Package ‘tab’

May 8, 2026

Type Package

Title Create Summary Tables for Statistical Reports

Version 5.1.1

Date 2021-08-01

Author Dane R. Van Domelen

Maintainer Dane R. Van Domelen <`vandomed@gmail.com`>

Description Contains functions for creating various types of summary tables, e.g. comparing characteristics across levels of a categorical variable and summarizing fitted generalized linear models, generalized estimating equations, and Cox proportional hazards models. Functions are available to handle data from simple random samples as well as complex surveys.

License GPL (>= 3)

LazyData true

Encoding UTF-8

Depends dplyr, knitr

Imports kableExtra, MASS, stats, survey (>= 4.1)

RoxygenNote 7.1.1

Suggests gee, rmarkdown, survival

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2021-08-02 04:30:02 UTC

Contents

`formatp` *Format P-values for Functions in the* **tab** *Package*

Description

Formats p-values for tables generated by the functions in the **tab** package. Handles rounding and presentation of p-values.

Usage

```
formatp(
  p,
  decimals = c(2, 3),
  cuts = 0.01,
  lowerbound = 0.001,
  leading0 = TRUE,
  avoid1 = FALSE
)
```

Arguments

`p`	Numeric vector of p-values.
`decimals`	Number of decimal places for p-values. If a vector is provided rather than a single value, number of decimal places will depend on what range the p-value lies in. See `cuts` input.
`cuts`	Cut-point(s) to control number of decimal places used for p-values. For example, by default `cuts = 0.1` and `decimals = c(2, 3)`. This means that p-values in the range [0.1, 1] will be printed to two decimal places, while p-values in the range [0, 0.1) will be printed to three decimal places.
`lowerbound`	Controls cut-point at which p-values are no longer printed as their value, but rather <lowerbound. For example, by default `lowerbound = 0.001`. Under this setting, p-values less than 0.001 are printed as `<0.001`.

`leading0`	If `TRUE`, p-values are printed with 0 before decimal place; if `FALSE`, the leading 0 is omitted.
`avoid1`	If `TRUE`, p-values rounded to 1 are not printed as 1, but as `>0.99` (or similarly depending on `decimals` and `cuts`).

Value

Character vector.

Examples

```
# Generate vector of numeric p-values
set.seed(123)
p <- c(runif(n = 5, min = 0, max = 1), 1, 0, 4e-7, 0.009)

# Round to nearest 2 decimals for p in (0.01, 1] and 3 decimals for p < 0.01
pvals <- formatp(p = p)

# Use 2 decimal places, a lower bound of 0.01, and omit the leading 0
pvals <- formatp(p = p, decimals = 2, lowerbound = 0.01, leading0 = FALSE)
```

`glm_v` *Print a GLM Summary Table to the RStudio Viewer*

Description

You can call this function as you would `glm` or pass a previously fitted `glm` object. Either way, the result is a summary table printed to the Viewer.

Usage

```
glm_v(...)
```

Arguments

`...`	Arguments to pass to glm.

Value

kable

Examples

```
# Fit and view
glm_v(death_1yr ~ Age + Sex + Race, data = tabdata, family = "binomial")

# Fit then view
fit <- glm(death_1yr ~ Age + Sex + Race, data = tabdata, family = "binomial")
glm_v(fit)

# Piping is OMG so cool Hashtag HexStickerz
fit %>% glm_v()
```

`tab` *Create Summary Tables for Statistical Reports*

Description

Contains functions for creating various types of summary tables, e.g. comparing characteristics across levels of a categorical variable and summarizing fitted generalized linear models, generalized estimating equations, and Cox proportional hazards models. Functions are available to handle data from simple random samples as well as complex surveys.

Details

Package:	tab
Type:	Package
Version:	5.1.1
Date:	2021-08-01
License:	GPL-3

See CRAN documentation for full list of functions.

Author(s)

Dane R. Van Domelen
`<vandomed@gmail.com>`

References

Acknowledgment: This material is based upon work supported by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-0940903.

`tabcoxph` *Create Summary Table for Fitted Cox Proportional Hazards Model*

Description

Creates a table summarizing a GEE fit using the `coxph` function.

