Package ‘TruncExpFam’

February 26, 2024

Title  Truncated Exponential Family
Version 1.1.1
Date 2024-02-26
Description Handles truncated members from the exponential family of probability distributions. Contains functions such as rtruncnorm() and dtruncpois(), which are truncated versions of rnorm() and dpois() from the stats package that also offer richer output containing, for example, the distribution parameters. It also provides functions to retrieve the original distribution parameters from a truncated sample by maximum-likelihood estimation.
License GPL-3
Encoding UTF-8
RoxygenNote 7.2.3
Imports methods, invgamma, rmutil
Suggests knitr, rmarkdown, testthat
URL https://ocbe-uio.github.io/TruncExpFam/
BugReports https://github.com/ocbe-uio/TruncExpFam/issues
VignetteBuilder knitr
NeedsCompilation no
Author René Holst [aut], Waldir Leoncio [cre, aut]
Maintainer Waldir Leoncio <w.l.netto@medisin.uio.no>
Repository CRAN
Date/Publication 2024-02-26 15:30:02 UTC

R topics documented:

.onAttach ................................................................. 2
averageT ............................................................... 2
dtruncbeta ............................................................ 3
Index 17

.onAttach  Prints welcome message on package load

Description

Prints package version number and welcome message on package load

Usage

.onAttach(libname, pkgname)

Arguments

libname  library location. See ?base::.onAttach for details
pkgname  package name. See ?base::.onAttach for details

averageT  Averages out the sufficient statistics \( T(y) \)

Description

Takes a vector of values and returns the column average of their sufficient statistic (determined by their class)

Usage

averageT(y)

Arguments

y  vector of values

Value

A vector with the average of the sufficient statistics
**dtruncbeta**  

*Probability Density Function*

### Description

Calculates the PDF for a given truncated distribution

### Usage

```r
dtruncbeta(y, shape1, shape2, eta, a = 0, b = 1, ...)
dtruncbinom(y, size, prob, eta, a = 0, b = attr(y, "parameters")$size, ...)
dtruncchisq(y, df, eta, a = 0, b = Inf, ...)
dtruncccontbern(y, lambda, eta, a = 0, b = 1, ...)
dtruncccontbern(y, lambda, eta, a = 0, b = 1, ...)
dtruncexp(y, rate = 1, eta, a = 0, b = Inf, ...)
dtruncgamma(y, shape, rate = 1, scale = 1/rate, eta, a = 0, b = Inf, ...)
dtrunc(y, ...)
dtruncinvgamma(y, shape, rate = 1, scale = 1/rate, eta, a = 0, b = Inf, ...)
dtruncinvgauss(y, m, s, eta, a = 0, b = Inf, ...)
dtrunclnorm(y, meanlog = 0, sdlog = 1, eta, a = 0, b = Inf, ...)
```

```r
## S3 method for class 'trunc_nbinom'
dtrunc(y, size, prob, eta, a = 0, b = Inf, ...)
dtruncnbinom(y, size, prob, eta, a = 0, b = Inf, ...)
dtruncnbinom(y, size, prob, eta, a = 0, b = Inf, ...)
dtruncnorm(y, mean = 0, sd = 1, eta, a = -Inf, b = Inf, ...)
dtruncpois(y, lambda, eta, a = 0, b = Inf, ...)
```

### Arguments

- **y**: output from rtrunc or any valid numeric value(s).
- **shape1**: positive shape parameter alpha
shape2  positive shape parameter beta
eta  vector of natural parameters
a  point of left truncation
b  point of right truncation
...  size
size  target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
prob  probability of success on each trial
df  degrees of freedom for "parent" distribution
lambda  mean and var of "parent" distribution
rate  inverse gamma rate parameter
shape  inverse gamma shape parameter
scale  inverse gamma scale parameter
m  vector of means
s  vector of dispersion parameters
meanlog  mean of un-truncated distribution
sdlog  standard deviation of un-truncated distribution
mean  mean of parent distribution
sd  standard deviation is parent distribution

Value

The density of y for the given values of the eta parameter.

