

Package ‘gamlss.dist’

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Author c(person("Mikis", "Stasinopoulos", role = c("aut", "cre", "cph"),
email = "d.stasinopoulos@londonmet.ac.uk"),
person("Bob", "Rigby", role = c("aut")),
person("Calliope", "Akantziliotou", role = "ctb"),
person("Vlasios", "Voudouris", role = "ctb",
email= "vlasios.voudouris@abm-analytics.com"),
person("Gillian", "Heller", role = "ctb"),
person("Raydonal", "Ospina", role = "ctb",
email= "rospina@ime.usp.br"),
person("Nicoletta", "Motpan", role = "ctb"),
person("Fiona", "McElduff", role = "ctb"),
person("Majid", "Djennad", role = "ctb"),
person("Marco", "Enea", role = "ctb"),
person("Alexios", "Ghalanos", role = "ctb"),
person("Christos", "Argyropoulos", role = "ctb"),
person("Almond", "Stocker", role = "ctb")
)

Maintainer Mikis Stasinopoulos <d.stasinopoulos@londonmet.ac.uk>

Depends R (>= 2.15.0), MASS, graphics, stats, methods

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.

License GPL-2 | GPL-3

URL <http://www.gamlss.org/>

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gamlss.dist-package *The GAMLSS distributions*

Description

This package contains all distributions to be used for GAMLSS models. Each distributions has its probability function, d , its commutative probability function, p , the inverse of the commutative probability function, q , its random generation function, r , and also the `gamlss.family` generating function

Details

Package: gamlss.dist
 Type: Package
 Version: 1.5.0
 Date: 2006-12-13
 License: GPL (version 2 or later)

This package is design to be used with the package **gamlss** but the d, p, q and r functions can be used separately.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby <r.rigby@londonmet.ac.uk> with contributions from Calliope Akantziliotou and Raydonal Ospina <rospina@ime.usp.br>.

Maintainer: Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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.

Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2003) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>)

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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#)

Examples

```

plot(function(y) dSICHEL(y, mu=10, sigma = 0.1 , nu=1 ), from=0, to=30, n=30+1, type="h") # pdf
# 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)

```

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 mu 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 sigma 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 p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
<code>fast</code>	a logical variable if <code>fast=TRUE</code> the <code>dBB</code> function is used in the calculation of the inverse c.d.f function. This is faster to the default <code>fast=FALSE</code> , where the <code>pBB{}</code> is used, but not always consistent with the results obtained from <code>pBB()</code> , for example if <code>p <- pBB(c(0,1,2,3,4,5), mu=.5, sigma=1, bd=5)</code> do not ensure that <code>qBB(p, mu=.5, sigma=1, bd=5)</code> will be <code>c(0,1,2,3,4,5)</code>

Details

Definition file for beta binomial distribution.

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

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

Value

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

Warning

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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

`mu.link` Defines the `mu.link`, with "identity" link as the default for the `mu` 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 sigma 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 nu 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 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 probability distribution function of the untruncated Box-Cox Cole and Green distribution, `BCCGuntr`, is defined as

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

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

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

Value

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

Warning

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

Note

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

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Kalliope Akantzi-Iotou

References

- Cole, T. J. and Green, P. J. (1992) Smoothing reference centile curves: the LMS method and penalized likelihood, *Statist. Med.* **11**, 1305–1319
- Rigby, R. A. and Stasinopoulos, D. M. (2004). Smooth centile curves for skew and kurtotic data modelled using the Box-Cox Power Exponential distribution. *Statistics in Medicine*, **23**: 3053-3076.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R.A. Stasinopoulos, D.M. (2006). Using the Box-Cox t distribution in GAMLSS to model skewness and kurtosis. to appear in *Statistical Modelling*.
- Stasinopoulos D. M., Rigby R.A. and Akantzi-Iotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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")
```

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 `dBCPE`, `pBCPE`, `qBCPE` and `rBCPE` define the density, distribution function, quantile function and random generation for the Box-Cox Power Exponential distribution. The function `checkBCPE` can be used, typically when a BCPE 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 BCPE distribution.] See Rigby and Stasinopoulos (2003) for details. The function `BCPEo` is identical to `BCPE` 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 mu 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 sigma 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 nu 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 tau 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 nu parameter values

<code>tau</code>	vector of 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 <code>length(n) > 1</code> , 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 $\tau > 0$.

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

- 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. and Stasinopoulos, D. M. (2004). Smooth centile curves for skew and kurtotic data modelled using the Box-Cox Power Exponential distribution. *Statistics in Medicine*, **23**: 3053-3076.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 `BCT` is identical to `BCT` but with log link for μ .

Usage

```

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

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <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 $\tau > 0$.

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

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

Note

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R.A. Stasinopoulos, D.M. (2006). Using the Box-Cox t distribution in GAMLSS to model skewness and kurtosis. to appear in *Statistical Modelling*.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

BE

The beta distribution for fitting a GAMLSS

Description

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

Usage

```
BE(mu.link = "logit", sigma.link = "logit")
dBET(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")
dBETo(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 <code>mu</code> link function with default <code>logit</code>
<code>sigma.link</code>	the <code>sigma</code> 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 <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, $P[X > x]$

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

Details

The original beta distributions distribution is given as

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

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

Value

returns a `gamlss.family` object which can be used to fit a normal 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

- 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

```

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

```

 BEINF

The beta inflated distribution for fitting a GAMLSS

Description

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

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

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

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

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

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

Usage

```

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

```

```

BEINF1(mu.link = "logit", sigma.link = "logit", nu.link = "log")

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

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

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

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

plotBEINF(mu = 0.5, sigma = 0.5, nu = 0.5, tau = 0.5,
         from = 0.001, to = 0.999, n = 101, ...)
plotBEINF0(mu = 0.5, sigma = 0.5, nu = 0.5,
         from = 1e-04, to = 0.9999, n = 101, ...)
plotBEINF1(mu = 0.5, sigma = 0.5, nu = 0.5,
         from = 1e-04, to = 0.9999, n = 101, ...)

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

```

Arguments

<code>mu.link</code>	the mu link function with default 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

tau	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 BEINF object
...	other graphical parameters for plotting

Details

The beta inflated distribution is given as

$$f(y) = p_0$$

if (y=0)

$$f(y) = p_1$$

if (y=1)

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

otherwise

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

Value

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

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Ospina R. and Ferrari S. L. P. (2010) Inflated beta distributions, *Statistical Papers*, **23**, 111-126.
- 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, <http://www.jstatsoft.org/v23/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.

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 logit
<code>sigma.link</code>	the sigma link function with default log
<code>nu.link</code>	the nu link function with default logit
<code>x,q</code>	vector of quantiles

<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of precision parameter values
<code>nu</code>	vector of parameter values modelling the probability at one
<code>log, log.p</code>	logical; if TRUE, probabilities <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 BEOI object
<code>...</code>	other graphical parameters for plotting

Details

The one-inflated beta distribution is given as

$$f(y) = \nu$$

if $(y = 1)$

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

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

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

Value

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

Note

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

Author(s)

Raydonal Ospina, Department of Statistics, University of Sao Paulo, Brazil.

<rospina@ime.usp.br>

References

- Ferrari, S.L.P., Cribari-Neto, F. (2004). Beta regression for modelling rates and proportions. *Journal of Applied Statistics*, **31** (1), 799-815.
- Ospina R. and Ferrari S. L. P. (2010) Inflated beta distributions, *Statistical Papers*, **23**, 111-126.
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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, <http://www.jstatsoft.org/v23/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.

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
```

