

Package ‘gamlss.dist’

March 8, 2022

Type Package

Title Distributions for Generalized Additive Models for Location Scale and Shape

Version 6.0-3

Date 2022-03-08

Description A set of distributions which can be used for modelling the response variables in Generalized Additive Models for Location Scale and Shape, Rigby and Stasinopoulos (2005), <[doi:10.1111/j.1467-9876.2005.00510.x](https://doi.org/10.1111/j.1467-9876.2005.00510.x)>. The distributions can be continuous, discrete or mixed distributions. Extra distributions can be created, by transforming, any continuous distribution defined on the real line, to a distribution defined on ranges 0 to infinity or 0 to 1, by using a "log" or a "logit" transformation respectively.

License GPL-2 | GPL-3

URL <https://www.gamlss.com/>

Depends R (>= 3.5.0), MASS, graphics, stats, methods, grDevices

Repository CRAN

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NeedsCompilation yes

Date/Publication 2022-03-08 16:40:07 UTC

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gamlss.dist-package	<i>Distributions for Generalized Additive Models for Location Scale and Shape</i>
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Description

A set of distributions which can be used for modelling the response variables in Generalized Additive Models for Location Scale and Shape, Rigby and Stasinopoulos (2005), <doi:10.1111/j.1467-9876.2005.00510.x>. The distributions can be continuous, discrete or mixed distributions. Extra distributions can be created, by transforming, any continuous distribution defined on the real line, to a distribution defined on ranges 0 to infinity or 0 to 1, by using a "log" or a "logit" transformation respectively.

Details

The DESCRIPTION file:

```
Package:      gamlss.dist
Type:         Package
Title:         Distributions for Generalized Additive Models for Location Scale and Shape
Version:       6.0-3
Date:          2022-03-08
Authors@R:     c(person("Mikis", "Stasinopoulos", role = c("aut", "cre", "cph"), email = "d.stasinopoulos@londonmet.ac.uk"),
Description:   A set of distributions which can be used for modelling the response variables in Generalized Additive Models
License:       GPL-2 | GPL-3
URL:           https://www.gamlss.com/
Depends:       R (>= 3.5.0), MASS, graphics, stats, methods, grDevices
Repository:    CRAN
Author:        Mikis Stasinopoulos [aut, cre, cph], Robert Rigby [aut], Calliope Akantziliotou [ctb], Vlasios Voudouris [ctb],
Maintainer:    Mikis Stasinopoulos <d.stasinopoulos@londonmet.ac.uk>
```

Index of help topics:

BB	Beta Binomial Distribution For Fitting a GAMLSS Model
BCCG	Box-Cox Cole and Green distribution (or Box-Cox normal) for fitting a GAMLSS
BCPE	Box-Cox Power Exponential distribution for fitting a GAMLSS
BCT	Box-Cox t distribution for fitting a GAMLSS
BE	The beta distribution for fitting a GAMLSS
BEINF	The beta inflated distribution for fitting a GAMLSS
BEOI	The one-inflated beta distribution for fitting a GAMLSS
BEZI	The zero-inflated beta distribution for fitting

	a GAMLSS
BI	Binomial distribution for fitting a GAMLSS
BNB	Beta Negative Binomial distribution for fitting a GAMLSS
DBI	The Double binomial distribution
DBURR12	The Discrete Burr type XII distribution for fitting a GAMLSS model
DEL	The Delaporte distribution for fitting a GAMLSS model
DPO	The Double Poisson distribution
EGB2	The exponential generalized Beta type 2 distribution for fitting a GAMLSS
EXP	Exponential distribution for fitting a GAMLSS
GA	Gamma distribution for fitting a GAMLSS
GAF	The Gamma distribution family
GB1	The generalized Beta type 1 distribution for fitting a GAMLSS
GB2	The generalized Beta type 2 and generalized Pareto distributions for fitting a GAMLSS
GEOM	Geometric distribution for fitting a GAMLSS model
GG	Generalized Gamma distribution for fitting a GAMLSS
GIG	Generalized Inverse Gaussian distribution for fitting a GAMLSS
GPO	The generalised Poisson distribution
GT	The generalized t distribution for fitting a GAMLSS
GU	The Gumbel distribution for fitting a GAMLSS
IG	Inverse Gaussian distribution for fitting a GAMLSS
IGAMMA	Inverse Gamma distribution for fitting a GAMLSS
JSU	The Johnson's Su distribution for fitting a GAMLSS
JSUo	The original Johnson's Su distribution for fitting a GAMLSS
LG	Logarithmic and zero adjusted logarithmic distributions for fitting a GAMLSS model
LNO	Log Normal distribution for fitting in GAMLSS
LO	Logistic distribution for fitting a GAMLSS
LOGITNO	Logit Normal distribution for fitting in GAMLSS
LQNO	Normal distribution with a specific mean and variance relationship for fitting a GAMLSS model
MN3	Multinomial distribution in GAMLSS
NBF	Negative Binomial Family distribution for fitting a GAMLSS
NBI	Negative Binomial type I distribution for

	fitting a GAMLSS
NBII	Negative Binomial type II distribution for fitting a GAMLSS
NET	Normal Exponential t distribution (NET) for fitting a GAMLSS
NO	Normal distribution for fitting a GAMLSS
NO2	Normal distribution (with variance as sigma parameter) for fitting a GAMLSS
NOF	Normal distribution family for fitting a GAMLSS
PARETO2	Pareto distributions for fitting in GAMLSS
PE	Power Exponential distribution for fitting a GAMLSS
PIG	The Poisson-inverse Gaussian distribution for fitting a GAMLSS model
PO	Poisson distribution for fitting a GAMLSS model
RG	The Reverse Gumbel distribution for fitting a GAMLSS
RGE	Reverse generalized extreme family distribution for fitting a GAMLSS
SEP	The Skew Power exponential (SEP) distribution for fitting a GAMLSS
SEP1	The Skew Power exponential type 1-4 distribution for fitting a GAMLSS
SHASH	The Sinh-Arcsinh (SHASH) distribution for fitting a GAMLSS
SI	The Sichel distribution for fitting a GAMLSS model
SICHEL	The Sichel distribution for fitting a GAMLSS model
SIMPLEX	The simplex distribution for fitting a GAMLSS
SN1	Skew Normal Type 1 distribution for fitting a GAMLSS
SN2	Skew Normal Type 2 distribution for fitting a GAMLSS
ST1	The skew t distributions, type 1 to 5
TF	t family distribution for fitting a GAMLSS
WARING	Waring distribution for fitting a GAMLSS model
WEI	Weibull distribution for fitting a GAMLSS
WEI2	A specific parameterization of the Weibull distribution for fitting a GAMLSS
WEI3	A specific parameterization of the Weibull distribution for fitting a GAMLSS
YULE	Yule distribution for fitting a GAMLSS model
ZABB	Zero inflated and zero adjusted Binomial distribution for fitting in GAMLSS
ZABI	Zero inflated and zero adjusted Binomial distribution for fitting in GAMLSS
ZAGA	The zero adjusted Gamma distribution for

	fitting a GAMLSS model
ZAIG	The zero adjusted Inverse Gaussian distribution for fitting a GAMLSS model
ZANBI	Zero inflated and zero adjusted negative binomial distributions for fitting a GAMLSS model
ZAP	Zero adjusted poisson distribution for fitting a GAMLSS model
ZIP	Zero inflated poisson distribution for fitting a GAMLSS model
ZIP2	Zero inflated poisson distribution for fitting a GAMLSS model
ZIPF	The zipf and zero adjusted zipf distributions for fitting a GAMLSS model
checklink	Set the Right Link Function for Specified Parameter and Distribution
count_1_31	A set of functions to plot gamlss.family distributions
exGAUS	The ex-Gaussian distribution
flexDist	Non-parametric pdf from limited information data
gamlss.dist-package	Distributions for Generalized Additive Models for Location Scale and Shape
gamlss.family	Family Objects for fitting a GAMLSS model
gen.Family	Functions to generate log and logit distributions from existing continuous gamlss.family distributions
hazardFun	Hazard functions for gamlss.family distributions
make.link.gamlss	Create a Link for GAMLSS families
momentSK	Sample and theoretical Moment and Centile Skewness and Kurtosis Functions

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References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/](https://doi.org/10.1201/)

9780429298547. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
# pdf plot
plot(function(y) dSICHEL(y, mu=10, sigma = 0.1 , nu=1 ),
      from=0, to=30, n=30+1, type="h")
# cdf plot
PPP <- par(mfrow=c(2,1))
plot(function(y) pSICHEL(y, mu=10, sigma =0.1, nu=1 ),
      from=0, to=30, n=30+1, type="h") # cdf
cdf<-pSICHEL(0:30, mu=10, sigma=0.1, nu=1)
sfun1 <- stepfun(1:30, cdf, f = 0)
plot(sfun1, xlim=c(0,30), main="cdf(x)")
par(PPP)
```

BB

Beta Binomial Distribution For Fitting a GAMLSS Model

Description

This function defines the beta binomial distribution, a two parameter distribution, for a `gamlss.family` object to be used in a GAMLSS fitting using the function `gamlss()`

Usage

```
BB(mu.link = "logit", sigma.link = "log")
dBB(x, mu = 0.5, sigma = 1, bd = 10, log = FALSE)
pBB(q, mu = 0.5, sigma = 1, bd = 10, lower.tail = TRUE,
    log.p = FALSE)
qBB(p, mu = 0.5, sigma = 1, bd = 10, lower.tail = TRUE,
    log.p = FALSE, fast = FALSE)
rBB(n, mu = 0.5, sigma = 1, bd = 10, fast = FALSE)
```


Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog" (complementary log-log)
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse", "identity" and "sqrt"
<code>mu</code>	vector of positive probabilities
<code>sigma</code>	the dispersion parameter
<code>bd</code>	vector of binomial denominators
<code>p</code>	vector of probabilities
<code>x,q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>fast</code>	a logical variable if <code>fast=TRUE</code> the <code>dbb</code> function is used in the calculation of the inverse c.d.f function. This is faster to the default <code>fast=FALSE</code> , where the <code>pBB{}</code> is used, but not always consistent with the results obtained from <code>pBB()</code> , for example if <code>p <- pBB(c(0,1,2,3,4,5), mu=.5, sigma=1, bd=5)</code> do not ensure that <code>qBB(p, mu=.5, sigma=1, bd=5)</code> will be <code>c(0,1,2,3,4,5)</code>

Details

Definition file for beta binomial distribution.

$$f(y|\mu, \sigma) = \frac{\Gamma(n+1)}{\Gamma(y+1)\Gamma(n-y+1)} \frac{\Gamma(\frac{1}{\sigma})\Gamma(y + \frac{\mu}{\sigma})\Gamma[n + \frac{(1-\mu)}{\sigma} - y]}{\Gamma(n + \frac{1}{\sigma})\Gamma(\frac{\mu}{\sigma})\Gamma(\frac{1-\mu}{\sigma})}$$

for $y = 0, 1, 2, \dots, n$, $0 < \mu < 1$ and $\sigma > 0$. For $\mu = 0.5$ and $\sigma = 0.5$ the distribution is uniform.

Value

Returns a `gamlss.family` object which can be used to fit a Beta Binomial distribution in the `gamlss()` function.

Warning

The functions `pBB` and `qBB` are calculated using a laborious procedure so they are relatively slow.

Note

The response variable should be a matrix containing two columns, the first with the count of successes and the second with the count of failures. The parameter `mu` represents a probability parameter with limits $0 < \mu < 1$. $n\mu$ is the mean of the distribution where n is the binomial denominator. $\{n\mu(1-\mu)[1 + (n-1)\sigma/(\sigma+1)]\}^{0.5}$ is the standard deviation of the Beta Binomial distribution. Hence σ is a dispersion type parameter

Author(s)

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References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BI](#),

Examples

```
# BB()# gives information about the default links for the Beta Binomial distribution
#plot the pdf
plot(function(y) dBB(y, mu = .5, sigma = 1, bd =40), from=0, to=40, n=40+1, type="h")
#calculate the cdf and plotting it
ppBB <- pBB(seq(from=0, to=40), mu=.2 , sigma=3, bd=40)
plot(0:40,ppBB, type="h")
#calculating quantiles and plotting them
qqBB <- qBB(ppBB, mu=.2 , sigma=3, bd=40)
plot(qqBB~ ppBB)
# when the argument fast is useful
p <- pBB(c(0,1,2,3,4,5), mu=.01 , sigma=1, bd=5)
qBB(p, mu=.01 , sigma=1, bd=5, fast=TRUE)
# 0 1 1 2 3 5
qBB(p, mu=.01 , sigma=1, bd=5, fast=FALSE)
# 0 1 2 3 4 5
# generate random sample
tN <- table(Ni <- rBB(1000, mu=.2, sigma=1, bd=20))
r <- barplot(tN, col='lightblue')
# fitting a model
# library(gamlss)
#data(aep)
# fits a Beta-Binomial model
#h<-gamlss(y~ward+loglos+year, sigma.formula=~year+ward, family=BB, data=aep)
```

BCCG

Box-Cox Cole and Green distribution (or Box-Cox normal) for fitting a GAMLSS

Description

The function BCCG defines the Box-Cox Cole and Green distribution (Box-Cox normal), a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dBCCG`, `pBCCG`, `qBCCG` and `rBCCG` define the density, distribution function, quantile function and random generation for the specific parameterization of the Box-Cox Cole and Green distribution. [The function `BCCGuntr()` is the original version of the function suitable only for the untruncated Box-Cox Cole and Green distribution See Cole and Green (1992) and Rigby and Stasinopoulos (2003a,2003b) for details. The function `BCCGo` is identical to `BCCG` but with `log link` for `mu`.

Usage

```
BCCG(mu.link = "identity", sigma.link = "log", nu.link = "identity")
BCCGo(mu.link = "log", sigma.link = "log", nu.link = "identity")
BCCGuntr(mu.link = "identity", sigma.link = "log", nu.link = "identity")
dBCCG(x, mu = 1, sigma = 0.1, nu = 1, log = FALSE)
pBCCG(q, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qBCCG(p, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
rBCCG(n, mu = 1, sigma = 0.1, nu = 1)
dBCCGo(x, mu = 1, sigma = 0.1, nu = 1, log = FALSE)
pBCCGo(q, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qBCCGo(p, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
rBCCGo(n, mu = 1, sigma = 0.1, nu = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter, other links are "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other links are "inverse", "identity" and "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter, other links are "inverse", "log" and "own"
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The probability distribution function of the untruncated Box-Cox Cole and Green distribution, `BCCGuntr`, is defined as

$$f(y|\mu, \sigma, \nu) = \frac{1}{\sqrt{2\pi}\sigma} \frac{y^{\nu-1}}{\mu^\nu} \exp\left(-\frac{z^2}{2}\right)$$

where if $\nu \neq 0$ then $z = [(y/\mu)^\nu - 1]/(\nu\sigma)$ else $z = \log(y/\mu)/\sigma$, for $y > 0$, $\mu > 0$, $\sigma > 0$ and $\nu = (-\infty, +\infty)$.

The Box-Cox Cole and Green distribution, BCCG, adjusts the above density $f(y|\mu, \sigma, \nu)$ for the truncation resulting from the condition $y > 0$. See Rigby and Stasinopoulos (2003a, 2003b) for details.

Value

`BCCG()` returns a `gamlss.family` object which can be used to fit a Cole and Green distribution in the `gamlss()` function. `dBCCG()` gives the density, `pBCCG()` gives the distribution function, `qBCCG()` gives the quantile function, and `rBCCG()` generates random deviates.

Warning

The `BCCGuntr` distribution may be unsuitable for some combinations of the parameters (mainly for large σ) where the integrating constant is less than 0.99. A warning will be given if this is the case. The BCCG distribution is suitable for all combinations of the distributional parameters within their range [i.e. $\mu > 0$, $\sigma > 0$, $\nu = (-\infty, +\infty)$]

Note

μ is the median of the distribution σ is approximately the coefficient of variation (for small values of σ), and ν controls the skewness.

The BCCG distribution is suitable for all combinations of the parameters within their ranges [i.e. $\mu > 0$, $\sigma > 0$, and $\nu = (-\infty, \infty)$]

Author(s)

Mikis Stasinopoulos, Bob Rigby and Kalliope Akantziliotou

References

- Cole, T. J. and Green, P. J. (1992) Smoothing reference centile curves: the LMS method and penalized likelihood, *Statist. Med.* **11**, 1305–1319
- Rigby, R. A. and Stasinopoulos, D. M. (2004). Smooth centile curves for skew and kurtotic data modelled using the Box-Cox Power Exponential distribution. *Statistics in Medicine*, **23**: 3053-3076.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R.A. Stasinopoulos, D.M. (2006). Using the Box-Cox t distribution in GAMLSS to model skewness and kurtosis. *Statistical Modelling*, 6(3) :209. doi: [10.1191/1471082X06st122oa](https://doi.org/10.1191/1471082X06st122oa)

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547) An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BCPE](#), [BCT](#)

Examples

```
BCCG() # gives information about the default links for the Cole and Green distribution
# library(gamlss)
# data(abdom)
# h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=BCCG, data=abdom)
# plot(h)
plot(function(x) dBCCG(x, mu=5,sigma=.5,nu=-1), 0.0, 20,
      main = "The BCCG density mu=5,sigma=.5,nu=-1")
plot(function(x) pBCCG(x, mu=5,sigma=.5,nu=-1), 0.0, 20,
      main = "The BCCG cdf mu=5, sigma=.5, nu=-1")
```

BCPE

Box-Cox Power Exponential distribution for fitting a GAMLSS

Description

This function defines the Box-Cox Power Exponential distribution, a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dBCE`, `pBCE`, `qBCE` and `rBCE` define the density, distribution function, quantile function and random generation for the Box-Cox Power Exponential distribution. The function `checkBCE` can be used, typically when a BCE model is fitted, to check whether there exit a turning point of the distribution close to zero. It give the number of values of the response below their minimum turning point and also the maximum probability of the lower tail below minimum turning point. [The function `Biventer()` is the original version of the function suitable only for the untruncated BCE distribution.] See Rigby and Stasinopoulos (2003) for details. The function `BCEo` is identical to BCE but with log link for mu.

Usage

```
BCPE(mu.link = "identity", sigma.link = "log", nu.link = "identity",
      tau.link = "log")
BCEo(mu.link = "log", sigma.link = "log", nu.link = "identity",
```

```

        tau.link = "log")
BCPEuntr(mu.link = "identity", sigma.link = "log", nu.link = "identity",
        tau.link = "log")
dBCPE(x, mu = 5, sigma = 0.1, nu = 1, tau = 2, log = FALSE)
pBCPE(q, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
qBCPE(p, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
rBCPE(n, mu = 5, sigma = 0.1, nu = 1, tau = 2)
dBCPEo(x, mu = 5, sigma = 0.1, nu = 1, tau = 2, log = FALSE)
pBCPEo(q, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE,
        log.p = FALSE)
qBCPEo(p, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE,
        log.p = FALSE)
rBCPEo(n, mu = 5, sigma = 0.1, nu = 1, tau = 2)
checkBCPE(obj = NULL, mu = 10, sigma = 0.1, nu = 0.5, tau = 2,...)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. Other links are "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse", "identity" and "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter. Other links are "inverse", "log" and "own"
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter. Other links are "logshifted", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of <code>nu</code> parameter values
<code>tau</code>	vector of <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required
<code>obj</code>	a <code>gamlss BCPE</code> family object
<code>...</code>	for extra arguments

Details

The probability density function of the untruncated Box Cox Power Exponential distribution, (`BCPE.untr`), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = \frac{y^{\nu-1} \tau \exp[-\frac{1}{2}|\frac{y}{\mu}|^{\tau}]}{\mu^{\nu} \sigma c 2^{(1+1/\tau)} \Gamma(\frac{1}{\tau})}$$

where $c = [2^{(-2/\tau)}\Gamma(1/\tau)/\Gamma(3/\tau)]^{0.5}$, where if $\nu \neq 0$ then $z = [(y/\mu)^\nu - 1]/(\nu\sigma)$ else $z = \log(y/\mu)/\sigma$, for $y > 0$, $\mu > 0$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$.

The Box-Cox Power Exponential, BCPE, adjusts the above density $f(y|\mu, \sigma, \nu, \tau)$ for the truncation resulting from the condition $y > 0$. See Rigby and Stasinopoulos (2003) for details.

Value

BCPE() returns a `gamlss.family` object which can be used to fit a Box Cox Power Exponential distribution in the `gamlss()` function. `dbcpe()` gives the density, `pbcpe()` gives the distribution function, `qbcpe()` gives the quantile function, and `rbcpe()` generates random deviates.

Warning

The BCPE.untr distribution may be unsuitable for some combinations of the parameters (mainly for large σ) where the integrating constant is less than 0.99. A warning will be given if this is the case.

The BCPE distribution is suitable for all combinations of the parameters within their ranges [i.e. $\mu > 0$, $\sigma > 0$, $\nu = (-\infty, \infty)$ and $\tau > 0$]

Note

μ , is the median of the distribution, σ is approximately the coefficient of variation (for small σ and moderate $\nu > 0$), ν controls the skewness and τ the kurtosis of the distribution

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BCT](#)

Examples

```
# BCPE() #
# library(gamlss)
# data(abdom)
#h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=BCPE, data=abdom)
#plot(h)
plot(function(x)dBCE(x, mu=5,sigma=.5,nu=1, tau=3), 0.0, 15,
      main = "The BCPE density mu=5,sigma=.5,nu=1, tau=3")
plot(function(x) pBCE(x, mu=5,sigma=.5,nu=1, tau=3), 0.0, 15,
      main = "The BCPE cdf mu=5, sigma=.5, nu=1, tau=3")
```

BCT

Box-Cox t distribution for fitting a GAMLSS

Description

The function `BCT()` defines the Box-Cox t distribution, a four parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dBCT`, `pBCT`, `qBCT` and `rBCT` define the density, distribution function, quantile function and random generation for the Box-Cox t distribution. [The function `BCTuntr()` is the original version of the function suitable only for the untruncated BCT distribution]. See Rigby and Stasinopoulos (2003) for details. The function `BCT` is identical to `BCT` but with log link for μ .

Usage

```
BCT(mu.link = "identity", sigma.link = "log", nu.link = "identity",
     tau.link = "log")
BCTo(mu.link = "log", sigma.link = "log", nu.link = "identity",
      tau.link = "log")
BCTuntr(mu.link = "identity", sigma.link = "log", nu.link = "identity",
         tau.link = "log")
dBCT(x, mu = 5, sigma = 0.1, nu = 1, tau = 2, log = FALSE)
pBCT(q, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
qBCT(p, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
rBCT(n, mu = 5, sigma = 0.1, nu = 1, tau = 2)
dBCTo(x, mu = 5, sigma = 0.1, nu = 1, tau = 2, log = FALSE)
pBCTo(q, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
qBCTo(p, mu = 5, sigma = 0.1, nu = 1, tau = 2, lower.tail = TRUE, log.p = FALSE)
rBCTo(n, mu = 5, sigma = 0.1, nu = 1, tau = 2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the μ parameter. Other links are "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the σ parameter. Other links are "inverse", "identity", "own"

<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter. Other links are "inverse", "log", "own"
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter. Other links are "inverse", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of <code>nu</code> parameter values
<code>tau</code>	vector of <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The probability density function of the untruncated Box-Cox t distribution, `BCTuntr`, is given by

$$f(y|\mu, \sigma, \nu, \tau) = \frac{y^{\nu-1}}{\mu^\nu \sigma} \frac{\Gamma[(\tau+1)/2]}{\Gamma(1/2)\Gamma(\tau/2)\tau^{0.5}} [1 + (1/\tau)z^2]^{-(\tau+1)/2}$$

where if $\nu \neq 0$ then $z = [(y/\mu)^\nu - 1]/(\nu\sigma)$ else $z = \log(y/\mu)/\sigma$, for $y > 0$, $\mu > 0$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$.

The Box-Cox t distribution, `BCT`, adjusts the above density $f(y|\mu, \sigma, \nu, \tau)$ for the truncation resulting from the condition $y > 0$. See Rigby and Stasinopoulos (2003) for details.

Value

`BCT()` returns a `gamlss.family` object which can be used to fit a Box Cox- t distribution in the `gamlss()` function. `dBCT()` gives the density, `pBCT()` gives the distribution function, `qBCT()` gives the quantile function, and `rBCT()` generates random deviates.

Warning

The use `BCTuntr` distribution may be unsuitable for some combinations of the parameters (mainly for large σ) where the integrating constant is less than 0.99. A warning will be given if this is the case.

The `BCT` distribution is suitable for all combinations of the parameters within their ranges [i.e. $\mu > 0$, $\sigma > 0$, $\nu = (-\infty, \infty)$ and $\tau > 0$]

Note

μ is the median of the distribution, $\sigma(\frac{\tau}{\tau-2})^{0.5}$ is approximate the coefficient of variation (for small σ and moderate $\nu > 0$ and moderate or large τ), ν controls the skewness and τ the kurtosis of the distribution

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BCPE](#), [BCCG](#)

Examples

```
BCT() # gives information about the default links for the Box Cox t distribution
# library(gamlss)
# data(abdom)
# h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=BCT, data=abdom) #
# plot(h)
plot(function(x)dBCT(x, mu=5,sigma=.5,nu=1, tau=2), 0.0, 20,
      main = "The BCT density mu=5,sigma=.5,nu=1, tau=2")
plot(function(x) pBCT(x, mu=5,sigma=.5,nu=1, tau=2), 0.0, 20,
      main = "The BCT cdf mu=5, sigma=.5, nu=1, tau=2")
```

 BE

The beta distribution for fitting a GAMLSS

Description

The functions `BE()` and `BEo()` define the beta distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. `BE()` has mean equal to the parameter `mu` and `sigma` as scale parameter, see below. `BEo()` is the original parameterizations of the beta distribution as in `dbeta()` with `shape1=mu` and `shape2=sigma`. The functions `dBET` and `dBETo`, `pBE` and `pBEo`, `qBE` and `qBEo` and finally `rBE` and `rBEo` define the density, distribution function, quantile function and random generation for the `BE` and `BEo` parameterizations respectively of the beta distribution.

Usage

```

BE(mu.link = "logit", sigma.link = "logit")
dBE(x, mu = 0.5, sigma = 0.2, log = FALSE)
pBE(q, mu = 0.5, sigma = 0.2, lower.tail = TRUE, log.p = FALSE)
qBE(p, mu = 0.5, sigma = 0.2, lower.tail = TRUE, log.p = FALSE)
rBE(n, mu = 0.5, sigma = 0.2)
BEo(mu.link = "log", sigma.link = "log")
dBEo(x, mu = 0.5, sigma = 0.2, log = FALSE)
pBEo(q, mu = 0.5, sigma = 0.2, lower.tail = TRUE, log.p = FALSE)
qBEo(p, mu = 0.5, sigma = 0.2, lower.tail = TRUE, log.p = FALSE)

```

Arguments

<code>mu.link</code>	the mu link function with default <code>logit</code>
<code>sigma.link</code>	the sigma link function with default <code>logit</code>
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The original beta distribution is given as

$$f(y|\alpha, \beta) = \frac{1}{B(\alpha, \beta)} y^{\alpha-1} (1-y)^{\beta-1}$$

for $y = (0, 1)$, $\alpha > 0$ and $\beta > 0$. In the `gamlss` implementation of `BEo` $\alpha = \mu$ and $\beta > \sigma$. The reparametrization in the function `BE()` is $\mu = \frac{\alpha}{\alpha+\beta}$ and $\sigma = (\frac{1}{(\alpha+\beta+1)^{1/2}})$ for $\mu = (0, 1)$ and $\sigma = (0, 1)$. The expected value of y is μ and the variance is $\sigma^2 \mu * (1 - \mu)$.

Value

`BE()` and `BEo()` return a `gamlss.family` object which can be used to fit a beta distribution in the `gamlss()` function.

Note

Note that for `BE`, `mu` is the mean and `sigma` a scale parameter contributing to the variance of y

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

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- Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <https://www.gamlss.com/>).
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BE](#), [LOGITNO](#), [GB1](#), [BEINF](#)

Examples

```
BE()# gives information about the default links for the beta distribution
dat1<-rBE(100, mu=.3, sigma=.5)
hist(dat1)
#library(gamlss)
# mod1<-gamlss(dat1~1,family=BE) # fits a constant for mu and sigma
#fitted(mod1)[1]
#fitted(mod1,"sigma")[1]
plot(function(y) dBE(y, mu=.1 ,sigma=.5), 0.001, .999)
plot(function(y) pBE(y, mu=.1 ,sigma=.5), 0.001, 0.999)
plot(function(y) qBE(y, mu=.1 ,sigma=.5), 0.001, 0.999)
plot(function(y) qBE(y, mu=.1 ,sigma=.5, lower.tail=FALSE), 0.001, .999)
dat2<-rBEo(100, mu=1, sigma=2)
#mod2<-gamlss(dat2~1,family=BEo) # fits a constant for mu and sigma
#fitted(mod2)[1]
#fitted(mod2,"sigma")[1]
```

BEINF

The beta inflated distribution for fitting a GAMLSS

Description

The function `BEINF()` defines the beta inflated distribution, a four parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The beta inflated is similar to the beta but allows zeros and ones as values for the response variable. The two extra parameters model the probabilities at zero and one.

The functions `BEINF0()` and `BEINF1()` are three parameter beta inflated distributions allowing zeros or ones only at the response respectively. `BEINF0()` and `BEINF1()` are re-parameterize versions of the distributions [BEZI](#) and [BEOI](#) contributed to `gamlss` by Raydonal Ospina (see Ospina and Ferrari (2010)).

The functions `dBEINF`, `pBEINF`, `qBEINF` and `rBEINF` define the density, distribution function, quantile function and random generation for the `BEINF` parametrization of the beta inflated distribution.

The functions `dBEINF0`, `pBEINF0`, `qBEINF0` and `rBEINF0` define the density, distribution function, quantile function and random generation for the `BEINF0` parametrization of the beta inflated at zero distribution.

The functions `dBEINF1`, `pBEINF1`, `qBEINF1` and `rBEINF1` define the density, distribution function, quantile function and random generation for the `BEINF1` parametrization of the beta inflated at one distribution.

`plotBEINF`, `plotBEINF0` and `plotBEINF1` can be used to plot the distributions. `meanBEINF`, `meanBEINF0` and `meanBEINF1` calculates the expected value of the response for a fitted model.

