

# Package: tldr (via r-universe)

November 3, 2024

**Title** T Loux Doing R: Functions to Simplify Data Analysis and Reporting

**Version** 0.4.0

**Description** Gives a number of functions to aid common data analysis processes and reporting statistical results in an 'RMarkdown' file. Data analysis functions combine multiple base R functions used to describe simple bivariate relationships into a single, easy to use function. Reporting functions will return character strings to report p-values, confidence intervals, and hypothesis test and regression results. Strings will be LaTeX-formatted as necessary and will knit pretty in an 'RMarkdown' document. The package also provides wrappers function in the 'tableone' package to make the results knit-able.

**Depends** R (>= 4.1.0)

**Imports** tableone, ggplot2, reshape2

**Suggests** knitr

**License** GPL-3

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.3.1

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

**RemoteUrl** <https://github.com/tloux/tldr>

**RemoteRef** HEAD

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as_perc	<i>Format a proportion as a percentage</i>
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### Description

as\_perc formats a proportion as a percentage to print in an RMarkdown document

### Usage

```
as_perc(p, digits = 0)
```

### Arguments

p	A length-1 numeric to be interpreted as a proportion
digits	Number of digits to round percentage to (default to 0)

### Details

Simply multiplies p by 100 and affixes a percent sign to the end after rounding.

### Value

Returns a string to report a percentage to the specified number of digits.

### Examples

```
as_perc(0.2345)
```

```
as_perc(0.000234)
```

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cat_compare	<i>Investigate association between two categorical variables</i>
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### Description

cat\_compare gives details about the association between two categorical variables.

### Usage

```
cat_compare(x, y, plot = TRUE)
```

### Arguments

x	A categorical variable: the predictor or group variable, if appropriate
y	A categorical variable: the outcome, if appropriate
plot	Logical. Whether a mosaic plot should be drawn

### Details

Strictly, x and y do not need to be factors but will be coerced into factors.

### Value

Returns a list including (1) two-way table of counts, (2) chi-squared test for independence, (3) Cramer's V standardized effect, and (4) ggplot2 column plot of proportions conditional on x, if requested.

The table of counts will include missing values of both variables, but these rows/columns are discarded prior to the chi-squared test and Cramer's V calculations.

### Examples

```
v1 = rbinom(n=50, size=1, p=0.5)
v2 = rbinom(n=50, size=2, p=0.3 + 0.2*v1)
cat_compare(x=v1, y=v2, plot=TRUE)
```

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cont_compare	<i>Compare a numerical variable across levels of a categorical variable</i>
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### Description

Deprecated. Use `'num_compare'` instead.

### Usage

```
cont_compare(y, grp, plot = c("density", "boxplot", "none"))
```

### Arguments

y	A numerical variable
grp	A categorical variable
plot	Type of plot to produce

### Value

Returns a list including (1) group-wise summary statistics, (2) ANOVA decomposition, (3) eta-squared effect size, and (4) ggplot2 object, if requested.

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cutp	<i>Cut a numeric vector into quantiles</i>
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### Description

cutp is a wrapper for the base `'cut'` function. The vector `'x'` will be categorized using the percentiles provided in `'p'` to create break values.

### Usage

```
cutp(x, p, ...)
```

### Arguments

x	A numeric vector to be discretized
p	A numeric vector of probabilities
...	Arguments passed to <code>'cut'</code>

### Details

Within the `'cutp'` function, `'p'` is passed to `'quantile'` as the `'probs'` input. The computed quantiles are then used as the `'breaks'` in `'cut'`.

The values `'-Inf'` and `'Inf'` are added to the beginning and end of the breaks vector, respectively, so quantiles for 0 and 1 do not need to be given explicitly.

**Value**

Returns the output from 'cut'. This is usually a factor unless otherwise specified.

#' @seealso [quantile](#); [cut](#)

**Examples**

```
myvals = rnorm(1000)
catx = cutp(x=myvals, p=c(0.25, 0.5, 0.75), labels=c('Q1', 'Q2', 'Q3', 'Q4'))
table(catx)
```

---

inline\_coef

*Report the coefficient from a regression model inline*

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**Description**

inline\_coef presents the results of a coefficient from a lm or glm model in LaTeX format to be reported inline in an RMarkdown document.