Description

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

Usage

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

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

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

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

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

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

meanBEZI(obj)
```

Arguments

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

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)

Raydonal Ospina, Department of Statistics, University of Sao Paulo, Brazil.
 <rospina@ime.usp.br>

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.

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

<code>mu.link</code>	Defines the <code>mu.link</code> , with "logit" link as the default for the <code>mu</code> parameter. Other links are "probit" and "cloglog"(complementary log-log)
<code>x</code>	vector of (non-negative integer) quantiles

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 $0 < \mu < 1$.

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

- 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.

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')

```

 BNB

Beta Negative Binomial distribution for fitting a GAMLSS

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

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

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

The distribution has mean μ .

Value

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

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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.

See Also

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

Examples

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

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

## End(Not run)
```

checklink

Set the Right Link Function for Specified Parameter and Distribution

Description

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

Usage

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

Arguments

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

Value

Defines the right link for each parameter

Author(s)

Calliope Akantziliotou

References

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

See Also

[gamlss.family](#)

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 <= 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:

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

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

Value

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

Author(s)

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

References

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

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)
```

DEL

The Delaporte distribution for fitting a GAMLSS model

Description

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

Usage

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

Arguments

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

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

where

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

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

Value

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

Note

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

Author(s)

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

References

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- Wimmer, G. and Altmann, G (1999). *Thesaurus of univariate discrete probability distributions* . Stamm Verlag, Essen, Germany

See Also

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

Examples

```
DEL()# gives information about the default links for the Delaportte 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))
```

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

- 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.
- 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, <http://www.jstatsoft.org/v23/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.

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

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

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

Value

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

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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, <http://www.jstatsoft.org/v23/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.

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

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

Details

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

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos and Bob Rigby

References

- Cousineau, D. Brown, S. and Heathcote A. (2004) Fitting distributions using maximum likelihood: Methods and packages, *Behavior Research Methods, Instruments and Computers*, **46**, 742-756.
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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.

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

mu.link	Defines the mu.link, with "log" link as the default for the mu parameter, other links are "inverse" and "identity"
x, q	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 $y > 0, \mu > 0$.

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 <mikis.stasinopoulos@gamlss.org>, 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.
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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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#)

Examples

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

flexDist

Non-parametric pdf from limited information data

Description

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

Usage

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

Arguments

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

Value

Returns a list with components

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

Author(s)

Mikis Stasinopoulos, Paul Eilers, Bob Rigby and Vlasios Voudouris

References

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

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.

See Also

[histSmo](#)

Examples

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

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

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 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 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 <code>length(n) > 1</code> , the length is taken to be the number required

Details

The specific parameterization of the gamma distribution used in GA is

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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)
```

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
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	GB1()	4
Generalized Beta type 2	GB2()	4
Generalized Gamma	GG()	3
Generalized Inverse Gaussian	GIG()	3
Generalized t	GT()	4
Geometric	GEOM()	1
Geometric (original)	GEOMo()	1
Gumbel	GU()	2
Inverse Gamma	IGAMMA()	2
Inverse Gaussian	IG()	2
Johnson's SU	JSU()	4
Logarithmic	LG()	1
Logistic	LO()	2
log-Normal	LOGNO()	2
log-Normal (Box-Cox)	LNO()	3 (1 fixed)
Negative Binomial type I	NBI()	2
Negative Binomial type II	NBII()	2
Negative Binomial family	NBF()	3
Normal Exponential t	NET()	4 (2 fixed)
Normal	NO()	2
Normal Family	NOF()	3 (1 fixed)
Normal Linear Quadratic	LQNO()	2
Pareto type 2	PARETO2()	2
Pareto type 2 original	PARETO2o()	2
Power Exponential	PE()	3
Power Exponential type 2	PE2()	3
Poisson	PO()	1
Poisson inverse Gaussian	PIG()	2
Reverse generalized extreme	RGE()	3
Reverse Gumbel	RG()	2
Skew Power Exponential type 1	SEP1()	4
Skew Power Exponential type 2	SEP2()	4
Skew Power Exponential type 3	SEP3()	4
Skew Power Exponential type 4	SEP4()	4
Shash	SHASH()	4
Shash original	SHASHo()	4
Shash original 2	SHASH()	4
Sichel (original)	SI()	3
Sichel (mu as the maen)	SICHEL()	3
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)	<code>WEI3()</code>	2
Yule	<code>YULE()</code>	1
Zero adjusted binomial	<code>ZABI()</code>	2
Zero adjusted beta neg. bin.	<code>ZABNB()</code>	4
Zero adjusted IG	<code>ZAIG()</code>	2
Zero adjusted logarithmic	<code>ZALG()</code>	2
Zero adjusted neg. bin.	<code>ZANBI()</code>	3
Zero adjusted poisson	<code>ZAP()</code>	2
Zero adjusted Sichel	<code>ZASICHEL()</code>	4
Zero adjusted Zipf	<code>ZAZIPF()</code>	2
Zero inflated binomial	<code>ZIBI()</code>	2
Zero inflated beta neg. bin.	<code>ZIBNB()</code>	4
Zero inflated neg. bin.	<code>ZINBI()</code>	3
Zero inflated poisson	<code>ZIP()</code>	2
Zero inf. poiss.(mu as mean)	<code>ZIP2()</code>	2
Zero inflated PIG	<code>ZIPIG()</code>	3
Zero inflated Sichel	<code>ZISICHEL()</code>	4
Zipf	<code>ZIPF()</code>	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)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

GB1

The generalized Beta type 1 distribution for fitting a GAMLSS

Description

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

Usage

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

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" link as the default for the <code>mu</code> parameter.
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" link as the default for the <code>sigma</code> parameter.
<code>nu.link</code>	Defines the <code>nu.link</code> , with "log" link as the default for the <code>nu</code> parameter.
<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the <code>tau</code> parameter.
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness <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 1, (GB1), is defined as

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

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

Value

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

Warning

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

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

GB2

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

Description

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

Usage

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

```

log.p = FALSE)
qGB2(p, mu = 1, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE,
log.p = FALSE)
rGB2(n, mu = 1, sigma = 1, nu = 1, tau = 0.5)

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

```

Arguments

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

Details

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

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

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

Value

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

Warning

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

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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, <http://www.jstatsoft.org/v23/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.

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 <code>gamlss.family</code> distribution
type	the type of transformation only "log" and "logit" are allowed
local	It is TRUE if is called within <code>gamlss()</code> 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 <mikis.stasinopoulos@gamlss.org> and Bob Rigby

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

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)
```

 GEOM

Geometric distribution for fitting a GAMLSS model

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 $P[X \leq x]$, 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 original geometric distribution in the function GE is

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

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

The parameterization of the geometric distribution in the function GEOM is

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

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

Value

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

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

- Johnson, N. L., Kemp, A. W., and Kotz, S. (2005). *Univariate discrete distributions*. Wiley.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, 54, part 3, pp 507-554.
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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.

