

Package ‘convdistr’

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Type Package

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Description Convolute probabilistic distributions using the random generator function of each distribution. A new random number generator function is created that perform the mathematical operation on the individual random samples from the random generator function of each distribution. See the documentation for examples.

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add_total	<i>Adds a total dimension</i>
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Description

This function returns a [DISTRIBUTION](#) with a new dimension created by row sum of the dimensions of the distribution.

Usage

```
add_total(p_distribution, p_totalname = "TOTAL")
```

Arguments

`p_distribution` an object of class [DISTRIBUTION](#)
`p_totalname` the name of the new dimension

Details

Only works with multidimensional distributions.

Value

a [DISTRIBUTION](#)

Author(s)

John J. Aponte

Examples

```
d1 <- new_DIRICHLET(c(0.2,0.5,0.3))
d2 <- add_total(d1)
```

BETA

Factory for a BETA distribution object

Description

Returns an BETA distribution object that produce random numbers from a beta distribution using the [rbeta](#) function

Usage

```
new_BETA(p_shape1, p_shape2, p_dimnames = "rvar")

new_BETA_lci(p_mean, p_lci, p_uci, p_dimnames = "rvar")

new_BETA_lci2(p_mean, p_lci, p_uci, p_dimnames = "rvar")
```

Arguments

`p_shape1` non-negative parameters of the Beta distribution
`p_shape2` non-negative parameters of the Beta distribution
`p_dimnames` A character that represents the name of the dimension
`p_mean` A numeric that represents the expected value of the proportion
`p_lci` A numeric for the lower 95% confidence interval
`p_uci` A numeric for the upper 95% confidence interval

Value

An object of class DISTRIBUTION, BETA

Functions

- `new_BETA_lci()`: Constructor based on confidence intervals. Preserve expected value.
- `new_BETA_lci2()`: Constructor based on ML confidence intervals

Note

When using confidence intervals, the shape parameters are obtained using the following formula:

$$varp = (p_{uci} - p_{lci})/4^2$$

$$shape1 = p_{mean} * (p_{mean} * (1 - p_{mean})/varp - 1)$$

$$shape2 = (1 - p_{mean}) * (p_{mean} * (1 - p_{mean})/varp - 1)$$

`new_BETA_lci2` estimate parameters using maximum likelihood `myDistr <- new_BETA_lci2(0.30,0.25,0.35)`
`myDistr$rfunc(10)`

Author(s)

John J. Aponte

Examples

```
myDistr <- new_BETA(1,1)
myDistr$rfunc(10)
myDistr <- new_BETA_lci(0.30,0.25,0.35)
myDistr$rfunc(10)
```

BETABINOMIAL

Factory for a BETABINOMIAL distribution object

Description

Returns an BETABINOMIAL distribution object that produce random numbers from a betabinomial distribution using the `rbbinom` function

Usage

```
new_BETABINOMIAL(p_size, p_shape1, p_shape2, p_dimnames = "rvar")

new_BETABINOMIAL_od(p_size, p_mu, p_od, p_dimnames = "rvar")

new_BETABINOMIAL_icc(p_size, p_mu, p_icc, p_dimnames = "rvar")
```

Arguments

<code>p_size</code>	a non-negative parameter for the number of trials
<code>p_shape1</code>	non-negative parameters of the Betabinomial distribution
<code>p_shape2</code>	non-negative parameters of the Betabinomial distribution
<code>p_dimnames</code>	A character that represents the name of the dimension
<code>p_mu</code>	mean proportion for the binomial part of the distribution
<code>p_od</code>	over dispersion parameter
<code>p_icc</code>	intra-class correlation parameter

Value

An object of class DISTRIBUTION, BETADISTRIBUTION

Functions

- `new_BETABINOMIAL_od()`: parametrization based on dispersion
- `new_BETABINOMIAL_icc()`: parametrization based on intra-class correlation

Note

There are several parametrization for the betabinomial distribution. The one based on `shape1` and `shape2` are parameters alpha and beta of the beta part of the distribution, but it can be parametrized as `mu`, and `od` where `mu` is the expected mean proportion and `od` is a measure of the overdispersion.

