." JOSS 1 (3). The Open Journal. <https://doi.org/10.21105/joss.00037>.

**See Also**

[combine\\_stopwords\(\)](#), [stopwords\\_miretrieve](#), [tidytext::stop\\_words](#)

Other stopword functions: [combine\\_stopwords\(\)](#)

---

get\_distinct\_mir\_df     *Identify top miRNA names distinct for one topic compared to another topic*

---

**Description**

Identify top miRNA names distinct for one topic compared to another topic in a data frame.

**Usage**

```
get_distinct_mir_df(  
  df,  
  distinct,  
  top = 5,  
  topic = NULL,  
  col.topic = Topic,  
  col.mir = miRNA,  
  col.pmid = PMID  
)
```

**Arguments**

df	Data frame containing at least two topics and miRNA names.
distinct	String. Name of topic top distinct miRNAs shall be identified for. distinct must be contained in the topic names provided in topic.
top	Integer. Number of top miRNA names to extract for both topics.

<code>topic</code>	String. Vector of strings containing topic names to compare miRNA names for. If <code>topic = NULL</code> , <code>topic</code> defaults to all topic names contained in <code>col.topic</code> in <code>df</code> . <code>topic</code> must only contain two topic names.
<code>col.topic</code>	Symbol. Column containing topic names.
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.

**Details**

Get top distinct miRNA names of one topic compared to another topic in a data frame. `get_distinct_mir_df()` compares the top miRNA names of two topics and returns the miRNA names that are exclusive for `distinct`.

**Value**

Character vector containing miRNA names distinct for `distinct` compared to the second topic provided in `topic`.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_mir\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#), [get\\_snp\(\)](#)

---

`get_distinct_mir_vec` *Identify miRNA names distinct for one vector compared to another vector*

---

**Description**

Identify miRNA names distinct for one vector compared to another vector.

**Usage**

```
get_distinct_mir_vec(mirna.vec.1, mirna.vec.2)
```

**Arguments**

<code>mirna.vec.1</code>	Character vector. First vector containing miRNA names.
<code>mirna.vec.2</code>	Character vector. Second vector containing miRNA names.

**Details**

Get distinct miRNA names of one vector compared to another vector. `get_distinct_mir()` compares two vectors containing miRNA names and returns the miRNA names that are exclusive for `mirna.vec.1`.

**Value**

Character vector containing miRNA names distinct for `mirna.vec.1` compared to `mirna.vec.2`.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_mir\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#), [get\\_snp\(\)](#)

---

 get\_mir

*Get miRNA names from a data frame*


---

**Description**

Get miRNA names from a data frame. These miRNA names can either be the most frequent ones, or the ones exceeding a threshold.

**Usage**

```
get_mir(
  df,
  top = NULL,
  threshold = NULL,
  topic = NULL,
  col.mir = miRNA,
  col.pmid = PMID,
  col.topic = Topic
)
```

**Arguments**

<code>df</code>	Data frame containing miRNA names. If <code>threshold</code> is set, <code>df</code> must also contain PubMed-IDs. If <code>topic</code> is set, <code>df</code> must also contain topic names.
<code>top</code>	Integer. Optional. Specifies number of most frequent miRNA names to return. If neither <code>top</code> nor <code>threshold</code> is set, <code>top</code> is automatically set to 5.
<code>threshold</code>	Integer or float. Optional. If <code>threshold &gt;= 1</code> , return miRNA names mentioned in at least <code>threshold</code> abstracts. If <code>threshold</code> is between 0 and 1, return miRNA names mentioned in at least <code>threshold</code> abstracts of all abstracts in <code>df</code> .
<code>topic</code>	String. Optional. Character vector specifying which topics to obtain miRNA names from.
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.
<code>col.topic</code>	Symbol. Column containing topic names.

**Details**

Get miRNA names from a data frame. These miRNA names can either be the most frequent ones, or the ones exceeding a threshold. Furthermore, if the data frame contains abstracts of different topics, only the miRNA names of specific topics can be obtained by setting the `topic` argument.

- To get the most frequent miRNA names, set the `top` argument. `top` determines how many most frequent miRNA names are returned, according to their rank. Ties among the most frequently mentioned miRNAs are treated as the same rank, e.g. if *miR-126*, *miR-34*, and *miR-29* were all mentioned the most often with the same frequency, they would all be returned by specifying `top = 1`, `top = 2`, and `top = 3`.
- To get the miRNA names exceeding a threshold, set the `threshold` argument. `threshold` can either be an absolute value, e.g. 3, or a float between 0 and 1, e.g. 0.2. If `threshold` is an absolute value, `get_mir()` returns only the miRNA names mentioned in at least `threshold` abstracts. If `threshold` is a float between 0 and 1, `get_mir()` returns only miRNA names mentioned in at least `threshold` abstracts of all abstracts. `threshold` requires the data frame to have a column with PubMed IDs.

If neither `top` nor `threshold` is set, `top` is automatically set to 5.

**Value**

Character vector containing miRNA names.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#), [get\\_snp\(\)](#)

---

get\_pmid

*Get PubMed-IDs of a data frame*

---

**Description**

Get PubMed-IDs of a data frame.

**Usage**

```
get_pmid(df, col.pmid = PMID, copy = TRUE)
```

**Arguments**

<code>df</code>	Data frame containing PubMed-IDs.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.
<code>copy</code>	Boolean. If <code>copy = FALSE</code> , <code>get_pmid()</code> returns a character vector, containing PubMed-IDs. If <code>copy = TRUE</code> , <code>get_pmid()</code> copies PubMed-IDs to clipboard.

**Details**

Get PubMed-IDs of a data frame. `get_pmid` returns either a character vector, containing PubMed-IDs, or copies PubMed-IDs to clipboard. If PubMed-IDs are copied to the clipboard, they can be used e.g. to search for abstracts on PubMed.

**Value**

Copy to clipboard or character vector. If `copy = TRUE`, `get_pmid()` copies PubMed-IDs to clipboard. If `copy = FALSE`, `get_pmid()` returns a character vector, containing PubMed-IDs.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_mir\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#), [get\\_snp\(\)](#)

---

<code>get_shared_mir_df</code>	<i>Get top miRNA names in common between two topics of a data frame</i>
--------------------------------	---

---

**Description**

Get top miRNA names in common between two topics of a data frame.

**Usage**

```
get_shared_mir_df(
  df,
  top = 5,
  topic = NULL,
  col.topic = Topic,
  col.mir = miRNA,
  col.pmid = PMID
)
```

**Arguments**

<code>df</code>	Data frame containing at least two topics and miRNA names.
<code>top</code>	Integer. Number of top miRNA names to extract for both topics.
<code>topic</code>	String. Vector of strings containing topic names to compare miRNA names for. If <code>topic = NULL</code> , <code>topic</code> defaults to all topic names contained in <code>col.topic</code> in <code>df</code> . <code>topic</code> must only contain two topic names.
<code>col.topic</code>	Symbol. Column containing topic names.
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.