Usage

```
BEINF(mu.link = "logit", sigma.link = "logit", nu.link = "log",
      tau.link = "log")
BEINF0(mu.link = "logit", sigma.link = "logit", nu.link = "log")
BEINF1(mu.link = "logit", sigma.link = "logit", nu.link = "log")

dBEINF(x, mu = 0.5, sigma = 0.1, nu = 0.1, tau = 0.1,
      log = FALSE)
dBEINF0(x, mu = 0.5, sigma = 0.1, nu = 0.1, log = FALSE)
dBEINF1(x, mu = 0.5, sigma = 0.1, nu = 0.1, log = FALSE)

pBEINF(q, mu = 0.5, sigma = 0.1, nu = 0.1, tau = 0.1,
      lower.tail = TRUE, log.p = FALSE)
pBEINF0(q, mu = 0.5, sigma = 0.1, nu = 0.1,
      lower.tail = TRUE, log.p = FALSE)
pBEINF1(q, mu = 0.5, sigma = 0.1, nu = 0.1,
      lower.tail = TRUE, log.p = FALSE)

qBEINF(p, mu = 0.5, sigma = 0.1, nu = 0.1, tau = 0.1,
      lower.tail = TRUE, log.p = FALSE)
qBEINF0(p, mu = 0.5, sigma = 0.1, nu = 0.1, tau = 0.1,
      lower.tail = TRUE, log.p = FALSE)
qBEINF1(p, mu = 0.5, sigma = 0.1, nu = 0.1,
      lower.tail = TRUE, log.p = FALSE)

rBEINF(n, mu = 0.5, sigma = 0.1, nu = 0.1, tau = 0.1)
rBEINF0(n, mu = 0.5, sigma = 0.1, nu = 0.1)
rBEINF1(n, mu = 0.5, sigma = 0.1, nu = 0.1)

plotBEINF(mu = 0.5, sigma = 0.5, nu = 0.5, tau = 0.5,
          from = 0.001, to = 0.999, n = 101, ...)
```

```

plotBEINF0(mu = 0.5, sigma = 0.5, nu = 0.5,
            from = 1e-04, to = 0.9999, n = 101, ...)
plotBEINF1(mu = 0.5, sigma = 0.5, nu = 0.5,
            from = 1e-04, to = 0.9999, n = 101, ...)

meanBEINF(obj)
meanBEINF0(obj)
meanBEINF1(obj)

```

Arguments

<code>mu.link</code>	the mu link function with default <code>logit</code>
<code>sigma.link</code>	the sigma link function with default <code>logit</code>
<code>nu.link</code>	the nu link function with default <code>log</code>
<code>tau.link</code>	the tau link function with default <code>log</code>
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of parameter values modelling the probability at zero
<code>tau</code>	vector of parameter values modelling the probability at one
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution
<code>obj</code>	a fitted BEINF object
<code>...</code>	other graphical parameters for plotting

Details

The beta inflated distribution is given as

$$f(y) = p_0$$

if (y=0)

$$f(y) = p_1$$

if (y=1)

$$f(y|\alpha, \beta) = \frac{1}{B(\alpha, \beta)} y^{\alpha-1} (1-y)^{\beta-1}$$

otherwise

for $y = (0, 1)$, $\alpha > 0$ and $\beta > 0$. The parametrization in the function `BEINF()` is $\mu = \frac{\alpha}{\alpha+\beta}$ and $\sigma = \frac{1}{\alpha+\beta+1}$ for $\mu = (0, 1)$ and $\sigma = (0, 1)$ and $\nu = \frac{p_0}{p_2}$, $\tau = \frac{p_1}{p_2}$ where $p_2 = 1 - p_0 - p_1$.

Value

returns a `gamlss.family` object which can be used to fit a beta inflated distribution in the `gamlss()` function. ...

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BE](#), [BEo](#), [BEZI](#), [BEOI](#)

Examples

```
BEINF()# gives information about the default links for the beta inflated distribution
BEINF0()
BEINF1()
# plotting the distributions
op<-par(mfrow=c(2,2))
plotBEINF( mu =.5 , sigma=.5, nu = 0.5, tau = 0.5, from = 0, to=1, n = 101)
plotBEINF0( mu =.5 , sigma=.5, nu = 0.5, from = 0, to=1, n = 101)
plotBEINF1( mu =.5 , sigma=.5, nu = 0.5, from = 0.001, to=1, n = 101)
curve(dBE(x, mu =.5, sigma=.5), 0.01, 0.999)
par(op)
# plotting the cdf
op<-par(mfrow=c(2,2))
plotBEINF( mu =.5 , sigma=.5, nu = 0.5, tau = 0.5, from = 0, to=1, n = 101, main="BEINF")
plotBEINF0( mu =.5 , sigma=.5, nu = 0.5, from = 0, to=1, n = 101, main="BEINF0")
plotBEINF1( mu =.5 , sigma=.5, nu = 0.5, from = 0.001, to=1, n = 101, main="BEINF1")
curve(dBE(x, mu =.5, sigma=.5), 0.01, 0.999, main="BE")
par(op)
#-----
op<-par(mfrow=c(2,2))
plotBEINF( mu =.5 , sigma=.5, nu = 0.5, tau = 0.5, from = 0, to=1, n = 101, main="BEINF")
```

```

plotBEINF0( mu =.5 , sigma=.5, nu = 0.5,  from = 0, to=1, n = 101, main="BEINF0")
plotBEINF1( mu =.5 , sigma=.5, nu = 0.5,  from = 0.001, to=1, n = 101, main="BEINF1")
curve(dBE(x, mu =.5, sigma=.5), 0.01, 0.999, main="BE")
par(op)
#-----
op<-par(mfrow=c(2,2))
curve( pBEINF(x, mu=.5 ,sigma=.5, nu = 0.5, tau = 0.5), 0, 1, ylim=c(0,1), main="BEINF" )
curve(pBEINF0(x, mu=.5 ,sigma=.5, nu = 0.5), 0, 1, ylim=c(0,1), main="BEINF0")
curve(pBEINF1(x, mu=.5 ,sigma=.5, nu = 0.5), 0, 1, ylim=c(0,1), main="BEINF1")
curve( pBE(x, mu=.5 ,sigma=.5), .001, .99, ylim=c(0,1), main="BE")
par(op)
#-----
op<-par(mfrow=c(2,2))
curve(qBEINF(x, mu=.5 ,sigma=.5, nu = 0.5, tau = 0.5), .01, .99, main="BEINF" )
curve(qBEINF0(x, mu=.5 ,sigma=.5, nu = 0.5), .01, .99, main="BEINF0" )
curve(qBEINF1(x, mu=.5 ,sigma=.5, nu = 0.5), .01, .99, main="BEINF1" )
curve(qBE(x, mu=.5 ,sigma=.5), .01, .99 , main="BE")
par(op)

#-----
op<-par(mfrow=c(2,2))
hist(rBEINF(200, mu=.5 ,sigma=.5, nu = 0.5, tau = 0.5))
hist(rBEINF0(200, mu=.5 ,sigma=.5, nu = 0.5))
hist(rBEINF1(200, mu=.5 ,sigma=.5, nu = 0.5))
hist(rBE(200, mu=.5 ,sigma=.5))
par(op)
# fit a model to the data
# library(gamlss)
#m1<-gamlss(dat~1,family=BEINF)
#meanBEINF(m1)[1]

```

BEOI

The one-inflated beta distribution for fitting a GAMLSS

Description

The function `BEOI()` defines the one-inflated beta distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The one-inflated beta is similar to the beta distribution but allows ones as y values. This distribution is an extension of the beta distribution using a parameterization of the beta law that is indexed by mean and precision parameters (Ferrari and Cribari-Neto, 2004). The extra parameter models the probability at one. The functions `dBEOI`, `pBEOI`, `qBEOI` and `rBEOI` define the density, distribution function, quantile function and random generation for the BEOI parameterization of the one-inflated beta distribution. `plotBEOI` can be used to plot the distribution. `meanBEOI` calculates the expected value of the response for a fitted model.

Usage

```
BEOI(mu.link = "logit", sigma.link = "log", nu.link = "logit")
```



```

dBEOI(x, mu = 0.5, sigma = 1, nu = 0.1, log = FALSE)

pBEOI(q, mu = 0.5, sigma = 1, nu = 0.1, lower.tail = TRUE, log.p = FALSE)

qBEOI(p, mu = 0.5, sigma = 1, nu = 0.1, lower.tail = TRUE,
      log.p = FALSE)

rBEOI(n, mu = 0.5, sigma = 1, nu = 0.1)

plotBEOI(mu = .5, sigma = 1, nu = 0.1, from = 0.001, to = 1, n = 101,
        ...)

meanBEOI(obj)

```

Arguments

<code>mu.link</code>	the mu link function with default <code>logit</code>
<code>sigma.link</code>	the sigma link function with default <code>log</code>
<code>nu.link</code>	the nu link function with default <code>logit</code>
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of precision parameter values
<code>nu</code>	vector of parameter values modelling the probability at one
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution
<code>obj</code>	a fitted BEOI object
<code>...</code>	other graphical parameters for plotting

Details

The one-inflated beta distribution is given as

$$f(y) = \nu$$

if $(y = 1)$

$$f(y|\mu, \sigma) = (1 - \nu) \frac{\Gamma(\sigma)}{\Gamma(\mu\sigma)\Gamma((1 - \mu)\sigma)} y^{\mu\sigma} (1 - y)^{((1 - \mu)\sigma) - 1}$$

if $y = (0, 1)$. The parameters satisfy $0 < \mu < 1$, $\sigma > 0$ and $0 < \nu < 1$.

Here $E(y) = \nu + (1 - \nu)\mu$ and $Var(y) = (1 - \nu)\frac{\mu(1 - \mu)}{\sigma + 1} + \nu(1 - \nu)(1 - \mu)^2$.

Value

returns a `gamlss.family` object which can be used to fit a one-inflated beta distribution in the `gamlss()` function.

Note

This work is part of my PhD project at the University of Sao Paulo under the supervision of Professor Silvia Ferrari. My thesis is concerned with regression modelling of rates and proportions with excess of zeros and/or ones

Author(s)

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References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BEOI](#)

Examples

```
BEOI())# gives information about the default links for the BEOI distribution
# plotting the distribution
plotBEOI( mu =0.5 , sigma=5, nu = 0.1, from = 0.001, to=1, n = 101)
# plotting the cdf
plot(function(y) pBEOI(y, mu=.5 ,sigma=5, nu=0.1), 0.001, 0.999)
# plotting the inverse cdf
plot(function(y) qBEOI(y, mu=.5 ,sigma=5, nu=0.1), 0.001, 0.999)
# generate random numbers
dat<-rBEOI(100, mu=.5, sigma=5, nu=0.1)
```

```
# fit a model to the data.
# library(gamlss)
#mod1<-gamlss(dat~1,sigma.formula=~1, nu.formula=~1, family=BEOI)
#fitted(mod1)[1]
#summary(mod1)
#fitted(mod1,"mu")[1]      #fitted mu
#fitted(mod1,"sigma")[1]   #fitted sigma
#fitted(mod1,"nu")[1]      #fitted nu
#meanBEOI(mod1)[1] # expected value of the response
```

BEZI

The zero-inflated beta distribution for fitting a GAMLSS

Description

The function `BEZI()` defines the zero-inflated beta distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The zero-inflated beta is similar to the beta distribution but allows zeros as y values. This distribution is an extension of the beta distribution using a parameterization of the beta law that is indexed by mean and precision parameters (Ferrari and Cribari-Neto, 2004). The extra parameter models the probability at zero. The functions `dBEZI`, `pBEZI`, `qBEZI` and `rBEZI` define the density, distribution function, quantile function and random generation for the BEZI parameterization of the zero-inflated beta distribution. `plotBEZI` can be used to plot the distribution. `meanBEZI` calculates the expected value of the response for a fitted model.

Usage

```
BEZI(mu.link = "logit", sigma.link = "log", nu.link = "logit")

dBEZI(x, mu = 0.5, sigma = 1, nu = 0.1, log = FALSE)

pBEZI(q, mu = 0.5, sigma = 1, nu = 0.1, lower.tail = TRUE, log.p = FALSE)

qBEZI(p, mu = 0.5, sigma = 1, nu = 0.1, lower.tail = TRUE,
      log.p = FALSE)

rBEZI(n, mu = 0.5, sigma = 1, nu = 0.1)

plotBEZI(mu = .5, sigma = 1, nu = 0.1, from = 0, to = 0.999, n = 101,
          ...)

meanBEZI(obj)
```

Arguments

<code>mu.link</code>	the mu link function with default <code>logit</code>
<code>sigma.link</code>	the sigma link function with default <code>log</code>

<code>nu.link</code>	the nu link function with default <code>logit</code>
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of precision parameter values
<code>nu</code>	vector of parameter values modelling the probability at zero
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution
<code>obj</code>	a fitted BEZI object
<code>...</code>	other graphical parameters for plotting

Details

The zero-inflated beta distribution is given as

$$f(y) = \nu$$

if $(y = 0)$

$$f(y|\mu, \sigma) = (1 - \nu) \frac{\Gamma(\sigma)}{\Gamma(\mu\sigma)\Gamma((1-\mu)\sigma)} y^{\mu\sigma} (1-y)^{((1-\mu)\sigma)-1}$$

if $y = (0, 1)$. The parameters satisfy $0 < \mu < 1, \sigma > 0$ and $0 < \nu < 1$.

Here $E(y) = (1 - \nu)\mu$ and $Var(y) = (1 - \nu) \frac{\mu(1-\mu)}{\sigma+1} + \nu(1 - \nu)\mu^2$.

Value

returns a `gamlss.family` object which can be used to fit a zero-inflated beta distribution in the `gamlss()` function.

Note

This work is part of my PhD project at the University of Sao Paulo under the supervision of Professor Silvia Ferrari. My thesis is concerned with regression modelling of rates and proportions with excess of zeros and/or ones

Author(s)

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BEZI](#)

Examples

```
BEZI()# gives information about the default links for the BEZI distribution
# plotting the distribution
plotBEZI( mu =0.5 , sigma=5, nu = 0.1, from = 0, to=0.99, n = 101)
# plotting the cdf
plot(function(y) pBEZI(y, mu=.5 ,sigma=5, nu=0.1), 0, 0.999)
# plotting the inverse cdf
plot(function(y) qBEZI(y, mu=.5 ,sigma=5, nu=0.1), 0, 0.999)
# generate random numbers
dat<-rBEZI(100, mu=.5, sigma=5, nu=0.1)
# fit a model to the data. Tits a constant for mu, sigma and nu
# library(gamlss)
#mod1<-gamlss(dat~1,sigma.formula=~1, nu.formula=~1, family=BEZI)
#fitted(mod1)[1]
#summary(mod1)
#fitted(mod1,"mu")[1]          #fitted mu
#fitted(mod1,"sigma")[1]      #fitted sigma
#fitted(mod1,"nu")[1]         #fitted nu
#meanBEZI(mod1)[1] # expected value of the response
```

Description

The `BI()` function defines the binomial distribution, a one parameter family distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dBI`, `pBI`, `qBI` and `rBI` define the density, distribution function, quantile function and random generation for the binomial, `BI()`, distribution.

Usage

```
BI(mu.link = "logit")
dBI(x, bd = 1, mu = 0.5, log = FALSE)
pBI(q, bd = 1, mu = 0.5, lower.tail = TRUE, log.p = FALSE)
qBI(p, bd = 1, mu = 0.5, lower.tail = TRUE, log.p = FALSE)
rBI(n, bd = 1, mu = 0.5)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive probabilities
<code>bd</code>	vector of binomial denominators
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Definition file for binomial distribution.

$$f(y|\mu) = \frac{\Gamma(n+1)}{\Gamma(y+1)\Gamma(n-y+1)} \mu^y (1-\mu)^{(n-y)}$$

for $y = 0, 1, 2, \dots, n$ and $0 < \mu < 1$.

Value

returns a `gamlss.family` object which can be used to fit a binomial distribution in the `gamlss()` function.

Note

The response variable should be a matrix containing two columns, the first with the count of successes and the second with the count of failures. The parameter μ represents a probability parameter with limits $0 < \mu < 1$. $n\mu$ is the mean of the distribution where n is the binomial denominator.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [ZABI](#), [ZIBI](#)

Examples

```
BI()# gives information about the default links for the Binomial distribution
# data(aep)
# library(gamlss)
# h<-gamlss(y~ward+loglos+year, family=BI, data=aep)
# plot of the binomial distribution
curve(dBI(x, mu = .5, bd=10), from=0, to=10, n=10+1, type="h")
tN <- table(Ni <- rBI(1000, mu=.2, bd=10))
r <- barplot(tN, col='lightblue')
```

Description

The `BNB()` function defines the beta negative binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`.

The functions `dbNB`, `pnNB`, `qnNB` and `rnNB` define the density, distribution function, quantile function and random generation for the beta negative binomial distribution, `BNB()`.

The functions `ZABNB()` and `ZIBNB()` are the zero adjusted (hurdle) and zero inflated versions of the beta negative binomial distribution, respectively. That is four parameter distributions.

The functions `dZABNB`, `dZIBNB`, `pZABNB`, `pZIBNB`, `qZABNB`, `qZIBNB`, `rZABNB` and `rZIBNB` define the probability, cumulative, quantile and random generation functions for the zero adjusted and zero inflated beta negative binomial distributions, `ZABNB()`, `ZIBNB()`, respectively.

Usage

```
BNB(mu.link = "log", sigma.link = "log", nu.link = "log")
dbNB(x, mu = 1, sigma = 1, nu = 1, log = FALSE)
pnNB(q, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qnNB(p, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE,
      max.value = 10000)
rnNB(n, mu = 1, sigma = 1, nu = 1, max.value = 10000)

ZABNB(mu.link = "log", sigma.link = "log", nu.link = "log",
       tau.link = "logit")
dZABNB(x, mu = 1, sigma = 1, nu = 1, tau = 0.1, log = FALSE)
pZABNB(q, mu = 1, sigma = 1, nu = 1, tau = 0.1, lower.tail = TRUE,
       log.p = FALSE)
qZABNB(p, mu = 1, sigma = 1, nu = 1, tau = 0.1, lower.tail = TRUE,
       log.p = FALSE, max.value = 10000)
rZABNB(n, mu = 1, sigma = 1, nu = 1, tau = 0.1, max.value = 10000)

ZIBNB(mu.link = "log", sigma.link = "log", nu.link = "log",
       tau.link = "logit")
dZIBNB(x, mu = 1, sigma = 1, nu = 1, tau = 0.1, log = FALSE)
pZIBNB(q, mu = 1, sigma = 1, nu = 1, tau = 0.1, lower.tail = TRUE,
       log.p = FALSE)
qZIBNB(p, mu = 1, sigma = 1, nu = 1, tau = 0.1, lower.tail = TRUE,
       log.p = FALSE, max.value = 10000)
rZIBNB(n, mu = 1, sigma = 1, nu = 1, tau = 0.1, max.value = 10000)
```

Arguments

<code>mu.link</code>	The link function for <code>mu</code>
<code>sigma.link</code>	The link function for <code>sigma</code>
<code>nu.link</code>	The link function for <code>nu</code>
<code>tau.link</code>	The link function for <code>tau</code>
<code>x</code>	vector of (non-negative integer)
<code>mu</code>	vector of positive means

<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of a positive parameter
<code>tau</code>	vector of probabilities
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>max.value</code>	a constant, set to the default value of 10000 for how far the algorithm should look for q

Details

The probability function of the BNB is

$$P(Y = y|\mu, \sigma, \nu) = \frac{\Gamma(y + \nu^{-1})}{\Gamma(y + 1)} \frac{B(y + \mu\sigma^{-1}\nu, \sigma^{-1} + \nu^{-1} + 1)}{\Gamma(\nu^{-1}) B(\mu\sigma^{-1}\nu, \sigma^{-1} + 1)}$$

for $y = 0, 1, 2, 3, \dots$, $\mu > 0$, $\sigma > 0$ and $\nu > 0$.

The distribution has mean μ .

Value

returns a `gamlss.family` object which can be used to fit a Poisson distribution in the `gamlss()` function.

Author(s)

Bob Rigby and Mikis Stasinopoulos <d.stasinopoulos@londonmrt.ac.uk>

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See Also[NBI, NBII](#)**Examples**

```
BNB() # gives information about the default links for the beta negative binomial
# plotting the distribution
plot(function(y) dBNB(y, mu = 10, sigma = 0.5, nu=2), from=0, to=40, n=40+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rBNB(1000, mu=5, sigma=0.5, nu=2))
r <- barplot(tN, col='lightblue')

ZABNB()
ZIBNB()
# plotting the distribution
plot(function(y) dZABNB(y, mu = 10, sigma = 0.5, nu=2, tau=.1),
      from=0, to=40, n=40+1, type="h")
plot(function(y) dZIBNB(y, mu = 10, sigma = 0.5, nu=2, tau=.1),
      from=0, to=40, n=40+1, type="h")
## Not run:
library(gamlss)
data(species)
species <- transform(species, x=log(lake))
m6 <- gamlss(fish~ pb(x), sigma.fo=~1, data=species, family=BNB)

## End(Not run)
```

checklink

*Set the Right Link Function for Specified Parameter and Distribution***Description**

This function is used within the distribution family specification of a GAMLSS model to define the right link for each of the parameters of the distribution. This function should not be called by the user unless he/she specify a new distribution family or wishes to change existing link functions in the parameters.

Usage

```
checklink(which.link = NULL, which.dist = NULL, link = NULL, link.List = NULL)
```

Arguments

which.link	which parameter link e.g. which.link="mu.link"
which.dist	which distribution family e.g. which.dist="Cole.Green"
link	a repetition of which.link e.g. link=substitute(mu.link)
link.List	what link function are required e.g. link.List=c("inverse", "log", "identity")

Value

Defines the right link for each parameter

Author(s)

Calliope Akantziliotou

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

count_1_31

A set of functions to plot gamlss.family distributions

Description

Those functions are used in the distribution book of gamlss, see Rigby et. al 2019.

Usage

```
binom_1_31(family = BI, mu = c(0.1, 0.5, 0.7), bd = NULL, miny = 0,
           maxy = 20, cex.axis = 1.2, cex.all = 1.5)
```

```
binom_2_33(family = BB, mu = c(0.1, 0.5, 0.8), sigma = c(0.5, 1, 2),
           bd = NULL, miny = 0, maxy = 10, cex.axis = 1.5,
           cex.all = 1.5)
```

```
binom_3_33(family = ZIBB, mu = c(0.1, 0.5, 0.8), sigma = c(0.5, 1, 2),
           nu = c(0.01, 0.3), bd = NULL, miny = 0, maxy = 10,
           cex.axis = 1.5, cex.all = 1.5, cols = c("darkgray", "black"),
           spacing = 0.3, legend.cex=1, legend.x="topright",
```

```

legend.where=c("left","right", "center"))

contr_2_12(family = "NO", mu = c(0, -1, 1), sigma = c(1, 0.5, 2),
  cols=c(gray(.1),gray(.2),gray(.3)),
  ltype = c(1, 2, 3), maxy = 7,
  no.points = 201, y.axis.lim = 1.1,
  cex.axis = 1.5, cex.all = 1.5,
  legend.cex=1, legend.x="topleft" )

contr_3_11(family = "PE", mu = 0, sigma = 1, nu = c(1, 2, 3),
  cols=c(gray(.1),gray(.2),gray(.3)), maxy = 7, no.points = 201,
  ltype = c(1, 2, 3), y.axis.lim = 1.1, cex.axis = 1.5,
  cex.all = 1.5, legend.cex=1, legend.x="topleft")

contr_4_13(family = "SEP3", mu = 0, sigma = 1, nu = c(0.5, 1, 2),
  tau = c(1, 2, 5), cols=c(gray(.1),gray(.2),gray(.3)), maxy = 7,
  no.points = 201, ltype = c(1, 2, 3),
  y.axis.lim = 1.1, cex.axis = 1.5, cex.all = 1.5,
  legend.cex=1, legend.x="topleft",
  legend.where=c("left","right"))

contrplus_2_11(family = GA, mu = 1, sigma = c(0.1, 0.6, 1),
  cols=c(gray(.1),gray(.2),gray(.3)),
  maxy = 4, no.points = 201,
  y.axis.lim = 1.1, ltype = c(1, 2, 3),
  cex.axis = 1.5, cex.all = 1.5,
  legend.cex=1, legend.x="topright")

contrplus_3_13(family = "BCCG", mu = 1, sigma = c(0.15, 0.2, 0.5),
  nu = c(-2, 0, 4),
  cols=c(gray(.1),gray(.2),gray(.3)),
  maxy = 4, ltype = c(1, 2, 3),
  no.points = 201, y.axis.lim = 1.1,
  cex.axis = 1.5, cex.all = 1.5,
  legend.cex=1, legend.x="topright",
  legend.where=c("left","right"))

contrplus_4_33(family = BCT, mu = 1, sigma = c(0.15, 0.2, 0.5),
  nu = c(-4, 0, 2), tau = c(100, 5, 1),
  cols=c(gray(.1),gray(.2),gray(.3)),
  maxy = 4, ltype = c(1, 2, 3),
  no.points = 201, y.axis.lim = 1.1,
  cex.axis = 1.5, cex.all = 1.5,
  legend.cex=1, legend.x="topright",
  legend.where=c("left","right"))

contr01_2_13(family = "BE", mu = c(0.2, 0.5, 0.8), sigma = c(0.2, 0.5, 0.8),
  cols=c(gray(.1),gray(.2),gray(.3)),

```

```

      ltype = c(1, 2, 3), maxy = 7, no.points = 201,
      y.axis.lim = 1.1, maxYlim = 10,
      cex.axis = 1.5, cex.all = 1.5,
      legend.cex=1, legend.x="topright",
      legend.where=c("left","right", "center"))

contr01_4_33(family = GB1, mu = c(0.5), sigma = c(0.2, 0.5, 0.7),
      nu = c(1, 2, 5), tau = c(0.5, 1, 2),
      cols=c(gray(.1),gray(.2),gray(.3)),
      maxy = 0.999, ltype = c(1, 2, 3),
      no.points = 201, y.axis.lim = 1.1,
      maxYlim = 10, cex.axis = 1.5, cex.all = 1.5,
      legend.cex=1, legend.x="topright",
      legend.where=c("left","right", "center"))

count_1_31(family = P0, mu = c(1, 2, 5), miny = 0, maxy = 10,
      cex.axis = 1.2, cex.all = 1.5)

count_1_22(family = P0, mu = c(1, 2, 5, 10), miny = 0,
      maxy = 20, cex.axis = 1.2, cex.all = 1.5)

count_2_32(family = NBI, mu = c(0.5, 1, 5), sigma = c(0.1, 2),
      miny = 0, maxy = 10, cex.axis = 1.5, cex.all = 1.5)

count_2_32R(family = NBI, mu = c(1, 2), sigma = c(0.1, 1, 2),
      miny = 0, maxy = 10, cex.axis = 1.5, cex.all = 1.5)

count_2_33(family = NBI, mu = c(0.1, 1, 2), sigma = c(0.5, 1, 2),
      miny = 0, maxy = 10, cex.axis = 1.5, cex.all = 1.5)

count_3_32(family = SICHEL, mu = c(1, 5, 10), sigma = c(0.5, 1),
      nu = c(-0.5, 0.5), miny = 0, maxy = 10, cex.axis = 1.5,
      cex.all = 1.5, cols = c("darkgray", "black"), spacing = 0.2,
      legend.cex=1, legend.x="topright",
      legend.where=c("left","right"))

count_3_33(family = SICHEL, mu = c(1, 5, 10), sigma = c(0.5, 1, 2),
      nu = c(-0.5, 0.5, 1), miny = 0, maxy = 10, cex.axis = 1.5,
      cex.all = 1.5, cols = c("darkgray", "black"), spacing = 0.3,
      legend.cex=1, legend.x="topright",
      legend.where=c("left","right", "center"))

```

Arguments

family	a gamlss family distribution
mu	the mu parameter values
sigma	The sigma parameter values

<code>nu</code>	the nu parameter values
<code>tau</code>	the tau parameter values
<code>bd</code>	the binomial denominator
<code>miny</code>	minimal value for the y axis
<code>maxy</code>	maximal value for the y axis
<code>cex.axis</code>	the size of the letters in the two axes
<code>cex.all</code>	the overall size of all plotting characters
<code>cols</code>	colours
<code>spacing</code>	spacing between plots
<code>ltype</code>	The type of lines used
<code>no.points</code>	the number of points in the curve
<code>y.axis.lim</code>	the maximum value for the y axis
<code>maxYlim</code>	the maximum permissible value for Y
<code>legend.cex</code>	the size of the legend
<code>legend.x</code>	where in the figure to put the legend
<code>legend.where</code>	where in the whole plot to put the legend

Details

The function plots different types of continuous and discrete distributions: i) `contR`: continuous distribution defined on minus infinity to plus infinity, ii) `contRplus`: continuous distribution defined from zero to plus infinity, iii) `contR01`: continuous distribution defined from zero to 1, iv) `bimom` binomial type discrete distributions, v) `count` count type discrete distributions.

The first number after the first underline in the name of the function indicates the number of parameters in the distribution. The two numbers after the second underline indicate how many rows and columns are in the plot.

Value

The result is a plot

Note

more notes

Author(s)

Mikis Stasinopoulos, Robert Rigby, Gillian Heller, Fernanda De Bastiani

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
count_1_31()
```

DBI

The Double binomial distribution

Description

The function `DBI()` defines the double binomial distribution, a two parameters distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dDBI`, `pDBI`, `qDBI` and `rDBI` define the density, distribution function, quantile function and random generation for the double binomial, `DBI()`, distribution. The function `GetBI_C` calculates numerically the constant of proportionality needed for the pdf to sum up to 1.

Usage

```
DBI(mu.link = "logit", sigma.link = "log")
dDBI(x, mu = 0.5, sigma = 1, bd = 2, log = FALSE)
pDBI(q, mu = 0.5, sigma = 1, bd = 2, lower.tail = TRUE,
     log.p = FALSE)
qDBI(p, mu = 0.5, sigma = 1, bd = 2, lower.tail = TRUE,
     log.p = FALSE)
rDBI(n, mu = 0.5, sigma = 1, bd = 2)
GetBI_C(mu, sigma, bd)
```

Arguments

<code>mu.link</code>	the link function for mu with default log
<code>sigma.link</code>	the link function for sigma with default log
<code>x, q</code>	vector of (non-negative integer) quantiles
<code>bd</code>	vector of binomial denominator
<code>p</code>	vector of probabilities
<code>mu</code>	the mu parameter
<code>sigma</code>	the sigma parameter
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p)
<code>n</code>	how many random values to generate

Details

The definition for the Double Poisson distribution first introduced by Efron (1986) is:

$$p_Y(y|n, \mu, \sigma) = \frac{\Gamma(n+1)}{\Gamma(y+1)\Gamma(n-y+1)} \frac{y^y (n-y)^{n-y}}{n^n} \frac{n^{n/\sigma} \mu^{y/\sigma} (1-\mu)^{(n-y)/\sigma}}{y^{y/\sigma} (n-y)^{(n-y)/\sigma}}$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$ and $\sigma > 0$ where C is the constant of proportionality which is calculated numerically using the function `GetBI_C()`.

Value

The function `DBI` returns a `gamlss.family` object which can be used to fit a double binomial distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby, Marco Enea and Fernanda de Bastiani

References

- Efron, B., 1986. Double exponential families and their use in generalized linear Regression. *Journal of the American Statistical Association* 81 (395), 709-721.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also[BI, BB](#)**Examples**

```

DBI()
x <- 0:20
# underdispersed DBI
plot(x, dDBI(x, mu=.5, sigma=.2, bd=20), type="h", col="green", lwd=2)
# binomial
lines(x+0.1, dDBI(x, mu=.5, sigma=1, bd=20), type="h", col="black", lwd=2)
# overdispersed DBI
lines(x+.2, dDBI(x, mu=.5, sigma=2, bd=20), type="h", col="red", lwd=2)

```

DBURR12

*The Discrete Burr type XII distribution for fitting a GAMLSS model***Description**

The DBURR12() function defines the discrete Burr type XII distribution, a three parameter discrete distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dDBURR12()`, `pDBURR12()`, `qDBURR12()` and `rDBURR12()` define the density, distribution function, quantile function and random generation for the discrete Burr type XII DBURR12(), distribution.

