Package ‘tableone’

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Type Package

Title Create ‘Table 1’ to Describe Baseline Characteristics with or without Propensity Score Weights

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Description Creates 'Table 1', i.e., description of baseline patient characteristics, which is essential in every medical research. Supports both continuous and categorical variables, as well as p-values and standardized mean differences. Weighted data are supported via the 'survey' package. See 'github' for a screen cast.

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Description

Creates "Table 1", i.e., description of baseline patient characteristics, which is essential in every medical research. Supports both continuous and categorical variables, as well as p-values and standardized mean differences. Weighted data are supported via the survey package. See github for a screencast. tableone was inspired by descriptive statistics functions in Deducer, a Java-based GUI package by Ian Fellows. This package does not require GUI or Java, and intended for command-line users. Most important functions are CreateTableOne and svyCreateTableOne.

Note

Acknowledgement:

Ian Fellows for developing the deducer package, which this package is based on.

Hadley Wickham for packaging advice and for creating tools this package was made with (roxygen2, devtools, testthat).

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Developmental repository is on github. Your contributions are appreciated.

https://github.com/kaz-yos/tableone

Author(s)

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See Also

CreateTableOne, svyCreateTableOne, print.TableOne, summary.TableOne, ShowRegTable

Examples

```r
## See examples for CreateTableOne and svyCreateTableOne
```

---

**CreateCatTable**

*Create an object summarizing categorical variables*

**Description**

Create an object summarizing categorical variables optionally stratifying by one or more stratifying variables and performing statistical tests. Usually, CreateTableOne should be used as the universal frontend for both continuous and categorical data.

**Usage**

```r
CreateCatTable(
  vars,
  strata,
  data,
  includeNA = FALSE,
  test = TRUE,
  testApprox = chisq.test,
  argsApprox = list(correct = TRUE),
  testExact = fisher.test,
  argsExact = list(workspace = 2 * 10^5),
  smd = TRUE,
  addOverall = FALSE
)
```
Arguments

vars Variable(s) to be summarized given as a character vector.
strata Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.
data A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
includeNA If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables.
test If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed. Both tests that require the large sample approximation and exact tests are performed. Either one of the result can be obtained from the print method.
testApprox A function used to perform the large sample approximation based tests. The default is chisq.test. This is not recommended when some of the cell have small counts like fewer than 5.
argsApprox A named list of arguments passed to the function specified in testApprox. The default is list(correct = TRUE), which turns on the continuity correction for chisq.test.
testExact A function used to perform the exact tests. The default is fisher.test. If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice.
argsExact A named list of arguments passed to the function specified in testExact. The default is list(workspace = 2*10^5), which specifies the memory space allocated for fisher.test.
smd If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.
addOverall (optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.

Value

An object of class CatTable.

Author(s)

Kazuki Yoshida (based on Deducer::frequencies()), Alexander Bartel

See Also

CreateTableOne, print.CatTable, summary.CatTable
Examples

```r
## Load
library(tableone)

## Load Mayo Clinic Primary Biliary Cirrhosis Data
library(survival)
data(pbc)
## Check variables
head(pbc)

## Create an overall table for categorical variables
catVars <- c("status","ascites","hepato","spiders","edema","stage")
catTableOverall <- CreateCatTable(vars = catVars, data = pbc)

## Simply typing the object name will invoke the print.CatTable method,
## which will show the sample size, frequencies and percentages.
## For 2-level variables, only the higher level is shown for simplicity
## unless the variables are specified in the cramVars argument.
catTableOverall

## If you need to show both levels for some 2-level factors, use cramVars
print(catTableOverall, cramVars = "hepato")

## Use the showAllLevels argument to see all levels for all variables.
print(catTableOverall, showAllLevels = TRUE)

## You can choose from frequencies ("f") and/or percentages ("p") or both.
## "fp" frequency (percentage) is the default. Row names change accordingly.
pD <- c("sex","trt")
print(catTableOverall, format = "f")
print(catTableOverall, format = "p")

## To further examine the variables, use the summary.CatTable method,
## which will show more details.
summary(catTableOverall)

## The table can be stratified by one or more variables
catTableBySexTrt <- CreateCatTable(vars = catVars,
                                  strata = c("sex","trt"), data = pbc)

## print now includes p-values which are by default calculated by chisq.test.
## It is formatted at the decimal place specified by the pDigits argument
## (3 by default). It is formatted like <0.001 if very small.
catTableBySexTrt

## The exact argument toggles the p-values to the exact test result from
## fisher.test. It will show which ones are from exact tests.
print(catTableBySexTrt, exact = "ascites")

## summary now includes both types of p-values
summary(catTableBySexTrt)
```
## If your work flow includes copying to Excel and Word when writing manuscripts, you may benefit from the quote argument. This will quote everything so that Excel does not mess up the cells.

```r
print(catTableBySexTrt, exact = "ascites", quote = TRUE)
```

## If you want to center-align values in Word, use noSpaces option.

```r
print(catTableBySexTrt, exact = "ascites", quote = TRUE, noSpaces = TRUE)
```

---

**CreateContTable**

*Create an object summarizing continuous variables*

**Description**

Create an object summarizing continuous variables optionally stratifying by one or more stratifying variables and performing statistical tests. Usually, **CreateTableOne** should be used as the universal frontend for both continuous and categorical data.

**Usage**

```r
CreateContTable(
  vars,
  strata,
  data,
  funcNames = c("n", "miss", "p.miss", "mean", "sd", "median", "p25", "p75", "min", "max", "skew", "kurt"),
  funcAdditional,
  test = TRUE,
  testNormal = oneway.test,
  argsNormal = list(var.equal = TRUE),
  testNonNormal = kruskal.test,
  argsNonNormal = list(NULL),
  smd = TRUE,
  addOverall = FALSE
)
```

**Arguments**

- **vars** Variable(s) to be summarized given as a character vector.
- **strata** Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.
- **data** A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.
- **funcNames** The functions to give the group size, number with missing values, proportion with missing values, mean, standard deviations, median, 25th percentile, 75th percentile, minimum, maximum, skewness (same definition as in SAS), kurtosis (same definition as in SAS). All of them can be seen in the summary method
output. The print method uses subset of these. You can choose subset of them or reorder them. They are all configure to omit NA values (na.rm = TRUE).