$$p_mu = p_shape1 / (p_shape1 + p_shape2)$$

$$p_od = p_shape1 + p_shape2$$

$$p_shape1 = p_mu * p_od$$

$$p_shape2 < -(1 - p_mu) * p_od$$

Another parametrization is based on `mu` and the `icc` where `mu` is the mean proportion and `icc` is the intra-class correlation.

$$p_mu = p_shape1 / (p_shape1 + p_shape2)$$

$$p_icc = 1 / (p_shape1 + p_shape2 + 1)$$

$$p_shape1 = p_mu * (1 - p_icc) / p_icc$$

$$p_shape2 = (1 - p_mu) * (1 - p_icc) / p_icc$$

Author(s)

John J. Aponte

Examples

```
myDistr <- new_BETABINOMIAL(10,1,1)
myDistr$rfunc(10)
```

 BINOMIAL

Factory for a BINOMIAL distribution object

Description

Returns a BINOMIAL distribution object that produce random numbers from a binomial distribution using the `rbinom` function

Usage

```
new_BINOMIAL(p_size, p_prob, p_dimnames = "rvar")
```

Arguments

<code>p_size</code>	integer that represent the number of trials
<code>p_prob</code>	probability of success
<code>p_dimnames</code>	A character that represents the name of the dimension

Value

An object of class `DISTRIBUTION`, BINOMIAL

Author(s)

John J. Aponte

Examples

```
myDistr <- new_BINOMIAL(1000,0.3)
myDistr$rfunc(10)
```

 cinqnum

cinqnum

Description

Produce 5 numbers of the distribution (mean_, sd_, lci_, uci_, median_).

Usage

```

cinqnum(x, ...)

## S3 method for class 'DISTRIBUTION'
cinqnum(x, n, ...)

## S3 method for class '`NA`'
cinqnum(x, n, ...)

## S3 method for class 'DIRAC'
cinqnum(x, n, ...)

```

Arguments

x	an object of class DISTRIBUTION
...	further parameters
n	number of draws

Details

Uses the stored seed to have the same sequence always and produce the same numbers This is an internal function for the summary function

Value

a vector with the mean, sd, lci, uci and median values

Methods (by class)

- `cinqnum(DISTRIBUTION)`: Generic method for a [DISTRIBUTION](#)
- `cinqnum(`NA`)`: Generic method for optimized for a NA distribution
- `cinqnum(DIRAC)`: Generic method optimized for a [DIRAC](#) distribution

Author(s)

John J. Aponte

CONVOLUTION

Make the convolution of two or more [DISTRIBUTION](#) objects

Description

The convolution of the simple algebraic operations is made by the operation of individual draws of the distributions. The [DISTRIBUTION](#) objects must have the same dimensions.

Usage

```

new_CONVOLUTION(listdistr, op, omit_NA = FALSE)

new_SUM(..., omit_NA = FALSE)

## S3 method for class 'DISTRIBUTION'
e1 + e2

new_SUBTRACTION(..., omit_NA = FALSE)

## S3 method for class 'DISTRIBUTION'
e1 - e2

new_MULTIPLICATION(..., omit_NA = FALSE)

## S3 method for class 'DISTRIBUTION'
e1 * e2

new_DIVISION(..., omit_NA = FALSE)

## S3 method for class 'DISTRIBUTION'
e1 / e2

```

Arguments

<code>listdistr</code>	a list of DISTRIBUTION objects
<code>op</code>	a function to convolute '+', '-', '*', '\'
<code>omit_NA</code>	if TRUE, NA distributions will be omitted
<code>...</code>	DISTRIBUTION objects or a list of distribution objects
<code>e1</code>	object of class DISTRIBUTION
<code>e2</code>	object of class DISTRIBUTION

Details

If any of the distributions is of class NA ([NA_DISTRIBUTION](#)) the result will be a new distribution of class NA unless the `omit_NA` option is set to TRUE

Value

and object of class CONVOLUTION, [DISTRIBUTION](#)

