Package ‘tangram’

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Title The Grammar of Tables

Version 0.8.2

Description Provides an extensible formula system to quickly and easily create production quality tables. The processing steps are a formula parser, statistical content generation from data as defined by formula, followed by rendering into a table. Each step of the processing is separate and user definable thus creating a set of composable building blocks for highly customizable table generation. A user is not limited by any of the choices of the package creator other than the formula grammar. For example, one could chose to add a different S3 rendering function and output a format not provided in the default package, or possibly one would rather have Gini coefficients for their statistical content in a resulting table. Routines to achieve New England Journal of Medicine style, Lancet style and \texttt{Hmisc::summaryM()} statistics are provided. The package contains rendering for HTML5, Rmarkdown and an indexing format for use in tracing and tracking are provided.

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'compile-clmm2.R' 'compile-operators.R' 'compile-post.R'
R topics documented:

'parser.R' 'compile.R' 'compile-rms.R' 'compile-typing.R'
'helper-format.R' 'hmisc-cut2.R' 'hmisc-lm.fit.qr.bare.R'
'hmisc-impute.R' 'hmisc-biVar.R' 'iify.R' 'render-csv.R'
'render-latex.R' 'render-index.R' 'render-latex-map.R'
'render-rtf.R' 'render-summary.R' 'smd.R' 'transform-hmisc.R'
'transform-lancet.R' 'transform-nejm.R' 'transform-proc-tab.R'
'transform-smd.R'

NeedsCompilation no

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Repository CRAN

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Provide a "+" operator for rbind of tangram tables

Description
The plus operator provides an rbind for tangram tables

Usage
## S3 method for class 'tangram'
x + y

Arguments
x  left argument for rbind
y  right argument for rbind

Value
A row wise merged tangram object
add_footnote

Add a footnote to a table

Description
Add a footnote to a table

Usage
add_footnote(table, footnote)

Arguments
- **table**: tangram; the tangram table to modify
- **footnote**: character; The footnote to add

Value
the modified table

add_indent
Add indentations to left column row headers

Description
Add indentations to left column row headers. Note: will only work on cell_header cells.

Usage
add_indent(table, amounts = 2, rows = NULL, columns = NULL)

Arguments
- **table**: Output of tangram::tangram()
- **amounts**: numeric; Specifies number of spaces to add. A vector that is either a single value or vector of the same size as the height of the table. If positions is specified then it must be the same length. Defaults to 2, which each pair of spaces converts naturally in rendering to HTML, LaTeX, etc..
- **rows**: numeric; A vector of numeric row numbers for the rows that need to be indented. Defaults to NULL which indents all.
- **columns**: numeric; Column to apply indent to, defaults to 1

Value
the modified table
as.categorical

Examples

x <- tangram(drug ~ bili + albumin, pbc)
add_indent(x)
add_indent(x, amounts=10)
add_indent(x, amounts=c(0, 0, 2, 4))
add_indent(x, rows=c(3))
add_indent(x, rows=c(3, 4), amounts=c(4, 2))

args_flatten

Flatten variable arguments

Description

Take variable arguments, flatten vectors and lists, but do not flatten cells (which are lists) e.g.

args_flatten(NA, list(1,2,3), 4:6, c(7,8,9))

Usage

args_flatten(...)

Arguments

... variable arguments

Value

a list of the arguments, with vectors and lists flattened

as.categorical

Convert data type to a factor if it's not already

Description

Convert data type to a factor if it's not already

Usage

as.categorical(x)

Arguments

x Data to convert to factor

Value

Data as a factor
Examples

```r
as.categorical(1:3)
```

Description

A left/right branch in an Abstract Syntrax Tree. This inherits from `ASTNode`, and is intended to be a base class as well. Should never be instantiated directly as once again the semantic information is contained in the class name.

A left/right branch in an Abstract Syntrax Tree. This inherits from `ASTNode`, and is intended to be a base class as well. Should never be instantiated directly as once again the semantic information is contained in the class name.

A left/right branch in an Abstract Syntrax Tree. This inherits from `ASTNode`, and is intended to be a base class as well. Should never be instantiated directly as once again the semantic information is contained in the class name.

Format

`R6Class` object.

Super class

`tangram::ASTNode` -> `ASTBranch`

Public fields

- `left` A pointer to the left node below this one
- `right` A pointer to the right node below this one

Methods

Public methods:

- `ASTBranch$distribute()`
- `ASTBranch$reduce()`
- `ASTBranch$clone()`

Method `distribute()`: Call to distribute multiplication nodes, just recursively calls left and right node distribute functions

Usage:

```r
ASTBranch$distribute()
```

Method `reduce()`: Attached data to nodes by processing `data.frame` appropriately. Recursively calls left and right nodes to reduces on `data.frame`
Usage:
ASTBranch$reduce(df)

Arguments:
df (data.frame) Data frame to reduce over

Method clone(): The objects of this class are cloneable with this method.
Usage:
ASTBranch$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

---

**ASTFunction**

A specified function call as an ASTNode

---

**Description**

A specified function call as an ASTNode
A specified function call as an ASTNode

**Format**

*R6Class* object.

**Super class**

*tangram::ASTNode* -> ASTFunction

**Public fields**

* r_expr A string containing the raw r expression from inside the parenthesis
* data Data stored as a result of reduction

**Methods**

**Public methods:**
- ASTFunction$new()
- ASTFunction$factors()
- ASTFunction$name()
- ASTFunction$string()
- ASTFunction$reduce()
- ASTFunction$clone()

**Method** new(): Construct a node representing a function call

*Usage:*
ASTFunction$new(value, r_expr)

Arguments:
value (character) The name of the function call
r_expr Any R expression to be evaluated inside the call

Method factors(): Returns all terminal nodes, this is a terminal node so returns self

Usage:
ASTFunction$factors()

Method name(): Returns the function call as character

Usage:
ASTFunction$name()

Method string(): Returns a re-parsable representation of the node

Usage:
ASTFunction$string()

Method reduce(): Given a data.frame execute the function in that environment and associate the result as data.

Usage:
ASTFunction$reduce(data)

Arguments:
data (data.frame) The data.frame to use as the environment for the function execution

Method clone(): The objects of this class are cloneable with this method.

Usage:
ASTFunction$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples
ASTFunction$new("log", "x+2")$string()
**Description**

The multiplication of two terms, as an ASTNode.

**Format**

R6Class object.

**Super classes**

tangram::ASTNode -> tangram::ASTBranch -> ASTMultiply

**Public fields**

- left  The AST tree to the left.
- right The AST tree to the right.
- type  The specified type of this node

**Methods**

**Public methods:**

- ASTMultiply$new()
- ASTMultiply$distribute()
- ASTMultiply$factors()
- ASTMultiply$string()
- ASTMultiply$clone()

**Method** new(): Construct a multiplication node

*Usage:*

ASTMultiply$new(left, right)

*Arguments:*

- left (ASTNode) nodes to the left of the multiplication
- right (ASTNode) nodes to the right of the multiplication

**Method** distribute(): Rearrange nodes distribution multiplication across parenthesis

*Usage:*

ASTMultiply$distribute()

**Method** factors(): return all terminal nodes on left and right

*Usage:*


ASTNode

ASTMultiply$factors()

**Method** string(): Return a re-parseable string

**Usage:**

ASTMultiply$string()

**Method** clone(): The objects of this class are cloneable with this method.

**Usage:**

ASTMultiply$clone(deep = FALSE)

**Arguments:**

depth Whether to make a deep clone.

**Examples**

ASTMultiply$new(ASTVariable$new("x"), ASTVariable$new("y"))$string()

---

**ASTNode**

A Node in an Abstract Syntax Tree (AST)

**Description**

A Node in an Abstract Syntax Tree (AST)

**Details**

This is the root R6 class of any term of the AST which is created when parsing a table formula. This should only be used as a base class as the class information carries the semantic meaning of a given node.

**Public fields**

- format Any formatting directive passed to this node.
- value A string of additional information contained by the node.

**Methods**

**Public methods:**

- ASTNode$terms()
- ASTNode$distribute()
- ASTNode$string()
- ASTNode$reduce()
- ASTNode$set_format()
- ASTNode$clone()
Method terms(): Returns this node
Usage:
ASTNode$terms()

Method distribute(): Distributes data across multiplications and rearranges nodes
Usage:
ASTNode$distribute()

Method string(): Returns string representation of node
Usage:
ASTNode$string()

Method reduce(): Given a set of data, associates it with AST nodes
Usage:
ASTNode$reduce(data)
Arguments:
data (data.frame) data to associate across nodes

Method set_format(): Override the formatting directive for this node
Usage:
ASTNode$set_format(x)
Arguments:
x (numeric, character) the formatting directive

Method clone(): The objects of this class are cloneable with this method.
Usage:
ASTNode$clone(deep = FALSE)
Arguments:
deep Whether to make a deep clone.

ASTPlus
The addition of two terms, in an ASTNode.

Description
The addition of two terms, in an ASTNode.
The addition of two terms, in an ASTNode.