`funcAdditional` Additional functions can be given as a named list. For example, `list(sum = sum)`.

`test` If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed. Both tests that assume normality and tests that do not are performed. Either one of the result can be obtained from the print method.

`testNormal` A function used to perform the normal assumption based tests. The default is `oneway.test`. This is equivalent of the t-test when there are only two groups.

`argsNormal` A named list of arguments passed to the function specified in `testNormal`. The default is `list(var.equal = TRUE)`, which makes it the ordinary ANOVA that assumes equal variance across groups.

`testNonNormal` A function used to perform the nonparametric tests. The default is `kruskal.test` (Kruskal-Wallis rank sum test). This is equivalent of the `wilcox.test` (Man-Whitney U test) when there are only two groups.

`argsNonNormal` A named list of arguments passed to the function specified in `testNonNormal`. The default is `list(NULL)`, which is just a placeholder.

`smd` If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.

`addOverall` (optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.

**Value**

An object of class `ContTable`.

**Author(s)**

Kazuki Yoshida (based on `Deducer::descriptive.table()`), Alexander Bartel

**See Also**

`CreateTableOne`, `print.ContTable`, `summary.ContTable`

**Examples**

```r
## Load
library(tableone)

## Load Mayo Clinic Primary Biliary Cirrhosis Data
library(survival)
data(pbc)
## Check variables
head(pbc)

## Create an overall table for continuous variables
contVars <- c("time","age","bili","chol","albumin","copper",
```
Create an object summarizing both continuous and categorical variables

```r
contTableOverall <- CreateContTable(vars = contVars, data = pbc)

## Simply typing the object name will invoke the print.ContTable method,
## which will show the sample size, means and standard deviations.
contTableOverall

## To further examine the variables, use the summary.ContTable method,
## which will show more details.
summary(contTableOverall)

## c("age","cholesterol","copper","alk.phos","trig","protime") appear highly skewed.
## Specify them in the nonnormal argument, and the display changes to the median,
## and the [25th, 75th] percentile.
nonNormalVars <- c("age","cholesterol","copper","alk.phos","trig","protime")
print(contTableOverall, nonnormal = nonNormalVars)

## To show median [min,max] for nonnormal variables, use minMax = TRUE
print(contTableOverall, nonnormal = nonNormalVars, minMax = TRUE)

## The table can be stratified by one or more variables
contTableBySexTrt <- CreateContTable(vars = contVars,
                                 strata = c("sex","trt"), data = pbc)

## print now includes p-values which are by default calculated by oneway.test (t-test
## equivalent in the two group case). It is formatted at the decimal place specified
## by the pDigits argument (3 by default). It does <0.001 for you.
contTableBySexTrt

## The nonnormal argument toggles the p-values to the nonparametric result from
## kruskal.test (wilcox.test equivalent for the two group case).
print(contTableBySexTrt, nonnormal = nonNormalVars)

## summary now includes both types of p-values
summary(contTableBySexTrt)

## If your work flow includes copying to Excel and Word when writing manuscripts,
## you may benefit from the quote argument. This will quote everything so that
## Excel does not mess up the cells.
pIint(contTableBySexTrt, nonnormal = nonNormalVars, quote = TRUE)

## If you want to center-align values in Word, use noSpaces option.
pIint(contTableBySexTrt, nonnormal = nonNormalVars, quote = TRUE, noSpaces = TRUE)
```
Description

Create an object summarizing all baseline variables (both continuous and categorical) optionally stratifying by one or more stratifying variables and performing statistical tests. The object gives a table that is easy to use in medical research papers.

Usage

CreateTableOne(
  vars,
  strata,
  data,
  factorVars,
  includeNA = FALSE,
  test = TRUE,
  testApprox = chisq.test,
  argsApprox = list(correct = TRUE),
  testExact = fisher.test,
  argsExact = list(workspace = 2 * 10^5),
  testNormal = oneway.test,
  argsNormal = list(var.equal = TRUE),
  testNonNormal = kruskal.test,
  argsNonNormal = list(NULL),
  smd = TRUE,
  addOverall = FALSE
)

Arguments

vars Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the data frame specified in the data argument are used.

strata Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.

data A data frame in which these variables exist. All variables (both vars and strata) must be in this data frame.

factorVars Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to rellevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the vars argument.

includeNA If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables.

test If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed.
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>testApprox</td>
<td>A function used to perform the large sample approximation based tests. The default is <code>chisq.test</code>. This is not recommended when some of the cell have small counts like fewer than 5.</td>
</tr>
<tr>
<td>argsApprox</td>
<td>A named list of arguments passed to the function specified in testApprox. The default is <code>list(correct = TRUE)</code>, which turns on the continuity correction for <code>chisq.test</code>.</td>
</tr>
<tr>
<td>testExact</td>
<td>A function used to perform the exact tests. The default is <code>fisher.test</code>. If the cells have large numbers, it will fail because of memory limitation. In this situation, the large sample approximation based should suffice.</td>
</tr>
<tr>
<td>argsExact</td>
<td>A named list of arguments passed to the function specified in testExact. The default is <code>list(workspace = 2*10^5)</code>, which specifies the memory space allocated for <code>fisher.test</code>.</td>
</tr>
<tr>
<td>testNormal</td>
<td>A function used to perform the normal assumption based tests. The default is <code>oneway.test</code>. This is equivalent of the t-test when there are only two groups.</td>
</tr>
<tr>
<td>argsNormal</td>
<td>A named list of arguments passed to the function specified in testNormal. The default is <code>list(var.equal = TRUE)</code>, which makes it the ordinary ANOVA that assumes equal variance across groups.</td>
</tr>
<tr>
<td>testNonNormal</td>
<td>A function used to perform the nonparametric tests. The default is <code>kruskal.test</code> (Kruskal-Wallis Rank Sum Test). This is equivalent of the <code>wilcox.test</code> (Man-Whitney U test) when there are only two groups.</td>
</tr>
<tr>
<td>argsNonNormal</td>
<td>A named list of arguments passed to the function specified in testNonNormal. The default is <code>list(NULL)</code>, which is just a placeholder.</td>
</tr>
<tr>
<td>smd</td>
<td>If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.</td>
</tr>
<tr>
<td>addOverall</td>
<td>(optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.</td>
</tr>
</tbody>
</table>

