Package 'jmv'

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Type Package

Title The 'jamovi' Analyses

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Maintainer Jonathon Love <jon@thon.cc>

Description A suite of common statistical methods such as descriptives, t-tests, ANOVAs, regression, correlation matrices, proportion tests, contingency tables, and factor analysis. This package is also useable from the 'jamovi' statistical spreadsheet (see <https://www.jamovi.org> for more information).

BugReports https://github.com/jamovi/jmv/issues

License GPL (>= 2)

Depends R (>= 3.2)

Imports jmvcore (>= 2.4.2), R6, car (>= 3.0.0), multcomp, ggplot2 (>= 2.2.1), PMCMR, emmeans (>= 1.4.2), vcd, vcdExtra, GGally, BayesFactor, psych (>= 1.7.5), GPArotation, afex (>= 0.28-0), mvnormtest, lavaan, ggridges, ROCR, nnet, MASS, ggrepel, dplyr, magrittr, matrixStats

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Author Ravi Selker [aut, cph],
Jonathon Love [aut, cre, cph],
Damian Dropmann [aut, cph],
Victor Moreno [ctb, cph],
Maurizio Agosti [ctb, cph],
Sebastian Jentschke [ctb, cph]

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Contents

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ancova *ANCOVA*

Description

The Analysis of Covariance (ANCOVA) is used to explore the relationship between a continuous dependent variable, one or more categorical explanatory variables, and one or more continuous explanatory variables (or covariates). It is essentially the same analysis as ANOVA, but with the addition of covariates.

Usage

```
ancova(data, dep, factors = NULL, covs = NULL, effectSize = NULL,
  modelTest = FALSE, modelTerms = NULL, ss = "3", homo = FALSE,
  norm = FALSE, qq = FALSE, contrasts = NULL, postHoc = NULL,
  postHocCorr = list("tukey"), postHocES = list(),
  postHocEsCi = FALSE, postHocEsCiWidth = 95, emMeans = list(list()),
  emmPlots = TRUE, emmPlotData = FALSE, emmPlotError = "ci",
  emmTables = FALSE, emmWeights = TRUE, ciWidthEmm = 95, formula)
```

Arguments

data	the data as a data frame
dep	the dependent variable from data, variable must be numeric (not necessary when providing a formula, see examples)
factors	the explanatory factors in data (not necessary when providing a formula, see examples)
covs	the explanatory covariates (not necessary when providing a formula, see examples)
effectSize	one or more of 'eta', 'partEta', or 'omega'; use eta², partial eta², and omega² effect sizes, respectively
modelTest	TRUE or FALSE (default); perform an overall model test
modelTerms	a formula describing the terms to go into the model (not necessary when providing a formula, see examples)
ss	'1', '2' or '3' (default), the sum of squares to use
homo	TRUE or FALSE (default), perform homogeneity tests
norm	TRUE or FALSE (default), perform Shapiro-Wilk tests of normality
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
contrasts	a list of lists specifying the factor and type of contrast to use, one of 'deviation', 'simple', 'difference', 'helmert', 'repeated' or 'polynomial'
postHoc	a formula containing the terms to perform post-hoc tests on (see the examples)
postHocCorr	one or more of 'none', 'tukey', 'scheffe', 'bonf', or 'holm'; provide no, Tukey, Scheffe, Bonferroni, and Holm Post Hoc corrections respectively
postHocES	a possible value of 'd'; provide cohen's d measure of effect size for the post-hoc tests
postHocEsCi	TRUE or FALSE (default), provide confidence intervals for the post-hoc effect sizes
postHocEsCiWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals for the post-hoc effect sizes
emMeans	a formula containing the terms to estimate marginal means for (see the examples)
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmPlotData	TRUE or FALSE (default), plot the data on top of the marginal means

emmPlotError	'none', 'ci' (default), or 'se'. Use no error bars, use confidence intervals, or use standard errors on the marginal mean plots, respectively
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
formula	(optional) the formula to use, see the examples

Value

A results object containing:

results$main	a table of ANCOVA results
results$model	The underlying aov object
results$assump$homo	a table of homogeneity tests
results$assump$norm	a table of normality tests
results$assump$qq	a q-q plot
results$contrasts	an array of contrasts tables
results$postHoc	an array of post-hoc tables
results$emm	an array of the estimated marginal means plots + tables
results$residsOV	an output

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$main$asDF

as.data.frame(results$main)
```

Examples

```
data('ToothGrowth')

ancova(formula = len ~ supp + dose, data = ToothGrowth)

#
#  ANCOVA
#
#  ANCOVA
#  ---------------------------------------------------------------------
#                 Sum of Squares    df    Mean Square    F        p
#  ---------------------------------------------------------------------
#    supp                    205     1          205.4     11.4     0.001
#    dose                   2224     1         2224.3    124.0    < .001
#    Residuals              1023    57           17.9
#  ---------------------------------------------------------------------
#

ancova(
```

```
  formula = len ~ supp + dose,
  data = ToothGrowth,
  postHoc = ~ supp,
  emMeans = ~ supp)
```

ANOVA *ANOVA*

Description

The Analysis of Variance (ANOVA) is used to explore the relationship between a continuous dependent variable, and one or more categorical explanatory variables.

Usage

```
ANOVA(data, dep, factors = NULL, effectSize = NULL,
  modelTest = FALSE, modelTerms = NULL, ss = "3", homo = FALSE,
  norm = FALSE, qq = FALSE, contrasts = NULL, postHoc = NULL,
  postHocCorr = list("tukey"), postHocES = list(),
  postHocEsCi = FALSE, postHocEsCiWidth = 95, emMeans = list(list()),
  emmPlots = TRUE, emmPlotData = FALSE, emmPlotError = "ci",
  emmTables = FALSE, emmWeights = TRUE, ciWidthEmm = 95, formula)
```

Arguments

data	the data as a data frame
dep	the dependent variable from data, variable must be numeric (not necessary when providing a formula, see examples)
factors	the explanatory factors in data (not necessary when providing a formula, see examples)
effectSize	one or more of 'eta', 'partEta', or 'omega'; use eta², partial eta², and omega² effect sizes, respectively
modelTest	TRUE or FALSE (default); perform an overall model test
modelTerms	a formula describing the terms to go into the model (not necessary when providing a formula, see examples)
ss	'1', '2' or '3' (default), the sum of squares to use
homo	TRUE or FALSE (default), perform homogeneity tests
norm	TRUE or FALSE (default), perform Shapiro-Wilk tests of normality
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
contrasts	a list of lists specifying the factor and type of contrast to use, one of 'deviation', 'simple', 'difference', 'helmert', 'repeated' or 'polynomial'
postHoc	a formula containing the terms to perform post-hoc tests on (see the examples)

postHocCorr	one or more of 'none', 'tukey', 'scheffe', 'bonf', or 'holm'; provide no, Tukey, Scheffe, Bonferroni, and Holm Post Hoc corrections respectively
postHocES	a possible value of 'd'; provide cohen's d measure of effect size for the post-hoc tests
postHocEsCi	TRUE or FALSE (default), provide confidence intervals for the post-hoc effect sizes
postHocEsCiWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals for the post-hoc effect sizes
emMeans	a formula containing the terms to estimate marginal means for (see the examples)
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmPlotData	TRUE or FALSE (default), plot the data on top of the marginal means
emmPlotError	'none', 'ci' (default), or 'se'. Use no error bars, use confidence intervals, or use standard errors on the marginal mean plots, respectively
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
formula	(optional) the formula to use, see the examples

Details

ANOVA assumes that the residuals are normally distributed, and that the variances of all groups are equal. If one is unwilling to assume that the variances are equal, then a Welch's test can be used instead (However, the Welch's test does not support more than one explanatory factor). Alternatively, if one is unwilling to assume that the data is normally distributed, a non-parametric approach (such as Kruskal-Wallis) can be used.

Value

A results object containing:

results$main	a table of ANOVA results
results$model	The underlying aov object
results$assump$homo	a table of homogeneity tests
results$assump$norm	a table of normality tests
results$assump$qq	a q-q plot
results$contrasts	an array of contrasts tables
results$postHoc	an array of post-hoc tables
results$emm	an array of the estimated marginal means plots + tables
results$residsOV	an output

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$main$asDF

as.data.frame(results$main)
```

Examples

```
data('ToothGrowth')

ANOVA(formula = len ~ dose * supp, data = ToothGrowth)

#
#  ANOVA
#
#  ANOVA
#  ---------------------------------------------------------------------------
#                 Sum of Squares    df    Mean Square    F        p
#  ---------------------------------------------------------------------------
#    dose                   2426     2         1213.2    92.00    < .001
#    supp                    205     1          205.4    15.57    < .001
#    dose:supp               108     2           54.2     4.11     0.022
#    Residuals               712    54           13.2
#  ---------------------------------------------------------------------------
#

ANOVA(
    formula = len ~ dose * supp,
    data = ToothGrowth,
    emMeans = ~ supp + dose:supp, # est. marginal means for supp and dose:supp
    emmPlots = TRUE,              # produce plots of those marginal means
    emmTables = TRUE)             # produce tables of those marginal means
```

---

anovaNP *One-Way ANOVA (Non-parametric)*

Description

The Kruskal-Wallis test is used to explore the relationship between a continuous dependent variable, and a categorical explanatory variable. It is analagous to ANOVA, but with the advantage of being non-parametric and having fewer assumptions. However, it has the limitation that it can only test a single explanatory variable at a time.

Usage

```
anovaNP(data, deps, group, es = FALSE, pairs = FALSE,
  pairsDunn = FALSE, formula)
```

Arguments

data	the data as a data frame
deps	a string naming the dependent variable in data
group	a string naming the grouping or independent variable in data
es	TRUE or FALSE (default), provide effect-sizes
pairs	TRUE or FALSE (default), perform pairwise comparisons
pairsDunn	TRUE or FALSE (default), perform pairwise comparisons
formula	(optional) the formula to use, see the examples

Value

A results object containing:

results$table	a table of the test results
results$comparisons	an array of pairwise comparison tables
results$comparisonsDunn	an array of pairwise comparison tables

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$table$asDF

as.data.frame(results$table)
```

Examples

```
data('ToothGrowth')

anovaNP(formula = len ~ dose, data=ToothGrowth)

#
#  ONE-WAY ANOVA (NON-PARAMETRIC)
#
#  Kruskal-Wallis
#  ------------------------------
#           X²      df    p
#  ------------------------------
#    len    40.7     2    < .001
#  ------------------------------
#
```

anovaOneW *One-Way ANOVA*

Description

The Analysis of Variance (ANOVA) is used to explore the relationship between a continuous dependent variable, and one or more categorical explanatory variables. This 'One-Way ANOVA' is a simplified version of the 'normal' ANOVA, allowing only a single explanatory factor, however also providing a Welch's ANOVA. The Welch's ANOVA has the advantage that it need not assume that the variances of all groups are equal.

Usage