Format
R6Class object.
Super classes

tangram::ASTNode -> tangram::ASTBranch -> ASTPlus

Public fields

data  Just returns the R6 name 'ASTPlus'
left  The node to the left of this node
right The node to the right of this node

Methods

Public methods:
• ASTPlus$new()
• ASTPlus/terms()
• ASTPlus$string()
• ASTPlus$clone()

Method new(): Construct a new node that represents addition

Usage:
ASTPlus$new(left, right)

Arguments:
left  (ASTNode) Node on the left side of the addition
right (ASTNode) Node on the right side of the addition

Method terms(): Returns a vector of the left and right terms

Usage:
ASTPlus/terms()

Method string(): A reparsable string representation of this node.

Usage:
ASTPlus$string()

Method clone(): The objects of this class are cloneable with this method.

Usage:
ASTPlus$clone(deep = FALSE)

Arguments:
deep  Whether to make a deep clone.

Examples

ASTPlus$new(ASTVariable$new("x"), ASTVariable$new("y"))$string()
ASTTableFormula

The root ASTNode of a formula.

Description
The root ASTNode of a formula.

The root ASTNode of a formula.

Format
R6Class object.

Super classes
tangram::ASTNode -> tangram::ASTBranch -> ASTTableFormula

Public fields
left The AST tree for the columns.
right The AST tree for the rows.

Methods

Public methods:
• ASTTableFormula$new()
• ASTTableFormula$terms()
• ASTTableFormula$string()
• ASTTableFormula$clone()

Method new(): Create a new formula node
Usage:
ASTTableFormula$new(left, right)
Arguments:
left The left side of the "~" as an AST
right The right side of the "~" as an AST

Method terms(): Returns all terminal nodes from left and right
Usage:
ASTTableFormula/terms()

Method string(): A re-parseable string representing the AST
Usage:
ASTTableFormula$string()

Method clone(): The objects of this class are cloneable with this method.
**Usage:**
ASTTableFormula$clone(deep = FALSE)

**Arguments:**
deep  Whether to make a deep clone.

**Examples**
ASTTableFormula$new(ASTVariable$new("x"), ASTVariable$new("y"))$string()

---

**ASTVariable**  
A Variable in an Abstract Syntax Tree (AST)

**Description**
A Variable in an Abstract Syntax Tree (AST)
A Variable in an Abstract Syntax Tree (AST)

**Format**
R6Class object.

**Details**
This node represents a variable of interest in the AST. A variable’s name is recorded in the value field, and must conform to the rules of identifiers in R. This class inherits from ASTNode.

**Methods**
new(identifier, format=NA, type=NA)
terms() Returns the node
distribute() Applies the distributive property to the node, and returns the resulting node.
string() Returns the string formula of the node
name() Return a human representation of a node
reduce(data) Given a set of data, perform the logical reduction of the current node.

**Super class**
tangram::ASTNode -> ASTVariable

**Public fields**

data  The associated data post reduction
type  The identified type of this node (defaults: Categorical, Numeric)
Methods

Public methods:

• ASTVariable$new()
• ASTVariable$factors()
• ASTVariable$name()
• ASTVariable$string()
• ASTVariable$reduce()
• ASTVariable$clone()

Method new(): This method creates an AST node representing a variable of a given identifier. An optional format consisting of a string of a number or a c-style printf string. An option type denoting a forced type cast of that variable.

Usage:
ASTVariable$new(identifier, format = NA, type = NA)

Arguments:
identifier (character) Variable name
format (character, numeric) Formatting directive
type (character) any additional type information

Method factors(): Returns all terminal nodes under this. Since this is a terminal node, returns self

Usage:
ASTVariable$factors()

Method name(): Returns the text name of this node. For an intercept, returns "All"

Usage:
ASTVariable$name()

Method string(): Returns name of variable with optional format and type information

Usage:
ASTVariable$string()

Method reduce(): Given a data.frame, associates correct variable with this node

Usage:
ASTVariable$reduce(d)

Arguments:
d (data.frame) data.frame to reduce

Method clone(): The objects of this class are cloneable with this method.

Usage:
ASTVariable$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

ASTVariable$new("x", "2", "Continuous")$string()
cbind.tangram

A cbind for generated table tangram objects.

Description

Execute the equivalent of an cbind for generated tables

Usage

## S3 method for class 'tangram'
cbind(..., deparse.level = 1)

Arguments

...   tangram objects to cbind
deparse.level numeric; not used

Value

A merged tangram object

cell

Construct a table cell from an object

Description

Any R object can be used as a cell value. Attributes are used to store additional classes of that cell attached to the object. This is a helper function to attach all the additional attributes to the provided object

Usage

cell(x, ...)

Arguments

x       R object to attach attributes too
...  Each additional argument becomes an attribute for the object

Details

Certain attributes have special meaning: - 'names' is appended to the front of a value, e.g. "P=" for a p-value. - 'sep' is used to join values, e.g. ", " for a list of values. - 'class' denotes special rendering handling, e.g. generally passed as CSS class to HTML5 - 'reference' a list of reference symbols to put inside the cell - 'row' and 'col' should refer to the row / column if key generation is needed - 'subrow' and 'subcol' further delineate the key value of a cell for key generation
cell_header  

Create a cell_header object of the given text.

Description

A cell_header object represents a label cell inside a table. It can also contain units.

Usage

cell_header(text, units = NULL, class = NULL, ...)

Arguments

text character; The text of the label. May include a subset of LaTeX greek or math.
units character; An optional field that contains units
class character; An optional field for additional S3 classes (e.g. could be used in html rendering for CSS)
...
optional extra information to attach

Value

A cell_header object

Examples

cell_header("Yahoo")
cell_header("Concentration", "mg/dl")
cell_header("Concentration", "mg/dl", src="A")


cell_label  

Create an cell_label (S3) object of the given text.

Description

A cell_label object represents a label cell inside a table. It can also contain units.

Usage

cell_label(text, units = NULL, class = NULL, ...)


Arguments

text character; The text of the label. May include a subset of LaTeX greek or math.
units character; An optional field that contains units
class character; An optional field for additional S3 classes (e.g. could be used in html rendering for CSS)
...

Value

A tangram object

Examples

cell_label("Compaction Method")
cell_label("Concentration", "mg/dl")
cell_label("Concentration", "mg/dl", subcol="A")

cell_n Create an cell_n (S3) object of the given statistic

Description

A cell_n object contains an n value. Essentially, this is just a helper that appends the cell_n class to the given object and makes sure it’s a cell S3 object as well.

Usage

cell_n(n, class = NULL, hdr = FALSE, possible = NULL, ...)

Arguments

n The numerical value
class character; An optional field for additional S3 classes (e.g. could be used in html rendering for CSS)
hdr logical; Construct an n value for a header (defaults to FALSE)
possible numerical; The total N that was possible
...

Value

A cell_n object.

Examples

cell_n(20)
**cell_subheader**  
*Create a cell_subheader object of the given text.*

**Description**

A cell_subheader object represents a label cell inside a table. It can also contain units.

**Usage**

```r
cell_subheader(text, units = NULL, class = NULL, ...)
```

**Arguments**

- `text`: character; The text of the label. May include a subset of LaTeX greek or math.
- `units`: character; An optional field that contains units.
- `class`: character; An optional field for additional S3 classes (e.g. could be used in html rendering for CSS).
- `...`: optional extra information to attach.

**Value**

A cell_subheader object.

**Examples**

```r
cell_subheader("Concentration")
cell_subheader("Concentration", "mg/dl")
cell_subheader("Concentration", "mg/dl", src="A")
```

---

**cell_transform**  
*Create a function to transform all cells of a table*

**Description**

Given a function that operates on a table cell and returns the modified cell, return a function that given a table applies that function to all cells and returns the modified table.

**Usage**

```r
cell_transform(FUN, ...)
```

**Arguments**

- `FUN`: function to apply, must return the modified cell.
- `...`: additional arguments to pass into function.
col_header

Value

a table modification function

---

col_header  A set of magrittr operators for tangram tables

Description

A set of magrittr operators for tangram tables

Usage

col_header(table, ..., sub = TRUE)
row_header(table, ..., sub = TRUE)
write_cell(table, x, ...)
home(table)
cursor_up(table, n = 1)
cursor_down(table, n = 1)
cursor_left(table, n = 1)
cursor_right(table, n = 1)
cursor_pos(table, nrow, ncol)
carriage_return(table)
line_feed(table, n = 1)
new_line(table)
new_row(table)
new_col(table)
table_apply(table, x, FUN, ...)
add_col(table, ...)
add_row(table, ...)
set_footnote(table, footnote)
set_id(table, id)
set_caption(table, caption)
set_style(table, style)
set_colspan(table, span)
set_rowspan(table, span)

Arguments

**table**  
tangram; The tangram table being built
**...**  
additional argument passed
**sub**  
logical; Is this a subheader
**x**  
object of focus in operation
**n**  
numeric; number of times to perform operation
**nrow**  
numeric; number of rows
**ncol**  
numeric; number of columns
**FUN**  
function; function to apply
**footnote**  
character; footnote to add
**id**  
character; id of table
**caption**  
character; caption of table
**style**  
character; styling in compiling table and in rendering
**span**  
numeric; number of rows or columns to span

---

csv  
*Generate an csv from a tangram or cell object*

Description

Given a tangram object create an index representation.