Note

Either the common or the natural parameters must be provided.

Examples

# Using the output of rtrunc
y <- rtrunc(50, mean = 5, sd = 2)
dtrunc(y, eta = c(0, -1))

# Directly-inputting values
dtruncnorm(y = c(5, 0, -10), eta = c(0, -0.05))
empiricalParameters  
*Calculate empirical parameters*

**Description**

Returns the empirical parameter estimate for a distribution

**Usage**

`empiricalParameters(y, ...)`

**Arguments**

- `y`: output of `rtrunc`
- `...`: other arguments passed to methods

**Value**

A vector of parameter estimates for the input sample

**Examples**

```r
# Normal distribution
sampNorm <- rtrunc(50, mean = 5, sd = 2)
empiricalParameters(sampNorm)

# Poisson distribution
sampPois <- rtrunc(10, lambda = 100, family = "Poisson")
empiricalParameters(sampPois)
```

empiricalParameters.numeric

*Extract parameters*

**Description**

Extract parameters

**Usage**

```r
## S3 method for class 'numeric'
empiricalParameters(y, family = "gaussian", natural = FALSE, ...)
```
Arguments

- **y**: Numeric vector containing observations from a random variable
- **family**: Distribution family to assume for y
- **natural**: Should output be in terms of the natural parameter eta?
- ... arguments passed to `empiricalParameters()`

Examples

```r
# Some random data
x <- c(4, 3, 6, 3, 3, 3, 4, 3, 2, 3, 0, 4, 2, 0, 1, 4, 3, 0, 0, 2, 3, 0, 3, 7,
      2, 1, 1, 2, 3, 2, 3, 3, 3, 2, 2, 2, 0, 2, 0, 2, 1, 0, 2, 3, 1, 0, 4, 2, 2,
      0, 1, 1, 2, 2, 3, 1, 3, 1, 1, 0, 3, 3, 2, 0, 2, 2, 3, 0, 2, 1, 0, 0, 1,
      0, 2, 4, 2, 3, 3, 0, 1, 0, 5, 2, 4, 2, 7, 4, 4, 1, 2, 4, 3, 2, 4, 3, 1, 3
)

# Extracting parameters under different distribution assumptions
empiricalParameters(x, family = "normal")
empiricalParameters(x, family = "normal", natural = TRUE)
empiricalParameters(x, family = "binomial", nsize = max(x))
empiricalParameters(x, family = "poisson", natural = FALSE)
empiricalParameters(x, family = "poisson", natural = TRUE)
```

genrtruncClass

**Generates an rtrunc-dispatchable class**

Description

Matches a list of arguments to an rtrunc method

Usage

```
genrtruncClass(n, family, parms)
```

Arguments

- **n**: sample size
- **family**: distribution family
- **parms**: list of parameters passed to rtrunc (through the ... element)

Value

A character string.

Author(s)

Waldir Leoncio
Description

ML-estimation of the parameters of the distribution of the specified family, truncated at y.min and y.max

Usage

```r
mlEstimationTruncDist(
  y,
  y.min = attr(y, "truncation_limits")$a,
  y.max = attr(y, "truncation_limits")$b,
  tol = 1e-05,
  max.it = 100,
  delta = 0.33,
  print.iter = 0,
  ny = 100,
  family = NULL,
  ...
)
```

Arguments

- **y**: Sequence spanning the domain of the truncated distribution
- **y.min**: Lower bound for y
- **y.max**: Upper bound for y
- **tol**: Error tolerance for parameter estimation
- **max.it**: Maximum number of iterations
- **delta**: Indirectly, the difference between consecutive iterations to compare with the error tolerance
- **print.iter**: Determines the frequency of printing (i.e., prints every print.iter iterations)
- **ny**: size of intermediate y range sequence. Higher values yield better estimations but slower iterations
- **family**: distribution family to use
- ... other parameters passed to subfunctions

Details

If print.iter = TRUE, the function prints the iteration, the sum of squares of delta.eta.j (delta.L2), and the current parameter estimates. The delta argument of this function is a factor in the calculation of delta.eta.j, which in turn is a factor in the calculation of delta.L2.
Value

A vector of class `trunc_*` containing the maximum-likelihood estimation of the underlying distribution parameters.