Functions

- `new_SUM()`: Sum of distributions
- `new_SUBTRACTION()`: Subtraction for distributions
- `new_MULTIPLICATION()`: Multiplication for distributions
- `new_DIVISION()`: DIVISION for distributions

Author(s)

John J. Aponte

Examples

```

x1 <- new_NORMAL(0,1)
x2 <- new_UNIFORM(1,2)
new_CONVOLUTION(list(x1,x2), `+`)
new_SUM(x1,x2)
x1 + x2
new_SUBTRACTION(x1,x2)
x1 - x2
new_MULTIPLICATION(list(x1,x2))
x1 * x2
new_DIVISION(list(x1,x2))
x1 / x2

```

CONVOLUTION_assoc

*Convolution with association of dimensions***Description**

In case of different dimensions of the distribution this function perform the operation on the common distributions and add without modifications the other dimensions of the distribution.

Usage

```

new_CONVOLUTION_assoc(dist1, dist2, op)

new_SUM_assoc(dist1, dist2)

new_SUBTRACTION_assoc(dist1, dist2)

new_MULTIPLICATION_assoc(dist1, dist2)

new_DIVISION_assoc(dist1, dist2)

```

Arguments

dist1	an object of class DISTRIBUTION
dist2	and object of class DISTRIBUTION
op	one of '+', '-', '*', '/'

Details

If distribution A have dimensions a and b and distribution B have dimensions b and c, the A + B would produce a distribution with dimensions a, c, b+b,

Value

an object of class `DISTRIBUTION`

Functions

- `new_SUM_assoc()`: Sum of distributions
- `new_SUBTRACTION_assoc()`: Subtraction of distributions
- `new_MULTIPLICATION_assoc()`: Multiplication of distributions
- `new_DIVISION_assoc()`: Division of distributions

Author(s)

John J. Aponte

Examples

```
x1 <- new_MULTINORMAL(c(0,1), matrix(c(1,0.5,0.5,1),ncol=2), p_dimnames = c("A","B"))
x2 <- new_MULTINORMAL(c(10,1), matrix(c(1,0.4,0.4,1),ncol=2), p_dimnames = c("B","C"))
new_CONVOLUTION_assoc(x1,x2, `+`)
new_SUM_assoc(x1,x2)
new_SUBTRACTION_assoc(x1,x2)
new_MULTIPLICATION_assoc(x1,x2)
new_DIVISION_assoc(x1,x2)
```

CONVOLUTION_comb

Convolution with combination of dimensions

Description

In case of different dimensions of the distribution this function perform the operation on the combination of the distributions of both distribution.

Usage

```
new_CONVOLUTION_comb(dist1, dist2, op, p_dimnames)
```

```
new_SUM_comb(dist1, dist2)
```

```
new_SUBTRACTION_comb(dist1, dist2)
```

```
new_MULTIPLICATION_comb(dist1, dist2)
```

```
new_DIVISION_comb(dist1, dist2)
```

Arguments

dist1	an object of class DISTRIBUTION
dist2	and object of class DISTRIBUTION
op	one of '+', '-', '*', '/'
p_dimnames	a character vector with the name of the dimensions. If missing the combination of the individual dimensions will be used

Details

If distribution A have dimensions a and b and distribution B have dimensions b and c, the A + B would produce a distribution with dimensions a_b,a_c,b_b, b_c

Value

an object of class [DISTRIBUTION](#)

Functions

- new_SUM_comb(): Sum of distributions
- new_SUBTRACTION_comb(): Subtraction of distributions
- new_MULTIPLICATION_comb(): Multiplication of distributions
- new_DIVISION_comb(): Division of distributions

Note

In case of the same dimensions, only the first combination is taken

Author(s)

John J. Aponte

Examples

```
x1 <- new_MULTINORMAL(c(0,1), matrix(c(1,0.5,0.5,1),ncol=2), p_dimnames = c("A","B"))
x2 <- new_MULTINORMAL(c(10,1), matrix(c(1,0.4,0.4,1),ncol=2), p_dimnames = c("B","C"))
new_CONVOLUTION_comb(x1,x2, `+`)
new_SUM_comb(x1,x2)
new_SUBTRACTION_comb(x1,x2)
new_MULTIPLICATION_comb(x1,x2)
new_DIVISION_comb(x1,x2)
```