Usage

```
tabcoxph(
  fit,
  columns = c("beta.se", "hr.ci", "p"),
  var.labels = NULL,
  factor.compression = 1,
  sep.char = ", ",
  decimals = 2,
  formatp.list = NULL
)
```

Arguments

`fit`	Fitted `coxph` object.
`columns`	Character vector specifying what columns to include. Choies for each element are `"events"`, `"beta"`, `"se"`, `"beta.se"`, `"beta.betaci"`, `"betaci"`, `"hr"`, `"hr.hrci"`, `"hrci"`, `"z"`, and `"p"`.
`var.labels`	Named list specifying labels to use for certain predictors. For example, if `fit` includes a predictor named "race" that you want to label "Race/ethnicity" and a predictor named "age_yrs" that you want to label "Age (years)", use `var.labels = list(race = "Race/ethnicity", age_yrs = "Age (years)"`.
`factor.compression`	Integer value from 1 to 5 controlling how much compression is applied to factor predictors (higher value = more compression). If 1, rows are Variable, Level 1 (ref), Level 2, ...; if 2, rows are Variable (ref = Level 1), Level 2, ...; if 3, rows are Level 1 (ref), Level 2, ...; if 4, rows are Level 2 (ref = Level 1), ...; if 5, rows are Level 2, ...
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.

Value

`kable`.

References

1. Therneau, T. (2015). A Package for Survival Analysis in S. R package version 2.38. https://cran.r-project.org/package=survival.

2. Therneau, T.M. and Grambsch, P.M. (2000). Modeling Survival Data: Extending the Cox Model. Springer, New York. ISBN 0-387-98784-3.

Examples

```
# Cox PH model with age, sex, race, and treatment
library("survival")
fit <- coxph(
  Surv(time = time, event = delta) ~ Age + Sex + Race + Group,
  data = tabdata
)
tabcoxph(fit)

# Can also use piping
fit %>% tabcoxph()

# Same as previous, but with custom labels for Age and Race and factors
# displayed in slightly more compressed format
fit %>%
  tabcoxph(
    var.labels = list(Age = "Age (years)", Race = "Race/ethnicity"),
    factor.compression = 2
  )

# Cox PH model with some higher-order terms
fit <- coxph(
  Surv(time = time, event = delta) ~
  poly(Age, 2, raw = TRUE) + Sex + Race + Group + Race*Group,
  data = tabdata
)
fit %>% tabcoxph()
```

`tabdata` *Sample Dataset for* **tab** *Package*

Description

Data frame with 15 variables, used to illustrate certain functions.

Source

Simulated data in R

`tabfreq` *Create Frequency Table*

Description

Creates an I-by-J frequency table comparing the distribution of `y` across levels of `x`.

Usage

```
tabfreq(
  formula = NULL,
  data = NULL,
  x = NULL,
  y = NULL,
  columns = c("xgroups", "p"),
  cell = "counts",
  parenth = "col.percent",
  sep.char = ", ",
  test = "chi.fisher",
  xlevels = NULL,
  yname = NULL,
  ylevels = NULL,
  compress.binary = FALSE,
  yname.row = TRUE,
  text.label = NULL,
  quantiles = NULL,
  quantile.vals = FALSE,
  decimals = 1,
  formatp.list = NULL,
  n.headings = FALSE,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `Sex ~ Group`.
`data`	Data frame containing variables named in `formula`.
`x`	Vector indicating group membership for columns of I-by-J table.
`y`	Vector indicating group membership for rows of I-by-J table.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall distribution of `y`, `"xgroups"` for distributions of `y` for each `x` group, `"test"` for test statistic, and `"p"` for p-value.
`cell`	Character string specifying what statistic to display in cells. Choices are `"counts"`, `"tot.percent"`, `"col.percent"`, and `"row.percent"`.

`parenth`	Character string specifying what statistic to display in parentheses. Choices are `"none"`, `"se"`, `"ci"`, `"counts"`, `"tot.percent"`, `"col.percent"`, and `"row.percent"`.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`test`	Character string specifying which test for association between `x` and `y` should be used. Choices are `"chi.fisher"` for Pearson's chi-squared test if its assumptions are met, otherwise Fisher's exact test; `"chi"`; `"fisher"`; `"z"` for z test without continuity correction; and `"z.continuity"` for z test with continuity correction. The last two only work if both `x` and `y` are binary.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yname`	Character string with a label for the `y` variable.
`ylevels`	Character vector with labels for the levels of `y`. Note that levels of `y` are listed in the order that they appear when you run `table(y, x)`.
`compress.binary`	Logical value for whether to compress binary `y` variable to a single row, excluding the first level rather than showing both.
`yname.row`	Logical value for whether to include a row displaying the name of the `y` variable and indent the factor levels.
`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent.
`quantiles`	Numeric value. If specified, table compares `y` across quantiles of `x` created on the fly.
`quantile.vals`	Logical value for whether labels for `x` quantiles should show quantile number and corresponding range, e.g. Q1 [0.00, 0.25), rather than just the quantile number.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Value

`kable`.

Examples