Author(s)

René Holst

References

Inspired by Salvador: Pueyo: "Algorithm for the maximum likelihood estimation of the parameters of the truncated normal and lognormal distributions"

Examples

```r
sample_size <- 1000
# Normal
sample.norm <- rtrunc(n = sample_size, mean = 2, sd = 1.5, a = -1)
mlEstimationTruncDist(
  sample.norm,
  y.min = -1, max.it = 500, delta = 0.33,
  print.iter = TRUE
)

# Log-Normal
sample.lognorm <- rtrunc(n = sample_size, family = "lognormal", meanlog = 2.5, sdlog = 0.5, a = 7
)
ml_lognormal <- mlEstimationTruncDist(
  sample.lognorm,
  y.min = 7, max.it = 500, tol = 1e-10, delta = 0.3,
  print.iter = FALSE
)
ml_lognormal

# Poisson
sample.pois <- rtrunc(n = sample_size, lambda = 10, a = 4, family = "Poisson"
)
mlEstimationTruncDist(
  sample.pois,
  y.min = 4, max.it = 500, delta = 0.33,
  print.iter = 5
)

# Gamma
sample.gamma <- rtrunc(n = sample_size, shape = 6, rate = 2, a = 2, family = "Gamma"
)
mlEstimationTruncDist(
  sample.gamma,
  y.min = 2, max.it = 1500, delta = 0.3,
)
print.iter = 10

# Negative binomial
sample.nbinom <- rtruncnbinom(
  sample_size, size = 50, prob = .3, a = 100, b = 120
)
mlEstimationTruncDist(sample.nbinom, r=10)

natural2parameters

Convert natural parameters to distribution parameters

Description
Convert natural parameters to distribution parameters

Usage
natural2parameters(eta, ...)

Arguments

- `eta` vector of natural parameters
- `...` other arguments passed to methods

Value
A vector of the original distribution parameters

See Also
parameters2natural()

Examples
samp <- rtrunc(n = 100, lambda = 2, family = "Poisson")
lambda_hat <- empiricalParameters(samp)
eta_hat <- parameters2natural(lambda_hat)
natural2parameters(eta_hat)  # yields back lambda
parameters2natural  Convert distribution parameters to natural parameters

Description

Convert distribution parameters to natural parameters

Usage

parameters2natural(parms, ...)

Arguments

parms  A vector of parameters in a distribution distribution
...
other arguments passed to methods

Value

A vector containing the natural parameters

See Also

natural2parameters()

Examples

# Poisson distribution
samp <- rtrunc(n = 100, lambda = 2, family = "Poisson")
parameters2natural(empiricalParameters(samp))

print.trunc  Print sample from truncated distribution

Description

Special printing methods for trunc_* classes.

Usage

## S3 method for class 'trunc'
print(x, details = FALSE, ...)

Arguments

x  object to print
details  if FALSE (default), hides the attributes of x
...
other arguments passed to print.default
Value

x with or without its attributes

Author(s)

Waldir Leoncio

---

**probdist-class**

*Probability distribution class*

---

**Description**

An R object describing the properties of a probability distribution.

**Value**

An RC class containing statistical properties of that distribution, namely its name, parameter names and values and natural parameter names and values.

**Author(s)**

Waldir Leoncio

**Examples**