Usage

csv(object, ...)

## S3 method for class 'tangram'
csv(object, file = NULL, sep = ",", ...)  

## Default S3 method:
csv(object, ...)
**custom_css**

**Arguments**

- **object**: The cell header to render to HTML5
- **...**: additional arguments to renderer. Unused
- **file**: File to write result into
- **sep**: separator to use

**Value**

A string containing the csv file

---

```r
custom_css(filename, id = NA)
```

**Description**

Given a filename, this function will load the file name from the current working directory. If it is not found from the current working directory it will search in the package for a a matching filename and load that instead. If an id is specified, that will be prepended to all CSS selectors (TODO: make this substitution more robust). The result is returned as a string.

**Usage**

```r
custom_css(filename, id = NA)
```

**Arguments**

- **filename**: Name of the CSS file to load
- **id**: CSS id to prepend to all entries

**Value**

String of possibly modified CSS file

**Examples**

```r
custom_css("lancet.css", "tbl1")
```
**del_col**  
*Delete given column(s) from a table*

**Description**
Given a table, remove the specified column

**Usage**
del_col(table, col)

**Arguments**
- **table**: the table to modify
- **col**: vector containing column(s) to drop

**Value**
the modified table

**del_row**  
*Delete a row(s) from a table*

**Description**
Given a table, remove the specified row

**Usage**
del_row(table, row)

**Arguments**
- **table**: the table to modify
- **row**: vector with row numbers to drop

**Value**
the modified table
**derive_label**

*Derive label of AST node.*

**Description**

Determine the label of a given AST node. NOTE: Should have data attached via reduce before calling.

**Usage**

```r
derive_label(node, capture_units = FALSE, ...)
```

**Arguments**

- `node`: Abstract syntax tree node.
- `capture_units`: logical; Capture units from parenthesis ending a label
- `...`: Other arguments, ignored

**Value**

A string with a label for the node

---

**drop_statistics**

*Drop all statistics columns from a table.*

**Description**

Delete from a table all columns that contain statistics

**Usage**

```r
drop_statistics(table)
```

**Arguments**

- `table`: the table to remove statistical columns

**Value**

the modified table
format_guess

Guess the best format for a given set of numerical data

Description
Given a vector of data, default to 3 significant digits or all if maximum is greater than zero

Usage
format_guess(x)

Arguments
x numeric; basic math and quantile function must work on data passed in

Value
numeric; the digits past the decimal recommended for display

Examples
format_guess(rnorm(100))
format_guess(rnorm(100, sd=1e-6))

hmisc_data_type

Determine data type of a vector loosely consistent with Hmisc.

Description
Determine data type of a vector loosely consistent with Hmisc.

Usage
hmisc_data_type(x, category_threshold = NA)

Arguments
x Vector to determine type of
category_threshold The upper threshold of unique values for which a vector is considered categorical.

Value
One of the following strings: Binomial, Categorical, or Numerical.
hmisc_intercept_cleanup

See Also

hmisc

Examples

hmisc_data_type(c(1,2,3))
hmisc_data_type(factor(c("A","B","C")))
hmisc_data_type(factor(c("A","B","B","A")))
hmisc_data_type(factor(c(TRUE, FALSE, TRUE, FALSE)))

hmisc_intercept_cleanup

Cleanup an intercept only model

Description

Cleanup an intercept only table that was generated from the hmisc default transform. This drops the statistics column, and modifies the header to eliminate blank space.

Usage

hmisc_intercept_cleanup(table)

Arguments

table the table to modify

Value

the modified table

hmisc_p

Cell Generation functions for hmisc default

Description

Each function here is called when a cell is generated. Overriding these in a formula call will allows one to customize exactly how each cell’s contents are generated. While this serves as the base template for transforms, it is by no means required if one develops their own bundle of data transforms. One can create ay number of cell level styling choices.
Usage

hmisc_p(p, pformat = "%1.3f", include_p = TRUE)

hmisc_iqr(
  x,
  format = NA,
  na.rm = TRUE,
  names = FALSE,
  type = 8,
  msd = FALSE,
  quant = c(0.25, 0.5, 0.75),
  ...
)

hmisc_fraction(numerator, denominator, format = 3, ...)

hmisc_fstat(f, df1, df2, p, class = NULL, ...)

hmisc_chi2(chi2, df, p, class = NULL, ...)

hmisc_spearman(S, rho, p, class = NULL, ...)

hmisc_wilcox(V, p, class = NULL, ...)

Arguments

p numeric; p-value to format
pformat numeric or character; Significant digits or fmt to pass to sprintf
include_p logical; include the leading P on the output string
x numeric; whose sample quantiles are wanted. NA and NaN values are not allowed in numeric vectors unless na.rm is TRUE.
format numeric or character; Significant digits or fmt to pass to sprintf
na.rm logical; if true, any NA and NaN's are removed from x before the quantiles are computed.
names logical; if true, the result has a names attribute. Set to FALSE for speedup with many probs.
type integer; specify algorithm to use in constructing quantile. See quantile for more information.
msd logical; compute an msd attribute containing mean and standard deviation
quant numeric; The quantiles to display. Should be an odd length vector, since the center value is highlighted.
... additional arguments passed
numerator numeric; The value of the numerator
**denominator** numeric; The value of the denominator  
**f** The value of the f-statistic  
**df1** 1st dimension degrees of freedom  
**df2** 2nd dimension degrees of freedom  
**class** character; An optional field for additional S3 classes (e.g. could be used in html rendering for CSS)  
**chi2** The value of the X^2 statistic  
**df** degrees of freedom  
**S** The value of the spearman statistic  
**rho** The rho value of the test  
**V** The value of the Wilcoxon statistic

**Format**

An object of class list of length 8.

**Value**

A formatted string or cell as appropriate

**hmisc_p**

Given a style in number of digits or a sprintf style specifier it renders the p-value and checks to see if it’s all zeros, then switches the output to a less than.

**hmisc_iqr**

Construct a cell which has the interquartile ranges specified.

**hmisc_fraction**

Construct a cell which has the fraction specified in an hmisc format

**hmisc_fstat**

Construct a cell which has the fstat specified in an hmisc format.

**hmisc_ch2**

Construct a cell which has the chi^2 specified in an hmisc format

**hmisc_spearman**

Construct a cell which has the spearman specified in an hmisc format

**hmisc_wilcoxon**

Construct a cell which has the Wilcoxon specified in an hmisc format
hmisc_cell

List of data transforms for a cell of a table.

hmisc_cell <- list(
  n = cell_n,
  iqr = hmisc_iqr,
  fraction = hmisc_fraction,
  fstat = hmisc_fstat,
  chi2 = hmisc_chi2,
  spearman = hmisc_spearman,
  wilcox = hmisc_wilcox,
  p = hmisc_p
)

See Also
hmisc

Examples

hmisc_p(1e-6)
hmisc_p(0.234)
hmisc_p(1.234e-6, 5)
hmisc_p(1.234e-6, 6)
require(stats)
hmisc_iqr(rnorm(100), '3')
hmisc_fraction(1, 4, 3)
hmisc_fstat(4.0, 10, 20, 0.004039541)
hmisc_chi2(5.33, 6, 0.2)
hmisc_spearman(20, 0.2, 0.05)
hmisc_wilcox(20, 0.2)

html5

S3 html5 Method function for use on a tangram to generate HTML5

Description

S3 html5 Method function for use on a tangram to generate HTML5

Usage

html5(object, id, ...)

Arguments

object The cell to render to HTML5
id A unique identifier for traceability in indexing
... additional arguments to renderer.
**html5.cell**

*Convert an abstract cell object into an HTML5 string*

**Description**

Given a cell class create an HTML5 representation.

**Usage**

```r
## S3 method for class 'cell'
html5(object, id, ..., class = NULL)
```

**Arguments**

- **object**
  The cell to render to HTML5
- **id**
  A unique identifier for traceability
- **...**
  Additional arguments to renderer. Unused
- **class**
  An additional class attribute for the HTML5 element

**Value**

A text string rendering of the given cell as a `<td>` with several `<span>`’s.

---

**html5.cell_header**

*Convert an abstract cell_header object into an HTML5 string*

**Description**

Given a cell_header class create an HTML5 representation.

**Usage**

```r
## S3 method for class 'cell_header'
html5(object, id, ..., class = NULL)
```

**Arguments**

- **object**
  The cell subheader to render to HTML5
- **id**
  A unique identifier for traceability
- **...**
  Additional arguments to renderer. Unused
- **class**
  Additional class attributes for CSS rendering

**Value**

A text string rendering of the given subheader as a `<td>` with several `<span>`’s.
html5.cell_label

Convert a cell_label object into an HTML5 string

Description
Given a cell_label class create an HTML5 representation.