**Details**

Get top miRNA names in common between two topics of a data frame. `get_shared_mir_df()` compares the top miRNA names of two topics in a data frame and returns the miRNA names in common.

**Value**

Character vector containing miRNA names in common between two topics.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_mir\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#), [get\\_snp\(\)](#)

---

<code>get_shared_mir_vec</code>	<i>Get miRNA names in common between two vectors</i>
---------------------------------	--

---

**Description**

Get miRNA names in common between two vectors.

**Usage**

```
get_shared_mir_vec(mirna.vec.1, mirna.vec.2)
```

**Arguments**

`mirna.vec.1` Character vector. First vector containing miRNA names.  
`mirna.vec.2` Character vector. Second vector containing miRNA names.

**Details**

Get miRNA names in common between two vectors. `get_shared_mir_vec()` compares two vectors containing miRNA names and returns the miRNA names that are in both vectors.

**Value**

Character vector containing miRNA names in common between two vectors.

**See Also**

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_mir\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_snp\(\)](#)



---

get_snp	<i>Get SNPs from a data frame</i>
---------	-----------------------------------

---

### Description

Get SNPs from a data frame.

### Usage

```
get_snp(df, row = NULL, top = NULL, col.snp = SNPs, col.pmid = PMID)
```

### Arguments

df	Data frame containing SNPs. If top is set, df must also contain PubMed IDs.
row	Integer. Optional. Specifies row from which SNP shall be obtained. Works best with a data frame listing counts only as from <a href="#">count_snp()</a> . If neither row nor top is given, row is automatically set to 1.
top	Integer. Optional. Specifies number of most frequent SNPs to return.
col.snp	Symbol. Column containing SNPs.
col.pmid	Symbol. Column containing PubMed IDs. Necessary if the data frame provided is not a count data frame.

### Details

Get SNPs from a data frame.

- If a data frame containing SNP counts as from [count\\_snp\(\)](#) is provided, these SNPs are specified by the row they are listed in. To get the SNPs by row, set the row argument.
- If a data frame with PubMed IDs is provided, these SNPs are specified by their top occurrence. To get the SNPs by frequency, set the top argument.

If neither row nor top is provided, row is automatically set to 1.

### Value

String or character vector containing SNPs.

### See Also

[extract\\_snp\(\)](#), [count\\_snp\(\)](#), [subset\\_snp\(\)](#)

Other get functions: [get\\_distinct\\_mir\\_df\(\)](#), [get\\_distinct\\_mir\\_vec\(\)](#), [get\\_mir\(\)](#), [get\\_pmid\(\)](#), [get\\_shared\\_mir\\_df\(\)](#), [get\\_shared\\_mir\\_vec\(\)](#)

---

indicate_mir	<i>Indicate if a miRNA name is contained in an abstract</i>
--------------	---

---

### Description

Indicate if a miRNA name is contained in an abstract with "Yes"/"No".

### Usage

```
indicate_mir(df, indicate.mir, col.mir = miRNA)
```

### Arguments

df	Data frame containing miRNA names.
indicate.mir	Character vector. Vector containing miRNA names to indicate.
col.mir	Symbol. Column containing miRNA names.

### Details

Indicate if a miRNA name is contained in an abstract with "Yes"/"No". This requires miRNA names already to be extracted, e.g. with `extract_mir_df()`, and to be stored in a separate column, specified by `col.mir`. `indicate_mir()` adds another column to a data frame which bears the name of the miRNA(s) of interest. Within this column, a "Yes" or "No" specifies if this miRNA name is contained in the corresponding abstract.

### Value

Data frame with as many columns added as miRNA names given in `indicate.mir`. Per column, a "Yes" or "No" indicates if the miRNA name of interest is present in the corresponding abstract.

### See Also

[extract\\_mir\\_df\(\)](#), [indicate\\_term\(\)](#)  
 Other indicate functions: [indicate\\_term\(\)](#)

---

indicate_term	<i>Indicate if a term is contained in abstracts</i>
---------------	---

---

### Description

Indicate if a term is contained in abstracts.

**Usage**

```
indicate_term(  
  df,  
  term,  
  threshold = 1,  
  case = FALSE,  
  discard = FALSE,  
  col.abstract = Abstract  
)
```

**Arguments**

df	Data frame containing abstracts.
term	Character vector. Vector containing terms to indicate.
threshold	Integer. Sets how often a term must be in an abstract to be considered "present".
case	Boolean. If case = TRUE, strings contained in term are case sensitive. If case = FALSE, strings contained in term are case insensitive.
discard	Boolean. If discard = TRUE, only abstracts containing the terms in term are kept.
col.abstract	Symbol. Column containing abstracts.

**Details**

Indicate if a term is contained in an abstract. Terms provided can either be case sensitive or insensitive. Per term, a new column is added to the data frame indicating if the term is present in an abstract. Furthermore, if a term is considered "present" in an abstract can be regulated via the threshold argument. threshold determines how often a term must be in an abstract to be considered "present".

**Value**

Data frame. If discard = FALSE, the original data frame with additional columns per term is returned. If discard = TRUE, only abstracts containing the terms in term are returned.

**See Also**

[indicate\\_mir\(\)](#)

Other indicate functions: [indicate\\_mir\(\)](#)

---

join_mirtarbase	<i>Add miRNA targets from miRTarBase version 8.0</i>
-----------------	--

---

## Description

Add miRNA targets from miRTarBase version 8.0 to a data frame.

## Usage

```
join_mirtarbase(
  df,
  col.pmid.df = PMID,
  col.topic.df = NULL,
  filter_na = TRUE,
  reduce = FALSE
)
```

## Arguments

df	Data frame containing PubMed-IDs that the miRNA targets shall be joined to.
col.pmid.df	Symbol. Column containing PubMed-IDs in df.
col.topic.df	Symbol. Optional. Only important if reduce = TRUE. If given, adds a topic column to the reduced data.frame.
filter_na	Boolean. If filter_na = TRUE, drops all rows containing NA in column Target.
reduce	Boolean. If reduce = FALSE, adds a new column containing miRNA targets to df. If reduce = TRUE, adds two new columns containing miRNA names and miRNA targets to df. All other columns except for the PubMed-ID column and (optionally) the topic column are dropped.

## Details

Add miRNA targets from miRTarBase version 8.0 to a data frame. `join_mirtarbase()` can return two different data frames, regulated by `reduce`:

1. If `reduce = FALSE`, `join_mirtarbase()` adds targets from miRTarBase 8.0 to the data frame in a new column. These targets then correspond to the targets determined in the research paper, but do not necessarily correspond to the miRNA names mentioned in the abstract.
2. If `reduce = TRUE`, `join_mirtarbase()` adds targets from miRTarBase 8.0 to the data frame in a new column. However, an altered data frame is returned, containing the PubMed-IDs, targets, and miRNAs from miRTarBase 8.0.

miRTarBase was published in

Hsi-Yuan Huang, Yang-Chi-Dung Lin, Jing Li, et al., miRTarBase 2020: updates to the experimentally validated microRNA–target interaction database, *Nucleic Acids Research*, Volume 48, Issue D1, 08 January 2020, Pages D148–D154, <https://doi.org/10.1093/nar/gkz896>

**Value**

Data frame containing miRNA targets.