DIRAC	<i>Factory for a DIRAC distribution object</i>
-------	--

Description

Returns an DIRAC distribution object that always return the same number, or the same matrix of numbers in case multiple dimensions are setup

Usage

```
new_DIRAC(p_scalar, p_dimnames = "rvar")
```

Arguments

p_scalar	A numeric that set the value for the distribution
p_dimnames	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, DIRAC

Author(s)

John J. Aponte

Examples

```
myDistr <- new_DIRAC(1)
myDistr$rfunc(10)
```

DIRICHLET	<i>Factory for a DIRICHLET distribution object</i>
-----------	--

Description

Returns an DIRICHLET distribution object that draw random numbers generated by the function [rdirichlet](#)

Usage

```
new_DIRICHLET(p_alpha, p_dimnames)
```

Arguments

p_alpha	k-value vector for concentration parameter. Must be positive
p_dimnames	A vector of characters for the names of the k-dimensions

Details

A name can be provided for the dimensions. Otherwise rvar1, rvar2, ..., rvark will be assigned

Value

An object of class DISTRIBUTION, p_distribution\$distribution, TRUNCATED

Author(s)

John J. Aponte

Examples

```
myDistr <- new_DIRICHLET(c(0.3,0.2,0.5), c("a","b","c"))
myDistr$rfunc(10)
```

DISCRETE

Factory for a DISCRETE distribution object

Description

Returns an DISCRETE distribution object that sample from the vector p_supp of options with probability the vector of probabilities p_prob.

Usage

```
new_DISCRETE(p_supp, p_prob, p_dimnames = "rvar")
```

Arguments

p_supp	A numeric vector of options
p_prob	A numeric vector of probabilities.
p_dimnames	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, DISCRETE

Note

If the second argument is missing, all options will be sample with equal probability. If provided, the second argument would add to 1 and must be the same length that the first argument

Author(s)

John J. Aponte

Examples

```
myDistr <- new_DISCRETE(p_supp=c(1,2,3,4), p_prob=c(0.40,0.30,0.20,0.10))
myDistr$rfunc(10)
```

DISTRIBUTION

*DISTRIBUTION class***Description**

DISTRIBUTION is a kind of abstract class (or interface) that the specific constructors should implement.

Details

It contains 4 fields

distribution A character with the name of the distribution implemented

seed A numerical that is used for details to produce reproducible details of the distribution

oval Observed value. Is the value expected. It is used as a number for the mathematical operations of the distributions as if they were a simple scalar

rfunc A function that generate random numbers from the distribution. Its only parameter n is the number of draws of the distribution. It returns a matrix with as many rows as n, and as many columns as the dimensions of the distributions

The DISTRIBUTION objects could support multidimensional distributions for example [DIRICHLET](#). The names of the dimensions should coincides with the names of the oval vector. If only one dimension, the default name is rvar.

It is expected that the rfunc is included in the creation of new distributions by convolution so the environment should be carefully controlled to avoid reference leaking that is possible within the R language. For that reason, rfunc should be created within a [restrict_environment](#) function

Once the object is instanced, the fields are immutable and should not be changed. If the seed needs to be modified, a new object can be created using the [set_seed](#) function

Objects are defined for the following distributions

- [UNIFORM](#)
- [NORMAL](#)
- [BETA](#)
- [TRIANGULAR](#)
- [POISSON](#)
- [EXPONENTIAL](#)
- [DISCRETE](#)
- [DIRAC](#)
- [DIRICHLET](#)
- [TRUNCATED](#)
- [NA_DISTRIBUTION](#)

Value

a DISTRIBUTION object

Author(s)

John J. Aponte

DISTRIBUTION_factory *A factory of [DISTRIBUTION](#) classes*

Description

Generate a function that creates [DISTRIBUTION](#) objects

Usage

```
DISTRIBUTION_factory(distname, rfunction, ovalfunc)
```

Arguments

distname	name of the distribution. By convention they are upper case
rfunction	a function to generate random numbers from the distribution
ovalfunc	a function that calculate the oval value, should used only the same arguments that the rfunction

Value

A function that is able to create [DISTRIBUTION](#) objects.