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, dGEMO(y), type="h")
q <- seq(0, 20, 1)
plot(q, pGEMO(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qGEMO(p), type="s")
dat <- rGEMO(100)
hist(dat)
#summary(gamlss(dat~1, family="GE"))

```

GG

*Generalized Gamma distribution for fitting a GAMLSS***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 <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

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

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

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

Value

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Nicoleta Motpan

References

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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.

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)

```

GIG

*Generalized Inverse Gaussian distribution for fitting a GAMLSS***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, $P[X > x]$

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

Value

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.
- Jorgensen B. (1982) Statistical properties of the generalized inverse Gaussian distribution, Series: Lecture notes in statistics; 9, New York : Springer-Verlag.

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 $\sigma > 0$.

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.

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, <http://www.jstatsoft.org/v23/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.

(see also <http://www.gamlss.org/>).

See Also

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

Examples

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

Description

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

Usage

```

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

```

Arguments

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

Details

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

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

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

Value

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

Warning

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

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 $\sigma > 0$.

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 <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziliotou

References

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

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Stasinopoulos D. M., Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/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.

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 <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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)
```

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 $\sigma > 0$.

Value

returns a `gamlss.family` object which can be used to fit a 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.
- 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 <http://www.gamlss.org/>)
- 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, <http://www.jstatsoft.org/v23/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.

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 link</code> 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 $\sigma > 0$.

Value

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

Note

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

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, 54, part 3, pp 507-554.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 = 0.5, log = FALSE)
pJSU(q, mu = 0, sigma = 1, nu = 1, tau = 0.5, lower.tail = TRUE, log.p = FALSE)
qJSU(p, mu = 0, sigma = 1, nu = 0, tau = 0.5, lower.tail = TRUE, log.p = FALSE)
rJSU(n, mu = 0, sigma = 1, nu = 0, tau = 0.5)
```

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

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

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

This is a reparameterization of the original Johnson Su distribution, Johnson (1954), so the parameters 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

```
JSUo()
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 ordinal Johnson's SU distribution, (JSU), is defined as

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

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

Value

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

Warning

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> 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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- 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, <http://www.jstatsoft.org/v23/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.

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

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

The parameterization of the logarithmic distribution in the function LM is

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

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

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

Value

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.

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 <http://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, <http://www.jstatsoft.org/v23/i07>.

Rigby, R. A. and Stasinopoulos D. M. (2010) The `gamlss.family` distributions, (distributed with this package or see <http://www.gamlss.org/>)

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.

See Also

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

Examples

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

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 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 probability density function in LOGNO is defined as

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

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

The probability density function in LNO is defined as

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

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

Value

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

Warning

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

Note

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Box, G. E. P. and Cox, D. R. (1964) An analysis of transformations (with discussion), *J. R. Statist. Soc. B.*, **26**, 211–252
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
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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, <http://www.jstatsoft.org/v23/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.

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 mu parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" 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>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

Definition file for Logistic distribution.

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.

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 <= 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 in LOGITNO is defined as

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

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

Value

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

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

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

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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

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

Author(s)

Christos Argyropoulos

References

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 bellow. `show.link` provides a way in which the user can identify the link functions available for each `gamlss` distribution. If your required link function is not available for any of the `gamlss` distributions you can add it in.

Usage

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

Arguments

link	character or numeric; one of "logit", "probit", "cloglog", "identity", "log", "sqrt", "1/mu^2", "inverse", "logshifted", "logitshifted", or number, say 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 defining 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", "Bo`

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.

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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#)

Examples

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

## bring the data
# library(gamlss)
#data(aep)
# fitting the model using "own"
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link="own"), data=aep)
# model h1 should be identical to the probit
```

```

# h2<-gamlss(y~ward+loglos+year, family=BI(mu.link="probit"), data=aep)
# now using a function instead of "own"
probittest <- function()
{
linkfun <- function(mu) { qNO(p=mu)}
linkinv <- function(eta)
  {
    thresh <- -qNO(.Machine$double.eps)
    eta <- pmin(thresh, pmax(eta, -thresh))
    pNO(eta)
  }
mu.eta <- function(eta) pmax(dNO(eta), .Machine$double.eps)
valideta <- function(eta) TRUE
link <- "probitTest"
structure(list(linkfun = linkfun, linkinv = linkinv, mu.eta = mu.eta,
  valideta = valideta, name = link), class = "link-gamlss")
}
# h3<-gamlss(y~ward+loglos+year, family=BI(mu.link=probittest()), data=aep)
# Second try the complementary log-log
# using the Gumbel distribution
own.linkfun <- function(mu) { qGU(p=mu)}
own.linkinv <- function(eta) {
  thresh <- -qGU(.Machine$double.eps)
  eta <- pmin(thresh, pmax(eta, -thresh))
  pGU(eta)}
own.mu.eta <- function(eta) pmax(dGU(eta), .Machine$double.eps)
own.valideta <- function(eta) TRUE
# h1 and h2 should be identical to cloglog
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link="own"), data=aep)
# h2<-gamlss(y~ward+loglos+year, family=BI(mu.link="cloglog"), data=aep)
# note that the Gumbel distribution is negatively skew
# for a positively skew link function we can use the Reverse Gumbel
revloglog <- function()
{
linkfun <- function(mu) { qRG(p=mu)}
linkinv <- function(eta) {
  thresh <- -qRG(.Machine$double.eps)
  eta <- pmin(thresh, pmax(eta, -thresh))
  pRG(eta)}
mu.eta <- function(eta) pmax(dRG(eta), .Machine$double.eps)
valideta <- function(eta) TRUE
link <- "revloglog"
structure(list(linkfun = linkfun, linkinv = linkinv, mu.eta = mu.eta,
  valideta = valideta, name = link), class = "link-gamlss")
}
# h1<-gamlss(y~ward+loglos+year, family=BI(mu.link=revloglog()), data=aep)
# a considerable improvement in the deviance
# try a shifted logit link function from -1, 1
own.linkfun <- function(mu)
  { shift = c(-1,1)
    log((mu-shift[1])/(shift[2]-mu))
  }
own.linkinv <- function(eta)

```

```

    {
      shift = c(-1,1)
      thresh <- -log(.Machine$double.eps)
      eta <- pmin(thresh, pmax(eta, -thresh))
      shift[2]-(shift[2]-shift[1])/(1 + exp(eta))
    }
  own.mu.eta <- function(eta)
  {
    shift = c(-1,1)
    thresh <- -log(.Machine$double.eps)
    res <- rep(.Machine$double.eps, length(eta))
    res[abs(eta) < thresh] <- ((shift[2]-shift[1])*exp(eta)/(1 +
      exp(eta))^2)[abs(eta) < thresh]
    res
  }
  own.valideta <- function(eta) TRUE
  #-----
  str(make.link.gamlss("own"))
  l2<-make.link.gamlss("own")
  l2$linkfun(0) # should be zero
  l2$linkfun(1) # should be Inf
  l2$linkinv(-5:5)