```r
probdist(shape = 2, scale = .25, family = "gamma")
probdist(mean = 2, sd = 10, family = "normal")
probdist(eta1 = 2, eta2 = -1, family = "normal")
```

---

**rtrunc**

*The Truncated Exponential Family*

---

**Description**

Random generation for the truncated exponential family distributions. Please refer to the "Details" and "Examples" section for more information on how to use this function.
Usage

rtrunc(n, family = "gaussian", faster = FALSE, ...)

rtrunc.beta(n, shape1, shape2, a = 0, b = 1)

rtruncbeta(n, shape1, shape2, a = 0, b = 1)

rtruncbinom(n, size, prob, a = 0, b = size)

rtruncchisq(n, df, a = 0, b = Inf)

rtrunccontbern(n, lambda, a = 0, b = 1)

rtruncexp(n, rate = 1, a = 0, b = Inf)

rtruncgamma(n, shape, rate = 1, scale = 1/rate, a = 0, b = Inf)

rtruncinvgamma(n, shape, rate = 1, scale = 1/rate, a = 0, b = Inf)

rtrunclnorm(n, meanlog, sdlog, a = 0, b = Inf)

rtruncnbinom(n, size, prob, mu, a = 0, b = Inf)

rtruncnorm(n, mean, sd, a = -Inf, b = Inf)

rtruncpois(n, lambda, a = 0, b = Inf)

rtrunc_direct(n, family = "gaussian", parms, ...)

Arguments

n sample size
family distribution family to use
faster if TRUE, samples directly from the truncated distribution (more info in details)
... individual arguments to each distribution
shape1 positive shape parameter alpha
shape2 positive shape parameter beta
a point of left truncation
b point of right truncation
size target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
prob probability of success on each trial
**rtrunc**

df degrees of freedom for "parent" distribution
lambda mean and var of "parent" distribution
rate inverse gamma rate parameter
shape inverse gamma shape parameter
scale inverse gamma scale parameter
m vector of means
s vector of dispersion parameters
meanlog mean of un-truncated distribution
sdlog standard deviation of un-truncated distribution
mu alternative parametrization via mean
mean mean of parent distribution
sd standard deviation is parent distribution
parms list of distribution parameters

**Details**

One way to use this function is by calling the rtrunc generic with the family parameter of your choice. You can also specifically call one of the methods (e.g. rtruncpois(10, lambda=3) instead of 'rtrunc(10, family="poisson", lambda=3)). The latter is more flexible (i.e., easily programmable) and more robust (i.e., it contains better error handling and validation procedures), while the former better conforms with the nomenclature from other distribution-related functions in the stats package.

Setting faster=TRUE uses a new algorithm that samples directly from the truncated distribution, as opposed to the old algorithm that samples from the untruncated distribution and then truncates the result. The advantage of the new algorithm is that it is way faster than the old one, particularly for highly-truncated distributions. On the other hand, the sample for untruncated distributions called through rtrunc() will no longer match their stats-package counterparts for the same seed.

**Value**

A sample of size n drawn from a truncated distribution
vector of one of the rtrunc_* classes containing the sample elements, as well as some attributes related to the chosen distribution.

**Note**

The current sample-generating algorithm may be slow if the distribution is largely represented by low-probability values. This will be fixed soon. Please follow https://github.com/ocbe-uiol-TruncExpFam/issues/72 for details.

**Author(s)**

René Holst, Waldir Leôncio
Examples

```r
# Truncated binomial distribution
sample.binom <- rtrunc(
  100, family = "binomial", prob = 0.6, size = 20, a = 4, b = 10
)
sample.binom
plot(
  table(sample.binom), ylab = "Frequency", main = "Freq. of sampled values"
)

# Truncated Log-Normal distribution
sample.lognorm <- rtrunc(
  n = 100, family = "lognormal", meanlog = 2.5, sdlog = 0.5, a = 7
)
sample.lognorm
summary(sample.lognorm)

hist(
  sample.lognorm,
  nclass = 35, xlim = c(0, 60), freq = FALSE,
  ylim = c(0, 0.15)
)

# Normal distribution
sample.norm <- rtrunc(n = 100, mean = 2, sd = 1.5, a = -1)
head(sample.norm)
hist(sample.norm, nclass = 25)