**See Also**

Other target functions: [count\\_target\(\)](#), [join\\_targets\(\)](#), [plot\\_target\\_count\(\)](#), [plot\\_target\\_mir\\_scatter\(\)](#)

---

<code>join_targets</code>	<i>Add miRNA targets from an excel-file to a data frame</i>
---------------------------	---

---

**Description**

Add miRNA targets from an external excel-file to a data frame.

**Usage**

```
join_targets(
  df,
  excel_file,
  col.pmid.excel,
  col.target.excel,
  col.mir.excel = NULL,
  col.pmid.df = PMID,
  col.topic.df = NULL,
  filter_na = TRUE,
  stem_mir_excel = TRUE,
  reduce = FALSE
)
```

**Arguments**

<code>df</code>	Data frame containing PubMed-IDs that the miRNA targets shall be joined to.
<code>excel_file</code>	excel-file. excel-file containing miRNA targets and PubMed-IDs.
<code>col.pmid.excel</code>	String. Column containing PubMed-IDs of the excel_file.
<code>col.target.excel</code>	String. Column containing targets of the excel_file.
<code>col.mir.excel</code>	String. Optional. Column containing miRNAs of the excel_file. Needed if <code>reduce = TRUE</code> .
<code>col.pmid.df</code>	Symbol. Column containing PubMed-IDs in df.
<code>col.topic.df</code>	Symbol. Optional. Only important if <code>reduce = TRUE</code> . If given, adds a topic column to the reduced data.frame.
<code>filter_na</code>	Boolean. If <code>filter_na = TRUE</code> , drops all rows containing NA in column Target.
<code>stem_mir_excel</code>	Boolean. If <code>stem_mir_excel = TRUE</code> , miRNA names provided in <code>col.mir.excel</code> are reduced to their stem, e.g. "miR-20a-5p" becomes "miR-20".

`reduce` Boolean. If `reduce = FALSE`, adds a new column containing miRNA targets to `df`. If `reduce = TRUE`, adds two new columns containing miRNA names and miRNA targets to `df`. All other columns except for the PubMed-ID column and (optionally) the topic column are dropped.

### Details

Add miRNA targets from an external xlsx-file to a data frame. To add the targets to the data frame, the xlsx-file and the data frame need to have one column in common, such as PubMed-IDs. `join_targets()` can return two different data frames, regulated by `reduce`:

1. If `reduce = FALSE`, `join_targets()` adds targets from an excel-file to the data frame in a new column. These targets then correspond to the targets determined in the research paper, but do not necessarily correspond to the miRNA names mentioned in the abstract.
2. If `reduce = TRUE`, `join_targets()` adds targets from an xlsx-file to the data frame in a new column. However, an altered data frame is returned, containing the PubMed-IDs, targets, and miRNAs from the excel-file. For `reduce = TRUE` to work, the xlsx-file provided must contain a column with miRNA names.

### Value

Data frame containing miRNA targets.

### See Also

Other target functions: [count\\_target\(\)](#), [join\\_mirtarbase\(\)](#), [plot\\_target\\_count\(\)](#), [plot\\_target\\_mir\\_scatter\(\)](#)

---

ngram\_stopwords      *Stop words for n-grams*

---

### Description

Vector containing stop words for n-grams, based on `tidytext::stop_words`.

### Usage

```
ngram_stopwords
```

### Format

Character vector.

### Source

`tidytext::stop_words`

---

patients_keywords	<i>Keywords - patients.</i>
-------------------	-----------------------------

---

**Description**

Keywords to identify abstracts investigating miRNAs in patients.

**Usage**

```
patients_keywords
```

**Format**

An object of class character of length 10.

---

plot_lda_term	<i>Plot terms associated with LDA-fitted topics</i>
---------------	---

---

**Description**

Plot terms associated with LDA-fitted topics.

**Usage**

```
plot_lda_term(lda_model, top.terms = 10, title = NULL)
```

**Arguments**

lda_model	LDA-model.
top.terms	Integer. Top terms to plot per topic.
title	String. Plot title.

**Details**

Plot terms associated with LDA-fitted topics. For each topic in the LDA-model, the top terms are plotted. Plotting top.terms for each topic can help identifying its subject.

**Value**

Bar plot with top terms per topic.

**See Also**

Other LDA functions: [assign\\_topic\\_lda\(\)](#), [fit\\_lda\(\)](#), [plot\\_perplexity\(\)](#)

---

plot_mir_count	<i>Plot count of most frequently mentioned miRNA names</i>
----------------	--

---

### Description

Plot count of most frequently mentioned miRNA names in a data frame.

### Usage

```
plot_mir_count(  
  df,  
  top = 10,  
  colour = "steelblue3",  
  col.mir = miRNA,  
  title = NULL  
)
```

### Arguments

df	Data frame containing miRNA names.
top	Integer. Specifies number of most frequent miRNA names to plot.
colour	String. Colour of bar plot.
col.mir	Symbol. Column containing miRNA names.
title	String. Plot title.

### Details

Plot count of most frequently mentioned miRNA names in a data frame. How many most frequently mentioned miRNAs are plotted is determined via the top argument. Ties among the most frequently mentioned miRNAs are treated as the same rank, e.g. if *miR-126*, *miR-34*, and *miR-29* were all mentioned the most often, they would all be plotted by specifying top = 1, top = 2, or top = 3.

### Value

Bar plot with the most frequently mentioned miRNAs names in df.

### See Also

[count\\_mir\(\)](#), [count\\_mir\\_threshold\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#)

Other count functions: [count\\_mir\\_threshold\(\)](#), [count\\_mir\(\)](#), [count\\_snp\(\)](#), [plot\\_mir\\_count\\_threshold\(\)](#)



---

`plot_mir_count_threshold`*Plot occurrence count of miRNA names over different thresholds*

---

## Description

Plot occurrence count of distinct miRNA names over different thresholds.

## Usage

```
plot_mir_count_threshold(  
  df,  
  start = 1,  
  end = 5,  
  bins = NULL,  
  colour = "steelblue3",  
  col.mir = miRNA,  
  col.pmid = PMID,  
  title = NULL  
)
```

## Arguments

<code>df</code>	Data frame containing columns with miRNAs and PubMed-IDs.
<code>start</code>	Integer or float. Must be greater than 0 and smaller than end.
<code>end</code>	Integer or float. Must be greater than 0 and greater than start. If <code>start &gt;= 1</code> , <code>plot_mir_count_threshold()</code> plots number of miRNAs above different absolute thresholds, ranging from <code>start</code> to <code>end</code> . If <code>start &gt;= 0</code> and <code>end &lt;= 1</code> , <code>bins</code> must be specified. If <code>bins</code> is not specified, <code>bins</code> is automatically set to 10. <code>plot_mir_count_threshold()</code> then plots number of miRNAs above different thresholds, ranging from <code>start</code> to <code>end</code> in <code>n</code> bins. If <code>start &gt;= 0</code> and <code>end &lt;= 1</code> and the value of <code>start</code> is too low for the number of miRNAs to be plotted, <code>plot_mir_count_threshold()</code> raises a warning, suggesting a more appropriate <code>start</code> value.
<code>bins</code>	Integer. Optional. Only necessary if <code>start &gt;= 0</code> and <code>end &lt;= 1</code> . Specifies number of bins between <code>start</code> and <code>end</code> . If <code>start &gt;= 0</code> , <code>end &lt;= 1</code> , and <code>bins</code> is not specified, <code>bins</code> is automatically set to 10.
<code>colour</code>	String. Colour of bar plot.
<code>col.mir</code>	Symbol. Column containing miRNAs.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.
<code>title</code>	String. Plot title.