```

Description

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

Usage

```

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

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

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

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

```

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

Arguments

<code>mu.link</code>	the link function for mu
<code>sigma.link</code>	the link function for sigma
<code>nu.link</code>	the link function for nu
<code>tau.link</code>	the link function for tau
<code>x</code>	the x variable
<code>q</code>	vector of quantiles
<code>p</code>	vector of probabilities
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$.
<code>log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$.
<code>log</code>	logical; if TRUE, probabilities p are given as $\log(p)$.
<code>n</code>	the number of observations
<code>mu</code>	the mu parameter
<code>sigma</code>	the sigma parameter
<code>nu</code>	the nu parameter
<code>tau</code>	the tau parameter
<code>type</code>	permitted values are 2 (Binomial), 3, 4, and 5
<code>model</code>	a <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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

NBF

Negative Binomial Family distribution for fitting a GAMLSS

Description

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

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

Usage

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

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

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

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

```

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

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

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

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

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

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

```

Arguments

<code>mu.link</code>	The link function for <code>mu</code>
<code>sigma.link</code>	The link function for <code>sigma</code>
<code>nu.link</code>	The link function for <code>nu</code>
<code>tau.link</code>	The link function for <code>tau</code>
<code>x</code>	vector of (non-negative integer)
<code>mu</code>	vector of positive means
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of power parameter
<code>tau</code>	vector of inflation 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>q</code>	vector of quantiles
<code>n</code>	number of random values to return

Details

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

Value

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

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- Anscombe, F. J. (1950) Sampling theory of the negative binomial and logarithmic distributions, *Biometrika*, **37**, 358-382.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.
- 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.

See Also

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

Examples

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

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

NBI

Negative Binomial type I distribution for fitting a GAMLSS

Description

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

Usage

```
NBI(mu.link = "log", sigma.link = "log")
dnBI(x, mu = 1, sigma = 1, log = FALSE)
pNBI(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qNBI(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rNBI(n, mu = 1, sigma = 1)
```

Arguments

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

Details

Definition file for Negative Binomial type I distribution.

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

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

Value

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

Warning

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziliotou

References

- Anscombe, F. J. (1950) Sampling theory of the negative binomial and logarithmic distribution, *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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

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

 NBII

Negative Binomial type II distribution for fitting a GAMLSS

Description

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

Usage

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

Arguments

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

Details

Definition file for Negative Binomial type II distribution.

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.

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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

NET

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

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

Usage

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

Arguments

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

Details

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

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

Value

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

References

- Rigby, R. A. and Stasinopoulos, D. M. (1994), Robust fitting of an additive model for variance heterogeneity, *COMPSTAT : Proceedings in Computational Statistics*, editors: R. Dutter and W. Grossmann, pp 263-268, Physica, Heidelberg.
- 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required

Details

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

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Calliope Akantziliotou

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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 $\sigma > 0$.

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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- 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.

See Also

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

Examples

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

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 in a GAMLSS fitting 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. The functions `dNOF`, `pNOF`, `qNOF` and `rNOF` define the density, distribution function, quantile function and random generation for the NOF parametrization of the normal distribution family.

Usage

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

Arguments

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

Details

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

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

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

Value

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

Note

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

- Davidian, M. and Carroll, R. J. (1987), Variance Function Estimation, *Journal of the American Statistical Association*, Vol. **82**, pp. 1079-1091
- 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

```
NOF()# gives information about the default links for the normal distribution family
# library(gamlss)
#data(abdom)
## the normal distribution fit with constant sigma
#m1<-gamlss(y~poly(x,2), sigma.fo=~1, family=NO, data=abdom)
## the normal family fit with variance proportional to mu
#m2<-gamlss(y~poly(x,2), sigma.fo=~1, family=NOF, data=abdom, method=mixed(1,20))
## a normal distribution fit with 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)
```

PARETO2

Pareto Type 2 distribution for fitting a GAMLSS

Description

The functions `PARETO2()` and `PARETO2o()` define the Pareto Type 2 distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The parameters are `mu` and `sigma` in both functions but the parameterisation different. The `mu` is identical for both `PARETO2()` and `PARETO2o()`. The `sigma` in `PARETO2o()` is the inverse of the `sigma` in `codePARETO2()` and corresponds to the usual parameter `alpha` 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

```

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 Pareto Type 2 distribution in the function PA2 is:

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

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

Value

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

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos

References

- Johnson, N., Kotz, S., and Balakrishnan, N. (1997). *Discrete Multivariate Distributions*. Wiley-Interscience, NY, USA.
- 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, <http://www.jstatsoft.org/v23/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.

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"))
```

Description

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

Usage

```

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

```

Arguments

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

Details

Power Exponential distribution (PE) is defined as

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

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

The Power Exponential distribution (PE2) is defined as

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

References

- Nelson, D.B. (1991) Conditional heteroskedasticity in asset returns: a new approach. *Econometrica*, **57**, 347-370.
- 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 functions dPIG, pPIG, qPIG and rPIG define the density, distribution function, quantile function and random generation for the Poisson-inverse Gaussian PIG(), distribution.

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 beta negative binomial 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)

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
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter
nu.link	Defines the mu.link, with "logit" link as the default for the nu parameter
x	vector of (non-negative integer) quantiles
mu	vector of positive means

sigma	vector of positive dispersion parameter
nu	vector of zero probability parameter
p	vector of probabilities
q	vector of quantiles
n	number of random values to return
log, log.p	logical; if TRUE, probabilities p are given as log(p)
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
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 Poisson-inverse Gaussian distribution, is given by

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

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

Value

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Marco Enea

References

- Dean, C., Lawless, J. F. and Willmot, G. E., A mixed poisson-inverse-Gaussian regression model, *Canadian J. Statist.*, **17**, 2, pp 171-181
- 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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

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

 PO

Poisson distribution for fitting a GAMLSS model

Description

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

Usage

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

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "log" link as the default for the mu 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 p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Definition file for Poisson distribution.

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

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

Value

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

Note

μ is the mean of the Poisson distribution

Author(s)

Bob Rigby, Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
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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, <http://www.jstatsoft.org/v23/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.

