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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.

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

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gamlss.dist-package *Distributions for Generalized Additive Models for Location Scale and Shape*

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:

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Version:     6.0-5
Date:       2022-08-28
Authors@R:  c(person("Mikis", "Stasinopoulos", role = c("aut", "cre", "cph"), email = "d.stasinopoulos@londonmet.ac.uk"),
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Author:     Mikis Stasinopoulos [aut, cre, cph], Robert Rigby [aut], Calliope Akantziliotou [ctb], Vlasios Voudouris [ctb],
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```

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 exponential power 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/)

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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.

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

(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>dB</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 $\sigma > 0$, see pp. 523-524 of Rigby *et al.* (2019). . 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. 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.

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

(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 $\log(p)$.
<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 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) or pp. 439-441 of Rigby et al. (2019) 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
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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.

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

(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` (very old) 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")
BCPEo(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

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

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 $\tau > 0$ see pp. 450-451 of Rigby et al. (2019).

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

[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)dBCPE(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) pBCPE(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 `BCTo` 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 <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", "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 $\log(p)$.
<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 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 $\tau > 0$ see pp. 450-451 of Rigby et al. (2019).

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, $\sigma\left(\frac{\tau}{\tau-2}\right)^{0.5}$ 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")
```

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 `dBE` and `dBEo`, `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 <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 standard parametrization of the 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 $\beta > 0$.

The first `gamlss` implementation the beta distribution is called `BEo`, and it is identical to the standard parametrization with $\alpha = \mu$ and $\beta = \sigma$, see pp. 460-461 of Rigby et al. (2019):

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

for $y \in (0, 1)$, $\mu > 0$ and $\sigma > 0$. The problem with this parametrization is that with mean $E(y) = \mu/(\mu + \sigma)$ it is not convenient for modelling the response y as function of the explanatory variables. The second parametrization, `BE` see pp. 461-463 of Rigby et al. (2019), is using

$$\mu = \frac{\alpha}{\alpha + \beta}$$

$$\sigma = \frac{1}{(\alpha + \beta + 1)^{1/2}}$$

(of the standard parametrization) and it is more convenient because μ now is the mean with variance equal to $Var(y) = \sigma^2 \mu(1 - \mu)$. Note however that $0 < \mu < 1$ and $0 < \sigma < 1$.

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.
- 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 (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]
```

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 logit
<code>sigma.link</code>	the sigma link function with default logit
<code>nu.link</code>	the nu link function with default log
<code>tau.link</code>	the tau link function with default 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 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 <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>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 defined as

$$\begin{aligned}
 f(y) &= p_0 \quad \text{if } y = 0 \\
 f(y) &= p_1 \quad \text{if } y = 1 \\
 f(y|\alpha, \beta) &= \frac{1}{B(\alpha, \beta)} y^{\alpha-1} (1-y)^{\beta-1} \quad \text{otherwise}
 \end{aligned}$$

for $0 \leq y \leq 1$, $\alpha > 0$, $\beta > 0$, $0 < p_0 < 1$, $0 < p_1 < 1$ and $0 < p_0 + p_1 < 1$.

The GAMLSS function `BEINF()` re-parametrize the parameters as

$$\begin{aligned}
 \mu &= \frac{\alpha}{\alpha + \beta} \\
 \sigma &= \frac{1}{\alpha + \beta + 1} \\
 \nu &= \frac{p_0}{p_2} \\
 \tau &= \frac{p_1}{p_2}
 \end{aligned}$$

where $p_2 = 1 - p_0 - p_1$ so $0 < \mu < 1$, $0 < \sigma < 1$, $\nu > 0$ and $\tau > 0$ see pp. 466-467 of Rigby et al. (2019).

The beta inflated at zero distribution is defined as

$$\begin{aligned}
 f(y) &= p_0 \quad \text{if } y = 0 \\
 f(y|\alpha, \beta) &= \frac{1}{B(\alpha, \beta)} y^{\alpha-1} (1-y)^{\beta-1} \quad \text{otherwise}
 \end{aligned}$$

for $0 \leq y < 1$, $\alpha > 0$, $\beta > 0$ and $0 < p_0 < 1$.

The GAMLSS function `BEINF0()` re-parametrize the parameters as

$$\begin{aligned}\mu &= \frac{\alpha}{\alpha + \beta} \\ \sigma &= \frac{1}{\alpha + \beta + 1} \\ \nu &= \frac{p_0}{1 - P_0}\end{aligned}$$

so $0 < \mu < 1$, $0 < \sigma < 1$ and $\nu > 0$ see pp. 467-468 of Rigby et al. (2019).