```
anovaOneW(data, deps, group, welchs = TRUE, fishers = FALSE,
  miss = "perAnalysis", desc = FALSE, descPlot = FALSE,
  norm = FALSE, qq = FALSE, eqv = FALSE, phMethod = "none",
  phMeanDif = TRUE, phSig = TRUE, phTest = FALSE, phFlag = FALSE,
  formula)
```

Arguments

data	the data as a data frame
deps	a string naming the dependent variables in data
group	a string naming the grouping or independent variable in data
welchs	TRUE (default) or FALSE, perform Welch's one-way ANOVA which does not assume equal variances
fishers	TRUE or FALSE (default), perform Fisher's one-way ANOVA which assumes equal variances
miss	'perAnalysis' or 'listwise', how to handle missing values; 'perAnalysis' excludes missing values for individual dependent variables, 'listwise' excludes a row from all analyses if one of its entries is missing.
desc	TRUE or FALSE (default), provide descriptive statistics
descPlot	TRUE or FALSE (default), provide descriptive plots
norm	TRUE or FALSE (default), perform Shapiro-Wilk test of normality
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
eqv	TRUE or FALSE (default), perform Levene's test for homogeneity of variances
phMethod	'none', 'gamesHowell' or 'tukey', which post-hoc tests to provide; 'none' shows no post-hoc tests, 'gamesHowell' shows Games-Howell post-hoc tests where no equivalence of variances is assumed, and 'tukey' shows Tukey post-hoc tests where equivalence of variances is assumed
phMeanDif	TRUE (default) or FALSE, provide mean differences for post-hoc tests
phSig	TRUE (default) or FALSE, provide significance levels for post-hoc tests

phTest	TRUE or FALSE (default), provide test results (t-value and degrees of freedom) for post-hoc tests
phFlag	TRUE or FALSE (default), flag significant post-hoc comparisons
formula	(optional) the formula to use, see the examples

Details

For convenience, this method allows specifying multiple dependent variables, resulting in multiple independent tests.

Note that the Welch's ANOVA is the same procedure as the Welch's independent samples t-test.

Value

A results object containing:

results$anova	a table of the test results
results$desc	a table containing the group descriptives
results$assump$norm	a table containing the normality tests
results$assump$eqv	a table of homogeneity of variances tests
results$plots	an array of groups of plots
results$postHoc	an array of post-hoc tables

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$anova$asDF
```

```
as.data.frame(results$anova)
```

Examples

```
data('ToothGrowth')
dat <- ToothGrowth
dat$dose <- factor(dat$dose)

anovaOneW(formula = len ~ dose, data = dat)

#
#  ONE-WAY ANOVA
#
#  One-Way ANOVA (Welch's)
#  ----------------------------------------
#           F       df1    df2     p
#  ----------------------------------------
#    len    68.4      2    37.7    < .001
#  ----------------------------------------
#
```

anovaRM *Repeated Measures ANOVA*

Description

The Repeated Measures ANOVA is used to explore the relationship between a continuous dependent variable and one or more categorical explanatory variables, where one or more of the explanatory variables are 'within subjects' (where multiple measurements are from the same subject). Additionally, this analysis allows the inclusion of covariates, allowing for repeated measures ANCOVAs as well.

Usage

```
anovaRM(data, rm = list(list(label = "RM Factor 1", levels =
  list("Level 1", "Level 2"))), rmCells = NULL, bs = NULL,
  cov = NULL, effectSize = NULL, depLabel = "Dependent",
  rmTerms = NULL, bsTerms = NULL, ss = "3", spherTests = FALSE,
  spherCorr = list("none"), leveneTest = FALSE, qq = FALSE,
  contrasts = NULL, postHoc = NULL, postHocCorr = list("tukey"),
  emMeans = list(list()), emmPlots = TRUE, emmTables = FALSE,
  emmWeights = TRUE, ciWidthEmm = 95, emmPlotData = FALSE,
  emmPlotError = "ci", groupSumm = FALSE)
```

Arguments

data	the data as a data frame
rm	a list of lists, where each list describes the label (as a string) and the levels (as vector of strings) of a particular repeated measures factor
rmCells	a list of lists, where each list decribes a repeated measure (as a string) from data defined as measure and the particular combination of levels from rm that it belongs to (as a vector of strings) defined as cell
bs	a vector of strings naming the between subjects factors from data
cov	a vector of strings naming the covariates from data. Variables must be numeric
effectSize	one or more of 'eta', 'partEta', or 'omega'; use eta², partial eta², and omega² effect sizes, respectively
depLabel	a string (default: 'Dependent') describing the label used for the dependent variable throughout the analysis
rmTerms	a list of character vectors describing the repeated measures terms to go into the model
bsTerms	a list of character vectors describing the between subjects terms to go into the model
ss	'2' or '3' (default), the sum of squares to use
spherTests	TRUE or FALSE (default), perform sphericity tests

spherCorr	one or more of 'none' (default), 'GG', or HF; use no p-value correction, the Greenhouse-Geisser p-value correction, and the Huynh-Feldt p-value correction for shericity, respectively
leveneTest	TRUE or FALSE (default), test for homogeneity of variances (i.e., Levene's test)
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
contrasts	in development
postHoc	a list of character vectors describing the post-hoc tests that need to be computed
postHocCorr	one or more of 'none', 'tukey' (default), 'scheffe', 'bonf', or 'holm'; use no, Tukey, Scheffe, Bonferroni and Holm posthoc corrections, respectively
emMeans	a list of lists specifying the variables for which the estimated marginal means need to be calculate. Supports up to three variables per term.
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
emmPlotData	TRUE or FALSE (default), plot the data on top of the marginal means
emmPlotError	'none', 'ci' (default), or 'se'. Use no error bars, use confidence intervals, or use standard errors on the marginal mean plots, respectively
groupSumm	TRUE or FALSE (default), report a summary of the different groups

Details

This analysis requires that the data be in 'wide format', where each row represents a subject (as opposed to long format, where each measurement of the dependent variable is represented as a row).

A non-parametric equivalent of the repeated measures ANOVA also exists; the Friedman test. However, it has the limitation of only being able to test a single factor.

Value

A results object containing:

results$rmTable	a table
results$bsTable	a table
results$assump$spherTable	a table
results$assump$leveneTable	a table
results$assump$qq	a q-q plot
results$contrasts	an array of tables
results$postHoc	an array of tables
results$emm	an array of the estimated marginal means plots + tables
results$groupSummary	a summary of the groups

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$rmTable$asDF

as.data.frame(results$rmTable)
```

Examples

```
data('bugs', package = 'jmv')

anovaRM(
    data = bugs,
    rm = list(
        list(
            label = 'Frightening',
            levels = c('Low', 'High'))),
    rmCells = list(
        list(
            measure = 'LDLF',
            cell = 'Low'),
        list(
            measure = 'LDHF',
            cell = 'High')),
    rmTerms = list(
        'Frightening'))

#
#  REPEATED MEASURES ANOVA
#
#  Within Subjects Effects
#  ------------------------------------------------------------------------
#                  Sum of Squares    df    Mean Square    F       p
#  ------------------------------------------------------------------------
#    Frightening              126     1         126.11    44.2    < .001
#    Residual                 257    90           2.85
#  ------------------------------------------------------------------------
#    Note. Type 3 Sums of Squares
#
#
#
#  Between Subjects Effects
#  ----------------------------------------------------------------
#                Sum of Squares    df    Mean Square    F    p
#  ----------------------------------------------------------------
#    Residual               954    90           10.6
#  ----------------------------------------------------------------
#    Note. Type 3 Sums of Squares
#
```

anovaRMNP *Repeated Measures ANOVA (Non-parametric)*

Description

The Friedman test is used to explore the relationship between a continuous dependent variable and a categorical explanatory variable, where the explanatory variable is 'within subjects' (where multiple measurements are from the same subject). It is analagous to Repeated Measures ANOVA, but with the advantage of being non-parametric, and not requiring the assumptions of normality or homogeneity of variances. However, it has the limitation that it can only test a single explanatory variable at a time.

Usage

```
anovaRMNP(data, measures, pairs = FALSE, desc = FALSE, plots = FALSE,
  plotType = "means")
```

Arguments

data	the data as a data frame
measures	a vector of strings naming the repeated measures variables
pairs	TRUE or FALSE (default), perform pairwise comparisons
desc	TRUE or FALSE (default), provide descriptive statistics
plots	TRUE or FALSE (default), provide a descriptive plot
plotType	'means' (default) or 'medians', the error bars to use in the plot

Value

A results object containing:

results$table	a table of the Friedman test results
results$comp	a table of the pairwise comparisons
results$desc	a table containing the descriptives
results$plot	a descriptives plot

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$table$asDF

as.data.frame(results$table)
```

Examples

```
data('bugs', package = 'jmv')

anovaRMNP(bugs, measures = vars(LDLF, LDHF, HDLF, HDHF))

#
#  REPEATED MEASURES ANOVA (NON-PARAMETRIC)
#
#  Friedman
#  ------------------------
#    X²      df    p
#  ------------------------
#    55.8     3    < .001
#  ------------------------
#
```

Big5 *Big 5*

Description

Big 5

---

bugs *bugs*

Description

bugs

Author(s)

Ryan, Wilde & Crist (2013)

References

https://faculty.kutztown.edu/rryan/RESEARCH/PUBS/Ryan,%20Wilde,%20%26%20Crist%202013%20Web%20exp%20vs%20lab.pdf

cfa *Confirmatory Factor Analysis*

Description

Confirmatory Factor Analysis

Usage

```
cfa(data, factors = list(list(label = "Factor 1", vars = list())),
  resCov, miss = "fiml", constrain = "facVar", estTest = TRUE,
  ci = FALSE, ciWidth = 95, stdEst = FALSE, factCovEst = TRUE,
  factInterceptEst = FALSE, resCovEst = FALSE,
  resInterceptEst = FALSE, fitMeasures = list("cfi", "tli", "rmsea"),
  modelTest = TRUE, pathDiagram = FALSE, corRes = FALSE,
  hlCorRes = 0.1, mi = FALSE, hlMI = 3)
```

Arguments

data	the data as a data frame
factors	a list containing named lists that define the label of the factor and the vars that belong to that factor
resCov	a list of lists specifying the residual covariances that need to be estimated
miss	'listwise' or 'fiml', how to handle missing values; 'listwise' excludes a row from all analyses if one of its entries is missing, 'fiml' uses a full information maximum likelihood method to estimate the model.
constrain	'facVar' or 'facInd', how to contrain the model; 'facVar' fixes the factor variances to one, 'facInd' fixes each factor to the scale of its first indicator.
estTest	TRUE (default) or FALSE, provide 'Z' and 'p' values for the model estimates
ci	TRUE or FALSE (default), provide a confidence interval for the model estimates
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width that is used as 'ci'
stdEst	TRUE or FALSE (default), provide a standardized estimate for the model estimates
factCovEst	TRUE (default) or FALSE, provide estimates for the factor (co)variances
factInterceptEst	TRUE or FALSE (default), provide estimates for the factor intercepts
resCovEst	TRUE (default) or FALSE, provide estimates for the residual (co)variances
resInterceptEst	TRUE or FALSE (default), provide estimates for the residual intercepts
fitMeasures	one or more of 'cfi', 'tli', 'srmr', 'rmsea', 'aic', or 'bic'; use CFI, TLI, SRMR, RMSEA + 90% confidence interval, adjusted AIC, and BIC model fit measures, respectively