### Details

Plot occurrence of distinct miRNA names over different thresholds. These thresholds can either be absolute values or floating values between 0 and 1. If the thresholds are absolute values, number of distinct miRNA names mentioned in at least *n* abstracts are plotted, where *n* is the range of thresholds defined by *start* and *end*. If the thresholds are floating values, bins must be specified as well. Then the number of distinct miRNA names mentioned in at least *n* abstracts over bins are plotted, where *n* is the range of thresholds between *start* and *end*. Overall, plotting can help in identifying if the abstracts at hand mention different miRNAs in a balanced way, or if there are few miRNAs dominating the field.

### Value

Bar plot counting the occurrence of miRNA names above different thresholds.

### See Also

[count\\_mir\\_threshold\(\)](#), [count\\_mir\(\)](#), [plot\\_mir\\_count\(\)](#)

Other count functions: [count\\_mir\\_threshold\(\)](#), [count\\_mir\(\)](#), [count\\_snp\(\)](#), [plot\\_mir\\_count\(\)](#)

---

plot\_mir\_development *Plot development of miRNA name mentioning over time*

---

### Description

Plot development of miRNA name mentioning over time.

### Usage

```
plot_mir_development(  
  df,  
  mir,  
  start = NULL,  
  end = NULL,  
  linetype = "miRNA",  
  alpha = 0.8,  
  width = 0.3,  
  col.mir = miRNA,  
  col.year = Year,  
  title = NULL  
)
```

### Arguments

<code>df</code>	Data frame containing miRNA names and publication years.
<code>mir</code>	Character vector. Vector containing miRNA names to plot.

start	Numeric. Optional. Specifies start year. If start = NULL, start is set to the oldest year in df.
end	Numeric. Optional. Specifies end year. If end = NULL, end is set to the youngest year in df.
linetype	String. Specifies linetype. linetype can take on values as mentioned in the geom_line documentation of <b>ggplot2</b> . Additionally, linetype can be set to "mirNA". If linetype = "mirNA", each miRNA name in mir has its own linetype.
alpha	Float. Opacity of lines.
width	Float. Width of dodging lines.
col.mir	Symbol. Column containing miRNA names.
col.year	Symbol. Column containing year.
title	String. Plot title.

### Details

Plot how often a miRNA name was mentioned per year.

### Value

Line plot displaying how often a miRNA name was mentioned per year..

### See Also

Other miR development functions: [plot\\_mir\\_new\(\)](#)

---

plot\_mir\_new

*Plot number of newly mentioned miRNA names/year*

---

### Description

Plot number of newly mentioned miRNA names/year.

### Usage

```
plot_mir_new(
  df,
  threshold = 1,
  start = NULL,
  end = NULL,
  colour = "steelblue3",
  col.mir = miRNA,
  col.year = Year,
  title = NULL
)
```

**Arguments**

df	Data frame containing miRNA names and publication years.
threshold	Integer. Specifies how often a miRNA must be mentioned in a year to be considered "mentioned".
start	Integer. Optional. Beginning of publication period. If start = NULL, start is set to the least recent year in df.
end	Integer. Optional. End of publication period. If end = NULL, end is set to the most recent year in df.
colour	String. Colour of bar plot.
col.mir	Symbol. Column containing miRNA names.
col.year	Symbol. Column containing publication year.
title	String. Plot title.

**Details**

Plot how many miRNAs are mentioned for the first time in different year. If a miRNA is considered to be "mentioned" in a year can be regulated via the threshold argument. If, for example, threshold is set to 3, but a miRNA is mentioned only twice in a year, it is not considered to be "mentioned" for this year.

**Value**

Bar plot displaying the number of newly mentioned miRNA names/year.

**See Also**

Other miR development functions: [plot\\_mir\\_development\(\)](#)

---

plot_mir_terms	<i>Plot count of top terms associated with a miRNA name</i>
----------------	---

---

**Description**

Plot count of top terms associated with a miRNA name.

**Usage**

```
plot_mir_terms(
  df,
  mir,
  top = 20,
  tf.idf = FALSE,
  token = "words",
  ...,
  stopwords = stopwords_miretrieve,
```

```

stopwords_ngram = TRUE,
normalize = TRUE,
colour = "steelblue3",
col.mir = miRNA,
col.abstract = Abstract,
col.pmid = PMID,
title = NULL
)

```

### Arguments

df	Data frame containing miRNA names, abstracts, and PubMed-IDs.
mir	String. miRNA name of interest.
top	Integer. Number of top terms to plot.
tf.idf	Boolean. If <code>tf.idf = TRUE</code> , terms are weighed in a tf-idf fashion. miRNA names are considered as separate documents and terms often associated with one miRNA, but not with other miRNAs get more weight.
token	String. Specifies how abstracts shall be split up. Taken from <code>unnest_tokens()</code> in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."
...	Additional arguments for tokenization, if necessary.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when <code>token = 'ngrams'</code> .
normalize	Boolean. If <code>normalize = TRUE</code> , normalizes the number of abstracts to the total number of abstracts with a miRNA name in a topic. Cannot be applied with <code>tf.idf = TRUE</code> .
colour	String. Colour of bar plot.
col.mir	Symbol. Column containing miRNA names
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Title plot.

### Details

Plot count of top terms associated with a miRNA name. Top terms associated with `mir` have to be in `df` as abstracts. Number of top terms to plot is regulated via the `top` argument. Terms can either be evaluated as their count or in a tf-idf fashion. If terms are evaluated as their count, they can either be evaluated as their raw count, e.g. in how many abstracts they are mentioned in conjunction with the miRNA name, or as their relative count, e.g. in how many abstracts containing the miRNA they are mentioned compared to all abstracts containing the miRNA. If terms are evaluated in a tf-idf

fashion, miRNA names are considered as separate documents and terms often associated with one miRNA, but not with other miRNAs get more weight. `plot_mir_terms()` is based on the tools available in the **tidytext** package.

### Value

Bar plot displaying the count of the top terms associated with a miRNA name.

### See Also

[plot\\_wordcloud\(\)](#), [tidytext::unnest\\_tokens\(\)](#)

Other miR term functions: [plot\\_wordcloud\(\)](#)

---

plot_perplexity	<i>Plot perplexity score of various LDA models</i>
-----------------	--

---

### Description

Plot perplexity score of various LDA models.

