uOneSample Function Descriptions
Version 20121110

This document contains help files for the one sample inference functions:

- `oneSample( )`: general one sample inference for an arbitrary functional (mean, geometric mean, proportion, ...) of a single variable, possibly subsetted.
- `print.uOneSample( )`: the print method for `uoneSample` objects returned by `oneSample()`.

Function Interface: oneSample

Description

Produces point estimates, interval estimates, and p values for an arbitrary functional (mean, geometric mean, proportion, median, quantile, odds) of a variable of class `integer, numeric, Surv,` or `Date`. A variety of inferential methods are provided, with the choices depending on the functional and the data type.

Usage

```
oneSample (fnctl, y, null.hypothesis=NA, test.type="two.sided", subset=rep(TRUE,N),
        conf.level=0.95, na.rm=TRUE, probs= 0.5, replaceZeroes=NULL, restriction=Inf,
        subjTime=rep(1,length(y)), method= NULL, above=NULL, below=NULL,
        labove=NULL, rbelow=NULL, interval=NULL, linterval=NULL, rinterval=NULL,
        lrinterval=NULL, g1=1, g2=0, dispersion=1, nbstrap=10000, resample="pairs",
        seed=0, ..., version=FALSE) {
```

Arguments

`fnctl`	a character string indicating the functional (summary measure of the distribution) for which inference is desired. Choices include `"mean", "geometric mean", "proportion", "median", "quantile", "odds", "rate"`. The character string may be shortened to a unique substring. Hence `"mea"` will suffice for `"mean"`.
`y`	a variable for whichone sample inference is desired. The variable may be of class `numeric`, `Surv`, or `Date`.
`null.hypothesis`	a numeric scalar indicating any null hypothesis to be tested.

`test.type`	a character string indicating whether a hypothesis test is to be of a one sided test of a lesser alternative hypothesis (`"less"`), a one sided test of a greater alternative hypothesis (`"greater"`),. or a test of a two sided alternative hypothesis (`"two.sided"`). The default value is `"two.sided"`.
`subset`	vector indicating a subset to be used for all inference.
`conf.level`	a numeric scalar indicating the level of confidence to be used in computing confidence intervals. The default is 0.95.
`probs`	a probability between 0 and 1 indicating the quantile used for inference. Default is to compute the 50th (median) percentile.
`replaceZeroes`	if not FALSE, this indicates a value to be used in place of zeroes when computing a geometric mean. If TRUE, a value equal to one-half the lowest nonzero value is used. If a numeric value is supplied, that value is used.
`restriction`	a value used for computing restricted means and geometric means with censored time to event data. The default value of `Inf` will cause restrictions at the highest observation.
`method`	a character string used to indicate inferential methods. Allowed choices depend on the variable type and the functional. Default values are `"t.test"` for means and geometric means, and `"exact"` for proportions of uncensored data, and `KM"` for censored survival data.
`above`	a value used to dichotomize variables. Inference will be on the proportion of measurements with values greater than `above`. Default is 0.
`below`	a value used to dichotomize variables. Inference will be on the proportion of measurements with values less than `below`.
`labove`	a vector of values used to dichotomize variables. Inference will be on the proportion of measurements with values greater than or equal to `labove`.
`rbelow`	a vector of values used to dichotomize variables. Inference will be on the proportion of measurements with values less than or equal to `rbelow`.

`interval`	a two column matrix of values in which each row is used to define intervals of interest to categorize variables. Inference will be on the proportion of measurements with values between the two values, with neither endpoint being included in each interval.
`linterval`	a two column matrix of values in which each row is used to define intervals of interest to categorize variables. Inference will be on the proportion of measurements with values between the two values, with the left hand endpoint being included in each interval.
`rinterval`	a two column matrix of values in which each row is used to define intervals of interest to categorize variables. Inference will be on the proportion of measurements with values between the two values, with the right hand endpoint being included in each interval.
`lrinterval`	a two column matrix of values in which each row is used to define intervals of interest to categorize variables. Inference will be on the proportion of measurements with values between the two values, with both endpoints being included in each interval.
`version`	if TRUE, the version of the function will be returned. No other computations will be performed.

Value

An object of class `uOneSample` is returned. Inferential statistics are contained in a vector named `$Inference` that includes the sample size, the point estimate, the lower and upper bounds of a confidence interval, any null hypothesis that was specified, and the p value. Also included is a vector named `$Statistics` that includes more technical information.

There is a print method that will format the descriptive statistics for the `Date` and `Surv` objects.

Details

Default values for inference correspond to the most commonly implemented methods. Additional methods are provided more for educational purposed than for purposes of statistical analysis.

Examples

```
# Sourcing the R code
source("http://www.emersonstatistics.com/courses/formal/b517_2012/uOneSample.txt")

# Reading in a dataset
mri <- read.table("http://www.emersonstatistics.com/datasets/mri.txt",header=T)

# Creating a Surv object to reflect time to death
mri$ttodth <- Surv(mri$obstime,mri$death)

# Reformatting an integer MMDDYY representation of date to be a Date object
mri$mridate <- as.Date(paste(trunc(mri$mridate/10000),trunc((mri$mridate %% 10000)/100),
               mri$mridate %% 100,sep="/"),"%m/%d/%y")
```

```
# Inference about the mean LDL: a two sample t test that mean LDL is 135 mg/dl
oneSample ("mean", mri$ldl, null.hypothesis=125)

# Inference about the mean LDL: a one sample t test of a lesser alternative
# that mean LDL is 125 mg/dl
oneSample ("mean", mri$ldl, null.hypothesis=125, test.type="less")

# Inference about the mean LDL: a one sample t test of a greater alternative
# that mean LDL is 125 mg/dl
oneSample ("mean", mri$ldl, null.hypothesis=125, test.type="greater")

# Inference about the geometric mean LDL: a one sample t test of a greater
# alternative that geometric mean LDL is 125 mg/dl
oneSample ("geom", mri$ldl, null.hypothesis=125, test.type="greater")

# Inference about the proportion of subjects with LDL greater than 128: exact binomial
# inference that 50\% of subjects have LDL greater than 128 mg/dl
oneSample ("prop", mri$ldl, null.hypothesis=0.5, above=128)
oneSample ("prop",mri$ldl>128, null.hypothesis=0.5)
```