Note

The function return a new function, that have as arguments the formals of the rfunction plus a new argument dimnames for the dimension names. If The distribution is unidimensional, the default value dimnames = "rvar" will works well, but if not, the dimnames argument should be specified when the generated function is used as in the example for the new_MyDIRICHLET

Author(s)

John J. Aponte

Examples

```

new_MYDISTR <- DISTRIBUTION_factory("MYDISTR", rnorm, function(){mean})
d1 <- new_MYDISTR(0,1)
summary(d1)
require(extraDistr)
new_MyDIRICHLET <- DISTRIBUTION_factory('rdirichlet',
                                         rdirichlet,
                                         function() {
                                           salpha = sum(alpha)
                                           alpha / salpha
                                         })
d2 <- new_MyDIRICHLET(c(10, 20, 70), dimnames = c("A", "B", "C"))
summary(d2)

```

EXPONENTIAL

*Factory for a EXPONENTIAL distribution using confidence intervals***Description**

Returns an EXPONENTIAL distribution object that produce random numbers from an exponential distribution using the [rexp](#) function

Usage

```
new_EXPONENTIAL(p_rate, p_dimnames = "rvar")
```

Arguments

<code>p_rate</code>	A numeric that represents the rate of events
<code>p_dimnames</code>	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, EXPONENTIAL

Author(s)

John J. Aponte

Examples

```

myDistr <- new_EXPONENTIAL(5)
myDistr$rfunc(10)

```

fitbeta

*Fits a beta distribution based on quantiles***Description**

Fits a beta distribution based on quantiles

Usage

```
fitbeta_ml(point, lci, uci)
```

```
fitbeta(point, lci, uci)
```

Arguments

point	Point estimates corresponding to the median
lci	Lower limit (quantile 0.025)
uci	Upper limit (quantile 0.975)

Value

parameters shape1 and shape2 of a beta distribution

Functions

- `fitbeta_ml()`: using ML to estimate parameters
- `fitbeta()`: preserve the expected value

Note

This is a wrap of the [fitdist](#) to obtain the best parameters for a beta distribution based on quantiles.

When using confidence intervals (not ML), the shape parameters are obtained using the following formula:

$$varp = (p_{uci} - p_{lci})/4^2$$

$$shape1 = p_{mean} * (p_{mean} * (1 - p_{mean})/varp - 1)$$

$$shape2 = (1 - p_{mean}) * (p_{mean} * (1 - p_{mean})/varp - 1)$$

Author(s)

John J. Aponte

See Also

[fitdist](#)

Examples

```
fitbeta_ml(0.45,0.40,0.50)
fitbeta(0.45,0.40,0.50)
```

fitdirichlet	<i>Fits a Dirichlet distribution,</i>
--------------	---------------------------------------

Description

Fits a Dirichlet distribution based on the parameters of Beta distributions

Usage

```
fitdirichlet(..., plotBeta = FALSE, n.fitted = "opt")
```

Arguments

...	named vectors with the distribution parameters shape1, shape2
plotBeta	if TRUE a ggplot of the densities are plotted
n.fitted	Method to fit the values

Details

Each one of the arguments is a named vector with values for shape1, shape2. Values from [fitbeta](#) are suitable for this. This is a wrap of [fitDirichlet](#)

Value

a vector with the parameters for a Dirichlet distribution

Author(s)

John J. Aponte

See Also

[fitDirichlet](#)

Examples

```
a <- fitbeta(0.3, 0.2, 0.4)
c <- fitbeta(0.2, 0.1, 0.3)
b <- fitbeta(0.5, 0.4, 0.6)
fitdirichlet(cat1=a,cat2=b,cat3=c)
```

ggDISTRIBUTION	<i>Plot of DISTRIBUTION objects using ggplot2</i>
----------------	---