The beta inflated at 1 distribution is defined as

$$\begin{aligned}f(y|\alpha, \beta) &= \frac{1}{B(\alpha, \beta)} y^{\alpha-1} (1-y)^{\beta-1} \quad \text{if } 0 < y < 1 \\ f(y) &= p_1 \quad \text{if } y = 1\end{aligned}$$

for $0 < y \leq 1$, $\alpha > 0$, $\beta > 0$ and $0 < p_1 < 1$.

The GAMLSS function `BEINF1()` re-parametrize the parameters as

$$\begin{aligned}\mu &= \frac{\alpha}{\alpha + \beta} \\ \sigma &= \frac{1}{\alpha + \beta + 1} \\ \nu &= \frac{p_1}{1 - P_1}\end{aligned}$$

so $0 < \mu < 1$, $0 < \sigma < 1$ and $\nu > 0$ see pp. 468-469 of Rigby et al. (2019).

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

[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

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
from	where to start plotting the distribution from
to	up to where to plot the distribution
obj	a fitted BEOI object
...	other graphical parameters for plotting

Details

The one-inflated beta distribution is given as

$$f(y) = \nu \quad \text{if } y = 1$$

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

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

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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

mu.link	the mu link function with default logit
sigma.link	the sigma link function with default log
nu.link	the nu link function with default logit
x,q	vector of quantiles
mu	vector of location parameter values
sigma	vector of precision parameter values
nu	vector of parameter values modelling the probability at zero
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
from	where to start plotting the distribution from
to	up to where to plot the distribution
obj	a fitted BEZI object
...	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
```

BI

*Binomial distribution for fitting a GAMLSS***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

mu.link	Defines the mu.link, with "logit" link as the default for the mu parameter. Other links are "probit" and "cloglog"(complementary log-log)
x	vector of (non-negative integer) quantiles
mu	vector of positive probabilities
bd	vector of binomial denominators
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 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 $0 < \mu < 1$ see pp. 521-522 of Rigby *et al.* (2019).

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 `mu` 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`, `pBNB`, `qBNB` and `rBNB` 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)
pBNB(q, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE)
qBNB(p, mu = 1, sigma = 1, nu = 1, lower.tail = TRUE, log.p = FALSE,
     max.value = 10000)
rBNB(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 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>	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 <= 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

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

for $y = 0, 1, 2, 3, \dots$, $\mu > 0$, $\sigma > 0$ and $\nu > 0$, see pp 502-503 of Rigby *et al.* (2019).

The distribution has mean μ .

The definition of the zero adjusted beta negative binomial distribution, ZABNB and the the zero inflated beta negative binomial distribution, ZIBNB, are given in p. 517 and pp. 519 of of Rigby *et al.* (2019), respectively.

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>

References

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

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)
```

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

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

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

See Also

[gamlss.family](#)

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"))

contrRplus_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"))

contrR01_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"))

contrR01_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 = PO, mu = c(1, 2, 5), miny = 0, maxy = 10,
  cex.axis = 1.2, cex.all = 1.5)

count_1_22(family = PO, 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
nu	the nu parameter values
tau	the tau parameter values
bd	the binomial denominator
miny	minimal value for the y axis
maxy	maximal value for the y axis
cex.axis	the size of the letters in the two axes
cex.all	the overall size of all plotting characters
cols	colours
spacing	spacing between plots
ltype	The type of lines used
no.points	the number of points in the curve
y.axis.lim	the maximum value for the y axis
maxYlim	the maximum permissible value for Y
legend.cex	the size of the legend
legend.x	where in the figure to put the legend
legend.where	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) 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, Fernada 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. 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.

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 (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:

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

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()`, see pp. 524-525 of Rigby *et al.* (2019).

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.
- 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. 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.

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

(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

x	vector of (non-negative integer) quantiles
p	vector of probabilities
q	vector of quantiles
mu	vector of positive mu
sigma	vector of positive dispersion parameter sigma
nu	vector of nu
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]
n	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 $\nu > 0$ see pp 504-505 of Rigby *et al.* (2019).

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. 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.

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 (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

sigma	vector of positive dispersion parameter
nu	vector of nu
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

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 $\rho = [1 + \mu\sigma(1 - \nu)]^{-1}$. For more details see pp 506-507 of Rigby *et al.* (2019).

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. 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.

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

Wimmer, G. and Altmann, G (1999). *Thesaurus of univariate discrete probability distributions*. Stamm 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 <= 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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(see also <https://www.gamlss.com/>).

See Also

[PO](#)

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

<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:

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

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), see also pp. 385-386 of Rigby et al. (2019).