**Details**

The definitions of the standardized mean difference (SMD) are available in Flury et al 1986 for the univariate case and the multivariate case (essentially the square root of the Mahalanobis distance). Extension to binary variables is discussed in Austin 2009 and extension to multinomival variables is suggested in Yang et al 2012. This multinomial extesion treats a single multinomial variable as multiple non-redundant dichotomous variables and use the Mahalanobis distance. The off diagonal elements of the covariance matrix on page 3 have an error, and need negation. In weighted data, the same definitions can be used except that the mean and standard deviation estimates are weighted estimates (Li et al 2013 and Austin et al 2015). In tableone, all weighted estimates are calculated by weighted estimation functions in the survey package.

**Value**

An object of class `TableOne`, which is a list of three objects.

- **ContTable** object of class `ContTable`, containing continuous variables only
- **CatTable** object of class `CatTable`, containing categorical variables only
- **MetaData** list of metadata regarding variables
Author(s)

Kazuki Yoshida, Justin Bohn, Alexander Bartel

References


See Also

`print.TableOne`, `summary.TableOne`

Examples

```r
## Load library(tableone)
## Load Mayo Clinic Primary Biliary Cirrhosis Data library(survival) data(pbc) ## Check variables head(pbc)
## Make categorical variables factors varsToFactor <- c("status","trt","ascites","hepato","spiders","edema","stage") pbc[varsToFactor] <- lapply(pbc[varsToFactor], factor)
## Create a variable list dput(names(pbc)) vars <- c("time","status","age","sex","ascites","hepato", "spiders","edema","bili","chol","albumin", "copper","alk.phos","ast","trig","platelet", "protime","stage")
## Create Table 1 stratified by trt tableOne <- CreateTableOne(vars = vars, strata = c("trt"), data = pbc)
## Just typing the object name will invoke the print.TableOne method
```
Specifying nonnormal variables will show the variables appropriately, and show nonparametric test p-values. Specify variables in the exact argument to obtain the exact test p-values. cramVars can be used to show both levels for a 2-level categorical variables.

```r
print(tableOne, nonnormal = c("bili","chol","copper","alk.phos","trig"),
      exact = c("status","stage"), cramVars = "hepato", smd = TRUE)
```

## Use the summary.TableOne method for detailed summary

```r
summary(tableOne)
```

## See the categorical part only using $ operator

```r
summary(tableOne$CatTable)
```

## See the continuous part only using $ operator

```r
summary(tableOne$ContTable)
```

## If your work flow includes copying to Excel and Word when writing manuscripts, you may benefit from the quote argument. This will quote everything so that Excel does not mess up the cells.

```r
print(tableOne, nonnormal = c("bili","chol","copper","alk.phos","trig"),
      exact = c("status","stage"), quote = TRUE)
```

## If you want to center-align values in Word, use noSpaces option.

```r
print(tableOne, nonnormal = c("bili","chol","copper","alk.phos","trig"),
      exact = c("status","stage"), quote = TRUE, noSpaces = TRUE)
```

## If SMDs are needed as numericals, use ExtractSmd()

```r
ExtractSmd(tableOne)
```

---

### Extract standardized mean differences from a (svy)TableOne object

#### Description

Extracts standardized mean differences data as a vector or matrix from a (svy)TableOne object

#### Usage

```r
ExtractSmd(x, varLabels = FALSE)
```

#### Arguments

- **x**: A stratified (svy)TableOne object containing standardized mean differences.
- **varLabels**: Whether to replace variable names with variable labels obtained from `labelled::var_label()` function.
kableone

Value
A vector or matrix containing the average standardized mean differences (if more than two contrasts exist) as well as the all possible pairwise standardized mean differences. Variables are ordered in the same order as the printed table.

Author(s)
Kazuki Yoshida

See Also
CreateTableOne, svyCreateTableOne

Examples
## See examples for CreateTableOne and svyCreateTableOne

```r
library(survival)
data(pbc)
tableOne <- CreateTableOne(data = pbc)
kableone(tableOne)
```

Description
Export TableOne Objects to Markdown

Usage
kableone(x, ...)

Arguments
- `x` an object created by a tableone function
- `...` arguments passed to `kable`

Value
A character vector of the table source code

Examples
```r
library(survival)
data(pbc)
tableOne <- CreateTableOne(data = pbc)
kableone(tableOne)
```
print.CatTable  

**Format and print CatTable class objects**

**Description**

print method for the CatTable class objects created by `CreateCatTable` function.