Description

Plot of DISTRIBUTION objects using ggplot2

Usage

```
ggDISTRIBUTION(x, n = 10000)
```

Arguments

x	an object of class DISTRIBUTION
n	number of observation

Value

a ggplot object with the density of the distribution

Examples

```
x <- new_NORMAL(0, 1)
ggDISTRIBUTION(x)
y <- new_DIRICHLET(c(10, 20, 70))
ggDISTRIBUTION(x)
```

LOGNORMAL	<i>Factory for a LOGNORMAL distribution object</i>
-----------	--

Description

Returns a LOGNORMAL distribution object that produce random numbers from a log normal distribution using the `rlnorm` function

Usage

```
new_LOGNORMAL(p_meanlog, p_sdlog, p_dimnames = "rvar")
```

Arguments

p_meanlog	mean of the distribution on the log scale
p_sdlog	A numeric that represents the standard deviation on the log scale
p_dimnames	A character that represents the name of the dimension

Value

An object of class `DISTRIBUTION`, `LOGNORMAL`

Author(s)

John J. Aponte

Examples

```
myDistr <- new_LOGNORMAL(0,1)
myDistr$rfunc(10)
```

metadata

Metadata for a DISTRIBUTION

Description

Shows the distribution and the oval values of a `DISTRIBUTION` object

Usage

```
metadata(x)

## S3 method for class 'DISTRIBUTION'
metadata(x)

## Default S3 method:
metadata(x)
```

Arguments

x a `DISTRIBUTION` object

Value

A `data.frame` with the metadata of the distributions

Methods (by class)

- `metadata(DISTRIBUTION)`: Metadata for `DISTRIBUTION` objects
- `metadata(default)`: Metadata for other objects

Note

The number of columns depends on the dimensions of the distribution. There will be one column distribution with the name of the distribution and one column for each dimension with the names from the oval field.

Author(s)

John J. Aponte

NA_DISTRIBUTION

*Factory for a NA distribution object***Description**

Returns an NA distribution object that always return NA_real_. This is useful to handle NA. By default only one dimension rvar is produced, but if several names are provided more columns will be added to the return matrix

Usage

```
new_NA(p_dimnames = "rvar")
```

Arguments

p_dimnames A character that represents the the names of the dimensions. By default only one dimension with name rvar

Value

An object of class DISTRIBUTION, NA

Author(s)

John J. Aponte

Examples

```
myDistr <- new_NA(p_dimnames = "rvar")
myDistr$rfunc(10)
```

new_MIXTURE

*Mixture of [DISTRIBUTION](#) objects***Description**

Produce a new distribution that obtain random draws of the mixture of the [DISTRIBUTION](#) objects

Usage

```
new_MIXTURE(listdistr, mixture)
```

Arguments

listdistr	a list of DISTRIBUTION objects
mixture	a vector of probabilities to mixture the distributions. Must add 1 If missing the draws are obtained from the distributions with the same probability

Value

an object of class MIXTURE, [DISTRIBUTION](#)

Author(s)

John J. Aponte

Examples

```
x1 <- new_NORMAL(0,1)
x2 <- new_NORMAL(4,1)
x3 <- new_NORMAL(6,1)
new_MIXTURE(list(x1,x2,x3))
```

new_MULTINORMAL	<i>Multivariate Normal Distribution</i>
-----------------	---

Description

Return a [DISTRIBUTION](#) object that draw random numbers from a multivariate normal distribution using the [mvrnorm](#) function.

Usage

```
new_MULTINORMAL(p_mu, p_sigma, p_dimnames, tol = 1e-06, empirical = FALSE)
```

Arguments

p_mu	a vector of means
p_sigma	a positive-definite symmetric matrix for the covariance matrix
p_dimnames	A character that represents the name of the dimension
tol	tolerance (relative to largest variance) for numerical lack of positive-definiteness in p_sigma.
empirical	logical. If true, mu and Sigma specify the empirical not population mean and covariance matrix.

