

# Package ‘TruncExpFam’

November 14, 2023

**Title** Truncated Exponential Family

**Version** 1.1.0

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**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, rmutl

**Suggests** knitr, rmarkdown, testthat

**URL** <https://ocbe-uio.github.io/TruncExpFam/>

**BugReports** <https://github.com/ocbe-uio/TruncExpFam/issues>

**VignetteBuilder** knitr

**NeedsCompilation** no

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`.onAttach` *Prints welcome message on package load*

---

### Description

Prints package version number and welcome message on package load

### Usage

```
.onAttach(libname, pkgname)
```

### Arguments

<code>libname</code>	library location. See <code>?base::.onAttach</code> for details
<code>pkgname</code>	package name. See <code>?base::.onAttach</code> 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

<code>y</code>	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

```
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, ...)
dtrunccontbern(y, lambda, eta, a = 0, b = 1, ...)
dtrunccontbern(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, ...)
## 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**

```
# 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**

```
## 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 <code>empiricalParameters()</code>

**Examples**

```
# Some random data
x <- c(
  4, 3, 6, 3, 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, 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	<i>Generates an rtrunc-dispatchable class</i>
----------------	---

---

**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

---

 mlEstimationTruncDist *ML Estimation of Distribution Parameters*


---

### Description

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

### Usage

```
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

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

```
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 <- rtruncbinom(
  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	<i>Probability distribution class</i>
----------------	---------------------------------------

---

**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**

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

---

rtrunc	<i>The Truncated Exponential Family</i>
--------	---

---

**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)

rtruncinvgauss(n, m, s, 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", ...)

```

**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

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

### 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-uio/TruncExpFam/issues/72> for details.

### Author(s)

René Holst, Waldir Leôncio

## Examples

```

# 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
)
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](mailto:w.l.netto@medisin.uio.no)>

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- René Holst <[rene.holst@medisin.uio.no](mailto:rene.holst@medisin.uio.no)>

### See Also

Useful links:

- <https://ocbe-uio.github.io/TruncExpFam/>
- Report bugs at <https://github.com/ocbe-uio/TruncExpFam/issues>

---

validateFamilyParms    *Validate family parameters*

---

**Description**

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

**Usage**

```
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



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