Package 'MCHT'

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.onAttach

Package Attach Hook Function

Description

Hook triggered when package attached

Usage

```
.onAttach(lib, pkg)
```

Arguments

1ib a character string giving the library directory where the package defining the

namespace was found

pkg a character string giving the name of the package

Examples

```
MCHT:::onAttach(.libPaths()[1], "MCHT")
```

```
check_params_in_functions
```

Check That Parameters Are In Functions

Description

Test that certain parameters are arguments for certain functions via **testthat** functions.

Usage

```
check_params_in_functions(params, func_list)
```

Arguments

params Character vector with parameter names

func_list List of functions to check

```
MCHT:::check_params_in_functions(c("x"), list(mean))
```

gen_memo_rng 3

gen_memo_rng

Memoised Random Variable Generation

Description

Creates a function that generates random numbers with memoization

Usage

```
gen_memo_rng(r, seed = NULL)
```

Arguments

r The random number generator

seed The seed value, to be passed to set.seed

Details

This is a function generator, with the returned function being one that can handle a set seed and will remember if it needs to regenerate a new set of random numbers. This allows both for control over random number generation and for faster performance.

Value

A function that generates random numbers with a set seed and with memoization; accepts seed and all other arguments that could be passed to the original random number generator

Examples

```
memo_runif <- MCHT:::gen_memo_rng(runif)
memo_runif(10)</pre>
```

```
get_MCHTest_settings Get Attributes of MCHTest Object
```

Description

Get the settings of an MCHTest-class object.

Usage

```
get_MCHTest_settings(x)
```

Arguments

x The MCHTest-class object

Value

A list with all the variables relevant to x

Examples

```
f <- MCHTest(mean, mean, seed = 100)
get_MCHTest_settings(f)</pre>
```

is.MCHTest

Is an Object of Type MCHTest?

Description

Checks whether its argument is an MCHTest-class object.

Usage

```
is.MCHTest(x)
```

Arguments

Х

An R object

Value

TRUE if x is an MCHTest-class objet, FALSE otherwise

Examples

```
f <- MCHTest(mean, mean, seed = 100)
is.MCHTest(1)
is.MCHTest(f)</pre>
```

MCHTest

Create an MCHTest Object

Description

This function creates an MCHTest-class object, an S3 object that defines a bootstrap or Monte Carlo test

Usage

```
MCHTest(test_stat, stat_gen, rand_gen = stats::runif, N = 10000,
    seed = NULL, memoise_sample = TRUE, pval_func = MCHT::pval,
    method = "Monte Carlo Test", test_params = NULL,
    fixed_params = NULL, nuisance_params = NULL, optim_control = NULL,
    tiebreaking = FALSE, lock_alternative = TRUE, threshold_pval = 1,
    suppress_threshold_warning = FALSE)
```

Arguments

test_stat A function that computes the test statistic from input data; x must be a parameter

of this function representing test data

stat_gen A function that generates values of the test statistic when given data; x (rep-

resenting a sample) must be a parameter of this function, and this function is expected to return one numeric output, but if n is a parameter, this will be interpreted as sample size information (this could be useful for allowing a "burn-in" period in random data, as is often the case when working with time series data)

rand_gen A function generating random data, accepting a parameter n (representing the

size of the data) or x (which would be the actual data)

N Integer representing the number of replications of stat_gen to generate

seed The random seed used to generate simulated statistic values; if NULL, the seed

 $will be \ randomly \ chosen \ each \ time \ the \ resulting \ function \ is \ called \ (unless \ memoise_sample$

is TRUE)

memoise_sample If TRUE, simulated statistic values are saved and will be used repeatedly if the

inputs to $stat_gen\ don't\ change\ (such\ as\ the\ sample\ size,\ n);$ this could be in conflict with seed if seed is NULL, so set to FALSE to allow for regeneration of

random samples for every call to the resulting function

pval_func A function that computes p-values from the test statistic computed by test_stat

using the simulated data generated via stat_gen; see pval for an example of

how this function should be specified

method A string labelling the test

test_params A character vector of the names of parameters with values specified under the

null hypothesis; both test_stat and stat_gen need to be able to recognize the contents of this vector as parameters (for example, if this argument is "mu", then mu needs to be an argument of both test_stat and stat_gen), and the resulting test will try to pass these parameters to rand_gen (but these *do not* need to be

parameters of rand_gen)