**Usage**

```
inline_coef(model, variable, coef = TRUE, stat = TRUE, pval = TRUE, digits = 2)
```

```
inline_coef_p(model, variable, digits = 2)
```

**Arguments**

model	A regression model
variable	A character string giving the name of the variable to be reported
coef	Logical, whether the coefficient value is to be reported (default TRUE)
stat	Logical, whether the test statistic for the coefficient should be reported (default TRUE)
pval	Logical, whether the p-value for the coefficient should be reported (default TRUE)
digits	Number of digits to round to (default to 2)

**Details**

This function currently only supports lm and glm objects. Suggestions and requests are welcomed.

inline\_coef\_p is a wrapper for inline\_coef to report only the p-value (sets all non-p-value logicals to FALSE).

**Value**

Returns a LaTeX-formatted result for use in RMarkdown document.

**Examples**

```
x1 = rnorm(20)
x2 = rnorm(20)
y = x1 + x2 + rnorm(20)
model1 = lm(y ~ x1 + x2)
inline_coef(model1, 'x1')
inline_coef_p(model1, 'x1')
```

---

inline\_reg

*Report the fit of a regression model inline*


---

**Description**

inline\_reg presents the fit of a coefficient from a lm or glm model in LaTeX format to be reported inline in an RMarkdown document.

**Usage**

```
inline_reg(model, fit = TRUE, stat = TRUE, pval = TRUE, digits = 2)
```

```
inline_reg_p(model, digits = 2)
```

```
inline_anova(model, stat = TRUE, pval = TRUE, digits = 2)
```

**Arguments**

model	A regression model
fit	Logical, whether the regression fit is to be reported (default TRUE, only applicable to lm objects)
stat	Logical, whether the test statistic for the coefficient should be reported (default TRUE)
pval	Logical, whether the p-value for the coefficient should be reported (default TRUE)
digits	Number of digits to round to (default to 2)

**Details**

For lm objects, results include R-squared, the F statistic, and the p-value. For glm objects, results include the chi-squared statistic and the p-value.

This function currently only supports lm and glm objects. Suggestions and requests are welcomed.

inline\_reg\_p is a wrapper for inline\_reg to report only the p-value (sets all non-p-value logicals to FALSE). inline\_anova is a wrapper to report a one-way ANOVA result in which fit is set to FALSE and other logical inputs (stat, pval, and digits) are allowed to be user-defined.

**Value**

Returns a LaTeX-formatted result for use in RMarkdown document.

## Examples

```
x1 = rnorm(20)
y1 = x1 + rnorm(20)
model1 = lm(y1 ~ x1)
inline_reg(model1)

x2 = rnorm(20)
y2 = rbinom(n=20, size=1, prob=pnorm(x2))
model2 = glm(y2 ~ x2, family=binomial('logit'))
inline_reg(model2)
```

---

inline_test	<i>Report a hypothesis test inline</i>
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## Description

`inline_test` formats the results of an `htest` object into LaTeX to be presented inline in an RMarkdown document.

## Usage

```
inline_test(test, stat = TRUE, pval = TRUE, digits = 2)

inline_test_p(test, digits = 2)
```

## Arguments

<code>test</code>	An <code>htest</code> object
<code>stat</code>	Logical, whether to report test statistic (default TRUE)
<code>pval</code>	Logical, whether to report p-value (default TRUE)
<code>digits</code>	Number of digits to round to (default to 2)

## Details

This function currently only supports t tests and chi-squared tests. Suggestions and requests are welcomed.

`inline_test_p` is a wrapper for `inline_test` to report only the p-value (sets all non-p-value logicals to FALSE).

## Value

Returns a LaTeX-formatted hypothesis test result for use in RMarkdown document.