### Usage

```
plot_perplexity(
  df,
  start = 2,
  end = 5,
  stopwords = stopwords_miretrieve,
  method = "gibbs",
  control = NULL,
  col.abstract = Abstract,
  col.pmid = PMID,
  title = NULL
)
```

### Arguments

<code>df</code>	Data frame containing abstracts and PubMed-IDs.
<code>start</code>	Integer. Minimum amount of k topics for the LDA model to fit. Must be $\geq 2$ .
<code>end</code>	Integer. Maximum amount of k topics for the LDA model to fit.
<code>stopwords</code>	Data frame containing stop words.
<code>method</code>	String. Either "gibbs" or "VEM".
<code>control</code>	Control parameters for LDA modeling. For more information, see the documentation of the <code>LDAcontrol</code> class in the <b>topicmodels</b> package.
<code>col.abstract</code>	Column containing abstracts.
<code>col.pmid</code>	Column containing PubMed-ID.
<code>title</code>	String. Plot title.

## Details

Plot perplexity score of various LDA models. `plot_perplexity()` fits different LDA models for `k` topics in the range between `start` and `end`. For each LDA model, the perplexity score is plotted against the corresponding value of `k`. Plotting the perplexity score of various LDA models can help in identifying the optimal number of topics to fit an LDA model for. `plot_perplexity()` is based on `LDA()` from the package **topicmodels**.

## Value

Elbow plot displaying perplexity scores of different LDA models.

## See Also

[fit\\_lda\(\)](#)

Other LDA functions: [assign\\_topic\\_lda\(\)](#), [fit\\_lda\(\)](#), [plot\\_lda\\_term\(\)](#)

---

`plot_score_animals`      *Plot frequency of animal model scores in abstracts*

---

## Description

Plot frequency of animal model scores in abstracts.

## Usage

```
plot_score_animals(  
  df,  
  keywords = animal_keywords,  
  case = FALSE,  
  bins = NULL,  
  colour = "steelblue3",  
  col.abstract = Abstract,  
  col.pmid = PMID,  
  title = NULL  
)
```

## Arguments

<code>df</code>	Data frame containing abstracts.
<code>keywords</code>	Character vector. Vector containing keywords. The animal model score is calculated based on these keywords. How much weight a keyword in keywords carries is determined how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score.
<code>case</code>	Boolean. If <code>case = TRUE</code> , terms contained in keywords are case sensitive. If <code>case = FALSE</code> , terms contained in keywords are case insensitive.

bins	Integer. Specifies how many bins are used to plot the distribution. If bins = NULL, bins are calculated over the whole range of scores, with one bin per score.
colour	String. Colour of histogram.
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

### Details

Plots a frequency distribution of animal model scores in abstracts of a data frame. The animal model score is influenced by the choice of terms in keywords. Plotting the distribution can help deciding if the terms are well-chosen, or in choosing the right threshold to decide which abstracts are considered to contain animal models.

### Value

Histogram displaying the distribution of animal scores in abstracts.

### See Also

[calculate\\_score\\_animals\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

plot\_score\_biomarker *Plot frequency of biomarker scores in abstracts*

---

### Description

Plot frequency of biomarker scores in abstracts.

### Usage

```
plot_score_biomarker(  
  df,  
  keywords = biomarker_keywords,  
  case = FALSE,  
  bins = NULL,  
  colour = "steelblue3",  
  col.abstract = Abstract,  
  col.pmid = PMID,  
  title = NULL  
)
```



**Arguments**

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. The biomarker score is calculated based on these keywords. How much weight a keyword in keywords carries is determined how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score.
case	Boolean. If case = TRUE, terms contained in keywords are case sensitive. If case = FALSE, terms contained in keywords are case insensitive.
bins	Integer. Specifies how many bins are used to plot the distribution. If bins = NULL, bins are calculated over the whole range of scores, with one bin per score.
colour	String. Colour of histogram.
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

**Details**

Plots a frequency distribution of biomarker scores in abstracts of a data frame. The biomarker score is influenced by the choice of terms in keywords. Plotting the distribution can help deciding if the terms are well-chosen, or in choosing the right threshold to decide which abstracts are considered to contain use of miRNAs as biomarker.

**Value**

Histogram displaying the distribution of biomarker scores in abstracts.

**See Also**

[calculate\\_score\\_biomarker\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_patients\(\)](#), [plot\\_score\\_topic\(\)](#)

---

plot\_score\_patients     *Plot frequency of patient scores in abstracts*

---

**Description**

Plot frequency of patient scores in abstracts.

**Usage**

```
plot_score_patients(
  df,
  keywords = patients_keywords,
  case = FALSE,
  bins = NULL,
  colour = "steelblue3",
  col.abstract = Abstract,
  col.pmid = PMID,
  title = NULL
)
```

**Arguments**

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. The score is calculated based on these keywords. How much weight a keyword in keywords carries is determined how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score.
case	Boolean. If case = TRUE, terms contained in keywords are case sensitive. If case = FALSE, terms contained in keywords are case insensitive.
bins	Integer. Specifies how many bins are used to plot the distribution. If bins = NULL, bins are calculated over the whole range of scores, with one bin per score.
colour	String. Colour of histogram.
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

**Details**

Plots a frequency distribution of patient scores in abstracts of a data frame. The patient score is influenced by the choice of terms in keywords. Plotting the distribution can help deciding if the terms are well-chosen, or in choosing the right threshold to decide which abstracts are considered to contain patient material

**Value**

Histogram displaying the distribution of patient scores in abstracts.

**See Also**

[calculate\\_score\\_patients\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_topic\(\)](#)

---

plot_score_topic	<i>Plot frequency of self-chosen topic scores in abstracts</i>
------------------	--

---

### Description

Plot frequency of self-chosen topic scores in abstracts.

### Usage

```
plot_score_topic(
  df,
  keywords,
  case = FALSE,
  name.topic = "TOPIC",
  bins = NULL,
  colour = "steelblue3",
  col.abstract = Abstract,
  col.pmid = PMID,
  title = NULL
)
```

### Arguments

df	Data frame containing abstracts.
keywords	Character vector. Vector containing keywords. How much weight a keyword in keywords carries is determined by how often it is present in keywords, e.g. if a keyword is mentioned twice in keywords and it is mentioned only once in an abstract, it adds 2 points to the score.
case	Boolean. If case = TRUE, terms contained in keywords are case sensitive. If case = FALSE, terms contained in keywords are case insensitive.
name.topic	String. Name of the topic.
bins	Integer. Specifies how many bins are used to plot the distribution. If bins = NULL, bins are calculated over the whole range of scores, with one bin per score.
colour	String. Colour of histogram.
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.

### Details

Plots a frequency distribution of self-chosen topic scores in abstracts of a data frame. The topic score is influenced by the choice of terms in keywords. Plotting the distribution can help in choosing the right threshold to decide which abstracts correspond to the self-chosen topic.

**Value**

Histogram displaying the distribution of self-chosen topic scores in abstracts.