`modelTest`	`TRUE` (default) or `FALSE`, provide a chi-square test for exact fit that compares the model with the perfect fitting model
`pathDiagram`	`TRUE` or `FALSE` (default), provide a path diagram of the model
`corRes`	`TRUE` or `FALSE` (default), provide the residuals for the observed correlation matrix (i.e., the difference between the expected correlation matrix and the observed correlation matrix)
`hlCorRes`	a number (default: 0.1), highlight values in the `'corRes'` table above this value
`mi`	`TRUE` or `FALSE` (default), provide modification indices for the parameters not included in the model
`hlMI`	a number (default: 3), highlight values in the `'modIndices'` tables above this value

Value

A results object containing:

`results$factorLoadings`	a table containing the factor loadings
`results$factorEst$factorCov`	a table containing factor covariances estimates
`results$factorEst$factorIntercept`	a table containing factor intercept estimates
`results$resEst$resCov`	a table containing residual covariances estimates
`results$resEst$resIntercept`	a table containing residual intercept estimates
`results$modelFit$test`	a table containing the chi-square test for exact fit
`results$modelFit$fitMeasures`	a table containing fit measures
`results$modelPerformance$corRes`	a table containing residuals for the observed correlation matrix
`results$modelPerformance$modIndices`	a group
`results$pathDiagram`	an image containing the model path diagram
`results$modelSyntax`	the lavaan syntax used to fit the model

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$factorLoadings$asDF
```

```
as.data.frame(results$factorLoadings)
```

Examples

```
data <- lavaan::HolzingerSwineford1939

jmv::cfa(
    data = data,
    factors = list(
        list(label="Visual", vars=c("x1", "x2", "x3")),
        list(label="Textual", vars=c("x4", "x5", "x6")),
        list(label="Speed", vars=c("x7", "x8", "x9"))),
    resCov = NULL)

#
#  CONFIRMATORY FACTOR ANALYSIS
#
```

```
#  Factor Loadings
#  ------------------------------------------------------------------
#    Factor     Indicator    Estimate    SE        Z        p
#  ------------------------------------------------------------------
#    Visual     x1              0.900    0.0832    10.81    < .001
#               x2              0.498    0.0808     6.16    < .001
#               x3              0.656    0.0776     8.46    < .001
#    Textual    x4              0.990    0.0567    17.46    < .001
#               x5              1.102    0.0626    17.60    < .001
#               x6              0.917    0.0538    17.05    < .001
#    Speed      x7              0.619    0.0743     8.34    < .001
#               x8              0.731    0.0755     9.68    < .001
#               x9              0.670    0.0775     8.64    < .001
#  ------------------------------------------------------------------
#
#
#  FACTOR ESTIMATES
#
#  Factor Covariances
#  ------------------------------------------------------------------
#                           Estimate    SE        Z       p
#  ------------------------------------------------------------------
#    Visual     Visual      1.000 a
#               Textual     0.459      0.0635    7.22    < .001
#               Speed       0.471      0.0862    5.46    < .001
#    Textual    Textual     1.000 a
#               Speed       0.283      0.0715    3.96    < .001
#    Speed      Speed       1.000 a
#  ------------------------------------------------------------------
#    a fixed parameter
#
#
#  MODEL FIT
#
#  Test for Exact Fit
#  ------------------------
#    X²      df    p
#  ------------------------
#    85.3    24    < .001
#  ------------------------
#
#
#  Fit Measures
#  -----------------------------------------------
#    CFI      TLI      RMSEA     Lower     Upper
#  -----------------------------------------------
#    0.931    0.896    0.0921    0.0714    0.114
#  -----------------------------------------------
#
```

contTables *Contingency Tables*

Description

The X^2 test of association (not to be confused with the X^2 goodness of fit) is used to test whether two categorical variables are independent or associated. If the p-value is low, it suggests the variables are not independent, and that there is a relationship between the two variables.

Usage

```
contTables(data, rows, cols, counts = NULL, layers = NULL,
  chiSq = TRUE, chiSqCorr = FALSE, zProp = FALSE, likeRat = FALSE,
  fisher = FALSE, contCoef = FALSE, phiCra = FALSE,
  diffProp = FALSE, logOdds = FALSE, odds = FALSE, relRisk = FALSE,
  ci = TRUE, ciWidth = 95, compare = "rows",
  hypothesis = "different", gamma = FALSE, taub = FALSE,
  mh = FALSE, obs = TRUE, exp = FALSE, pcRow = FALSE,
  pcCol = FALSE, pcTot = FALSE, barplot = FALSE, yaxis = "ycounts",
  yaxisPc = "total_pc", xaxis = "xrows", bartype = "dodge",
  resU = FALSE, resP = FALSE, hlresP = 2, resS = FALSE,
  hlresS = 2, resA = FALSE, hlresA = 2, formula)
```

Arguments

data	the data as a data frame
rows	the variable to use as the rows in the contingency table (not necessary when providing a formula, see the examples)
cols	the variable to use as the columns in the contingency table (not necessary when providing a formula, see the examples)
counts	the variable to use as the counts in the contingency table (not necessary when providing a formula, see the examples)
layers	the variables to use to split the contingency table (not necessary when providing a formula, see the examples)
chiSq	TRUE (default) or FALSE, provide X^2
chiSqCorr	TRUE or FALSE (default), provide X^2 with continuity correction
zProp	TRUE or FALSE (default), provide a z test for differences between two proportions
likeRat	TRUE or FALSE (default), provide the likelihood ratio
fisher	TRUE or FALSE (default), provide Fisher's exact test
contCoef	TRUE or FALSE (default), provide the contingency coefficient
phiCra	TRUE or FALSE (default), provide Phi and Cramer's V
diffProp	TRUE or FALSE (default), provide the differences in proportions (only available for 2x2 tables)

logOdds	TRUE or FALSE (default), provide the log odds ratio (only available for 2x2 tables)
odds	TRUE or FALSE (default), provide the odds ratio (only available for 2x2 tables)
relRisk	TRUE or FALSE (default), provide the relative risk (only available for 2x2 tables)
ci	TRUE or FALSE (default), provide confidence intervals for the comparative measures
ciWidth	a number between 50 and 99.9 (default: 95), width of the confidence intervals to provide
compare	columns or rows (default), compare columns/rows in difference of proportions or relative risks (2x2 tables)
hypothesis	'different' (default), 'oneGreater' or 'twoGreater', the alternative hypothesis; group 1 different to group 2, group 1 greater than group 2, and group 2 greater than group 1 respectively
gamma	TRUE or FALSE (default), provide gamma
taub	TRUE or FALSE (default), provide Kendall's tau-b
mh	TRUE or FALSE (default), provide Mantel-Haenszel test for trend
obs	TRUE or FALSE (default), provide the observed counts
exp	TRUE or FALSE (default), provide the expected counts
pcRow	TRUE or FALSE (default), provide row percentages
pcCol	TRUE or FALSE (default), provide column percentages
pcTot	TRUE or FALSE (default), provide total percentages
barplot	TRUE or FALSE (default), show barplots
yaxis	ycounts (default) or ypc. Use respectively counts or percentages for the bar plot y-axis
yaxisPc	total_pc (default), column_pc, or row_pc. Use respectively percentages of total, within columns, or within rows for the bar plot y-axis.
xaxis	rows (default), or columns in bar plot X axis
bartype	stack or side by side (default), barplot type
resU	TRUE or FALSE (default), display unstandardized residuals in the post hoc tests table.
resP	TRUE or FALSE (default), display Pearson residuals in the post hoc tests table.
hlresP	A numeric value (default: 2.0), highlight Pearson residuals above this threshold in the post hoc tests table.
resS	TRUE or FALSE (default), display standardized residuals (adjusted Pearson) in the post hoc tests table.
hlresS	A numeric value (default: 2.0), highlight standardized residuals above this threshold in the post hoc tests table.
resA	TRUE or FALSE (default), display deviance residuals from a Poisson GLM in the post hoc tests table.
hlresA	A numeric value (default: 2.0), highlight deviance residuals above this threshold in the post hoc tests table.
formula	(optional) the formula to use, see the examples

Value

A results object containing:

`results$freqs`	a table of proportions
`results$chiSq`	a table of X^2 test results
`results$odds`	a table of comparative measures
`results$nom`	a table of the 'nominal' test results
`results$gamma`	a table of the gamma test results
`results$taub`	a table of the Kendall's tau-b test results
`results$mh`	a table of the Mantel-Haenszel test for trend
`results$postHoc`	a table of post-hoc residuals
`results$barplot`	an image

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$freqs$asDF
```

```
as.data.frame(results$freqs)
```

Examples

```
data('HairEyeColor')
dat <- as.data.frame(HairEyeColor)

contTables(formula = Freq ~ Hair:Eye, dat)

#
#  CONTINGENCY TABLES
#
#  Contingency Tables
#  ---------------------------------------------------
#    Hair     Brown    Blue    Hazel    Green    Total
#  ---------------------------------------------------
#    Black       68      20       15        5      108
#    Brown      119      84       54       29      286
#    Red         26      17       14       14       71
#    Blond        7      94       10       16      127
#    Total      220     215       93       64      592
#  ---------------------------------------------------
#
#
#  X² Tests
#  ------------------------------
#           Value    df    p
#  ------------------------------
#    X²      138     9    < .001
#    N       592
#  ------------------------------
#

# Alternatively, omit the left of the formula (`Freq`) if each row
```

```
# represents a single observation:

contTables(formula = ~ Hair:Eye, dat)
```

`contTablesPaired` *Paired Samples Contingency Tables*

Description

McNemar test

Usage

```
contTablesPaired(data, rows, cols, counts = NULL, chiSq = TRUE,
  chiSqCorr = FALSE, exact = FALSE, pcRow = FALSE, pcCol = FALSE,
  formula)
```

Arguments

`data`	the data as a data frame
`rows`	the variable to use as the rows in the contingency table (not necessary when providing a formula, see the examples)
`cols`	the variable to use as the columns in the contingency table (not necessary when providing a formula, see the examples)
`counts`	the variable to use as the counts in the contingency table (not necessary when providing a formula, see the examples)
`chiSq`	`TRUE` (default) or `FALSE`, provide X^2
`chiSqCorr`	`TRUE` or `FALSE` (default), provide X^2 with continuity correction
`exact`	`TRUE` or `FALSE` (default), provide an exact log odds ratio (requires exact2x2 to be installed)
`pcRow`	`TRUE` or `FALSE` (default), provide row percentages
`pcCol`	`TRUE` or `FALSE` (default), provide column percentages
`formula`	(optional) the formula to use, see the examples

Value

A results object containing:

`results$freqs`	a proportions table
`results$test`	a table of test results

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$freqs$asDF

as.data.frame(results$freqs)
```

Examples

```
dat <- data.frame(
    `1st survey` = c('Approve', 'Approve', 'Disapprove', 'Disapprove'),
    `2nd survey` = c('Approve', 'Disapprove', 'Approve', 'Disapprove'),
    `Counts` = c(794, 150, 86, 570),
    check.names=FALSE)

contTablesPaired(formula = Counts ~ `1st survey`:`2nd survey`, data = dat)