Usage

```

DBURR12(mu.link = "log", sigma.link = "log", nu.link = "log")
dDBURR12(x, mu = 5, sigma = 2, nu = 2, log = FALSE)
pDBURR12(q, mu = 5, sigma = 2, nu = 2, lower.tail = TRUE,
          log.p = FALSE)
qDBURR12(p, mu = 5, sigma = 2, nu = 2, lower.tail = TRUE,
          log.p = FALSE)
rDBURR12(n, mu = 5, sigma = 2, nu = 2)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>mu</code>	vector of positive <code>mu</code>
<code>sigma</code>	vector of positive dispersion parameter <code>sigma</code>

<code>nu</code>	vector of ν
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>n</code>	number of random values to return

Details

The probability function of the discrete Burr XII distribution is given by

$$f(y|\mu, \sigma, \nu) = (1 + (y/\mu)^\sigma)^\nu - (1 + ((y+1)/\mu)^\sigma)^\nu$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$, $\sigma > 0$ and $\nu > 0$.

Note that the above parametrization is different from Para and Jan (2016).

Value

The function `DBURR12()` Returns a `gamlss.family` object which can be used to fit a discrete Burr XII distribution in the `gamlss()` function.

Note

The parameters of the distributions are highly correlated so the argument of `gamlss method=mixed(10,100)` may have to be used.

The distribution can be under/over dispersed and also with long tails.

Author(s)

Rigby, R. A., Stasinopoulos D. M., Fernanda De Bastiani.

References

- Para, B. A. and Jan, T. R. (2016). On discrete three parameter Burr type XII and discrete Lomax distributions and their applications to model count data from medical science. *Biometrics and Biostatistics International Journal*, **54**, part 3, pp 507-554.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **4**, pp 1-15.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [DPO](#)

Examples

```
DBURR12()#
#plot the pdf using plot
plot(function(y) dDBURR12(y, mu=10, sigma=1, nu=1), from=0, to=100, n=100+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=100),pDBURR12(seq(from=0,to=100), mu=10, sigma=1, nu=1), type="h") # cdf
# generate random sample
tN <- table(Ni <- rDBURR12(100, mu=5, sigma=1, nu=1))
r <- barplot(tN, col='lightblue')
```

DEL

The Delaporte distribution for fitting a GAMLSS model

Description

The `DEL()` function defines the Delaporte distribution, a three parameter discrete distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dDEL`, `pDEL`, `qDEL` and `rDEL` define the density, distribution function, quantile function and random generation for the Delaporte `DEL()`, distribution.

Usage

```
DEL(mu.link = "log", sigma.link = "log", nu.link = "logit")
dDEL(x, mu=1, sigma=1, nu=0.5, log=FALSE)
pDEL(q, mu=1, sigma=1, nu=0.5, lower.tail = TRUE,
      log.p = FALSE)
qDEL(p, mu=1, sigma=1, nu=0.5, lower.tail = TRUE,
      log.p = FALSE, max.value = 10000)
rDEL(n, mu=1, sigma=1, nu=0.5, max.value = 10000)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the mu parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "logit" link as the default for the nu parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive mu
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of nu
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles

n	number of random values to return
log, log.p	logical; if TRUE, probabilities p are given as log(p)
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
max.value	a constant, set to the default value of 10000 for how far the algorithm should look for q

Details

The probability function of the Delaporte distribution is given by

$$f(y|\mu, \sigma, \nu) = \frac{e^{-\mu\nu}}{\Gamma(1/\sigma)} [1 + \mu\sigma(1 - \nu)]^{-1/\sigma} S$$

where

$$S = \sum_{j=0}^y \binom{y}{j} \frac{\mu^y \nu^{y-j}}{y!} \left[\mu + \frac{1}{\sigma(1 - \nu)} \right]^{-j} \Gamma\left(\frac{1}{\sigma} + j\right)$$

for $y = 0, 1, 2, \dots, \infty$ where $\mu > 0$, $\sigma > 0$ and $0 < \nu < 1$. This distribution is a parametrization of the distribution given by Wimmer and Altmann (1999) p 515-516 where $\alpha = \mu\nu$, $k = 1/\sigma$ and $\rho = [1 + \mu\sigma(1 - \nu)]^{-1}$

Value

Returns a `gamlss.family` object which can be used to fit a Delaporte distribution in the `gamlss()` function.

Note

The mean of Y is given by $E(Y) = \mu$ and the variance by $V(Y) = \mu + \mu^2\sigma(1 - \nu)^2$.

Author(s)

Rigby, R. A., Stasinopoulos D. M. and Marco Enea

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC,doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
- Wimmer, G. and Altmann, G (1999). *Thesaurus of univariate discrete probability distributions* . Stann Verlag, Essen, Germany
- (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [SI](#), [SICHEL](#)

Examples

```
DEL()# gives information about the default links for the Delaporte distribution
#plot the pdf using plot
plot(function(y) dDEL(y, mu=10, sigma=1, nu=.5), from=0, to=100, n=100+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=100),pDEL(seq(from=0,to=100), mu=10, sigma=1, nu=0.5), type="h") # cdf
# generate random sample
tN <- table(Ni <- rDEL(100, mu=10, sigma=1, nu=0.5))
r <- barplot(tN, col='lightblue')
# fit a model to the data
# library(gamlss)
# gamlss(Ni~1,family=DEL, control=gamlss.control(n.cyc=50))
```

DPO

The Double Poisson distribution

Description

The function `DPO()` defines the double Poisson distribution, a two parameters distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dDPO`, `pDPO`, `qDPO` and `rDPO` define the density, distribution function, quantile function and random generation for the double Poisson, `DPO()`, distribution. The function `get_C()` calculates numerically the constant of proportionality needed for the pdf to sum up to 1.

Usage

```
DPO(mu.link = "log", sigma.link = "log")
dDPO(x, mu = 1, sigma = 1, log = FALSE)
pDPO(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qDPO(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
rDPO(n, mu = 1, sigma = 1, max.value = 10000)
get_C(x, mu, sigma)
```

Arguments

<code>mu.link</code>	the link function for mu with default log
<code>sigma.link</code>	the link function for sigma with default log
<code>x, q</code>	vector of (non-negative integer) quantiles
<code>p</code>	vector of probabilities
<code>mu</code>	the mu parameter
<code>sigma</code>	the sigma parameter

<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$
<code>max.value</code>	a constant, set to the default value of 10000 for how far the algorithm should look for q
<code>n</code>	how many random values to generate

Details

The definition for the Double Poisson distribution first introduced by Efron (1986) is:

$$f(y|\mu, \sigma) = \left(\frac{1}{\sigma}\right)^{1/2} e^{-\mu/\sigma} \left(\frac{e^{-y} y^y}{y!}\right) \left(\frac{e\mu}{y}\right)^{y/\sigma} C$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$ and $\sigma > 0$ where C is the constant of proportionality which is calculated numerically using the function `get_C`.

Value

The function `DPO` returns a `gamlss.family` object which can be used to fit a double Poisson distribution in the `gamlss()` function.

Note

The distributons calculates the constant of proportionality numerically therefore it can be slow for large data

Author(s)

Mikis Stasinopoulos, Bob Rigby and Marco Enea

References

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- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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(see also <https://www.gamlss.com/>).

See Also[P0](#)**Examples**

```

DPO()
# overdispersed DPO
x <- 0:20
plot(x, dDPO(x, mu=5, sigma=3), type="h", col="red")
# underdispersed DPO
plot(x, dDPO(x, mu=5, sigma=.3), type="h", col="red")
# generate random sample
Y <- rDPO(100,5,.5)
plot(table(Y))
points(0:20, 100*dDPO(0:20, mu=5, sigma=.5)+0.2, col="red")
# fit a model to the data
# library(gamlss)
# gamlss(Y~1,family=DPO)

```

EGB2

The exponential generalized Beta type 2 distribution for fitting a GAMLSS

Description

This function defines the generalized t distribution, a four parameter distribution. The response variable is in the range from minus infinity to plus infinity. The functions dEGB2, pEGB2, qEGB2 and rEGB2 define the density, distribution function, quantile function and random generation for the generalized beta type 2 distribution.

Usage

```

EGB2(mu.link = "identity", sigma.link = "log", nu.link = "log",
      tau.link = "log")
dEGB2(x, mu = 0, sigma = 1, nu = 1, tau = 0.5, log = FALSE)
pEGB2(q, mu = 0, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE,
      log.p = FALSE)
qEGB2(p, mu = 0, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE,
      log.p = FALSE)
rEGB2(n, mu = 0, sigma = 1, nu = 1, tau = 0.5)

```

Arguments

mu.link	Defines the mu.link, with "identity" link as the default for the mu parameter.
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter.
nu.link	Defines the nu.link, with "log" link as the default for the nu parameter.
tau.link	Defines the tau.link, with "log" link as the default for the tau parameter.

x, q	vector of quantiles
mu	vector of location parameter values
sigma	vector of scale parameter values
nu	vector of skewness nu parameter values
tau	vector of kurtosis tau parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required

Details

The probability density function of the Generalized Beta type 2, (GB2), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = e^{\nu z} \{ |\sigma| B(\nu, \tau) [1 + e^z]^{\nu+\tau} \}^{-1}$$

for $-\infty < y < \infty$, where $z = (y - \mu)/\sigma$ and $-\infty < \mu < \infty$, $-\infty < \sigma < \infty$, $\nu > 0$ and $\tau > 0$, McDonald and Xu (1995).

Value

EGB2() returns a `gamlss.family` object which can be used to fit the EGB2 distribution in the `gamlss()` function. `dEGB2()` gives the density, `pEGB2()` gives the distribution function, `qEGB2()` gives the quantile function, and `rEGB2()` generates random deviates.

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
EGB2() #
y<- rEGB2(200, mu=5, sigma=2, nu=1, tau=4)
library(MASS)
truehist(y)
fx<-dEGB2(seq(min(y), 20, length=200), mu=5 ,sigma=2, nu=1, tau=4)
lines(seq(min(y),20,length=200),fx)
# something funny here
# library(gamlss)
# histDist(y, family=EGB2, n.cyc=60)
integrate(function(x) x*dEGB2(x=x, mu=5, sigma=2, nu=1, tau=4), -Inf, Inf)
curve(dEGB2(x, mu=5 ,sigma=2, nu=1, tau=4), -10, 10, main = "The EGB2 density
      mu=5, sigma=2, nu=1, tau=4")
```

exGAUS

The ex-Gaussian distribution

Description

The ex-Gaussian distribution is often used by psychologists to model response time (RT). It is defined by adding two random variables, one from a normal distribution and the other from an exponential. The parameters `mu` and `sigma` are the mean and standard deviation from the normal distribution variable while the parameter `nu` is the mean of the exponential variable. The functions `dexGAUS`, `pexGAUS`, `qexGAUS` and `rexGAUS` define the density, distribution function, quantile function and random generation for the ex-Gaussian distribution.

Usage

```
exGAUS(mu.link = "identity", sigma.link = "log", nu.link = "log")
dexGAUS(x, mu = 5, sigma = 1, nu = 1, log = FALSE)
pexGAUS(q, mu = 5, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qexGAUS(p, mu = 5, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
rexGAUS(n, mu = 5, sigma = 1, nu = 1, ...)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter. Other links are "inverse", "identity", "logshifted" (shifted from one) and "own"
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of <code>mu</code> parameter values

<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of nu parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>...</code>	for extra arguments

Details

The probability density function of the ex-Gaussian distribution, (exGAUS), is defined as

$$f(y|\mu, \sigma, \nu) = \frac{1}{\nu} e^{\frac{\mu-y}{\nu} + \frac{\sigma^2}{2\nu^2}} \Phi\left(\frac{y-\mu}{\sigma} - \frac{\sigma}{\nu}\right)$$

where Φ is the cdf of the standard normal distribution, for $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$ and $\nu > 0$.

Value

`exGAUS()` returns a `gamlss.family` object which can be used to fit ex-Gaussian distribution in the `gamlss()` function. `dexGAUS()` gives the density, `pexGAUS()` gives the distribution function, `qexGAUS()` gives the quantile function, and `rexGAUS()` generates random deviates.

Note

The mean of the ex-Gaussian is $\mu + \nu$ and the variance is $\sigma^2 + \nu^2$.

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

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See Also

[gamlss.family](#), [BCCG](#), [GA](#), [IG LNO](#)

Examples

```
exGAUS() #
y<- rexGAUS(100, mu=300, nu=100, sigma=35)
hist(y)
# library(gamlss)
# m1<-gamlss(y~1, family=exGAUS)
# plot(m1)
curve(dexGAUS(x, mu=300 ,sigma=35,nu=100), 100, 600,
      main = "The ex-GAUS density mu=300 ,sigma=35,nu=100")
plot(function(x) pexGAUS(x, mu=300,sigma=35,nu=100), 100, 600,
      main = "The ex-GAUS cdf mu=300, sigma=35, nu=100")
```

EXP

*Exponential distribution for fitting a GAMLSS***Description**

The function EXP defines the exponential distribution, a one parameter distribution for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The `mu` parameter represents the mean of the distribution. The functions `dEXP`, `pEXP`, `qEXP` and `rEXP` define the density, distribution function, quantile function and random generation for the specific parameterization of the exponential distribution defined by function EXP.

Usage

```
EXP(mu.link = "log")
dEXP(x, mu = 1, log = FALSE)
pEXP(q, mu = 1, lower.tail = TRUE, log.p = FALSE)
qEXP(p, mu = 1, lower.tail = TRUE, log.p = FALSE)
rEXP(n, mu = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter, other links are "inverse" and "identity"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The specific parameterization of the exponential distribution used in EXP is

$$f(y|\mu) = \frac{1}{\mu} \exp \left\{ -\frac{y}{\mu} \right\}$$

, for $y > 0$, $\mu > 0$.

Value

EXP() returns a `gamlss.family` object which can be used to fit an exponential distribution in the `gamlss()` function. `dEXP()` gives the density, `pEXP()` gives the distribution function, `qEXP()` gives the quantile function, and `rEXP()` generates random deviates.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Nicoleta Motpan

References

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
y<-rEXP(1000,mu=1) # generates 1000 random observations
hist(y)
# library(gamlss)
# histDist(y, family=EXP)
```

flexDist

*Non-parametric pdf from limited information data***Description**

This is an attempt to create a distribution function if the only existing information is the quantiles or expectiles of the distribution.

Usage

```
flexDist(quantiles = list(values=c(-1.96,0,1.96), prob=c(0.05, .50, 0.95)),
        expectiles = list(), lambda = 10,
        kappa = 10, delta = 1e-07, order = 3, n.iter = 200,
        plot = TRUE, no.inter = 100, lower = NULL,
        upper = NULL, perc.quant = 0.3, ...)
```

Arguments

quantiles	a list with components values and prob
expectiles	a list with components values and prob
lambda	smoothing parameter for the log-pdf
kappa	smoothing parameter for log concavity
delta	smoothing parameter for ridge penalty
order	the order of the penalty for log-pdf
n.iter	maximum number of iterations
plot	whether to plot the result
no.inter	How many discrete probabilities to evaluate
lower	the lower value of the x
upper	the upper value of the x
perc.quant	how far from the quantile should go out to define the limit of x if not set by lower or upper
...	additional arguments

Value

Returns a list with components

pdf	the heights of the fitted pdf, the sum of it multiplied by the Dx should add up to 1 i.e. <code>sum(object\$pdf*diff(object\$x)[1])</code>
cdf	the fitted cdf
x	the values of x where the discretise distribution is defined
pFun	the cdf of the fitted non-parametric distribution
qFun	the inverse cdf function of the fitted non-parametric distribution
rFun	a function to generate a random sample from the fitted non-parametric distribution

Author(s)

Mikis Stasinopoulos, Paul Eilers, Bob Rigby and Vlasios Voudouris

References

Eilers, P. H. C., Voudouris, V., Rigby R. A., Stasinopoulos D. M. (2012) Estimation of nonparametric density from sparse summary information, under review.

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See Also

[histSmo](#)

Examples

```
# Normal
r1<-flexDist(quantiles=list(values=qN0(c(0.05, 0.25, 0.5,0.75, 0.95), mu=0,
      sigma=1), prob=c( 0.05, 0.25, 0.5,0.75,0.95 )),
      no.inter=200, lambda=10, kappa=10, perc.quant=0.3)

# GAMMA
r1<-flexDist(quantiles=list(values=qGA(c(0.05,0.25, 0.5,0.75,0.95), mu=1,
      sigma=.8), prob=c(0.05,0.25, 0.5,0.75,0.95)),
      expectiles=list(values=1, prob=0.5), lambda=10,
      kappa=10, lower=0, upper=5)#
```

GA

Gamma distribution for fitting a GAMLSS

Description

The function GA defines the gamma distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The parameterization used has the mean of the distribution equal to μ and the variance equal to $\sigma^2\mu^2$. The functions `dGA`, `pGA`, `qGA` and `rGA` define the density, distribution function, quantile function and random generation for the specific parameterization of the gamma distribution defined by function GA.

Usage

```
GA(mu.link = "log", sigma.link = "log")
dGA(x, mu = 1, sigma = 1, log = FALSE)
pGA(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qGA(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rGA(n, mu = 1, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter, other links are "inverse", "identity" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other link is the "inverse", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The specific parameterization of the gamma distribution used in GA is

$$f(y|\mu, \sigma) = \frac{y^{(1/\sigma^2)-1} \exp[-y/(\sigma^2\mu)]}{(\sigma^2\mu)^{(1/\sigma^2)} \Gamma(1/\sigma^2)}$$

for $y > 0$, $\mu > 0$ and $\sigma > 0$.

Value

`GA()` returns a `gamlss.family` object which can be used to fit a gamma distribution in the `gamlss()` function. `dGA()` gives the density, `pGA()` gives the distribution function, `qGA()` gives the quantile function, and `rGA()` generates random deviates. The latest functions are based on the equivalent R functions for gamma distribution.

Note

μ is the mean of the distribution in GA. In the function GA, σ is the square root of the usual dispersion parameter for a GLM gamma model. Hence $\sigma\mu$ is the standard deviation of the distribution defined in GA.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
GA()# gives information about the default links for the gamma distribution
# dat<-rgamma(100, shape=1, scale=10) # generates 100 random observations
# fit a gamlss model
# gamlss(dat~1,family=GA)
# fits a constant for each parameter mu and sigma of the gamma distribution
newdata<-rGA(1000,mu=1,sigma=1) # generates 1000 random observations
hist(newdata)
rm(dat,newdata)
```

GAF

The Gamma distribution family

Description

The function `GAF()` defines a gamma distribution family, which has three parameters. This is not the generalised gamma distribution which is called GG. The third parameter here is to model the mean and variance relationship. The distribution can be fitted using the function `gamlss()`. The mean of GAF is equal to μ . The variance is equal to $\sigma^2 \mu^\nu$ so the standard deviation is $\sigma \mu^{\nu/2}$. The function is design for cases where the variance is proportional to a power of the mean. This is an instance of the Taylor's power law, see Enki et al. (2017). The functions `dGAF`, `pGAF`, `qGAF` and `rGAF` define the density, distribution function, quantile function and random generation for the GAF parametrization of the gamma family.

Usage

```
GAF(mu.link = "log", sigma.link = "log", nu.link = "identity")
dGAF(x, mu = 1, sigma = 1, nu = 2, log = FALSE)
pGAF(q, mu = 1, sigma = 1, nu = 2, lower.tail = TRUE,
     log.p = FALSE)
qGAF(p, mu = 1, sigma = 1, nu = 2, lower.tail = TRUE,
     log.p = FALSE)
rGAF(n, mu = 1, sigma = 1, nu = 2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> with "identity" link as the default for the <code>nu</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of power parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parametrization of the gamma family given in the function `GAF()` is:

$$f(y|\mu, \sigma_1) = \frac{y^{(1/\sigma_1^2 - 1)} \exp[-y/(\sigma_1^2 \mu)]}{(\sigma_1^2 \mu)^{(1/\sigma_1^2)} \Gamma(1/\sigma_1^2)}$$

for $y > 0$, $\mu > 0$ where $\sigma_1 = \sigma \mu^{(\nu/1 - 1)}$.

Value

`GAF()` returns a `gamlss.family` object which can be used to fit the gamma family in the `gamlss()` function.

Note

For the function `GAF()`, μ is the mean and $\sigma \mu^{\nu/2}$ is the standard deviation of the gamma family. The GAF is design for fitting regression type models where the variance is proportional to a power of the mean.

Note that because the high correlation between the `sigma` and the `nu` parameter the `mixed()` method should be used in the fitting.

Author(s)

Mikis Stasinopoulos, Robert Rigby and Fernanda De Bastiani

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [GA](#), [GG](#)

Examples

```
GAF()
## Not run:
m1<-gamlss(y~poly(x,2),data=abdom,family=GAF, method=mixed(1,100),
           c.crit=0.00001)
# using RS()
m2<-gamlss(y~poly(x,2),data=abdom,family=GAF, n.cyc=5000, c.crit=0.00001)
# the estimates of nu slightly different
fitted(m1, "nu")[1]
fitted(m2, "nu")[1]
# global deviance almost identical
AIC(m1, m2)

## End(Not run)
```

gamlss.family

Family Objects for fitting a GAMLSS model

Description

GAMLSS families are the current available distributions that can be fitted using the `gamlss()` function.

Usage

```
gamlss.family(object,...)
as.gamlss.family(object)
as.family(object)
## S3 method for class 'gamlss.family'
print(x,...)
```

Arguments

```
object      a gamlss family object e.g. BCT
x           a gamlss family object e.g. BCT
...         further arguments passed to or from other methods.
```

Details

There are several distributions available for the response variable in the `gamlss` function. The following table display their names and their abbreviations in R. Note that the different distributions can be fitted using their R abbreviations (and optionally excluding the brackets) i.e. `family=BI()`, `family=BI` are equivalent.

Distributions	R names	No of parameters
Beta	<code>BE()</code>	2
Beta Binomial	<code>BB()</code>	2
Beta negative binomial	<code>BNB()</code>	3
Beta one inflated	<code>BEOI()</code>	3
Beta zero inflated	<code>BEZI()</code>	3
Beta inflated	<code>BEINF()</code>	4
Binomial	<code>BI()</code>	1
Box-Cox Cole and Green	<code>BCCG()</code>	3
Box-Cox Power Exponential	<code>BCPE()</code>	4
Box-Cox-t	<code>BCT()</code>	4
Delaport	<code>DEL()</code>	3
Discrete Burr XII	<code>DBURR12()</code>	3
Double Poisson	<code>DPO()</code>	2
Double binomial	<code>DBI()</code>	2
Exponential	<code>EXP()</code>	1
Exponential Gaussian	<code>exGAUS()</code>	3
Exponential generalized Beta type 2	<code>EGB2()</code>	4
Gamma	<code>GA()</code>	2
Generalized Beta type 1	<code>GB1()</code>	4
Generalized Beta type 2	<code>GB2()</code>	4
Generalized Gamma	<code>GG()</code>	3
Generalized Inverse Gaussian	<code>GIG()</code>	3
Generalized t	<code>GT()</code>	4
Geometric	<code>GEOM()</code>	1
Geometric (original)	<code>GEOMo()</code>	1
Gumbel	<code>GU()</code>	2
Inverse Gamma	<code>IGAMMA()</code>	2

Inverse Gaussian	IG()	2
Johnson's SU	JSU()	4
Logarithmic	LG()	1
Logistic	LO()	2
Logit-Normal	LOGITNO()	2
log-Normal	LOGNO()	2
log-Normal (Box-Cox)	LNO()	3 (1 fixed)
Negative Binomial type I	NBI()	2
Negative Binomial type II	NBII()	2
Negative Binomial family	NBF()	3
Normal Exponential t	NET()	4 (2 fixed)
Normal	NO()	2
Normal Family	NOF()	3 (1 fixed)
Normal Linear Quadratic	LQNO()	2
Pareto type 2	PARETO2()	2
Pareto type 2 original	PARETO2o()	2
Power Exponential	PE()	3
Power Exponential type 2	PE2()	3
Poisson	PO()	1
Poisson inverse Gaussian	PIG()	2
Reverse generalized extreme	RGE()	3
Reverse Gumbel	RG()	2
Skew Power Exponential type 1	SEP1()	4
Skew Power Exponential type 2	SEP2()	4
Skew Power Exponential type 3	SEP3()	4
Skew Power Exponential type 4	SEP4()	4
Shash	SHASH()	4
Shash original	SHASHo()	4
Shash original 2	SHASH()	4
Sichel (original)	SI()	3
Sichel (mu as the mean)	SICHEL()	3
Simplex	SIMPLEX()	2
Skew t type 1	ST1()	3
Skew t type 2	ST2()	3
Skew t type 3	ST3()	3
Skew t type 4	ST4()	3
Skew t type 5	ST5()	3
t-distribution	TF()	3
Waring	WARING()	1
Weibull	WEI()	2
Weibull(PH parameterization)	WEI2()	2
Weibull (mu as mean)	WEI3()	2
Yule	YULE()	1
Zero adjusted binomial	ZABI()	2
Zero adjusted beta neg. bin.	ZABNB()	4
Zero adjusted IG	ZAIG()	2
Zero adjusted logarithmic	ZALG()	2
Zero adjusted neg. bin.	ZANBI()	3

Zero adjusted poisson	ZAP()	2
Zero adjusted Sichel	ZASICHEL()	4
Zero adjusted Zipf	ZAZIPF()	2
Zero inflated binomial	ZIBI()	2
Zero inflated beta neg. bin.	ZIBNB()	4
Zero inflated neg. bin.	ZINBI()	3
Zero inflated poisson	ZIP()	2
Zero inf. poiss.(mu as mean)	ZIP2()	2
Zero inflated PIG	ZIPIG()	3
Zero inflated Sichel	ZISICHEL()	4
Zipf	ZIPF()	1

Note that some of the distributions are in the package `gamlss.dist`. The parameters of the distributions are in order, `mu` for location, `sigma` for scale (or dispersion), and `nu` and `tau` for shape. More specifically for the BCCG family `mu` is the median, `sigma` approximately the coefficient of variation, and `nu` the skewness parameter. The parameters for BCPE distribution have the same interpretation with the extra fourth parameter `tau` modelling the kurtosis of the distribution. The parameters for BCT have the same interpretation except that $\sigma[(\tau/(\tau - 2))^{0.5}]$ is approximately the coefficient of variation.

All of the distribution in the above list are also provided with the corresponding `d`, `p`, `q` and `r` functions for density (pdf), distribution function (cdf), quantile function and random generation function respectively, (see individual distribution for details).

Value

The above GAMLSS families return an object which is of type `gamlss.family`. This object is used to define the family in the `gamlss()` fit.

Note

More distributions will be documented in later GAMLSS releases. Further user defined distributions can be incorporate relatively easy, see, for example, the help documentation accompanying the `gamlss` library.

Author(s)

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(see also <https://www.gamlss.com/>).

See Also

[BE](#), [BB](#), [BEINF](#), [BI](#), [LNO](#), [BCT](#), [BCPE](#), [BCCG](#), [GA](#), [GU](#), [JSU](#), [IG](#), [LO](#), [NBI](#), [NBII](#), [NO](#), [PE](#), [PO](#), [RG](#), [PIG](#), [TF](#), [WEI](#), [WEI2](#), [ZIP](#)

Examples

```
normal<-N0(mu.link="log", sigma.link="log")
normal
```

GB1

The generalized Beta type 1 distribution for fitting a GAMLSS

Description

This function defines the generalized beta type 1 distribution, a four parameter distribution. The function GB1 creates a `gamlss.family` object which can be used to fit the distribution using the function `gamlss()`. Note the range of the response variable is from zero to one. The functions `dGB1`, `GB1`, `qGB1` and `rGB1` define the density, distribution function, quantile function and random generation for the generalized beta type 1 distribution.

Usage

```
GB1(mu.link = "logit", sigma.link = "logit", nu.link = "log",
    tau.link = "log")
dGB1(x, mu = 0.5, sigma = 0.4, nu = 1, tau = 1, log = FALSE)
pGB1(q, mu = 0.5, sigma = 0.4, nu = 1, tau = 1, lower.tail = TRUE,
    log.p = FALSE)
qGB1(p, mu = 0.5, sigma = 0.4, nu = 1, tau = 1, lower.tail = TRUE,
    log.p = FALSE)
rGB1(n, mu = 0.5, sigma = 0.4, nu = 1, tau = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter.
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter.
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values

<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness nu parameter values
<code>tau</code>	vector of kurtosis tau parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the Generalized Beta type 1, (GB1), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = \frac{\tau \nu^\beta y^{\tau\alpha-1} (1-y^\tau)^{\beta-1}}{B(\alpha, \beta) [\nu + (1-\nu)y^\tau]^{\alpha+\beta}}$$

where $0 < y < 1$, $\alpha = \mu(1 - \sigma^2)/\sigma^2$ and $\beta = (1 - \mu)(1 - \sigma^2)/\sigma^2$, and $\alpha > 0$, $\beta > 0$. Note the $\mu = \alpha/(\alpha + \beta)$, $\sigma = (\alpha + \beta + 1)^{-1/2}$.

Value

`GB1()` returns a `gamlss.family` object which can be used to fit the GB1 distribution in the `gamlss()` function. `dGB1()` gives the density, `pGB1()` gives the distribution function, `qGB1()` gives the quantile function, and `rGB1()` generates random deviates.