**See Also**

[calculate\\_score\\_topic\(\)](#), [assign\\_topic\(\)](#)

Other score functions: [assign\\_topic\(\)](#), [calculate\\_score\\_animals\(\)](#), [calculate\\_score\\_biomarker\(\)](#), [calculate\\_score\\_patients\(\)](#), [calculate\\_score\\_topic\(\)](#), [plot\\_score\\_animals\(\)](#), [plot\\_score\\_biomarker\(\)](#), [plot\\_score\\_patients\(\)](#)

---

plot_target_count	<i>Plot count of miRNA targets</i>
-------------------	------------------------------------

---

**Description**

Plot count of miRNA targets.

**Usage**

```
plot_target_count(
  df,
  top = NULL,
  threshold = NULL,
  colour = "steelblue3",
  col.target = Target,
  title = NULL
)
```

**Arguments**

df	Data frame with miRNA targets.
top	Numeric. Specifies number of top targets to be plotted.
threshold	Numeric. Specifies how often a target must be in col.target to be plotted.
colour	String. Colour of bar plot.
col.target	Symbol. Column containing miRNA targets.
title	String. Plot title.

**Details**

Plot count of miRNA targets as a bar plot. How many targets are plotted is determined either by the top or by the threshold argument. If top is given, targets with the highest count are plotted. Ties among targets with the highest count are treated as the same rank, e.g. if *PTEN*, *AKT*, and *VEGFA* all had the highest count, they would all be plotted by specifying top = 1, top = 2, and top = 3. If threshold is given, only targets with a count of at least threshold are plotted. If neither top nor threshold is given, top is automatically set to 5.

**Value**

Bar plot with target counts.

**See Also**

[count\\_target\(\)](#), [join\\_targets\(\)](#)

Other target functions: [count\\_target\(\)](#), [join\\_mirtarbase\(\)](#), [join\\_targets\(\)](#), [plot\\_target\\_mir\\_scatter\(\)](#)

---

plot\_target\_mir\_scatter

*Plot targets and corresponding miRNAs as a scatter plot*

---

**Description**

Plot targets and corresponding miRNAs as a scatter plot.

**Usage**

```
plot_target_mir_scatter(
  df,
  mir = NULL,
  target = NULL,
  top = NULL,
  threshold = NULL,
  filter_for = "target",
  col.target = Target,
  col.mir = miRNA,
  col.topic = Topic,
  col.pmid = PMID,
  title = NULL,
  height = 0.05,
  width = 0.05,
  alpha = 0.6
)
```

**Arguments**

df	Data frame containing targets and miRNA names.
mir	String or character vector. Specifies which miRNAs to plot.
target	String or character vector. Specifies which targets to plot.
top	Numeric. Specifies number of top targets/miRNA names to be plotted.
threshold	Numeric. Specifies how often a target/miRNA name must be in df to be plotted.
filter_for	String. Must either be "target" or "miRNA". Specifies if threshold/top shall be applied to targets or miRNA names.
col.target	Symbol. Column containing miRNA targets.

col.mir	Symbol. Column containing miRNA names.
col.topic	Symbol. Column containing topic names.
col.pmid	Symbol. Column containing PubMed-IDs.
title	String. Plot title.
height	Double. Specifies height of jitter.
width	Double. Specifies width of jitter.
alpha	Double. Specifies opacity of points.

### Details

Plot targets and corresponding miRNAs as a scatter plot. With `filter_for`, it can be determined if the focus shall be on the top targets to plot their corresponding miRNAs, or if the focus shall be on the top miRNA names to plot their corresponding targets. What "top targets" or "top miRNA names" mean can be determined via the `top` and `threshold` arguments.

- If `top` is given, `df` is filtered for the most frequent targets/miRNA names.
- If `threshold` is given, data frame is filtered for all targets/miRNA names mentioned at least `threshold` times.
- If neither `top` nor `threshold` is given, `top` is automatically set to 5.

By plotting miRNAs against their targets, it is visualized if one miRNA regulates many targets, or if one target is regulated by many miRNAs. Furthermore, the miRNA-target interactions are labelled according to their topic in `col.topic`, thereby facilitating comparison of miRNA-target interactions across different topics.

### Value

Scatter plot with targets and corresponding miRNAs.

### See Also

[join\\_targets\(\)](#)

Other target functions: [count\\_target\(\)](#), [join\\_mirtarbase\(\)](#), [join\\_targets\(\)](#), [plot\\_target\\_count\(\)](#)

---

plot\_wordcloud

*Create wordcloud of terms associated with a miRNA name*

---

### Description

Create wordcloud of terms associated with a miRNA name.

**Usage**

```
plot_wordcloud(
  df,
  mir,
  min.freq = 1,
  max.terms = 20,
  tf.idf = FALSE,
  token = "words",
  ...,
  stopwords = stopwords_miretrieve,
  stopwords_ngram = TRUE,
  colours = "black",
  random.colour = TRUE,
  ordered.colour = FALSE,
  col.mir = miRNA,
  col.abstract = Abstract,
  col.pmid = PMID
)
```

**Arguments**

df	Data frame containing miRNA names, abstracts, and PubMed-IDs.
mir	String. miRNA name of interest.
min.freq	Integer. Specifies least number of times a term must be associated with mir to be plotted.
max.terms	Integer. Maximum number of terms to plot.
tf.idf	Boolean. If tf.idf = TRUE, terms are weighed in a tf-idf fashion. miRNA names are considered as separate documents, and terms often associated with one miRNA, but not with other miRNAs get more weight. Cannot be used if normalize = TRUE. If tf.idf = TRUE and normalize = TRUE, tf.idf = TRUE is ignored.
token	String. Specifies how abstracts shall be split up. Taken from unnest_tokens() in the <b>tidytext</b> package: "Unit for tokenizing, or a custom tokenizing function. Built-in options are "words" (default), "characters", "character_shingles", "ngrams", "skip_ngrams", "sentences", "lines", "paragraphs", "regex", (...), and "ptb" (Penn Treebank). If a function, should take a character vector and return a list of character vectors of the same length."
...	Additional arguments for tokenization, if necessary.
stopwords	Data frame containing stop words.
stopwords_ngram	Boolean. Specifies if stop words shall be removed from abstracts when using ngrams. Only applied when token = 'ngrams'.
colours	Vector of strings. Colours for wordcloud.
random.colour	Boolean. Taken from wordcloud() in the <b>wordcloud</b> package: "Choose colours randomly from colours. If false, the colour is chosen based on the frequency."

ordered.colour	Boolean. Taken from wordcloud() in the <b>wordcloud</b> package: "If true, then colours are assigned to words in order."
col.mir	Symbol. Column containing miRNA names.
col.abstract	Symbol. Column containing abstracts.
col.pmid	Symbol. Column containing PubMed-IDs.

