

# Package: tern.rbmi (via r-universe)

September 3, 2024

**Title** Create interface for rbmi and tern

**Version** 0.1.3.9005

**Date** 2024-09-03

**Description** `RBMI` tabulation with `rtables` and `tern` packages.

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**URL** <https://github.com/insightengineering/tern.rbmi>,  
<https://insightengineering.github.io/tern.rbmi/>

**BugReports** <https://github.com/insightengineering/tern.rbmi/issues>

**Depends** R (>= 3.6), rbmi (>= 1.2.5), tern (>= 0.9.4)

**Imports** broom (>= 0.5.4), checkmate (>= 2.1.0), formatters (>= 0.5.6),  
lifecycle (>= 0.2.0), magrittr (>= 1.5), rtables (>= 0.6.7)

**Suggests** dplyr (>= 1.0.3), knitr (>= 1.42), Matrix, rmarkdown (>= 2.23), testthat (>= 3.0.4), tidyr (>= 0.8.3)

**VignetteBuilder** knitr, rmarkdown

**Remotes** insightengineering/tern@\*release

**Config/Needs/verdepcheck** insightengineering/rbmi,  
insightengineering/tern, tidymodels/broom, mllg/checkmate,  
insightengineering/formatters, r-lib/lifecycle,  
tidyverse/magrittr, insightengineering/rtables,  
tidyverse/dplyr, yihui/knitr, rstudio/rmarkdown,  
r-lib/testthat, tidyverse/tidyr

**Config/Needs/website** insightengineering/nesttemplate

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Collate** 'tabulate\_rbmi.R' 'tern.rbmi-package.R'

**Repository** <https://pharmaverse.r-universe.dev>

**RemoteUrl** <https://github.com/insightsengineering/tern.rbmi>

**RemoteRef** HEAD

**RemoteSha** 5b432cb342150b04a78c6e4a876e0d37cb51de4d

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a_rbmi_lsmeans	<i>Formatted Analysis function which can be further customized by calling <code>rtables::make_afun()</code> on it. It is used as afun in <code>rtables::analyze()</code>.</i>
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## Description

**[Experimental]**

## Usage

```
a_rbmi_lsmeans(df, .in_ref_col, show_relative = c("reduction", "increase"))
```

## Arguments

df	input dataframe
.in_ref_col	boolean variable, if reference column is specified
show_relative	"reduction" if (control - treatment, default) or "increase" (treatment - control) of relative change from baseline?

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h_tidy_pool	<i>Helper function to produce data frame with results of pool for a single visit</i>
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**Description****[Experimental]****Usage**

```
h_tidy_pool(x)
```

**Arguments**

x (pool) is a list of pooled object from rbmi analysis results. This list includes analysis results, confidence level, hypothesis testing type.

**Examples**

```
data("rbmi_test_data")
pool_obj <- rbmi_test_data

h_tidy_pool(pool_obj$pars[1:3])
```

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rbmi_test_data	<i>Example dataset for tern.rbmi package. This is an pool object from the rbmi analysis, see <code>browseVignettes(package = "tern.rbmi")</code></i>
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**Description****[Experimental]****Usage**

```
rbmi_test_data
```

**Format**

An object of class pool of length 5.

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summarize_rbmi	<i>Analyze function for tabulating LS means estimates from tidied rbmi pool results.</i>
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## Description

**[Experimental]**

## Usage

```
summarize_rbmi(
  lyt,
  ...,
  table_names = "rbmi_summary",
  .stats = NULL,
  .formats = NULL,
  .indent_mods = NULL,
  .labels = NULL
)
```

## Arguments

lyt	(layout) input layout where analyses will be added to.
...	additional argument.
table_names	(character) this can be customized in case that the same vars are analyzed multiple times, to avoid warnings from rtables.
.stats	(character) statistics to select for the table.
.formats	(named character or list) formats for the statistics.
.indent_mods	(named integer) indent modifiers for the labels.
.labels	(named character) labels for the statistics (without indent).

## Examples

```
library(rtables)
library(dplyr)
library(broom)

data("rbmi_test_data")
pool_obj <- rbmi_test_data
```

```
df <- tidy(pool_obj)

basic_table() %>%
  split_cols_by("group", ref_group = levels(df$group)[1]) %>%
  split_rows_by("visit", split_label = "Visit", label_pos = "topleft") %>%
  summarize_rbmi() %>%
  build_table(df)
```

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s_rbmi_lsmeans	<i>Statistics function which is extracting estimates from a tidied LS means data frame.</i>
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## Description

[Experimental]

## Usage

```
s_rbmi_lsmeans(df, .in_ref_col, show_relative = c("reduction", "increase"))
```

## Arguments

df	input dataframe
.in_ref_col	boolean variable, if reference column is specified
show_relative	"reduction" if (control - treatment, default) or "increase" (treatment - control) of relative change from baseline?

## Examples

```
library(rtables)
library(dplyr)
library(broom)

data("rbmi_test_data")
pool_obj <- rbmi_test_data
df <- tidy(pool_obj)

s_rbmi_lsmeans(df[1, ], .in_ref_col = TRUE)

s_rbmi_lsmeans(df[2, ], .in_ref_col = FALSE)
```

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tidy.pool	<i>Helper method (for <code>broom::tidy()</code>) to prepare a data frame from an pool rbmi object containing the LS means and contrasts and multiple visits</i>
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**Description****[Experimental]****Usage**

```
## S3 method for class 'pool'  
tidy(x, ...)
```

**Arguments**

x	(pool) is a list of pooled object from rbmi analysis results. This list includes analysis results, confidence level, hypothesis testing type.
...	Additional arguments. Not used. Needed to match generic signature only.

**Value**

A dataframe

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