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)
```

RG

*The Reverse Gumbel distribution for fitting a GAMLSS***Description**

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

Usage

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

Arguments

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

Details

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

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

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

Value

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

Note

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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](#)

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

Details

Definition file for reverse generalized extreme family distribution.

The probability density function of the generalized extreme value distribution is obtained from Johnson *et al.* (1995), Volume 2, p76, equation (22.184) [where $(\xi, \theta, \gamma) \rightarrow (\mu, \sigma, \nu)$].

The probability density function of the reverse generalized extreme value distribution is then obtained by replacing `y` by `-y` and `μ` by `$-\mu$` .

Hence the probability density function of the reverse generalized extreme value distribution with $\nu > 0$ is given by

$$f(y|\mu, \sigma, \nu) = \frac{1}{\sigma} \left[1 + \frac{\nu(y - \mu)}{\sigma} \right]^{\frac{1}{\nu} - 1} S_1(y|\mu, \sigma, \nu)$$

for

$$\mu - \frac{\sigma}{\nu} < y < \infty$$

where

$$S_1(y|\mu, \sigma, \nu) = \exp \left\{ - \left[1 + \frac{\nu(y - \mu)}{\sigma} \right]^{\frac{1}{\nu}} \right\}$$

and where $-\infty < \mu < y + \frac{\sigma}{\nu}$, $\sigma > 0$ and $\nu > 0$. Note that only the case $\nu > 0$ is allowed here. The reverse generalized extreme value distribution is denoted as $RGE(\mu, \sigma, \nu)$ or as `ReverseGeneralized.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 <mikis.stasinopoulos@gamlss.org> 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.

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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, <http://www.jstatsoft.org/v23/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.

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
```

SEP

The Skew Power exponential (SEP) distribution for fitting a GAMLSS

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

<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 "1/mu ² " 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/nu ² " and "log"

<code>tau.link</code>	Defines the <code>tau.link</code> , with "log" link as the default for the tau parameter. Other links are "1/tau ² ", and "identity"
<code>x,q</code>	vector of quantiles
<code>mu</code>	vector of location parameter values
<code>sigma</code>	vector of scale parameter values
<code>nu</code>	vector of skewness 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 <code>length(n) > 1</code> , the length is taken to be the number required
<code>lower.limit</code>	lower limit for the golden search to find quantiles from probabilities
<code>upper.limit</code>	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 <mikis.stasinopoulos@gamlss.org>

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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

See Also

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

Examples

```
SEP() #
plot(function(x)dSEP(x, mu=0,sigma=1, nu=1, tau=2), -5, 5,
      main = "The SEP density mu=0,sigma=1,nu=1, tau=2")
plot(function(x) pSEP(x, mu=0,sigma=1,nu=1, tau=2), -5, 5,
      main = "The BCPE cdf mu=0, sigma=1, nu=1, tau=2")
dat <- rSEP(100,mu=10,sigma=1,nu=-1,tau=1.5)
# library(gamlss)
# gamlss(dat~1,family=SEP, control=gamlss.control(n.cyc=30))
```

SEPI	<i>The Skew Power exponential type 1-4 distribution for fitting a GAMLSS</i>
------	--

Description

These functions define the Skew Power exponential type 1 to 4 distributions. All of them are four parameter distributions and can be used to fit a GAMLSS model. The functions dSEP1, dSEP2, dSEP3 and dSEP4 define the probability distribution functions, the functions pSEP1, pSEP2, pSEP3 and pSEP4 define the cumulative distribution functions the functions qSEP1, qSEP2, qSEP3 and qSEP4 define the inverse cumulative distribution functions and the functions rSEP1, rSEP2, rSEP3 and rSEP4 define the random generation for the Skew exponential power distributions.

Usage

```
SEP1(mu.link = "identity", sigma.link = "log", nu.link = "identity",
     tau.link = "log")
dSEP1(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pSEP1(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
qSEP1(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
     log.p = FALSE)
rSEP1(n, mu = 0, sigma = 1, nu = 0, tau = 2)
```

```

SEP2(mu.link = "identity", sigma.link = "log", nu.link = "identity",
      tau.link = "log")
dSEP2(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pSEP2(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
      log.p = FALSE)
qSEP2(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE,
      log.p = FALSE)
rSEP2(n, mu = 0, sigma = 1, nu = 0, tau = 2)

SEP3(mu.link = "identity", sigma.link = "log", nu.link = "log",
      tau.link = "log")
dSEP3(x, mu = 0, sigma = 1, nu = 2, tau = 2, log = FALSE)
pSEP3(q, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
      log.p = FALSE)
qSEP3(p, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
      log.p = FALSE)

SEP4(mu.link = "identity", sigma.link = "log", nu.link = "log",
      tau.link = "log")
dSEP4(x, mu = 0, sigma = 1, nu = 2, tau = 2, log = FALSE)
pSEP4(q, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
      log.p = FALSE)
qSEP4(p, mu = 0, sigma = 1, nu = 2, tau = 2, lower.tail = TRUE,
      log.p = FALSE)
rSEP4(n, mu = 0, sigma = 1, nu = 2, tau = 2)

```

Arguments

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

Details

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

$$f_Y(y|\mu, \sigma, \nu, \tau) = \frac{\nu}{\sigma(1+\nu^2)^{2^{1/\tau}}\Gamma(1+1/\tau)} \left\{ \exp\left(-\frac{1}{2}\left|\frac{\nu(y-\mu)}{\sigma}\right|^\tau\right) I(y < \mu) + \exp\left(-\frac{1}{2}\left|\frac{(y-\mu)}{\sigma\nu}\right|^\tau\right) I(y \geq \mu) \right\}$$

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

Value

SEP2() returns a `gamlss.family` object which can be used to fit the SEP2 distribution in the `gamlss()` function. `dSEP2()` gives the density, `pSEP2()` gives the distribution function, `qSEP2()` gives the quantile function, and `rSEP2()` generates random deviates.

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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, <http://www.jstatsoft.org/v23/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.

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.

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 Sinh-Arcsinh distribution, (SHASH), Jones(2005), is defined as

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

where

$$r = \frac{1}{2} \{ \exp [\tau \sinh^{-1}(z)] - \exp [-\nu \sinh^{-1}(z)] \}$$

and

$$c = \frac{1}{2} \{ \tau \exp [\tau \sinh^{-1}(z)] + \nu \exp [-\nu \sinh^{-1}(z)] \}$$

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

The parameters μ and σ are the location and scale of the distribution. The parameter ν determines the left hand tail of the distribution with $\nu > 1$ indicating a lighter tail than the normal and $\nu < 1$ heavier tail than the normal. The parameter τ determines the right hand tail of the distribution in the same way.

The second form of the Sinh-Arcsinh distribution can be found in Jones and Pewsey (2009, p.2) denoted by SHASHo and the probability density function is defined as,

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

where

$$r = \sinh(\tau \arcsin(z) - \nu)$$

and

$$c = \cosh(\tau \arcsin(z) - \nu)$$

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

The third form of the Sinh-Arcsinh distribution (Jones and Pewsey, 2009, p.8) divides the distribution by sigma for the density of the unstandardized variable. This distribution is denoted by SHASHo2 and has pdf

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

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 <mikis.stasinopoulos@gamlss.org> 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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- 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.

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 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 "identity" link as the default for the nu parameter
<code>x</code>	vector of (non-negative integer) quantiles
<code>mu</code>	vector of positive mu
<code>sigma</code>	vector of positive dispersion parameter
<code>nu</code>	vector of nu

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

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

where $\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu}{\sigma}$, for $y = 0, 1, 2, \dots, \infty$ where $\mu > 0$, $\sigma > 0$ and $-\infty < \nu < \infty$ and $K_\lambda(t) = \frac{1}{2} \int_0^\infty x^{\lambda-1} \exp\{-\frac{1}{2}t(x + x^{-1})\} dx$ is the modified Bessel function of the third kind. Note that the above parameterization is different from Stein, Zucchini and Juritz (1988) who use the above probability function but treat μ , α and ν as the parameters. Note that $\sigma = [(\mu^2 + \alpha^2)^{\frac{1}{2}} - \mu]^{-1}$.