```
# Compare sex distribution by group
(freqtable1 <- tabfreq(Sex ~ Group, data = tabdata))

# Same as previous, but showing male row only and % (SE) rather than n (%)
(freqtable2 <- tabfreq(Sex ~ Group, data = tabdata,
                       cell = "col.percent", parenth = "se",
                       compress.binary = TRUE))
```

`tabfreq.svy` *Create Frequency Table (for Complex Survey Data)*

Description

Creates an I-by-J frequency table comparing the distribution of `y` across levels of `x`.

Usage

```
tabfreq.svy(
  formula,
  design,
  columns = c("xgroups", "p"),
  cell = "col.percent",
  parenth = "se",
  sep.char = ", ",
  xlevels = NULL,
  yname = NULL,
  ylevels = NULL,
  compress.binary = FALSE,
  yname.row = TRUE,
  text.label = NULL,
  decimals = 1,
  svychisq.list = NULL,
  formatp.list = NULL,
  n.headings = FALSE,
  N.headings = FALSE,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `Race ~ Sex`.
`design`	Survey design object from `svydesign`.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total unweighted sample size, `"N"` for total weighted sample size, `"overall"` for overall distribution of `y`, `"xgroups"` for distributions of `y` for each `x` group, and `"p"` for Chi-square p-value.
`cell`	Character string specifying what statistic to display in cells. Choices are `"n"`, `"N"`, and `"col.percent"`.
`parenth`	Character string specifying what statistic to display in parentheses. Choices are `"none"`, `"n"`, `"N"`, `"col.percent"`, `"se"`, and `"ci"`.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.

`yname`	Character string with a label for the `y` variable.
`ylevels`	Character vector with labels for the levels of `y`. Note that levels of `y` are listed in the order that they appear when you run `table(y, x)`.
`compress.binary`	Logical value for whether to compress binary `y` variable to a single row, excluding the first level rather than showing both.
`yname.row`	Logical value for whether to include a row displaying the name of the `y` variable.
`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`svychisq.list`	List of arguments to pass to `svychisq`.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display unweighted sample sizes in parentheses in column headings.
`N.headings`	Logical value for whether to display weighted sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Details

Basically `tabmedians` for complex survey data. Relies heavily on the **survey** package.

Value

`kable` or character matrix.

Examples

```
# Create survey design object
library("survey")
design <- svydesign(
  data = tabsvydata,
  ids = ~sdmvpsu,
  strata = ~sdmvstra,
  weights = ~wtmec2yr,
  nest = TRUE
)

# Compare race distribution by sex
tabfreq.svy(Race ~ Sex, design)
```

`tabgee` *Create Summary Table for Fitted Generalized Estimating Equation Model*

Description

Creates a table summarizing a GEE fit using the `gee` function.

Usage

```
tabgee(
  fit,
  data = NULL,
  columns = NULL,
  robust = TRUE,
  var.labels = NULL,
  factor.compression = 1,
  sep.char = ", ",
  decimals = 2,
  formatp.list = NULL
)
```

Arguments

`fit`	Fitted `gee` object.
`data`	Data frame that served as 'data' in function call to `gee`. Only needs to be specified if one or more of the predictors is a factor and `factor.compression` is 1, 2, 3, or 4.
`columns`	Character vector specifying what columns to include. Choices for each element are `"beta"`, `"se"`, `"betaci"` for 95% CI for Beta, `"beta.se"` for Beta (SE), `"beta.ci"` for Beta (95% CI), `"or"`, `"orci"` for 95% CI for OR, `"or.ci"` for OR (95% CI), `"hr"`, `"hrci"` for 95% CI for HR, `"hr.ci"` for HR (95% CI), `"z"` for z statistic, and `"p"`. If OR's or HR's are requested, the function will trust that exponentiated betas correspond to these quantities.
`robust`	Logical value for whether to use robust standard errors.
`var.labels`	Named list specifying labels to use for certain predictors. For example, if `fit` includes a predictor named "race" that you want to label "Race/ethnicity" and a predictor named "age_yrs" that you want to label "Age (years)", use `var.labels = list(race = "Race/ethnicity", age_yrs = "Age (years)"`.
`factor.compression`	Integer value from 1 to 5 controlling how much compression is applied to factor predictors (higher value = more compression). If 1, rows are Variable, Level 1 (ref), Level 2, ...; if 2, rows are Variable (ref = Level 1), Level 2, ...; if 3, rows are Level 1 (ref), Level 2, ...; if 4, rows are Level 2 (ref = Level 1), ...; if 5, rows are Level 2, ...