#
#  PAIRED SAMPLES CONTINGENCY TABLES
#
#  Contingency Tables
#  -------------------------------------------------
#    1st survey    Approve    Disapprove    Total
#  -------------------------------------------------
#    Approve           794           150      944
#    Disapprove         86           570      656
#    Total             880           720     1600
#  -------------------------------------------------
#
#
#  McNemar Test
#  -----------------------------------------------------
#                                Value    df    p
#  -----------------------------------------------------
#    X²                           17.4     1    < .001
#    X² continuity correction     16.8     1    < .001
#  -----------------------------------------------------
#


# Alternatively, omit the left of the formula (`Counts`) from the
# formula if each row represents a single observation:

contTablesPaired(formula = ~ `1st survey`:`2nd survey`, data = dat)
```

---

corrMatrix *Correlation Matrix*

Description

Correlation matrices are a way to examine linear relationships between two or more continuous variables.

Usage

```
corrMatrix(data, vars, pearson = TRUE, spearman = FALSE,
  kendall = FALSE, sig = TRUE, flag = FALSE, n = FALSE,
```

```
    ci = FALSE, ciWidth = 95, plots = FALSE, plotDens = FALSE,
    plotStats = FALSE, hypothesis = "corr")
```

Arguments

data	the data as a data frame
vars	a vector of strings naming the variables to correlate in data
pearson	TRUE (default) or FALSE, provide Pearson's R
spearman	TRUE or FALSE (default), provide Spearman's rho
kendall	TRUE or FALSE (default), provide Kendall's tau-b
sig	TRUE (default) or FALSE, provide significance levels
flag	TRUE or FALSE (default), flag significant correlations
n	TRUE or FALSE (default), provide the number of cases
ci	TRUE or FALSE (default), provide confidence intervals
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals to provide
plots	TRUE or FALSE (default), provide a correlation matrix plot
plotDens	TRUE or FALSE (default), provide densities in the correlation matrix plot
plotStats	TRUE or FALSE (default), provide statistics in the correlation matrix plot
hypothesis	one of 'corr' (default), 'pos', 'neg' specifying the alernative hypothesis; correlated, correlated positively, correlated negatively respectively.

Details

For each pair of variables, a Pearson's r value indicates the strength and direction of the relationship between those two variables. A positive value indicates a positive relationship (higher values of one variable predict higher values of the other variable). A negative Pearson's r indicates a negative relationship (higher values of one variable predict lower values of the other variable, and vice-versa). A value of zero indicates no relationship (whether a variable is high or low, does not tell us anything about the value of the other variable).

More formally, it is possible to test the null hypothesis that the correlation is zero and calculate a p-value. If the p-value is low, it suggests the correlation co-efficient is not zero, and there is a linear (or more complex) relationship between the two variables.

Value

A results object containing:

results$matrix	a correlation matrix table
results$plot	a correlation matrix plot

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$matrix$asDF

as.data.frame(results$matrix)
```

Examples

```
data('mtcars')

corrMatrix(mtcars, vars = vars(mpg, cyl, disp, hp))

#
#  CORRELATION MATRIX
#
#  Correlation Matrix
#  ------------------------------------------------------------
#                            mpg      cyl       disp      hp
#  ------------------------------------------------------------
#    mpg     Pearson's r        —    -0.852    -0.848    -0.776
#            p-value            —    < .001    < .001    < .001
#
#    cyl     Pearson's r             —     0.902     0.832
#            p-value                 —    < .001    < .001
#
#    disp    Pearson's r                   —     0.791
#            p-value                       —    < .001
#
#    hp      Pearson's r                           —
#            p-value                               —
#  ------------------------------------------------------------
#
```

`corrPart` *Partial Correlation*

Description

Partial correlation matrices are a way to examine linear relationships between two or more continuous variables while controlling for other variables

Usage

```
corrPart(data, vars, controls, pearson = TRUE, spearman = FALSE,
  kendall = FALSE, type = "part", sig = TRUE, flag = FALSE,
  n = FALSE, hypothesis = "corr")
```

Arguments

`data`	the data as a data frame
`vars`	a vector of strings naming the variables to correlate in `data`
`controls`	a vector of strings naming the control variables in `data`
`pearson`	`TRUE` (default) or `FALSE`, provide Pearson's R
`spearman`	`TRUE` or `FALSE` (default), provide Spearman's rho

kendall	TRUE or FALSE (default), provide Kendall's tau-b
type	one of 'part' (default) or 'semi' specifying the type of partial correlation to calculate; partial or semipartial correlation.
sig	TRUE (default) or FALSE, provide significance levels
flag	TRUE or FALSE (default), flag significant correlations
n	TRUE or FALSE (default), provide the number of cases
hypothesis	one of 'corr' (default), 'pos', 'neg' specifying the alernative hypothesis; correlated, correlated positively, correlated negatively respectively.

Details

For each pair of variables, a Pearson's r value indicates the strength and direction of the relationship between those two variables. A positive value indicates a positive relationship (higher values of one variable predict higher values of the other variable). A negative Pearson's r indicates a negative relationship (higher values of one variable predict lower values of the other variable, and vice-versa). A value of zero indicates no relationship (whether a variable is high or low, does not tell us anything about the value of the other variable).

More formally, it is possible to test the null hypothesis that the correlation is zero and calculate a p-value. If the p-value is low, it suggests the correlation co-efficient is not zero, and there is a linear (or more complex) relationship between the two variables.

Value

A results object containing:

results$matrix	a (semi)partial correlation matrix table

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$matrix$asDF

as.data.frame(results$matrix)
```

Examples

```
data('mtcars')

corrPart(mtcars, vars = vars(mpg, cyl, disp), controls = vars(hp))

#
#  PARTIAL CORRELATION
#
#  Partial Correlation
#  ---------------------------------------------------
#                           mpg       cyl       disp
#  ---------------------------------------------------
#    mpg     Pearson's r         —
#            p-value             —
#
```

```
#    cyl     Pearson's r    -0.590         —
#            p-value        < .001         —
#
#    disp    Pearson's r    -0.606     0.719        —
#            p-value        < .001    < .001        —
#  ---------------------------------------------------
#    Note. controlling for 'hp'
#
```

---

descriptives *Descriptives*

Description

Descriptives are an assortment of summarising statistics, and visualizations which allow exploring the shape and distribution of data. It is good practice to explore your data with descriptives before proceeding to more formal tests.

Usage

```
descriptives(data, vars, splitBy = NULL, freq = FALSE,
  desc = "columns", hist = FALSE, dens = FALSE, bar = FALSE,
  barCounts = FALSE, box = FALSE, violin = FALSE, dot = FALSE,
  dotType = "jitter", boxMean = FALSE, boxLabelOutliers = TRUE,
  qq = FALSE, n = TRUE, missing = TRUE, mean = TRUE,
  median = TRUE, mode = FALSE, sum = FALSE, sd = TRUE,
  variance = FALSE, range = FALSE, min = TRUE, max = TRUE,
  se = FALSE, ci = FALSE, ciWidth = 95, iqr = FALSE,
  skew = FALSE, kurt = FALSE, sw = FALSE, pcEqGr = FALSE,
  pcNEqGr = 4, pc = FALSE, pcValues = "25,50,75", extreme = FALSE,
  extremeN = 5, formula)
```

Arguments

data	the data as a data frame
vars	a vector of strings naming the variables of interest in data
splitBy	a vector of strings naming the variables used to split vars
freq	TRUE or FALSE (default), provide frequency tables (nominal, ordinal variables only)
desc	'rows' or 'columns' (default), display the variables across the rows or across the columns (default)
hist	TRUE or FALSE (default), provide histograms (continuous variables only)
dens	TRUE or FALSE (default), provide density plots (continuous variables only)
bar	TRUE or FALSE (default), provide bar plots (nominal, ordinal variables only)

barCounts	TRUE or FALSE (default), add counts to the bar plots
box	TRUE or FALSE (default), provide box plots (continuous variables only)
violin	TRUE or FALSE (default), provide violin plots (continuous variables only)
dot	TRUE or FALSE (default), provide dot plots (continuous variables only)
dotType	.
boxMean	TRUE or FALSE (default), add mean to box plot
boxLabelOutliers	TRUE (default) or FALSE, add labels with the row number to the outliers in the box plot
qq	TRUE or FALSE (default), provide Q-Q plots (continuous variables only)
n	TRUE (default) or FALSE, provide the sample size
missing	TRUE (default) or FALSE, provide the number of missing values
mean	TRUE (default) or FALSE, provide the mean
median	TRUE (default) or FALSE, provide the median
mode	TRUE or FALSE (default), provide the mode
sum	TRUE or FALSE (default), provide the sum
sd	TRUE (default) or FALSE, provide the standard deviation
variance	TRUE or FALSE (default), provide the variance
range	TRUE or FALSE (default), provide the range
min	TRUE or FALSE (default), provide the minimum
max	TRUE or FALSE (default), provide the maximum
se	TRUE or FALSE (default), provide the standard error
ci	TRUE or FALSE (default), provide confidence intervals for the mean
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
iqr	TRUE or FALSE (default), provide the interquartile range
skew	TRUE or FALSE (default), provide the skewness
kurt	TRUE or FALSE (default), provide the kurtosis
sw	TRUE or FALSE (default), provide Shapiro-Wilk p-value
pcEqGr	TRUE or FALSE (default), provide quantiles
pcNEqGr	an integer (default: 4) specifying the number of equal groups
pc	TRUE or FALSE (default), provide percentiles
pcValues	a comma-sepated list (default: 25,50,75) specifying the percentiles
extreme	TRUE or FALSE (default), provide N most extreme (highest and lowest) values
extremeN	an integer (default: 5) specifying the number of extreme values
formula	(optional) the formula to use, see the examples

Value

A results object containing:

`results$descriptives`	a table of the descriptive statistics
`results$descriptivesT`	a table of the descriptive statistics
`results$frequencies`	an array of frequency tables
`results$extremeValues`	an array of extreme values tables
`results$plots`	an array of descriptive plots

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$descriptives$asDF
```

```
as.data.frame(results$descriptives)
```

Examples

```
data('mtcars')
dat <- mtcars

# frequency tables can be provided for factors
dat$gear <- as.factor(dat$gear)

descriptives(dat, vars = vars(mpg, cyl, disp, gear), freq = TRUE)

#
#  DESCRIPTIVES
#
#  Descriptives
#  ---------------------------------------------
#                mpg     cyl     disp    gear
#  ---------------------------------------------
#    N            32      32      32      32
#    Missing       0       0       0       0
#    Mean       20.1    6.19     231    3.69
#    Median     19.2    6.00     196    4.00
#    Minimum    10.4    4.00    71.1       3
#    Maximum    33.9    8.00     472       5
#  ---------------------------------------------
#
#
#  FREQUENCIES
#
#  Frequencies of gear
#  --------------------
#    Levels    Counts
#  --------------------
#    3             15
#    4             12
#    5              5
#  --------------------
```

```
#

# spliting by a variable
descriptives(formula = disp + mpg ~ cyl, dat,
    median=FALSE, min=FALSE, max=FALSE, n=FALSE,
    missing=FALSE)

# providing histograms
descriptives(formula = mpg ~ cyl, dat, hist=TRUE,
    median=FALSE, min=FALSE, max=FALSE, n=FALSE,
    missing=FALSE)

# splitting by multiple variables
descriptives(formula = mpg ~ cyl:gear, dat,
    median=FALSE, min=FALSE, max=FALSE,
    missing=FALSE)
```