Usage
## S3 method for class 'cell_label'
html5(object, id, ..., class = NULL)

Arguments
- **object**: The cell label to render to HTML5
- **id**: A unique identifier for traceability
- **...**: additional arguments to renderer. Unused
- **class**: An additional class attribute for the HTML5 element

Value
A text string rendering of the given label as a <td> with several <span>’s.

html5.cell_n

Convert an abstract cell_n object into an HTML5 string

Description
Given a cell_n class create an HTML5 representation.

Usage
## S3 method for class 'cell_n'
html5(object, id, ..., class = NULL)

Arguments
- **object**: The cell n to render to HTML5
- **id**: A unique identifier for traceability
- **...**: additional arguments to renderer. Unused
- **class**: An additional class attribute for the HTML5 element

Value
A text string rendering of the given n as a <td> with several <span>’s.
Convert an abstract cell_subheader object into an HTML5 string

Description
Given a cell_subheader class create an HTML5 representation.

Usage

```r
## S3 method for class 'cell_subheader'
html5(object, id, ..., class = NULL)
```

Arguments

- `object`  The cell subheader to render to HTML5
- `id`  A unique identifier for traceability
- `...`  additional arguments to renderer. Unused
- `class`  additional class attributes for CSS rendering

Value
An text string rendering of the given subheader as a `<td>` with several `<span>`’s.

Default conversion to HTML5 for a character cell

Description
Produces table cell

Usage

```r
## S3 method for class 'character'
html5(object, id, ..., class = NA)
```

Arguments

- `object`  The cell to render to HTML5
- `id`  A unique identifier for traceability
- `...`  additional arguments to renderer. Unused
- `class`  An additional class attribute for the HTML5 element

Value
An empty html5 td of the given class
**html5.default**  
*Default conversion to HTML5 for an abstract table element*

**Description**

Gives a warning and produces an empty `<td></td>` cell

**Usage**

```r
## Default S3 method:
html5(object, id, ..., class = NA)
```

**Arguments**

- `object` The cell to render to HTML5
- `id` A unique identifier for traceability
- `...` additional arguments to renderer. Unused
- `class` An additional class attribute for the HTML5 element

**Value**

An empty html5 td of the given class

---

**html5.logical**  
*Default conversion to HTML5 for a logical cell*

**Description**

Produces table cell or nothing if it’s an NA. This is useful for dealing with rowspan and colspan.

**Usage**

```r
## S3 method for class 'logical'
html5(object, id, ..., class = NA)
```

**Arguments**

- `object` The cell to render to HTML5
- `id` A unique identifier for traceability
- `...` additional arguments to renderer. Unused
- `class` An additional class attribute for the HTML5 element

**Value**

An empty html5 td of the given class
Convert a tangram class into an HTML5 string

Description

Given a tangram class, a series of conversion creates an HTML5 representation of the table. It may be an HTML5 fragment or it may be a complete web page.

Usage

```r
## S3 method for class 'tangram'
html5(
  object,
  id = NULL,
  caption = NULL,
  fragment = NULL,
  style = NULL,
  footnote = NULL,
  inline = NULL,
  fixed_thead = NULL,
  ...
)
```

Arguments

- `object` The cell table to render to HTML5
- `id` A unique identifier for the table (strongly recommended). If not provided, caption will be used.
- `caption` A string caption for the table
- `fragment` A boolean flag that determines whether a fragment or a complete HTML5 document is generated
- `style` A string containing a style filename to include as inline CSS. It first searches the drive for the file, if that fails it looks inside the package for a matching css file.
- `footnote` Any footnotes to include under the table.
- `inline` DEPRECATED
- `fixed_thead` logical; fixes the header using position sticky in CSS defaults to FALSE
- `...` additional arguments to renderer. Unused

Details

The package includes several css files for styling. At present the following exist: 'hmisc.css', 'lancet.css', 'lancet-stripped.css' and 'nejm.css'

Value

A text string rendering of the given table in HTML5
index

Generate an index from a tangram or cell object

Description

Given a tangram object create an index representation.

Usage

```r
index(object, ...)  
```

Arguments

- `object` The cell header to render to HTML5
- `...` additional arguments to renderer. Unused

Value

A matrix or list of strings containing key, source and value

index.cell_label

Generate an index from a label object

Description

Overrides to generate no indexing on labels

Usage

```r
## S3 method for class 'cell_label'
index(object, id = "tangram", key.len = 4, ...)  
```

Arguments

- `object` cell; The cell for indexing
- `id` character; an additional specifier for the object key
- `key.len` numeric; length of key to generate
- `...` additional arguments to renderer. Unused

Value

A list of strings containing key, source and value
index.default

*Generate an index from a cell object*

**Description**

Given a cell class create an index representation. If no source is specified no index will be generated.

**Usage**

```r
## Default S3 method:
index(object, id = "tangram", name = NULL, key.len = 4, ...)
```

**Arguments**

- `object`: cell; The cell for indexing
- `id`: character; an additional specifier for the object key
- `name`: character; optional names of elements inside object
- `key.len`: numeric; length of generated key
- `...`: additional arguments to renderer. Unused

**Value**

A list of strings containing key, source and value

---

index.list

*Generate an index from a list object*

**Description**

Given a cell class create an index representation. If no source is specified no index will be generated.

**Usage**

```r
## S3 method for class 'list'
index(object, id = "tangram", key.len = 4, ...)
```

**Arguments**

- `object`: cell; The cell for indexing
- `id`: character; an additional specifier for the object key
- `key.len`: numeric; length of key to generate
- `...`: additional arguments to renderer. Unused

**Value**

A list of strings containing key, source and value
index.tangram

Generate an index from a tangram object

Description

Given a tangram class create an index representation.

Usage

```r
## S3 method for class 'tangram'
index(object, id = "tangram", key.len = 4, ...)
```

Arguments

- `object` The tangram for indexing
- `id` an additional specifier for the object key
- `key.len` numeric; length of keys generated (affects collision probability)
- `...` additional arguments to renderer. Unused

Value

A matrix of strings containing key, source and value

insert_column

Insert a column into a tangram table

Description

Insert a column into a tangram table. Will fill with empty cells is not enough cells are specified.

Usage

```r
insert_column(table, after, ..., class = NULL)
```

Arguments

- `table` the table to modify
- `after` numeric; The column to position the new row after. Can be zero for inserting a new first row.
- `...` Table cells to insert. Cannot be larger than existing table.
- `class` character; Classes to apply as directives to renderers

Value

the modified table
insert_row  

Insert a row into a tangram table

Description

Insert a row into a tangram table. Will fill with empty cells is not enough cells are specified.

Usage

`insert_row(table, after, ..., class = NULL)`

Arguments

table  
the table to modify

after  
numeric; The row to position the new row after. Can be zero for inserting a new first row.

...  
Table cells to insert. Cannot be larger than existing table.

class  
character; Classes to apply as directives to renderers

Value

the modified table

is.binomial  

Determine if a vector is binomial or not

Description

Determine if a vector is binomial or not

Usage

`is.binomial(x, threshold = NA)`

Arguments

x  
Vector to determine type of

threshold  
The upper threshold of unique values for which a vector is considered categorical.

Value

a Boolean: TRUE / FALSE
Examples

```r
is.binomial(c(1, 2, 3))
is.binomial(factor(c("A", "B", "C")))
is.binomial(factor(c("A", "B", "B", "A")))
is.binomial(factor(c(TRUE, FALSE, TRUE, FALSE)))
is.binomial(c('M', 'F', 'M', 'F'), 10)
```

is.categorical

Determine if a vector is categorical or not

Description

Determine if a vector is categorical or not

Usage

```r
is.categorical(x, threshold = NA)
```

Arguments

- `x`: Vector to determine type of
- `threshold`: The upper threshold of unique values for which a vector is considered categorical.

Value

A Boolean: TRUE / FALSE

Examples

```r
is.categorical(c(1, 2, 3))
is.categorical(c(rep(1, 20), rep(2, 20), rep(3, 20)), threshold=5)
is.categorical(c("A", "B", "B"))
is.categorical(factor(c("A", "B", "C")))
is.categorical(factor(c("A", "B", "B", "A")))
is.categorical(factor(c(TRUE, FALSE, TRUE, FALSE)))
```
**key**

*Key derivation helper function*

**Description**

This function should generate a string that uniquely identifies a piece of data present in a table. In a report with multiple tables the id is used to preserve uniqueness.

**Usage**

`key(x, id)`

**Arguments**

- `x` : cell object to derive key for
- `id` : the unique id of the table being keyed

**Details**

This function relies on the object being keyed having at a minimum character attributes for `row` and `col`. Additional specifies for embedded tables are given with `subrow` and `subcol`. The `row` and `col` are automatically appended when using a `table_builder`. However the `subrow` and `subcol` must be added by the user to a cell of a table.

---

**lancet**

*Style Bundle for Lancet style*

**Description**

List of lists, should contain a "Type" entry with a function to determine type of vector passed in. Next entries are keyed off returned types from function, and represent the type of a row. The returned list should contain the same list of types, and represents the type of a column. Thus it now returns a function to process the intersection of those two types.

**Usage**

`lancet`

**Format**

An object of class `list` of length 5.
lancet_cell  
*Cell Generation functions for Lancet styling*

**Description**

Each function here is called when a cell is generated. Overriding these in a formula call will allow one to customize exactly how each cell’s contents are generated.