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 μ and σ are the mean and standard deviation from the normal distribution variable while the parameter ν 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

`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. Other links are "inverse", "identity", "logshifted" (shifted from one) and "own"
x,q	vector of quantiles
mu	vector of mu parameter values
sigma	vector of scale parameter values
nu	vector of nu 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
...	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 $\nu > 0$ see pp. 372-373 of Rigby et al. (2019).

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

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

mu	vector of location 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 specific parameterization of the exponential distribution used in EXP is

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

for $y > 0$, $\mu > 0$ see pp. 422-23 of Rigby et al. (2019).

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

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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

[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. $\text{sum}(\text{object}\$pdf * \text{diff}(\text{object}\$x)[1])$
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)),
      exptiles=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 $\sigma > 0$, see pp. 423-424 of Rigby et al. (2019).

Value

`GA()` returns a `glmss.family` object which can be used to fit a gamma distribution in the `glmss()` 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)
```

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 $\sigma_1 = \sigma\mu^{(\nu/2)-1}$ $\sigma > 0$ and $-\infty < \nu < \infty$ see pp. 442-443 of Rigby et al. (2019).

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

[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	PARET02()	2
Pareto type 2 original	PARET02o()	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 maen)	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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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. 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.

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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<-NO(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 <= x], otherwise, P[X > x]
<code>p</code>	vector of probabilities.
<code>n</code>	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 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 $0 < y < 1$, $0 < \mu < 1$, $0 < \sigma < 1$, $\nu > 0$, $\tau > 0$ and where $\alpha = \mu(1 - \sigma^2)/\sigma^2$ and $\beta = (1 - \mu)(1 - \sigma^2)/\sigma^2$, and $\alpha > 0$, $\beta > 0$. Note the $\mu = \alpha/(\alpha + \beta)$, $\sigma = (\alpha + \beta + 1)^{-1/2}$ see pp. 464-465 of Rigby et al. (2019).

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 $y > 0$, $\mu > 0$, $\sigma > 0$, $\nu > 0$ and $\tau > 0$ see pp. 452-453 of Rigby et al. (2019).

Note that by setting $\sigma = 1$ we have the Pearson type VI, by setting $\nu = 1$ we have the Burr type XII and by setting $\tau = 1$ the Burr type III.

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.
- 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. An older version can be found in <https://www.gamlss.com/>.
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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 `mu`. 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 <code>log</code> 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 <code>TRUE</code> , probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if <code>TRUE</code> (default), probabilities are <code>P[X <= x]</code> , otherwise <code>P[X > x]</code>
<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 original geometric distribution in the function `GEOM` is:

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

for $y = 0, 1, 2, 3, \dots$ and $\mu > 0$, see pp 472-473 of Rigby et al. (2019).

The parameterization of the original geometric distribution, `GEOMo` is

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

for $y=0,1,2,3,\dots$ and $\mu > 0$, see pp 473-474 of Rigby et al. (2019).

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.
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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
(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 $-\infty < \nu < +\infty$ see pp. 443-444 of Rigby et al. (2019). 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. 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

$$f(y|\mu, \sigma, \nu) = \left(\frac{b}{\mu}\right)^\nu \left[\frac{y^{\nu-1}}{2K_\nu(\sigma^{-2})}\right] \exp\left[-\frac{1}{2\sigma^2} \left(\frac{by}{\mu} + \frac{\mu}{by}\right)\right]$$

where $b = \frac{K_{\nu+1}(\frac{1}{\sigma^2})}{K_\nu(\frac{1}{\sigma^2})}$, for $y > 0$, $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < +\infty$ see pp 445-446 of Rigby et al. (2019).

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. 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.
- 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
- 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

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 mu
sigma	vector of positive dispersion parameter sigma
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

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 $\sigma > 0$ see pp. 481-483 of Rigby *et al.* (2019).

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

See Also

[gamlss.family](#), [PO](#), [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 <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 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 $\tau > 0$, see pp. 387-388 of Rigby et al. (2019).

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.
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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. (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 $\log(p)$.
<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 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 $\sigma > 0$, see pp. 366-367 of Rigby et al. (2019).

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

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

for $y > 0$, $\mu > 0$ and $\sigma > 0$ see pp. 426-427 of Rigby et al. (2019).

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. 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, doi10.18637/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 (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 <code>log</code> link as the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with <code>log</code> 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 <code>TRUE</code> , probabilities <code>p</code> are given as <code>log(p)</code>
<code>lower.tail</code>	logical; if <code>TRUE</code> (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 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 $\sigma > 0$ see pp. 424-426 of Rigby et al. (2019).

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()`, `mu` 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. An older version can be found in <https://www.gamlss.com/>.
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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"))
```