**Usage**

```r
## S3 method for class 'CatTable'
print(
  x,
  digits = 1,
  pDigits = 3,
  quote = FALSE,
  missing = FALSE,
  explain = TRUE,
  printToggle = TRUE,
  noSpaces = FALSE,
  format = c("fp", "f", "p", "pf")[1],
  showAllLevels = FALSE,
  cramVars = NULL,
  dropEqual = FALSE,
  test = TRUE,
  exact = NULL,
  smd = FALSE,
  CrossTable = FALSE,
  formatOptions = list(scientific = FALSE),
  ...
)
```

**Arguments**

- **x**: Object returned by `CreateCatTable` function.
- **digits**: Number of digits to print in the table.
- **pDigits**: Number of digits to print for p-values (also used for standardized mean differences).
- **quote**: Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.
- **missing**: Whether to show missing data information.
- **explain**: Whether to add explanation to the variable names, i.e., (%) is added to the variable names when percentage is shown.
- **printToggle**: Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned.
print.CatTable

noSpaces  Whether to remove spaces added for alignment. Use this option if you prefer to align numbers yourself in other software.

format  The default is "fp" frequency (percentage). You can also choose from "f" frequency only, "p" percentage only, and "pf" percentage (frequency).

showAllLevels  Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information.

cramVars  A character vector to specify the two-level categorical variables, for which both levels should be shown in one row.

dropEqual  Whether to drop " = second level name" description indicating which level is shown for two-level categorical variables.

test  Whether to show p-values. TRUE by default. If FALSE, only the numerical summaries are shown.

exact  A character vector to specify the variables for which the p-values should be those of exact tests. By default all p-values are from large sample approximation tests (chisq.test).

smd  Whether to show standardized mean differences. FALSE by default. If there are more than one contrasts, the average of all possible standardized mean differences is shown. For individual contrasts, use summary.

CrossTable  Whether to show the cross table objects held internally using gmodels::CrossTable function. This will give an output similar to the PROC FREQ in SAS.

formatOptions  A list of options, which will be passed to format. Can be used to modify the big.mark, decimal.mark, big.interval etc. The default is list(scientific = FALSE). The options digits, nsmall, justify and trim are not available. (Experimental)

...  For compatibility with generic. Ignored.

Value

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via write.csv.

Author(s)

Kazuki Yoshida, Alexander Bartel

See Also

CreateTableOne, CreateCatTable, summary.CatTable

Examples

```r
# Load
library(tableone)

# Load Mayo Clinic Primary Biliary Cirrhosis Data
library(survival)
```
```
data(pbc)
# Check variables
head(pbc)

# Create an overall table for categorical variables
catVars <- c("status","ascites","hepato","spiders","edema","stage")
catTableOverall <- CreateCatTable(vars = catVars, data = pbc)

# Simply typing the object name will invoke the print.CatTable method,
# which will show the sample size, frequencies and percentages.
# For 2-level variables, only the higher level is shown for simplicity.
catTableOverall

# If you need to show both levels for some 2-level factors, use cramVars
print(catTableOverall, cramVars = "hepato")

# Use the showAllLevels argument to see all levels for all variables.
print(catTableOverall, showAllLevels = TRUE)

# You can choose form frequencies ("f") and/or percentages ("p") or both.
# "fp" frequency (percentage) is the default. Row names change accordingly.
print(catTableOverall, format = "f")
print(catTableOverall, format = "p")

# To further examine the variables, use the summary.CatTable method,
# which will show more details.
summary(catTableOverall)

# The table can be stratified by one or more variables
catTableBySexTrt <- CreateCatTable(vars = catVars,
                                      strata = c("sex","trt"), data = pbc)

# print now includes p-values which are by default calculated by chisq.test.
# It is formatted at the decimal place specified by the pDigits argument
# (3 by default). It does <0.001 for you.
catTableBySexTrt

# The exact argument toggles the p-values to the exact test result from
# fisher.test. It will show which ones are from exact tests.
print(catTableBySexTrt, exact = "ascites")

# summary now includes both types of p-values
summary(catTableBySexTrt)

# If your work flow includes copying to Excel and Word when writing manuscripts,
# you may benefit from the quote argument. This will quote everything so that
# Excel does not mess up the cells.
print(catTableBySexTrt, exact = "ascites", quote = TRUE)

# If you want to center-align values in Word, use noSpaces option.
print(catTableBySexTrt, exact = "ascites", quote = TRUE, noSpaces = TRUE)
```
print.ContTable  Format and print ContTable class objects

Description

print method for the ContTable class objects created by CreateContTable function.

Usage

```r
## S3 method for class 'ContTable'
print(
  x,
  digits = 2,
  pDigits = 3,
  quote = FALSE,
  missing = FALSE,
  explain = TRUE,
  printToggle = TRUE,
  noSpaces = FALSE,
  nonnormal = NULL,
  minMax = FALSE,
  insertLevel = FALSE,
  test = TRUE,
  smd = FALSE,
  formatOptions = list(scientific = FALSE),
  ...
)
```

Arguments

- `x`: Object returned by CreateContTable function.
- `digits`: Number of digits to print in the table.
- `pDigits`: Number of digits to print for p-values (also used for standardized mean differences).
- `quote`: Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.
- `missing`: Whether to show missing data information.
- `explain`: Whether to add explanation to the variable names, i.e., (mean (SD) or median [IQR]) is added to the variable names.
- `printToggle`: Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned.
- `noSpaces`: Whether to remove spaces added for alignment. Use this option if you prefer to align numbers yourself in other software.
nonnormal A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test).

minMax Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.

insertLevel Whether to add an empty level column to the left of strata.

test Whether to show p-values. TRUE by default. If FALSE, only the numerical summaries are shown.

smd Whether to show standardized mean differences. FALSE by default. If there are more than one contrasts, the average of all possible standardized mean differences is shown. For individual contrasts, use summary.

formatOptions A list of options, which will be passed to format. Can be used to modify the big.mark, decimal.mark, big.interval etc. The default is list(scientific = FALSE). The options digits, nsmall, justify and trim are not available. (Experimental)

... For compatibility with generic. Ignored.

Value
A matrix object containing what you see is also invisibly returned. This can be assinged a name and exported via write.csv.