`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.

Value

`kable`.

Examples

```
# Load in sample dataset and convert to long format
tabdata2 <- reshape(data = tabdata,
                    varying = c("bp.1", "bp.2", "bp.3", "highbp.1",
                                "highbp.2", "highbp.3"),
                    timevar = "bp.visit", direction = "long")
tabdata2 <- tabdata2[order(tabdata2$id), ]

# Blood pressure at 1, 2, and 3 months vs. age, sex, race, and treatment
library("gee")
fit <- gee(bp ~ Age + Sex + Race + Group, id = id, data = tabdata2,
           corstr = "unstructured")
tabgee(fit)

# Can also use piping
fit %>% tabgee(data = tabdata2)

# Same as previous, but with custom labels for Age and Race and factors
# displayed in slightly more compressed format
fit %>%
  tabgee(
    data = tabdata2,
    var.labels = list(Age = "Age (years)", Race = "Race/ethnicity"),
    factor.compression = 2
  )

# GEE with some higher-order terms
# higher-order terms
fit <- gee(
  highbp ~ poly(Age, 2, raw = TRUE) + Sex + Race + Group + Race*Group,
  id = id,
  data = tabdata2,
  family = "binomial",
  corstr = "unstructured"
)
fit %>% tabgee(data = tabdata2)
```

`tabglm` *Create Summary Table for Fitted Generalized Linear Model*

Description

Creates a table summarizing a GLM fit using `glm`.

Usage

```
tabglm(
  fit,
  columns = NULL,
  xvarlabels = NULL,
  factor.compression = 1,
  sep.char = ", ",
  decimals = 2,
  formatp.list = NULL
)
```

Arguments

`fit`	Fitted `glm` object.
`columns`	Character vector specifying what columns to include. Choices for each element are `"beta"`, `"se"`, `"betaci"` for 95% CI for Beta, `"beta.se"` for Beta (SE), `"beta.ci"` for Beta (95% CI), `"or"`, `"orci"` for 95% CI for OR, `"or.ci"` for OR (95% CI), `"hr"`, `"hrci"` for 95% CI for HR, `"hr.ci"` for HR (95% CI), `"test"` for z/t statistic, and `"p"`. If OR's or HR's are requested, the function will trust that exponentiated betas correspond to these quantities.
`xvarlabels`	Named list specifying labels to use for certain predictors. For example, if `fit` includes a predictor named "race" that you want to label "Race/ethnicity" and a predictor named "age_yrs" that you want to label "Age (years)", use `xvarlabels = list(race = "Race/ethnicity", age_yrs = "Age (years)"`.
`factor.compression`	Integer value from 1 to 5 controlling how much compression is applied to factor predictors (higher value = more compression). If 1, rows are Variable, Level 1 (ref), Level 2, ...; if 2, rows are Variable (ref = Level 1), Level 2, ...; if 3, rows are Level 1 (ref), Level 2, ...; if 4, rows are Level 2 (ref = Level 1), ...; if 5, rows are Level 2, ...
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`. `kable`.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.

Value

kable.

Examples

```
# Linear regression: BMI vs. age, sex, race, and treatment
fit <- glm(BMI ~ Age + Sex + Race + Group, data = tabdata)
tabglm(fit)

# Can also use piping
fit %>% tabglm()

# Logistic regression: 1-year mortality vs. age, sex, race, and treatment
fit <- glm(
  death_1yr ~ Age + Sex + Race + Group,
  data = tabdata,
  family = binomial
)
fit %>% tabglm()

# Same as previous, but with custom labels for Age and Race and factors
# displayed in slightly more compressed format
fit %>%
  tabglm(
    xvarlabels = list(Age = "Age (years)", Race = "Race/ethnicity"),
    factor.compression = 2
  )

# Logistic regression model with some higher-order terms
fit <- glm(
  death_1yr ~ poly(Age, 2, raw = TRUE) + Sex + BMI + Sex * BMI,
  data = tabdata,
  family = "binomial"
)
fit %>% tabglm()
```

---

tabmeans *Create Table Comparing Group Means*

Description

Creates a table comparing the mean of `y` across levels of `x`.

