

Package: coreStatsNMR (via r-universe)

September 30, 2024

Title Statistical Functions for Core Analysis Tasks at NMR

Version 1.3.6-7

Description A set of statistical functions for use at NMR Group when completing core analysis tasks: frequency tables, cross-tabs, t-tests, proportion tests, etc.

Depends R (>= 4.2.0)

Imports dplyr, tidyr, purrr, data.table, broom, wrapr, scales, magrittr, weights

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests testthat, knitr, rmarkdown,forcats, ggplot2

VignetteBuilder knitr

Repository <https://nmrgroup.r-universe.dev>

RemoteUrl <https://gitlab.com/NMRgroup/corestatsnmr>

RemoteRef HEAD

RemoteSha fd4a8effcf4460036c026fffc6ddb3653f20015a

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aggRval	<i>Area-weighted R-value</i>
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Description

Returns a single area-weighted R-value from the two vectors it accepts as arguments: one vector of R-values, and the other of areas associated with each R-value

Usage

```
aggRval(r_val, area)
```

Arguments

r_val	Vector of r-values
area	Vector of area associated with each r-value

Value

Single area-weighted r-value

Examples

```
aggRval(c(2,5,20), c(10,10,50))
```

confInterval	<i>Calculate confidence interval (using normal distribution)</i>
---------------------	--

Description

Calculate confidence interval (using normal distribution)

Usage

```
confInterval(x, conf_lvl = 0.9)
```

Arguments

- | | |
|----------|--|
| x | Numerical vector |
| conf_lvl | A number from 0 to 1 indicating confidence level, defaults to 0.9 or 90% |

Value

A dataframe summarizing the sample mean and confidence interval

Examples

```
confInterval(runif(100)); confInterval(runif(1e3))
```

designEffect	<i>Calculate the design effect for adjusting cluster sampling sizes</i>
--------------	---

Description

Calculate the design effect for adjusting cluster sampling sizes

Usage

```
designEffect(n_obs, icc)
```

Arguments

- | | |
|-------|--|
| n_obs | number. Observations in a cluster (e.g. average lamps in a home) |
| icc | number. Intraclass correlation (similarity of clustered data) |

Value

A correction factor for sample sizes drawn from clustered units.

References

<http://faculty.smu.edu/slstokes/stat6380/deffdoc.pdf>

Examples

```
designEffect(35, 0.75)
```

makeWeights*Generate weights for data from sample and population counts***Description**

Assumes data is provided in columns listing each category that is part of the weighting scheme, then a column for the sample n and a column for the general population.

Usage

```
makeWeights(data, sampleVal, populationVal, digits = 5, checkCols = FALSE)

## S3 method for class 'data.frame'
makeWeights(data, sampleVal, populationVal, digits = 5, checkCols = FALSE)
```

Arguments

- `data` A data.frame (or data.table) to add weights to.
- `sampleVal` A string selecting the column in the data with sample counts
- `populationVal` A string selecting the column in the data with population counts
- `digits` A number of digits to use when rounding proportion weights
- `checkCols` A boolean that toggles whether to calculate checks on proportion and population (included as additional columns)

Value

A dataframe with population and proportion weights, as well as optional intermediate calculations.

Examples

```
myData <- data.frame(HairEyeColor)

myData$Population <- round(runif(nrow(myData), 10000, 20000), 0)

makeWeights(data=myData, sampleVal="Freq", populationVal = "Population")
```

mode	<i>Get the mode of a vector of values</i>
------	---

Description

Get the mode of a vector of values

Usage

```
mode(x, show_all = FALSE)
```

Arguments

- | | |
|----------|---|
| x | A vector of values to calculate the mode from |
| show_all | A boolean, if FALSE (default) returns a single mode or NA if there are none/multiple.
If TRUE, returns multiple modes, if they exist |

Value

The mode(s) of the supplied vector.