`efa` *Exploratory Factor Analysis*

Description

Exploratory Factor Analysis

Usage

```
efa(data, vars, nFactorMethod = "parallel", nFactors = 1,
  minEigen = 0, extraction = "minres", rotation = "oblimin",
  hideLoadings = 0.3, sortLoadings = FALSE, screePlot = FALSE,
  eigen = FALSE, factorCor = FALSE, factorSummary = FALSE,
  modelFit = FALSE, kmo = FALSE, bartlett = FALSE,
  factorScoreMethod = "Thurstone")
```

Arguments

`data`	the data as a data frame
`vars`	a vector of strings naming the variables of interest in `data`
`nFactorMethod`	`'parallel'` (default), `'eigen'` or `'fixed'`, the way to determine the number of factors
`nFactors`	an integer (default: 1), the number of factors in the model
`minEigen`	a number (default: 0), the minimal eigenvalue for a factor to be included in the model
`extraction`	`'minres'` (default), `'ml'`, or `'pa'` use respectively 'minimum residual', 'maximum likelihood', or 'prinicipal axis' as the factor extraction method
`rotation`	`'none'`, `'varimax'`, `'quartimax'`, `'promax'`, `'oblimin'` (default), or `'simplimax'`, the rotation to use in estimation

hideLoadings	a number (default: 0.3), hide factor loadings below this value
sortLoadings	TRUE or FALSE (default), sort the factor loadings by size
screePlot	TRUE or FALSE (default), show scree plot
eigen	TRUE or FALSE (default), show eigenvalue table
factorCor	TRUE or FALSE (default), show inter-factor correlations
factorSummary	TRUE or FALSE (default), show factor summary
modelFit	TRUE or FALSE (default), show model fit measures and test
kmo	TRUE or FALSE (default), show Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (MSA) results
bartlett	TRUE or FALSE (default), show Bartlett's test of sphericity results
factorScoreMethod	'Thurstone' (default), 'Bartlett', 'tenBerge', 'Anderson', or 'Harman' use respectively 'Thurstone', 'Bartlett', 'ten Berge', 'Anderson & Rubin', or 'Harman' method for estimating factor scores

Value

A results object containing:

results$text	a preformatted

Examples

```
data('iris')

efa(iris, vars = vars(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width))

#
#  EXPLORATORY FACTOR ANALYSIS
#
#  Factor Loadings
#  ------------------------------------------------
#                    1        2        Uniqueness
#  ------------------------------------------------
#    Sepal.Length    0.993                0.10181
#    Sepal.Width              0.725       0.42199
#    Petal.Length    0.933                0.00483
#    Petal.Width     0.897                0.07088
#  ------------------------------------------------
#    Note. 'oblimin' rotation was used
#
```

iris *iris*

Description

iris

linReg *Linear Regression*

Description

Linear regression is used to explore the relationship between a continuous dependent variable, and one or more continuous and/or categorical explanatory variables. Other statistical methods, such as ANOVA and ANCOVA, are in reality just forms of linear regression.

Usage

```
linReg(data, dep, covs = NULL, factors = NULL, weights = NULL,
  blocks = list(list()), refLevels = NULL, intercept = "refLevel",
  r = TRUE, r2 = TRUE, r2Adj = FALSE, aic = FALSE, bic = FALSE,
  rmse = FALSE, modelTest = FALSE, anova = FALSE, ci = FALSE,
  ciWidth = 95, stdEst = FALSE, ciStdEst = FALSE,
  ciWidthStdEst = 95, norm = FALSE, qqPlot = FALSE,
  resPlots = FALSE, durbin = FALSE, collin = FALSE, cooks = FALSE,
  mahal = FALSE, mahalp = "0.001", emMeans = list(list()),
  ciEmm = TRUE, ciWidthEmm = 95, emmPlots = TRUE,
  emmTables = FALSE, emmWeights = TRUE)
```

Arguments

data	the data as a data frame
dep	the dependent variable from data, variable must be numeric
covs	the covariates from data
factors	the fixed factors from data
weights	the (optional) weights from data to be used in the fitting process
blocks	a list containing vectors of strings that name the predictors that are added to the model. The elements are added to the model according to their order in the list
refLevels	a list of lists specifying reference levels of the dependent variable and all the factors
intercept	'refLevel' (default) or 'grandMean', coding of the intercept. Either creates contrast so that the intercept represents the reference level or the grand mean
r	TRUE (default) or FALSE, provide the statistical measure R for the models

r2	TRUE (default) or FALSE, provide the statistical measure R-squared for the models
r2Adj	TRUE or FALSE (default), provide the statistical measure adjusted R-squared for the models
aic	TRUE or FALSE (default), provide Aikaike's Information Criterion (AIC) for the models
bic	TRUE or FALSE (default), provide Bayesian Information Criterion (BIC) for the models
rmse	TRUE or FALSE (default), provide RMSE for the models
modelTest	TRUE (default) or FALSE, provide the model comparison between the models and the NULL model
anova	TRUE or FALSE (default), provide the omnibus ANOVA test for the predictors
ci	TRUE or FALSE (default), provide a confidence interval for the model coefficients
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
stdEst	TRUE or FALSE (default), provide a standardized estimate for the model coefficients
ciStdEst	TRUE or FALSE (default), provide a confidence interval for the model coefficient standardized estimates
ciWidthStdEst	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
norm	TRUE or FALSE (default), perform a Shapiro-Wilk test on the residuals
qqPlot	TRUE or FALSE (default), provide a Q-Q plot of residuals
resPlots	TRUE or FALSE (default), provide residual plots where the dependent variable and each covariate is plotted against the standardized residuals.
durbin	TRUE or FALSE (default), provide results of the Durbin- Watson test for autocorrelation
collin	TRUE or FALSE (default), provide VIF and tolerence collinearity statistics
cooks	TRUE or FALSE (default), provide summary statistics for the Cook's distance
mahal	TRUE or FALSE (default), provide a summary table reporting (significant) Mahalanobis distances
mahalp	'0.05', '0.01' or '0.001' (default), p-threshold to be used for selecting entries in the summary table that reports Mahalanobis distances that are significant at that p-threshold
emMeans	a formula containing the terms to estimate marginal means for, supports up to three variables per term
ciEmm	TRUE (default) or FALSE, provide a confidence interval for the estimated marginal means
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency

Value

A results object containing:

`results$modelFit`	a table
`results$modelComp`	a table
`results$models`	an array of model specific results
`results$predictOV`	an output
`results$residsOV`	an output
`results$cooksOV`	an output
`results$mahalOV`	an output

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$modelFit$asDF
as.data.frame(results$modelFit)
```

Examples

```
data('Prestige', package='carData')

linReg(data = Prestige, dep = income,
       covs = vars(education, prestige, women),
       blocks = list(list('education', 'prestige', 'women')))

#
#  LINEAR REGRESSION
#
#  Model Fit Measures
#  ---------------------------
#    Model    R        R²
#  ---------------------------
#        1    0.802    0.643
#  ---------------------------
#
#
#  MODEL SPECIFIC RESULTS
#
#  MODEL 1
#
#
#  Model Coefficients
#  -----------------------------------------------------------
#    Predictor    Estimate    SE         t         p
#  -----------------------------------------------------------
#    Intercept      -253.8    1086.16    -0.234     0.816
#    women           -50.9       8.56    -5.948    < .001
#    prestige        141.4      29.91     4.729    < .001
#    education       177.2     187.63     0.944     0.347
#  -----------------------------------------------------------
#
```

logLinear *Log-Linear Regression*

Description

Log-Linear Regression

Usage

```
logLinear(data, factors = NULL, counts = NULL, blocks = list(list()),
  refLevels = NULL, modelTest = FALSE, dev = TRUE, aic = TRUE,
  bic = FALSE, pseudoR2 = list("r2mf"), omni = FALSE, ci = FALSE,
  ciWidth = 95, RR = FALSE, ciRR = FALSE, ciWidthRR = 95,
  emMeans = list(list()), ciEmm = TRUE, ciWidthEmm = 95,
  emmPlots = TRUE, emmTables = FALSE, emmWeights = TRUE)
```

Arguments

data	the data as a data frame
factors	a vector of strings naming the factors from data
counts	a string naming a variable in data containing counts, or NULL if each row represents a single observation
blocks	a list containing vectors of strings that name the predictors that are added to the model. The elements are added to the model according to their order in the list
refLevels	a list of lists specifying reference levels of the dependent variable and all the factors
modelTest	TRUE or FALSE (default), provide the model comparison between the models and the NULL model
dev	TRUE (default) or FALSE, provide the deviance (or -2LogLikelihood) for the models
aic	TRUE (default) or FALSE, provide Aikaike's Information Criterion (AIC) for the models
bic	TRUE or FALSE (default), provide Bayesian Information Criterion (BIC) for the models
pseudoR2	one or more of 'r2mf', 'r2cs', or 'r2n'; use McFadden's, Cox & Snell, and Nagelkerke pseudo-R^2, respectively
omni	TRUE or FALSE (default), provide the omnibus likelihood ratio tests for the predictors
ci	TRUE or FALSE (default), provide a confidence interval for the model coefficient estimates
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width

RR	TRUE or FALSE (default), provide the exponential of the log-rate ratio estimate, or the rate ratio estimate
ciRR	TRUE or FALSE (default), provide a confidence interval for the model coefficient rate ratio estimates
ciWidthRR	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
emMeans	a list of lists specifying the variables for which the estimated marginal means need to be calculate. Supports up to three variables per term.
ciEmm	TRUE (default) or FALSE, provide a confidence interval for the estimated marginal means
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency

Value

A results object containing:

results$modelFit	a table
results$modelComp	a table
results$models	an array of model specific results

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$modelFit$asDF
```

```
as.data.frame(results$modelFit)
```

Examples

```
data('mtcars')

tab <- table('gear'=mtcars$gear, 'cyl'=mtcars$cyl)
dat <- as.data.frame(tab)

logLinear(data = dat, factors = vars(gear, cyl),  counts = Freq,
          blocks = list(list("gear", "cyl", c("gear", "cyl"))),
          refLevels = list(
              list(var="gear", ref="3"),
              list(var="cyl", ref="4")))

#
#  LOG-LINEAR REGRESSION
#
#  Model Fit Measures
```

```
#  ---------------------------------------
#    Model    Deviance    AIC     R²-McF
#  ---------------------------------------
#        1    4.12e-10    41.4     1.000
#  ---------------------------------------
#
#
#  MODEL SPECIFIC RESULTS
#
#  MODEL 1
#
#  Model Coefficients
#  ---------------------------------------------------------------------
#    Predictor          Estimate     SE          Z            p
#  ---------------------------------------------------------------------
#    Intercept          -4.71e-16        1.00    -4.71e-16    1.000
#    gear:
#    4 - 3                  2.079        1.06        1.961    0.050
#    5 - 3                  0.693        1.22        0.566    0.571
#    cyl:
#    6 - 4                  0.693        1.22        0.566    0.571
#    8 - 4                  2.485        1.04        2.387    0.017
#    gear:cyl:
#    (4 - 3):(6 - 4)       -1.386        1.37       -1.012    0.311
#    (5 - 3):(6 - 4)       -1.386        1.73       -0.800    0.423
#    (4 - 3):(8 - 4)      -26.867    42247.17    -6.36e -4    0.999
#    (5 - 3):(8 - 4)       -2.485        1.44       -1.722    0.085
#  ---------------------------------------------------------------------
#
#
```