**Usage**

lancet_cell

**Format**

An object of class `list` of length 8.

---

lancet_fraction  
*Create an cell_fraction (S3) in NEJM style of the given data*

**Description**

A cell object contains a statistical result of a fraction/percentage in nejm style

**Usage**

lancet_fraction(numerator, denominator, format = NULL, ...)

**Arguments**

- **numerator**: numeric; The value of the numerator
- **denominator**: numeric; The value of the denominator
- **format**: numeric or character; a string formatting directive
- **...**: optional extra information to attach

**Value**

A cell_fraction object.

**Examples**

lancet_fraction(1, 4, 3)
lancet_mean_sd  Create a mean/sd cell object of the given data in Lancet style

Description

Create a mean/sd cell object of the given data in Lancet style.

Usage

lancet_mean_sd(
  x,
  format = NA,
  na.rm = TRUE,
  names = FALSE,
  type = 8,
  msd = FALSE,
  quant = c(0.25, 0.5, 0.75),
  ...
)

Arguments

  x  numeric vector whose sample quantiles are wanted. NA and NaN values are not
      allowed in numeric vectors unless na.rm is TRUE.
  format  numeric or character; Significant digits or fmt to pass to sprintf
  na.rm  logical; if true, any NA and NaN's are removed from x before the quantiles are
          computed.
  names  logical; ignored. For compatibility with hmisc_iqr
  type  integer; ignored. For compatibility with hmisc_iqr
  msd  logical; ignored. For compatibility with hmisc_iqr
  quant  numeric; ignored. For compatibility with hmisc_iqr
  ...  additional arguments to constructing cell

Value

A cell object.

Examples

require(stats)
lancet_mean_sd(rnorm(100), '3')
latex

Render to LaTeX methods for tangram cell objects

Description

Each of these methods will render the cell object as a LaTeX fragment

Usage

latex(object, ...)

## Default S3 method:
latex(object, ...)

## S3 method for class 'cell'
l latex(object, na.blank = TRUE, ...)

## S3 method for class 'cell_label'
l latex(object, ...)

## S3 method for class 'logical'
l latex(object, ...)

## S3 method for class 'cell_header'
l latex(object, ...)

## S3 method for class 'cell_subheader'
l latex(object, ...)

## S3 method for class 'tangram'
l latex(object, fragment = TRUE, filename = NULL, append = FALSE, ...)

Arguments

object object; the item to render to latex
...
additional arguments
na.blank logical; Dispaly NAs as blanks.
fragment logical; Is this a complete LaTeX document or just the table fragment
filename character; filename to write LaTeX into
append logical; Should the write be an append operation or overwrite

Details

There are addition arguments possible to control the rendering, but due to some oddities between CRAN requirements and how R handles defaults (for full details see the source code) they are as follows
latexify

* cgroup.just character; The text of the column justification used in the table
* arraystretch numeric; The arraystretch parameter used for vertical spacing
* style character; can be null or "nejm" for different table styling
* rel_size numeric; a scaling to be applied to the entire table, e.g. rel_size=-2
* placement character; placement directive, defaults to "H"

**Value**

the LaTeX rendering

**Examples**

```r
latex(cell_label("123"))
l latex(hmisc_iqr(rnorm(20)))
l latex(hmisc_fraction(45, 137))
tbl <- tangram(drug~bili, pbc, "tbl")
l latex(tbl)
```

---

**latexify**

*LaTeX safe string conversion*

**Description**

LaTeX safe string conversion. This transforms a string handling Markdown characters and UNICODE as best it can with an automated pass.

**Usage**

```r
latexify(x)
```

**Arguments**

- `x`
  
  string to make LaTeX safe

**Value**

valid LaTeX code
latex_template \hspace{1cm} \textit{Return a \LaTeX\ template that works with tangram}

\begin{description}
\item[Description] Pandoc in the current version of RStudio does not allow for setting package options to xcolor and this has made it incompatible with the \LaTeX\ generated by this package. This provides a known working template.
\end{description}

\begin{description}
\item[Usage] latex_template()
\end{description}

\begin{description}
\item[Details] An example header would look like the following:
\begin{verbatim}
— title: "A Document Full of Beautiful Tables" output: pdf_document: "'r tangram::latex_template()"
\end{verbatim}
\end{description}

\begin{description}
\item[Value] filename of \LaTeX\ template
\end{description}

\begin{description}
\item[nejm] \hspace{1cm} \textit{Style Bundle for Closer to NEJM style}
\end{description}

\begin{description}
\item[Description] List of lists, should contain a "Type" entry with a function to determine type of vector passed in. Next entries are keyed off returned types from function, and represent the type of a row. The returned list should contain the same list of types, and represents the type of a column. Thus it now returns a function to process the intersection of those two types.
\end{description}

\begin{description}
\item[Usage] nejm
\end{description}

\begin{description}
\item[Format] An object of class list of length 5.
\end{description}
**Description**

Each function here is called when a cell is generated. Overriding these in a formula call will allow
one to customize exactly how each cell’s contents are generated.

**Usage**

```r
nejm_cell
```

**Format**

An object of class `list` of length 9.

**Details**

While this serves as the base template for transforms, it is by no means required if one develops
their own bundle of data transforms. One can create any number of cell level styling choices.

**nejm_fraction**

**Create an cell_fraction (S3) in NEJM style of the given data**

**Description**

A cell object contains a statistical result of a fraction/percentage in nejm style

**Usage**

```r
nejm_fraction(numerator, denominator, format = NULL, ...)
```

**Arguments**

- `numerator`: numeric; The value of the numerator
- `denominator`: numeric; The value of the denominator
- `format`: numeric or character; a string formatting directive
- `...`: optional extra information to attach

**Value**

A cell_fraction object.

**Examples**

```r
nejm_fraction(1, 4, 3)
```
Description

Construct a cell which has the 3 interquartile ranges specified.

Usage

```r
nejm_iqr(
  x,
  format = NA,
  na.rm = TRUE,
  names = FALSE,
  type = 8,
  msd = FALSE,
  quant = c(0.25, 0.5, 0.75),
  ...
)
```

Arguments

- `x` numeric vector whose sample quantiles are wanted. NA and NaN values are not allowed in numeric vectors unless `na.rm` is `TRUE`.
- `format` numeric or character; Significant digits or fmt to pass to `sprintf`
- `na.rm` logical; if true, any NA and NaN's are removed from `x` before the quantiles are computed.
- `names` logical; if true, the result has a names attribute. Set to FALSE for speedup with many probs.
- `type` integer; specify algorithm to use in constructing quantile. See quantile for more information.
- `msd` logical; compute an msd attribute containing mean and standard deviation
- `quant` numeric; The quantiles to display. Should be an odd length vector, since the center value is highlighted.
- `...` additional arguments to constructing cell

Value

A `cell_quantile` object.

Examples

```r
require(stats)
nejm_iqr(rnorm(100), '3')
```
nejm_range  

Create a NEJM style range

Description

Construct a cell which has the range of the given data in NEJM style

Usage

nejm_range(x, format, ...)

Arguments

- **x**: numeric vector whose range is desired
- **format**: numeric or character; an argument to pass to the formatting function
- **...**: additional arguments to passed to cell()

Parser

The parser class for generating abstract syntax trees for given table formulas.

Description

The parser class for generating abstract syntax trees for given table formulas.

The parser class for generating abstract syntax trees for given table formulas.

Format

R6Class object.

References


Public fields

- **input**: Storage for input string of a formula
- **pos**: The current parsing position
- **len**: The length of the input
Methods

**Public methods:**

- `Parser$new()`
- `Parser$expect()`
- `Parser$peek()`
- `Parser$eat_whitespace()`
- `Parser$next_token()`
- `Parser$format()`
- `Parser$r_expression()`
- `Parser$factor()`
- `Parser$term()`
- `Parser$expression()`
- `Parser$table_formula()`
- `Parser$run()`
- `Parser$clone()`

**Method new():** Create a parser

*Usage:*

`Parser$new()`

**Method expect():** Specify expectation of next token from lexer

*Usage:*

`Parser$expect(id)`

*Arguments:*

- `id` The token id expected in stream, otherwise it’s an error

**Method peek():** Peek at the next token from parser

*Usage:*

`Parser$peek()`

**Method eat_whitespace():** Remove white space to find start of next token

*Usage:*

`Parser$eat_whitespace()`

**Method next_token():** Returns next lexical token

*Usage:*

`Parser$next_token()`

**Method format():** Return format string as token from lexical stream

*Usage:*

`Parser$format()`

**Method r_expression():** Return R expression as token from lexical stream

*Usage:*

...
Parser$r_expression()

**Method** factor(): Return next factor as token.

*Usage:*
Parser$factor()

**Method** term(): Parse and return next term in stream

*Usage:*
Parser$term()

**Method** expression(): Parse and return next expression in stream

*Usage:*
Parser$expression()

**Method** table_formula(): Parse and return table formula from stream

*Usage:*
Parser$table_formula()

**Method** run(): Run the parser

*Usage:*
Parser$run(x)

*Arguments:*

  x  (character,formula) The table specification to parse

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*
Parser$clone(deep = FALSE)

*Arguments:*

  deep  Whether to make a deep clone.