Usage

```
tabmeans(
  formula = NULL,
```

```
  data = NULL,
  x = NULL,
  y = NULL,
  columns = c("xgroups", "p"),
  parenth = "sd",
  sep.char = ", ",
  variance = "unequal",
  xlevels = NULL,
  yname = NULL,
  text.label = NULL,
  quantiles = NULL,
  quantile.vals = FALSE,
  decimals = NULL,
  formatp.list = NULL,
  n.headings = TRUE,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `BMI ~ Group`.
`data`	Data frame containing variables named in `formula`.
`x`	Vector of values for the categorical `x` variable.
`y`	Vector of values for the continuous `y` variable.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall mean, `"xgroups"` for `x` group means, `"diff"` for difference in `x` group means (this one and the next two are only available for binary `x`), `"diffci"` for 95 `x` group means, `"diff.ci"` for difference in group means and 95 confidence interval, `"test"` for test statistic, and `"p"` for p-value.
`parenth`	Character string specifying what statistic to display in parentheses after the means. Choices are `"none"`, `"sd"`, `"se"`, `"t.ci"`, `"z.ci"`, `"range"`, and `"minmax"`.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`variance`	Character string specifying which version of the two-sample t-test to use if `x` has 2 levels. Choices are `"equal"` for equal variance t-test, `"unequal"` for unequal variance t-test, and `"f"` for F test to determine which to use.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yname`	Character string with a label for the `y` variable.
`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent.
`quantiles`	Numeric value. If specified, table compares `y` across quantiles of `x` created on the fly.
`quantile.vals`	Logical value for whether labels for `x` quantiles should show quantile number and corresponding range, e.g. Q1 [0.00, 0.25), rather than just the quantile number.

`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Details

A t-test is used to compare means if `x` has two levels, and a one-way analysis of variance is used if `x` has more than two levels. Observations with missing values for `x` and/or `y` are dropped.

Value

`kable` or character matrix.

Examples

```
# Compare mean BMI in control vs. treatment group in sample dataset
(meanstable1 <- tabmeans(BMI ~ Group, data = tabdata))

# Compare mean baseline systolic BP across tertiles of BMI
(meanstable2 <- tabmeans(bp.1 ~ BMI, data = tabdata,
                         quantiles = 3, yname = "Systolic BP"))
```

`tabmeans.svy` *Create Table Comparing Group Means (for Complex Survey Data)*

Description

Creates a table comparing the mean of `y` across levels of `x`.

Usage

```
tabmeans.svy(
  formula,
  design,
  columns = c("xgroups", "p"),
  parenth = "sd",
  sep.char = ", ",
  xlevels = NULL,
  yname = NULL,
  text.label = NULL,
  decimals = 1,
  anova.svyglm.list = NULL,
  formatp.list = NULL,
```

```
    n.headings = FALSE,
    N.headings = FALSE,
    kable = TRUE
  )
```

Arguments

`formula`	Formula, e.g. `BMI ~ Sex`.
`design`	Survey design object from `svydesign`.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall mean, `"xgroups"` for `x` group means, `"diff"` for difference in `x` group means (this one and the next two are only available for binary `x`), `"diffci"` for 95 `x` group means, `"diff.ci"` for difference in group means and 95 confidence interval, and `"p"` for p-value.
`parenth`	Character string specifying what statistic to display in parentheses after the means. Choices are `"none"`, `"sd"`, `"se"`, `"t.ci"`, `"z.ci"`, `"range"`, and `"minmax"`.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yname`	Character string with a label for the `y` variable.
`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`anova.svyglm.list`	List of arguments to pass to `anova.svyglm`. Only used if `x` has three or more levels.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`N.headings`	Logical value for whether to display weighted sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Details

Basically `tabmeans` for complex survey data. Relies heavily on the **survey** package.

Value

`kable` or character matrix.

Examples

```
# Create survey design object
library("survey")
design <- svydesign(
  data = tabsvydata,
  ids = ~sdmvpsu,
  strata = ~sdmvstra,
  weights = ~wtmec2yr,
  nest = TRUE
)

# Compare mean BMI by sex
(meanstable <- tabmeans.svy(BMI ~ Sex, design = design))
```

`tabmedians` *Create Table Comparing Group Medians*

Description

Creates a table comparing the median of `y` across levels of `x`.

Usage

```
tabmedians(
  formula = NULL,
  data = NULL,
  x = NULL,
  y = NULL,
  columns = c("xgroups", "p"),
  parenth = "iqr",
  sep.char = ", ",
  xlevels = NULL,
  yname = NULL,
  text.label = NULL,
  quantiles = NULL,
  quantile.vals = FALSE,
  decimals = NULL,
  formatp.list = NULL,
  n.headings = TRUE,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `BMI ~ Group`.
`data`	Data frame containing variables named in `formula`.