`logRegBin` *Binomial Logistic Regression*

Description

Binomial Logistic Regression

Usage

```
logRegBin(data, dep, covs = NULL, factors = NULL,
  blocks = list(list()), refLevels = NULL, modelTest = FALSE,
  dev = TRUE, aic = TRUE, bic = FALSE, pseudoR2 = list("r2mf"),
  omni = FALSE, ci = FALSE, ciWidth = 95, OR = FALSE,
  ciOR = FALSE, ciWidthOR = 95, emMeans = list(list()),
  ciEmm = TRUE, ciWidthEmm = 95, emmPlots = TRUE,
  emmTables = FALSE, emmWeights = TRUE, class = FALSE, acc = FALSE,
  spec = FALSE, sens = FALSE, auc = FALSE, rocPlot = FALSE,
  cutOff = 0.5, cutOffPlot = FALSE, collin = FALSE,
  boxTidwell = FALSE, cooks = FALSE)
```

Arguments

data	the data as a data frame
dep	a string naming the dependent variable from data, variable must be a factor
covs	a vector of strings naming the covariates from data
factors	a vector of strings naming the fixed factors from data
blocks	a list containing vectors of strings that name the predictors that are added to the model. The elements are added to the model according to their order in the list
refLevels	a list of lists specifying reference levels of the dependent variable and all the factors
modelTest	TRUE or FALSE (default), provide the model comparison between the models and the NULL model
dev	TRUE (default) or FALSE, provide the deviance (or -2LogLikelihood) for the models
aic	TRUE (default) or FALSE, provide Aikaike's Information Criterion (AIC) for the models
bic	TRUE or FALSE (default), provide Bayesian Information Criterion (BIC) for the models
pseudoR2	one or more of 'r2mf', 'r2cs', or 'r2n'; use McFadden's, Cox & Snell, and Nagelkerke pseudo-R^2, respectively
omni	TRUE or FALSE (default), provide the omnibus likelihood ratio tests for the predictors
ci	TRUE or FALSE (default), provide a confidence interval for the model coefficient estimates
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
OR	TRUE or FALSE (default), provide the exponential of the log-odds ratio estimate, or the odds ratio estimate
ciOR	TRUE or FALSE (default), provide a confidence interval for the model coefficient odds ratio estimates
ciWidthOR	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
emMeans	a list of lists specifying the variables for which the estimated marginal means need to be calculate. Supports up to three variables per term.
ciEmm	TRUE (default) or FALSE, provide a confidence interval for the estimated marginal means
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency

class	TRUE or FALSE (default), provide a predicted classification table (or confusion matrix)
acc	TRUE or FALSE (default), provide the predicted accuracy of outcomes grouped by the cut-off value
spec	TRUE or FALSE (default), provide the predicted specificity of outcomes grouped by the cut-off value
sens	TRUE or FALSE (default), provide the predicted sensitivity of outcomes grouped by the cut-off value
auc	TRUE or FALSE (default), provide the area under the ROC curve (AUC)
rocPlot	TRUE or FALSE (default), provide a ROC curve plot
cutOff	TRUE or FALSE (default), set a cut-off used for the predictions
cutOffPlot	TRUE or FALSE (default), provide a cut-off plot
collin	TRUE or FALSE (default), provide VIF and tolerence collinearity statistics
boxTidwell	TRUE or FALSE (default), provide Box-Tidwell test for linearity of the logit
cooks	TRUE or FALSE (default), provide summary statistics for the Cook's distance

Value

A results object containing:

results$modelFit	a table
results$modelComp	a table
results$models	an array of model specific results
results$predictOV	an output
results$residsOV	an output
results$cooksOV	an output

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$modelFit$asDF
```

```
as.data.frame(results$modelFit)
```

Examples

```
data('birthwt', package='MASS')

dat <- data.frame(
            low = factor(birthwt$low),
            age = birthwt$age,
            bwt = birthwt$bwt)

logRegBin(data = dat, dep = low,
          covs = vars(age, bwt),
          blocks = list(list("age", "bwt")),
          refLevels = list(list(var="low", ref="0")))
```

```
#
#  BINOMIAL LOGISTIC REGRESSION
#
#  Model Fit Measures
#  ---------------------------------------
#    Model    Deviance    AIC     R²-McF
#  ---------------------------------------
#        1     4.97e-7    6.00     1.000
#  ---------------------------------------
#
#
#  MODEL SPECIFIC RESULTS
#
#  MODEL 1
#
#  Model Coefficients
#  ------------------------------------------------------------
#    Predictor    Estimate      SE          Z           p
#  ------------------------------------------------------------
#    Intercept    2974.73225    218237.2      0.0136    0.989
#    age            -0.00653       482.7    -1.35e-5    1.000
#    bwt            -1.18532        87.0     -0.0136    0.989
#  ------------------------------------------------------------
#    Note. Estimates represent the log odds of "low = 1"
#    vs. "low = 0"
#
#
```

---

logRegMulti *Multinomial Logistic Regression*

Description

Multinomial Logistic Regression

Usage

```
logRegMulti(data, dep, covs = NULL, factors = NULL,
  blocks = list(list()), refLevels = NULL, modelTest = FALSE,
  dev = TRUE, aic = TRUE, bic = FALSE, pseudoR2 = list("r2mf"),
  omni = FALSE, ci = FALSE, ciWidth = 95, OR = FALSE,
  ciOR = FALSE, ciWidthOR = 95, emMeans = list(list()),
  ciEmm = TRUE, ciWidthEmm = 95, emmPlots = TRUE,
  emmTables = FALSE, emmWeights = TRUE)
```

Arguments

data	the data as a data frame

dep	a string naming the dependent variable from data, variable must be a factor
covs	a vector of strings naming the covariates from data
factors	a vector of strings naming the fixed factors from data
blocks	a list containing vectors of strings that name the predictors that are added to the model. The elements are added to the model according to their order in the list
refLevels	a list of lists specifying reference levels of the dependent variable and all the factors
modelTest	TRUE or FALSE (default), provide the model comparison between the models and the NULL model
dev	TRUE (default) or FALSE, provide the deviance (or -2LogLikelihood) for the models
aic	TRUE (default) or FALSE, provide Aikaike's Information Criterion (AIC) for the models
bic	TRUE or FALSE (default), provide Bayesian Information Criterion (BIC) for the models
pseudoR2	one or more of 'r2mf', 'r2cs', or 'r2n'; use McFadden's, Cox & Snell, and Nagelkerke pseudo-R^2, respectively
omni	TRUE or FALSE (default), provide the omnibus likelihood ratio tests for the predictors
ci	TRUE or FALSE (default), provide a confidence interval for the model coefficient estimates
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
OR	TRUE or FALSE (default), provide the exponential of the log-odds ratio estimate, or the odds ratio estimate
ciOR	TRUE or FALSE (default), provide a confidence interval for the model coefficient odds ratio estimates
ciWidthOR	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
emMeans	a list of lists specifying the variables for which the estimated marginal means need to be calculate. Supports up to three variables per term.
ciEmm	TRUE (default) or FALSE, provide a confidence interval for the estimated marginal means
ciWidthEmm	a number between 50 and 99.9 (default: 95) specifying the confidence interval width for the estimated marginal means
emmPlots	TRUE (default) or FALSE, provide estimated marginal means plots
emmTables	TRUE or FALSE (default), provide estimated marginal means tables
emmWeights	TRUE (default) or FALSE, weigh each cell equally or weigh them according to the cell frequency

Value

A results object containing:

`results$modelFit`	a table
`results$modelComp`	a table
`results$models`	an array of model specific results

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$modelFit$asDF
```

```
as.data.frame(results$modelFit)
```

Examples

```
data('birthwt', package='MASS')

dat <- data.frame(
            race = factor(birthwt$race),
            age = birthwt$age,
            low = factor(birthwt$low))

logRegMulti(data = dat, dep = race,
            covs = age, factors = low,
            blocks = list(list("age", "low")),
            refLevels = list(
                list(var="race", ref="1"),
                list(var="low", ref="0")))

#
#  MULTINOMIAL LOGISTIC REGRESSION
#
#  Model Fit Measures
#  -------------------------------------
#    Model    Deviance    AIC    R²-McF
#  -------------------------------------
#        1         360    372    0.0333
#  -------------------------------------
#
#
#  MODEL SPECIFIC RESULTS
#
#  MODEL 1
#
#  Model Coefficients
#  ---------------------------------------------------------------------
#    race     Predictor    Estimate    SE        Z         p
#  ---------------------------------------------------------------------
#    2 - 1    Intercept      0.8155    1.1186     0.729    0.466
#             age           -0.1038    0.0487    -2.131    0.033
#             low:
```

```
#             1 - 0          0.7527    0.4700     1.601    0.109
#    3 - 1    Intercept      1.0123    0.7798     1.298    0.194
#             age           -0.0663    0.0324    -2.047    0.041
#             low:
#             1 - 0          0.5677    0.3522     1.612    0.107
#  ------------------------------------------------------------
#
#
```

---

logRegOrd *Ordinal Logistic Regression*

Description

Ordinal Logistic Regression

Usage

```
logRegOrd(data, dep, covs = NULL, factors = NULL,
  blocks = list(list()), refLevels = NULL, modelTest = FALSE,
  dev = TRUE, aic = TRUE, bic = FALSE, pseudoR2 = list("r2mf"),
  omni = FALSE, thres = FALSE, ci = FALSE, ciWidth = 95,
  OR = FALSE, ciOR = FALSE, ciWidthOR = 95)
```

Arguments

data	the data as a data frame
dep	a string naming the dependent variable from data, variable must be a factor
covs	a vector of strings naming the covariates from data
factors	a vector of strings naming the fixed factors from data
blocks	a list containing vectors of strings that name the predictors that are added to the model. The elements are added to the model according to their order in the list
refLevels	a list of lists specifying reference levels of the dependent variable and all the factors
modelTest	TRUE or FALSE (default), provide the model comparison between the models and the NULL model
dev	TRUE (default) or FALSE, provide the deviance (or -2LogLikelihood) for the models
aic	TRUE (default) or FALSE, provide Aikaike's Information Criterion (AIC) for the models
bic	TRUE or FALSE (default), provide Bayesian Information Criterion (BIC) for the models
pseudoR2	one or more of 'r2mf', 'r2cs', or 'r2n'; use McFadden's, Cox & Snell, and Nagelkerke pseudo-R^2, respectively

omni	TRUE or FALSE (default), provide the omnibus likelihood ratio tests for the predictors
thres	TRUE or FALSE (default), provide the thresholds that are used as cut-off scores for the levels of the dependent variable
ci	TRUE or FALSE (default), provide a confidence interval for the model coefficient estimates
ciWidth	a number between 50 and 99.9 (default: 95) specifying the confidence interval width
OR	TRUE or FALSE (default), provide the exponential of the log-odds ratio estimate, or the odds ratio estimate
ciOR	TRUE or FALSE (default), provide a confidence interval for the model coefficient odds ratio estimates
ciWidthOR	a number between 50 and 99.9 (default: 95) specifying the confidence interval width