Warning

The `qSHASH` and `rSHASH` are slow since they are relying on golden section for finding the quantiles

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
GB1() #
y<- rGB1(200, mu=.1, sigma=.6, nu=1, tau=4)
hist(y)
# library(gamlss)
# histDist(y, family=GB1, n.cyc=60)
curve(dGB1(x, mu=.1, sigma=.6, nu=1, tau=4), 0.01, 0.99, main = "The GB1
      density mu=0.1, sigma=.6, nu=1, tau=4")
```

GB2

The generalized Beta type 2 and generalized Pareto distributions for fitting a GAMLSS

Description

This function defines the generalized beta type 2 distribution, a four parameter distribution. The function GB2 creates a `gamlss.family` object which can be used to fit the distribution using the function `gamlss()`. The response variable is in the range from zero to infinity. The functions `dGB2`, `GB2`, `qGB2` and `rGB2` define the density, distribution function, quantile function and random generation for the generalized beta type 2 distribution. The generalised Pareto GP distribution is defined by setting the parameters `sigma` and `nu` of the GB2 distribution to 1.

Usage

```
GB2(mu.link = "log", sigma.link = "log", nu.link = "log",
    tau.link = "log")
dGB2(x, mu = 1, sigma = 1, nu = 1, tau = 0.5, log = FALSE)
pGB2(q, mu = 1, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE,
    log.p = FALSE)
qGB2(p, mu = 1, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE,
    log.p = FALSE)
rGB2(n, mu = 1, sigma = 1, nu = 1, tau = 0.5)

GP(mu.link = "log", sigma.link = "log")
dGP(x, mu = 1, sigma = 1, log = FALSE)
pGP(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qGP(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rGP(n, mu = 1, sigma = 1)
```


Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter.
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter.
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <code>nu</code> parameter values
<code>tau</code>	vector of kurtosis <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the Generalized Beta type 2, (GB2), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = |\sigma| y^{\sigma\nu-1} \{ \mu^{\sigma\nu} B(\nu, \tau) [1 + (y/\mu)^\sigma]^{\nu+\tau} \}^{-1}$$

where $y > 0$, $\mu > 0$, $-\infty < \sigma < \infty$, $\nu > 0$ and $\tau > 0$.

Value

`GB2()` returns a `gamlss.family` object which can be used to fit the GB2 distribution in the `gamlss()` function. `dGB2()` gives the density, `pGB2()` gives the distribution function, `qGB2()` gives the quantile function, and `rGB2()` generates random deviates.

Warning

The `qSHASH` and `rSHASH` are slow since they are relying on golden section for finding the quantiles

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
GB2() #
y<- rGB2(200, mu=5, sigma=2, nu=1, tau=1)
library(MASS)
truehist(y)
fx<-dGB2(seq(0.01, 20, length=200), mu=5 ,sigma=2, nu=1, tau=1)
lines(seq(0.01,20,length=200),fx)
integrate(function(x) x*dGB2(x=x, mu=5, sigma=2, nu=1, tau=1), 0, Inf)
mean(y)
curve(dGB2(x, mu=5 ,sigma=2, nu=1, tau=1), 0.01, 20,
      main = "The GB2 density mu=5, sigma=2, nu=1, tau=4")
```

gen.Family

Functions to generate log and logit distributions from existing continuous gamlss.family distributions

Description

There are five functions here. Only the functions Family and gen.Family should be used (see details).

Usage

```
Family.d(family = "NO", type = c("log", "logit"), ...)
Family.p(family = "NO", type = c("log", "logit"), ...)
Family.q(family = "NO", type = c("log", "logit"), ...)
Family.r(family = "NO", type = c("log", "logit"), ...)
Family(family = "NO", type = c("log", "logit"), local = TRUE, ...)
gen.Family(family = "NO", type = c("log", "logit"), ...)
```

Arguments

family	a continuous gamlss.family distribution
type	the type of transformation only "log" and "logit" are allowed
local	It is TRUE if is called within gamlss() otherwise is FALSE
...	for passing extra arguments

Details

The function gen.Family creates the standard d,p,q,r functions for the distribution plus the fitting gamlss.family. For example gen.Family("NO","logit") will generate the functions dlogitNO(), plogitNO(), qlogitNO(), rlogitNO() and dlogitNO(). The latest function can be used in family argument of gamlss() to fit a logic-Normal distribution i.e. family=logitNO. The same fitting can be achieved by using family=Family("NO","logit"). Here the required dlogitNO(), plogitNO() and logitNO() functions are generated locally within the gamlss() environment.

Value

The function gen.Family returns the d, p, q r functions plus the fitting function.

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

Examples

```
# generating a log t distribution
gen.Family("TF")
# plotting the d, p, q, and r functions
op<-par(mfrow=c(2,2))
curve(dlogTF(x, mu=0), 0, 10)
curve(plogTF(x, mu=0), 0, 10)
curve(qlogTF(x, mu=0), 0, 1)
```

```

Y<- rlogTF(200)
hist(Y)
par(op)

# different mu
curve(dlogTF(x, mu=-1, sigma=1, nu=10), 0, 5, ylim=c(0,1))
curve(dlogTF(x, mu=0, sigma=1, nu=10), 0, 5, add=TRUE, col="red", lty=2)
curve(dlogTF(x, mu=1, sigma=1, nu=10), 0, 5, add=TRUE, col="blue", lty=3)

# different sigma
curve(dlogTF(x, mu=0, sigma=.5, nu=10), 0, 5, ylim=c(0,1))
curve(dlogTF(x, mu=0, sigma=1, nu=10), 0, 5, add=TRUE, col="red", lty=2)
curve(dlogTF(x, mu=0, sigma=2, nu=10), 0, 5, add=TRUE, col="blue", lty=3)

# different degrees of freedom nu
curve(dlogTF(x, mu=0, sigma=1, nu=1), 0, 5, ylim=c(0,.8), n = 1001)
curve(dlogTF(x, mu=0, sigma=1, nu=2), 0, 5, add=TRUE, col="red", lty=2)
curve(dlogTF(x, mu=0, sigma=1, nu=5), 0, 5, add=TRUE, col="blue", lty=3)

# generating a logit t distribution
gen.Family("TF", "logit")
# plotting the d, p, q, and r functions
op<-par(mfrow=c(2,2))
curve(dlogitTF(x, mu=0), 0, 1)
curve(plogitTF(x, mu=0), 0, 1)
curve(qlogitTF(x, mu=0), 0, 1)
abline(v=1)
Y<- rlogitTF(200)
hist(Y)
par(op)

# different mu
curve(dlogitTF(x, mu=-2, sigma=1, nu=10), 0, 1, ylim=c(0,5))
curve(dlogitTF(x, mu=0, sigma=1, nu=10), 0, 1, add=TRUE, col="red", lty=2)
curve(dlogitTF(x, mu=2, sigma=1, nu=10), 0, 1, add=TRUE, col="blue", lty=3)

# different sigma
curve(dlogitTF(x, mu=0, sigma=1, nu=10), 0, 1, ylim=c(0,2.5))
curve(dlogitTF(x, mu=0, sigma=2, nu=10), 0, 1, add=TRUE, col="red", lty=2)
curve(dlogitTF(x, mu=0, sigma=.7, nu=10), 0, 1, add=TRUE, col="blue", lty=3)

# different degrees of freedom nu
curve(dlogitTF(x, mu=0, sigma=1, nu=1), 0, 1, ylim=c(0,1.6))
curve(dlogitTF(x, mu=0, sigma=1, nu=2), 0, 1, add=TRUE, col="red", lty=2)
curve(dlogitTF(x, mu=0, sigma=1, nu=5), 0, 1, add=TRUE, col="blue", lty=3)

```

Description

The functions `GEOMo()` and `GEOM()` define two parametrizations of the geometric distribution. The geometric distribution is a one parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The mean of `GEOM()` is equal to the parameter μ . The functions `dGEOM`, `pGEOM`, `qGEOM` and `rGEOM` define the density, distribution function, quantile function and random generation for the `GEOM` parameterization of the Geometric distribution.

Usage

```
GEOM(mu.link = "log")
dGEOM(x, mu = 2, log = FALSE)
pGEOM(q, mu = 2, lower.tail = TRUE, log.p = FALSE)
qGEOM(p, mu = 2, lower.tail = TRUE, log.p = FALSE)
rGEOM(n, mu = 2)
GEOMo(mu.link = "logit")
dGEOMo(x, mu = 0.5, log = FALSE)
pGEOMo(q, mu = 0.5, lower.tail = TRUE, log.p = FALSE)
qGEOMo(p, mu = 0.5, lower.tail = TRUE, log.p = FALSE)
rGEOMo(n, mu = 0.5)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with log link as the default for the <code>mu</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the original geometric distribution in the function `GE` is

$$f(y|\mu) = (1 - \mu)^y \mu$$

for $y \geq 0$ and $\mu > 0$.

The parameterization of the geometric distribution in the function `GEOM` is

$$f(y|\mu) = \mu^y / (\mu + 1)^{y+1}$$

where for $y \geq 0$ and $\mu > 0$.

Value

returns a `gamlss.family` object which can be used to fit a Geometric distribution in the `gamlss()` function.

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

- Johnson, N. L., Kemp, A. W., and Kotz, S. (2005). *Univariate discrete distributions*. Wiley.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, 54, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. 23, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(0,20,1)
plot(y, dGEOM(y), type="h")
q <- seq(0, 20, 1)
plot(q, pGEOM(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qGEOM(p), type="s")
dat <- rGEOM(100)
hist(dat)
#summary(gamlss(dat~1, family=GEOM))
par(mfrow=c(2,2))
y<-seq(0,20,1)
plot(y, dGEOMo(y), type="h")
q <- seq(0, 20, 1)
plot(q, pGEOMo(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qGEOMo(p), type="s")
dat <- rGEOMo(100)
hist(dat)
#summary(gamlss(dat~1, family="GE"))
```

Description

The function GG defines the generalized gamma distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The parameterization used has the mean of the distribution equal to μ and the variance equal to $(\sigma^2)(\mu^2)$. The functions `dGG`, `pGG`, `qGG` and `rGG` define the density, distribution function, quantile function and random generation for the specific parameterization of the generalized gamma distribution defined by function GG.

Usage

```
GG(mu.link = "log", sigma.link = "log",
   nu.link = "identity")
dGG(x, mu=1, sigma=0.5, nu=1,
    log = FALSE)
pGG(q, mu=1, sigma=0.5, nu=1, lower.tail = TRUE,
    log.p = FALSE)
qGG(p, mu=1, sigma=0.5, nu=1, lower.tail = TRUE,
    log.p = FALSE )
rGG(n, mu=1, sigma=0.5, nu=1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter, other links are "inverse" and "identity"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other links are "inverse" and "identity"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>sigma</code> parameter, other links are $1/nu^2$ and "log"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of shape parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The specific parameterization of the generalized gamma distribution used in GG is

$$f(y|\mu, \sigma, \nu) = \frac{\theta^\theta z^\theta \nu e^{(-\theta z)}}{(\Gamma(\theta)y)}$$

where $z = (y/\mu)^\nu$, $\theta = 1/(\sigma^2|\nu|^2)$ for $y > 0$, $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < +\infty$. Note that for $\nu = 0$ the distribution is log normal.

Value

GG() returns a `gamlss.family` object which can be used to fit a generalized gamma distribution in the `gamlss()` function. `dGG()` gives the density, `pGG()` gives the distribution function, `qGG()` gives the quantile function, and `rGG()` generates random deviates.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Nicoleta Motpan

References

- Lopatzidis, A. and Green, P. J. (2000), Nonparametric quantile regression using the gamma distribution, unpublished.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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See Also

[gamlss.family](#), [GA](#)

Examples

```
y<-rGG(100,mu=1,sigma=0.1, nu=-.5) # generates 100 random observations
hist(y)
# library(gamlss)
# histDist(y, family=GG)
# m1 <-gamlss(y~1,family=GG)
# prof.dev(m1, "nu", min=-2, max=2, step=0.2)
```


Description

The function GIG defines the generalized inverse gaussian distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions DIG, pGIG, GIG and rGIG define the density, distribution function, quantile function and random generation for the specific parameterization of the generalized inverse gaussian distribution defined by function GIG.

Usage

```
GIG(mu.link = "log", sigma.link = "log",
    nu.link = "identity")
dGIG(x, mu=1, sigma=1, nu=1,
     log = FALSE)
pGIG(q, mu=1, sigma=1, nu=1, lower.tail = TRUE,
     log.p = FALSE)
qGIG(p, mu=1, sigma=1, nu=1, lower.tail = TRUE,
     log.p = FALSE)
rGIG(n, mu=1, sigma=1, nu=1, ...)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter, other links are "inverse" and "identity"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other links are "inverse" and "identity"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter, other links are "inverse" and "log"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of shape parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required
<code>...</code>	for extra arguments

Details

The specific parameterization of the generalized inverse gaussian distribution used in GIG is $f(y|\mu, \sigma, \nu) = (\frac{c}{\mu})^\nu (\frac{y^{\nu-1}}{2K(\frac{1}{\sigma}, \nu)}) (\exp((\frac{-1}{2\sigma})(\frac{cy}{\mu} + \frac{\mu}{cy})))$ where $c = \frac{K(\frac{1}{\sigma}, \nu+1)}{K(\frac{1}{\sigma}, \nu)}$, for $y > 0$, $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < +\infty$.

Value

GIG() returns a `gamlss.family` object which can be used to fit a generalized inverse gaussian distribution in the `gamlss()` function. DIG() gives the density, pGIG() gives the distribution function, GIG() gives the quantile function, and rGIG() generates random deviates.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Nicoleta Motpan

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

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Jorgensen B. (1982) Statistical properties of the generalized inverse Gaussian distribution, Series: Lecture notes in statistics; 9, New York : Springer-Verlag.

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [IG](#)

Examples

```
y<-rGIG(100,mu=1,sigma=1, nu=-0.5) # generates 1000 random observations
hist(y)
# library(gamlss)
# histDist(y, family=GIG)
```

Description

The `GPO()` function defines the generalised Poisson distribution, a two parameter discrete distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dGPO`, `pGPO`, `qGPO` and `rGPO` define the density, distribution function, quantile function and random generation for the Delaporte `GPO()`, distribution.

Usage

```
GPO(mu.link = "log", sigma.link = "log")

dGPO(x, mu = 1, sigma = 1, log = FALSE)

pGPO(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)

qGPO(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE, max.value = 10000)

rGPO(n, mu = 1, sigma = 1, max.value = 10000)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive <code>mu</code>
<code>sigma</code>	vector of positive dispersion parameter <code>sigma</code>
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>max.value</code>	a constant, set to the default value of 10000 for how far the algorithm should look for <code>q</code>

Details

The probability function of the Generalised Poisson distribution is given by

$$P(Y = y | \mu, \sigma) = \left(\frac{\mu}{1 + \sigma\mu} \right)^y \frac{(1 + \sigma y)^{y-1}}{y!} \exp \left[\frac{-\mu(1 + \sigma y)}{1 + \sigma\mu} \right]$$

for $y = 0, 1, 2, \dots, \infty$ where $\mu > 0$ and $\sigma > 0$.

Value

Returns a `gamlss.family` object which can be used to fit a Generalised Poisson distribution in the `gamlss()` function.

Author(s)

Rigby, R. A., Stasinopoulos D. M.

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [P0](#), [DPO](#)

Examples

```
GPO()# gives information about the default links for the
#plot the pdf using plot
plot(function(y) dGPO(y, mu=10, sigma=1 ), from=0, to=100, n=100+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=100),pGPO(seq(from=0,to=100), mu=10, sigma=1), type="h") # cdf
# generate random sample
tN <- table(Ni <- rGPO(100, mu=5, sigma=1))
r <- barplot(tN, col='lightblue')
```

Description

This function defines the generalized t distribution, a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dGT`, `pGT`, `qGT` and `rGT` define the density, distribution function, quantile function and random generation for the generalized t distribution.

Usage

```

GT(mu.link = "identity", sigma.link = "log", nu.link = "log",
   tau.link = "log")
dGT(x, mu = 0, sigma = 1, nu = 3, tau = 1.5, log = FALSE)
pGT(q, mu = 0, sigma = 1, nu = 3, tau = 1.5, lower.tail = TRUE,
    log.p = FALSE)
qGT(p, mu = 0, sigma = 1, nu = 3, tau = 1.5, lower.tail = TRUE,
    log.p = FALSE)
rGT(n, mu = 0, sigma = 1, nu = 3, tau = 1.5)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter.
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter.
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <code>nu</code> parameter values
<code>tau</code>	vector of kurtosis <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the generalized t distribution, (GT), , is defined as

$$f(y|\mu, \sigma, \nu, \tau) = \tau \left\{ 2\sigma\nu^{1/\tau} B\left(\frac{1}{\tau}, \nu\right) [1 + |z|^\tau/\nu]^{\nu+1/\tau} \right\}^{-1}$$

where $-\infty < y < \infty$, $z = (y - \mu)/\sigma$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu > 0$ and $\tau > 0$.

Value

`GT()` returns a `gamlss.family` object which can be used to fit the GT distribution in the `gamlss()` function. `dGT()` gives the density, `pGT()` gives the distribution function, `qGT()` gives the quantile function, and `rGT()` generates random deviates.

Warning

The `qGT` and `rGT` are slow since they are relying on optimization for finding the quantiles

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
GT() #
y<- rGT(200, mu=5, sigma=1, nu=1, tau=4)
hist(y)
curve(dGT(x, mu=5 ,sigma=2,nu=1, tau=4), -2, 11,
      main = "The GT density mu=5 ,sigma=1, nu=1, tau=4")
# library(gamlss)
# m1<-gamlss(y~1, family=GT)
```

 GU

The Gumbel distribution for fitting a GAMLSS

Description

The function GU defines the Gumbel distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dGU`, `pGU`, `qGU` and `rGU` define the density, distribution function, quantile function and random generation for the specific parameterization of the Gumbel distribution.

Usage

```
GU(mu.link = "identity", sigma.link = "log")
dGU(x, mu = 0, sigma = 1, log = FALSE)
pGU(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qGU(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rGU(n, mu = 0, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. other available link is "inverse", "log" and "own")
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other links are the "inverse", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The specific parameterization of the Gumbel distribution used in GU is

$$f(y|\mu, \sigma) = \frac{1}{\sigma} \exp \left\{ \left(\frac{y - \mu}{\sigma} \right) - \exp \left(\frac{y - \mu}{\sigma} \right) \right\}$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$.

Value

`GU()` returns a `gamlss.family` object which can be used to fit a Gumbel distribution in the `gamlss()` function. `dGU()` gives the density, `pGU()` gives the distribution function, `qGU()` gives the quantile function, and `rGU()` generates random deviates.

Note

The mean of the distribution is $\mu - 0.57722\sigma$ and the variance is $\pi^2\sigma^2/6$.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [RG](#)

Examples

```
plot(function(x) dGU(x, mu=0,sigma=1), -6, 3,
      main = "{Gumbel density mu=0,sigma=1}")
GU()# gives information about the default links for the Gumbel distribution
dat<-rGU(100, mu=10, sigma=2) # generates 100 random observations
hist(dat)
# library(gamlss)
# gamlss(dat~1,family=GU) # fits a constant for each parameter mu and sigma
```

hazardFun

Hazard functions for gamlss.family distributions

Description

The function `hazardFun()` takes as an argument a `gamlss.family` object and creates the hazard function for it. The function `gen.hazard()` generates a hazard function called `hNAME` where `NAME` is a `gamlss.family` i.e. `hGA()`.

Usage

```
hazardFun(family = "NO", ...)
gen.hazard(family = "NO", ...)
```

Arguments

<code>family</code>	a <code>gamlss.family</code> object
<code>...</code>	for passing extra arguments

Value

A hazard function.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Vlasios Voudouris

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
gen.hazard("WEI2")
y<-seq(0,10,by=0.01)
plot(hWEI2(y, mu=1, sigma=1)~y, type="l", col="black", ylab="h(y)", ylim=c(0,2.5))
lines(hWEI2(y, mu=1, sigma=1.2)~y, col="red",lt=2,lw=2)
lines(hWEI2(y, mu=1, sigma=.5)~y, col="blue",lt=3,lw=2)
```

IG

Inverse Gaussian distribution for fitting a GAMLSS

Description

The function `IG()`, or equivalently `Inverse.Gaussian()`, defines the inverse Gaussian distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dIG`, `pIG`, `qIG` and `rIG` define the density, distribution function, quantile function and random generation for the specific parameterization of the Inverse Gaussian distribution defined by function `IG`.

Usage

```
IG(mu.link = "log", sigma.link = "log")
dIG(x, mu = 1, sigma = 1, log = FALSE)
pIG(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qIG(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rIG(n, mu = 1, sigma = 1, ...)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required
<code>...</code>	<code>...</code> can be used to pass the <code>uppr.limit</code> argument to <code>qIG</code>

Details

Definition file for inverse Gaussian distribution.

$$f(y|\mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2 y^3}} \exp \left\{ -\frac{1}{2\mu^2 \sigma^2 y} (y - \mu)^2 \right\}$$

for $y > 0$, $\mu > 0$ and $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit an inverse Gaussian distribution in the `gamlss()` function.

Note

μ is the mean and $\sigma^2 \mu^3$ is the variance of the inverse Gaussian

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [GA](#), [GIG](#)

Examples

```
IG()# gives information about the default links for the normal distribution
# library(gamlss)
# data(rent)
# gamlss(R~cs(F1),family=IG, data=rent) #
plot(function(x)dIG(x, mu=1,sigma=.5), 0.01, 6,
      main = "{Inverse Gaussian density mu=1,sigma=0.5}")
plot(function(x)pIG(x, mu=1,sigma=.5), 0.01, 6,
      main = "{Inverse Gaussian cdf mu=1,sigma=0.5}")
```

IGAMMA

Inverse Gamma distribution for fitting a GAMLSS

Description

The function `IGAMMA()` defines the Inverse Gamma distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with parameters `mu` (the mode) and `sigma`. The functions `dIGAMMA`, `pIGAMMA`, `qIGAMMA` and `rIGAMMA` define the density, distribution function, quantile function and random generation for the IGAMMA parameterization of the Inverse Gamma distribution.

Usage

```
IGAMMA(mu.link = "log", sigma.link="log")
dIGAMMA(x, mu = 1, sigma = .5, log = FALSE)
pIGAMMA(q, mu = 1, sigma = .5, lower.tail = TRUE, log.p = FALSE)
qIGAMMA(p, mu = 1, sigma = .5, lower.tail = TRUE, log.p = FALSE)
rIGAMMA(n, mu = 1, sigma = .5)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with log link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with log as the default for the <code>sigma</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the Inverse Gamma distribution in the function IGAMMA is

$$f(y|\mu, \sigma) = \frac{[\mu(\alpha + 1)]^\alpha}{\Gamma(\alpha)} y^{-(\alpha+1)} \exp\left[-\frac{\mu(\alpha + 1)}{y}\right]$$

where $\alpha = 1/(\sigma^2)$ for $y > 0$, $\mu > 0$ and $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit an Inverse Gamma distribution in the `gamlss()` function.

Note

For the function `IGAMMA()`, μ is the mode of the Inverse Gamma distribution.

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, 54, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [GA](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(0.2,20,0.2)
plot(y, dIGAMMA(y), type="l")
q <- seq(0.2, 20, 0.2)
plot(q, pIGAMMA(q), type="l")
p<-seq(0.0001,0.999,0.05)
plot(p, qIGAMMA(p), type="l")
dat <- rIGAMMA(50)
```

```
hist(dat)
#summary(gamlss(dat~1, family="IGAMMA"))
```

JSU

The Johnson's Su distribution for fitting a GAMLSS

Description

This function defines the , a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dJSU`, `pJSU`, `qJSU` and `rJSU` define the density, distribution function, quantile function and random generation for the the Johnson's Su distribution.

Usage

```
JSU(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dJSU(x, mu = 0, sigma = 1, nu = 1, tau = 1, log = FALSE)
pJSU(q, mu = 0, sigma = 1, nu = 1, tau = 1, lower.tail = TRUE, log.p = FALSE)
qJSU(p, mu = 0, sigma = 1, nu = 1, tau = 1, lower.tail = TRUE, log.p = FALSE)
rJSU(n, mu = 0, sigma = 1, nu = 1, tau = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. Other links are "inverse" "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse", "identity" and "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter. Other links are "onverse", "log" and "own"
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter. Other links are "onverse", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <code>nu</code> parameter values
<code>tau</code>	vector of kurtosis <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the Jonhson's SU distribution, (JSU), is defined as

$$f(y|n, \mu, \sigma, \nu, \tau) = \frac{1}{c\sigma} \frac{1}{\tau(z^2 + 1)^{\frac{1}{2}}} \frac{1}{\sqrt{2\pi}} \exp \left[-\frac{1}{2} r^2 \right]$$

for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$. where $r = -\nu + \frac{1}{\tau} \sinh^{-1}(z)$, $z = \frac{y - (\mu + c\sigma w^{\frac{1}{2}} \sinh \Omega)}{c\sigma}$, $c = [\frac{1}{2}(w - 1)(w \cosh 2\Omega + 1)]^{\frac{1}{2}}$, $w = e^{\tau^2}$ and $\Omega = -\nu\tau$.

This is a reparameterization of the original Johnson Su distribution, Johnson (1954), so the parameters `mu` and `sigma` are the mean and the standard deviation of the distribution. The parameter `nu` determines the skewness of the distribution with `nu>0` indicating positive skewness and `nu<0` negative. The parameter `tau` determines the kurtosis of the distribution. `tau` should be positive and most likely in the region from zero to 1. As `tau` goes to 0 (and for `nu=0`) the distribution approaches the the Normal density function. The distribution is appropriate for leptokurtic data that is data with kurtosis larger that the Normal distribution one.

Value

`JSU()` returns a `gamlss.family` object which can be used to fit a Johnson's Su distribution in the `gamlss()` function. `dJSU()` gives the density, `pJSU()` gives the distribution function, `qJSU()` gives the quantile function, and `rJSU()` generates random deviates.

Warning

The function `JSU` uses first derivatives square in the fitting procedure so standard errors should be interpreted with caution

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Johnson, N. L. (1954). Systems of frequency curves derived from the first law of Laplace., *Trabajos de Estadística*, **5**, 283-291.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R. A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <https://www.gamlss.com/>).
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [JSUo](#), [BCT](#)

Examples

```
JSUo()
plot(function(x)dJSUo(x, mu=0,sigma=1,nu=-1, tau=.5), -4, 4,
     main = "The JSU density mu=0,sigma=1,nu=-1, tau=.5")
plot(function(x) pJSUo(x, mu=0,sigma=1,nu=-1, tau=.5), -4, 4,
     main = "The JSU cdf mu=0, sigma=1, nu=-1, tau=.5")
# library(gamlss)
# data(abdom)
# h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=JSU, data=abdom)
```

JSUo

The original Johnson's Su distribution for fitting a GAMLSS

Description

This function defines the , a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dJSUo`, `pJSUo`, `qJSUo` and `rJSUo` define the density, distribution function, quantile function and random generation for the the Johnson's Su distribution.

Usage

```
JSUo(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dJSUo(x, mu = 0, sigma = 1, nu = 0, tau = 1, log = FALSE)
pJSUo(q, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
qJSUo(p, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
rJSUo(n, mu = 0, sigma = 1, nu = 0, tau = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. Other links are "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse", "identity" and "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter. Other links are "inverse", "log" and "own"
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter. Other links are "inverse", "identity" and "own"

<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness nu parameter values
<code>tau</code>	vector of kurtosis tau parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the orininal Jonhson's SU distribution, (JSU), is defined as

$$f(y|n, \mu, \sigma, \nu, \tau) = \frac{\tau}{\sigma} \frac{1}{(z^2 + 1)^{\frac{1}{2}}} \frac{1}{\sqrt{2\pi}} \exp \left[-\frac{1}{2} r^2 \right]$$

for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$. where $z = \frac{(y-\mu)}{\sigma}$, $r = \nu + \tau \sinh^{-1}(z)$.

Value

`JSUo()` returns a `gamlss.family` object which can be used to fit a Johnson's Su distribution in the `gamlss()` function. `dJSUo()` gives the density, `pJSUo()` gives the distribution function, `qJSUo()` gives the quantile function, and `rJSUo()` generates random deviates.