Value

An object of class [DISTRIBUTION](#), MULTINORMAL

Author(s)

John J. Aponte

See Also

[mvnrm](#)

Examples

```
msigma <- matrix(c(1,0,0,1), ncol=2)
d1 <- new_MULTINORMAL(c(0,1), msigma)
rfunc(d1, 10)
```

NORMAL

Factory for a NORMAL distribution object

Description

Returns a NORMAL distribution object that produce random numbers from a normal distribution using the [rnorm](#) function

Usage

```
new_NORMAL(p_mean, p_sd, p_dimnames = "rvar")
```

Arguments

p_mean	A numeric that represents the mean value
p_sd	A numeric that represents the standard deviation
p_dimnames	A character that represents the name of the dimension

Value

An object of class [DISTRIBUTION](#), NORMAL

Author(s)

John J. Aponte

Examples

```
myDistr <- new_NORMAL(0,1)
myDistr$rfunc(10)
```

omit_NA	<i>Omit NA distributions from a list of distributions</i>
---------	---

Description

Omit NA distributions from a list of distributions

Usage

```
omit_NA(listdistr)
```

Arguments

listdistr a list of [DISTRIBUTION](#) objects

Value

the list without the [NA_DISTRIBUTION](#)

Author(s)

John J. Aponte

plot.DISTRIBUTION	<i>plot of DISTRIBUTION objects</i>
-------------------	---

Description

Plot an histogram of the density of the distribution using random numbers from the distribution

Usage

```
## S3 method for class 'DISTRIBUTION'
plot(x, n = 10000, ...)
```

Arguments

x an object of class [DISTRIBUTION](#)
 n number of observations
 ... other parameters to the [hist](#) function

Value

No return value. Side effect plot the histogram.

Examples

```
x <- new_NORMAL(0,1)
plot(x)
y <- new_DIRICHLET(c(10,20,70))
plot(x)
```

POISSON*Factory for a POISSON distribution using confidence intervals*

Description

Returns an POISSON distribution object that produce random numbers from a Poisson distribution using the [rpois](#) function

Usage

```
new_POISSON(p_lambda, p_dimnames = "rvar")
```

Arguments

p_lambda	A numeric that represents the expected number of events
p_dimnames	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, POISSON

Author(s)

John J. Aponte

Examples

```
myDistr <- new_POISSON(5)
myDistr$rfunc(10)
```

restrict_environment *Build a new function with a smaller environment*

Description

As standard feature, R include in the environment of a function all the variables that are available when the function is created. This, however is prompt to leak reference when you have a factory of function and they are created within a list.. it will include all the component of the list in the function environment. To prevent that, the random generator functions are encapsulated with a restricted environment where only the variables that the function requires to work are included

Usage

```
restrict_environment(f, ...)
```

Arguments

f	input function
...	define the set of variables to be included as variable = value.

Value

new function with a restricted environment

Author(s)

John J. Aponte

Examples

```
a = 0
b = 1
myfunc <- restrict_environment(
  function(n) {
    rnorm(meanvalue, sdvalue)
  },
  meanvalue = a, sdvalue = b)

myfunc(10)
ls(envir=environment(myfunc))
```

rfunc	<i>Generate random numbers from a DISTRIBUTION object</i>
-------	---

Description

This is a generic method that calls the rfunc slot of the object

Usage

```
rfunc(x, n)
```

Arguments

x	an object
n	the number of random samples

Value

a matrix with as many rows as n and as many columns as dimensions have distribution

Author(s)

John J. Aponte

rfunc.default	<i>Default function</i>
---------------	-------------------------

Description

Default function

Usage

```
## Default S3 method:
rfunc(x, n)
```

Arguments

x	an object of class different from DISTRIBUTION
n	the number of random samples

Value

No return value. Raise an error message.

