

# Package ‘cheese’

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**Title** Tools for Intuitive and Flexible Statistical Analysis Workflows

**Description** Contains flexible and intuitive functions to assist in carrying out tasks in a statistical analysis and to get from the raw data to presentation-ready results. A user-friendly interface is used in specialized functions that are aimed at common tasks such as building a univariate descriptive table for variables in a dataset. These high-level functions are built on a collection of low(er)-level functions that may be useful for aspects of a custom statistical analysis workflow or for general programming use.

**URL** <https://github.com/zajichek/cheese>

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**Depends** R (>= 3.4.0)

**Imports** dplyr (>= 0.7.7), forcats (>= 0.3.0), kableExtra (>= 1.0.1), knitr (>= 1.20), magrittr (>= 1.5), methods (>= 3.4.1), purrr (>= 0.2.4), rlang (>= 0.3.0.1), stringr (>= 1.3.1), tibble (>= 1.4.2), tidyr (>= 0.8.1), tidyselect (>= 0.2.4)

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absorb	<i>Absorb values of a key-value pair into an arbitrary character string containing keys</i>
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---

## Description

Populates user-specified string templates containing keys as placeholders, with the values. The keys are interpreted as regular expressions. Results can optionally be evaluated as R expressions.

## Usage

```
absorb(
  key,
  value,
  text,
  sep = "|",
  print = FALSE,
  evaluate = FALSE
)
```

## Arguments

key	Vector of keys that can be coerced to type character.
value	Vector of values with positions corresponding to the key.
text	Vector of character strings containing sequences of characters and keys/patterns where values should be filled.
sep	Character to separate values by in the placeholder in the event of duplicate keys (patterns). Defaults to " "
print	Should the recursion results be printed to the console each iteration? Defaults to FALSE.
evaluate	Should the resulting strings be evaluated as R expressions? Defaults to FALSE.

## Details

The algorithm iterates the provided value vector (in sequential order) and recursively replaces substrings where there is a matching pattern of a key. Thus, it is possible that a subsequent key could match with a previous value, and hence be replaced more than once. If duplicate keys exist, the placeholder will be filled with a collapsed string of all the values for that key.

## Value

If `evaluate = FALSE` (default), a character vector the same length as `text` with all matching patterns replaced by their value. If `evaluate = TRUE`, a list with the same length as `text` is returned with the result of the evaluation of each string.

## Author(s)

Alex Zajichek

## Examples

```
require(tidyverse)

#1) Simple example
absorb(
  key = c("mean", "sd", "var"),
  value = c("10", "2", "4"),
  text =
    c("MEAN: mean, SD: sd",
      "VAR: var = sd^2",
      "MEAN = mean"
    )
)

#2) Evaluating results
absorb(
  key = c("mean", "mean", "sd", "var"),
  value = c("10", "20", "2", "4"),
  text = c("(mean)/2", "sd^2"),
  sep = "+",
  evaluate = TRUE
) %>%
  flatten_dbl()
```

**Description**

Computes a number of common descriptive statistics for different types of data. The user can specify an unlimited number of additional functions to compute and the types of data that each set (including the default) of functions will be applied to.

**Usage**

```
descriptives(
  data,
  f_all = NULL,
  f_numeric = NULL,
  numeric_types = "numeric",
  f_categorical = NULL,
  categorical_types = "factor",
  f_other = NULL,
  na.rm = TRUE,
  useNA = c("ifany", "no", "always"),
  round = 2
)
```

**Arguments**

<code>data</code>	A data.frame. Could also be a list.
<code>f_all</code>	Functions to apply to all columns. Should return a scalar. See "Details" for information computed by default.
<code>f_numeric</code>	Functions to apply to columns conforming to <code>numeric_types</code> . Should return a scalar. See "Details" for information computed by default.
<code>numeric_types</code>	Character vector of data types that should be evaluated with <code>f_numeric</code> .
<code>f_categorical</code>	Functions to apply to columns conforming to <code>categorical_types</code> . Should return a named vector where the names correspond to the levels. See "Details" for information computed by default.
<code>categorical_types</code>	Character vector of data types that should be evaluated with <code>f_categorical</code> .
<code>f_other</code>	Functions to apply to remaining columns.
<code>na.rm</code>	Logical argument supplied to <code>f_numeric</code> . Defaults to TRUE.
<code>useNA</code>	Supplied to <code>f_categorical</code> . See <code>?base::table</code> for details. Defaults to "ifany".
<code>round</code>	Digit to round numeric data. Defaults to 2.