fixed_params A character vector of the names of parameters treated as fixed values; this isn't

needed but if these parameters are being used then test output is more informative and errors will be raised if test_stat and stat_gen don't accept these parameters—which is safer—and the resulting test will try to pass these param-

eters to rand_gen (but these *do not* need to be parameters of rand_gen)

nuisance_params

A character vector of the names of parameters to be treated as nuisance parameters which must be chosen via optimization (see (Dufour 2006)); must be parameters of test_stat and stat_gen, but these *will not* be viewed as param-

eters of rand_gen, and cannot be non-NULL if codeoptim_control is NULL

optim_control A list of arguments to be passed to GenSA, containing at least lower and upper

elements as named vectors, with the names being identical to nuisance_params, but could also include other arguments to be passed to GenSA; the fn parameter will be set, and parameters of that function will be the parameters mentioned in nuisance_params, and this argument will be ignored if nuisance_params is

NULL

tiebreaking Break ties using the method as described in Dufour (2006); won't work if pval_func

doesn't support it via a unif_gen argument, and should only be used for test

statistics not computed on continuously-distributed data

lock_alternative

If TRUE, then the resulting function will effectively ignore the alternative parameter, while if FALSE, the resulting function will be sensitive to values of alternative; this argument exists to prevent shooting yourself in the foot and accidentally computing p-values in inappropriate ways

threshold_pval A numeric value that represents a threshold *p*-value that, if surpassed by the optimization algorithm, will cause the algorithm to terminate; will override the threshold.stop argument in the control list that's used by GenSA

suppress_threshold_warning

If TRUE, user will not be warned if the threshold p-value was surpassed by the optimization algorithm

Value

A MCHTest-class object, a function with parameters x, alternative, and ..., with other parameters being passed to functions such as those passed to test_stat and stat_gen, controlling what's tested and how; depending on lock_alternative, the alternative argument may be ignored

```
dat <- c(0.16, 1.00, 0.67, 1.28, 0.31, 1.16, 1.25, 0.93, 0.66, 0.54)
# Monte Carlo t-test for exponentially distributed data
mc.t.test <- MCHTest(test_stat = function(x, mu = 1) {</pre>
                        sqrt(length(x)) * (mean(x) - mu)/sd(x)
                      }, stat_gen = function(x, mu = 1) {
                        x \leftarrow x * mu
                        sqrt(length(x)) * (mean(x) - mu)/sd(x)
                      }, rand_gen = rexp, seed = 123,
                      method = "Monte Carlo t-Test", test_params = "mu",
                      lock_alternative = FALSE)
mc.t.test(dat)
mc.t.test(dat, mu = 0.1, alternative = "two.sided")
# Testing for the scale parameter of a Weibull distribution
# Two-sided test for location of scale parameter
library(MASS)
library(fitdistrplus)
ts <- function(x, scale = 1) {</pre>
  fit_null <- coef(fitdist(x, "weibull", fix.arg = list("scale" = scale)))</pre>
  kt <- fit_null[["shape"]]</pre>
  10 <- scale
  fit_all <- coef(fitdist(x, "weibull"))</pre>
  kh <- fit_all[["shape"]]</pre>
  lh <- fit_all[["scale"]]</pre>
  n \leftarrow length(x)
  # Test statistic, based on the negative-log-likelihood ratio
  suppressWarnings(n * ((kt - 1) * log(l0) - (kh - 1) * log(lh) -
      log(kt/kh) - log(lh/l0)) - (kt - kh) * sum(log(x)) + l0^(-kt) *
      sum(x^kt) - lh^(-kh) * sum(x^kh)
}
sg <- function(x, scale = 1, shape = 1) {</pre>
 x <- qweibull(x, shape = shape, scale = scale)</pre>
  ts(x, scale = scale)
```

```
}
mc.wei.shape.test <- MCHTest(ts, sg, seed = 123, test_params = "scale",</pre>
                               nuisance_params = "shape",
                               optim_control = list(
                                 lower = c("shape" = 0),
                                 upper = c("shape" = 100),
                                 control = list("max.time" = 10)
                               ), threshold_pval = .2, N = 1000)
mc.wei.shape.test(rweibull(100, scale = 4, shape = 2), scale = 2)
# Bootstrap hypothesis test
# Kolmogorov-Smirnov test for Weibull distribution via parametric botstrap
# hypothesis test
ts <- function(x) {</pre>
  param <- coef(fitdist(x, "weibull"))</pre>
  shape <- param[['shape']]; scale <- param[['scale']]</pre>
 ks.test(x, pweibull, shape = shape, scale = scale,
          alternative = "two.sided")$statistic[[1]]
rg <- function(x) {</pre>
 n <- length(x)</pre>
  param <- coef(fitdist(x, "weibull"))</pre>
  shape <- param[['shape']]; scale <- param[['scale']]</pre>
  rweibull(n, shape = shape, scale = scale)
b.ks.test <- MCHTest(test_stat = ts, stat_gen = ts, rand_gen = rg,</pre>
                      seed = 123, N = 1000)
b.ks.test(rbeta(100, 2, 2))
# Permutation test
df <- data.frame(</pre>
 val = c(rnorm(5, mean = 2, sd = 3), rnorm(10, mean = 1, sd = 2)),
  group = rep(c("x", "y"), times = c(5, 10))
ts <- function(x) {</pre>
  means <- aggregate(val ~ group, data = x, mean)</pre>
  vars <- aggregate(val ~ group, data = x, var)</pre>
  counts <- aggregate(val ~ group, data = x, length)</pre>
  (means$val[1] - means$val[2])/sum(vars$val / sqrt(counts$val))
rg <- function(x) {</pre>
 x$group <- sample(x$group)</pre>
}
permute.test <- MCHTest(ts, ts, rg, seed = 123, N = 1000,
                          lock_alternative = FALSE)
```