Warning

The function JSU uses first derivatives square in the fitting procedure so standard errors should be interpreted with caution. It is recomented to be used only with `method=mixed(2, 20)`

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

- Johnson, N. L. (1954). Systems of frequency curves derived from the first law of Laplace., *Trabajos de Estadistica*, **5**, 283-291.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
JSU()
plot(function(x)dJSUo(x, mu=0,sigma=1,nu=-1, tau=.5), -4, 15,
      main = "The JSUo density mu=0,sigma=1,nu=-1, tau=.5")
plot(function(x) pJSUo(x, mu=0,sigma=1,nu=-1, tau=.5), -4, 15,
      main = "The JSUo cdf mu=0, sigma=1, nu=-1, tau=.5")
# library(gamlss)
# data(abdom)
# h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=JSUo,
#           data=abdom, method=mixed(2,20))
# plot(h)
```

LG

Logarithmic and zero adjusted logarithmic distributions for fitting a GAMLSS model

Description

The function LG defines the logarithmic distribution, a one parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dLG`, `pLG`, `qLG` and `rLG` define the density, distribution function, quantile function and random generation for the logarithmic , `LG()`, distribution.

The function ZALG defines the zero adjusted logarithmic distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZALG`, `pZALG`, `qZALG` and `rZALG` define the density, distribution function, quantile function and random generation for the inflated logarithmic , `ZALG()`, distribution.

Usage

```
LG(mu.link = "logit")
dLG(x, mu = 0.5, log = FALSE)
pLG(q, mu = 0.5, lower.tail = TRUE, log.p = FALSE)
qLG(p, mu = 0.5, lower.tail = TRUE, log.p = FALSE, max.value = 10000)
rLG(n, mu = 0.5)
ZALG(mu.link = "logit", sigma.link = "logit")
```

```

dZALG(x, mu = 0.5, sigma = 0.1, log = FALSE)
pZALG(q, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZALG(p, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZALG(n, mu = 0.5, sigma = 0.1)

```

Arguments

<code>mu.link</code>	defines the <code>mu.link</code> , with <code>logit</code> link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	defines the <code>sigma.link</code> , with <code>logit</code> link as the default for the <code>sigma</code> parameter which in this case is the probability at zero.
<code>x</code>	vector of (non-negative integer)
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of probabilities at zero
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>max.value</code>	valued needed for the numerical calculation of the q-function

Details

For the definition of the distributions see Rigby and Stasinopoulos (2010) below.

The parameterization of the logarithmic distribution in the function `LM` is

$$f(y|\mu) = \alpha \mu^y / y$$

where for $y \geq 1$ and $\mu > 0$ and

$$\alpha = -[\log(1 - \mu)]^{-1}$$

Value

The function `LG` and `ZALG` return a `gamlss.family` object which can be used to fit a logarithmic and a zero inflated logarithmic distributions respectively in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

Johnson, Norman Lloyd; Kemp, Adrienne W; Kotz, Samuel (2005). "Chapter 7: Logarithmic and Lagrangian distributions". *Univariate discrete distributions* (3 ed.). John Wiley & Sons. ISBN 9780471272465.

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See Also

[gamlss.family](#), [P0](#), [ZAP](#)

Examples

```
LG()
ZAP()
# creating data and plotting them
dat <- rLG(1000, mu=.3)
r <- barplot(table(dat), col='lightblue')
dat1 <- rZALG(1000, mu=.3, sigma=.1)
r1 <- barplot(table(dat1), col='lightblue')
```

LNO

Log Normal distribution for fitting in GAMLSS

Description

The functions LOGNO and LOGNO2 define a `gamlss.family` distribution to fits the log-Normal distribution. The difference between them is that while LOGNO retains the original parametrization for μ , (identical to the normal distribution NO) and therefore $\mu = (-\infty, +\infty)$, the function LOGNO2 use μ as the median, so $\mu = (0, +\infty)$.

The function LNO is more general and can fit a Box-Cox transformation to data using the `gamlss()` function. In the LOGNO (and LOGNO2) there are two parameters involved μ σ , while in the LNO there are three parameters μ σ , and the transformation parameter ν . The transformation parameter ν in LNO is a 'fixed' parameter (not estimated) and it has its default value equal to zero allowing the fitting of the log-normal distribution as in LOGNO. See the example below on how to fix ν to be a particular value. In order to estimate (or model) the parameter ν , use the [gamlss.family BCCG](#) distribution which uses a reparameterized version of the the Box-Cox transformation. The functions dLOGNO, pLOGNO, qLOGNO and rLOGNO define the density, distribution function, quantile function and random generation for the specific parameterization of the log-normal distribution.

The functions dLOGNO2, pLOGNO2, qLOGNO2 and rLOGNO2 define the density, distribution function, quantile function and random generation when μ is the median of the log-normal distribution.

The functions dLNO, pLNO, qLNO and rLNO define the density, distribution function, quantile function and random generation for the specific parameterization of the log-normal distribution and more generally a Box-Cox transformation.

Usage

```
LNO(mu.link = "identity", sigma.link = "log")
LOGNO(mu.link = "identity", sigma.link = "log")
LOGNO2(mu.link = "log", sigma.link = "log")
dLNO(x, mu = 1, sigma = 0.1, nu = 0, log = FALSE)
dLOGNO(x, mu = 0, sigma = 1, log = FALSE)
dLOGNO2(x, mu = 1, sigma = 1, log = FALSE)
pLNO(q, mu = 1, sigma = 0.1, nu = 0, lower.tail = TRUE, log.p = FALSE)
pLOGNO(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
pLOGNO2(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qLNO(p, mu = 1, sigma = 0.1, nu = 0, lower.tail = TRUE, log.p = FALSE)
qLOGNO(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qLOGNO2(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rLNO(n, mu = 1, sigma = 0.1, nu = 0)
rLOGNO(n, mu = 0, sigma = 1)
rLOGNO2(n, mu = 1, sigma = 1)
```

Arguments

mu.link	Defines the mu.link, with "identity" or "log" link depending on the parametrization
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter. Other links are "inverse", "identity" and "own"
x, q	vector of quantiles
mu	vector of location parameter values
sigma	vector of scale parameter values
nu	vector of shape parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required

Details

The probability density function in LOGNO is defined as

$$f(y|\mu, \sigma) = \frac{1}{y\sqrt{2\pi}\sigma} \exp\left[-\frac{1}{2\sigma^2}(\log(y) - \mu)^2\right]$$

for $y > 0$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$.

The probability density function in LNO is defined as

$$f(y|\mu, \sigma, \nu) = \frac{1}{\sqrt{2\pi}\sigma} y^{\nu-1} \exp\left[-\frac{1}{2\sigma^2}(z - \mu)^2\right]$$

where if $\nu \neq 0$ $z = (y^\nu - 1)/\nu$ else $z = \log(y)$ and $z \sim N(0, \sigma^2)$, for $y > 0$, $\mu > 0$, $\sigma > 0$ and $\nu = (-\infty, +\infty)$.

Value

LNO() returns a `gamlss.family` object which can be used to fit a log-normal distribution in the `gamlss()` function. `dLNO()` gives the density, `pLNO()` gives the distribution function, `qLNO()` gives the quantile function, and `rLNO()` generates random deviates.

Warning

This is a two parameter fit for μ and σ while ν is fixed. If you wish to model ν use the `gamlss` family `BCCG`.

Note

μ is the mean of z (and also the median of y), the Box-Cox transformed variable and σ is the standard deviation of z and approximate the coefficient of variation of y

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Box, G. E. P. and Cox, D. R. (1964) An analysis of transformations (with discussion), *J. R. Statist. Soc. B.*, **26**, 211–252
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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- (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BCCG](#)

Examples

```
LOGNO()# gives information about the default links for the log normal distribution
LOGNO2()
LNO()# gives information about the default links for the Box Cox distribution

# plotting the d, p, q, and r functions
op<-par(mfrow=c(2,2))
curve(dLOGNO(x, mu=0), 0, 10)
curve(pLOGNO(x, mu=0), 0, 10)
curve(qLOGNO(x, mu=0), 0, 1)
Y<- rLOGNO(200)
hist(Y)
par(op)

# plotting the d, p, q, and r functions
op<-par(mfrow=c(2,2))
curve(dLOGNO2(x, mu=1), 0, 10)
curve(pLOGNO2(x, mu=1), 0, 10)
curve(qLOGNO2(x, mu=1), 0, 1)
Y<- rLOGNO(200)
hist(Y)
par(op)

# library(gamlss)
# data(abdom)
# h1<-gamlss(y~cs(x), family=LOGNO, data=abdom)#fits the log-Normal distribution
# h2<-gamlss(y~cs(x), family=LNO, data=abdom) #should be identical to the one above
# to change to square root transformation, i.e. fix nu=0.5
# h3<-gamlss(y~cs(x), family=LNO, data=abdom, nu.fix=TRUE, nu.start=0.5)
```

LO

Logistic distribution for fitting a GAMLSS

Description

The function `LO()`, or equivalently `Logistic()`, defines the logistic distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`

Usage

```
LO(mu.link = "identity", sigma.link = "log")
dLO(x, mu = 0, sigma = 1, log = FALSE)
pLO(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qLO(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rLO(n, mu = 0, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

Definition file for Logistic distribution.

$$f(y|\mu, \sigma) = \frac{1}{\sigma} e^{-\frac{y-\mu}{\sigma}} [1 + e^{-\frac{y-\mu}{\sigma}}]^{-2}$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, \infty)$ and $\sigma > 0$.

Value

`LO()` returns a `gamlss.family` object which can be used to fit a logistic distribution in the `gamlss()` function. `dLO()` gives the density, `pLO()` gives the distribution function, `qLO()` gives the quantile function, and `rLO()` generates random deviates for the logistic distribution. The latest functions are based on the equivalent R functions for logistic distribution.

Note

μ is the mean and $\sigma\pi/\sqrt{3}$ is the standard deviation for the logistic distribution

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NO](#), [TF](#)

Examples

```
L0()# gives information about the default links for the Logistic distribution
plot(function(y) dL0(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) pL0(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) qL0(y, mu=10 ,sigma=2), 0, 1)
# library(gamlss)
# data(abdom)
# h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=L0, data=abdom) # fits
# plot(h)
```

LOGITNO

Logit Normal distribution for fitting in GAMLSS

Description

The functions dLOGITNO, pLOGITNO, qLOGITNO and rLOGITNO define the density, distribution function, quantile function and random generation for the logit-normal distribution. The function LOGITNO can be used for fitting the distribution in `gamlss()`.

Usage

```
LOGITNO(mu.link = "logit", sigma.link = "log")
dLOGITNO(x, mu = 0.5, sigma = 1, log = FALSE)
pLOGITNO(q, mu = 0.5, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qLOGITNO(p, mu = 0.5, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rLOGITNO(n, mu = 0.5, sigma = 1)
```

Arguments

<code>mu.link</code>	the link function for mu
<code>sigma.link</code>	the link function for sigma
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function in LOGITNO is defined as

$$f(y|\mu, \sigma) = \frac{1}{y(1-y)\sqrt{2\pi}\sigma} \exp\left[-\frac{1}{2\sigma^2}(\log(y/(1-y)) - \log(\mu/(1-\mu)))^2\right]$$

for $0 < y < 1$, $\mu \in (0, 1)$ and $\sigma > 0$.

Value

LOGITNO() returns a `gamlss.family` object which can be used to fit a logit-normal distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [LOGNO](#)

Examples

```
# plotting the d, p, q, and r functions
op<-par(mfrow=c(2,2))
curve(dLOGITNO(x), 0, 1)
curve(pLOGITNO(x), 0, 1)
curve(qLOGITNO(x), 0, 1)
Y<- rLOGITNO(200)
hist(Y)
par(op)

# plotting the d, p, q, and r functions
# sigma 3
op<-par(mfrow=c(2,2))
curve(dLOGITNO(x, sigma=3), 0, 1)
```

```

curve(pLOGITNO(x, sigma=3), 0, 1)
curve(qLOGITNO(x, sigma=3), 0, 1)
Y<- rLOGITNO(200, sigma=3)
hist(Y)
par(op)

```

LQNO

Normal distribution with a specific mean and variance relationship for fitting a GAMLSS model

Description

The function `LQNO()` defines a normal distribution family, which has a specific mean and variance relationship. The distribution can be used in a GAMLSS fitting using the function `gamlss()`. The mean of `LQNO` is equal to μ . The variance is equal to $\mu \cdot (1 + \sigma \cdot \mu)$ so the standard deviation is $\sqrt{\mu \cdot (1 + \sigma \cdot \mu)}$. The function is found useful in modelling small RNA sequencing experiments. The functions `dLQNO`, `pLQNO`, `qLQNO` and `rLQNO` define the density, distribution function, quantile function (inverse cdf) and random generation for the `LQNO()` parametrization of the normal distribution.

Usage

```

LQNO(mu.link = "log", sigma.link = "log")
dLQNO(x, mu = 1, sigma = 1, log = FALSE)
pLQNO(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qLQNO(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rLQNO(n, mu = 1, sigma = 1)

```

Arguments

<code>mu.link</code>	mu link function with "log" as default
<code>sigma.link</code>	mu link function with "log" as default
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$
<code>lower.tail</code>	if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

LQNO stands for Linear Quadratic Normal Family, in which the variance is a linear quadratic function of the mean: $\text{Var}(Y) = \mu \cdot (1 + \sigma \cdot \mu)$. This is created to facilitate the analysis of data coming from small RNA sequencing experiments, basically counts of short RNAs that one isolates from cells or biofluids such as urine, plasma or cerebrospinal fluid. Argyropoulos *et al.* (2017) showing that the LQNO distribution (and the Negative Binomial which implements the same mean- variance relationship) are highly accurate approximations to the generative models of the signals in these experiments

Value

The function LQNO returns a `gamlss.family` object which can be used to fit this specific form of the normal distribution family in the `gamlss()` function.

Note

The μ parameters must be positive so for the relationship $\text{Var}(Y) = \mu \cdot (1 + \sigma \cdot \mu)$ to be valid.

Author(s)

Christos Argyropoulos

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Argyropoulos C, Etheridge A, Sakhanenko N, Galas D. (2017) Modeling bias and variation in the stochastic processes of small RNA sequencing. *Nucleic Acids Res.* 2017 Mar 27. doi: 10.1093/nar/gkx199. [Epub ahead of print] PubMed PMID: 28369495.

See Also

[NO](#), [NO2](#), [NOF](#)

Examples

```
LQNO()# gives information about the default links for the normal distribution
# a comparison of different Normal models
#m1 <- gamlss(y~pb(x), sigma.fo=~pb(x), data=abdom, family=NO(mu.link="log"))
#m2 <- gamlss(y~pb(x), sigma.fo=~pb(x), data=abdom, family=LQNO)
#m3 <- gamlss(y~pb(x), sigma.fo=~pb(x), data=abdom, family=NOF(mu.link="log"))
#AIC(m1,m2,m3)
```

Description

The function `make.link.gamlss()` is used with `gamlss.family` distributions in package **gamlss()**. Given a link, it returns a link function, an inverse link function, the derivative `dpar/deta` where 'par' is the appropriate distribution parameter and a function for checking the domain. It differs from the usual `make.link` of `glm()` by having extra links as the `logshift1`, and the `own`. For the use of the `own` link see the example bellow. `show.link` provides a way in which the user can identify the link functions available for each `gamlss` distribution. If your required link function is not available for any of the `gamlss` distributions you can add it in.

Usage

```
make.link.gamlss(link)
show.link(family = "NO")
```

Arguments

link	character or numeric; one of "logit", "probit", "cloglog", "identity", "log", "sqrt", "1/mu^2", "inverse", "logshifted", "logitshifted", or number, say λ resulting in power link μ^λ .
family	a <code>gamlss</code> distribution family

Details

The `own` link function is added to allow the user greater flexibility. In order to use the `own` link function for any of the parameters of the distribution the `own` link should appear in the available links for this parameter. You can check this using the function `show.link`. If the `own` does not appear in the list you can create a new function for the distribution in which `own` is added in the list. For example the first line of the code of the binomial distribution, `BI`, has changed from

```
"mstats <- checklink("mu.link", "Binomial", substitute(mu.link), c("logit", "probit", "cloglog", "log")),
in version 1.0-0 of gamlss, to
```

```
"mstats <- checklink("mu.link", "Binomial", substitute(mu.link), c("logit", "probit", "cloglog", "log",
"own"))
```

in version 1.0-1. Given that the parameter has `own` as an option the user needs also to define the following four new functions in order to use an `own` link.

- i) `own.linkfun`
- ii) `own.linkinv`
- iii) `own.mu.eta` and
- iv) `own.valideta`.

An example is given below.

Only one parameter of the distribution at a time is allowed to have its own link, (unless the same four own functions above are suitable for more than one parameter of the distribution).

Note that from **gamlss** version 1.9-0 the user can introduce its own link function by define an appropriate function, (see the example below).

Value

For the `make.link.gamlss` a list with components

`linkfun`: Link function `function(parameter)`

`linkinv`: Inverse link function `function(eta)`

`mu.eta`: Derivative function `function(eta) dparameter/deta`

`valideta`: `function(eta)` TRUE if all of eta is in the domain of `linkinv`.

For the `show.link` a list with components the available links for the distribution parameters

Note

For the links involving parameters as in `logshifted` and `logitshifted` the parameters can be passed in the definition of the distribution by calling the `checklink` function, for example in the definition of the tau parameter in BCPE distribution the following call is made: `tstats <-checklink("tau.link", "Box Cox Power Exponential", substitute(tau.link), c("logshifted", "log", "identity"), par.link = c(1))`

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```

str(make.link.gamlss("logshiftt01"))
l2<-make.link.gamlss("logshiftt01")
l2$linkfun(2) # should close to zero (Note that 0.00001 is added)
l2$linkfun(1-0.00001) # should be -Inf but it is large negative
#-----
# now use the own link function
# first if the distribution allows you
show.link(BI)
# seems OK now define the four own functions
# First try the probit link using the own link function
# 1: the linkfun function
own.linkfun <- function(mu) { qNO(p=mu)}
# 2: the inverse link function
own.linkinv <- function(eta) {
  thresh <- -qNO(.Machine$double.eps)
  eta <- pmin(thresh, pmax(eta, -thresh))
  pNO(eta)}
# 3: the dmu/deta function
own.mu.eta <- function(eta) pmax(dNO(eta), .Machine$double.eps)
# 4: the valideta function
own.valideta <- function(eta) TRUE

## bring the data
# library(gamlss)
#data(aep)
# fitting the model using "own"
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link="own"), data=aep)
# model h1 should be identical to the probit
# h2<-gamlss(y~ward+loglos+year, family=BI(mu.link="probit"), data=aep)
# now using a function instead of "own"
probittest <- function()
{
  linkfun <- function(mu) { qNO(p=mu)}
  linkinv <- function(eta)
  {
    thresh <- -qNO(.Machine$double.eps)
    eta <- pmin(thresh, pmax(eta, -thresh))
    pNO(eta)
  }
  mu.eta <- function(eta) pmax(dNO(eta), .Machine$double.eps)
  valideta <- function(eta) TRUE
  link <- "probitTest"
  structure(list(linkfun = linkfun, linkinv = linkinv, mu.eta = mu.eta,
    valideta = valideta, name = link), class = "link-gamlss")
}
# h3<-gamlss(y~ward+loglos+year, family=BI(mu.link=probittest()), data=aep)
# Second try the complementary log-log
# using the Gumbel distribution
own.linkfun <- function(mu) { qGU(p=mu)}
own.linkinv <- function(eta) {
  thresh <- -qGU(.Machine$double.eps)

```

```

        eta <- pmin(thresh, pmax(eta, -thresh))
        pGU(eta)}
own.mu.eta <- function(eta) pmax(dGU(eta), .Machine$double.eps)
own.valideta <- function(eta) TRUE
# h1 and h2 should be identical to cloglog
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link="own"), data=aep)
# h2<-gamlss(y~ward+loglos+year, family=BI(mu.link="cloglog"), data=aep)
# note that the Gumbel distribution is negatively skew
# for a positively skew link function we can use the Reverse Gumbel
revloglog <- function()
{
linkfun <- function(mu) { qRG(p=mu)}
linkinv <- function(eta) {
        thresh <- -qRG(.Machine$double.eps)
        eta <- pmin(thresh, pmax(eta, -thresh))
        pRG(eta)}
mu.eta <- function(eta) pmax(dRG(eta), .Machine$double.eps)
valideta <- function(eta) TRUE
link <- "revloglog"
structure(list(linkfun = linkfun, linkinv = linkinv, mu.eta = mu.eta,
        valideta = valideta, name = link), class = "link-gamlss")
}
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link=revloglog()), data=aep)
# a considerable improvement in the deviance
# try a shifted logit link function from -1, 1
own.linkfun <- function(mu)
{ shift = c(-1,1)
  log((mu-shift[1])/(shift[2]-mu))
}
own.linkinv <- function(eta)
{
  shift = c(-1,1)
  thresh <- -log(.Machine$double.eps)
  eta <- pmin(thresh, pmax(eta, -thresh))
  shift[2]-(shift[2]-shift[1])/(1 + exp(eta))
}
own.mu.eta <- function(eta)
{
  shift = c(-1,1)
  thresh <- -log(.Machine$double.eps)
  res <- rep(.Machine$double.eps, length(eta))
  res[abs(eta) < thresh] <- ((shift[2]-shift[1])*exp(eta)/(1 +
    exp(eta))^2)[abs(eta) < thresh]
  res
}
own.valideta <- function(eta) TRUE
#-----
str(make.link.gamlss("own"))
l2<-make.link.gamlss("own")
l2$linkfun(0) # should be zero
l2$linkfun(1) # should be Inf
l2$linkinv(-5:5)

```

Description

The set of function presented here is useful for fitting multinomial regression within gamlss.

Usage

```
MN3(mu.link = "log", sigma.link = "log")
MN4(mu.link = "log", sigma.link = "log", nu.link = "log")
MN5(mu.link = "log", sigma.link = "log", nu.link = "log", tau.link = "log")
MULTIN(type = "3")
fittedMN(model)

dMN3(x, mu = 1, sigma = 1, log = FALSE)
dMN4(x, mu = 1, sigma = 1, nu = 1, log = FALSE)
dMN5(x, mu = 1, sigma = 1, nu = 1, tau = 1, log = FALSE)

pMN3(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
pMN4(q, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
pMN5(q, mu = 1, sigma = 1, nu = 1, tau = 1, lower.tail = TRUE, log.p = FALSE)

qMN3(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qMN4(p, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qMN5(p, mu = 1, sigma = 1, nu = 1, tau = 1, lower.tail = TRUE, log.p = FALSE)

rMN3(n, mu = 1, sigma = 1)
rMN4(n, mu = 1, sigma = 1, nu = 1)
rMN5(n, mu = 1, sigma = 1, nu = 1, tau = 1)
```

Arguments

<code>mu.link</code>	the link function for mu
<code>sigma.link</code>	the link function for sigma
<code>nu.link</code>	the link function for nu
<code>tau.link</code>	the link function for tau
<code>x</code>	the x variable
<code>q</code>	vector of quantiles
<code>p</code>	vector of probabilities
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$.
<code>log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$.
<code>log</code>	logical; if TRUE, probabilities p are given as $\log(p)$.
<code>n</code>	the number of observations

<code>mu</code>	the mu parameter
<code>sigma</code>	the sigma parameter
<code>nu</code>	the nu parameter
<code>tau</code>	the tau parameter
<code>type</code>	permitted values are 2 (Binomial), 3, 4, and 5
<code>model</code>	a gamlss multinomial fitted model

Details

GAMLSS is in general not suitable for multinomial regression. Nevertheless multinomial regression can be fitted within GAMLSS if the response variable y has less than five categories. The function here provide the facilities to do so. The functions `MN3()`, `MN4()` and `MN5()` fit multinomial responses with 3, 4 and 5 categories respectively. The function `MULTIN()` can be used instead of `codeMN3()`, `MN4()` and `MN5()` by specifying the number of levels of the response. Note that `MULTIN(2)` will produce a binomial fit.

Value

returns a `gamlss.family` object which can be used to fit a binomial distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Vlasios Voudouris

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BI](#)

Examples

```
dMN3(3)
pMN3(2)
qMN3(.6)
rMN3(10)
```

momentSK

Sample and theoretical Moment and Centile Skewness and Kurtosis Functions

Description

The functions `momentSK()`, `centileSK()`, `centileSkew()` and `centileKurt()`, calculate sample statistics related to skewness and kurtosis. The function `theoCentileSK()` calculates the theoretical centile statistics from a given `gamlss.family` distribution. The `plotCentileSK()` plots the theoretical centile skewness and kurtosis against `p` (see below).

The function `checkMomentSK()` can be use to check (a) whether the moment skewness and kurtosis of a fitted model are modelled adequately (the residuals of the model are used). (b) whether a given sample display skewness or kurtosis.

Usage

```
momentSK(x, weights=NULL)
centileSK(x, cent = c(1, 25), weights=NULL)
centileSkew(x, cent = 1, weights=NULL)
centileKurt(x, cent = 1, weights=NULL)

theoCentileSK(fam = "NO", p = 0.01, ...)
plotCentileSK(fam = "NO", plotting = c("skew", "kurt", "standKurt"),
              add = FALSE, col = 1, lty = 1, lwd = 1, ylim = NULL, ...)

checkMomentSK(x, weights=NULL, add = FALSE, bootstrap = TRUE, no.bootstrap = 99,
              col.bootstrap = "lightblue", pch.bootstrap = 21,
              asCharacter = TRUE, col.point = "black", pch.point = 4,
              lwd.point = 2, text.to.show = NULL, cex.text = 1.5,
              col.text = "black", show.legend = TRUE)

checkCentileSK(x, weights=NULL, type = c("central", "tail"), add = FALSE,
              bootstrap = TRUE, no.bootstrap = 99,
              col.bootstrap = "lightblue", pch.bootstrap = 21,
              asCharacter = TRUE, col.point = "black", pch.point = 4,
              lwd.point = 2, text.to.show = NULL, cex.text = 1.5,
              col.text = "black", show.legend = TRUE)
```

Arguments

<code>x</code>	data vector or gamlss model
<code>weights</code>	prior weights for the x
<code>cent</code>	the centile required
<code>type</code>	For centile skewness and kurtosis only whether "central" (default) or "tail"
<code>fam</code>	A gamlss distribution family
<code>plotting</code>	what to plot
<code>add</code>	whether to add the line to the existing plot
<code>col</code>	the colour of the line
<code>lty</code>	the type of the line
<code>lwd</code>	the width of the line
<code>ylim</code>	the y limit of the graph
<code>p</code>	the value determining the centile skewness or kurtosis
<code>...</code>	additional arguments pass to <code>theoCentileSK()</code> function i.e. the values of the distribution parameters
<code>bootstrap</code>	whether a plot of the bootstrap skewness and kurtosis measures should be added in the plot
<code>no.bootstrap</code>	the number of bootstrap skewness and kurtosis measures
<code>col.bootstrap</code>	the colour for bootstraps
<code>pch.bootstrap</code>	the point type of bootstraps
<code>asCharacter</code>	whether to plot the estimated skewness and kurtosis measure as character or as point
<code>col.point</code>	the colour of the skewness and kurtosis measure
<code>pch.point</code>	the point type of the skewness and kurtosis measure
<code>lwd.point</code>	the width of the plotted point
<code>text.to.show</code>	to display text different from variable or model
<code>cex.text</code>	the size of the text
<code>col.text</code>	the colour of the text
<code>show.legend</code>	whether to show the legend

Details

Those function calculate sample moment and centile skewness and kurtosis statistics and theoretical centile values for a specific distribution.

Value

Different functions produce different output: The function `momentSK()` produce:

`mom.skew:` sample moment skewness

trans.mom.skew: sample transformed moment skewness
 mom.kurt: sample moment kurtosis
 excess.mom.kurt: sample excess moment kurtosis
 trans.mom.kurt: sample transformed moment excess kurtosis
 jarque.bera.test: the value of the Jarque-Bera test for testing whether skewness and excess kurtosis are zero or not

The function centileSK() produces:

S0.25: sample centile central skewness
 S0.01: sample centile tail skewness
 K0.01: sample centile kurtosis
 standK0.01: standardised centile kurtosis, $(K0.01/3.449)$
 exc.K0.01: excess centile kurtosis, $(K0.01-3.449)$
 trans.K0.01: transformed excess centile kurtosis, $(exc.K0.01/(1+abs(exc.K0.01)))$

The function centileSkew() for a given argument p produces:

p: the value determining the centile skewness
 Sp: sample centile skewness at p

The function centileKurt() for a given argument p produces:

p: the value determining the centile kurtosis
 Kp: sample centile kurtosis at p
 sKp: sample standardised centile kurtosis at p
 ex.Kp: sample excess centile kurtosis at p
 teKp: sample transformed excess centile kurtosis at p

The function theoCentileSK for a given gamlss.family produces:

IR: the interquartile range of the distribution
 SIR: the semi interquartile range of the distribution
 S_0.25: the central skewness of the distribution
 S_0.01: the tail skewness of the distribution
 K_0.01: the centile kurtosis of the distribution
 sK_0.01: the standardised centile kurtosis of the distribution

Author(s)

Mikis Stasinopoulos, Robert Rigby, Gillain Heller and Fernanda De Bastiani.

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
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See Also

[gamlss.family](#)

Examples

```
Y <- rSEP3(1000)
momentSK(Y)
centileSK(Y)
centileSkew(Y, cent=20)
centileKurt(Y, cent=30)

theoCentileSK("BCCG", mu=2, sigma=.2, nu=2)
plotCentileSK(fam="BCCG", mu=2, sigma=.2, nu=2)

checkMomentSK(Y)
checkCentileSK(Y)
checkCentileSK(Y, type="tail")
```

NBF

Negative Binomial Family distribution for fitting a GAMLSS

Description

The `NBF()` function defines the Negative Binomial family distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dnBF`, `pnBF`, `qnBF` and `rnBF` define the density, distribution function, quantile function and random generation for the negative binomial family, `NBF()`, distribution.

The functions `dZINBF`, `pZINBF`, `qZINBF` and `rZINBF` define the density, distribution function, quantile function and random generation for the zero inflated negative binomial family, `ZINBF()`, distribution a four parameter distribution.

Usage

```

NBF(mu.link = "log", sigma.link = "log", nu.link = "log")

dNBF(x, mu = 1, sigma = 1, nu = 2, log = FALSE)

pNBF(q, mu = 1, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)

qNBF(p, mu = 1, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)

rNBF(n, mu = 1, sigma = 1, nu = 2)

ZINBF(mu.link = "log", sigma.link = "log", nu.link = "log",
      tau.link = "logit")

dZINBF(x, mu = 1, sigma = 1, nu = 2, tau = 0.1, log = FALSE)

pZINBF(q, mu = 1, sigma = 1, nu = 2, tau = 0.1, lower.tail = TRUE,
      log.p = FALSE)

qZINBF(p, mu = 1, sigma = 1, nu = 2, tau = 0.1, lower.tail = TRUE,
      log.p = FALSE)

rZINBF(n, mu = 1, sigma = 1, nu = 2, tau = 0.1)

```

Arguments

<code>mu.link</code>	The link function for μ
<code>sigma.link</code>	The link function for σ
<code>nu.link</code>	The link function for ν
<code>tau.link</code>	The link function for τ
<code>x</code>	vector of (non-negative integer)
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of power parameter
<code>tau</code>	vector of inflation parameter
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return

Details

The definition for Negative Binomial Family distribution, NBF, is similar to the Negative Binomial type I. The probability function of the NBF can be obtained by replacing σ with $\sigma\mu^{\nu-2}$ where ν is a power parameter. The distribution has mean μ and variance $\mu + \sigma\mu^\nu$.

Value

returns a `gamlss.family` object which can be used to fit a Negative Binomial Family distribution in the `gamlss()` function.

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

Anscombe, F. J. (1950) Sampling theory of the negative binomial and logarithmic distributions, *Biometrika*, **37**, 358-382.

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[NBI](#), [NBII](#)

Examples

```
NBF() # default link functions for the Negative Binomial Family
# plotting the distribution
plot(function(y) dNBF(y, mu = 10, sigma = 0.5, nu=2 ), from=0,
      to=40, n=40+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rNBF(1000, mu=5, sigma=0.5, nu=2))
r <- barplot(tN, col='lightblue')
# zero inflated NBF
ZINBF() # default link functions for the zero inflated NBF
# plotting the distribution
plot(function(y) dZINBF(y, mu = 10, sigma = 0.5, nu=2, tau=.1 ),
      from=0, to=40, n=40+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rZINBF(1000, mu=5, sigma=0.5, nu=2, tau=0.1))
r <- barplot(tN, col='lightblue')
## Not run:
library(gamlss)
data(species)
species <- transform(species, x=log(lake))
m6 <- gamlss(fish~poly(x,2), sigma.fo=~1, data=species, family=NBF,
             n.cyc=200)
fitted(m6, "nu")[1]
```

```
## End(Not run)
```

NBI

Negative Binomial type I distribution for fitting a GAMLSS

Description

The `NBI()` function defines the Negative Binomial type I distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dnBI`, `pnBI`, `qnBI` and `rnBI` define the density, distribution function, quantile function and random generation for the Negative Binomial type I, `NBI()`, distribution.

Usage

```
NBI(mu.link = "log", sigma.link = "log")
dnBI(x, mu = 1, sigma = 1, log = FALSE)
pnBI(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qnBI(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rnBI(n, mu = 1, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of positive dispersion parameter
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Definition file for Negative Binomial type I distribution.

$$P(Y = y | \mu, \sigma) = \frac{\Gamma(y + \frac{1}{\sigma})}{\Gamma(\frac{1}{\sigma})\Gamma(y + 1)} \left(\frac{\sigma\mu}{1 + \sigma\mu} \right)^y \left(\frac{1}{1 + \sigma\mu} \right)^{1/\sigma}$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$ and $\sigma > 0$. This parameterization is equivalent to that used by Anscombe (1950) except he used $\alpha = 1/\sigma$ instead of σ .

Value

returns a `gamlss.family` object which can be used to fit a Negative Binomial type I distribution in the `gamlss()` function.

Warning

For values of $\sigma < 0.0001$ the `d,p,q,r` functions switch to the Poisson distribution

Note

μ is the mean and $(\mu + \sigma\mu^2)^{0.5}$ is the standard deviation of the Negative Binomial type I distribution (so σ is the dispersion parameter in the usual GLM for the negative binomial type I distribution)

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

Anscombe, F. J. (1950) Sampling theory of the negative binomial and logarithmic distributiona, *Biometrika*, **37**, 358-382.

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NBII](#), [PIG](#), [SI](#)

Examples

```
NBI() # gives information about the default links for the Negative Binomial type I distribution
# plotting the distribution
plot(function(y) dNBI(y, mu = 10, sigma = 0.5 ), from=0, to=40, n=40+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rNBI(1000, mu=5, sigma=0.5))
r <- barplot(tN, col='lightblue')
# library(gamlss)
# data(aids)
# h<-gamlss(y~cs(x,df=7)+qrt, family=NBI, data=aids) # fits the model
```

```
# plot(h)
# pdf.plot(family=NBII, mu=10, sigma=0.5, min=0, max=40, step=1)
```

NBII

Negative Binomial type II distribution for fitting a GAMLSS

Description

The NBII() function defines the Negative Binomial type II distribution, a two parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(). The functions dNBII, pNBII, qNBII and rNBII define the density, distribution function, quantile function and random generation for the Negative Binomial type II, NBII(), distribution.