# Gamma distribution
sample.gamma <- rtrunc(n = 100, family = "gamma", shape = 6, rate = 2, a = 2)
hist(sample.gamma, nclass = 15)

# Poisson distribution
sample.pois <- rtrunc(n = 10, family = "poisson", lambda = 10, a = 4)
sample.pois
plot(table(sample.pois))
```

---

**TruncExpFam**

**Truncated Exponential Family**

**Description**

TruncExpFam is an R package to handle truncated members from the exponential family.

**Details**

This package offers truncated counterparts of the density-, distribution-, quantile- and sampling-functions for a broad range of distributions from the exponential family, as implemented in the stats package.
The package also provides functions for estimating the parameters of the distributions from data, given the truncation limits.

For more info, please check `rtrunc()`, `dtrunc()` and `print.trunc()`. Counterparts for density and probability functions are on the roadmap for a future release.

### Supported distributions

- Beta
- Binomial
- Chi-Square
- Continuous Bernoulli
- Exponential
- Gamma
- Inverse Gamma
- Inverse Gaussian
- Log-normal
- Negative Binomial
- Normal
- Poisson

### Note

Found a bug? Want to suggest a feature? Contribute to the scientific and open source communities by opening an issue on our home page. Check the "BugReports" field on `packageDescription("TruncExpFam")` for the URL.

### Author(s)

**Maintainer:** Waldir Leoncio <w.l.netto@medisin.uio.no>

Authors:

- René Holst <rene.holst@medisin.uio.no>

### See Also

Useful links:

- [https://ocbe-uio.github.io/TruncExpFam/](https://ocbe-uio.github.io/TruncExpFam/)
validateFamilyParms  

**Validate family parameters**

**Description**

Checks if a combination of distribution family and parameters is valid.

**Usage**

```r
validateFamilyParms(family, parms)
```

**Arguments**

- `family` character with family distribution name
- `parms` character vector with distribution parameter names

**Value**

list telling if family-parm combo is valid + the family name

**Author(s)**

Waldir Leoncio
Index

.onAttach, 2
averageT, 2
dtrunc (dtruncbeta), 3
dtrunc(), 15
dtruncbeta, 3
dtruncbinom (dtruncbeta), 3
dtrunchnorm (dtruncbeta), 3
dtruncexp (dtruncbeta), 3
dtrungamma (dtruncbeta), 3
dtruncinvgamma (dtruncbeta), 3
dtruncinvgauss (dtruncbeta), 3
dtrunchnorm (dtruncbeta), 3
dtruncbinom (dtruncbeta), 3
dtruncpois (dtruncbeta), 3

empiricalParameters, 5
empiricalParameters(). 6
empiricalParameters.numeric, 5

genrtruncClass, 6

mleEstimationTruncDist, 7

natural2parameters, 9
natural2parameters(), 10

parameters2natural, 10
parameters2natural(), 9

print.trunc, 10
print.trunc(), 15
print.trunc_beta (print.trunc), 10
print.trunc_binomial (print.trunc), 10
print.trunc_chisq (print.trunc), 10
print.trunc_contbern (print.trunc), 10
print.trunc_exp (print.trunc), 10
print.trunc_gamma (print.trunc), 10
print.trunc_invgauss (print.trunc), 10

rtrunc, 11
rtrunc(), 15
rtrunc_direct (rtrunc), 11
rtruncbeta (rtrunc), 11
rtruncbinom (rtrunc), 11
rtruncchisq (rtrunc), 11
rtrunccontbern (rtrunc), 11
rtruncexp (rtrunc), 11
rtrungamma (rtrunc), 11
rtruncinvgamma (rtrunc), 11
rtruncinvgauss (rtrunc), 11
rtrunchnorm (rtrunc), 11
rtruncbinom (rtrunc), 11
rtrunchnorm (rtrunc), 11
rtruncpois (rtrunc), 11

stats, 14
TruncExpFam, 14
TruncExpFam-package (TruncExpFam), 14

validateFamilyParms, 16