**Details**

The `min`, `max`, `median`, `iqr`, `mean`, `sd` are automatically computed for numeric data and `table`, `prop.table*100` for categorical data. The sample size, number of missing values, number of nonmissing values, the number of unique values, the `class` are automatically computed on all columns.

**Value**

A long tibble with columns `.variable` (for the variable name), `.key` (for the statistic or attribute), `.value` (for numeric results), `.label` (for non-numeric results), and `.combo` (convenient combination of `.value` and `.label` coerced to a character vector). If categorical variables exist, additional columns `.level` (for the factor levels) and `.order` (to retain order of the levels).

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#1) Default
heart_disease %>%
  descriptives()

#2) Allow logicals as categorical
heart_disease %>%
  descriptives(
    categorical_types = c("logical", "factor")
  )

#3) Only apply "other" functions to numeric types
heart_disease %>%
  descriptives(
    numeric_types = NULL
  )

#4) Compute a custom function
heart_disease %>%
  descriptives(
    f_numeric =
      list(
        cv = function(x, na.rm) sd(x, na.rm = na.rm)/mean(x, na.rm = na.rm)
      )
  )
```

---

dish

*Dish out a function to combinations of variables*

---

**Description**

Evaluates a two argument function on subsets of a data frame by evaluating each combination of columns or subsets.

**Usage**

```
dish(
  data,
  f,
  left = NULL,
  right = NULL,
  each_left = TRUE,
  each_right = TRUE,
  bind = FALSE,
  ...
)
```

**Arguments**

<code>data</code>	A <code>data.frame</code> .
<code>f</code>	Any function that takes a vector and/or <code>data.frame</code> in the first two arguments.
<code>left</code>	Variables to be used in the first argument of <code>f</code> . If <code>NULL</code> (default), all variables except those in <code>right</code> are used. Has <code>tidyselect::vars_select</code> capabilities.
<code>right</code>	Variables to be used in the second argument of <code>f</code> . If <code>NULL</code> (default), all variables except those in <code>left</code> are used. Has <code>tidyselect::vars_select</code> capabilities.
<code>each_left</code>	Should each <code>left</code> variable be separately evaluated in <code>f</code> ? Defaults to <code>TRUE</code> . If <code>FALSE</code> , <code>left</code> is entered into <code>f</code> as a <code>data.frame</code> .
<code>each_right</code>	Should each <code>right</code> variable be separately evaluated in <code>f</code> ? Defaults to <code>TRUE</code> . If <code>FALSE</code> , <code>right</code> is entered into <code>f</code> as a <code>data.frame</code> .
<code>bind</code>	Should results be binded into a single <code>data.frame</code> ? Defaults to <code>FALSE</code> .
<code>...</code>	Additional arguments to be passed to <code>f</code> .

**Value**

A list (if `bind = FALSE`) or a tibble (if `bind = TRUE`) with the results of `f` evaluated on data subsets.

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#1) Default uses every variable on both sides
heart_disease %>%
  select_if(
    is.numeric
  ) %>%
  dish(
```

```

    f = cor
  )

#2) Simple regression of Age and BP on each variable
heart_disease %>%
  dish(
    f =
      function(y, x) {
        mod <- lm(y ~ x)
        tibble(
          Parameter = names(mod$coef),
          Estimate = mod$coef
        )
      },
    left = c("Age", "BP"),
    bind = TRUE
  )

#3) Multiple regression with Age, BP on all variables simultaneously
heart_disease %>%
  dish(
    f =
      function(y, x) {
        mod <- lm(y ~ ., data = x)
        tibble(
          Parameter = names(mod$coef),
          Estimate = mod$coef
        )
      },
    left = c("Age", "BP"),
    each_right = FALSE,
    bind = TRUE
  )

```

---

 divide

---

*Divide a data frame into a list by any number of variables.*


---

### Description

Separates a data frame by one or more stratification variables into a list of data frames whose names are the strata. Removes stratification variables from each frame.