Usage

```
NBII(mu.link = "log", sigma.link = "log")
dNBII(x, mu = 1, sigma = 1, log = FALSE)
pNBII(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qNBII(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rNBII(n, mu = 1, sigma = 1)
```

Arguments

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter
x	vector of (non-negative integer) quantiles
mu	vector of positive means
sigma	vector of positive dispersion parameter
p	vector of probabilities
q	vector of quantiles
n	number of random values to return
log, log.p	logical; if TRUE, probabilities p are given as log(p)
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]

Details

Definition file for Negative Binomial type II distribution.

$$P(Y = y | \mu, \sigma) = \frac{\Gamma(y + \frac{\mu}{\sigma}) \sigma^y}{\Gamma(\frac{\mu}{\sigma}) \Gamma(y + 1) (1 + \sigma)^{y + \mu/\sigma}}$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$ and $\sigma > 0$. This parameterization was used by Evans (1953) and also by Johnson *et al.* (1993) p 200.

Value

returns a `gamlss.family` object which can be used to fit a Negative Binomial type II distribution in the `gamlss()` function.

Note

μ is the mean and $[(1 + \sigma)\mu]^{0.5}$ is the standard deviation of the Negative Binomial type II distribution, so σ is a dispersion parameter

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NBI](#), [PIG](#), [SI](#)

Examples

```
NBII() # gives information about the default links for the Negative Binomial type II distribution
# plotting the distribution
plot(function(y) dNBII(y, mu = 10, sigma = 0.5 ), from=0, to=40, n=40+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rNBII(1000, mu=5, sigma=0.5))
r <- barplot(tN, col='lightblue')
# library(gamlss)
# data(aids)
# h<-gamlss(y~cs(x,df=7)+qrt, family=NBII, data=aids) # fits a model
# plot(h)
# pdf.plot(family=NBII, mu=10, sigma=0.5, min=0, max=40, step=1)
```

NET

*Normal Exponential t distribution (NET) for fitting a GAMLSS***Description**

This function defines the Power Exponential t distribution (NET), a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dNET`, `pNET` define the density and distribution function the NET distribution.

Usage

```
NET(mu.link = "identity", sigma.link = "log", nu.link = "identity",
    tau.link = "identity")
pNET(q, mu=0, sigma=1, nu=1.5, tau=2, lower.tail = TRUE, log.p = FALSE)
dNET(x, mu=0, sigma=1, nu=1.5, tau=2, log=FALSE)
qNET(p, mu=0, sigma=1, nu=1.5, tau=2, lower.tail = TRUE, log.p = FALSE)
rNET(n, mu=0, sigma=1, nu=1.5, tau=2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. Other links are "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse", "identity" and "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , and because <code>nu</code> is fixed we use "identity" link
<code>tau.link</code>	Defines the <code>tau.link</code> , and because <code>tau</code> is fixed we use "identity" link
<code>x, q</code>	vector of quantiles
<code>p</code>	vector of probabilities
<code>n</code>	number of observations.
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of <code>nu</code> parameter values
<code>tau</code>	vector of <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

The NET distribution was introduced by Rigby and Stasinopoulos (1994) as a robust distribution for a response variable with heavier tails than the normal. The NET distribution is the abbreviation of the Normal Exponential Student t distribution. The NET distribution is a four parameter continuous distribution, although in the GAMLSS implementation only the two parameters, `mu` and `sigma`, of

the distribution are modelled with ν and τ fixed. The distribution takes its names because it is normal up to ν , Exponential from ν to τ (hence $\text{abs}(\nu) \leq \text{abs}(\tau)$) and Student-t with $\nu \cdot \tau - 1$ degrees of freedom after τ . Maximum likelihood estimator of the third and forth parameter can be obtained, using the GAMLSS functions, `find.hyper` or `prof.dev`.

Value

`NET()` returns a `gamlss.family` object which can be used to fit a Box Cox Power Exponential distribution in the `gamlss()` function. `dNET()` gives the density, `pNET()` gives the distribution function.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

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See Also

[gamlss.family](#), [BCPE](#)

Examples

```
NET()  #
data(abdom)
plot(function(x)dNET(x, mu=0,sigma=1,nu=2, tau=3), -5, 5)
plot(function(x)pNET(x, mu=0,sigma=1,nu=2, tau=3), -5, 5)
# fit NET with nu=1 and tau=3
# library(gamlss)
#h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=NET,
#         data=abdom, nu.start=2, tau.start=3)
#plot(h)
```

NO	<i>Normal distribution for fitting a GAMLSS</i>
----	---

Description

The function `NO()` defines the normal distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with mean equal to the parameter `mu` and `sigma` equal the standard deviation. The functions `dNO`, `pNO`, `qNO` and `rNO` define the density, distribution function, quantile function and random generation for the NO parameterization of the normal distribution. [A alternative parameterization with `sigma` equal to the variance is given in the function `NO2()`]

Usage

```
NO(mu.link = "identity", sigma.link = "log")
dNO(x, mu = 0, sigma = 1, log = FALSE)
pNO(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qNO(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rNO(n, mu = 0, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The parametrization of the normal distribution given in the function `NO()` is

$$f(y|\mu, \sigma) = \frac{1}{\sqrt{2\pi}\sigma} \exp \left[-\frac{1}{2} \left(\frac{y - \mu}{\sigma} \right)^2 \right]$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit a normal distribution in the `gamlss()` function.

Note

For the function `NO()`, μ is the mean and σ is the standard deviation (not the variance) of the normal distribution.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

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Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NO2](#)

Examples

```
NO()# gives information about the default links for the normal distribution
plot(function(y) dNO(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) pNO(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) qNO(y, mu=10 ,sigma=2), 0, 1)
dat<-rNO(100)
hist(dat)
# library(gamlss)
# gamlss(dat~1,family=NO) # fits a constant for mu and sigma
```

Description

The function `NO2()` defines the normal distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()` with mean equal to `mu` and variance equal to `sigma`. The functions `dNO2`, `pNO2`, `qNO2` and `rNO2` define the density, distribution function, quantile function and random generation for this specific parameterization of the normal distribution.

[A alternative parameterization with `sigma` as the standard deviation is given in the function `NO()`]

Usage

```
NO2(mu.link = "identity", sigma.link = "log")
dNO2(x, mu = 0, sigma = 1, log = FALSE)
pNO2(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qNO2(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rNO2(n, mu = 0, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parametrization of the normal distribution given in the function `NO2()` is

$$f(y|\mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma}} \exp \left[-\frac{1}{2} \frac{(y - \mu)^2}{\sigma} \right]$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit a normal distribution in the `gamlss()` function.

Note

For the function `NO()`, μ is the mean and σ is the standard deviation (not the variance) of the normal distribution. [The function `NO2()` defines the normal distribution with σ as the variance.]

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NO](#)

Examples

```
NO()# gives information about the default links for the normal distribution
dat<-rNO(100)
hist(dat)
plot(function(y) dNO(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) pNO(y, mu=10 ,sigma=2), 0, 20)
plot(function(y) qNO(y, mu=10 ,sigma=2), 0, 1)
# library(gamlss)
# gamlss(dat~1,family=NO) # fits a constant for mu and sigma
```

Description

The function `NOF()` defines a normal distribution family, which has three parameters. The distribution can be used using the function `gamlss()`. The mean of NOF is equal to μ . The variance is equal to $\sigma^2 \mu^\nu$ so the standard deviation is $\sigma \mu^{\nu/2}$. The function is design for cases where the variance is proportional to a power of the mean. This is an instance of the Taylor's power law, see Enki et al. (2017). The functions `dNOF`, `pNOF`, `qNOF` and `rNOF` define the density, distribution function, quantile function and random generation for the NOF parametrization of the normal distribution family.

Usage

```
NOF(mu.link = "identity", sigma.link = "log", nu.link = "identity")
dNOF(x, mu = 0, sigma = 1, nu = 0, log = FALSE)
pNOF(q, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
qNOF(p, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
rNOF(n, mu = 0, sigma = 1, nu = 0)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> with "identity" link as the default for the <code>nu</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of power parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parametrization of the normal distribution given in the function `NOF()` is

$$f(y|\mu, \sigma, \nu) = \frac{1}{\sqrt{2\pi}\sigma\mu^{\nu/2}} \exp \left[-\frac{1}{2} \frac{(y - \mu)^2}{\sigma^2\mu^\nu} \right]$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, \infty)$, $\sigma > 0$ and $\nu = (-\infty, +\infty)$.

Value

returns a `gamlss.family` object which can be used to fit a normal distribution family in the `gamlss()` function.

Note

For the function `NOF()`, μ is the mean and $\sigma\mu^{\nu/2}$ is the standard deviation of the normal distribution family. The NOF is design for fitting regression type models where the variance is proportional to a power of the mean. Models of this type are also related to the "pseudo likelihood" models of Carroll and Rubert (1987) but here a proper likelihood is maximised.

Note that because the high correlation between the `sigma` and the `nu` parameter the `mixed()` method should be used in the fitting.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [N0](#), [N02](#)

Examples

```
NOF()# gives information about the default links for the normal distribution family
## Not run:
## the normal distribution, fitting a constant sigma
m1<-gamlss(y~poly(x,2), sigma.fo=~1, family=N0, data=abdom)
## the normal family, fitting a variance proportional to the mean (mu)
m2<-gamlss(y~poly(x,2), sigma.fo=~1, family=NOF, data=abdom, method=mixed(1,20))
## the normal distribution fitting the variance as a function of x
m3 <-gamlss(y~poly(x,2), sigma.fo=~x, family=N0, data=abdom, method=mixed(1,20))
GAIC(m1,m2,m3)

## End(Not run)
```

Description

The functions `PARETO()` defines the one parameter Pareto distribution for $y > 1$.

The functions `PARETO1()` defines the one parameter Pareto distribution for $y > 0$.

The functions `PARETOo1()` defines the one parameter Pareto distribution for $y > \mu$ therefor requires μ to be fixed.

The functions `PARETO2()` and `PARETO2o()` define the Pareto Type 2 distribution, for $y > 0$, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The parameters are μ and σ in both functions but the parameterisation different. The μ is identical for both `PARETO2()` and `PARETO2o()`. The σ in `PARETO2o()` is the inverse of the σ in `codePARETO2()` and correspond to the usual parameter α of the Pareto distribution. The functions `dPARETO2`, `pPARETO2`, `qPARETO2` and `rPARETO2` define the density, distribution function, quantile function and random generation for the `PARETO2` parameterization of the Pareto type 2 distribution while the functions `dPARETO2o`, `pPARETO2o`, `qPARETO2o` and `rPARETO2o` define the density, distribution function, quantile function and random generation for the original `PARETO2o` parameterization of the Pareto type 2 distribution

Usage

```
PARETO(mu.link = "log")
dPARETO(x, mu = 1, log = FALSE)
pPARETO(q, mu = 1, lower.tail = TRUE, log.p = FALSE)
qPARETO(p, mu = 1, lower.tail = TRUE, log.p = FALSE)
rPARETO(n, mu = 1)

PARETO1(mu.link = "log")
dPARETO1(x, mu = 1, log = FALSE)
pPARETO1(q, mu = 1, lower.tail = TRUE, log.p = FALSE)
qPARETO1(p, mu = 1, lower.tail = TRUE, log.p = FALSE)
rPARETO1(n, mu = 1)

PARETO1o(mu.link = "log", sigma.link = "log")
dPARETO1o(x, mu = 1, sigma = 0.5, log = FALSE)
pPARETO1o(q, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
qPARETO1o(p, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
rPARETO1o(n, mu = 1, sigma = 0.5)

PARETO2(mu.link = "log", sigma.link = "log")
dPARETO2(x, mu = 1, sigma = 0.5, log = FALSE)
pPARETO2(q, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
qPARETO2(p, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
rPARETO2(n, mu = 1, sigma = 0.5)
```

```

PARETO2o(mu.link = "log", sigma.link = "log")
dPARETO2o(x, mu = 1, sigma = 0.5, log = FALSE)
pPARETO2o(q, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
qPARETO2o(p, mu = 1, sigma = 0.5, lower.tail = TRUE, log.p = FALSE)
rPARETO2o(n, mu = 1, sigma = 0.5)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" as the default for the <code>sigma</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the one parameter Pareto distribution in the function `PARETO` is:

$$f(y|\mu) = \mu y^{\mu+1}$$

for $y > 1$ and $\mu > 0$.

The parameterization of the Pareto Type 2 distribution in the function `PARETO2` is:

$$f(y|\mu, \sigma) = \frac{1}{\sigma} \mu^{\frac{1}{\sigma}} (y + \mu)^{-\frac{1}{\sigma+1}}$$

for $y \geq 0$, $\mu > 0$ and $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit a Pareto type 2 distribution in the `gamlss()` function.

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(0.2,20,0.2)
plot(y, dPARET02(y), type="l" , lwd=2)
q<-seq(0,20,0.2)
plot(q, pPARET02(q), ylim=c(0,1), type="l", lwd=2)
p<-seq(0.0001,0.999,0.05)
plot(p, qPARET02(p), type="l", lwd=2)
dat <- rPARET02(100)
hist(rPARET02(100), nclass=30)
#summary(gamlss(a~1, family="PARET02"))
```

PE

Power Exponential distribution for fitting a GAMLSS

Description

The functions define the Power Exponential distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dPE`, `pPE`, `qPE` and `rPE` define the density, distribution function, quantile function and random generation for the specific parameterization of the power exponential distribution showing below. The functions `dPE2`, `pPE2`, `qPE2` and `rPE2` define the density, distribution function, quantile function and random generation of a standard parameterization of the power exponential distribution.

Usage

```

PE(mu.link = "identity", sigma.link = "log", nu.link = "log")
dPE(x, mu = 0, sigma = 1, nu = 2, log = FALSE)
pPE(q, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
qPE(p, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
rPE(n, mu = 0, sigma = 1, nu = 2)
PE2(mu.link = "identity", sigma.link = "log", nu.link = "log")
dPE2(x, mu = 0, sigma = 1, nu = 2, log = FALSE)
pPE2(q, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
qPE2(p, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
rPE2(n, mu = 0, sigma = 1, nu = 2)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of kurtosis parameter
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

Power Exponential distribution (PE) is defined as

$$f(y|\mu, \sigma, \nu) = \frac{\nu \exp[-(\frac{1}{2})|\frac{z}{c}|^\nu]}{\sigma c 2^{(1+1/\nu)} \Gamma(\frac{1}{\nu})}$$

where $c = [2^{-2/\nu} \Gamma(1/\nu) / \Gamma(3/\nu)]^{0.5}$, for $y = (-\infty, +\infty)$, $\mu = (-\infty, +\infty)$, $\sigma > 0$ and $\nu > 0$. This parametrization was used by Nelson (1991) and ensures μ is the mean and σ is the standard deviation of y (for all parameter values of μ , σ and ν within the ranges above)

The Power Exponential distribution (PE2) is defined as

$$f(y|\mu, \sigma, \nu) = \frac{\nu \exp[-|z|^\nu]}{2\sigma \Gamma(\frac{1}{\nu})}$$

Value

returns a `gamlss.family` object which can be used to fit a Power Exponential distribution in the `gamlss()` function.

Note

μ is the mean and σ is the standard deviation of the Power Exponential distribution

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

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Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BCPE](#)

Examples

```
PE()# gives information about the default links for the Power Exponential distribution
# library(gamlss)
# data(abdom)
# h1<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=PE, data=abdom) # fit
# h2<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=PE2, data=abdom) # fit
# plot(h1)
# plot(h2)
# leptokurtotic
plot(function(x) dPE(x, mu=10,sigma=2,nu=1), 0.0, 20,
     main = "The PE density mu=10,sigma=2,nu=1")
# platykurtotic
plot(function(x) dPE(x, mu=10,sigma=2,nu=4), 0.0, 20,
     main = "The PE density mu=10,sigma=2,nu=4")
```


Description

The PIG() function defines the Poisson-inverse Gaussian distribution, a two parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(). The PIG2() function is a reparametrization of PIG() where mu and sigma are orthogonal see Heller *et al.* (2018).

The functions dPIG, pPIG, qPIG and rPIG define the density, distribution function, quantile function and random generation for the Poisson-inverse Gaussian PIG(), distribution. Also codedPIG2, pPIG2, qPIG2 and rPIG2 are the equivalent functions for codePIG2()

The functions ZAPIG() and ZIPIG() are the zero adjusted (hurdle) and zero inflated versions of the Poisson-inverse Gaussian distribution, respectively. That is three parameter distributions.

The functions dZAPIG, dZIPIG, pZAPIG, pZIPIG, qZAPIG, qZIPIG, rZAPIG and rZIPIG define the probability, cumulative, quantile and random generation functions for the zero adjusted and zero inflated Poisson Inverse Gaussian distributions, ZAPIG(), ZIPIG(), respectively.

Usage

```
PIG(mu.link = "log", sigma.link = "log")
dPIG(x, mu = 1, sigma = 1, log = FALSE)
pPIG(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qPIG(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
rPIG(n, mu = 1, sigma = 1, max.value = 10000)

PIG2(mu.link = "log", sigma.link = "log")
dPIG2(x, mu=0.5, sigma=0.02, log = FALSE)
pPIG2(q, mu=0.5, sigma=0.02, lower.tail = TRUE, log.p = FALSE)
qPIG2(p, mu=0.5, sigma=0.02, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
rPIG2(n, mu=0.5, sigma=0.02)

ZIPIG(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZIPIG(x, mu = 1, sigma = 1, nu = 0.3, log = FALSE)
pZIPIG(q, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
qZIPIG(p, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
rZIPIG(n, mu = 1, sigma = 1, nu = 0.3, max.value = 10000)

ZAPIG(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZAPIG(x, mu = 1, sigma = 1, nu = 0.3, log = FALSE)
pZAPIG(q, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
qZAPIG(p, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
```

```
rZAPIG(n, mu = 1, sigma = 1, nu = 0.3, max.value = 10000)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>nu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of zero probability parameter
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>max.value</code>	a constant, set to the default value of 10000 for how far the algorithm should look for <code>q</code>

Details

The probability function of the Poisson-inverse Gaussian distribution, is given by

$$f(y|\mu, \sigma) = \left(\frac{2\alpha^{\frac{1}{2}}}{\pi} \right) \frac{\mu^y e^{\frac{1}{\sigma}} K_{y-\frac{1}{2}}(\alpha)}{(\alpha\sigma)^y y!}$$

where $\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu}{\sigma}$, for $y = 0, 1, 2, \dots, \infty$ where $\mu > 0$ and $\sigma > 0$ and $K_\lambda(t) = \frac{1}{2} \int_0^\infty x^{\lambda-1} \exp\{-\frac{1}{2}t(x+x^{-1})\}dx$ is the modified Bessel function of the third kind. [Note that the above parameterization was used by Dean, Lawless and Willmot(1989). It is also a special case of the Sichel distribution $SI()$ when $\nu = -\frac{1}{2}$.]

Value

Returns a `gamlss.family` object which can be used to fit a Poisson-inverse Gaussian distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Marco Enea

References

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See Also

[gamlss.family](#), [NBI](#), [NBII](#), [SI](#), [SICHEL](#)

Examples

```
PIG()# gives information about the default links for the Poisson-inverse Gaussian distribution
#plot the pdf using plot
plot(function(y) dPIG(y, mu=10, sigma = 1 ), from=0, to=50, n=50+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=50),pPIG(seq(from=0,to=50), mu=10, sigma=1), type="h") # cdf
# generate random sample
tN <- table(Ni <- rPIG(100, mu=5, sigma=1))
r <- barplot(tN, col='lightblue')
# fit a model to the data
# library(gamlss)
# gamlss(Ni~1,family=PIG)
ZIPIG()
ZAPIG()
```

PO

Poisson distribution for fitting a GAMLSS model

Description

This function PO defines the Poisson distribution, an one parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dPO`, `pPO`, `qPO` and `rPO` define the density, distribution function, quantile function and random generation for the Poisson, `PO()`, distribution.

Usage

```
PO(mu.link = "log")
dPO(x, mu = 1, log = FALSE)
pPO(q, mu = 1, lower.tail = TRUE, log.p = FALSE)
qPO(p, mu = 1, lower.tail = TRUE, log.p = FALSE)
rPO(n, mu = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Definition file for Poisson distribution.

$$f(y|\mu) = \frac{e^{-\mu} \mu^y}{\Gamma(y+1)}$$

for $y = 0, 1, 2, \dots$ and $\mu > 0$.

Value

returns a `gamlss.family` object which can be used to fit a Poisson distribution in the `gamlss()` function.

Note

μ is the mean of the Poisson distribution

Author(s)

Bob Rigby, Mikis Stasinopoulos, and Kalliope Akantziliotou

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NBI](#), [NBII](#), [SI](#), [SICHEL](#)

Examples

```
P0()# gives information about the default links for the Poisson distribution
# fitting data using P0()

# plotting the distribution
plot(function(y) dP0(y, mu=10 ), from=0, to=20, n=20+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rP0(1000, mu=5))
r <- barplot(tN, col='lightblue')
# library(gamlss)
# data(aids)
# h<-gamlss(y~cs(x,df=7)+qrt, family=P0, data=aids) # fits the constant+x+qrt model
# plot(h)
# pdf.plot(family=P0, mu=10, min=0, max=20, step=1)
```

RG

The Reverse Gumbel distribution for fitting a GAMLSS

Description

The function RG defines the reverse Gumbel distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dRG`, `pRG`, `qRG` and `rRG` define the density, distribution function, quantile function and random generation for the specific parameterization of the reverse Gumbel distribution.

Usage

```
RG(mu.link = "identity", sigma.link = "log")
dRG(x, mu = 0, sigma = 1, log = FALSE)
pRG(q, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qRG(p, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rRG(n, mu = 0, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. other available link is "inverse", "log" and "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter, other links are the "inverse", "identity" and "own"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The specific parameterization of the reverse Gumbel distribution used in RG is

$$f(y|\mu, \sigma) = \frac{1}{\sigma} \exp \left\{ - \left(\frac{y - \mu}{\sigma} \right) - \exp \left[- \frac{(y - \mu)}{\sigma} \right] \right\}$$

for $y = (-\infty, \infty)$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$.

Value

`RG()` returns a `gamlss.family` object which can be used to fit a Gumbel distribution in the `gamlss()` function. `dRG()` gives the density, `pGU()` gives the distribution function, `qRG()` gives the quantile function, and `rRG()` generates random deviates.

Note

The mean of the distribution is $\mu + 0.57722\sigma$ and the variance is $\pi^2\sigma^2/6$.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
plot(function(x) dRG(x, mu=0,sigma=1), -3, 6,
      main = "{Reverse Gumbel density mu=0,sigma=1}")
RG()# gives information about the default links for the Gumbel distribution
dat<-rRG(100, mu=10, sigma=2) # generates 100 random observations
# library(gamlss)
# gamlss(dat~1,family=RG) # fits a constant for each parameter mu and sigma
```

RGE	<i>Reverse generalized extreme family distribution for fitting a GAMLSS</i>
-----	---

Description

The function RGE defines the reverse generalized extreme family distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dRGE`, `pRGE`, `qRGE` and `rRGE` define the density, distribution function, quantile function and random generation for the specific parameterization of the reverse generalized extreme distribution given in details below.

Usage

```
RGE(mu.link = "identity", sigma.link = "log", nu.link = "log")
dRGE(x, mu = 1, sigma = 0.1, nu = 1, log = FALSE)
pRGE(q, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qRGE(p, mu = 1, sigma = 0.1, nu = 1, lower.tail = TRUE, log.p = FALSE)
rRGE(n, mu = 1, sigma = 0.1, nu = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values

<code>nu</code>	vector of the shape parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

Definition file for reverse generalized extreme family distribution.

The probability density function of the generalized extreme value distribution is obtained from Johnson *et al.* (1995), Volume 2, p76, equation (22.184) [where $(\xi, \theta, \gamma) \rightarrow (\mu, \sigma, \nu)$].

The probability density function of the reverse generalized extreme value distribution is then obtained by replacing y by $-y$ and μ by $-\mu$.

Hence the probability density function of the reverse generalized extreme value distribution with $\nu > 0$ is given by

$$f(y|\mu, \sigma, \nu) = \frac{1}{\sigma} \left[1 + \frac{\nu(y - \mu)}{\sigma} \right]^{\frac{1}{\nu} - 1} S_1(y|\mu, \sigma, \nu)$$

for

$$\mu - \frac{\sigma}{\nu} < y < \infty$$

where

$$S_1(y|\mu, \sigma, \nu) = \exp \left\{ - \left[1 + \frac{\nu(y - \mu)}{\sigma} \right]^{\frac{1}{\nu}} \right\}$$

and where $-\infty < \mu < y + \frac{\sigma}{\nu}$, $\sigma > 0$ and $\nu > 0$. Note that only the case $\nu > 0$ is allowed here. The reverse generalized extreme value distribution is denoted as $\text{RGE}(\mu, \sigma, \nu)$ or as $\text{Reverse Generalized.Extreme.Family}(\mu, \sigma, \nu)$.

Note the the above distribution is a reparameterization of the three parameter Weibull distribution given by

$$f(y|\alpha_1, \alpha_2, \alpha_3) = \frac{\alpha_3}{\alpha_2} \left[\frac{y - \alpha_1}{\alpha_2} \right]^{\alpha_3 - 1} \exp \left[- \left(\frac{y - \alpha_1}{\alpha_2} \right)^{\alpha_3} \right]$$

given by setting $\alpha_1 = \mu - \sigma/\nu$, $\alpha_2 = \sigma/\nu$, $\alpha_3 = 1/\nu$.

Value

`RGE()` returns a `gamlss.family` object which can be used to fit a reverse generalized extreme distribution in the `gamlss()` function. `drGE()` gives the density, `prGE()` gives the distribution function, `qrGE()` gives the quantile function, and `rRGE()` generates random deviates.

Note

This distribution is very difficult to fit because the y values depends on the parameter values. The `RS()` and `CG()` algorithms are not appropriate for this type of problem.

Author(s)

Bob Rigby, Mikis Stasinopoulos and Kalliope Akantziliotou

References

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Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
RGE()# default links for the reverse generalized extreme family distribution
newdata<-rRGE(100,mu=0,sigma=1,nu=5) # generates 100 random observations
# library(gamlss)
# gamlss(newdata~1, family=RGE, method=mixed(5,50)) # difficult to converse
```

Description

This function defines the Skew Power exponential (SEP) distribution, a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dSEP`, `pSEP`, `qSEP` and `rSEP` define the density, distribution function, quantile function and random generation for the Skew Power exponential (SEP) distribution.

Usage

```

SEP(mu.link = "identity", sigma.link = "log", nu.link = "identity",
    tau.link = "log")
dSEP(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pSEP(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
    log.p = FALSE)
qSEP(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
    log.p = FALSE, lower.limit = mu - 5 * sigma,
    upper.limit = mu + 5 * sigma)
rSEP(n, mu = 0, sigma = 1, nu = 0, tau = 2)

```

Arguments

mu.link	Defines the mu.link, with "identity" link as the default for the mu parameter. Other links are "1/mu ² " and "log"
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter. Other links are "inverse" and "identity"
nu.link	Defines the nu.link, with "identity" link as the default for the nu parameter. Other links are "1/nu ² " and "log"
tau.link	Defines the tau.link, with "log" link as the default for the tau parameter. Other links are "1/tau ² ", and "identity"
x,q	vector of quantiles
mu	vector of location parameter values
sigma	vector of scale parameter values
nu	vector of skewness nu parameter values
tau	vector of kurtosis tau parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required
lower.limit	lower limit for the golden search to find quantiles from probabilities
upper.limit	upper limit for the golden search to find quantiles from probabilities

Details

The probability density function of the Skew Power exponential distribution, (SEP), is defined as

$$f(y|n, \mu, \sigma, \nu, \tau) == \frac{z}{\sigma} \Phi(\omega) f_{EP}(z, 0, 1, \tau)$$

for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$. where $z = \frac{y-\mu}{\sigma}$, $\omega = \text{sign}(z)|z|^{\tau/2}\nu\sqrt{2/\tau}$ and $f_{EP}(z, 0, 1, \tau)$ is the pdf of an Exponential Power distribution.

Value

SEP() returns a `gamlss.family` object which can be used to fit the SEP distribution in the `gamlss()` function. `dSEP()` gives the density, `pSEP()` gives the distribution function, `qSEP()` gives the quantile function, and `rSEP()` generates random deviates.

Warning

The `qSEP` and `rSEP` are slow since they are relying on golden section for finding the quantiles

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

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- (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
SEP() #
plot(function(x)dSEP(x, mu=0,sigma=1, nu=1, tau=2), -5, 5,
      main = "The SEP density mu=0,sigma=1,nu=1, tau=2")
plot(function(x) pSEP(x, mu=0,sigma=1,nu=1, tau=2), -5, 5,
      main = "The BCPE cdf mu=0, sigma=1, nu=1, tau=2")
dat <- rSEP(100,mu=10,sigma=1,nu=-1,tau=1.5)
# library(gamlss)
# gamlss(dat~1,family=SEP, control=gamlss.control(n.cyc=30))
```

SEPI	<i>The Skew Power exponential type 1-4 distribution for fitting a GAMLSS</i>
------	--

Description

These functions define the Skew Power exponential type 1 to 4 distributions. All of them are four parameter distributions and can be used to fit a GAMLSS model. The functions dSEP1, dSEP2, dSEP3 and dSEP4 define the probability distribution functions, the functions pSEP1, pSEP2, pSEP3 and pSEP4 define the cumulative distribution functions the functions qSEP1, qSEP2, qSEP3 and qSEP4 define the inverse cumulative distribution functions and the functions rSEP1, rSEP2, rSEP3 and rSEP4 define the random generation for the Skew exponential power distributions.