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 mu parameter. Other links are "inverse" "log" ans "own"
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma parameter. Other links are "inverse", "identity" ans "own"
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" link as the default for the nu 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 tau parameter. Other links are "onverse", "identity" ans "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 <code>length(n) > 1</code> , the length is taken to be the number required

Details

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

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

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

$$z = -\nu + \tau \sinh^{-1}(s)$$

,

$$s = \frac{y - \mu + c\sigma w^{\frac{1}{2}} \sinh(\nu/\tau)}{c\sigma}$$

,

$$c = \left\{ \frac{1}{2}(w - 1) [w \cosh(2\nu/\tau) + 1] \right\}^{-\frac{1}{2}}$$

and

$$w = e^{1/\tau^2}$$

see pp. 393-394 of Rigby et al. (2019).

This is a reparameterization of the original Johnson Su distribution, Johnson (1954), so the parameters μ and σ are the mean and the standard deviation of the distribution. The parameter ν determines the skewness of the distribution with $\nu > 0$ indicating positive skewness and $\nu < 0$ negative. The parameter τ determines the kurtosis of the distribution. τ should be positive and most likely in the region from zero to 1. As τ 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 than 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. 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.

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

See Also

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

Examples

```
JSU()
plot(function(x)dJSU(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) pJSU(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 <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 original Johnson's SU distribution, (JSUo), is defined as

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

for $-\infty < y < \infty$, $\mu = (-\infty, +\infty)$, $\sigma > 0$, $\nu = (-\infty, +\infty)$ and $\tau > 0$. where $z = \frac{(y-\mu)}{\sigma}$, $r = \nu + \tau \sinh^{-1}(z)$, see pp. 389-390 of Rigby et al. (2019).

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 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.

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(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 $\log(p)$
<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

The parameterization of the logarithmic distribution in the function LG is

$$P(Y = y|\mu) = \alpha\mu^y/y$$

where for $y = 1, 2, 3, \dots$ with $0 < \mu < 1$ and

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

see pp 474-475 of Rigby *et al.* (2019).

For the zero adjusted logarithmic distribution ZALG which is defined for $y = 0, 1, 2, 3, \dots$ see pp 492-494 of Rigby *et al.* (2019).

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.
- 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](#), [PO](#), [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

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" or "log" link depending on the parametrization
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma 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 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 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 $y > 0$, $-\infty < \mu < \infty$ and $\sigma > 0$ see pp. 428-429 of Rigby et al. (2019).

The probability density function in LOGNO2 is defined as

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

for $y > 0$, $-\infty < \mu < \infty$ and $\sigma > 0$ see pp. 429-430 of Rigby et al. (2019).

The probability density function in LNO is defined as

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

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 $\nu = (-\infty, +\infty)$. This is not a proper distribution see for example p. 447 of Rigby et al. (2019).

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. 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.
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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, $P[X > x]$

p	vector of probabilities.
n	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

Definition file for Logistic distribution.

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

for $y = (-\infty, \infty)$, $\mu = (-\infty, \infty)$ and $\sigma > 0$, see page 368 of Rigby et al. (2019).

Value

`L0()` returns a `gamlss.family` object which can be used to fit a logistic distribution in the `gamlss()` function. `dL0()` gives the density, `pL0()` gives the distribution function, `qL0()` gives the quantile function, and `rL0()` 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.
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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 (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

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

for $0 < y < 1$, $0 < \mu < 1$ and $\sigma > 0$ see p 463 of Rigby et al. (2019).

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.

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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, \doi10.18637/jss.v023.i07.

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(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	<i>Normal distribution with a specific mean and variance relationship for fitting a GAMLSS model</i>
------	--

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 mu 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. 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)
```

make.link.gamlss

Create a Link for GAMLSS families

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 $d\text{par}/d\text{eta}$ 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 `logshift01`, and the `own`. For the use of the `own` link see the example below. `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 lambda resulting in power link μ^λ .
family	a gamlss 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(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.
- 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. 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 (see also <https://www.gamlss.com/>).

See Also

[gamlss.family](#)

Examples

```
str(make.link.gamlss("logshiftto1"))
l2<-make.link.gamlss("logshiftto1")
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 used 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 <code>gamlss</code> 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. 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.

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

(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