### Usage

```

divide(
  data,
  by,
  sep = "|"
)

```

**Arguments**

<code>data</code>	Any <code>data.frame</code> .
<code>by</code>	Character vector of variable names or a <code>tidyselect::select_helper</code> .
<code>sep</code>	String to separate values of each stratification variable by. Defaults to <code>" "</code> .

**Value**

A named list of `data.frame` objects

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#1) Exact match
heart_disease %>%
  divide(
    by = "Sex"
  )

#2) Regular expression
heart_disease %>%
  divide(
    by = matches("^(S|H)")
  )

#3) Beginning character
heart_disease %>%
  divide(
    by = starts_with("S")
  )

#4) Negation
heart_disease %>%
  select(
    Sex,
    HeartDisease,
    BloodSugar
  ) %>%
  divide(
    by = -matches("^(S|H)")
  )
```



---

heart_disease	<i>Heart Disease</i>
---------------	----------------------

---

**Description**

This is a cleaned up version of the "heart disease data set" found in the UCI Machine Learning Repository (<https://archive.ics.uci.edu/ml/datasets/Heart+Disease>), containing a subset of the default variables.

**Usage**

```
heart_disease
```

**Format**

See "Source" for link to dataset home page

**Source**

```
https://archive.ics.uci.edu/ml/datasets/Heart+Disease
```

---

stratiply	<i>Stratify a data frame, apply a function to each strata, and collect results</i>
-----------	--

---

**Description**

Calls "[divide](#)" to separate a data frame into one or more stratified frames, applies a function to each strata, and optionally collects the results and returns strata to their original columns.

**Usage**

```
stratiply(  
  data,  
  strata,  
  f,  
  delimiter = "|",  
  bind = FALSE,  
  separate = FALSE,  
  ...  
)
```

**Arguments**

<code>data</code>	Any <code>data.frame</code> .
<code>strata</code>	See the <code>by</code> argument in " <code>divide</code> ".
<code>f</code>	Any function that takes a <code>data.frame</code> as an argument.
<code>delimiter</code>	See the <code>sep</code> argument in " <code>divide</code> ". Also used for salvaging original columns.
<code>bind</code>	Should the results be binded back to a single <code>data.frame</code> ? Defaults to <code>FALSE</code> .
<code>separate</code>	If <code>bind = TRUE</code> , should the stratification variables be separated back to their original columns? Defaults to <code>FALSE</code> .
<code>...</code>	Additional arguments passed to <code>f</code> .

**Value**

If `bind = FALSE`, a named list with the results of `f` for each `strata`. Otherwise the results are binded to a single frame.

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#1) Return a list
heart_disease %>%
  stratiplly(
    strata = c("Sex", "HeartDisease"),
    f = head
  )

#2) Unseparated strata column
heart_disease %>%
  stratiplly(
    strata = c("Sex", "HeartDisease"),
    f = head,
    bind = TRUE
  )

#3) Separated strata column
heart_disease %>%
  stratiplly(
    strata = c("Sex", "HeartDisease"),
    f = head,
    bind = TRUE,
    separate = TRUE
  )

#4) Custom function
heart_disease %>%
```

```

stratiplay(
  strata = c("Sex", "HeartDisease"),
  f = function(x)
    x %>%
    select_if(is.numeric) %>%
    map(mean, na.rm = TRUE),
  bind = TRUE,
  separate = TRUE
)

#5) Regular expression
heart_disease %>%
  stratiplay(
    strata = matches("^(S|H)"),
    f = function(x)
      x %>%
      select_if(is.numeric) %>%
      map(mean, na.rm = TRUE),
    bind = TRUE,
    separate = TRUE
  )

```

---

stretch

*Stretch one or variables over many columns by one or more keys*


---

### Description

Provides similar functionality to `tidyr::spread` or `reshape2::dcast` but allows for an unlimited number of variables to be spanned across the columns.