**Examples**

Parser$new()$run("col1 + col2 + col3 ~ drug*age+spiders")
Mayo Clinic Primary Biliary Cirrhosis Data

Description

This data is from the Mayo Clinic trial in primary biliary cirrhosis (PBC) of the liver conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

Usage

pbc

Format

An object of class data.frame with 418 rows and 19 columns.

Details

A nearly identical data set found in appendix D of Fleming and Harrington; this version has fewer missing values.

Included for use in example from Hmisc.

Provide a "|" operator for cbind of tangram tables

Description

The pipe operator provides an cbind for tangram tables

Usage

## S3 method for class 'tangram'

x | y

Arguments

x left argument for rbind

y right argument for rbind
Value

A column wise merged tangram object

print.cell

## S3 method for class 'cell'
print(x, ...)

## S3 method for class 'tangram'
print(x, ...)

## S3 method for class 'summary.tangram'
print(x, ...)

Arguments

x object; the item to render

... additional arguments passed to summary

Value

the text summary

Examples

print(cell_label("123"))
print(hmisc_iqr(rnorm(20)))
print(hmisc_fraction(45, 137))
print(tangram(1,1) %>%
  row_header("row") %>%
  col_header(1,2,3) %>%
  add_col("A","B","C"))
print(tangram(drug~bili, pbc))
proc_tab

**Tangram transform for proc_tab style summaries via a function**

**Description**

Given a function that produces a vector of tangram cells, will generate a table

**Usage**

```r
proc_tab(table, row, column, fun = NULL, overall = FALSE, ...) 
```

**Arguments**

- `table`: The table builder object
- `row`: The row from the abstract syntax tree that parsed the formula
- `column`: The column from the abstract syntax tree that parsed the formula
- `fun`: The function to apply to the broken out categories
- `overall`: Provide a summary of categorical breakdowns
- `...`: additional arguments to pass to `fun`

**rbind.tangram**

*An rbind for generated tables tangram objects.*

**Description**

Execute the equivalent of an rbind for generated tables

**Usage**

```r
## S3 method for class 'tangram'
rbind(..., deparse.level = 1) 
```

**Arguments**

- `...`: tangram objects to rbind
- `deparse.level`: numeric; not used

**Value**

A merged tangram object
render_f

Format a vector of provided numeric values

Description
Given a vector of data return as strings formatted as requested

Usage
render_f(x, format)

Arguments
x numeric; the data to format. Must work with quantile function.
format numeric or character; If numeric preserve that many position past the decimal, if character pass directly into sprintf as format string

Value
character; formatted values as character strings

Examples
render_f(rnorm(5), 3)
render_f(round(rnorm(5), 2), "%010.03f")

render_route_tangram
Router for rendering method

Description
This function detects if knitr is loaded, and does its best to determine the output format from knitr and returns the appropriate rendering function.

Usage
render_route_tangram()

Value
A rendering function to use
**replace_cell**

Replace a cell’s contents

**Description**

Replace a cell in a table

**Usage**

replace_cell(table, row, col, object, ...)

**Arguments**

- **table**: the tangram table to modify
- **row**: numeric; The row to modify
- **col**: numeric; The column to modify
- **object**: The cell or object to replace in a table
- **...**: Additional parameters passed to cell function if not given a cell object

**Value**

the modified table

---

**rmd**

Generate an Rmd table entry from a cell object

**Description**

Given a cell object generate the corresponding piece of an Rmd table

**Usage**

rmd(object, key = FALSE, ...)

## Default S3 method:
rmd(object, key = FALSE, ...)

## S3 method for class 'cell'
rmd(object, key = FALSE, ...)

## S3 method for class 'cell_n'
rmd(object, key = FALSE, ...)

## S3 method for class 'tangram'
rmd(object, key = NULL, append = FALSE, pad = 10, ...)

---
**Arguments**

- **object**  
  The `cell_fstat` for indexing

- **key**  
  A filename to write key values into. Can be false if no key file is desired.

- **...**  
  additional arguments to renderer. Unused

- **append**  
  logical; Should the key file be appended too, or overwritten

- **pad**  
  numeric; Minimum width of columns can be a single or vector of numerics.

**Value**

A string representation of the table

**Examples**

```r
rmd(tangram(drug ~ bili, pbc))
```

---

**Description**

Number of rows/cols in provided object

**Usage**

```r
rows(x)
```

```r
cols(x)
```

```r
# S3 method for class 'list'
rows(x)
```

```r
# S3 method for class 'list'
cols(x)
```

**Arguments**

- **x**  
  object; object to determine requested count
Description

S3 rtf Method function for use on abstract table class

Usage

```
rtf(object, id, ...)
```

Arguments

- `object`: The cell to render to RTF
- `id`: A unique identifier for the table (strongly recommended). If not provided, caption will be used.
- `...`: additional arguments to renderer. Unused at present.

Value

A text string rendering of the given table

Description

Given a cell class create an RTF representation.

Usage

```
## S3 method for class 'cell'
rtf(object, id, ...)
```

Arguments

- `object`: The cell to render to RTF
- `id`: A unique identifier for traceability
- `...`: additional arguments to renderer. Unused

Value

An RTF string rendering of the given cell.
rtf.cell_ch2  

Convert an abstract cell_ch2 object into an rtf string

Description
Given a cell_ch2 class create an rtf representation.

Usage
```r
## S3 method for class 'cell_ch2'
rtf(object, id, ...)
```

Arguments
- ```object``` The cell ch2 to render to HTML5
- ```id``` A unique identifier for traceability
- `...` additional arguments to renderer. Unused

Value
A text string rendering of the given chi2 in rtf

---

rtf.cell_fstat  

Convert an abstract cell_fstat object into an RTF string

Description
Given a cell_fstat class create an RTF representation.

Usage
```r
## S3 method for class 'cell_fstat'
rtf(object, id, ...)
```

Arguments
- ```object``` The cell fstat to render to RTF
- ```id``` A unique identifier for traceability
- `...` additional arguments to renderer. Unused

Value
A text string rendering of the given fstat as a `<td>` with several `<span>`’s.
**rtf.cell_header**

Convert an abstract cell_header object into an RTF string

**Description**

Given a cell_header class create an RTF representation.

**Usage**

```r
## S3 method for class 'cell_header'
rtf(object, id, ...)  
```

**Arguments**

- `object`: The cell header to render to RTF
- `id`: A unique identifier for traceability
- `...`: additional arguments to renderer. Unused

**Value**

An RTF string rendering of the given header

---

**rtf.cell_iqr**

Convert an abstract cell_iqr object into an RTF string

**Description**

Given a cell_quantile class create an RTF representation.

**Usage**

```r
## S3 method for class 'cell_iqr'
rtf(object, id, ..., point = 9)
```

**Arguments**

- `object`: The cell quantile to render to RTF
- `id`: A unique identifier for traceability
- `...`: additional arguments to renderer. Unused
- `point`: numeric; The font point size to use in display

**Value**

An RTF string rendering of the given quantile.
rtf.cell_label  

Given a cell_label class create an RTF representation.

Description

Given a cell_label class create an RTF representation.

Usage

```r
## S3 method for class 'cell_label'
rtf(object, id, ..., point = 18)
```

Arguments

- `object`  The cell label to render to RTF
- `id`  A unique identifier for traceability
- `...`  additional arguments to renderer. Unused
- `point`  size of main font for cell label

Value

An RTF text string rendering of the given label.

---

rtf.cell_n  

Convert an abstract cell_n object into an RTF string

Description

Given a cell_n class create an RTF representation.

Usage

```r
## S3 method for class 'cell_n'
rtf(object, id, ...)
```

Arguments

- `object`  The cell n to render to RTF
- `id`  A unique identifier for traceability
- `...`  additional arguments to renderer. Unused

Value

An RTF string rendering of the given n.
Convert an abstract cell_subheader object into an RTF string

Description
Given a cell_subheader class create an RTF representation.

Usage
## S3 method for class 'cell_subheader'
rtf(object, id, ..., point = 9)

Arguments
- object: The cell header to render to RTF
- id: A unique identifier for traceability
- ...: additional arguments to renderer. Unused
- point: numeric; The font point size to use in display

Value
An RTF string rendering of the given header

Default conversion to RTF for an abstract table element

Description
Gives a warning and produces an empty cell

Usage
## Default S3 method:
rtf(object, id, ...)

Arguments
- object: The cell to render to RTF
- id: A unique identifier for traceability
- ...: additional arguments to renderer. Unused

Value
A RTF string rendering of the given cell
rtf.tangram Convert a tangram into an RTF string or file

Description

Given a tangram class, a series of conversion creates an rtf representation of the table.