Source

https://stackoverflow.com/questions/56552709/r-no-mode-and-exclude-na?noredirect=1#comment99692066_56552709

pairPropTest	<i>Pairwise proportion comparisons</i>
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Description

Pairwise proportion comparisons

Usage

```
pairPropTest(  
  data,  
  indexVar,  
  valVar,  
  grpVar,  
  alpha = 0.1,  
  n.min = 10,  
  p.adjust.method = p.adjust.methods,  
  counts = FALSE  
)
```

Arguments

<code>data</code>	A dataset to calculate proportions for and test for statistically significant differences.
<code>indexVar</code>	string. Selects an index column for the dataset
<code>valVar</code>	string. Selects the column containing counts of successes in data
<code>grpVar</code>	string. Selects the column containing counts of trials in data
<code>alpha</code>	number. Significance level (e.g. 0.05 for 95-pct confidence level)
<code>n.min</code>	number. Minimum counts to consider
<code>p.adjust.method</code>	string. Method for adjusting p-values. See ?p.adjust for more details.
<code>counts</code>	Boolean. Toggles whether function returns significance results or counts (for diagnostic purposes)

Value

A dataframe showing p-values and statistically significant differences for the pairs of variables chosen

pairTtest*Pairwise T-test comparisons***Description**

Pairwise T-test comparisons

Usage

```
pairTtest(
  data,
  valVar,
  grpVar,
  alpha = 0.1,
  n.min = 10,
  p.adjust.method = p.adjust.methods
)
```

Arguments

<code>data</code>	A dataset to calculate difference testing for and test for statistically significant differences.
<code>valVar</code>	string. Selects the column containing counts of successes in data
<code>grpVar</code>	string. Selects the column containing counts of trials in data
<code>alpha</code>	number. Significance level (e.g. 0.05 for 95-pct confidence level)
<code>n.min</code>	number. Minimum counts to consider
<code>p.adjust.method</code>	string. Method for adjusting p-values. See ?p.adjust for more details.

Value

A dataframe showing p-values and statistically significant differences for the pairs of variables chosen

penTable	<i>Generating a penetration table</i>
----------	---------------------------------------

Description

Generating a penetration table
Generating a weighted proportion table (2-way)

Usage

```
penTable(  
  data,  
  index,  
  x,  
  y,  
  totWeightVar = NULL,  
  inGroupWeightVar = NULL,  
  only_ns,  
  accuracy,  
  normwt = TRUE,  
  tot.label = "Total"  
)  
  
## S3 method for class 'data.frame'  
penTable(  
  data,  
  index,  
  x,  
  y,  
  totWeightVar = NULL,  
  inGroupWeightVar = NULL,  
  only_ns = FALSE,  
  accuracy = 1,  
  normwt = TRUE,  
  tot.label = "Total"  
)
```

Arguments

data	A dataset to calculate weighted proportions
index	string. Selects an index column for the dataset
x	string. Selects the first variable to find proportions for

<code>y</code>	string. Selects the second variable to find proportions for
<code>totWeightVar</code>	string. A string selecting the column to weight the population
<code>inGroupWeightVar</code>	string. A string selecting the column to use for in-group weights
<code>only_ns</code>	Boolean. Toggles whether to return penetration table or intermediate table of n's.
<code>accuracy</code>	number. A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values.
<code>normwt</code>	Boolean. if TRUE, normalize weights so that the total weighted count is the same as the unweighted one
<code>tot.label</code>	string. A string label for totals column

Value

A data.frame or data.table showing a penetration table

<code>propTest</code>	<i>Proportion comparisons</i>
-----------------------	-------------------------------

Description

Proportion comparisons

Usage

```
propTest(
  data,
  indexVar,
  valVar,
  grpVar,
  counts = NULL,
  alpha = 0.1,
  n.min = 10,
  alternative = c("two.sided", "less", "greater")
)
```

Arguments

<code>data</code>	A dataset to calculate proportions for and test for statistically significant differences.
<code>valVar</code>	string. Selects the column containing counts of successes in data
<code>grpVar</code>	string. Selects the column containing counts of trials in data

counts	vector. Optional vector of strings containing columns counts for successes and trials (otherwise, function calculates counts from valVar and grpVar)
alpha	number. Significance level (e.g. 0.05 for 95-pct confidence level)
n.min	number. Minimum counts to consider
alternative	string. Specifies the alternative hypothesis. See ?prop.test