Value

A results object containing:

results$modelFit	a table
results$modelComp	a table
results$models	an array of model specific results

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$modelFit$asDF
```

```
as.data.frame(results$modelFit)
```

Examples

```
set.seed(1337)

y <- factor(sample(1:3, 100, replace = TRUE))
x1 <- rnorm(100)
x2 <- rnorm(100)

df <- data.frame(y=y, x1=x1, x2=x2)

logRegOrd(data = df, dep = y,
          covs = vars(x1, x2),
          blocks = list(list("x1", "x2")))

#
#  ORDINAL LOGISTIC REGRESSION
#
#  Model Fit Measures
#  ---------------------------------------
#    Model    Deviance    AIC    R²-McF
```

```
#  ---------------------------------------
#        1         218    226    5.68e-4
#  ---------------------------------------
#
#
#  MODEL SPECIFIC RESULTS
#
#  MODEL 1
#
#  Model Coefficients
#  ---------------------------------------------------
#    Predictor    Estimate    SE       Z        p
#  ---------------------------------------------------
#    x1             0.0579    0.193    0.300    0.764
#    x2             0.0330    0.172    0.192    0.848
#  ---------------------------------------------------
#
#
```

---

mancova *MANCOVA*

Description

Multivariate Analysis of (Co)Variance (MANCOVA) is used to explore the relationship between multiple dependent variables, and one or more categorical and/or continuous explanatory variables.

Usage

```
mancova(data, deps, factors = NULL, covs = NULL,
  multivar = list("pillai", "wilks", "hotel", "roy"), boxM = FALSE,
  shapiro = FALSE, qqPlot = FALSE)
```

Arguments

data	the data as a data frame
deps	a string naming the dependent variable from data, variable must be numeric
factors	a vector of strings naming the factors from data
covs	a vector of strings naming the covariates from data
multivar	one or more of 'pillai', 'wilks', 'hotel', or 'roy'; use Pillai's Trace, Wilks' Lambda, Hotelling's Trace, and Roy's Largest Root multivariate statistics, respectively
boxM	TRUE or FALSE (default), provide Box's M test
shapiro	TRUE or FALSE (default), provide Shapiro-Wilk test
qqPlot	TRUE or FALSE (default), provide a Q-Q plot of multivariate normality

Value

A results object containing:

results$multivar	a table
results$univar	a table
results$assump$boxM	a table
results$assump$shapiro	a table
results$assump$qqPlot	an image

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$multivar$asDF
as.data.frame(results$multivar)
```

Examples

```
data('iris')

mancova(data = iris,
    deps = vars(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width),
    factors = Species)

#
#  MANCOVA
#
#  Multivariate Tests
#  ---------------------------------------------------------------------------
#                                   value     F       df1    df2    p
#  ---------------------------------------------------------------------------
#    Species    Pillai's Trace          1.19    53.5      8    290    < .001
#               Wilks' Lambda         0.0234     199      8    288    < .001
#               Hotelling's Trace       32.5     581      8    286    < .001
#               Roy's Largest Root      32.2    1167      4    145    < .001
#  ---------------------------------------------------------------------------
#
#
#  Univariate Tests
#  ------------------------------------------------------------------------------------------------
#                Dependent Variable    Sum of Squares    df     Mean Square    F         p
#  ------------------------------------------------------------------------------------------------
#    Species     Sepal.Length                63.21     2       31.6061     119.3    < .001
#               Sepal.Width                  11.34     2        5.6725      49.2    < .001
#               Petal.Length                437.10     2      218.5514    1180.2    < .001
#               Petal.Width                  80.41     2       40.2067     960.0    < .001
#    Residuals    Sepal.Length                    38.96    147         0.2650
#                 Sepal.Width                     16.96    147         0.1154
#                 Petal.Length                    27.22    147         0.1852
#                 Petal.Width                      6.16    147         0.0419
#  ------------------------------------------------------------------------------------------------
#
```

pca *Principal Component Analysis*

Description

Principal Component Analysis

Usage

```
pca(data, vars, nFactorMethod = "parallel", nFactors = 1,
  minEigen = 1, rotation = "varimax", hideLoadings = 0.3,
  sortLoadings = FALSE, screePlot = FALSE, eigen = FALSE,
  factorCor = FALSE, factorSummary = FALSE, kmo = FALSE,
  bartlett = FALSE)
```

Arguments

data	the data as a data frame
vars	a vector of strings naming the variables of interest in data
nFactorMethod	'parallel' (default), 'eigen' or 'fixed', the way to determine the number of factors
nFactors	an integer (default: 1), the number of components in the model
minEigen	a number (default: 1), the minimal eigenvalue for a component to be included in the model
rotation	'none', 'varimax' (default), 'quartimax', 'promax', 'oblimin', or 'simplimax', the rotation to use in estimation
hideLoadings	a number (default: 0.3), hide loadings below this value
sortLoadings	TRUE or FALSE (default), sort the factor loadings by size
screePlot	TRUE or FALSE (default), show scree plot
eigen	TRUE or FALSE (default), show eigenvalue table
factorCor	TRUE or FALSE (default), show inter-factor correlations
factorSummary	TRUE or FALSE (default), show factor summary
kmo	TRUE or FALSE (default), show Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (MSA) results
bartlett	TRUE or FALSE (default), show Bartlett's test of sphericity results

Value

A results object containing:

results$loadings	a table
results$factorStats$factorSummary	a table
results$factorStats$factorCor	a table

results$modelFit$fit	a table
results$assump$bartlett	a table
results$assump$kmo	a table
results$eigen$initEigen	a table
results$eigen$screePlot	an image
results$factorScoresOV	an output

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$loadings$asDF

as.data.frame(results$loadings)
```

Examples

```
data('iris')

pca(iris, vars = vars(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width))

#
#  PRINCIPAL COMPONENT ANALYSIS
#
#  Component Loadings
#  ----------------------------------------
#                     1         Uniqueness
#  ----------------------------------------
#    Sepal.Length     0.890        0.2076
#    Sepal.Width     -0.460        0.7883
#    Petal.Length     0.992        0.0168
#    Petal.Width      0.965        0.0688
#  ----------------------------------------
#    Note. 'varimax' rotation was used
#
```

---

propTest2 *Proportion Test (2 Outcomes)*

Description

The Binomial test is used to test the Null hypothesis that the proportion of observations match some expected value. If the p-value is low, this suggests that the Null hypothesis is false, and that the true proportion must be some other value.

Usage

```
propTest2(data, vars, areCounts = FALSE, testValue = 0.5,
  hypothesis = "notequal", ci = FALSE, ciWidth = 95, bf = FALSE,
  priorA = 1, priorB = 1, ciBayes = FALSE, ciBayesWidth = 95,
  postPlots = FALSE)
```

Arguments

`data`	the data as a data frame
`vars`	a vector of strings naming the variables of interest in `data`
`areCounts`	`TRUE` or `FALSE` (default), the variables are counts
`testValue`	a number (default: 0.5), the value for the null hypothesis
`hypothesis`	`'notequal'` (default), `'greater'` or `'less'`, the alternative hypothesis
`ci`	`TRUE` or `FALSE` (default), provide confidence intervals
`ciWidth`	a number between 50 and 99.9 (default: 95), the confidence interval width
`bf`	`TRUE` or `FALSE` (default), provide Bayes factors
`priorA`	a number (default: 1), the beta prior 'a' parameter
`priorB`	a number (default: 1), the beta prior 'b' parameter
`ciBayes`	`TRUE` or `FALSE` (default), provide Bayesian credible intervals
`ciBayesWidth`	a number between 50 and 99.9 (default: 95), the credible interval width
`postPlots`	`TRUE` or `FALSE` (default), provide posterior plots

Value

A results object containing:

`results$table`	a table of the proportions and test results
`results$postPlots`	an array of the posterior plots

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

```
results$table$asDF
as.data.frame(results$table)
```

Examples

```
dat <- data.frame(x=c(8, 15))

propTest2(dat, vars = x, areCounts = TRUE)

#
#  PROPORTION TEST (2 OUTCOMES)
#
#  Binomial Test
#  ---------------------------------------------------------
#         Level    Count    Total    Proportion    p
#  ---------------------------------------------------------
#    x    1            8       23         0.348    0.210
#         2           15       23         0.652    0.210
#  ---------------------------------------------------------
#    Note. Ha is proportion != 0.5
#
```

propTestN *Proportion Test (N Outcomes)*

Description

The X² Goodness of fit test (not to be confused with the X² test of independence), tests the Null hypothesis that the proportions of observations match some expected proportions. If the p-value is low, this suggests that the Null hypothesis is false, and that the true proportions are different to those tested.

Usage

```
propTestN(data, var, counts = NULL, expected = FALSE, ratio = NULL,
  formula)
```

Arguments

data	the data as a data frame
var	the variable of interest in data (not necessary when using a formula, see the examples)
counts	the counts in data
expected	TRUE or FALSE (default), whether expected counts should be displayed
ratio	a vector of numbers: the expected proportions
formula	(optional) the formula to use, see the examples

Value

A results object containing:

results$props	a table of the proportions
results$tests	a table of the test results

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$props$asDF
```

```
as.data.frame(results$props)
```

Examples

```
data('HairEyeColor')
dat <- as.data.frame(HairEyeColor)

propTestN(formula = Freq ~ Eye, data = dat, ratio = c(1,1,1,1))

#
```

```
#  PROPORTION TEST (N OUTCOMES)
#
#  Proportions
#  --------------------------------
#    Level    Count    Proportion
#  --------------------------------
#    Brown      220         0.372
#    Blue       215         0.363
#    Hazel       93         0.157
#    Green       64         0.108
#  --------------------------------
#
#
#  X² Goodness of Fit
#  ----------------------
#    X²     df    p
#  ----------------------
#    133     3    < .001
#  ----------------------
#
```

`reliability` *Reliability Analysis*

Description

Reliability Analysis

Usage

```
reliability(data, vars, alphaScale = TRUE, omegaScale = FALSE,
  meanScale = FALSE, sdScale = FALSE, corPlot = FALSE,
  alphaItems = FALSE, omegaItems = FALSE, meanItems = FALSE,
  sdItems = FALSE, itemRestCor = FALSE, revItems = NULL)
```

Arguments

`data`	the data as a data frame
`vars`	a vector of strings naming the variables of interest in `data`
`alphaScale`	`TRUE` (default) or `FALSE`, provide Cronbach's alpha
`omegaScale`	`TRUE` or `FALSE` (default), provide McDonald's omega
`meanScale`	`TRUE` or `FALSE` (default), provide the mean
`sdScale`	`TRUE` or `FALSE` (default), provide the standard deviation
`corPlot`	`TRUE` or `FALSE` (default), provide a correlation plot
`alphaItems`	`TRUE` or `FALSE` (default), provide what the Cronbach's alpha would be if the item was dropped

omegaItems	TRUE or FALSE (default), provide what the McDonald's omega would be if the item was dropped
meanItems	TRUE or FALSE (default), provide item means
sdItems	TRUE or FALSE (default), provide item standard deviations
itemRestCor	TRUE or FALSE (default), provide item-rest correlations
revItems	a vector containing strings naming the varibales that are reverse scaled