Usage

```r
## S3 method for class 'tangram'
rtf(
  object,  # The cell table to render to RTF
  id = NA,  # A unique identifier for the table (strongly recommended).
  caption = NA,  # A string caption for the table
  fragment = FALSE,  # A boolean flag that determines whether a fragment or a complete RTF document is generated
  widths = NA,  # RTF requires specified left margin and column widths, this allows user control over these (inches)
  footnote = NA,  # Any footnotes to include under the table.
  filename = NA,  # A filename to write resulting rtf file to
  append = FALSE,  # A boolean for whether or not to append to given filename
  point = 9,  # Main font point size
  ...  # additional arguments to renderer. Unused
)
```

Arguments

object The cell table to render to RTF
id A unique identifier for the table (strongly recommended).
caption A string caption for the table
fragment A boolean flag that determines whether a fragment or a complete RTF document is generated
widths RTF requires specified left margin and column widths, this allows user control over these (inches)
footnote Any footnotes to include under the table.
filename A filename to write resulting rtf file to
append A boolean for whether or not to append to given filename
point Main font point size
... additional arguments to renderer. Unused

Value

A text string rendering of the given table
select_col  
Select given column(s) from a table

Description
Given a table, select the specified column(s)

Usage
select_col(table, col)

Arguments
- table: the table to modify
- col: vector containing column(s) to select

Value
the modified table

select_row  
Select given row(s) from a table

Description
Given a table, select the specified rows

Usage
select_row(table, row)

Arguments
- table: the table to modify
- row: vector with row numbers to select

Value
the modified table
List of lists, should contain a "Type" entry with a function to determine type of vector passed in. Next entries are keyed off returned types from function, and represent the type of a row. The returned list should contain the same list of types, and represents the type of a column. Thus it now returns a function to process the intersection of those two types.

Description

List of lists, should contain a "Type" entry with a function to determine type of vector passed in. Next entries are keyed off returned types from function, and represent the type of a row. The returned list should contain the same list of types, and represents the type of a column. Thus it now returns a function to process the intersection of those two types.

Usage

smd

Format

An object of class list of length 5.

Cell Generation functions for SMD comparisons of categorical to numerical

Description

Each function here is called when a cell is generated. Overriding these in a formula call will allows one to customize exactly how each cell’s contents are generated.

Usage

smd_cell

Format

An object of class list of length 7.

Details

While this serves as the base template for transforms, it is by no means required if one develops their own bundle of data transforms. One can create ay number of cell level styling choices.
Create a SMD for a categorical set of column versus a numerical row

Description

Given a row and column object from the parser apply a Kruskal test and output the results horizontally. \( 1 \times (n + \text{no. categories} + \text{test statistic}) \)

Usage

```r
smd_compare(
  table,
  row,
  column,
  cell_style,
  style,
  smdformat = NULL,
  pformat = NULL,
  weight = NULL,
  test = FALSE,
  ...
)
```

Arguments

- `table`: The table object to modify
- `row`: The row variable object to use (numerical)
- `column`: The column variable to use (categorical)
- `cell_style`: list; cell styling functions
- `style`: character; chosen styling to final table
- `smdformat`: numeric, character or function; A formatting directive to be applied to smd
- `pformat`: numeric, character or function; A formatting directive to be applied to p-values
- `weight`: numeric; Vector of weights to apply to data when computing SMD
- `test`: logical; include statistical test results
- `...`: absorbs additional arguments. Unused at present.

Value

The modified table object
smd_contingency

Create a contingency table with SMD given a row column of a formula

Description

Create a contingency table with SMD given a row column of a formula

Usage

smd_contingency(
  table,
  row,
  column,
  cell_style,
  style,
  smdformat = NULL,
  collapse_single = TRUE,
  weight = NULL,
  test = FALSE,
  pformat = NULL,
  ...
)

Arguments

table The tablebuilder object
row The row node from the parser of the formula
column The column node provided by the parser of the formula
cell_style A list of all individual cell stylings to apply
style The global style to apply.
smdformat The format command to apply to smd
collapse_single Should single factor variables be collapsed
weight Any weighting to apply to data for computation of SMD
test logical; include statistical test results
pformat numeric, character or function; A formatting directive to be applied to p-values
... Additional arguments to provide cell generation functions

Value

The resulting sub table constructed
smd_dist

Create an SMD distance cell

Description

Create an SMD distance cell. It calls the smd function then formats the result. If the result rounds to all zeros then it appends a less than sign and bumps the least significant digit to one.

Usage

smd_dist(x, group, format, weight = NULL, ...)

Arguments

- x: vector; variable to evaluate with smd
- group: factor; A grouping to apply. Must have 2 levels.
- format: formatting to apply to result
- weight: numeric; Weighting to apply to computation. Defaults to NULL.
- ... additional arguments to pass to cell generation

Value

a tangram cell

smd_fraction

Create a fraction cell in the smd transform

Description

Create a fraction cell in the smd transform. In this instance it print the numerator followed by percentage in parenthesis.

Usage

smd_fraction(num, den, format, ...)

Arguments

- num: numerator of fraction
- den: denominator of fraction
- format: formatting to apply to result
- ... additional arguments to pass to cell generation

Value

a tangram cell
smd_meansd

Create an SMD mean and standard deviation cell

Description
Create an SMD mean and standard deviation cell. In this case it prints the mean with the standard deviation in parenthesis

Usage
smd_meansd(x, format, ...)

Arguments
- x: vector; variable to evaluate with smd
- format: formatting to apply to result
- ...: additional arguments to pass to cell generation

Value
a tangram cell

standard_difference
Compute the standardized mean distance between 2 groups for numerical or categorical information. Using method described in 'A unified approach to measuring the effect size between two groups using SAS' by Dongsheng Yand and Jarrod E. Dalton, 2012. SAS Global Forum 2012

Description
Compute the standardized mean distance between 2 groups for numerical or categorical information. Using method described in 'A unified approach to measuring the effect size between two groups using SAS' by Dongsheng Yand and Jarrod E. Dalton, 2012. SAS Global Forum 2012

Usage
standard_difference(x, group, weight = NULL)

Arguments
- x: vector; data to estimate effect size for groups
- group: vector; the grouping variable.
- weight: vector; weighting information for x
summarize_kruskal_horz

Description

List of lists, should contain a "Type" entry with a function to determine type of vector passed in. Next entries are keyed off returned types from function, and represent the type of a row. The returned list should contain the same list of types, and represents the type of a column. Thus it now returns a function to process the intersection of those two types. There are additionally a list of cell transforms that can be overridden and a default footnote if none is specified.

Usage

```r
summarize_kruskal_horz(
  table,
  row,
  column,
  cell_style,
  pformat = NULL,
  msd = FALSE,
  quant = c(0.25, 0.5, 0.75),
  overall = NULL,
  test = FALSE,
  ...
)

summarize_kruskal_vert(
  table,
  row,
  column,
  cell_style,
  collapse_single = TRUE,
  pformat = NULL,
  msd = FALSE,
  test = FALSE,
  ...
)

summarize_chisq(
  table,
  row,
  column,
  cell_style,
  pformat = NULL,
  collapse_single = TRUE,
  overall = NULL,
)```
Arguments

table       The table object to modify
row         The row variable object to use (numerical)
column      The column variable to use (categorical)
cell_style  list; cell styling functions
pformat     numeric, character or function; A formatting directive to be applied to p-values
msd         logical; Include mean and standard deviation with quantile statistics
quant       numeric; Vector of quantiles to include. Should be an odd number since the middle value is highlighted on display.
overall     logical or character; Include overall summary statistics for a categorical column. Character values are assumed to be true and used as column header.
test        logical or function; include statistical test results. Function signature must be function(row, col, cell_style, ...)
            absorbs additional arguments. Unused at present.
collapse_single logical; default TRUE. Categorical variables with a two values collapse to single row.
row_percents logical; use denominator across rows instead of columns.
useNA       character; Specifies whether to include NA counts in the table. The allowed values correspond to never "no" (Default), only if the count is positive "ifany" and even for zero counts "always". An NA column is always excluded.

Format

An object of class list of length 5.
**Value**

The modified table object

**summarize_kruskal_horz**

Given a row and column object apply a Kruskal test and output the results horizontally. $1 \times (n + \text{no. categories} + \text{test statistic})$

**summarize_kruskal_vert**

Given a row and column object from the parser apply a Kruskal test and output the results vertically (#Categories+1) $\times (N, \text{Summary}, \text{Statistic})$

**summarize_chisq**

Given a row and column object from the parser apply a chi^2 test and output the results

**summarize_spearman**

Given a row and column object from the parser apply a Spearman test and output the results in a 1X3 format.

**hmisc**

```r
hmisc <- list(
  Type = hmisc_data_type,
  Numerical = list(
    Numerical = summarize_spearman,
    Categorical = summarize_kruskal_horz
  ),
  Categorical = list(
    Numerical = summarize_kruskal_vert,
    Categorical = summarize_chisq
  ),
  Cell = hmisc_cell,
  Footnote = "N is the number of non-missing value. ^1^Kruskal-Wallis. ^2^Pearson. ^3^Wilcoxon."
)
```

**See Also**

`hmisc_data_type, tangram, hmisc_cell`
**summarize_nejm_horz**

Create a summarization for a categorical set of column versus a numerical row in NEJM style

**Description**

Given a row and column object from the parser apply a Kruskal test and output the results horizontally. 5 X (n + no. categories + test statistic)

**Usage**