Usage

```
SEP1(mu.link = "identity", sigma.link = "log", nu.link = "identity",
     tau.link = "log")
dSEP1(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pSEP1(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
qSEP1(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
rSEP1(n, mu = 0, sigma = 1, nu = 0, tau = 2)

SEP2(mu.link = "identity", sigma.link = "log", nu.link = "identity",
     tau.link = "log")
dSEP2(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pSEP2(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
qSEP2(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
rSEP2(n, mu = 0, sigma = 1, nu = 0, tau = 2)

SEP3(mu.link = "identity", sigma.link = "log", nu.link = "log",
     tau.link = "log")
dSEP3(x, mu = 0, sigma = 1, nu = 2, tau = 2, log = FALSE)
pSEP3(q, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
qSEP3(p, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
     log.p = FALSE)

SEP4(mu.link = "identity", sigma.link = "log", nu.link = "log",
     tau.link = "log")
dSEP4(x, mu = 0, sigma = 1, nu = 2, tau = 2, log = FALSE)
pSEP4(q, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
qSEP4(p, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
```

```
log.p = FALSE)
rSEP4(n, mu = 0, sigma = 1, nu = 2, tau = 2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter. Other links are "inverse" and "log"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter. Other links are "inverse" and "identity"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter. Other links are "identity" and "inverse"
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter. Other links are "inverse", and "identity"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <code>nu</code> parameter values
<code>tau</code>	vector of kurtosis <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the Skew Power exponential distribution type 2, (SEP2), is defined as

$$f_Y(y|\mu, \sigma, \nu, \tau) = \frac{\nu}{\sigma(1+\nu^2)2^{1/\tau}\Gamma(1+1/\tau)} \left\{ \exp\left(-\frac{1}{2}\left|\frac{\nu(y-\mu)}{\sigma}\right|^\tau\right) I(y < \mu) + \exp\left(-\frac{1}{2}\left|\frac{(y-\mu)}{\sigma\nu}\right|^\tau\right) I(y \geq \mu) \right\}$$

for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu > 0$ and $\tau > 0$.

Value

`SEP2()` returns a `gamlss.family` object which can be used to fit the SEP2 distribution in the `gamlss()` function. `dSEP2()` gives the density, `pSEP2()` gives the distribution function, `qSEP2()` gives the quantile function, and `rSEP2()` generates random deviates.

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [SEP](#)

Examples

```
SEP1()
curve(dSEP4(x, mu=5 ,sigma=1, nu=2, tau=1.5), -2, 10,
      main = "The SEP4 density mu=5 ,sigma=1, nu=1, tau=1.5")
# library(gamlss)
#y<- rSEP4(100, mu=5, sigma=1, nu=2, tau=1.5);hist(y)
#m1<-gamlss(y~1, family=SEP1, n.cyc=50)
#m2<-gamlss(y~1, family=SEP2, n.cyc=50)
#m3<-gamlss(y~1, family=SEP3, n.cyc=50)
#m4<-gamlss(y~1, family=SEP4, n.cyc=50)
#GAIC(m1,m2,m3,m4)
```

SHASH

The Sinh-Arcsinh (SHASH) distribution for fitting a GAMLSS

Description

The Sinh-Arcsinh (SHASH) distribution is a four parameter distribution, for a `gamlss.family` object to be used for a GAMLSS fitting using the function `gamlss()`. The functions `dSHASH`, `pSHASH`, `qSHASH` and `rSHASH` define the density, distribution function, quantile function and random generation for the Sinh-Arcsinh (SHASH) distribution.

There are 3 different SHASH distributions implemented in GAMLSS.

Usage

```

SHASH(mu.link = "identity", sigma.link = "log", nu.link = "log",
      tau.link = "log")
dSHASH(x, mu = 0, sigma = 1, nu = 0.5, tau = 0.5, log = FALSE)
pSHASH(q, mu = 0, sigma = 1, nu = 0.5, tau = 0.5, lower.tail = TRUE,
      log.p = FALSE)
qSHASH(p, mu = 0, sigma = 1, nu = 0.5, tau = 0.5, lower.tail = TRUE,
      log.p = FALSE)
rSHASH(n, mu = 0, sigma = 1, nu = 0.5, tau = 0.5)

SHASHo(mu.link = "identity", sigma.link = "log", nu.link = "identity",
      tau.link = "log")
dSHASHo(x, mu = 0, sigma = 1, nu = 0, tau = 1, log = FALSE)
pSHASHo(q, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE,
      log.p = FALSE)
qSHASHo(p, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE,
      log.p = FALSE)
rSHASHo(n, mu = 0, sigma = 1, nu = 0, tau = 1)

SHASHo2(mu.link = "identity", sigma.link = "log", nu.link = "identity",
      tau.link = "log")
dSHASHo2(x, mu = 0, sigma = 1, nu = 0, tau = 1, log = FALSE)
pSHASHo2(q, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE,
      log.p = FALSE)
qSHASHo2(p, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE,
      log.p = FALSE)
rSHASHo2(n, mu = 0, sigma = 1, nu = 0, tau = 1)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter.
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter.
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <code>nu</code> parameter values
<code>tau</code>	vector of kurtosis <code>tau</code> parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The probability density function of the Sinh-Arcsinh distribution, (SHASH), Jones(2005), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = \frac{c}{\sqrt{2\pi}\sigma(1+z^2)^{1/2}} e^{-r^2/2}$$

where

$$r = \frac{1}{2} \{ \exp [\tau \sinh^{-1}(z)] - \exp [-\nu \sinh^{-1}(z)] \}$$

and

$$c = \frac{1}{2} \{ \tau \exp [\tau \sinh^{-1}(z)] + \nu \exp [-\nu \sinh^{-1}(z)] \}$$

and $z = (y - \mu)/\sigma$ for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu > 0$ and $\tau > 0$.

The parameters μ and σ are the location and scale of the distribution. The parameter ν determines the left hand tail of the distribution with $\nu > 1$ indicating a lighter tail than the normal and $\nu < 1$ heavier tail than the normal. The parameter τ determines the right hand tail of the distribution in the same way.

The second form of the Sinh-Arcsinh distribution can be found in Jones and Pewsey (2009, p.2) denoted by SHASHo and the probability density function is defined as,

$$f(y|\mu, \sigma, \nu, \tau) = \frac{\tau}{\sigma} \frac{c}{\sqrt{2\pi}} \frac{1}{2\sqrt{1+z^2}} \exp\left(-\frac{r^2}{2}\right)$$

where

$$r = \sinh(\tau \arcsin(z) - \nu)$$

and

$$c = \cosh(\tau \arcsin(z) - \nu)$$

and $z = (y - \mu)/\sigma$ for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$.

The third form of the Sinh-Arcsinh distribution (Jones and Pewsey, 2009, p.8) divides the distribution by sigma for the density of the unstandardized variable. This distribution is denoted by SHASHo2 and has pdf

$$f(y|\mu, \sigma, \nu, \tau) = \frac{c}{\sigma} \frac{\tau}{\sqrt{2\pi}} \frac{1}{\sqrt{1+z^2}} \exp\left(-\frac{r^2}{2}\right)$$

where $z = (y - \mu)/(\sigma\tau)$, with r and c as for the pdf of the SHASHo distribution, for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$.

Value

SHASH() returns a `gamlss.family` object which can be used to fit the SHASH distribution in the `gamlss()` function. `dSHASH()` gives the density, `pSHASH()` gives the distribution function, `qSHASH()` gives the quantile function, and `rSHASH()` generates random deviates.

Warning

The `qSHASH` and `rSHASH` are slow since they are relying on golden section for finding the quantiles

Author(s)

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See Also

[gamlss.family](#), [JSU](#), [BCT](#)

Examples

```
SHASH() #
plot(function(x)dSHASH(x, mu=0,sigma=1, nu=1, tau=2), -5, 5,
      main = "The SHASH density mu=0,sigma=1,nu=1, tau=2")
plot(function(x) pSHASH(x, mu=0,sigma=1,nu=1, tau=2), -5, 5,
      main = "The BCPE cdf mu=0, sigma=1, nu=1, tau=2")
dat<-rSHASH(100,mu=10,sigma=1,nu=1,tau=1.5)
hist(dat)
# library(gamlss)
# gamlss(dat~1,family=SHASH, control=gamlss.control(n.cyc=30))
```

Description

The `SI()` function defines the Sichel distribution, a three parameter discrete distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dSI`, `pSI`, `qSI` and `rSI` define the density, distribution function, quantile function and random generation for the Sichel `SI()`, distribution.

Usage

```
SI(mu.link = "log", sigma.link = "log", nu.link = "identity")
dSI(x, mu = 0.5, sigma = 0.02, nu = -0.5, log = FALSE)
pSI(q, mu = 0.5, sigma = 0.02, nu = -0.5, lower.tail = TRUE,
    log.p = FALSE)
qSI(p, mu = 0.5, sigma = 0.02, nu = -0.5, lower.tail = TRUE,
    log.p = FALSE, max.value = 10000)
rSI(n, mu = 0.5, sigma = 0.02, nu = -0.5)
tofyS(y, mu, sigma, nu, what = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the <code>nu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive <code>mu</code>
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of <code>nu</code>
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>max.value</code>	a constant, set to the default value of 10000 for how far the algorithm should look for <code>q</code>
<code>y</code>	the <code>y</code> variable. The function <code>tofyS()</code> should be not used on its own.
<code>what</code>	take values 1 or 2, for function <code>tofyS()</code> .

Details

The probability function of the Sichel distribution is given by

$$f(y|\mu, \sigma, \nu) = \frac{\mu^y K_{y+\nu}(\alpha)}{(\alpha\sigma)^{y+\nu} y! K_\nu(\frac{1}{\sigma})}$$

where $\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu}{\sigma}$, for $y = 0, 1, 2, \dots, \infty$ where $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < \infty$ and $K_\lambda(t) = \frac{1}{2} \int_0^\infty x^{\lambda-1} \exp\{-\frac{1}{2}t(x + x^{-1})\} dx$ is the modified Bessel function of the third kind. Note that the above parameterization is different from Stein, Zucchini and Juritz (1988) who use the above probability function but treat μ , α and ν as the parameters. Note that $\sigma = [(\mu^2 + \alpha^2)^{\frac{1}{2}} - \mu]^{-1}$.

Value

Returns a `gamlss.family` object which can be used to fit a Sichel distribution in the `gamlss()` function.

Author(s)

Akantziliotou C., Rigby, R. A., Stasinopoulos D. M. and Marco Enea

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- Stein, G. Z., Zucchini, W. and Juritz, J. M. (1987). Parameter Estimation of the Sichel Distribution and its Multivariate Extension. *Journal of American Statistical Association*, **82**, 938-944.
- (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [PIG](#), [NBI](#), [NBII](#)

Examples

```
SI()# gives information about the default links for the Sichel distribution
#plot the pdf using plot
plot(function(y) dSI(y, mu=10, sigma=1, nu=1), from=0, to=100, n=100+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=100),pSI(seq(from=0,to=100), mu=10, sigma=1, nu=1), type="h") # cdf
# generate random sample
tN <- table(Ni <- rSI(100, mu=5, sigma=1, nu=1))
```

```

r <- barplot(tN, col='lightblue')
# fit a model to the data
# library(gamlss)
# gamlss(Ni~1,family=SI, control=gamlss.control(n.cyc=50))

```

SICHEL

The Sichel distribution for fitting a GAMLSS model

Description

The `SICHEL()` function defines the Sichel distribution, a three parameter discrete distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dSICHEL`, `pSICHEL`, `qSICHEL` and `rSICHEL` define the density, distribution function, quantile function and random generation for the Sichel `SICHEL()`, distribution. The function `VSICHEL` gives the variance of a fitted Sichel model.

The functions `ZASICHEL()` and `ZISICHEL()` are the zero adjusted (hurdle) and zero inflated versions of the Sichel distribution, respectively. That is four parameter distributions.

The functions `dZASICHEL`, `dZISICHEL`, `pZASICHEL`, `pZISICHEL`, `qZASICHEL`, `qZISICHEL`, `rZASICHEL` and `rZISICHEL` define the probability, cumulative, quantile and random generation functions for the zero adjusted and zero inflated Sichel distributions, `ZASICHEL()`, `ZISICHEL()`, respectively.

Usage

```

SICHEL(mu.link = "log", sigma.link = "log", nu.link = "identity")
dSICHEL(x, mu=1, sigma=1, nu=-0.5, log=FALSE)
pSICHEL(q, mu=1, sigma=1, nu=-0.5, lower.tail = TRUE,
        log.p = FALSE)
qSICHEL(p, mu=1, sigma=1, nu=-0.5, lower.tail = TRUE,
        log.p = FALSE, max.value = 10000)
rSICHEL(n, mu=1, sigma=1, nu=-0.5, max.value = 10000)
VSICHEL(obj)
tofySICHEL(y, mu, sigma, nu)

ZASICHEL(mu.link = "log", sigma.link = "log", nu.link = "identity",
        tau.link = "logit")
dZASICHEL(x, mu = 1, sigma = 1, nu = -0.5, tau = 0.1, log = FALSE)
pZASICHEL(q, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,
        lower.tail = TRUE, log.p = FALSE)
qZASICHEL(p, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,
        lower.tail = TRUE, log.p = FALSE, max.value = 10000)
rZASICHEL(n, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,
        max.value = 10000)

ZISICHEL(mu.link = "log", sigma.link = "log", nu.link = "identity",
        tau.link = "logit")
dZISICHEL(x, mu = 1, sigma = 1, nu = -0.5, tau = 0.1, log = FALSE)
pZISICHEL(q, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,

```

```

        lower.tail = TRUE, log.p = FALSE)
qZISICHEL(p, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,
        lower.tail = TRUE, log.p = FALSE, max.value = 10000)
rZISICHEL(n, mu = 1, sigma = 1, nu = -0.5, tau = 0.1,
        max.value = 10000)

```

Arguments

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter
nu.link	Defines the nu.link, with "identity" link as the default for the nu parameter
tau.link	Defines the tau.link, with "logit" link as the default for the tau parameter
x	vector of (non-negative integer) quantiles
mu	vector of positive mu
sigma	vector of positive dispersion parameter sigma
nu	vector of nu
tau	vector of probabilities tau
p	vector of probabilities
q	vector of quantiles
n	number of random values to return
log, log.p	logical; if TRUE, probabilities p are given as log(p)
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
max.value	a constant, set to the default value of 10000 for how far the algorithm should look for q
obj	a fitted Sichel gamlss model
y	the y variable, the tofySICHEL() should not be used on its own.

Details

The probability function of the Sichel distribution is given by

$$f(y|\mu, \sigma, \nu) = \frac{\mu^y K_{y+\nu}(\alpha)}{y! (\alpha\sigma)^{y+\nu} K_\nu(\frac{1}{\sigma})}$$

for $y = 0, 1, 2, \dots, \infty$, $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < \infty$ where

$$\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu}{\sigma}$$

$$c = K_{\nu+1}(1/\sigma)/K_\nu(1/\sigma)$$

and $K_\lambda(t)$ is the modified Bessel function of the third kind. Note that the above parametrization is different from Stein, Zucchini and Juritz (1988) who use the above probability function but treat μ , α and ν as the parameters.

Value

Returns a `gamlss.family` object which can be used to fit a Sichel distribution in the `gamlss()` function.

Note

The mean of the above Sichel distribution is μ and the variance is $\mu^2 \left[\frac{2\sigma(\nu+1)}{c} + \frac{1}{c^2} - 1 \right]$

Author(s)

Rigby, R. A., Stasinopoulos D. M., Akantziliotou C and Marco Enea.

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Rigby, R. A., Stasinopoulos, D. M., & Akantziliotou, C. (2008). A framework for modelling overdispersed count data, including the Poisson-shifted generalized inverse Gaussian distribution. *Computational Statistics & Data Analysis*, 53(2), 381-393.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

Stein, G. Z., Zucchini, W. and Juritz, J. M. (1987). Parameter Estimation of the Sichel Distribution and its Multivariate Extension. *Journal of American Statistical Association*, **82**, 938-944.

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [PIG](#), [SI](#)

Examples

```
SICHEL()# gives information about the default links for the Sichel distribution
#plot the pdf using plot
plot(function(y) dSICHEL(y, mu=10, sigma=1, nu=1), from=0, to=100, n=100+1, type="h") # pdf
# plot the cdf
plot(seq(from=0,to=100),pSICHEL(seq(from=0,to=100), mu=10, sigma=1, nu=1), type="h") # cdf
# generate random sample
tN <- table(Ni <- rSICHEL(100, mu=5, sigma=1, nu=1))
r <- barplot(tN, col='lightblue')
# fit a model to the data
# library(gamlss)
# gamlss(Ni~1,family=SICHEL, control=gamlss.control(n.cyc=50))
```

SIMPLEX

*The simplex distribution for fitting a GAMLSS***Description**

The functions SIMPLEX() define the simplex distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. SIMPLEX() has mean equal to the parameter `mu` and `sigma` as scale parameter, see below. The functions `dSIMPLEX`, `pSIMPLEX`, `qSIMPLEX` and `rSIMPLEX` define the density, cumulative distribution function, quantile function and random generation for the simplex distribution.

Usage

```
SIMPLEX(mu.link = "logit", sigma.link = "log")
dSIMPLEX(x, mu = 0.5, sigma = 1, log = FALSE)
pSIMPLEX(q, mu = 0.5, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qSIMPLEX(p, mu = 0.5, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rSIMPLEX(n = 1, mu = 0.5, sigma = 1)
```

Arguments

<code>mu.link</code>	the mu link function with default <code>logit</code>
<code>sigma.link</code>	the sigma link function with default <code>log</code>
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The simplex distribution is given as

$$f(y|\mu, \sigma) = \frac{1}{(2\pi\sigma^2(y(1-y))^3)^{1/2}} \exp\left(-\frac{1}{2\sigma^2} \frac{(y-\mu)^2}{y(1-y)\mu^2(1-\mu)^2}\right)$$

for y in $(0,1)$, $0 < \mu < 1$ and $\sigma > 0$.

Value

SIMPLEX() returns a `gamlss.family` object which can be used to fit a simplex distribution in the `gamlss()` function.

Author(s)

Bob Rigby, Mikis Stasinopoulos and Fernanda De Bastiani

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

Examples

```
SIMPLEX()# default links for the simplex distribution
plot(function(y) dSIMPLEX(y, mu=.5 ,sigma=1), 0.001, .999)
plot(function(y) pSIMPLEX(y, mu=.5 ,sigma=1), 0.001, 0.999)
plot(function(y) qSIMPLEX(y, mu=.5 ,sigma=1), 0.001, 0.999)
plot(function(y) qSIMPLEX(y, mu=.5 ,sigma=1, lower.tail=FALSE), 0.001, .999)
```

SN1

Skew Normal Type 1 distribution for fitting a GAMLSS

Description

The function SN1() defines the Skew Normal Type 1 distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with parameters `mu`, `sigma` and `nu`. The functions `dSN1`, `pSN1`, `qSN1` and `rSN1` define the density, distribution function, quantile function and random generation for the SN1 parameterization of the Skew Normal Type 1 distribution.

Usage

```
SN1(mu.link = "identity", sigma.link = "log", nu.link="identity")
dSN1(x, mu = 0, sigma = 1, nu = 0, log = FALSE)
pSN1(q, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
qSN1(p, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
rSN1(n, mu = 0, sigma = 1, nu = 0)
```


Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" links the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" as the default for the <code>sigma</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of scale parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the Skew Normal Type 1 distribution in the function SN1 is ...

Value

returns a `gamlss.family` object which can be used to fit a Skew Normal Type 1 distribution in the `gamlss()` function.

Note

This is a special case of the Skew Exponential Power type 1 distribution (SEP1) where $\tau=2$.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fiona McElduff

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(-3,3,0.2)
plot(y, dSN1(y), type="l" , lwd=2)
q<-seq(-3,3,0.2)
plot(q, pSN1(q), ylim=c(0,1), type="l", lwd=2)
p<-seq(0.0001,0.999,0.05)
plot(p, qSN1(p), type="l", lwd=2)
dat <- rSN1(100)
hist(rSN1(100), nclass=30)
```

SN2	<i>Skew Normal Type 2 distribution for fitting a GAMLSS</i>
-----	---

Description

The function SN2() defines the Skew Normal Type 2 distribution, a three parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(), with parameters mu, sigma and nu. The functions dSN2, pSN2, qSN2 and rSN2 define the density, distribution function, quantile function and random generation for the SN2 parameterization of the Skew Normal Type 2 distribution.

Usage

```
SN2(mu.link = "identity", sigma.link = "log", nu.link = "log")
dSN2(x, mu = 0, sigma = 1, nu = 2, log = FALSE)
pSN2(q, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
qSN2(p, mu = 0, sigma = 1, nu = 2, lower.tail = TRUE, log.p = FALSE)
rSN2(n, mu = 0, sigma = 1, nu = 2)
```

Arguments

mu.link	Defines the mu.link, with "identity" links the default for the mu parameter
sigma.link	Defines the sigma.link, with "log" as the default for the sigma parameter
nu.link	Defines the nu.link, with "log" as the default for the sigma parameter
x, q	vector of quantiles
mu	vector of location parameter values
sigma	vector of scale parameter values
nu	vector of scale parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p)

<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The parameterization of the Skew Normal Type 2 distribution in the function SN2 is ...

Value

returns a `gamlss.family` object which can be used to fit a Skew Normal Type 2 distribution in the `gamlss()` function.

Note

This is a special case of the Skew Exponential Power type 3 distribution (SEP3) where $\tau=2$.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fiona McElduff.

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(-3,3,0.2)
plot(y, dSN2(y), type="l" , lwd=2)
q<-seq(-3,3,0.2)
plot(q, pSN2(q), ylim=c(0,1), type="l", lwd=2)
p<-seq(0.0001,0.999,0.05)
plot(p, qSN2(p), type="l", lwd=2)
```

```
dat <- rSN2(100)
hist(rSN2(100), nclass=30)
```

ST1

The skew t distributions, type 1 to 5

Description

There are 5 different skew t distributions implemented in GAMLSS.

The Skew t type 1 distribution, ST1, is based on Azzalini (1986).

The skew t type 2 distribution, ST2, is based on Azzalini and Capitanio (2003).

The skew t type 3, ST3 and ST3C, distribution is based on Fernandez and Steel (1998). The difference between the ST3 and ST3C is that the first is written entirely in R while the second is in C.

The skew t type 4 distribution, ST4, is a spliced-shape distribution.

The skew t type 5 distribution, ST5, is based on Jones and Faddy (2003).

The SST is a reparametrised version of dST3 where sigma is the standard deviation of the distribution.

Usage

```
ST1(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dST1(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pST1(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
qST1(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
rST1(n, mu = 0, sigma = 1, nu = 0, tau = 2)
```

```
ST2(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dST2(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pST2(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
qST2(p, mu = 1, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
rST2(n, mu = 0, sigma = 1, nu = 0, tau = 2)
```

```
ST3(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST3(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST3(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST3(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST3(n, mu = 0, sigma = 1, nu = 1, tau = 10)
```

```
ST3C(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST3C(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST3C(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST3C(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST3C(n, mu = 0, sigma = 1, nu = 1, tau = 10)
```

```
SST(mu.link = "identity", sigma.link = "log", nu.link = "log",
```

```

    tau.link = "logshiftto2")
dSST(x, mu = 0, sigma = 1, nu = 0.8, tau = 7, log = FALSE)
pSST(q, mu = 0, sigma = 1, nu = 0.8, tau = 7, lower.tail = TRUE, log.p = FALSE)
qSST(p, mu = 0, sigma = 1, nu = 0.8, tau = 7, lower.tail = TRUE, log.p = FALSE)
rSST(n, mu = 0, sigma = 1, nu = 0.8, tau = 7)

ST4(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST4(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST4(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST4(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST4(n, mu = 0, sigma = 1, nu = 1, tau = 10)

ST5(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dST5(x, mu = 0, sigma = 1, nu = 0, tau = 1, log = FALSE)
pST5(q, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
qST5(p, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
rST5(n, mu = 0, sigma = 1, nu = 0, tau = 1)

```

Arguments

mu.link	Defines the mu.link, with "identity" link as the default for the mu parameter. Other links are "1/mu ² " and "log"
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter. Other links are "inverse" and "identity"
nu.link	Defines the nu.link, with "identity" link as the default for the nu parameter. Other links are "1/mu ² " and "log"
tau.link	Defines the tau.link, with "log" link as the default for the tau parameter. Other links are "inverse", "identity"
x, q	vector of quantiles
mu	vector of mu parameter values
sigma	vector of scale parameter values
nu	vector of nu parameter values
tau	vector of tau parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are P[X ≤ x], otherwise, P[X > x]
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required

Details

$$f(y|\mu, \sigma, \nu, \frac{z}{\sigma}) f_{z_1}(z) F_{z_2}(w)\tau =$$

for $-\infty < y < \infty$, where $z = (y - \mu)/\sigma$, $w = \nu\lambda^{1/2}z$, $\lambda = (\tau + 1)/(\tau + z^2)$ and $z_1 \sim TF(0, 1, \tau)$ and $z_2 \sim TF(0, 1, \tau + 1)$.

The probability density function of the skew t distribution type q, (ST3), is defined in Chapter 10 of the GAMLSS manual.

The probability density function of the skew t distribution type q, (ST4), is defined in Chapter of the GAMLSS manual.

The probability density function of the skew t distribution type 5, (ST5), is defined as

$$f(y|\mu, \sigma, \nu, \tau) = \frac{1}{c} \left[1 + \frac{z}{(a+b+z^2)^{1/2}} \right]^{a+1/2} \left[1 - \frac{z}{(a+b+z^2)^{1/2}} \right]^{b+1/2}$$

where $c = 2^{a+b-1}(a+b)^{1/2}B(a,b)$, and $B(a,b) = \Gamma(a)\Gamma(b)/\Gamma(a+b)$ and $z = (y - \mu)/\sigma$ and $\nu = (a-b)/[ab(a+b)]^{1/2}$ and $\tau = 2/(a+b)$ for $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$, $-\infty < \nu < \infty$ and $\tau > 0$.

Value

The functions ST1(), ST2(), ST3(), ST4() and ST5() return a `gamlss.family` object which can be used to fit the skew t type 1-5 distribution in the `gamlss()` function.

The functions dST1(), dST2(), dST3(), dST4() and dST5() give the density functions.

The functions pST1(), pST2(), pST3(), pST4() and pST5() give the cumulative distribution functions.

The functions qST1(), qST2(), qST3(), qST4() and qST5() give the quantile function, and rST1(), rST2(), rST3(), rST4() and rST5() generates random deviates.

Note

The mean of the ex-Gaussian is $\mu + \nu$ and the variance is $\sigma^2 + \nu^2$.

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

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Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973) (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [SEP1](#), [SHASH](#)

Examples

```
y<- rST5(200, mu=5, sigma=1, nu=.1)
hist(y)
curve(dST5(x, mu=30, sigma=5, nu=-1), -50, 50, main = "The ST5 density mu=30, sigma=5, nu=1")
# library(gamlss)
# m1<-gamlss(y~1, family=ST1)
# m2<-gamlss(y~1, family=ST2)
# m3<-gamlss(y~1, family=ST3)
# m4<-gamlss(y~1, family=ST4)
# m5<-gamlss(y~1, family=ST5)
# GAIC(m1,m2,m3,m4,m5)
```

TF

t family distribution for fitting a GAMLSS

Description

The function TF defines the t-family distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dTF`, `pTF`, `qTF` and `rTF` define the density, distribution function, quantile function and random generation for the specific parameterization of the t distribution given in details below, with mean equal to μ and standard deviation equal to $\sigma(\frac{\nu}{\nu-2})^{0.5}$ with the degrees of freedom ν . The function `TF2` is a different parametrization where `sigma` is the standard deviation.

Usage

```
TF(mu.link = "identity", sigma.link = "log", nu.link = "log")
dTF(x, mu = 0, sigma = 1, nu = 10, log = FALSE)
pTF(q, mu = 0, sigma = 1, nu = 10, lower.tail = TRUE, log.p = FALSE)
qTF(p, mu = 0, sigma = 1, nu = 10, lower.tail = TRUE, log.p = FALSE)
rTF(n, mu = 0, sigma = 1, nu = 10)
```

```

TF2(mu.link = "identity", sigma.link = "log", nu.link = "logshiftto2")
dTF2(x, mu = 0, sigma = 1, nu = 10, log = FALSE)
pTF2(q, mu = 0, sigma = 1, nu = 10, lower.tail = TRUE, log.p = FALSE)
qTF2(p, mu = 0, sigma = 1, nu = 10, lower.tail = TRUE, log.p = FALSE)
rTF2(n, mu = 0, sigma = 1, nu = 10)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of the degrees of freedom parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$.
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

Definition file for t family distribution.

$$f(y|\mu, \sigma, \nu) = \frac{\Gamma((\nu + 1)/2)}{\sigma \Gamma(1/2) \Gamma(\nu/2) \nu^{0.5}} \left[1 + \frac{(y - \mu)^2}{\nu \sigma^2} \right]^{-(\nu+1)/2}$$

$y = (-\infty, +\infty)$, $\mu = (-\infty, +\infty)$, $\sigma > 0$ and $\nu > 0$. Note that $z = (y - \mu)/\sigma$ has a standard t distribution with degrees of freedom ν .

Value

`TF()` returns a `gamlss.family` object which can be used to fit a t distribution in the `gamlss()` function. `dTF()` gives the density, `pTF()` gives the distribution function, `qTF()` gives the quantile function, and `rTF()` generates random deviates. The latest functions are based on the equivalent R functions for gamma distribution.

Note

μ is the mean and $\sigma[\nu/(\nu - 2)]^{0.5}$ is the standard deviation of the t family distribution. $\nu > 0$ is a positive real valued parameter.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Kalliope Akantziliotou

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

See Also

[gamlss.family](#)

Examples

```
TF()# gives information about the default links for the t-family distribution
# library(gamlss)
#data(abdom)
#h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=TF, data=abdom) # fits
#plot(h)
newdata<-rTF(1000,mu=0,sigma=1,nu=5) # generates 1000 random observations
hist(newdata)
```

WARING

Waring distribution for fitting a GAMLSS model

Description

The function `WARING()` defines the Waring distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with mean equal to the parameter `mu` and scale parameter `sigma`. The functions `dWARING`, `pWARING`, `qWARING` and `rWARING` define the density, distribution function, quantile function and random generation for the `WARING` parameterization of the Waring distribution.

Usage

```
WARING(mu.link = "log", sigma.link = "log")
dWARING(x, mu = 2, sigma = 2, log = FALSE)
pWARING(q, mu = 2, sigma = 2, lower.tail = TRUE, log.p = FALSE)
qWARING(p, mu = 2, sigma = 2, lower.tail = TRUE, log.p = FALSE,
        max.value = 10000)
rWARING(n, mu = 2, sigma = 2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles.
<code>q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of random values to return.
<code>mu</code>	vector of positive <code>mu</code> values.
<code>sigma</code>	vector of positive <code>sigma</code> values.
<code>lower.tail</code>	logical; if TRUE (default) probabilities are $P[Y \leq y]$, otherwise, $P[Y > y]$.
<code>log, log.p</code>	logical; if TRUE probabilities <code>p</code> are given as $\log(p)$.
<code>max.value</code>	constant; generates a sequence of values for the cdf function.

Details

The Waring distribution has density,

$$f(y|\mu, \sigma) = \frac{(1 + \sigma) \Gamma(y + \frac{\mu}{\sigma}) \Gamma(\frac{\mu + \sigma + 1}{\sigma})}{\sigma \Gamma(y + \frac{\mu + 1}{\sigma} + 2) \Gamma(\frac{\mu}{\sigma})}$$

for $y = 0, 1, 2, \dots$, $\mu > 0$ and $\sigma > 0$.

Value

Returns a `gamlss.family` object which can be used to fit a Waring distribution in the `gamlss()` function.

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos. <f.mcelduff@ich.ucl.ac.uk>

References

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See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(0,20,1)
plot(y, dWARING(y), type="h")
q <- seq(0, 20, 1)
plot(q, pWARING(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qWARING(p), type="s")
dat <- rWARING(100)
hist(dat)
#summary(gamlss(dat~1, family=WARING))
```

WEI

Weibull distribution for fitting a GAMLSS

Description

The function WEI can be used to define the Weibull distribution, a two parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(). [Note that the GAMLSS function WEI2 uses a different parameterization for fitting the Weibull distribution.] The functions dWEI, pWEI, qWEI and rWEI define the density, distribution function, quantile function and random generation for the specific parameterization of the Weibull distribution.