Value

A results object containing:

results$scale	a table
results$items	a table
results$corPlot	an image
results$meanScoreOV	an output
results$sumScoreOV	an output

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$scale$asDF
```

```
as.data.frame(results$scale)
```

Examples

```
data('iris')

reliability(iris, vars = c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width'),
            omegaScale = TRUE)

#
#  RELIABILITY ANALYSIS
#
#  Scale Reliability Statistics
#  ----------------------------------------
#              Cronbach's alpha    McDonald's omega
#  ----------------------------------------
#    scale           0.708           0.848
#  ----------------------------------------
#
```

summarizeAnovaModel *Summarize an Anova object from a repeated measures model into a single table*

Description

Summarize an Anova object from a repeated measures model into a single table

Usage

```
summarizeAnovaModel(object, aov_table)
```

Arguments

object	An Anova object from a repeated measures model
aov_table	The ANOVA table from the model containing the generalized eta squared

Value

A data frame containing all the relevant ANOVA statistics

ToothGrowth *Tooth Growth*

Description

Tooth Growth

ttestIS *Independent Samples T-Test*

Description

The Student's Independent samples t-test (sometimes called a two-samples t-test) is used to test the null hypothesis that two groups have the same mean. A low p-value suggests that the null hypothesis is not true, and therefore the group means are different.

Usage

```
ttestIS(data, vars, group, students = TRUE, bf = FALSE,
  bfPrior = 0.707, welchs = FALSE, mann = FALSE,
  hypothesis = "different", norm = FALSE, qq = FALSE, eqv = FALSE,
  meanDiff = FALSE, ci = FALSE, ciWidth = 95, effectSize = FALSE,
  ciES = FALSE, ciWidthES = 95, desc = FALSE, plots = FALSE,
  miss = "perAnalysis", formula)
```

Arguments

data	the data as a data frame
vars	the dependent variables (not necessary when using a formula, see the examples)
group	the grouping variable with two levels (not necessary when using a formula, see the examples)
students	TRUE (default) or FALSE, perform Student's t-tests
bf	TRUE or FALSE (default), provide Bayes factors
bfPrior	a number between 0.01 and 2 (default 0.707), the prior width to use in calculating Bayes factors
welchs	TRUE or FALSE (default), perform Welch's t-tests
mann	TRUE or FALSE (default), perform Mann-Whitney U tests
hypothesis	'different' (default), 'oneGreater' or 'twoGreater', the alternative hypothesis; group 1 different to group 2, group 1 greater than group 2, and group 2 greater than group 1 respectively
norm	TRUE or FALSE (default), perform Shapiro-Wilk tests of normality
qq	TRUE or FALSE (default), provide Q-Q plots of residuals
eqv	TRUE or FALSE (default), perform Levene's tests for homogeneity of variances
meanDiff	TRUE or FALSE (default), provide means and standard errors
ci	TRUE or FALSE (default), provide confidence intervals
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
effectSize	TRUE or FALSE (default), provide effect sizes
ciES	TRUE or FALSE (default), provide confidence intervals for the effect-sizes
ciWidthES	a number between 50 and 99.9 (default: 95), the width of confidence intervals for the effect sizes
desc	TRUE or FALSE (default), provide descriptive statistics
plots	TRUE or FALSE (default), provide descriptive plots
miss	'perAnalysis' or 'listwise', how to handle missing values; 'perAnalysis' excludes missing values for individual dependent variables, 'listwise' excludes a row from all analyses if one of its entries is missing.
formula	(optional) the formula to use, see the examples

Details

The Student's independent t-test assumes that the data from each group are from a normal distribution, and that the variances of these groups are equal. If unwilling to assume the groups have equal variances, the Welch's t-test can be used in it's place. If one is additionally unwilling to assume the data from each group are from a normal distribution, the non-parametric Mann-Whitney U test can be used instead (However, note that the Mann-Whitney U test has a slightly different null hypothesis; that the distributions of each group is equal).

Value

A results object containing:

`results$ttest`	a table containing the t-test results
`results$assum$norm`	a table containing the normality tests
`results$assum$eqv`	a table containing the homogeneity of variances tests
`results$desc`	a table containing the group descriptives
`results$plots`	an array of groups of plots

Tables can be converted to data frames with `asDF` or `as.data.frame`. For example:

`results$ttest$asDF`

`as.data.frame(results$ttest)`

Examples

```
data('ToothGrowth')

ttestIS(formula = len ~ supp, data = ToothGrowth)

#
#  INDEPENDENT SAMPLES T-TEST
#
#  Independent Samples T-Test
#  ---------------------------------------------------
#                          statistic    df      p
#  ---------------------------------------------------
#    len    Student's t         1.92    58.0    0.060
#  ---------------------------------------------------
#
```

---

ttestOneS *One Sample T-Test*

Description

The Student's One-sample t-test is used to test the null hypothesis that the true mean is equal to a particular value (typically zero). A low p-value suggests that the null hypothesis is not true, and therefore the true mean must be different from the test value.

Usage

```
ttestOneS(data, vars, students = TRUE, bf = FALSE, bfPrior = 0.707,
  wilcoxon = FALSE, testValue = 0, hypothesis = "dt", norm = FALSE,
  qq = FALSE, meanDiff = FALSE, ci = FALSE, ciWidth = 95,
  effectSize = FALSE, ciES = FALSE, ciWidthES = 95, desc = FALSE,
  plots = FALSE, miss = "perAnalysis", mann = FALSE)
```

Arguments

data	the data as a data frame
vars	a vector of strings naming the variables of interest in data
students	TRUE (default) or FALSE, perform Student's t-tests
bf	TRUE or FALSE (default), provide Bayes factors
bfPrior	a number between 0.5 and 2.0 (default 0.707), the prior width to use in calculating Bayes factors
wilcoxon	TRUE or FALSE (default), perform Wilcoxon signed rank tests
testValue	a number specifying the value of the null hypothesis
hypothesis	'dt' (default), 'gt' or 'lt', the alternative hypothesis; different to testValue, greater than testValue, and less than testValue respectively
norm	TRUE or FALSE (default), perform Shapiro-wilk tests of normality
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
meanDiff	TRUE or FALSE (default), provide means and standard deviations
ci	TRUE or FALSE (default), provide confidence intervals for the mean difference
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
effectSize	TRUE or FALSE (default), provide Cohen's d effect sizes
ciES	TRUE or FALSE (default), provide confidence intervals for the effect-sizes
ciWidthES	a number between 50 and 99.9 (default: 95), the width of confidence intervals for the effect sizes
desc	TRUE or FALSE (default), provide descriptive statistics
plots	TRUE or FALSE (default), provide descriptive plots
miss	'perAnalysis' or 'listwise', how to handle missing values; 'perAnalysis' excludes missing values for individual dependent variables, 'listwise' excludes a row from all analyses if one of its entries is missing.
mann	deprecated

Details

The Student's One-sample t-test assumes that the data are from a normal distribution – in the case that one is unwilling to assume this, the non-parametric Wilcoxon signed-rank can be used in it's place (However, note that the Wilcoxon signed-rank has a slightly different null hypothesis; that the *median* is equal to the test value).

Value

A results object containing:

results$ttest	a table containing the t-test results
results$normality	a table containing the normality test results
results$descriptives	a table containing the descriptives
results$plots	an image of the descriptive plots

results$qq	an array of Q-Q plots

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$ttest$asDF

as.data.frame(results$ttest)
```

Examples

```
data('ToothGrowth')

ttestOneS(ToothGrowth, vars = vars(len, dose))

#
#  ONE SAMPLE T-TEST
#
#  One Sample T-Test
#  ---------------------------------------------------------
#                            statistic    df      p
#  ---------------------------------------------------------
#    len     Student's t         19.1    59.0    < .001
#    dose    Student's t         14.4    59.0    < .001
#  ---------------------------------------------------------
#
```

---

ttestPS *Paired Samples T-Test*

Description

The Student's paired samples t-test (sometimes called a dependent-samples t-test) is used to test the null hypothesis that the difference between pairs of measurements is equal to zero. A low p-value suggests that the null hypothesis is not true, and that the difference between the measurement pairs is not zero.

Usage

```
ttestPS(data, pairs, students = TRUE, bf = FALSE, bfPrior = 0.707,
  wilcoxon = FALSE, hypothesis = "different", norm = FALSE,
  qq = FALSE, meanDiff = FALSE, ci = FALSE, ciWidth = 95,
  effectSize = FALSE, ciES = FALSE, ciWidthES = 95, desc = FALSE,
  plots = FALSE, miss = "perAnalysis")
```

Arguments

data	the data as a data frame
pairs	a list of lists specifying the pairs of measurement in data
students	TRUE (default) or FALSE, perform Student's t-tests
bf	TRUE or FALSE (default), provide Bayes factors
bfPrior	a number between 0.5 and 2 (default 0.707), the prior width to use in calculating Bayes factors
wilcoxon	TRUE or FALSE (default), perform Wilcoxon signed rank tests
hypothesis	'different' (default), 'oneGreater' or 'twoGreater', the alternative hypothesis; measure 1 different to measure 2, measure 1 greater than measure 2, and measure 2 greater than measure 1 respectively
norm	TRUE or FALSE (default), perform Shapiro-wilk normality tests
qq	TRUE or FALSE (default), provide a Q-Q plot of residuals
meanDiff	TRUE or FALSE (default), provide means and standard errors
ci	TRUE or FALSE (default), provide confidence intervals
ciWidth	a number between 50 and 99.9 (default: 95), the width of confidence intervals
effectSize	TRUE or FALSE (default), provide effect sizes
ciES	TRUE or FALSE (default), provide confidence intervals for the effect-sizes
ciWidthES	a number between 50 and 99.9 (default: 95), the width of confidence intervals for the effect sizes
desc	TRUE or FALSE (default), provide descriptive statistics
plots	TRUE or FALSE (default), provide descriptive plots
miss	'perAnalysis' or 'listwise', how to handle missing values; 'perAnalysis' excludes missing values for individual dependent variables, 'listwise' excludes a row from all analyses if one of its entries is missing

Details

The Student's paired samples t-test assumes that pair differences follow a normal distribution – in the case that one is unwilling to assume this, the non-parametric Wilcoxon signed-rank can be used in it's place (However, note that the Wilcoxon signed-rank has a slightly different null hypothesis; that the two groups of measurements follow the same distribution).

Value

A results object containing:

results$ttest	a table containing the t-test results
results$norm	a table containing the normality test results
results$desc	a table containing the descriptives
results$plots	an array of the descriptive plots

Tables can be converted to data frames with asDF or as.data.frame. For example:

```
results$ttest$asDF

as.data.frame(results$ttest)
```

Examples

```
data('bugs', package = 'jmv')

ttestPS(bugs, pairs = list(
        list(i1 = 'LDLF', i2 = 'LDHF')))

#
#  PAIRED SAMPLES T-TEST
#
#  Paired Samples T-Test
#  ---------------------------------------------------------------
#                                  statistic    df      p
#  ---------------------------------------------------------------
#    LDLF    LDHF    Student's t        -6.65    90.0    < .001
#  ---------------------------------------------------------------
#
```

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