```

momentsSK(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

x	data vector or gamlss model
weights	prior weights for the x
cent	the centile required
type	For centile skewness and kurtosis only whether "central" (default) or "tail"
fam	A gamlss distribution family
plotting	what to plot
add	whether to add the line to the existing plot
col	the colour of the line
lty	the type of the line
lwd	the width of the line
ylim	the y limit of the graph
p	the value determining the centile skewness or kurtosis
...	additional arguments pass to theoCentileSK() function i.e. the values of the distribution parameters
bootstrap	whether a plot of the bootstrap skewness and kurtosis measures should be added in the plot
no.bootstrap	the number of bootstrap skewness and kurtosis measures
col.bootstrap	the colour for bootstraps

pch.bootstrap	the point type of bootstraps
asCharacter	whether to plot the estimated skewness and kurtosis measure as character or as point
col.point	the colour of the skewness and kurtosis measure
pch.point	the point type of the skewness and kurtosis measure
lwd.point	the width of the plotted point
text.to.show	to display text different from variable or model
cex.text	the size of the text
col.text	the colour of the text
show.legend	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 ransformed 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:	transfomed 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:

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

The function `theoCentileSK` for a given `gamlss.family` produces:

<code>IR</code>	the interquartile range of the distribution
<code>SIR</code>	the semi interquartile range of the distribution
<code>S_0.25</code>	the central skewness of the distribution
<code>S_0.01</code> :	the tail skewness of the distribution
<code>K_0.01</code> :	the centile kurtosis of the distribution
<code>sK_0.01</code> :	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. 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 (see also <https://www.gamlss.com/>).

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")

```

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 $\mu + \sigma\mu^\nu$. For more details see pp 507-508 of Rigby *et al.* (2019).

The zero inflated negative binomial family ZINBF is defined as an inflated at zero NBF.

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. 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 (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 mu parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma 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 p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are P[X <= 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 , see also pp. 483-485 of Rigby *et al.* (2019).

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.
- 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. 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.
- 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
(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=NBII, 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

<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 $\log(p)$
<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 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, see also pp. 485-487 of Rigby *et al.* (2019).

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

- Evans, D. A. (1953). Experimental evidence concerning contagious distributions in ecology. *Biometrika*, **40**: 186-211.
- Johnson, N. L., Kotz, S. and Kemp, A. W. (1993). *Univariate Discrete Distributions*, 2nd edn. Wiley, New York.
- 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. 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.
- 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 (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)
```

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

For more details about the NET distribution please refer to pp. 393-396 of Rigby et al. (2019).

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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SStasinopoulos 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

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

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

Normal distribution for fitting a GAMLSS

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 $\log(p)$.
<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 `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 $\sigma > 0$ see pp. 369-370 of Rigby et al. (2019).

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

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](#), [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
```

NO2

Normal distribution (with variance as sigma parameter) for fitting a GAMLSS

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 $\sigma > 0$ see p. 370 of Rigby et al. (2019).

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

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, NO](#)

Examples

```
NOF()# 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
```

NOF

Normal distribution family for fitting a GAMLSS

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 <code>log(p)</code> .

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 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 $\nu = (-\infty, +\infty)$ see pp. 373-374 of Rigby et al. (2019).

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

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

[gamlss.family](#), [NO](#), [NO2](#)

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=NO, 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=NO, data=abdom, method=mixed(1,20))
GAIC(m1,m2,m3)

## End(Not run)
```

PARETO2

Pareto distributions for fitting in GAMLSS

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 $y > \mu$ therefore 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 corresponds 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 1 original distribution in the function PARETO1o is:

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

for $y \geq 0$, $\mu > 0$ and $\sigma > 0$ see pp. 430-431 of Rigby et al. (2019).

The parameterization of the Pareto Type 2 original distribution in the function PARETO2o is:

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

for $y \geq 0$, $\mu > 0$ and $\sigma > 0$ see pp. 432-433 of Rigby et al. (2019).

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 $\sigma > 0$ see pp.433-434 The parameterization of the Pareto Type 1 original distribution in the function PARETO1o is:

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

for $y \geq 0$, $\mu > 0$ and $\sigma > 0$ see pp. 430-431 of Rigby et al. (2019).

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

References

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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. 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.