Author(s)
Kazuki Yoshida, Alexander Bartel

See Also
CreateTableOne, CreateContTable, summary.ContTable

Examples

```r
## Load library(tableone)
## Load Mayo Clinic Primary Biliary Cirrhosis Data library(survival) data(pbc) ## Check variables head(pbc)

## Create an overall table for continuous variables contVars <- c("time","age","bili","chol","albumin","copper", "alk.phos","ast","trig","platelet","protime") contTableOverall <- CreateContTable(vars = contVars, data = pbc)

## Simply typing the object name will invoke the print.ContTable method, ## which will show the sample size, means and standard deviations.
```
To further examine the variables, use the summary.ContTable method, which will show more details.

```r
table <- summary(contTableOverall)
```


```r
nonNormalVars <- c("age", "chol", "copper", "alk.phos", "trig", "protime")
print(contTableOverall, nonnormal = nonNormalVars)
```

To show median [min, max] for nonnormal variables, use `minMax = TRUE`

```r
print(contTableOverall, nonnormal = nonNormalVars, minMax = TRUE)
```

The table can be stratified by one or more variables

```r
contTableBySexTrt <- CreateContTable(vars = contVars,
                                     strata = c("sex", "trt"), data = pbc)
```

Print now includes p-values which are by default calculated by `oneway.test` (t-test equivalent in the two group case). It is formatted at the decimal place specified by the `pDigits` argument (3 by default). It does <0.001 for you.

```r
contTableBySexTrt
```

The nonnormal argument toggles the p-values to the nonparametric result from `kruskal.test` (wilcox.test equivalent for the two group case).

```r
print(contTableBySexTrt, nonnormal = nonNormalVars)
```

The `minMax` argument toggles whether to show median [range]

```r
print(contTableBySexTrt, nonnormal = nonNormalVars, minMax = TRUE)
```

Summary now includes both types of p-values

```r
summary(contTableBySexTrt)
```

If your workflow includes copying to Excel and Word when writing manuscripts, you may benefit from the `quote` argument. This will quote everything so that Excel does not mess up the cells.

```r
print(contTableBySexTrt, nonnormal = nonNormalVars, quote = TRUE)
```

If you want to center-align values in Word, use the `noSpaces` option.

```r
print(contTableBySexTrt, nonnormal = nonNormalVars, quote = TRUE, noSpaces = TRUE)
```
## Usage

```r
## S3 method for class 'svyCatTable'
print(
  x,
  digits = 1,
  pDigits = 3,
  quote = FALSE,
  missing = FALSE,
  explain = TRUE,
  printToggle = TRUE,
  noSpaces = FALSE,
  format = c("fp", "f", "p", "pf")[1],
  showAllLevels = FALSE,
  cramVars = NULL,
  dropEqual = FALSE,
  test = TRUE,
  exact = NULL,
  smd = FALSE,
  CrossTable = FALSE,
  formatOptions = list(scientific = FALSE),
  ...
)
```

## Arguments

- `x` The result of a call to the `svyCreateCatTable` function.
- `digits` Number of digits to print in the table.
- `pDigits` Number of digits to print for p-values (also used for standardized mean differences).
- `quote` Whether to show everything in quotes. The default is `FALSE`. If `TRUE`, everything including the row and column names are quoted so that you can copy it to Excel easily.
- `missing` Whether to show missing data information.
- `explain` Whether to add explanation to the variable names, i.e., (%) is added to the variable names when percentage is shown.
- `printToggle` Whether to print the output. If `FALSE`, no output is created, and a matrix is invisibly returned.
- `noSpaces` Whether to remove spaces added for alignment. Use this option if you prefer to align numbers yourself in other software.
- `format` The default is "fp" frequency (percentage). You can also choose from "f" frequency only, "p" percentage only, and "pf" percentage (frequency).
- `showAllLevels` Whether to show all levels. `FALSE` by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information.
- `cramVars` A character vector to specify the two-level categorical variables, for which both levels should be shown in one row.
print.svyContTable

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dropEqual</td>
<td>Whether to drop &quot; = second level name&quot; description indicating which level is shown for two-level categorical variables.</td>
</tr>
<tr>
<td>test</td>
<td>Whether to show p-values. TRUE by default. If FALSE, only the numerical summaries are shown.</td>
</tr>
<tr>
<td>exact</td>
<td>This option is not available for tables from weighted data.</td>
</tr>
<tr>
<td>smd</td>
<td>Whether to show standardized mean differences. FALSE by default. If there are more than one contrasts, the average of all possible standardized mean differences is shown. For individual contrasts, use summary.</td>
</tr>
<tr>
<td>CrossTable</td>
<td>Whether to show the cross table objects held internally using gmodels::CrossTable function. This will give an output similar to the PROC FREQ in SAS.</td>
</tr>
<tr>
<td>formatOptions</td>
<td>A list of options, which will be passed to format. Can be used to modify the big.mark, decimal.mark, big.interval etc. The default is list(scientific = FALSE). The options digits, nsmall, justify and trim are not available. (Experimental)</td>
</tr>
<tr>
<td>...</td>
<td>For compatibility with generic. Ignored.</td>
</tr>
</tbody>
</table>

Value

A matrix object containing what you see is also invisibly returned. This can be assigned a name and exported via write.csv.