```r
summarize_nejm_horz(
  table,
  row,
  column,
  cell_style,
  pformat = NULL,
  msd = FALSE,
  quant = c(0.25, 0.5, 0.75),
  overall = NULL,
  test = FALSE,
  useNA = "no",
  ...
)
```

**Arguments**

- **table**  The table object to modify
- **row**    The row variable object to use (numerical)
- **column** The column variable to use (categorical)
- **cell_style** list; cell styling functions
- **pformat** numeric, character or function; A formatting directive to be applied to p-values
- **msd**    logical; Include mean and standard deviation with quantile statistics
- **quant**  numeric; Vector of quantiles to include. Should be an odd number since the middle value is highlighted on display.
- **overall** logical or character; Include overall summary statistics for a categorical column. Character values are assumed to be true and used as column header.
- **test**   logical or function; include statistical test results. Function signature must be function(row, col, cell_style, ...)
- **useNA** character; Specifies whether to include NA counts in the table. The allowed values correspond to never "no" (Default), only if the count is positive "ifany" and even for zero counts "always". An NA column is always excluded.
- **...**    absorbs additional arugments. Unused at present.
summarize_nejm_vert

Create a summarization for a categorical row versus X numerical column

Description

Given a row and column object from the parser apply a Kruskal test and output the results vertically (#Categories+1) X (N, Summary, Statistic)

Usage

summarize_nejm_vert(
  table,  
  row,    
  column, 
  cell_style, 
  collapse_single = TRUE, 
  pformat = NULL, 
  msd = FALSE, 
  test = FALSE, 
  quant = c(0.25, 0.5, 0.75),
  ...
)

Arguments

table  The table object to modify
row    The row variable object to use (categorical)
column The column variable to use (numerical)
cell_style list; cell styling functions
collapse_single logical; default TRUE. Categorical variables with a two values collapse to single row.
pformat numeric, character or function; A formatting directive to be applied to p-values
msd    logical; include msd in summary
test   logical; include statistical test results
quant numeric; vector of quantiles to include. Should be an odd number since the middle value is highlighted on display.
...    absorbs additional arguments. Unused at present.

Value

The modified table object
Summary.tangram

The default method for rendering tangram objects

Description

A tangram is a summary, so it returns itself. Otherwise convert to a text representation.

Usage

```r
## S3 method for class 'tangram'
summary(object, ...)

## S3 method for class 'cell'
summary(object, ...)
```

Arguments

- `object`: object; the item to render
- `...`: additional arguments passed to `summary`

Value

the text summary

Examples

```r
summary(cell_label("123"))
summary(hmisc_iqr(rnorm(20)))
summary(hmisc_fraction(45, 137))
summary(tangram(1,1) %>%
  row_header("row") %>%
  col_header(1,2,3) %>%
  add_col("A","B","C"))
summary(tangram(drug~bili, pbc))
```

table_flatten

Given a tangram object with embedded tables, flattens to a single table.

Description

Flattening function to expanded embedded tables inside table cells.

Usage

```r
table_flatten(table)
```
Arguments

table the table object to flatten

Value

the flattened table object

tangram.clmm2  Table creation methods

Description

The tangram method is the principal method to create tables. It uses R3 method dispatch. If one specifies rows and columns, one gets an empty table of the given size. A formula or character will invoke the parser and process the specified data into a table like `Hmisc::summaryM`. Given an `rms` object it will summarize that model in a table. A `data.frame` is converted directly into a table as well for later rendering. Can create tables from `summary.rms()`, `anova.rms()`, and other `rms` object info to create a single pretty table of model results. The `rms` and `Hmisc` packages are required.

Usage

```r
## S3 method for class 'clmm2'
tangram(
  x,
  id = NULL,
  style = "hmisc",
  caption = NULL,
  footnote = NULL,
  digits = NULL,
  ...
)

## S3 method for class 'summary.clmm2'
tangram(
  x,
  id = NULL,
  style = "hmisc",
  caption = NULL,
  footnote = NULL,
  digits = NULL,
  pformat = "%1.3f",
  include_p = FALSE,
  ...
)

tangram(x, ...)
```
## S3 method for class 'numeric'
tangram(
  x,
  cols,
  id = NULL,
  caption = NULL,
  style = "hmisc",
  footnote = NULL,
  fixed_thead = NULL,
  ...
)

## S3 method for class 'anova.lme'
tangram(
  x,
  id = NULL,
  style = "hmisc",
  caption = NULL,
  footnote = NULL,
  digits = NULL,
  fixed_thead = NULL,
  ...
)

## S3 method for class 'data.frame'
tangram(
  x,
  id = NULL,
  colheader = NA,
  caption = NULL,
  style = "hmisc",
  footnote = NULL,
  after = NA,
  quant = seq(0, 1, 0.25),
  msd = TRUE,
  as.character = NULL,
  fixed_thead = NULL,
  exclude = NULL,
  ...
)

## S3 method for class 'formula'
tangram(
  x,
  data = NULL,
  id = NULL,
  transforms = NULL,
  caption = NULL,
style = "hmisc",
footnote = NULL,
after = NA,
digits = NA,
fixed_thead = NULL,
exclude = NULL,
...}
}
}

## S3 method for class 'character'
tangram(x, ...)

## S3 method for class 'table'
tangram(
x,
id = NULL,
percents = FALSE,
digits = 1,
test = FALSE,
footnote = NULL,
...}
)

## S3 method for class 'ftable'
tangram(x, id = NULL, ...)

## S3 method for class 'matrix'
tangram(x, digits = NULL, ...)

## S3 method for class 'tbl_df'
tangram(x, ...)

## S3 method for class 'lm'
tangram(x, ...)

## S3 method for class 'summary.lm'
tangram(x, id = NULL, format = NULL, pformat = NULL, tformat = NULL, ...)

## S3 method for class 'rms'
tangram(
x,
data = NULL,
short.labels = NULL,
footnote = NULL,
rnd.digits = 2,
rnd.stats = rnd.digits,
...}
)
Arguments

- **x**: object; depends on S3 type, could be rows, formula, string of a formula, data.frame or numerical rows, an rms.model
- **id**: character; A unique character id used to identify this table over multiple runs. No spaces.
- **style**: character; Desired rendering style, currently supports "hmisc", "nejm", and "lancet". Defaults to "hmisc"
- **caption**: character; A string with the desired caption
- **footnote**: character; A vector of character strings as footnotes
- **digits**: numeric; default number of digits to use for display of numerics
- **cols**: numeric; An integer of the number of cols to create
- **fixed_thead**: logical; On conversion to HTML5 should headers be treated as fixed?
- **colheader**: character; Use as column headers in final table
- **after**: function or list of functions; one or more functions to further process an abstract table
- **quant**: numeric; A vector of quantiles to use for summaries
- **msd**: logical; Include mean and standard deviation in numeric summary
- **as.character**: logical; if true data.frames all variables are passed through as.character and no numerical summary is provided.
- **exclude**: vector or list; When x is a data.frame this exclusion criteria is applied to the data. If this is a list then each list pair is the (column name, criteria). It is preferred to use a list to be specific.
- **data**: data.frame; data to use for rendering tangram object
- **transforms**: list of lists of functions; that contain the transformation to apply for summarization
- **percents**: logical; Display percents when rendering a table object. Defaults to FALSE
- **test**: logical or function; Perform default test or a statistical function that will return a test result when passed a row and column
- **format**: numeric or character; Format to apply to statistic
- **tformat**: numeric or character; format to apply to t-value
- **short.labels**: numeric; Named vector of variable labels to replace in interaction rows. Must be in format c("variable name" = "shortened label").
- **rnd.digits**: numeric; Digits to round reference, comparison, result and CI values to. Defaults to 2.
- **rnd.stats**: numeric; Digits to round model LR, R2, etc to. Defaults to rnd.digits.
Details

Note that additional arguments are passed to any subsequent transform. This means that a lot of possible arguments are not documented here but in the transform applied. Examine their documentations for additional possible arguments if needed.

Value

A tangram object (a table).

See Also

Possible transforms are (see hmisc) (*default*), nejm and lancet.

Examples

tangram(1, 1)
tangram(data.frame(x=1:3, y=c('a','b','c')), id="mytbl1")
tangram(drug ~ bili + albumin + protime + sex + age + spiders, pbc, id="mytbl2")
tangram("drug~bili+albumin+stage::Categorical+protime+sex+age+spiders", pbc,"mytbl3")

---

Token

A token in the formula grammar

Description

A token in the formula grammar

A token in the formula grammar

Format

R6Class object.

Public fields

id The token identifier, E.g. "LPAREN"

name Information about the token, useful with IDENTIFIERs.

Methods

Public methods:

- Token$new()
- Token$clone()

Method new(): Construct a lexical token

Usage:

Token$new(id, name = "")
Arguments:

id (character) The lexical id of the token
name (character) Additional token information if needed

Method clone(): The objects of this class are cloneable with this method.

Usage:
Token$clone(deep = FALSE)

Arguments:

deepl Whether to make a deep clone.
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