`x`	Vector of values for the categorical `x` variable.
`y`	Vector of values for the continuous `y` variable.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall median, `"xgroups"` for `x` group medians, `"diff"` for difference in `x` group medians (only available for binary `x`), `"test"` for test statistic, and `"p"` for p-value.
`parenth`	Character string specifying what values are shown in parentheses after the medians in each cell. Choices are `"none"`, `"iqr"`, `"q1q3"` for first and third quartiles, `"range"`, `"minmax"`, and `"ci"` for 95% confidence interval for the medians based on normal approximation to binomial.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yname`	Character string with a label for the `y` variable.
`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent.
`quantiles`	Numeric value. If specified, table compares `y` across quantiles of `x` created on the fly.
`quantile.vals`	Logical value for whether labels for `x` quantiles should show quantile number and corresponding range, e.g. Q1 [0.00, 0.25), rather than just the quantile number.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Details

If `x` has 2 levels, a Mann-Whitney U (also known as Wilcoxon rank-sum) test is used to test whether the distribution of `y` differs in the two groups; if `x` has more than 2 levels, a Kruskal-Wallis test is used to test whether the distribution of `y` differs across at least two of the groups. Observations with missing values for `x` and/or `y` are dropped.

Value

`kable`.

Examples

```
# Compare median BMI in control group vs. treatment group in sample dataset
(medtable1 <- tabmedians(BMI ~ Group, data = tabdata))

# Compare median baseline systolic BP across tertiles of BMI
```

```
(medtable2 <- tabmedians(bp.1 ~ BMI, data = tabdata,
                         quantiles = 3, yname = "Systolic BP"))
```

`tabmedians.svy` *Create Table Comparing Group Medians (for Complex Survey Data)*

Description

Creates a table comparing the median of `y` across levels of `x`.

Usage

```
tabmedians.svy(
  formula,
  design,
  columns = c("xgroups", "p"),
  parenth = "iqr",
  sep.char = ", ",
  xlevels = NULL,
  yname = NULL,
  text.label = NULL,
  decimals = NULL,
  svyranktest.list = NULL,
  formatp.list = NULL,
  n.headings = FALSE,
  N.headings = FALSE,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `BMI ~ Sex`.
`design`	Survey design object from `svydesign`.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall median, `"xgroups"` for `x` group medians, `"diff"` for difference in `x` group medians (only available for binary `x`), and `"p"` for p-value.
`parenth`	Character string specifying what values are shown in parentheses after the medians in each cell. Choices are `"none"`, `"iqr"`, `"q1q3"` for first and third quartiles, `"range"`, `"minmax"`, and `"ci"` for 95% confidence interval for the median.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yname`	Character string with a label for the `y` variable.

`text.label`	Character string with text to put after the `y` variable name, identifying what cell values and parentheses represent.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`svyranktest.list`	List of arguments to pass to `svyranktest`.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`N.headings`	Logical value for whether to display weighted sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.

Details

Basically `tabmedians` for complex survey data. Relies heavily on the **survey** package.

Value

`kable` or character matrix.

Examples

```
# Create survey design object
library("survey")
design <- svydesign(
  data = tabsvydata,
  ids = ~sdmvpsu,
  strata = ~sdmvstra,
  weights = ~wtmec2yr,
  nest = TRUE
)

# Compare median BMI by sex
(medtable1 <- tabmedians.svy(BMI ~ Sex, design = design))
```

`tabmulti` *Create Table Comparing Characteristics Across Levels of a Categorical Variable*

Description

Creates a table comparing multiple characteristics (e.g. median age, mean BMI, and race/ethnicity distribution) across levels of `x`.

Usage