Author(s)

Kazuki Yoshida, Alexander Bartel

See Also

svyCreateTableOne, svyCreateCatTable, summary.svyCatTable

Examples

## See the examples for svyCreateTableOne()

print.svyContTable | Format and print svyContTable class objects

Description

print method for the svyContTable class objects created by CreateContTable function.
Usage

```r
## S3 method for class 'svyContTable'
print(
  x,
  digits = 2,
  pDigits = 3,
  quote = FALSE,
  missing = FALSE,
  explain = TRUE,
  printToggle = TRUE,
  noSpaces = FALSE,
  nonnormal = NULL,
  minMax = FALSE,
  insertLevel = FALSE,
  test = TRUE,
  smd = FALSE,
  formatOptions = list(scientific = FALSE),
  ...
)
```

Arguments

- `x`: Object returned by `svyCreateContTable` function.
- `digits`: Number of digits to print in the table.
- `pDigits`: Number of digits to print for p-values (also used for standardized mean differences).
- `quote`: Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.
- `missing`: Whether to show missing data information.
- `explain`: Whether to add explanation to the variable names, i.e., (mean (SD) or median [IQR]) is added to the variable names.
- `printToggle`: Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned.
- `noSpaces`: Whether to remove spaces added for alignment. Use this option if you prefer to align numbers yourself in other software.
- `nonnormal`: A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test).
- `minMax`: Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.
- `insertLevel`: Whether to add an empty level column to the left of strata.
- `test`: Whether to show p-values. TRUE by default. If FALSE, only the numerical summaries are shown.
smd
Whether to show standardized mean differences. FALSE by default. If there are more than one contrasts, the average of all possible standardized mean differences is shown. For individual contrasts, use `summary`.

formatOptions
A list of options, which will be passed to `format`. Can be used to modify the `big.mark`, `decimal.mark`, `big.interval` etc. The default is `list(scientific = FALSE)`. The options `digits`, `nsmall`, `justify` and `trim` are not available. (Experimental)

... For compatibility with generic. Ignored.

Value
A matrix object containing what you see is also invisibly returned. This can be assinged a name and exported via `write.csv`.

Author(s)
Kazuki Yoshida, Alexander Bartel

See Also
`svyCreateTableOne`, `svyCreateCatTable`, `summary.svyCatTable`

Examples

```r
## See the examples for svyCreateTableOne()
```

---

### print.TableOne

**Format and print TableOne class objects**

#### Description

print method for the TableOne class objects created by ` CreateTableOne` function.

#### Usage

```r
## S3 method for class 'TableOne'
print(  
  x,  
  catDigits = 1,  
  contDigits = 2,  
  pDigits = 3,  
  quote = FALSE,  
  missing = FALSE,  
  explain = TRUE,  
  printToggle = TRUE,
```

```
test = TRUE,
smd = FALSE,
noSpaces = FALSE,
padColnames = FALSE,
varLabels = FALSE,
format = c("fp", "f", "p", "pf")[1],
showAllLevels = FALSE,
cramVars = NULL,
dropEqual = FALSE,
exact = NULL,
nonnormal = NULL,
minMax = FALSE,
formatOptions = list(scientific = FALSE),
...)

Arguments
x Object returned by CreateTableOne function.
catDigits Number of digits to print for proportions. Default 1.
contDigits Number of digits to print for continuous variables. Default 2.
pDigits Number of digits to print for p-values (also used for standardized mean differences). Default 3.
quote Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.
missing Whether to show missing data information.
explain Whether to add explanation to the variable names, i.e., (%) is added to the variable names when percentage is shown.
printToggle Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned.
test Whether to show p-values. TRUE by default. If FALSE, only the numerical summaries are shown.
smd Whether to show standardized mean differences. FALSE by default. If there are more than one contrasts, the average of all possible standardized mean differences is shown. For individual contrasts, use summary.
noSpaces Whether to remove spaces added for alignment. Use this option if you prefer to align numbers yourself in other software.
padColnames Whether to pad column names with spaces to center justify. The default is FALSE. It is not conducted if noSpaces = TRUE.
varLabels Whether to replace variable names with variable labels obtained from labelled::var_label() function.
format The default is "fp" frequency (percentage). You can also choose from "f" frequency only, "p" percentage only, and "pf" percentage (frequency).
showAllLevels  Whether to show all levels. FALSE by default, i.e., for 2-level categorical variables, only the higher level is shown to avoid redundant information.

cramVars  A character vector to specify the two-level categorical variables, for which both levels should be shown in one row.

dropEqual  Whether to drop " = second level name" description indicating which level is shown for two-level categorical variables.

exact  A character vector to specify the variables for which the p-values should be those of exact tests. By default all p-values are from large sample approximation tests (chisq.test).

nonnormal  A character vector to specify the variables for which the p-values should be those of nonparametric tests. By default all p-values are from normal assumption-based tests (oneway.test).

minMax  Whether to use [min,max] instead of [p25,p75] for nonnormal variables. The default is FALSE.

formatOptions  A list of options, which will be passed to format. Can be used to modify the big.mark, decimal.mark, big.interval etc. The default is list(scientific = FALSE). The options digits, nsmall, justify and trim are not available. (Experimental)

...  For compatibility with generic. Ignored.

Value

A matrix object containing what you see is also invisibly returned. This can be assinged a name and exported via write.csv.

Author(s)

Kazuki Yoshida, Justin Bohn, Alexander Bartel

See Also

CreateTableOne, CreateTableOne, summary.TableOne

Examples

## See examples for CreateTableOne and svyCreateTableOne
ShowRegTable  

Format regression results in medically decent format

Description

It shows the regression result in the HR [95% CI] p-value format, which is usually the form used in medical research papers.

Usage

ShowRegTable(
  model,
  exp = TRUE,
  digits = 2,
  pDigits = 3,
  printToggle = TRUE,
  quote = FALSE,
  ciFun = confint
)

Arguments

model  Regression model result objects that have the summary and confint methods.
exp  TRUE by default. You need to specify exp = FALSE if your model is has the identity link function (linear regression, etc).
digits  Number of digits to print for the main part.
pDigits  Number of digits to print for the p-values.
printToggle  Whether to print the output. If FALSE, no output is created, and a matrix is invisibly returned.
quote  Whether to show everything in quotes. The default is FALSE. If TRUE, everything including the row and column names are quoted so that you can copy it to Excel easily.
ciFun  Function used for calculation. confint is the default. For generalized linear models this gives the profile likelihood-based calculation, which may take too much time for large models, use confint.default for simple normal approximation method (+/- 1.96 * standard error).

Value

A matrix containing what you see is returned invisibly. You can capture it by assignment to an object.

Author(s)

Kazuki Yoshida
Examples