Usage

```
WEI(mu.link = "log", sigma.link = "log")
dWEI(x, mu = 1, sigma = 1, log = FALSE)
pWEI(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qWEI(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rWEI(n, mu = 1, sigma = 1)
```

Arguments

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter, other links are "inverse", "identity" and "own"
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter, other link is the "inverse", "identity" and "own"
x,q	vector of quantiles
mu	vector of the mu parameter
sigma	vector of sigma parameter
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the function WEI is given by

$$f(y|\mu, \sigma) = \frac{\sigma y^{\sigma-1}}{\mu^\sigma} \exp \left[- \left(\frac{y}{\mu} \right)^\sigma \right]$$

for $y > 0$, $\mu > 0$ and $\sigma > 0$. The GAMLSS functions dWEI, pWEI, qWEI, and rWEI can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument mu, and sigma. [See the GAMLSS function WEI2 for a different parameterization of the Weibull.]

Value

WEI() returns a gamlss.family object which can be used to fit a Weibull distribution in the gamlss() function. dWEI() gives the density, pWEI() gives the distribution function, qWEI() gives the quantile function, and rWEI() generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Note

The mean in WEI is given by $\mu\Gamma(\frac{1}{\sigma} + 1)$ and the variance $\mu^2 [\Gamma(\frac{2}{\sigma} + 1) - (\Gamma(\frac{1}{\sigma} + 1))^2]$

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [WEI2](#), [WEI3](#)

Examples

```
WEI()
dat<-rWEI(100, mu=10, sigma=2)
# library(gamlss)
# gamlss(dat~1, family=WEI)
```

WEI2

A specific parameterization of the Weibull distribution for fitting a GAMLSS

Description

The function WEI2 can be used to define the Weibull distribution, a two parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(). This is the parameterization of the Weibull distribution usually used in proportional hazard models and is defined in details below. [Note that the GAMLSS function WEI uses a different parameterization for fitting the Weibull distribution.] The functions dWEI2, pWEI2, qWEI2 and rWEI2 define the density, distribution function, quantile function and random generation for the specific parameterization of the Weibull distribution.

Usage

```
WEI2(mu.link = "log", sigma.link = "log")
dWEI2(x, mu = 1, sigma = 1, log = FALSE)
pWEI2(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qWEI2(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rWEI2(n, mu = 1, sigma = 1)
```

Arguments

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter, other links are "inverse" and "identity"
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter, other link is the "inverse" and "identity"
x,q	vector of quantiles
mu	vector of the mu parameter values
sigma	vector of sigma parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required

Details

The parameterization of the function WEI2 is given by

$$f(y|\mu, \sigma) = \sigma \mu y^{\sigma-1} e^{-\mu y^\sigma}$$

for $y > 0$, $\mu > 0$ and $\sigma > 0$. The GAMLSS functions dWEI2, pWEI2, qWEI2, and rWEI2 can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument mu, and sigma. [See the GAMLSS function WEI for a different parameterization of the Weibull.]

Value

WEI2() returns a gamlss.family object which can be used to fit a Weibull distribution in the gamlss() function. dWEI2() gives the density, pWEI2() gives the distribution function, qWEI2() gives the quantile function, and rWEI2() generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Warning

In WEI2 the estimated parameters mu and sigma can be highly correlated so it is advisable to use the CG() method for fitting [as the RS() method can be very slow in this situation.]

Note

The mean in WEI2 is given by $\mu^{-1/\sigma} \Gamma(\frac{1}{\sigma} + 1)$ and the variance $\mu^{-2/\sigma} (\Gamma(\frac{2}{\sigma} + 1) - [\Gamma(\frac{1}{\sigma} + 1)]^2)$

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [WEI](#), [WEI3](#),

Examples

```
WEI2()
dat<-rWEI(100, mu=.1, sigma=2)
hist(dat)
# library(gamlss)
# gamlss(dat~1, family=WEI2, method=CG())
```

WEI3

A specific parameterization of the Weibull distribution for fitting a GAMLSS

Description

The function WEI3 can be used to define the Weibull distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss\(\)`. This is a parameterization of the Weibull distribution where μ is the mean of the distribution. [Note that the GAMLSS functions [WEI](#) and [WEI2](#) use different parameterizations for fitting the Weibull distribution.] The functions `dWEI3`, `pWEI3`, `qWEI3` and `rWEI3` define the density, distribution function, quantile function and random generation for the specific parameterization of the Weibull distribution.

Usage

```
WEI3(mu.link = "log", sigma.link = "log")
dWEI3(x, mu = 1, sigma = 1, log = FALSE)
pWEI3(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qWEI3(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rWEI3(n, mu = 1, sigma = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the mu parameter, other links are "inverse" and "identity"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma parameter, other link is the "inverse" and "identity"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of the mu parameter values
<code>sigma</code>	vector of sigma parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

The parameterization of the function WEI3 is given by

$$f(y|\mu, \sigma) = \frac{\sigma}{\beta} \left(\frac{y}{\beta} \right)^{\sigma-1} e^{-\left(\frac{y}{\beta}\right)^{\sigma}}$$

where $\beta = \frac{\mu}{\Gamma((1/\sigma)+1)}$ for $y > 0$, $\mu > 0$ and $\sigma > 0$. The GAMLSS functions dWEI3, pWEI3, qWEI3, and rWEI3 can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument mu, and sigma. [See the GAMLSS function WEI for a different parameterization of the Weibull.]

Value

WEI3() returns a `gamlss.family` object which can be used to fit a Weibull distribution in the `gamlss()` function. `dWEI3()` gives the density, `pWEI3()` gives the distribution function, `qWEI3()` gives the quantile function, and `rWEI3()` generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Warning

In WEI3 the estimated parameters mu and sigma can be highly correlated so it is advisable to use the `CG()` method for fitting [as the `RS()` method can be very slow in this situation.]

Note

The mean in WEI3 is given by μ and the variance $\mu^2 \left\{ \Gamma(2/\sigma + 1) / [\Gamma(1/\sigma + 1)]^2 - 1 \right\}$

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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See Also

[gamlss.family](#), [WEI](#), [WEI2](#)

Examples

```
WEI3()
dat<-rWEI(100, mu=.1, sigma=2)
# library(gamlss)
# gamlss(dat~1, family=WEI3, method=CG())
```

YULE

*Yule distribution for fitting a GAMLSS model***Description**

The function YULE defines the Yule distribution, a one parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with mean equal to the parameter `mu`. The functions `dYULE`, `pYULE`, `qYULE` and `rYULE` define the density, distribution function, quantile function and random generation for the YULE parameterization of the Yule distribution.

Usage

```
YULE(mu.link = "log")
dYULE(x, mu = 2, log = FALSE)
pYULE(q, mu = 2, lower.tail = TRUE, log.p = FALSE)
qYULE(p, mu = 2, lower.tail = TRUE, log.p = FALSE,
      max.value = 10000)
rYULE(n, mu = 2)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles.
<code>q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of random values to return.
<code>mu</code>	vector of positive <code>mu</code> values.
<code>lower.tail</code>	logical; if TRUE (default) probabilities are $P[Y \leq y]$, otherwise, $P[Y > y]$.
<code>log, log.p</code>	logical; if TRUE probabilities <code>p</code> are given as $\log(p)$.
<code>max.value</code>	constant; generates a sequence of values for the cdf function.

Details

The Yule distribution has density

$$P(Y = y|\mu) = (\mu^{-1} + 1)B(y + 1, \mu^{-1} + 2)$$

for $y = 0, 1, 2, \dots$ and $\mu > 0$.

Value

Returns a `gamlss.family` object which can be used to fit a Yule distribution in the `gamlss()` function.

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

Wimmer, G. and Altmann, G. (1999) *Thesaurus of univariate discrete probability distributions*. Stamm.

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(0,20,1)
plot(y, dYULE(y), type="h")
q <- seq(0, 20, 1)
plot(q, pYULE(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qYULE(p), type="s")
dat <- rYULE(100)
hist(dat)
#summary(gamlss(dat~1, family=YULE))
```

ZABB

Zero inflated and zero adjusted Binomial distribution for fitting in GAMLSS

Description

The function ZIBB defines the zero inflated beta binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIBB`, `pZIBB`, `qZIBB` and `rZINN` define the density, distribution function, quantile function and random generation for the zero inflated beta binomial, ZIBB, distribution.

The function ZABB defines the zero adjusted beta binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZABB`, `pZABB`, `qZABB` and `rZABB` define the density, distribution function, quantile function and random generation for the zero inflated beta binomial, `ZABB()`, distribution.

Usage

```
ZABB(mu.link = "logit", sigma.link = "log", nu.link = "logit")
ZIBB(mu.link = "logit", sigma.link = "log", nu.link = "logit")

dZIBB(x, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1, log = FALSE)
dZABB(x, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1, log = FALSE)

pZIBB(q, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1, lower.tail = TRUE, log.p = FALSE)
pZABB(q, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1, lower.tail = TRUE, log.p = FALSE)

qZIBB(p, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1, lower.tail = TRUE, log.p = FALSE)
qZABB(p, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1, lower.tail = TRUE, log.p = FALSE)

rZIBB(n, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1)
rZABB(n, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog" (complementary log-log)
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>sigma.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog" (complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive probabilities
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of positive probabilities
<code>bd</code>	vector of binomial denominators
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

For the definition of the distributions see Rigby and Stasinopoulos (2010) below.

Value

The functions ZIBB and ZABB return a `gamlss.family` object which can be used to fit a zero inflated or zero adjusted beta binomial distribution respectively in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) Distributions for modeling location, scale, and shape: Using GAMLSS in R, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07)..

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NBI](#), [NBII](#)

Examples

```
ZIBB()
ZABB()
# creating data and plotting them
dat <- rZIBB(1000, mu=.5, sigma=.5, nu=0.1, bd=10)
r <- barplot(table(dat), col='lightblue')
dat1 <- rZABB(1000, mu=.5, sigma=.2, nu=0.1, bd=10)
r1 <- barplot(table(dat1), col='lightblue')
```

Description

The `ZABI()` function defines the zero adjusted binomial distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZABI`, `pZABI`, `qZABI` and `rZABI` define the density, distribution function, quantile function and random generation for the zero adjusted binomial, `ZABI()`, distribution.

The `ZIBI()` function defines the zero inflated binomial distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIBI`, `pZIBI`, `qZIBI` and `rZIBI` define the density, distribution function, quantile function and random generation for the zero inflated binomial, `ZIBI()`, distribution.

Usage

```
ZABI(mu.link = "logit", sigma.link = "logit")
dZABI(x, bd = 1, mu = 0.5, sigma = 0.1, log = FALSE)
pZABI(q, bd = 1, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZABI(p, bd = 1, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZABI(n, bd = 1, mu = 0.5, sigma = 0.1)

ZIBI(mu.link = "logit", sigma.link = "logit")
dZIBI(x, bd = 1, mu = 0.5, sigma = 0.1, log = FALSE)
pZIBI(q, bd = 1, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZIBI(p, bd = 1, mu = 0.5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZIBI(n, bd = 1, mu = 0.5, sigma = 0.1)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog"(complementary log-log)
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive probabilities
<code>sigma</code>	vector of positive probabilities
<code>bd</code>	vector of binomial denominators
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

For the definition of the distributions see Rigby and Stasinopoulos (2010) below.

Value

The functions ZABI and ZIBI return a `gamlss.family` object which can be used to fit a binomial distribution in the `gamlss()` function.

Note

The response variable should be a matrix containing two columns, the first with the count of successes and the second with the count of failures.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [BI](#)

Examples

```
ZABI()
curve(dZABI(x, mu = .5, bd=10), from=0, to=10, n=10+1, type="h")
tN <- table(Ni <- rZABI(1000, mu=.2, sigma=.3, bd=10))
r <- barplot(tN, col='lightblue')
```

```
ZIBI()
curve(dZIBI(x, mu = .5, bd=10), from=0, to=10, n=10+1, type="h")
tN <- table(Ni <- rZIBI(1000, mu=.2, sigma=.3, bd=10))
r <- barplot(tN, col='lightblue')
```

Description

The function `ZAGA()` defines the zero adjusted Gamma distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The zero adjusted Gamma distribution is similar to the Gamma distribution but allows zeros as y values. The extra parameter `nu` models the probabilities at zero. The functions `dZAGA`, `pZAGA`, `qZAGA` and `rZAGA` define the density, distribution function, quartile function and random generation for the ZAGA parameterization of the zero adjusted Gamma distribution. `plotZAGA` can be used to plot the distribution. `meanZAGA` calculates the expected value of the response for a fitted model.

Usage

```
ZAGA(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZAGA(x, mu = 1, sigma = 1, nu = 0.1, log = FALSE)
pZAGA(q, mu = 1, sigma = 1, nu = 0.1, lower.tail = TRUE,
      log.p = FALSE)
qZAGA(p, mu = 1, sigma = 1, nu = 0.1, lower.tail = TRUE,
      log.p = FALSE)
rZAGA(n, mu = 1, sigma = 1, nu = 0.1, ...)
plotZAGA(mu = 5, sigma = 1, nu = 0.1, from = 0, to = 10,
          n = 101, main=NULL, ...)
meanZAGA(obj)
```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the mu parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "logit" link as the default for the sigma parameter
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of probability at zero parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as log(p).
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution

obj a fitted `gamlss` object
 main for title in the plot
 can be used to pass the `uppr.limit` argument to `qIG`

Details

The Zero adjusted GA distribution is given as

$$f(y|\mu, \sigma, \nu) = \nu$$

if ($y=0$)

$$f(y|\mu, \sigma, \nu) = (1 - \nu) \left[\frac{1}{(\sigma^2 \mu)^{1/\sigma^2}} \frac{y^{\frac{1}{\sigma^2}-1} e^{-y/(\sigma^2 \mu)}}{\Gamma(1/\sigma^2)} \right]$$

otherwise

for $y = (0, \infty)$, $\mu > 0$, $\sigma > 0$ and $0 < \nu < 1$. $E(y) = (1 - \nu)\mu$ and $Var(y) = (1 - \nu)\mu^2(\nu + \sigma^2)$.

Value

The function `ZAGA` returns a `gamlss.family` object which can be used to fit a zero adjusted Gamma distribution in the `gamlss()` function.

Author(s)

Bob Rigby, Mikis Stasinopoulos and Almond Stocker

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <https://www.gamlss.com/>).
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
 (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [GA](#), [ZAIG](#)

Examples

```
ZAGA()# gives information about the default links for the ZAGA distribution
# plotting the function
PPP <- par(mfrow=c(2,2))
plotZAGA(mu=1, sigma=.5, nu=.2, from=0,to=3)
#curve(dZAGA(x,mu=1, sigma=.5, nu=.2), 0,3) # pdf
curve(pZAGA(x,mu=1, sigma=.5, nu=.2), 0,3, ylim=c(0,1)) # cdf
curve(qZAGA(x,mu=1, sigma=.5, nu=.2), 0,.99) # inverse cdf
y<-rZAGA(100, mu=1, sigma=.5, nu=.2) # randomly generated values
hist(y)
par(PPP)
# check that the positive part sums up to .8 (since nu=0.2)
integrate(function(x) dZAGA(x,mu=1, sigma=.5, nu=.2), 0,Inf)
```

ZAIG

The zero adjusted Inverse Gaussian distribution for fitting a GAMLSS model

Description

The function ZAIG() defines the zero adjusted Inverse Gaussian distribution, a three parameter distribution, for a gamlss.family object to be used in GAMLSS fitting using the function gamlss(). The zero adjusted Inverse Gaussian distribution is similar to the Inverse Gaussian distribution but allows zeros as y values. The extra parameter models the probabilities at zero. The functions dZAIG, pZAIG, qZAIG and rZAIG define the density, distribution function, quantile function and random generation for the ZAIG parameterization of the zero adjusted Inverse Gaussian distribution. plotZAIG can be used to plot the distribution. meanZAIG calculates the expected value of the response for a fitted model.

Usage

```
ZAIG(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZAIG(x, mu = 1, sigma = 1, nu = 0.1, log = FALSE)
pZAIG(q, mu = 1, sigma = 1, nu = 0.1, lower.tail = TRUE, log.p = FALSE)
qZAIG(p, mu = 1, sigma = 1, nu = 0.1, lower.tail = TRUE, log.p = FALSE)
rZAIG(n, mu = 1, sigma = 1, nu = 0.1, ...)
plotZAIG(mu = 5, sigma = 1, nu = 0.1, from = 0, to = 10, n = 101,
         main = NULL,...)
meanZAIG(obj)
```

Arguments

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter
nu.link	Defines the nu.link, with "logit" link as the default for the sigma parameter
x,q	vector of quantiles
mu	vector of location parameter values

<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of probability at zero parameter values
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution
<code>obj</code>	a fitted BEINF object
<code>main</code>	for title in the plot
<code>...</code>	<code>...</code> can be used to pass the <code>uppr.limit</code> argument to <code>qIG</code>

Details

The Zero adjusted IG distribution is given as

$$f(y|\mu, \sigma, \nu) = \nu$$

if ($y=0$)

$$f(y|\mu, \sigma, \nu) = (1 - \nu) \frac{1}{\sqrt{2\pi\sigma^2 y^3}} \exp\left(-\frac{(y - \mu)^2}{2\mu^2\sigma^2 y}\right)$$

otherwise

for $y = (0, \infty)$, $\mu > 0$, $\sigma > 0$ and $0 < \nu < 1$. $E(y) = (1 - \nu)\mu$ and $Var(y) = (1 - \nu)\mu^2(\nu + \mu\sigma^2)$.

Value

returns a `gamlss.family` object which can be used to fit a zero adjusted inverse Gaussian distribution in the `gamlss()` function.

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Heller, G. Stasinopoulos M and Rigby R.A. (2006) The zero-adjusted Inverse Gaussian distribution as a model for insurance claims. in *Proceedings of the 21th International Workshop on Statistical Modelling*, eds J. Hinde, J. Einbeck and J. Newell, pp 226-233, Galway, Ireland.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M., Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)

(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [IG](#)

Examples

```
ZAIG())# gives information about the default links for the ZAIG distribution
# plotting the distribution
plotZAIG( mu =10 , sigma=.5, nu = 0.1, from = 0, to=10, n = 101)
# plotting the cdf
plot(function(y) pZAIG(y, mu=10 ,sigma=.5, nu = 0.1 ), 0, 1)
# plotting the inverse cdf
plot(function(y) qZAIG(y, mu=10 ,sigma=.5, nu = 0.1 ), 0.001, .99)
# generate random numbers
dat <- rZAIG(100,mu=10,sigma=.5, nu=.1)
# fit a model to the data
# library(gamlss)
# m1<-gamlss(dat~1,family=ZAIG)
# meanZAIG(m1)[1]
```

ZANBI

Zero inflated and zero adjusted negative binomial distributions for fitting a GAMLSS model

Description

The function ZINBI defines the zero inflated negative binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZINBI`, `pZINBI`, `qZINBI` and `rZINBI` define the density, distribution function, quantile function and random generation for the zero inflated negative binomial, ZINBI(), distribution.

The function ZANBI defines the zero adjusted negative binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZANBI`, `pZANBI`, `qZANBI` and `rZANBI` define the density, distribution function, quantile function and random generation for the zero inflated negative binomial, ZANBI(), distribution.

Usage

```

ZINBI(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZINBI(x, mu = 1, sigma = 1, nu = 0.3, log = FALSE)
pZINBI(q, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
qZINBI(p, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
rZINBI(n, mu = 1, sigma = 1, nu = 0.3)
ZANBI(mu.link = "log", sigma.link = "log", nu.link = "logit")
dZANBI(x, mu = 1, sigma = 1, nu = 0.3, log = FALSE)
pZANBI(q, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
qZANBI(p, mu = 1, sigma = 1, nu = 0.3, lower.tail = TRUE, log.p = FALSE)
rZANBI(n, mu = 1, sigma = 1, nu = 0.3)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "logit" link as the default for the <code>nu</code> parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of zero probability parameter
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

The definition for the zero inflated Negative Binomial type I distribution and for the zero adjusted Negative Binomial type I distribution is given in Rigby and Stasinopoulos (2010) below

Value

The functions `ZINBI` and `ZANBI` return a `gamlss.family` object which can be used to fit a zero inflated or zero adjusted Negative Binomial type I distribution respectively in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [NBI](#), [NBII](#)

Examples

```
ZINBI()
ZANBI()
# creating data and plotting them
dat <- rZINBI(1000, mu=5, sigma=.5, nu=0.1)
r <- barplot(table(dat), col='lightblue')
dat1 <- rZANBI(1000, mu=5, sigma=.5, nu=0.1)
r1 <- barplot(table(dat1), col='lightblue')
```

ZAP

Zero adjusted poisson distribution for fitting a GAMLSS model

Description

The function ZAP defines the zero adjusted Poisson distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZAP`, `pZAP`, `qZAP` and `rZAP` define the density, distribution function, quantile function and random generation for the inflated poisson, `ZAP()`, distribution.

Usage

```
ZAP(mu.link = "log", sigma.link = "logit")
dZAP(x, mu = 5, sigma = 0.1, log = FALSE)
pZAP(q, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZAP(p, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZAP(n, mu = 5, sigma = 0.1)
```

Arguments

<code>mu.link</code>	defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	defines the <code>sigma.link</code> , with "logit" link as the default for the <code>sigma</code> parameter which in this case is the probability at zero. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer)
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of probabilities at zero
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

For the definition of the distribution see Rigby and Stasinopoulos (2010) below.

Value

The function `ZAP` returns a `gamlss.family` object which can be used to fit a zero inflated poisson distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>)..

See Also

[gamlss.family](#), [P0](#), [ZIP](#), [ZIP2](#), [ZALG](#)

Examples

```
ZAP()
# creating data and plotting them
dat<-rZAP(1000, mu=5, sigma=.1)
r <- barplot(table(dat), col='lightblue')
```

ZIP

Zero inflated poisson distribution for fitting a GAMLSS model

Description

The function ZIP defines the zero inflated Poisson distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIP`, `pZIP`, `qZIP` and `rZIP` define the density, distribution function, quantile function and random generation for the inflated poisson, `ZIP()`, distribution.

Usage

```
ZIP(mu.link = "log", sigma.link = "logit")
dZIP(x, mu = 5, sigma = 0.1, log = FALSE)
pZIP(q, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZIP(p, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZIP(n, mu = 5, sigma = 0.1)
```

Arguments

<code>mu.link</code>	defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	defines the <code>sigma.link</code> , with "logit" link as the default for the <code>sigma</code> parameter which in this case is the probability at zero. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of probabilities at zero
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Let $Y = 0$ with probability σ and $Y \sim Po(\mu)$ with probability $(1 - \sigma)$ the Y has a Zero inflated Poisson Distribution given by

$$f(y) = \sigma + (1 - \sigma)e^{-\mu}$$

if ($y=0$)

$$f(y) = (1 - \sigma) \frac{e^{-\mu} \mu^y}{y!}$$

if ($y>0$) for $y = 0, 1, \dots$.

Value

returns a `gamlss.family` object which can be used to fit a zero inflated poisson distribution in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

- Lambert, D. (1992), Zero-inflated Poisson Regression with an application to defects in Manufacturing, *Technometrics*, **34**, pp 1-14.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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(see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [P0](#), [ZIP2](#)

Examples

```
ZIP()# gives information about the default links for the normal distribution
# creating data and plotting them
dat<-rZIP(1000, mu=5, sigma=.1)
r <- barplot(table(dat), col='lightblue')
# library(gamlss)
```



```
# fit the distribution
# mod1<-gamlss(dat~1, family=ZIP)# fits a constant for mu and sigma
# fitted(mod1)[1]
# fitted(mod1,"sigma")[1]
```

ZIP2

Zero inflated poisson distribution for fitting a GAMLSS model

Description

The function ZIP2 defines the zero inflated Poisson type 2 distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIP2`, `pZIP2`, `qZIP2` and `rZIP2` define the density, distribution function, quantile function and random generation for the inflated poisson, ZIP2(), distribution. The ZIP2 is a different parameterization of the ZIP distribution. In the ZIP2 the `mu` is the mean of the distribution.

Usage

```
ZIP2(mu.link = "log", sigma.link = "logit")
dZIP2(x, mu = 5, sigma = 0.1, log = FALSE)
pZIP2(q, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZIP2(p, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZIP2(n, mu = 5, sigma = 0.1)
```

Arguments

<code>mu.link</code>	defines the <code>mu.link</code> , with "log" link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	defines the <code>sigma.link</code> , with "logit" link as the default for the <code>sigma</code> parameter which in this case is the probability at zero. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of probabilities at zero
<code>p</code>	vector of probabilities
<code>q</code>	vector of quantiles
<code>n</code>	number of random values to return
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Let $Y = 0$ with probability σ and $Y \sim Po(\mu/[1 - \sigma])$ with probability $(1 - \sigma)$ then Y has a Zero inflated Poisson type 2 distribution given by

$$f(y|\mu, \sigma) = \sigma + (1 - \sigma)e^{-\mu/(1-\sigma)} \quad \text{if } y = 0$$

$$f(y|\mu, \sigma) = (1 - \sigma) \frac{e^{-\mu/(1-\sigma)} [\mu/(1 - \sigma)]^y}{y!} \quad \text{if } y = 1, 2, 3, \dots$$

The mean of the distribution in this parameterization is μ .

Value

returns a `gamlss.family` object which can be used to fit a zero inflated poisson distribution in the `gamlss()` function.

Author(s)

Bob Rigby, Gillian Heller and Mikis Stasinopoulos

References

- Lambert, D. (1992), Zero-inflated Poisson Regression with an application to defects in Manufacturing, *Technometrics*, **34**, pp 1-14.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
- (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#), [ZIP](#)

Examples

```
ZIP2())# gives information about the default links for the normal distribution
# creating data and plotting them
dat<-rZIP2(1000, mu=5, sigma=.1)
r <- barplot(table(dat), col='lightblue')
# fit the disteibution
# library(gamlss)
```

```
# mod1<-gamlss(dat~1, family=ZIP2)# fits a constant for mu and sigma
# fitted(mod1)[1]
# fitted(mod1,"sigma")[1]
```

ZIPF

The zipf and zero adjusted zipf distributions for fitting a GAMLSS model

Description

This function `ZIPF()` defines the zipf distribution, Johnson et. al., (2005), sections 11.2.20, p 527-528. The zipf distribution is an one parameter distribution with long tails (a discrete version of the Pareto distribution). The function `ZIPF()` creates a `gamlss.family` object to be used in GAMLSS fitting. The functions `dZIPF`, `pZIPF`, `qZIPF` and `rZIPF` define the density, distribution function, quantile function and random generation for the zipf, `ZIPF()`, distribution. The function `zetaP()` defines the zeta function and it is based on the zeta function defined on the VGAM package of Thomas Yee, see Yee (2017).

The distribution zipf is defined on $y = 1, 2, 3, \dots, \infty$, the zero adjusted zipf permits values on $y = 0, 1, 2, \dots, \infty$. The function `ZAZIPF()` defines the zero adjusted zipf distribution. The function `ZAZIPF()` creates a `gamlss.family` object to be used in GAMLSS fitting. The functions `dZAZIPF`, `pZAZIPF`, `qZAZIPF` and `rZAZIPF` define the density, distribution function, quantile function and random generation for the zero adjusted zipf, `ZAZIPF()`, distribution.

Usage

```
ZIPF(mu.link = "log")
dZIPF(x, mu = 1, log = FALSE)
pZIPF(q, mu = 1, lower.tail = TRUE, log.p = FALSE)
qZIPF(p, mu = 1, lower.tail = TRUE, log.p = FALSE,
      max.value = 10000)
rZIPF(n, mu = 1, max.value = 10000)
zetaP(x)
ZAZIPF(mu.link = "log", sigma.link = "logit")
dZAZIPF(x, mu = 0.5, sigma = 0.1, log = FALSE)
pZAZIPF(q, mu = 0.5, sigma = 0.1, lower.tail = TRUE,
        log.p = FALSE)
qZAZIPF(p, mu = 0.5, sigma = 0.1, lower.tail = TRUE,
        log.p = FALSE, max.value = 10000)
rZAZIPF(n, mu = 0.5, sigma = 0.1, max.value = 10000)
```

Arguments

<code>mu.link</code>	the link function for the parameter mu with default log
<code>x, q</code>	vectors of (non-negative integer) quantiles
<code>p</code>	vector of probabilities
<code>mu</code>	vector of positive parameter

<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>n</code>	number of random values to return
<code>max.value</code>	a constant, set to the default value of 10000, It is used in the <code>q</code> function which numerically calculates how far the algorithm should look for <code>q</code> . Maybe for zipf data the values has to increase at a considerable computational cost.
<code>sigma.link</code>	the link function for the parameter <code>sigma</code> with default <code>logit</code>
<code>sigma</code>	a vector of probabilities of zero

Details

The probability density for the zipf distribution, ZIPF, is:

$$f(y|\mu) = \frac{y^{-(\mu+1)}}{\zeta(\mu+1)}$$

for $y = 1, 2, \dots, \infty$, $\mu > 0$ and where $\zeta()$ is the (Reimann) zeta function.

The distribution has mean $\zeta(\mu)/\zeta(\mu+1)$ and variance $\zeta(\mu+1)\zeta(\mu-1) - [\zeta(\mu)]^2/[\zeta(\mu+1)]^2$.

Value

The function `ZIPF()` returns a `gamlss.family` object which can be used to fit a zipf distribution in the `gamlss()` function.

Note

Because the zipf distribution has very long tails the `max.value` in the `q` and `r`, may need to increase.

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

- N. L. Johnson, A. W. Kemp, and S. Kotz. (2005) *Univariate Discrete Distributions*. Wiley, New York, 3rd edition.
- Thomas W. Yee (2017). VGAM: Vector Generalized Linear and Additive Models. R package version 1.0-3. <https://CRAN.R-project.org/package=VGAM>
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi: [10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi: [10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi: [10.1201/b21973](https://doi.org/10.1201/b21973)
(see also <https://www.gamlss.com/>).

See Also

[PO](#), [LG](#), [GEOM](#), [YULE](#)

Examples

```
# ZIPF
par(mfrow=c(2,2))
y<-seq(1,20,1)
plot(y, dZIPF(y), type="h")
q <- seq(1, 20, 1)
plot(q, pZIPF(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qZIPF(p), type="s")
dat <- rZIPF(100)
hist(dat)

# ZAZIPF
y<-seq(0,20,1)
plot(y, dZAZIPF(y, mu=.9, sigma=.1), type="h")
q <- seq(1, 20, 1)
plot(q, pZAZIPF(q, mu=.9, sigma=.1), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p, qZAZIPF(p, mu=.9, sigma=.1), type="s")
dat <- rZAZIPF(100, mu=.9, sigma=.1)
hist(dat)
```

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