### Usage

```

stretch(
  data,
  keys,
  keep = NULL,
  send = NULL,
  join = dplyr::full_join,
  .sep = "_",
  extract_keys_as_header = FALSE,
  keep_keys_in_header = TRUE,
  ...
)

```

### Arguments

`data` A `data.frame` object.

`keys` Variables to be used as keys. See the `by` argument in "[divide](#)".

keep	Variables to remain as their own columns. If NULL (default), all variables except those in send are chosen, excluding the keys. Has <code>tidyselect::vars_select</code> capabilities.
send	Variables to send into new columns for each key. If NULL (default), all variables except those in keep are chosen, excluding the keys. Has <code>tidyselect::vars_select</code> capabilities.
join	Function that joins on keep across the keys. Defaults to <code>dplyr::full_join</code> . See <code>?dplyr::join</code> for choices.
.sep	Character to separate and identify keys values over the columns. Defaults to "_".
extract_keys_as_header	Should the keys labels be returned as a separate character vector? Defaults to FALSE. Has no effect when there is only 1 send column.
keep_keys_in_header	If <code>extract_keys_as_header = TRUE</code> , should the keys be left in the result columns? Defaults to TRUE. Useful to set to FALSE if a call to <code>knitr::kable</code> follows.
...	Additional arguments to be passed to join.

**Value**

A wide `data.frame` with variables spread over the columns. If `extract_keys_as_header = TRUE`, the result is a two-element `list` with the transformed data in 1 element and the top-level header in the other. If only 1 send variable exists, the original names are removed.

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#Make data frame with multiple summary columns
temp_summary <-

  heart_disease %>%
  group_by(
    Sex,
    HeartDisease,
    BloodSugar
  ) %>%
  summarise(
    Mean = mean(Age, na.rm = TRUE),
    SD = sd(Age, na.rm = TRUE),
    Median = median(Age, na.rm = TRUE)
  ) %>%
  ungroup()
```

```

#1) Span summaries for each combination of Sex and BloodSugar
temp_summary %>%
  stretch(
    keys = c("Sex", "BloodSugar"),
    keep = "HeartDisease"
  )

#2) If "HeartDisease" wasn't fully crossed, use different joining to get only matching groups
temp_summary %>%
  stretch(
    keys = c("Sex", "BloodSugar"),
    keep = "HeartDisease",
    join = inner_join
  )

#3) Only send two of the summaries
temp_summary %>%
  stretch(
    keys = c("Sex", "BloodSugar"),
    keep = "HeartDisease",
    send = c("Mean", "Median")
  )

#4) Clean HTML table with keys spanned over columns
result <-
  temp_summary %>%
  stretch(
    keys = c("Sex", "BloodSugar"),
    keep = "HeartDisease",
    extract_keys_as_header = TRUE,
    keep_keys_in_header = FALSE
  )
result$result %>%
  knitr::kable(format = "html") %>%
  kableExtra::kable_styling() %>%
  kableExtra::add_header_above(
    kableExtra::auto_index(result$header)
  )

```

---

type\_match

*Check if an object is at least one (or none) of the specified types*


---

## Description

This is a utility function to assess whether an object inherits at least one (or none) of the user-specified classes.

**Usage**

```
type_match(  
  object,  
  types,  
  negated = FALSE  
)
```

**Arguments**

object	Any R object.
types	A character vector of classes to check against object.
negated	Should TRUE be returned if object inherits no types? Defaults to FALSE.

**Value**

A logical indicator

**Author(s)**

Alex Zajichok

**Examples**

```
require(tidyverse)  
  
#1) Default  
heart_disease %>%  
  map_lgl(  
    type_match,  
    types = "numeric"  
  )  
  
#2) Use negation  
heart_disease %>%  
  map_lgl(  
    type_match,  
    types = "numeric",  
    negated = TRUE  
  )  
  
#3) Multiple types  
heart_disease %>%  
  map_lgl(  
    type_match,  
    types = c("numeric", "factor")  
  )  
  