### Details

Create wordcloud of terms associated with a miRNA name. miRNA names must be in a data frame `df`, while terms are taken from abstracts contained in `df`. Number of terms to plot is regulated by `max.terms`, while `min.freq` regulates the least number of times a term must be mentioned to be plotted. Terms can either be evaluated as their raw count, e.g. how often they are mentioned in conjunction with the miRNA of interest, or weighed in a tf-idf fashion. If `tf.idf = TRUE`, miRNA names are considered as separate documents, and terms often associated with one miRNA, but not with other miRNAs get more weight. `plot_wordcloud()` is based on the tools available in the **wordcloud** package.

### Value

Wordcloud of terms associated with a miRNA name.

### See Also

`plot_mir_terms()`, `wordcloud::wordcloud()`, `tidytext::unnest_tokens()`

Other miR term functions: `plot_mir_terms()`

---

read\_pubmed

*Convert PubMed-file from PubMed into a data frame*

---

### Description

Convert PubMed-file from PubMed into a data frame.

### Usage

```
read_pubmed(pubmed_file, topic = NULL)
```

### Arguments

pubmed_file	PubMed-file as .txt, downloaded from PubMed.
topic	String. Optional. If provided, adds a "Topic" column containing topic.



## Details

Convert an PubMed-file from PubMed into a data frame. The PubMed-file should contain PubMed-IDs, abstracts from research articles, abstract title, publication year, abstract language, and article type. The data frame created holds at least six columns, namely

- PMID, containing the PubMed-ID,
- Year, containing the publication year,
- Title, containing the title of the abstracts,
- Abstract, containing the actual abstract,
- Language, containing the language(s) of the paper,
- Type, containing the article type.

If topic is provided, a "Topic" column is added, assigning all abstracts in df to topic.

read\_pubmed() is faster than read\_pubmed\_jats() and thus recommended.

## Value

Data frame containing PubMed-IDs, abstracts, abstract titles, publication years, languages, and article types.

## See Also

[read\\_pubmed\\_jats\(\)](#)

Other external data functions: [read\\_pubmed\\_jats\(\)](#), [save\\_excel\(\)](#), [save\\_plot\(\)](#)

---

read_pubmed_jats	<i>Convert JATS-file from PubMed into a data frame</i>
------------------	--

---

## Description

Convert JATS-file from PubMed into a data frame.

## Usage

```
read_pubmed_jats(jats_file, topic = NULL)
```

## Arguments

jats_file	JATS-file, downloaded from PubMed.
topic	String. Optional. If provided, adds a "Topic" column containing topic.

**Details**

Converts an JATS-file from PubMed into a data frame. The JATS-file should contain PubMed-IDs, abstracts from research articles, abstract title, publication year, abstract language, and article type. The data frame created holds at least six columns, namely

- PMID, containing the PubMed-ID,
- Year, containing the publication year,
- Title, containing the title of the abstracts,
- Abstract, containing the actual abstract,
- Language, containing the language(s) of the paper,
- Type, containing the article type.

If topic is provided, a "Topic" column is added, assigning all abstracts in df to topic.

read\_pubmed() is faster than read\_pubmed\_jats() and thus recommended.

**Value**

Data frame containing PubMed-IDs, abstracts, abstract titles, publication years, languages, and article types.

**See Also**

[read\\_pubmed\(\)](#)

Other external data functions: [read\\_pubmed\(\)](#), [save\\_excel\(\)](#), [save\\_plot\(\)](#)

---

save_excel	<i>Save data frame(s) as xlsx-file</i>
------------	--

---

**Description**

Save data frame(s) locally as an xlsx-file.

**Usage**

```
save_excel(..., excel_file = "miRetrieve_data.xlsx")
```

**Arguments**

...	Data frame(s) to save.
excel_file	String. File name that ... shall be saved to. Must end in ".xlsx".

**Details**

Saves data frame locally as an xlsx-file. If more than one data frame is provided, data frames are saved in an xlsx-file with one sheet per data frame.

Wrapper function of write.xlsx() from **openxlsx**.

**Value**

xlsx-file, locally saved.

**See Also**

[openxlsx::write.xlsx\(\)](#)

Other external data functions: [read\\_pubmed\\_jats\(\)](#), [read\\_pubmed\(\)](#), [save\\_plot\(\)](#)

---

save_plot	<i>Save the last generated figure</i>
-----------	---------------------------------------

---

**Description**

Save the last generated figure locally.

**Usage**

```
save_plot(
  plot_file,
  width = NULL,
  height = NULL,
  units = "in",
  dpi = 300,
  device = NULL
)
```

**Arguments**

plot_file	String. File name that the figure shall be saved to. Can end in either ".png", ".tiff", ".pdf", ".jpeg", or ".bmp". For more information, see the documentation of <a href="#">ggplot2::ggsave()</a> .
width	Integer. Optional. Plot width. If width = NULL, width is set to the width of the plotting window.
height	Integer. Optional. Plot height. If height = NULL, height is set to the height of the plotting window.
units	String. Units for width and height.
dpi	Integer. Resolution for raster graphics such as .pdf-files.
device	String or function. Specifies which device to use (such as "pdf" or cairo_pdf)

**Details**

Saves the last generated figure locally. Wrapper function of [ggsave\(\)](#) from **ggplot2**. For further details, please see [?ggplot2::ggsave](#).

**Value**

Plot, locally saved.

**See Also**

[ggplot2::ggsave\(\)](#)

Other external data functions: [read\\_pubmed\\_jats\(\)](#), [read\\_pubmed\(\)](#), [save\\_excel\(\)](#)

---

stopwords\_2gram      *Stop words for text mining with common PubMed 2-grams*

---

**Description**

Data frame containing PubMed 2-gram stop words, manually curated from PubMed abstracts

**Usage**

```
stopwords_2gram
```

**Format**

Tibble.

- word: Column containing stop words. Pulled from various PubMed abstracts.
- lexicon: Column specifying lexicon.

**Source**

Manually created from various PubMed abstracts.

---

stopwords\_miretrieve      *Stop words for text mining with miRetrieve*

---

**Description**

Data frame containing English stop words, PubMed stop words, and common 2-gram stopwords. English stop words are based on tidytext::stop\_words, while PubMed stop words are manually curated from PubMed abstracts

**Usage**

```
stopwords_miretrieve
```

**Format**

Tibble.

- word: Column containing stop words. Pulled from various PubMed abstracts.
- lexicon: Column specifying lexicon.

**Source**

tidytext::stop\_words; manually created from various PubMed abstracts.

---

stopwords_pubmed	<i>Stop words for text mining from PubMed abstracts</i>
------------------	---

---

**Description**

Data frame containing PubMed stop words, manually curated from PubMed abstracts

**Usage**

```
stopwords_pubmed
```

**Format**

Tibble.

- word: Column containing stop words. Pulled from various PubMed abstracts.
- lexicon: Column specifying lexicon.

**Source**

Manually created from various PubMed abstracts.

---

subset_df	<i>Subset data frame for a term</i>
-----------	-------------------------------------

---

**Description**

Subset data frame for a term in a specified column.

**Usage**

```
subset_df(df, col.filter, filter_for = "Yes")
```

**Arguments**

df	Data frame to subset.
col.filter	String. Name of column to filter.
filter_for	String. Term to filter for.