```r
## Load
library(tableone)

## Load Mayo Clinic Primary Biliary Cirrhosis Data
library(survival)
data(pbc)

## Check variables
head(pbc)

## Fit a Cox regression model
objCoxph <- coxph(formula = Surv(time, status == 2) ~ trt + age + albumin + ascites,
data = pbc)

## Show the simple table
ShowRegTable(objCoxph)

## Show with quote to ease copy and paste
ShowRegTable(objCoxph, quote = TRUE)
```

**summary.CatTable**  
*Shows all results in a CatTable class object*

Description

Shows all data a CatTable class object has. This includes the (optionally stratified) part with summary statistics and, if available, p-values from the approximation method test (`chisq.test` by default) and exact method test (`fisher.test` by default) and standardized mean differences of all possible pairwise contrasts.

Usage

```r
## S3 method for class 'CatTable'
summary(object, digits = 1, ...)
```

Arguments

- `object` An object that has the CatTable class to be shown.
- `digits` Number of digits to print.
- `...` For compatibility with generic. Ignored.

Value

None. Results are printed.
Author(s)

Kazuki Yoshida

See Also

CreateTableOne, CreateCatTable, print.CatTable.

Examples

## See examples for CreateTableOne

---

summary.ContTable  
*Shows all results in a ContTable class object*

Description

Shows all data a ContTable class object has. This includes the (optionally stratified) part with summary statistics and, if available, p-values from the normal assumption-based test (oneway.test by default) and nonparametric test (kruskal.test by default) and standardized mean differences of all possible pairwise contrasts.

Usage

## S3 method for class 'ContTable'
summary(object, digits = 2, ...)

Arguments

- **object**: An object that has the ContTable class to be shown.
- **digits**: Number of digits to print.
- **...**: For compatibility with generic. Ignored.

Value

None. Results are printed.

Author(s)

Kazuki Yoshida

See Also

CreateTableOne, CreateContTable, print.ContTable
Examples

```r
## See examples for CreateTableOne
```

### Description

Shows all data a `svyCatTable` class object has. This includes the (optionally stratified) part with summary statistics and, if available, p-values from the approximation method test (`chisq.test` by default) and exact method test (`fisher.test` by default) and standardized mean differences of all possible pairwise contrasts.

### Usage

```r
## S3 method for class 'svyCatTable'
summary(object, digits = 1, ...)
```

### Arguments

- `object`: An object that has the `svyCatTable` class to be shown.
- `digits`: Number of digits to print.
- `...`: For compatibility with generic. Ignored.

### Value

None. Results are printed.

### Author(s)

Kazuki Yoshida

### See Also

- `svyCreateTableOne`, `svyCreateCatTable`, `print.svyCatTable`

### Examples

```r
## See the examples for svyCreateTableOne()
```
summary.svyContTable  
*Shows all results in a svyContTable class object*

**Description**

Shows all data a svyContTable class object has. This includes the (optionally stratified) part with summary statistics and, if available, p-values from the normal assumption-based test (regTermTest with svyglm by default) and nonparametric test (svyranktest by default) and standardized mean differences of all possible pairwise contrasts.

**Usage**

```r
## S3 method for class 'svyContTable'
summary(object, digits = 2, ...)
```

**Arguments**

- `object` An object that has the svyContTable class to be shown.
- `digits` Number of digits to print.
- `...` For compatibility with generic. Ignored.

**Value**

None. Results are printed.

**Author(s)**

Kazuki Yoshida

**See Also**

- `svyCreateTableOne`, `svyCreateContTable`, `print.svyContTable`

**Examples**

```r
## See the examples for svyCreateTableOne()
```
**summary.TableOne**

*Shows all results in a (svy)TableOne class object*

---

**Description**

Shows all data a (svy)TableOne class object has. This includes the (optionally stratified) part with summary statistics and p-values and/or standardized mean differences.

**Usage**

```r
## S3 method for class 'TableOne'
summary(object, digits = 1, ...)
```

**Arguments**

- `object` An object that has the (svy)TableOne class to be shown.
- `digits` Number of digits to print.
- `...` For compatibility with generic. Ignored.

**Value**

None. Results are printed.

**Author(s)**

Kazuki Yoshida

**See Also**

`CreateTableOne`, `svyCreateCatTable`

**Examples**

```r
## See examples for CreateTableOne and svyCreateTableOne
```
svyCreateCatTable

Create an object summarizing categorical variables for weighted data

Description

Create an object summarizing categorical variables optionally stratifying by one or more stratifying variables and performing statistical tests. Usually, `svyCreateTableOne` should be used as the universal frontend for both continuous and categorical data.

Usage