Value

A dataframe showing p-values and statistically significant differences for the chosen variables

statsTable

Generate a statistical summary table, with optional grouping

Description

Generate a statistical summary table, with optional grouping

Usage

```
statsTable(  
  data,  
  summVar,  
  groupVar = NULL,  
  stats,  
  accuracy = NULL,  
  totCol = TRUE,  
  totWeightVar = NULL,  
  inGroupWeightVar = NULL,  
  drop0trailing = FALSE,  
  colOrder = NULL  
)  
  
## S3 method for class 'data.frame'  
statsTable(  
  data,  
  summVar,  
  groupVar = NULL,  
  stats,  
  accuracy = 1,  
  totCol = TRUE,  
  totWeightVar = NULL,  
  inGroupWeightVar = NULL,  
  drop0trailing = FALSE,  
  colOrder = NULL  
)
```

```
## S3 method for class 'data.table'
statsTable(
  data,
  summVar,
  groupVar = NULL,
  stats,
  accuracy = 1,
  totCol = TRUE,
  totWeightVar = NULL,
  inGroupWeightVar = NULL,
  drop0trailing = FALSE,
  colOrder = NULL
)
```

Arguments

<code>data</code>	A <code>data.frame</code> (or <code>data.table</code>) to use for statistical summary
<code>summVar</code>	A string selecting the column in ‘ <code>data</code> ’ to summarize
<code>groupVar</code>	A string or list of strings selecting the (optional) columns in ‘ <code>data</code> ’ to group by
<code>stats</code>	A list of strings selecting summary stats functions (i.e. <code>mean</code> , <code>sd</code> , <code>sum</code>)
<code>accuracy</code>	A number to round to. Use (e.g.) <code>0.01</code> to show 2 decimal places of precision. If <code>NULL</code> , the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values.
<code>totCol</code>	A boolean toggling whether to include a total column
<code>totWeightVar</code>	A string selecting the column to weight the population
<code>inGroupWeightVar</code>	A string selecting the column to use for in-group weights
<code>drop0trailing</code>	A boolean toggling whether to include trailing zeros in the output (converts to strings)
<code>colOrder</code>	To be deprecated

Value

A `data.frame` with statistical summary results describing the selected variable.

Examples

```
library(dplyr)

statsTable(iris,
  summVar = "Sepal.Length",
  groupVar = "Species",
  stats = c("n", "min", "max", "weighted.mean", "median", "sd"),
  accuracy = 2)
```

stratRandSample *Conducting stratified random sampling*

Description

Conducting stratified random sampling
Stratified random sampling

Usage

```
stratRandSample(  
  data,  
  group,  
  size,  
  select = NULL,  
  replace = FALSE,  
  bothSets = FALSE,  
  keep.rownames = FALSE  
)  
  
## S3 method for class 'data.frame'  
stratRandSample(  
  data,  
  group,  
  size,  
  select = NULL,  
  replace = FALSE,  
  bothSets = FALSE,  
  keep.rownames = NULL  
)  
  
## S3 method for class 'data.table'  
stratRandSample(  
  data,  
  group,  
  size,  
  select = NULL,  
  replace = FALSE,  
  bothSets = FALSE,  
  keep.rownames = FALSE  
)
```

Arguments

data	A data.frame (or data.table) to use for allocating sample
group	string. The column(s) that represent strata

size	number. If <1, the proportion to take from each stratum. If an integer 1+, the number of samples to take from each stratum. If size is a vector of integers, the number of samples taken for each stratum. Recommended in latter case to use a named vector
select	list. Named list specifying a subset of strata to use in sampling
replace	boolean. Toggling whether to sample with replacement
bothSets	boolean. Toggling whether to return list of sampled and unsampled portions of data
keep.rownames	For data.tables only. See ?data.table.

Adapted from <https://gist.github.com/mrdwab/6424112> and <https://gist.github.com/mrdwab/933ffea7a1c>

Value

A sample of the data passed to the function, optionally accounting for strata.

`tidy.wtd.chi.sq`

Tidy a weighted chi-squared contingency table test

Description

Tidy a weighted chi-squared contingency table test

Usage

```
## S3 method for class 'wtd.chi.sq'
tidy(x)
```

Arguments

x	An htest object, such as those created by weights::wtd.chi.sq
---	---

Value

A tibble::tibble() with columns for method, coefficients, estimated values, p-value, and other statistics

tidy.wtd.t.test *Tidy a weighted t-test object*

Description

Tidy a weighted t-test object

Usage

```
## S3 method for class 'wtd.t.test'  
tidy(x)
```

Arguments

x An htest object, such as those created by weights::wtd.t.test()

Value

A tibble::tibble() with columns for method, coefficients, estimated values, p-value, and other statistics

wtdFreqTable *Generating a weighted frequency table (2-way)*

Description

Generating a weighted frequency table (2-way)

Generating a weighted frequency table (2-way)