```
tabmulti(
  formula = NULL,
  data,
  xvarname = NULL,
  yvarnames = NULL,
  ymeasures = NULL,
  columns = c("xgroups", "p"),
  listwise.deletion = FALSE,
  sep.char = ", ",
  xlevels = NULL,
  yvarlabels = NULL,
  ylevels = NULL,
  quantiles = NULL,
  quantile.vals = FALSE,
  decimals = NULL,
  formatp.list = NULL,
  n.headings = FALSE,
  tabmeans.list = NULL,
  tabmedians.list = NULL,
  tabfreq.list = NULL,
  kable = TRUE
)
```

Arguments

`formula`	Formula, e.g. `Age + Sex + Race + BMI ~ Group`.
`data`	Data frame containing variables named in `formula`.
`xvarname`	Character string with name of column variable. Should be one of `names(data)`.
`yvarnames`	Character vector with names of row variables. Each element should be one of `names(data)`.
`ymeasures`	Character vector specifying whether each `y` variable should be summarized by mean, median, or frequency. For example, if you want to compare frequencies for the first variable, means for the second, and medians for the third, you would set `ymeasures = c("freq", "mean", "median")`. If unspecified, function compares means for numeric variables and frequencies for factor and character variables.
`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for total sample size, `"overall"` for overall statistics, `"xgroups"` for `x` group statistics, `"test"` for test statistic, and `"p"` for p-value.
`listwise.deletion`	Logical value for whether observations with missing values for any `y` variable should be excluded entirely (as opposed to using all available data for each comparison).
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.

`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yvarlabels`	Named list specifying labels for certain `y` variables. For example, if you want variables named "race" and "age_yrs" to print as "Race/ethnicity" and "Age (years)", use \codeyvarlabels = list(race = "Race/ethnicity", age_yrs = "Age (years)").
`ylevels`	Character vector (if only 1 frequency comparison) or list of character vectors with labels for the levels of each categorical `y` variable.
`quantiles`	Numeric value. If specified, function compares `y` variables across quantiles of `x`. For example, if `x` contains BMI values and `yvarnames` includes HDL and race, setting `quantiles = 3` compares mean BMI and distribution of race across BMI tertiles.
`quantile.vals`	Logical value for whether labels for `x` quantiles should show quantile number and corresponding range, e.g. Q1 [0.00, 0.25), rather than just the quantile number.
`decimals`	Numeric vector specifying number of decimal places for numbers other than p-values for each `y` variable. Can be a single value to use for all `y` variables.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display group sample sizes in parentheses in column headings.
`tabmeans.list`	List of arguments to pass to `tabmeans`.
`tabmedians.list`	List of arguments to pass to `tabmedians`.
`tabfreq.list`	List of arguments to pass to `tabfreq`.
`kable`	Logical value for whether to return a `kable`.

Value

`kable` or character matrix.

Examples

```
# Compare age, sex, race, and BMI in control vs. treatment group
tabmulti(Age + Sex + Race + BMI ~ Group, data = tabdata)

# Same as previous, but compare medians rather than means for BMI
tabmulti(Age + Sex + Race + BMI ~ Group, data = tabdata,
         ymeasures = c(”mean”, ”freq”, ”freq”, ”median”))
```

`tabmulti.svy` *Create Table Comparing Characteristics Across Levels of a Categorical Variable (for Complex Survey Data)*

Description

Creates a table comparing multiple characteristics (e.g. median age, mean BMI, and race/ethnicity distribution) across levels of `x`.

Usage