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

(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, dPARETO2(y), type="l" , lwd=2)
q<-seq(0,20,0.2)
plot(q, pPARETO2(q), ylim=c(0,1), type="l", lwd=2)
p<-seq(0.0001,0.999,0.05)
plot(p, qPARETO2(p), type="l", lwd=2)
dat <- rPARETO2(100)
hist(rPARETO2(100), nclass=30)
#summary(gamlss(a~1, family="PARETO2"))
```

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:

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

where $z = (y - \mu)/c\sigma$ and $c^2 = \Gamma(1/\nu) [\Gamma(3/\nu)]^{-1}$, 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), see p. 374 of Rigby et al. (2019)

The Power Exponential distribution (PE2) is defined as

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

see p. 376 of Rigby et al. (2019)

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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(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

`mu.link` Defines the `mu.link`, 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>mu.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 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 p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are P[X <= 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 q

Details

The probability function of the Poisson-inverse Gaussian distribution PIG, 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, see also pp. 487-489 of Rigby *et al.* (2019). [Note that the above parameterization was used by Dean, Lawless and Willmot(1989). It is also a special case of the Sichel distribution SI(ν) when $\nu = -\frac{1}{2}$.]

The probability function of the Poisson-inverse Gaussian distribution PIG2, is given by

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

for $y = 0, 1, 2, \dots, \infty, \mu > 0$ and $\sigma > 0$ and $\alpha = [(\mu^2 + \sigma^2)^{0.5} - \mu]^{-1}$, $K_\lambda(t) = \frac{1}{2} \int_0^\infty x^{\lambda-1} \exp\{-\frac{1}{2}t(x+x^{-1})\} dx$ is the modified Bessel function of the third kind, see pp. 487-489 of Rigby *et al.* (2019).

The definition of the zero adjusted Poisson inverse Gaussian distribution, ZAPIG and the zero inflated Poisson inverse Gaussian distribution, ZIPIG, are given in p. 513 and pp. 514-515 of Rigby *et al.* (2019), respectively.

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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- Heller, G. Z., Couturier, D.L. and Heritier, S. R. (2018) Beyond mean modelling: Bias due to misspecification of dispersion in Poisson-inverse Gaussian regression *Biometrical Journal*, **2**, pp 333-342.
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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()
```

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 $\mu > 0$ see ee pp 476-477 of Rigby et al. (2019).

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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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.

(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

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

See Also

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

Examples

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

# plotting the distribution
plot(function(y) dPO(y, mu=10 ), from=0, to=20, n=20+1, type="h")
# creating random variables and plot them
tN <- table(Ni <- rPO(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)
```

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

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

for $y = (-\infty, \infty)$, $\mu = (-\infty, +\infty)$ and $\sigma > 0$ see pp. 370-371 of Rigby et al. (2019).

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

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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

Reverse generalized extreme family distribution for fitting a GAMLSS

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 <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

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 `RGE(μ, σ, ν)` or as `Reverse.Generalized.Extreme.Family(μ, σ, ν)`.

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 Akantziotou

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
(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 *The Skew exponential power type 1-4 distribution for fitting a GAMLSS*

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

mu.link	Defines the mu.link, with "identity" link as the default for the mu parameter. Other links are "inverse" 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 "log" link as the default for the nu parameter. Other links are "identity" and "inverse"
tau.link	Defines the tau.link, with "log" link as the default for the tau parameter. Other links are "inverse", 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

Details

The probability density function of the Skew Power exponential distribution type 1, (SEP1), is defined as

$$f_Y(y|\mu, \sigma, \nu, \tau) = \frac{2}{\sigma} f_{Z_1}(z) F_{Z_1}(\nu z)$$

for $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$, $-\infty < \nu < \infty$, and $\tau > 0$ where $z = (y - \mu)/\sigma$, and $Z_1 \sim \text{PE2}(0, \tau^{1/\tau}, \tau)$, see pp 401-402 of Rigby et al. (2019).

The probability density function of the Skew Power exponential distribution type 2, (SEP2), is defined as

$$f_Y(y|\mu, \sigma, \nu, \tau) = \frac{2}{\sigma} f_{Z_1}(z) \Phi_{Z_1}(\omega)$$

for $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$, $-\infty < \nu < \infty$, and $\tau > 0$ where $z = (y - \mu)/\sigma$, and $\omega = \text{sign}(z)|z|^{\tau/2}\nu\sqrt{2/\tau}$, and $Z_1 \sim \text{PE2}(0, \tau^{1/\tau}, \tau)$, see pp 402-404 of Rigby et al. (2019).

For SEP3 and SEP3 see pp 404-406 and pp 407-408 of Rigby et al. (2019), respectively.

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 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 <= x], otherwise, P[X > x]
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If 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 $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$, $\nu > 0$ and $\tau > 0$, see pp. 396-397 of Rigby et al. (2019).

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,

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

where

$$r = \sinh(\tau \sinh^{-1}(z) - \nu)$$

and

$$c = \cosh(\tau \sinh^{-1}(z) - \nu)$$

and $z = (y - \mu)/\sigma$ for $-\infty < y < \infty$, $-\infty < \mu < +\infty$, $\sigma > 0$, $-\infty < \nu < +\infty$ and $\tau > 0$, see pp. 398-400 of Rigby et al. (2019)

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

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

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)

Bob Rigby, Mikis Stasinopoulos and Fiona McElduff

References

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- Jones and Pewsey (2009) Sinh-arcsinh distributions. *Biometrika*. **96**(4), pp. 761-780.
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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))
```

SI

The Sichel distribution for fitting a GAMLSS model

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>

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
y	the y variable. The function tofyS() should be not used on its own.
what	take values 1 or 2, for function tofyS().