Value

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

Author(s)

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

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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- 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

[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 is given by

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

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

$$\alpha^2 = \frac{1}{\sigma^2} + \frac{2\mu}{\sigma}$$

$$c = K_{\nu+1}(1/\sigma)/K_{\nu}(1/\sigma)$$

and $K_{\lambda}(t)$ is the modified Bessel function of the third kind. Note that the above parametrization is different from Stein, Zucchini and Juritz (1988) who use the above probability function but treat μ , α and ν as the parameters.

Value

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

Note

The mean of the above Sichel distribution is μ and the variance is $\mu^2 \left[\frac{2\sigma(\nu+1)}{c} + \frac{1}{c^2} - 1 \right]$

Author(s)

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

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos D. M. and Akantziliotou, C. (2006) Modelling the parameters of a family of mixed Poisson distributions including the Sichel and Delaptorte. Submitted for publication.
- Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2003) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.
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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

[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))

```

SN1

*Skew Normal Type 1 distribution for fitting a GAMLSS***Description**

The function SN1() defines the Skew Normal Type 1 distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with parameters `mu`, `sigma` and `nu`. The functions `dSN1`, `pSN1`, `qSN1` and `rSN1` define the density, distribution function, quantile function and random generation for the SN1 parameterization of the Skew Normal Type 1 distribution.

Usage

```

SN1(mu.link = "identity", sigma.link = "log", nu.link="identity")
dSN1(x, mu = 0, sigma = 1, nu = 0, log = FALSE)
pSN1(q, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
qSN1(p, mu = 0, sigma = 1, nu = 0, lower.tail = TRUE, log.p = FALSE)
rSN1(n, mu = 0, sigma = 1, nu = 0)

```

Arguments

<code>mu.link</code>	Defines the <code>mu.link</code> , with "identity" links the default for the <code>mu</code> parameter
<code>sigma.link</code>	Defines the <code>sigma.link</code> , with "log" as the default for the <code>sigma</code> parameter
<code>nu.link</code>	Defines the <code>nu.link</code> , with "identity" as the default for the <code>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 ...

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.

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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

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)
```

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 $\log(p)$
<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 2 distribution in the function `SN2` is ...

Value

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

Note

This is a special case of the Skew Exponential Power type 3 distribution (SEP3) where $\tau=2$.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fiona McElduff.

References

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

See Also

[gamlss.family](#)

Examples

```
par(mfrow=c(2,2))
y<-seq(-3,3,0.2)
plot(y, dSN2(y), type="l" , lwd=2)
q<-seq(-3,3,0.2)
plot(q, pSN2(q), ylim=c(0,1), type="l", lwd=2)
p<-seq(0.0001,0.999,0.05)
plot(p, qSN2(p), type="l", lwd=2)
dat <- rSN2(100)
hist(rSN2(100), nclass=30)
```

 ST1

The skew t distributions, type 1 to 5

Description

There are 5 different skew t distributions implemented in GAMLSS.

The Skew t type 1 distribution, ST1, is based on Azzalini (1986).

The skew t type 2 distribution, ST2, is based on Azzalini and Capitanio (2003).

The skew t type 3, ST3 and ST3C, distribution is based Fernande and Steel (1998). The difference between the ST3 and ST3C is that the first is written entirely in R while the second is in C.

The skew t type 4 distribution , ST4, is a spliced-shape distribution.

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

The SST is a reparametrised version of dST3 where sigma is the standard deviation of the distribution.

Usage

```
ST1(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link="log")
dST1(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pST1(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
qST1(p, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
rST1(n, mu = 0, sigma = 1, nu = 0, tau = 2)
```

```
ST2(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dST2(x, mu = 0, sigma = 1, nu = 0, tau = 2, log = FALSE)
pST2(q, mu = 0, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
qST2(p, mu = 1, sigma = 1, nu = 0, tau = 2, lower.tail = TRUE, log.p = FALSE)
rST2(n, mu = 0, sigma = 1, nu = 0, tau = 2)
```

```
ST3(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST3(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST3(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST3(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST3(n, mu = 0, sigma = 1, nu = 1, tau = 10)
```

```
ST3C(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST3C(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST3C(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST3C(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST3C(n, mu = 0, sigma = 1, nu = 1, tau = 10)
```

```
SST(mu.link = "identity", sigma.link = "log", nu.link = "log",
    tau.link = "logshiftto2")
dSST(x, mu = 0, sigma = 1, nu = 0.8, tau = 7, log = FALSE)
pSST(q, mu = 0, sigma = 1, nu = 0.8, tau = 7, lower.tail = TRUE, log.p = FALSE)
qSST(p, mu = 0, sigma = 1, nu = 0.8, tau = 7, lower.tail = TRUE, log.p = FALSE)
rSST(n, mu = 0, sigma = 1, nu = 0.8, tau = 7)
```

```
ST4(mu.link = "identity", sigma.link = "log", nu.link = "log", tau.link = "log")
dST4(x, mu = 0, sigma = 1, nu = 1, tau = 10, log = FALSE)
pST4(q, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
qST4(p, mu = 0, sigma = 1, nu = 1, tau = 10, lower.tail = TRUE, log.p = FALSE)
rST4(n, mu = 0, sigma = 1, nu = 1, tau = 10)
```

```
ST5(mu.link = "identity", sigma.link = "log", nu.link = "identity", tau.link = "log")
dST5(x, mu = 0, sigma = 1, nu = 0, tau = 1, log = FALSE)
pST5(q, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
qST5(p, mu = 0, sigma = 1, nu = 0, tau = 1, lower.tail = TRUE, log.p = FALSE)
```

rST5(n, mu = 0, sigma = 1, nu = 0, tau = 1)

Arguments

mu.link	Defines the mu.link, with "identity" link as the default for the mu parameter. Other links are "1/mu ² " and "log"
sigma.link	Defines the sigma.link, with "log" link as the default for the sigma parameter. Other links are "inverse" and "identity"
nu.link	Defines the nu.link, with "identity" link as the default for the nu parameter. Other links are "1/mu ² " and "log"
tau.link	Defines the nu.link, with "log" link as the default for the nu parameter. Other links are "inverse", "identity"
x, q	vector of quantiles
mu	vector of mu parameter values
sigma	vector of scale parameter values
nu	vector of nu parameter values
tau	vector of tau parameter values
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x]
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required
...	for extra arguments

Details

$$f(y|\mu, \sigma, \nu, \frac{z}{\sigma} f_{z_1}(z) F_{z_2}(w)\tau) =$$

for $-\infty < y < \infty$, where $z = (y - \mu)/\sigma$, $w = \nu\lambda^{1/2}z$, $\lambda = (\tau + 1)/(\tau + z^2)$ and $z_1 \sim TF(0, 1, \tau)$ and $z_2 \sim TF(0, 1, \tau + 1)$.

The probability density function of the skew t distribution type q, (ST3), is defined in Chapter 10 of the GAMLSS manual.

