

Package: trdist (via r-universe)

August 21, 2024

Type Package

Title Univariate Probability Distributions with Truncation

Version 1.0.1

Date 2024-07-17

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Depends R (>= 3.6.0)

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Description Truncation of univariate probability distributions. The probability distribution can come from other packages so long as the function names follow the standard d, p, q, r naming format. Also other univariate probability distributions are included.

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RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

Date/Publication 2024-07-21 09:00:02 UTC

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`getDistributionFunction`*Get Distribution Functions*

Description

Determines if the distribution functions are available. This is intended for internal use only.

Usage

```
getDistributionFunction(type, distr, ...)
```

Arguments

<code>type</code>	Character, typically either 'r', 'q', 'p', or 'd'.
<code>distr</code>	Character, typically something like 'norm', 'gamma', etc.
<code>...</code>	Currently ignored.

Details

It is determined that `paste0(type, distr)` is a function and returns that function. The nature of the returned function is not verified.

Value

Function, the first function in the search path that matches the name `paste0(type, distr)`.

Examples

```
fun <- getDistributionFunction(type="q",distr="norm")
```

`LogLogistic`*Log-Logistic Distribution*

Description

The probability density function, cumulative density function, inverse cumulative density function, random generation for the log logistic distribution.

Usage

```

dllog(x, shape = 1, scale = 1, log = FALSE, ...)

llogSummaryStats(shape, scale, ...)

pllog(q, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE, ...)

qllog(p, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE, ...)

rlllog(n, shape = 1, scale = 1, ...)

```

Arguments

x	Vector of quantiles.
shape	Shape parameter.
scale	Scale parameter.
log	Logical; if TRUE, log densities are returned.
...	Currently ignored.
q	Vector of quantiles.
lower.tail	Logical; if TRUE (default), probabilities are P(X <= x) otherwise, P(X > x).
log.p	Logical; if TRUE, probabilities p are given as log(p).
p	Vector of probabilities.
n	Number of observations. If length(n) > 1, the length is taken to be the number required.

Details

If X is a random variable distributed according to a logistic distribution, then Y = exp(X) has a log-logistic distribution.

The log-logistic distribution with parameters shape = a and scale = s has density

$$f(x) = \frac{\left(\frac{1}{a \cdot \exp(s)}\right) \left(\frac{x}{\exp s}\right)^{\frac{1}{a}-1}}{\left(1 + \left(\frac{x}{\exp s}\right)^{1/a}\right)^2}$$

for $x \geq 0$, $a > 1$, and $s > 0$.

The median is $\exp(s)$, mean is

$$\frac{a\pi \cdot \exp(s)}{\sin(a \cdot \pi)}$$

for $1/a > 1$. The variance is

$$(\exp(s))^2 \left(\frac{2 \cdot \pi \cdot a}{\sin(2 \cdot \pi \cdot a)} - \frac{(a \cdot \pi)^2}{\sin^2(a \cdot \pi)} \right)$$

for $1/a > 2$. The mode is

$$\exp(s) \left(\frac{1/a - 1}{1/a + 1} \right)^a$$

for $1/a > 1$ otherwise it is zero.

Value

dllog returns vector of the densities.

llogSummaryStats returns a data frame of summary statistics.

pllog returns a vector of probabilities.

qllog returns a vector of quantiles.

rllog returns a vector of random log-logistic variates.

See Also

[Logistic](#)

Examples

```
y <- rllog(5, shape=1, scale=1/3)
dllog(x=y, shape=1, scale=1/3)
dlogis(x=log(y), location=1/3, scale=1)/y

pllog(q=y, shape=1, scale=1/3)
qllog(p=seq(0, 1, by=.25), shape=1, scale=1/3)
```

trdist

Univariate Probability Distributions with Truncation

Description

Truncation of univariate probability distributions. The probability distribution can come from other packages so long as the function names follow the standard d, p, q, r naming format. Also other univariate probability distributions are included.

Author(s)

Maintainer: Jared Studyvin <studyvinstat@gmail.com>

truncatedDistribution *Truncated Distributions*

Description

Truncated probability density function, truncated cumulative density function, inverse truncated cumulative density function, and random variates from a truncated distribution.

Usage

```
dtrunc(x, distr, ..., low = -Inf, high = Inf, log = FALSE)
```

```
ptrunc(q, distr, ..., low = -Inf, high = Inf, lower.tail = TRUE, log.p = FALSE)
```

```
qtrunc(p, distr, ..., low = -Inf, high = Inf, lower.tail = TRUE, log.p = FALSE)
```

```
rtrunc(n, distr, ..., low = -Inf, high = Inf)
```

Arguments

x	Vector of quantiles.
distr	Character value specifying the desired probability distribution.
...	Additional arguments passed to the non-truncated distribution functions.
low	Numeric value specifying the lower truncation bound.
high	Numeric value specifying the upper truncation bound.
log	Logical; if TRUE, log densities are returned.
q	Vector of quantiles.
lower.tail	Logical; if TRUE (default), probabilities are $P(X \leq x)$ otherwise, $P(X > x)$.
log.p	Currently ignored.
p	Vector of probabilities.
n	A positive integer specifying the desired number of random variates.

Details

The non truncated distribution functions are assumed to be available. For example if the normal distribution is desired then used `distr='norm'`, the functions then look for `'qnorm'`, `'pnorm'`, etc.

The truncation interval is $(low, high]$, which only matters for discrete distribution.

The random variates are produced using the direct method (see Casella and Berger 2002).

Value

`dtrunc` returns a vector of densities.

`ptrunc` returns a vector of probabilities.

`qtrunc` returns a vector of quantiles.

`rtrunc` returns a vector of random variates.

References

G. Casella and R. L. Berger. Statistical inference. Vol. 2. Duxbury Pacific Grove, CA, 2002.

Examples

```
## dtrunc
# not truncated
dnorm(5,mean=5)
dtrunc(x=5,distr='norm',mean=5)
# truncated
dtrunc(x=5,distr='norm',mean=5,low=4, high=5.5)

## ptrunc
#not truncated
pgamma(2, shape=3, rate=2)
ptrunc(2, distr = 'gamma', shape=3, rate=2)
# truncated
ptrunc(2, distr = 'gamma', shape=3, rate=2, low=1, high=5)

## upper tail
# not truncated
pgamma(2, shape=3, rate=2,lower.tail=FALSE)
ptrunc(2, distr='gamma', shape=3, rate=2, lower.tail=FALSE)
# truncated
ptrunc(2, distr='gamma', shape=3, rate=2, low=1, high=5, lower.tail=FALSE)

## qtrunc
#not truncated
qnorm(p=.975)
qtrunc(p=.975,distr='norm')
# truncated
qtrunc(p=.975,distr='norm', low=0, high=1)

## upper tail
# not truncated
qnorm(p=.975,lower.tail=FALSE)
qtrunc(p=.975, distr='norm', lower.tail=FALSE)
# truncated
qtrunc(p=.975, distr='norm', low=0, high=1, lower.tail=FALSE)

## rtrunc
rtrunc(n=5, distr = 'gamma', shape=3, rate=2, low=2, high=5)
```

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