```
tabmulti.svy(
  formula = NULL,
  design,
  xvarname = NULL,
  yvarnames = NULL,
  ymeasures = NULL,
  columns = c("xgroups", "p"),
  listwise.deletion = FALSE,
  sep.char = ", ",
  xlevels = NULL,
  yvarlabels = NULL,
  ylevels = NULL,
  decimals = NULL,
  formatp.list = NULL,
  n.headings = FALSE,
  N.headings = FALSE,
  kable = TRUE,
  tabmeans.svy.list = NULL,
  tabmedians.svy.list = NULL,
  tabfreq.svy.list = NULL
)
```

Arguments

`formula`	Formula, e.g. `Age + Race + BMI ~ Sex`.
`design`	Survey design object from `svydesign`.
`xvarname`	Character string with name of column variable. Should be one of `names(design$variables)`.
`yvarnames`	Character vector with names of row variables. Each element should be one of `names(design$variables)`.
`ymeasures`	Character vector specifying whether each `y` variable should be summarized by mean, median, or frequency. For example, if you want to compare frequencies for the first variable, means for the second, and medians for the third, you would set `ymeasures = c("freq", "mean", "median")`. If unspecified, function compares means for numeric variables and frequencies for factor and character variables.

`columns`	Character vector specifying what columns to include. Choices for each element are `"n"` for unweighted sample size, `"N"` for weighted sample size, `"overall"` for overall statistics, `"xgroups"` for `x` group statistics, and `"p"` for p-value.
`listwise.deletion`	Logical value for whether observations with missing values for any `y` variable should be excluded entirely (as opposed to using all available data for each comparison).
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`xlevels`	Character vector with labels for the levels of `x`, used in column headings.
`yvarlabels`	Named list specifying labels for certain `y` variables. For example, if you want variables named "race" and "age_yrs" to print as "Race/ethnicity" and "Age (years)", use \codeyvarlabels = list(race = "Race/ethnicity", age_yrs = "Age (years)").
`ylevels`	Character vector (if only 1 frequency comparison) or list of character vectors with labels for the levels of each categorical `y` variable.
`decimals`	Numeric vector specifying number of decimal places for numbers other than p-values for each `y` variable. Can be a single value to use for all `y` variables.
`formatp.list`	List of arguments to pass to `formatp`.
`n.headings`	Logical value for whether to display unweighted sample sizes in parentheses in column headings.
`N.headings`	Logical value for whether to display weighted sample sizes in parentheses in column headings.
`kable`	Logical value for whether to return a `kable`.
`tabmeans.svy.list`	List of arguments to pass to `tabmeans.svy`.
`tabmedians.svy.list`	List of arguments to pass to `tabmedians.svy`.
`tabfreq.svy.list`	List of arguments to pass to `tabfreq.svy`.

Details

Basically `tabmulti` for complex survey data. Relies heavily on the **survey** package.

Value

`kable` or character matrix.

Examples

```
# Create survey design object
library("survey")
design <- svydesign(
  data = tabsvydata,
  ids = ~sdmvpsu,
```

```
  strata = ~sdmvstra,
  weights = ~wtmec2yr,
  nest = TRUE
)

# Compare age, race, and BMI by sex
tabmulti.svy(Age + Race + BMI ~ Sex, design)
```

`tabreg` *Create Regression Table from Betas and Standard Errors*

Description

Useful for quickly creating a summary table.

Usage

```
tabreg(
  betas,
  ses = NULL,
  varcov = NULL,
  columns = c("beta.se", "p"),
  sep.char = ", ",
  decimals = NULL,
  formatp.list = NULL,
  labels = NULL
)
```

Arguments

`betas`	Numeric vector.
`ses`	Numeric vector.
`varcov`	Numeric matrix.
`columns`	Character vector specifying what columns to include. Choices are `"beta"`, `"se"`, `"betaci"`, `"beta.se"`, `"beta.ci"`, `"or"`, `"orci"`, `"or.ci"`, and `"p"`.
`sep.char`	Character string with separator to place between lower and upper bound of confidence intervals. Typically `"-"` or `", "`.
`decimals`	Numeric value specifying number of decimal places for numbers other than p-values.
`formatp.list`	List of arguments to pass to `formatp`.
`labels`	Character vector.

Value

`kable`.

Examples

```
# Create summary table for mtcars regression
fit <- lm(mpg ~ wt + hp + drat, data = mtcars)
tabreg(
  betas = fit$coef,
  varcov = vcov(fit),
  labels = c("Intercept", "Weight", "HP", "Rear axle ratio")
)
```

`tabsvydata` *Sample Survey Dataset for* **tab** *Package*

Description

Data frame with with 9 variables, used to illustrate certain functions. Data are derived from the National Health and Nutrition Examination Survey, years 2003-2004, although the variables 'time' and 'event' are simulated (fake).

Source

https://wwwn.cdc.gov/Nchs/Nhanes/2003-2004/DEMO_C.htm

References

Centers for Disease Control and Prevention (CDC). National Center for Health Statistics (NCHS). National Health and Nutrition Examination Survey Data. Hyattsville, MD: US Department of Health and Human Services, Centers for Disease Control and Prevention, 2003-2004. https://wwwn.cdc.gov/nchs/nhanes/con Accessed June 8, 2019.

`toviewer` *Output a Table to the RStudio Viewer*

Description

Does some basic formatting and then calls `kable` and `kable_styling` to print table to Viewer.

Usage

```
toviewer(x)
```

Arguments

`x`	Character matrix

Index