The probability density function of the skew t distribution type q, (ST4), is defined in Chapter of the GAMLSS manual.

The probability density function of the skew t distribution type 5, (ST5), is defined as

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

where $c = 2^{a+b-1}(a+b)^{1/2}B(a, b)$, and $B(a, b) = \Gamma(a)\Gamma(b)/\Gamma(a+b)$ and $z = (y - \mu)/\sigma$ and $\nu = (a - b)/[ab(a+b)]^{1/2}$ and $\tau = 2/(a+b)$ for $-\infty < y < \infty$, $-\infty < \mu < \infty$, $\sigma > 0$, $-\infty < \nu < \infty$ and $\tau > 0$.

Value

ST1(), ST2(), ST3(), ST4() and ST5() return a `gamlss.family` object which can be used to fit the skew t type 1-5 distribution in the `gamlss()` function. `dST1()`, `dST2()`, `dST3()`, `dST4()` and `dST5()` give the density functions, `pST1()`, `pST2()`, `pST3()`, `pST4()` and `pST5()` give the cumulative distribution functions, `qST1()`, `qST2()`, `qST3()`, `qST4()` and `qST5()` give the quantile function, and `rST1()`, `rST2()`, `rST3()`, `rST4()` and `rST3()` generates random deviates.

Note

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

Author(s)

Bob Rigby and Mikis Stasinopoulos

References

- 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.
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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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.

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 <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 t family distribution.

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

$y = (-\infty, +\infty)$, $\mu = (-\infty, +\infty)$, $\sigma > 0$ and $\nu > 0$. Note that $z = (y - \mu)/\sigma$ has a standard t distribution with degrees of freedom ν .

Value

TF() returns a `gamlss.family` object which can be used to fit a t distribution in the `gamlss()` function. `dTF()` gives the density, `pTF()` gives the distribution function, `qTF()` gives the quantile function, and `rTF()` generates random deviates. The latest functions are based on the equivalent R functions for gamma distribution.

Note

μ is the mean and $\sigma[\nu/(\nu - 2)]^{0.5}$ is the standard deviation of the t family distribution. $\nu > 0$ is a positive real valued parameter.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#)

Examples

```
TF()# gives information about the default links for the t-family distribution
# library(gamlss)
#data(abdom)
#h<-gamlss(y~cs(x,df=3), sigma.formula=~cs(x,1), family=TF, data=abdom) # fits
```

```
#plot(h)
newdata<-rTF(1000,mu=0,sigma=1,nu=5) # generates 1000 random observations
hist(newdata)
```

 WARING

Waring distribution for fitting a GAMLSS model

Description

The function `WARING()` defines the Waring distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with mean equal to the parameter `mu` and scale parameter `sigma`. The functions `dWARING`, `pWARING`, `qWARING` and `rWARING` define the density, distribution function, quantile function and random generation for the WARING parameterization of the Waring distribution.

Usage

```
WARING(mu.link = "log", sigma.link = "log")
dWARING(x, mu = 2, sigma = 2, log = FALSE)
pWARING(q, mu = 2, sigma = 2, lower.tail = TRUE, log.p = FALSE)
qWARING(p, mu = 2, sigma = 2, lower.tail = TRUE, log.p = FALSE,
        max.value = 10000)
rWARING(n, mu = 2, sigma = 2)
```

Arguments

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

Details

The Waring distribution has density,

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

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

Value

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

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos. <f.mcelduff@ich.ucl.ac.uk>

References

Wimmer, G. and Altmann, G. (1999) *Thesaurus of univariate discrete probability distributions*. Stamm.

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.

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))
```

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 <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 the <code>mu</code> parameter
<code>sigma</code>	vector of <code>sigma</code> 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

The parameterization of the function WEI is given by

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

for $y > 0$, $\mu > 0$ and $\sigma > 0$. The GAMLSS functions `dWEI`, `pWEI`, `qWEI`, and `rWEI` can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument `mu`, and `sigma`. [See the GAMLSS function `WEI2` for a different parameterization of the Weibull.]

Value

`WEI()` returns a `gamlss.family` object which can be used to fit a Weibull distribution in the `gamlss()` function. `dWEI()` gives the density, `pWEI()` gives the distribution function, `qWEI()` gives the quantile function, and `rWEI()` generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Note

The mean in WEI is given by $\mu \Gamma(\frac{1}{\sigma} + 1)$ and the variance $\mu^2 [\Gamma(\frac{2}{\sigma} + 1) - (\Gamma(\frac{1}{\sigma} + 1))^2]$

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziotiou

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.

Stasinopoulos D. M., Rigby R.A. and Akantziotiou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#), [WEI2](#), [WEI3](#)

Examples

```
WEI()
dat<-rWEI(100, mu=10, sigma=2)
# library(gamlss)
# gamlss(dat~1, family=WEI)
```

WEI2

A specific parameterization of the Weibull distribution for fitting a GAMLSS

Description

The function WEI2 can be used to define the Weibull distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. This is the parameterization of the Weibull distribution usually used in proportional hazard models and is defined in details below. [Note that the GAMLSS function WEI uses a different parameterization for fitting the Weibull distribution.] The functions `dWEI2`, `pWEI2`, `qWEI2` and `rWEI2` define the density, distribution function, quantile function and random generation for the specific parameterization of the Weibull distribution.

Usage

```
WEI2(mu.link = "log", sigma.link = "log")
dWEI2(x, mu = 1, sigma = 1, log = FALSE)
pWEI2(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qWEI2(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rWEI2(n, mu = 1, sigma = 1)
```

Arguments

<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 link is the "inverse" and "identity"
<code>x, q</code>	vector of quantiles
<code>mu</code>	vector of the <code>mu</code> parameter values
<code>sigma</code>	vector of <code>sigma</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 parameterization of the function WEI2 is given by

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

for $y > 0$, $\mu > 0$ and $\sigma > 0$. The GAMLSS functions `dWEI2`, `pWEI2`, `qWEI2`, and `rWEI2` can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument `mu`, and `sigma`. [See the GAMLSS function `WEI` for a different parameterization of the Weibull.]

Value

`WEI2()` returns a `gamlss.family` object which can be used to fit a Weibull distribution in the `gamlss()` function. `dWEI2()` gives the density, `pWEI2()` gives the distribution function, `qWEI2()` gives the quantile function, and `rWEI2()` generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Warning

In `WEI2` the estimated parameters `mu` and `sigma` can be highly correlated so it is advisable to use the `CG()` method for fitting [as the `RS()` method can be very slow in this situation.]

Note

The mean in `WEI2` is given by $\mu^{-1/\sigma} \Gamma(\frac{1}{\sigma} + 1)$ and the variance $\mu^{-2/\sigma} (\Gamma(\frac{2}{\sigma} + 1) - [\Gamma(\frac{1}{\sigma} + 1)]^2)$

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#), [WEI](#), [WEI3](#),

Examples