#4) Check other objects  
heart_disease %>%  
  glm(Sex ~ Age, data = ., family = "binomial") %>%  
  type_match(
```

```

    types = "glm"
  )

```

typly

*Apply function(s) to elements conforming to specified type(s)*

### Description

Evaluates a function or a list of function on all elements of `list` or `data.frame` that inherit at least one of the allowable types specified by the user. An option is available to evaluate the function(s) on all elements that do not match.

### Usage

```

typly(
  data,
  types,
  f,
  negated = FALSE,
  keep = FALSE,
  ...
)

```

### Arguments

<code>data</code>	A <code>data.frame</code> or <code>list</code> .
<code>types</code>	A character vector of allowable data types identifying columns in which function(s) should be applied.
<code>f</code>	A function or list of functions.
<code>negated</code>	Should the function(s) be applied to columns that don't match any types? Defaults to FALSE.
<code>keep</code>	Should the non-matching columns be kept as is? Defaults to FALSE.
<code>...</code>	Additional arguments to be passed to <code>f</code> .

### Value

A list with the result(s) of `f` for each applicable column.

### Author(s)

Alex Zajichek

**Examples**

```
require(tidyverse)

heart_disease %>%

  #Compute means and medians on numeric data
  tply(
    c("numeric", "logical"),
    list(
      mean = mean,
      median = median
    ),
    keep = TRUE,
    na.rm = TRUE
  ) %>%

  #Compute table
  tply(
    "factor",
    table,
    keep = TRUE
  )
```

---

 univariate\_associations

*Compute association metrics between any number of variables*

---

**Description**

Evaluates a list of scalar functions on any number of "responses" for each individual variable and gathers results.

**Usage**

```
univariate_associations(
  data,
  f,
  responses = NULL,
  predictors = NULL
)
```

**Arguments**

data	Any data.frame.
f	A function or a list of functions (preferably named) that take a vector as input in the first two arguments and return an atomic scalar.
responses	Response or outcome variables. See " <a href="#">dish</a> ".
predictors	Predictors or covariates. See " <a href="#">dish</a> ".



**Value**

A tibble with the variables in the rows and the results of the functions in the columns. The names of the columns will be the names provided in `f`.

**Author(s)**

Alex Zajichek

**Examples**

```
require(tidyverse)

#Make a list of functions
f <-
  list(

    #Compute a univariate p-value
    `P-value` =

      function(x, y) {

        if(type_match(y, c("factor", "character"))) {

          p <- fisher.test(factor(x), factor(y), simulate.p.value = TRUE)$p.value

        } else {

          p <- kruskal.test(y, factor(x))$p.value

        }

        if_else(
          p < 0.001, "<0.001", as.character(round(p, 2))
        )

      },

    #Compute difference in AIC model between null model and one predictor model
    `AIC Difference` =
      function(x, y) {

        glm(factor(x)~1, family = "binomial")$aic -
        glm(factor(x)~y, family = "binomial")$aic

      }

  )

#1) Apply functions to Sex/HeartDisease by all other variables
heart_disease %>%
  univariate_associations(
    f = f,
    responses = c("Sex", "HeartDisease")
  )
```

```

#2) Only use two variables on RHS
heart_disease %>%
  univariate_associations(
    f = f,
    responses = c("Sex", "HeartDisease"),
    predictors = c("Age", "ChestPain")
  )

#3) Use all combinations
heart_disease %>%
  univariate_associations(
    f = f
  )

```

---

univariate\_table

*Create a custom univariate summary for a dataset*


---

## Description

Produces a formatted table of univariate summary statistics with options allowing for stratification by 1 or more variables, computing of custom summary/association statistics, custom string templates for results, etc.

## Usage

```

univariate_table(
  data,
  strata = NULL,
  associations = NULL,
  numeric_summary = c(Summary = "median (iqr)"),
  categorical_summary = c(Summary = "count (percent%)"),
  other_summary = c(Summary = "unique"),
  all_summary = NULL,
  evaluate = FALSE,
  add_n = FALSE,
  order = NULL,
  labels = NULL,
  levels = NULL,
  format = c("html", "latex", "markdown", "pandoc", "none"),
  variableName = "Variable",
  levelName = "Level",
  na_string = "(missing)",
  strata_sep = "/",
  summary_strata_sep = "_",
  fill_blanks = "",
  caption = ""
)

```