Details

The probability function of the Sichel distribution is given by

$$f(y|\mu, \sigma, \nu) = \frac{\mu^y K_{y+\nu}(\alpha)}{y!(\alpha\sigma)^{y+\nu} K_\nu(\frac{1}{\sigma})}$$

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 $\sigma = [(\mu^2 + \alpha^2)^{\frac{1}{2}} - \mu]^{-1}$. See also pp 510-511 of Rigby *et al.* (2019).

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

References

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- (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

<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>tau.link</code>	Defines the <code>tau.link</code> , with "logit" link as the default for the <code>tau</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>nu</code>	vector of <code>nu</code>
<code>tau</code>	vector of probabilities <code>tau</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>obj</code>	a fitted Sichel <code>gamlss</code> model
<code>y</code>	the <code>y</code> variable, the <code>tofySICHEL()</code> should not be used on its own.

Details

The probability function of the Sichel distribution SICHEL is given by

$$f(y|\mu, \sigma, \nu) = \frac{(\mu/b)^y K_{y+\nu}(\alpha)}{y!(\alpha\sigma)^{y+\nu} K_\nu(\frac{1}{\sigma})}$$

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 see pp 508-510 of Rigby *et al.* (2019). 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.

The definition of the zero adjusted Sichel distribution, ZASICHEL and the the zero inflated Sichel distribution, ZISICHEL, are given in pp. 517-518 and pp. 519-520 of of Rigby *et al.* (2019), respectively.

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. An older version can be found in <https://www.gamlss.com/>.
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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](#), [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, SIMPLEX, is given as

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

for $0 < y < 1$, $0 < \mu < 1$ and $\sigma > 0$ see p 464 of Rigby et al. (2019).

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. 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.

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

(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)
```

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>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 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

$$f(y|\mu, \sigma, \nu) = \frac{2}{\sigma} \phi(z) \Phi(\nu z)$$

for $(-\infty < y < +\infty)$, $(-\infty < \mu < +\infty)$, $\sigma > 0$ and $(-\infty < \nu < +\infty)$ where $z = (y - \mu)/\sigma$ and $\phi()$ and $\Phi()$ are the pdf and cdf of the standard normal distribution, respectively, see pp. 378-379 of Rigby et al. (2019).

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. 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 (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

Skew Normal Type 2 distribution for fitting a GAMLSS

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

<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 "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>nu</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 parameterization of the Skew Normal Type 2 distribution in the function `SN2` is

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

if $y < \mu$

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

if $y \geq \mu$

for $(-\infty < y < +\infty)$, $(-\infty < \mu < +\infty)$, $\sigma > 0$ and $\nu > 0$ where $z = (y - \mu)/\sigma$ and $c = \sqrt{2\nu} / [\sqrt{\pi}(1 + \nu^2)]$ see pp. 380-381 of Rigby et al. (2019).

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.
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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.
- 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 (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), see pp. 411-412 of Rigby et al. (2019).

The skew t type 2 distribution, ST2, is based on Azzalini and Capitanio (2003) see pp. 412-414 of Rigby et al. (2019).

The skew t type 3 , ST3 and ST3C, distribution is based Fernande and Steel (1998) see pp 413-415 of Rigby et al. (2019). 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 see see pp 413-415 of Rigby et al. (2019).

The skew t type 5 distribution , ST5, is Jones and Faddy (2003).

The SST is a reparametrised version of ST3 where σ 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/mu²" 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 "identity" link as the default for the <code>nu</code> parameter. Other links are " $1/\mu^2$ " and "log"
<code>tau.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"
<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 <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

Details

The definitions of all Skew t distributions is given in pp.409-420 of of Rigby et al. (2019).

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

- Azzalini A. (1986) Further results on a class of distributions which includes the normal ones, *Statistica*, **46**, pp. 199-208.
- Azzalini A. and Capitanio, A. Distributions generated by perturbation of symmetry with emphasis on a multivariate skew t-distribution, *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **65**, pp. 367-389.
- Jones, M.C. and Faddy, M. J. (2003) A skew extension of the t distribution, with applications. *Journal of the Royal Statistical Society, Series B*, **65**, pp 159-174.
- Fernandez, C. and Steel, M. F. (1998) On Bayesian modeling of fat tails and skewness. *Journal of the American Statistical Association*, **93**, pp. 359-371.
- 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. 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.

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

(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 `TF()`:

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

for $-\infty < y < +\infty$, $-\infty < \mu < +\infty$, $\sigma > 0$ and $\nu > 0$ see pp. 382-383 of Rigby et al. (2019). Note that $z = (y - \mu)/\sigma$ has a standard t distribution with degrees of freedom ν see pp. 382-383 of Rigby et al. (2019).

Definition file for t family distribution `TF2()`:

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

for $-\infty < y < +\infty$, $-\infty < \mu < +\infty$, $\sigma > 0$ and $\nu > 2$ see pp. 382-383 of Rigby et al. (2019). Note that $z = (y - \mu)/\sigma$ has a standard t distribution with degrees of freedom ν see pp. 383-384 of Rigby et al. (2019).

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.
- 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

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 mu parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the sigma 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 mu values.
<code>sigma</code>	vector of positive sigma 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 p are given as $\log(p)$.
<code>max.value</code>	constant; generates a sequence of values for the cdf function.

Details

The Waring distribution, `WARING`, has density,

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

for $y = 0, 1, 2, \dots$, $\mu > 0$ and $\sigma > 0$ see pp. 490-492 of Rigby *et al.* (2019).

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

- Wimmer, G. and Altmann, G. (1999) *Thesaurus of univariate discrete probability distributions*. Stamm.
- 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. 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 (see also <https://www.gamlss.com/>).

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

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the mu 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 sigma parameter, other link is the "inverse", "identity" and "own"
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of the mu parameter
<code>sigma</code>	vector of sigma 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>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 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 $\sigma > 0$ see pp. 435-436 of Rigby et al. (2019). 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.

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. 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.

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 (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	<i>A specific parameterization of the Weibull distribution for fitting a GAMLSS</i>
------	---

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

<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 WEI2 is given by

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

for $y > 0$, $\mu > 0$ and $\sigma > 0$, see pp. 436-437 of Rigby et al. (2019). 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 Akantziotou

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. 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.

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

(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	<i>A specific parameterization of the Weibull distribution for fitting a GAMLSS</i>
------	---

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 <= 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 $\sigma > 0$ see pp. 437-438 of Rigby et al. (2019). 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 $\mu^2 \left\{ \Gamma(2/\sigma + 1) / [\Gamma(1/\sigma + 1)]^2 - 1 \right\}$ see pp. 438 of Rigby et al. (2019)

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. 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.

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

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

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	<i>Yule distribution for fitting a GAMLSS model</i>
------	---

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 $\mu > 0$, see pp 477-478 of Rigby et al. (2019).

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. 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

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

The definition of the zero adjusted beta binomial distribution, ZABB and the the zero inflated beta binomial distribution, ZIBB, are given in p. 527 and p. 528 of of Rigby *et al.* (2019), respectively.

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..
- 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
(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')
```