```
svyCreateCatTable(
  vars,
  strata,
  data,
  includeNA = FALSE,
  test = TRUE,
  testApprox = svyTestChisq,
  argsApprox = NULL,
  smd = TRUE,
  addOverall = FALSE
)
```

Arguments

- **vars**: Variable(s) to be summarized given as a character vector.
- **strata**: Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.
- **data**: A survey design object in which these variables exist. All variables (both vars and strata) must be in this survey design object. It is created with the `svydesign` function in the `survey` package.
- **includeNA**: If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables.
- **test**: If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed. Both tests that require the large sample approximation and exact tests are performed. Either one of the result can be obtained from the print method.
- **testApprox**: A function used to perform the large sample approximation based tests. The default is `svychisq`.
- **argsApprox**: A named list of arguments passed to the function specified in `testApprox`.
- **smd**: If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.
- **addOverall**: (optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.
svyCreateContTable

Value

An object of class svyCatTable.

Author(s)

Kazuki Yoshida, Alexander Bartel

See Also

svyCreateTableOne, print.svyCatTable, summary.svyCatTable.

Examples

## See the examples for svyCreateTableOne()

svyCreateContTable

Create an object summarizing continuous variables for weighted dataset

Description

Create an object summarizing continuous variables optionally stratifying by one or more stratifying variables and performing statistical tests. Usually, svyCreateTableOne should be used as the universal frontend for both continuous and categorical data.

Usage

svyCreateContTable(
  vars,
  strata,
  data,
  test = TRUE,
  testNormal = svyTestNormal,
  argsNormal = list(method = "Wald"),
  testNonNormal = svyTestNonNormal,
  argsNonNormal = NULL,
  smd = TRUE,
  addOverall = FALSE
)
svyCreateContTable

Arguments

vars Variable(s) to be summarized given as a character vector.

strata Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.

data A survey design object in which these variables exist. All variables (both vars and strata) must be in this survey design object. It is created with the svydesign function in the survey package.

test If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed. Both tests that assume normality and tests that do not are performed. Either one of the result can be obtained from the print method.

testNormal A function used to perform the normal assumption based tests. The default is multiple degrees of freedom test using svyglm and regTermTest. This is equivalent of the svytest when there are only two groups.

argsNormal A named list of arguments passed to the function specified in testNormal.

testNonNormal A function used to perform the nonparametric tests. The default is svyranktest.

argsNonNormal A named list of arguments passed to the function specified in testNonNormal.

smd If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.

addOverall (optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.

Value

An object of class svyContTable.

Author(s)

Kazuki Yoshida, Alexander Bartel

See Also

svyCreateTableOne, print.svyContTable, summary.svyContTable.

Examples

## See the examples for svyCreateTableOne()
svyCreateTableOne

Create an object summarizing both continuous and categorical variables for weighted data

**Description**

Create an object summarizing all baseline variables (both continuous and categorical) optionally stratifying by one or more stratifying variables and performing statistical tests. The object gives a table that is easy to use in medical research papers.

**Usage**

```r
svyCreateTableOne(
  vars,
  strata,
  data,
  factorVars,
  includeNA = FALSE,
  test = TRUE,
  testApprox = svyTestChisq,
  argsApprox = NULL,
  testNormal = svyTestNormal,
  argsNormal = list(method = "Wald"),
  testNonNormal = svyTestNonNormal,
  argsNonNormal = NULL,
  smd = TRUE,
  addOverall = FALSE
)
```

**Arguments**

- **vars**: Variables to be summarized given as a character vector. Factors are handled as categorical variables, whereas numeric variables are handled as continuous variables. If empty, all variables in the survey design object specified in the data argument are used.

- **strata**: Stratifying (grouping) variable name(s) given as a character vector. If omitted, the overall results are returned.

- **data**: A survey design object in which these variables exist. All variables (both vars and strata) must be in this survey design object. It is created with the `svydesign` function in the `survey` package.

- **factorVars**: Numerically coded variables that should be handled as categorical variables given as a character vector. Do not include factors, unless you need to relevel them by removing empty levels. If omitted, only factors are considered categorical variables. The variables specified here must also be specified in the `vars` argument.
includeNA  If TRUE, NA is handled as a regular factor level rather than missing. NA is shown as the last factor level in the table. Only effective for categorical variables.
test  If TRUE, as in the default and there are more than two groups, groupwise comparisons are performed.
testApprox  A function used to perform the large sample approximation based tests. The default is svychisq.
argsApprox  A named list of arguments passed to the function specified in testApprox.
testNormal  A function used to perform the normal assumption based tests. The default is multiple degrees of freedom test using svyglm and regTermTest. This is equivalent of the svyttest when there are only two groups.
argsNormal  A named list of arguments passed to the function specified in testNormal.
testNonNormal  A function used to perform the nonparametric tests. The default is svyranktest.
argsNonNormal  A named list of arguments passed to the function specified in testNonNormal.
smd  If TRUE, as in the default and there are more than two groups, standardized mean differences for all pairwise comparisons are calculated.
addOverall  (optional, only used if strata are supplied) Adds an overall column to the table. Smd and p-value calculations are performed using only the stratified columns.

Details
See the details for CreateTableOne.

Value
An object of class svyTableOne, which is a list of three objects.

ContTable  an object of class svyContTable, containing continuous variables only
CatTable  an object of class svyCatTable, containing categorical variables only
MetaData  list of metadata regarding variables

Author(s)
Kazuki Yoshida

See Also
print.TableOne, summary.TableOne

Examples

## Load packages
library(tableone)
library(survey)

## Create a weighted survey design object
svyCreateTableOne

data(nhanes)

nhanesSvy <- svydesign(ids = ~ SDMVPSU, strata = ~ SDMVSTRA, weights = ~ WTMEC2YR, 
est = TRUE, data = nhanes)

## Create a table object
## factorVars are converted to factors; no need for variables already factors
## strata will stratify summaries; leave it unspecified for overall summaries

tab1 <- svyCreateTableOne(vars = c("HI_CHOL","race","agecat","RIAGENDR"),
                         strata = "RIAGENDR", data = nhanesSvy, 
factorVars = c("race","RIAGENDR"))

## Detailed output
summary(tab1)

## Default formatted printing

print(tab1)

## nonnormal specifies variables to be shown as median [IQR]
print(tab1, nonnormal = "HI_CHOL", contDigits = 3, catDigits = 2, 
pDigits = 4, smd = TRUE)

## minMax changes it to median [min, max]
print(tab1, nonnormal = "HI_CHOL", minMax = TRUE, contDigits = 3, 
catDigits = 2, pDigits = 4, smd = TRUE)

## showAllLevels can be used to show levels for all categorical variables
print(tab1, showAllLevels = TRUE, smd = TRUE)

## To see all printing options
?print.TableOne

## To examine categorical variables only

tab1$CatTable

## To examine continuous variables only

tab1$ContTable

## If SMDs are needed as numericals, use ExtractSmd()

ExtractSmd(tab1)
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