```
    ...
  )
```

## Arguments

<code>data</code>	A <code>data.frame</code> to summarise.
<code>strata</code>	A formula specifying one or more stratification variables. LHS variables go to rows, RHS variables go to columns. Defaults to <code>NULL</code> .
<code>associations</code>	A named list of functions to evaluate with column <code>strata</code> and each variable. Defaults to <code>NULL</code> .
<code>numeric_summary</code>	A (preferably named) character vector containing string templates of how results for numeric data should be presented. See details for a list of what is available by default. Defaults to <code>c(Summary = "median (iqr)")</code> .
<code>categorical_summary</code>	A (preferably named) character vector containing string templates of how results for categorical data should be presented. See details for a list of what is available by default. Defaults to <code>c(Summary = "count (percent%)")</code> .
<code>other_summary</code>	A (preferably named) character vector containing string templates of how results for non-numeric and non-categorical data should be presented. See details for a list of what is available by default. Defaults to <code>c(Summary = "unique")</code> .
<code>all_summary</code>	A (preferably named) character vector containing string templates of additional results for all variables should be presented. See details for a list of what is available by default. Defaults to <code>NULL</code> .
<code>evaluate</code>	Should the results of the string templates be evaluated as an R expression after filled with their values? See " <code>absorb</code> " for details. Defaults to <code>FALSE</code> .
<code>add_n</code>	Should the sample size for each stratification level be added to the result? Defaults to <code>FALSE</code> .
<code>order</code>	Character vector of 1 or more variables to reorder the result by from top to bottom. If <code>NULL</code> (default), the result is sorted according to <code>names(data)</code> .
<code>labels</code>	Named character vector for re-labeling variables in the result. Defaults to <code>NULL</code> .
<code>levels</code>	Named list of character vectors for re-labeling factor levels in the result. Defaults to <code>NULL</code> .
<code>format</code>	The format that the result should be rendered as. Must be one of <code>c("html", "latex", "markdown", "pandoc")</code> . Defaults to <code>"html"</code> .
<code>variableName</code>	Header for the variable column in the result. Defaults to <code>"Variable"</code> .
<code>levelName</code>	Header for the factor level column in the result. Defaults to <code>"Level"</code> .
<code>na_string</code>	String for NA factor levels in the result. Defaults to <code>"(missing)"</code> .
<code>strata_sep</code>	Delimiter to separate stratification levels by in the result. Defaults to <code>"/"</code> .
<code>summary_strata_sep</code>	Delimiter to separate summary column names with the strata groups. Defaults to <code>"_"</code> .
<code>fill_blanks</code>	String to fill in blank spaces in the result. Defaults to <code>""</code> .
<code>caption</code>	Caption for resulting table passed to <code>knitr::kable</code> . Defaults to <code>NULL</code> .
<code>...</code>	Additional arguments to pass to " <code>descriptives</code> ".

## Details

The following statistics are available by default for each data type:

Numeric: "min", "max", "median", "iqr", "mean", "sd"

Categorical: "count", "percent"

All variables: "length", "missing", "available", "class", "unique"

These strings are typed explicitly in the `._summary` arguments and serve as placeholders for where the actual value will appear. Custom functions can be entered in a named list, where the names are what provide access to the values in string templates. See "[descriptives](#)" and "[absorb](#)".

The names of the `._summary` arguments are what become the column headers in the result. If unnamed, an arbitrary name (i.e. "VX") will appear in the column header.

## Value

A table of summary statistics according to the specified format. A tibble is returned if `format = "none"`.

## Author(s)

Alex Zajichek

## Examples

```
require(tidyverse)

#1) Default summary
heart_disease %>%
  univariate_table()

#2) Stratified summary
heart_disease %>%
  univariate_table(
    strata = ~Sex,
    add_n = TRUE
  )

#See vignette("cheese") for more examples
```

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