**Examples**

```
x = rnorm(20)
test1 = t.test(x)
inline_test(test1)
inline_test_p(test1)
```

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KcreateTableOne	<i>Create a table of descriptive statistics formatted for knitr::kable</i>
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**Description**

KcreateTableOne is a wrapper for `tableone::CreateTableOne` which formats the original plain text table as a data.frame of character columns. `KnitableTableOne` is a wrapper for `tableone::print.TableOne` which allows for more versatility in printing options. The output of both functions can be printed in an RMarkdown document in a number of ways, e.g., using `knitr::kable`. `svyKcreateTableOne` does the same with `tableone::svyCreateTableOne` for complex survey data.

**Usage**

```
KcreateTableOne(...)
svyKcreateTableOne(...)
KnitableTableOne(x, ...)
```

**Arguments**

...	Parameters to be passed to <code>tableone::CreateTableOne</code> ( <code>KcreateTableOne</code> ) or <code>tableone::print.TableOne</code> ( <code>KnitableTableOne</code> ).
x	A <code>TableOne</code> object created from <code>tableone::CreateTableOne</code> .

**Details**

These are very hacky functions. If used within an RMarkdown document, `KcreateTableOne` and `KnitableTableOne` should be called in a code chunk with `results='hide'` to hide the plain test results printed from `tableone::CreateTableOne`. The resulting data frame should be saved as an object and used in a second code chunk for formatted printing. Suggestions for improvement are welcomed.

The function is written to work with `knitr::kable`, but should be able to work with other functions such as `xtable::xtable`.

**Value**

Returns a data frame of character columns.

**See Also**

[CreateTableOne](#) [print.TableOne](#)

**Examples**

```
table1 = CreateTableOne(data=mtcars, strata='am', factorVars='vs')
table1
knitr::kable(table1)
```

---

num_compare	<i>Compare a numerical variable across levels of a categorical variable</i>
-------------	---

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**Description**

num\_compare gives details about the distribution of a numeric variable across subsets of the dataset

**Usage**

```
num_compare(y, grp, plot = c("density", "boxplot", "none"))
```

**Arguments**

y	A numerical variable
grp	A categorical variable
plot	Type of plot to produce

**Value**

Returns a list including (1) group-wise summary statistics, (2) ANOVA decomposition, (3) eta-squared effect size, and (4) ggplot2 object, if requested.

**Examples**

```
v1 = rbinom(n=50, size=1, p=0.5)
v2 = rnorm(50)
num_compare(y=v2, grp=v1, plot='density')
```

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write_int	<i>Format an interval for display</i>
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**Description**

write\_int formats a numeric input into an interval to be printed, e.g., in an RMarkdown document.

**Usage**

```
write_int(x, delim = "(", digits = 2)
```

**Arguments**

x	A length-2 numeric vector consisting of the endpoints of the interval or an n-row by 2-column matrix of endpoints.
delim	The bracket delimiters to surround the interval. Must be either a round bracket, square bracket, curly bracket, or angled bracket.
digits	Number of digits to round to (default to 2). Will keep trailing zeros.

**Details**

If a matrix is provided, the values in each row will be used to create a formatted interval.

**Value**

Returns a character string of the form " $x[1]$ ,  $x[2]$ " (or supplied bracket delimiter).

**Examples**

```
write_int(x=c(1.2, 2.345))
write_int(x=c(1.2, 2.345), delim='[')
```

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write_p	<i>Format a p-value for display</i>
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**Description**

write\_p formats a p-value for display in an RMarkdown document.

**Usage**

```
write_p(x, digits = 2)
```

**Arguments**

<code>x</code>	A length-1 numeric or a list-like object with element named <code>p.value</code> (such as an <code>hstest</code> object)
<code>digits</code>	Number of digits to round to (default to 2)

**Details**

If  $x < 10^{-(\text{digits})}$ , then the result is the string  $p < 10^{-(\text{digits})}$  in decimal notation.

**Value**

Returns a LaTeX-formatted string to report a p-value to the specified number of digits.

**Examples**

```
write_p(0.2345)
```

```
write_p(0.000234)
```

```
x = rnorm(10)
test1 = t.test(x)
write_p(test1)
```

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