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```
permute.test(df, alternative = "two.sided")
```

Description

Makes package startup message.

Usage

```
MCHT_startup_message()
```

Examples

```
MCHT:::MCHT_startup_message()
```

print.MCHTest

Print MCHTest-Class Object

Description

Print an link{MCHTest}-class object.

Usage

```
## S3 method for class 'MCHTest' print(x, ...)
```

Arguments

```
x The MCHTest-class object
```

Other arguments, such as prefix (a string wrapped around the first line; by default, "\t")

```
f <- MCHTest(mean, mean, seed = 100)
print(f)</pre>
```

pval 9

pval

Compute p-Value For a Test Statistic

Description

Compute the p-value of a test statistic for Monte Carlo tests.

Usage

```
pval(S, sample_S, alternative = NULL, unif_gen = NULL)
```

Arguments

S	The value of the test statistic
sample_S	Simulated values of the
alternative	A string specifying the alternative hypothesis, or NULL
unif_gen	If not NULL, the function generating uniformly-distributed random variables for breaking ties; if NULL, no tie breaking is done

Details

Let S be a test statistic and S_i be simulated values of that test statistic under the null hypothesis, with $1 \le i \le N$. If unif_gen is not NULL, this function computes p-values via

$$p = \hat{p} = \frac{1}{N} \sum_{i=1}^{N} I_{\{(S,U_0) \le (S_i,U_i)\}}$$

where $I_{\{S \in A\}} = 1$ if $S \in A$ and is 0 otherwise, U_i are uniformly distributed random variables, and the ordering over tuples is lexicographical ordering, as described by Dufour (2006).

If unif_gen is NULL, then the random variables are not generated and not used to break ties.

This function is designed to handle an alternative parameter similar to what appears in other stats functions like t.test. If alternative is "less", then $p=\hat{p}$; if alternative is "greater", then $p=1-\hat{p}$; and if alternative is "two.sided", then $p=2\min(\hat{p},1-\hat{p})$. Any other value raises an error.

The parameter S is S, and the vector sample_S is the vector containing the values S_i .

Value

A number representing the p-value.

```
sample_S <- rnorm(10)
pval(1.01, sample_S)
pval(1.01, sample_S, alternative = "greater")</pre>
```

10 %s0%

%s%

Concatenate (With Space)

Description

Concatenate and form strings (with space separation)

Usage

```
x %s% y
```

Arguments

```
x One objecty Another object
```

Value

A string combining x and y with a space separating them

Examples

```
`%s%` <- MCHT:::`%s%`
"Hello" %s% "world"
```

%s0%

Concatenate (Without Space)

Description

Concatenate and form strings (no space separation)

Usage

```
x %s0% y
```

Arguments

```
x One objecty Another object
```

Value

A string combining x and y

```
`%s0%` <- MCHT:::`%s0%`
"Hello" %s0% "world"
```

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