**Details**

Subset data frame for a term in a specified column. `subset_df()` filters a data frame for a certain term in a specified column. All rows containing the term in the specified column are kept, while the other rows are silently dropped. Here, `col.filter` is a string rather than a symbol to facilitate filtering in columns that carry special characters such as '-' in their name.

**Value**

Data frame, subset for rows where `filter_for` was present in `col.filter`.

**See Also**

[indicate\\_term\(\)](#), [indicate\\_mir\(\)](#), [extract\\_snp\(\)](#)

Other subset functions: [subset\\_mir\\_threshold\(\)](#), [subset\\_mir\(\)](#), [subset\\_research\(\)](#), [subset\\_review\(\)](#), [subset\\_snp\(\)](#), [subset\\_year\(\)](#)

---

subset\_mir

*Subset data frame for specific miRNA names*

---

**Description**

Subset data frame for specific miRNA names only.

**Usage**

```
subset_mir(df, mir.retain, col.mir = miRNA)
```

**Arguments**

df	Data frame containing a miRNA names.
mir.retain	Character vector. Vector specifying which miRNA names to keep. miRNA names in <code>mir.retain</code> must match miRNA names in <code>col.mir</code> in <code>df</code> .
col.mir	Symbol. Column containing miRNA names.

**Details**

Subset data frame for specific miRNA names only.

**Value**

Data frame containing only specified miRNA names. If no miRNA name in `mir.retain` matches a miRNA name in `col.mir`, `subset_mir()` stops with a warning saying *"No miRNA name in 'mir.retain' matches a miRNA name in 'col.mir'. Could not filter for miRNA name."*

**See Also**

[get\\_mir\(\)](#), [subset\\_mir\\_threshold\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\\_threshold\(\)](#), [subset\\_research\(\)](#), [subset\\_review\(\)](#), [subset\\_snp\(\)](#), [subset\\_year\(\)](#)

---

subset\_mir\_threshold    *Subset data frame for miRNA names exceeding a threshold*

---

**Description**

Subset data frame for miRNA names whose frequency exceeds a threshold.

**Usage**

```
subset_mir_threshold(df, threshold = 1, col.mir = miRNA, col.pmid = PMID)
```

**Arguments**

<code>df</code>	Data frame containing miRNA names and a PubMed-IDs.
<code>threshold</code>	Integer or float. If <code>threshold &gt;= 1</code> , retains miRNA names in at least <code>threshold</code> abstracts. If <code>threshold</code> is between 0 and 1, retains miRNA names mentioned in at least <code>threshold</code> abstracts of all abstracts in <code>df</code> .
<code>col.mir</code>	Symbol. Column containing miRNA names.
<code>col.pmid</code>	Symbol. Column containing PubMed-IDs.

**Details**

Subset data frame for miRNA names whose frequency exceeds a threshold. This threshold can either be an absolute value, e.g. 3, or a float between 0 and 1, e.g. 0.2. If `threshold` is an absolute value, `subset_mir_threshold()` retains miRNA names mentioned in at least `threshold` abstracts. If `threshold` is a float between 0 and 1, `subset_mir_threshold()` retains miRNA names mentioned in at least `threshold` abstracts of all abstracts in `df`.

**Value**

Data frame, subset for miRNA names whose frequency exceeds a threshold.

**See Also**

[get\\_mir\(\)](#), [subset\\_mir\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\(\)](#), [subset\\_research\(\)](#), [subset\\_review\(\)](#), [subset\\_snp\(\)](#), [subset\\_year\(\)](#)

---

subset_research	<i>Subset data frame for abstracts of research articles</i>
-----------------	---

---

**Description**

Subset data frame for abstracts of research articles only.

**Usage**

```
subset_research(df, col.type = Type)
```

**Arguments**

df	Data frame containing article types.
col.type	Symbol. Column containing articles types.

**Details**

Subset data frame for abstracts of research articles only. At the same time, abstracts from other article types such as *Review*, *Letter*, etc. are dropped.

**Value**

Data frame containing abstracts of research articles only.

**See Also**

[subset\\_review\(\)](#), [subset\\_year\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\\_threshold\(\)](#), [subset\\_mir\(\)](#), [subset\\_review\(\)](#), [subset\\_snp\(\)](#), [subset\\_year\(\)](#)

---

subset_review	<i>Subset data frame for abstracts of review articles</i>
---------------	---

---

**Description**

Subset data frame for abstracts of review articles only.

**Usage**

```
subset_review(df, col.type = Type)
```

**Arguments**

df	Data frame containing article types.
col.type	Symbol. Column containing articles types.



**Details**

Subset data frame for abstracts of review articles only. At the same time, abstracts from other article types such as *Journal Article*, *Letter*, etc. are dropped.

**Value**

Data frame containing abstracts of review articles only.

**See Also**

[subset\\_research\(\)](#), [subset\\_year\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\\_threshold\(\)](#), [subset\\_mir\(\)](#), [subset\\_research\(\)](#), [subset\\_snp\(\)](#), [subset\\_year\(\)](#)

---

subset\_snp

*Subset data frame for specific SNPs*

---

**Description**

Subset data frame for specific SNPs only.

**Usage**

```
subset_snp(df, snp.retain, col.snp = SNPs)
```

**Arguments**

df	Data frame containing SNPs.
snp.retain	Character vector. Vector specifying which SNPs to keep. SNPs in snp.retain must match SNPs in col.snp in df.
col.snp	Symbol. Column containing SNPs.

**Details**

Subset data frame for specific SNPs only.

**Value**

Data frame containing only specified SNPs. If no SNP in snp.retain matches a SNP in col.snp, subset\_snp() stops with a warning saying *"No SNP in 'snp.retain' matches a SNP in 'col.snp'. Could not filter for SNP."*

**See Also**

[extract\\_snp\(\)](#), [count\\_snp\(\)](#), [get\\_snp\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\\_threshold\(\)](#), [subset\\_mir\(\)](#), [subset\\_research\(\)](#), [subset\\_review\(\)](#), [subset\\_year\(\)](#)

---

subset_year	<i>Subset data frame for abstracts published in a specific period</i>
-------------	---

---

**Description**

Subset data frame for abstracts published in a specific period only.

**Usage**

```
subset_year(df, col.year = Year, start = NULL, end = NULL)
```

**Arguments**

df	Data frame containing publication years.
col.year	Symbol. Column containing publication years.
start	Integer. Optional. Beginning of publication period. If start = NULL, start is set to the least recent year in df.
end	Integer. Optional. End of publication period. If end = NULL, end is set to the most recent year in df.

**Details**

Subset data frame for abstracts published in a specific period only. All other abstracts published not within this period are silently dropped.

**Value**

Data frame containing abstracts published in a specific period only.

**See Also**

[subset\\_research\(\)](#), [subset\\_review\(\)](#)

Other subset functions: [subset\\_df\(\)](#), [subset\\_mir\\_threshold\(\)](#), [subset\\_mir\(\)](#), [subset\\_research\(\)](#), [subset\\_review\(\)](#), [subset\\_snp\(\)](#)

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