ZABI

Zero inflated and zero adjusted Binomial distribution for fitting in GAMLSS

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

The definition of the zero adjusted binomial distribution, ZABI and the zero inflated binomial distribution, ZIBI, are given in p. 526 and p. 527 of Rigby *et al.* (2019), respectively.

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. 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.

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

(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 <= 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 <code>gamLSS</code> object
<code>main</code>	for title in the plot
<code>...</code>	... can be used to pass the <code>uppr.limit</code> argument to <code>qIG</code>

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. 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.

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

(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

<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
<code>obj</code>	a fitted BEINF object
<code>main</code>	for title in the plot
<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. 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.
- 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 (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 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 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 of the zero adjusted Negative Binomial type I distribution, ZANBI and the the zero inflated Negative Binomial type I distribution, ZINBI, are given in p. 512 and pp. 513-514 of of Rigby *et al.* (2019), respectively.

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. 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.
- 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 (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')
```

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

Details about the zero adjusted Poisson, ZAP can be found pp 494-496 of Rigby *et al.* (2019).

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. 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.

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

(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 $y = 0, 1, \dots$ see pp 498-500 of Rigby *et al.* (2019). .

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.
- 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. 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.

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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

The parametrization used for this version of the zero inflated Poisson distribution ZIP2 can be found in pp 500-501 of Rigby *et al.* (2019). Note that 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.
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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 distribution
# 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 <code>mu</code> with default <code>log</code>
<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 <code>log(p)</code>
<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 $\zeta() = \sum_i^n i^{-b}$ is the (Reimann) zeta function.

The distribution has mean $\zeta(\mu)/\zeta(\mu+1)$ and variance $\zeta(\mu+1)\zeta(\mu-1) - [\zeta(\mu)]^2/[\zeta(\mu+1)]^2$, see pp 479-480 of Rigby et al. (2019)

For more details about the zero-adjusted Zipf distributions, ZAZIPF, see see pp 496-498 of Rigby et al. (2019).

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>
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(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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