Usage

```
wtdFreqTable(  
  data,  
  x,  
  y,  
  totWeightVar = NULL,  
  inGroupWeightVar = NULL,  
  accuracy = 1,  
  normwt = TRUE,  
  tot.label = "Statewide",  
  colOrder = NULL  
)  
  
## S3 method for class 'data.frame'  
wtdFreqTable(
```

```

    data,
    x,
    y,
    totWeightVar = NULL,
    inGroupWeightVar = NULL,
    accuracy = 1,
    normwt = TRUE,
    tot.label = "Total",
    colOrder = NULL
)

```

Arguments

data	A dataset to calculate weighted frequencies. Only operational for data.frame for now
x	string. Selects the first variable to find frequencies for
y	string. Selects the second variable to find frequencies for
totWeightVar	string. A string selecting the column to weight the population
inGroupWeightVar	string. A string selecting the column to use for in-group weights
accuracy	number. A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values.
normwt	Boolean. if TRUE, normalize weights so that the total weighted count is the same as the unweighted one
tot.label	string. Label for totals column
colOrder	vector. Vector of strings to set the order for the colum given by variable x

Value

A data.frame showing a two-way weighted frequency table

Description

Weighted pairwise proportion comparisons

Usage

```
wtdPairPropTest(
  data,
  indexVar,
  valVar,
  grpVar,
  weightVar,
  alpha = 0.1,
  n.min = 10,
  p.adjust.method = p.adjust.methods,
  counts = FALSE
)
```

Arguments

<code>data</code>	A dataset to calculate proportions for and test for statistically significant differences.
<code>indexVar</code>	string. Selects an index column for the dataset
<code>valVar</code>	string. Selects the column containing counts of successes in data
<code>grpVar</code>	string. Selects the column containing counts of trials in data
<code>weightVar</code>	string. Selects the column containing weights in the data
<code>alpha</code>	number. Significance level (e.g. 0.05 for 95-pct confidence level)
<code>n.min</code>	number. Minimum counts to consider
<code>p.adjust.method</code>	string. Method for adjusting p-values. See <code>?p.adjust</code> for more details.
<code>counts</code>	Boolean. Toggles whether function returns significance results or counts (for diagnostic purposes)

Value

A dataframe showing p-values and statistically significant differences for the pairs of variables chosen

Description

Pairwise Weighted T-Test comparisons

Usage

```
wtdPairTtest(
  data,
  valVar,
  grpVar,
  weightVar,
  alpha = 0.1,
  n.min = 10,
  p.adjust.method = p.adjust.methods
)
```

Arguments

data	A dataset to calculate difference testing for and test for statistically significant differences.
valVar	string. Selects the column containing counts of successes in data
grpVar	string. Selects the column containing counts of trials in data
weightVar	string. Selects the column containing weights in the data
alpha	number. Significance level (e.g. 0.05 for 95-pct confidence level)
n.min	number. Minimum counts to consider
p.adjust.method	string. Method for adjusting p-values. See ?p.adjust for more details.

Value

A dataframe showing p-values and statistically significant differences for the pairs of variables chosen

wtdPropTable

*Generating a weighted proportion table (2-way)***Description**

Generating a weighted proportion table (2-way)
 Generating a weighted proportion table (2-way)

Usage

```
wtdPropTable(
  data,
  x,
  y,
  totWeightVar = NULL,
  inGroupWeightVar = NULL,
  pct_format = TRUE,
```

```

accuracy = 0.1,
normwt = TRUE,
tot.label = "Total",
colOrder = NULL
)

## S3 method for class 'data.frame'
wtdPropTable(
  data,
  x,
  y,
  totWeightVar = NULL,
  inGroupWeightVar = NULL,
  pct_format = TRUE,
  accuracy = 0.1,
  normwt = TRUE,
  tot.label = "Total",
  colOrder = NULL
)

```

Arguments

data	A dataset to calculate weighted proportions
x	string. Selects the first variable to find proportions for
y	string. Selects the second variable to find proportions for
totWeightVar	string. A string selecting the column to weight the population
inGroupWeightVar	string. A string selecting the column to use for in-group weights
pct_format	boolean. Toggles whether proportions are given as decimals or percents (converts to strings)
accuracy	number. A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values.
normwt	Boolean. if TRUE, normalize weights so that the total weighted count is the same as the unweighted one
tot.label	string. A string label for totals column
colOrder	vector. A vector of strings to set the order for the column given by variable x

Value

A data.frame or data.table showing a two-way weighted proportion table

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