Author(s)

John J. Aponte

<code>rfunc.DISTRIBUTION</code>	<i>Generic function for a DISTRIBUTION object</i>
---------------------------------	---

Description

Generic function for a [DISTRIBUTION](#) object

Usage

```
## S3 method for class 'DISTRIBUTION'  
rfunc(x, n)
```

Arguments

<code>x</code>	an object of class DISTRIBUTION
<code>n</code>	the number of random samples

Value

a matrix with as many rows as `n` and as many columns as

Author(s)

John J. Aponte

<code>same_dimensions</code>	<i>Check the dimensions of a list of distributions</i>
------------------------------	--

Description

Check the dimensions of a list of distributions

Usage

```
same_dimensions(listdistr)
```

Arguments

<code>listdistr</code>	a list of DISTRIBUTION objects
------------------------	--

Value

return TRUE if all the dimensions are the same

`set_seed`*Modify a the seed of a Distribution object*

Description

This create a new [DISTRIBUTION](#) object but with the specified seed

Usage

```
set_seed(distribution, seed)
```

Arguments

<code>distribution</code>	a DISTRIBUTION object
<code>seed</code>	the new seed

Value

a [DISTRIBUTION](#) object of the same class

Author(s)

John J. Aponte

`summary.DISTRIBUTION`*Summary of Distributions*

Description

Summary of Distributions

Usage

```
## S3 method for class 'DISTRIBUTION'  
summary(object, n = 10000, ...)
```

Arguments

<code>object</code>	object of class DISTRIBUTION
<code>n</code>	the number of random samples from the distribution
<code>...</code>	other parameters. Not used

Value

A `data.frame` with as many rows as dimensions had the distribution and with the following columns

- distribution name
- varname name of the dimension
- oval value
- nsample number of random samples
- mean_ mean value of the sample
- sd_ standard deviation of the sample
- lci_ lower 95
- median_ median value of the sample
- uci_ upper 95

Note

The sample uses the seed saved in the object those it will provide the same values fir an n value

Author(s)

John J. Aponte

TRIANGULAR

Factory for a TRIANGULAR distribution object

Description

Returns an TRIANGULAR distribution object that produce random numbers from a triangular distribution using the `rtriang` function

Usage

```
new_TRIANGULAR(p_min, p_max, p_mode, p_dimnames = "rvar")
```

Arguments

<code>p_min</code>	A numeric that represents the lower limit
<code>p_max</code>	A numeric that represents the upper limit
<code>p_mode</code>	A numeric that represents the mode
<code>p_dimnames</code>	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, TRIANGULAR

Author(s)

John J. Aponte

Examples

```
myDistr <- new_TRIANGULAR(-1,1,0)
myDistr$rfunc(10)
```

TRUNCATED

Factory for a TRUNCATED distribution object

Description

Returns an TRUNCATED distribution object that limits the values that are generated by the distribution to be in the limits `p_min`, `p_max`

Usage

```
new_TRUNCATED(p_distribution, p_min = -Inf, p_max = Inf)
```

Arguments

`p_distribution` An object of class `DISTRIBUTION` to truncate
`p_min` A numeric that set the lower limit of the distribution
`p_max` A numeric that set the upper limit of the distribution

Value

An object of class `DISTRIBUTION`, `p_distribution$distribution`, `TRUNCATED`

Note

The expected value of a truncated distribution could be very different from the expected value of the unrestricted distribution. Be careful as the `oval` field is not changed and may not represent any more the expected value of the distribution.

If the distribution is multidimensional, the limits will apply to all dimensions.

Author(s)

John J. Aponte

Examples

```
myDistr <- new_TRUNCATED(p_distribution = new_NORMAL(0,1), p_min = -1, p_max = 1)
myDistr$rfunc(10)
```

UNIFORM*Factory for a UNIFORM distribution object*

Description

Returns an UNIFORM distribution object that produce random numbers from a uniform distribution using the [runif](#) function

Usage

```
new_UNIFORM(p_min, p_max, p_dimnames = "rvar")
```

Arguments

<code>p_min</code>	A numeric that represents the lower limit
<code>p_max</code>	A numeric that represents the upper limit
<code>p_dimnames</code>	A character that represents the name of the dimension

Value

An object of class DISTRIBUTION, UNIFORM

Author(s)

John J. Aponte

Examples

```
myDistr <- new_UNIFORM(0,1)
myDistr$rfunc(10)
```

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