```
WEI2()
dat<-rWEI(100, mu=.1, sigma=2)
hist(dat)
# library(gamlss)
# gamlss(dat~1, family=WEI2, method=CG())
```

WEI3

A specific parameterization of the Weibull distribution for fitting a GAMLSS

Description

The function WEI3 can be used to define the Weibull distribution, a two parameter distribution, for a [gamlss.family](#) object to be used in GAMLSS fitting using the function `gamlss()`. This is a parameterization of the Weibull distribution where μ is the mean of the distribution. [Note that the GAMLSS functions [WEI](#) and [WEI2](#) use different parameterizations for fitting the Weibull distribution.] The functions `dWEI3`, `pWEI3`, `qWEI3` and `rWEI3` define the density, distribution function, quantile function and random generation for the specific parameterization of the Weibull distribution.

Usage

```
WEI3(mu.link = "log", sigma.link = "log")
dWEI3(x, mu = 1, sigma = 1, log = FALSE)
pWEI3(q, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qWEI3(p, mu = 1, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rWEI3(n, mu = 1, sigma = 1)
```

Arguments

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

Details

The parameterization of the function WEI3 is given by

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

where $\beta = \frac{\mu}{\Gamma((1/\sigma)+1)}$ for $y > 0, \mu > 0$ and $\sigma > 0$. The GAMLSS functions `dWEI3`, `pWEI3`, `qWEI3`, and `rWEI3` can be used to provide the pdf, the cdf, the quantiles and random generated numbers for the Weibull distribution with argument `mu`, and `sigma`. [See the GAMLSS function `WEI` for a different parameterization of the Weibull.]

Value

`WEI3()` returns a `gamlss.family` object which can be used to fit a Weibull distribution in the `gamlss()` function. `dWEI3()` gives the density, `pWEI3()` gives the distribution function, `qWEI3()` gives the quantile function, and `rWEI3()` generates random deviates. The latest functions are based on the equivalent R functions for Weibull distribution.

Warning

In `WEI3` the estimated parameters `mu` and `sigma` can be highly correlated so it is advisable to use the `CG()` method for fitting [as the `RS()` method can be very slow in this situation.]

Note

The mean in WEI3 is given by μ and the variance $\mu^2 \left\{ \frac{\Gamma(2/\sigma + 1)}{[\Gamma(1/\sigma + 1)]^2} - 1 \right\}$

Author(s)

Bob Rigby and Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

See Also

[gamlss.family](#), [WEI](#), [WEI2](#)

Examples

```
WEI3()
dat<-rWEI(100, mu=.1, sigma=2)
# library(gamlss)
# gamlss(dat~1, family=WEI3, method=CG())
```

YULE

Yule distribution for fitting a GAMLSS model

Description

The function YULE defines the Yule distribution, a one parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`, with mean equal to the parameter `mu`. The functions `dYULE`, `pYULE`, `qYULE` and `rYULE` define the density, distribution function, quantile function and random generation for the YULE parameterization of the Yule distribution.

Usage

```

YULE(mu.link = "log")
dYULE(x, mu = 2, log = FALSE)
pYULE(q, mu = 2, lower.tail = TRUE, log.p = FALSE)
qYULE(p, mu = 2, lower.tail = TRUE, log.p = FALSE,
      max.value = 10000)
rYULE(n, mu = 2)

```

Arguments

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

Details

The Yule distribution has density

$$P(Y = y|\mu) = (\mu^{-1} + 1)B(y + 1, \mu^{-1} + 2)$$

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

Value

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

Author(s)

Fiona McElduff, Bob Rigby and Mikis Stasinopoulos.

References

Wimmer, G. and Altmann, G. (1999) *Thesaurus of univariate discrete probability distributions*. Stamm.

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.

See Also

[gamlss.family](#)

Examples

```

par(mfrow=c(2,2))
y<-seq(0,20,1)
plot(y, dYULE(y), type="h")
q <- seq(0, 20, 1)
plot(q, pYULE(q), type="h")
p<-seq(0.0001,0.999,0.05)
plot(p , qYULE(p), type="s")
dat <- rYULE(100)
hist(dat)
#summary(gamlss(dat~1, family=YULE))

```

ZABB

Zero inflated and zero adjusted Binomial distribution for fitting in GAMLSS

Description

The function ZIBB defines the zero inflated beta binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIBB`, `pZIBB`, `qZIBB` and `rZINN` define the density, distribution function, quantile function and random generation for the zero inflated beta binomial, ZIBB, distribution.

The function ZABB defines the zero adjusted beta binomial distribution, a three parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZABB`, `pZABB`, `qZABB` and `rZABB` define the density, distribution function, quantile function and random generation for the zero inflated beta binomial, ZABB(), distribution.

Usage

```

ZABB(mu.link = "logit", sigma.link = "log", nu.link = "logit")
ZIBB(mu.link = "logit", sigma.link = "log", nu.link = "logit")

dZIBB(x, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1, log = FALSE)
dZABB(x, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1, log = FALSE)

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

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

rZIBB(n, mu = 0.5, sigma = 0.5, nu = 0.1, bd = 1)
rZABB(n, mu = 0.5, sigma = 0.1, nu = 0.1, bd = 1)

```

Arguments

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

Details

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

Value

The functions ZIBB and ZABB return a `gamlss.family` object which can be used to fit a zero inflated or zero adjusted beta binomial distribution respectively in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.
- Rigby, R. A. and Stasinopoulos D. M. (2010) The `gamlss.family` distributions, (distributed with this package or see <http://www.gamlss.org/>)
- 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.

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

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

Value

The functions ZABI and ZIBI return a `gamlss.family` object which can be used to fit a binomial distribution in the `gamlss()` function.

Note

The response variable should be a matrix containing two columns, the first with the count of successes and the second with the count of failures.

Author(s)

Mikis Stasinopoulos, Bob Rigby

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.
- Rigby, R. A. and Stasinopoulos D. M. (2010) The `gamlss.family` distributions, (distributed with this package or see <http://www.gamlss.org/>)

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.

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')
```

ZAGA

The zero adjusted Gamma distribution for fitting a GAMLSS model

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>	<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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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,
      upper.limit = mu + 10 * sqrt(sigma^2 * mu^3))
rZAIG(n, mu = 1, sigma = 1, nu = 0.1, ...)
plotZAIG(mu = 5, sigma = 1, nu = 0.1, from = 0, to = 10, n = 101, ...)
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 <= x], otherwise, P[X > x]
<code>upper.limit</code>	the argument <code>upper.limit</code> sets the upper limit in the golden section search for q, the default is 10 time its standard deviation
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required
<code>from</code>	where to start plotting the distribution from
<code>to</code>	up to where to plot the distribution
<code>obj</code>	a fitted BEINF object
<code>...</code>	... 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/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.

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 p are given as log(p)
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

The definition for the zero inflated Negative Binomial type I distribution and for the zero adjusted Negative Binomial type I distribution is given in Rigby and Stasinopoulos (2010) below

Value

The functions ZINBI and ZANBI return a `gamlss.family` object which can be used to fit a zero inflated or zero adjusted Negative Binomial type I distribution respectively in the `gamlss()` function.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.
- Rigby, R. A. and Stasinopoulos D. M. (2010) The `gamlss.family` distributions, (distributed with this package or see <http://www.gamlss.org/>)
- 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.

See Also

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

Examples

```
ZINBI()
ZANBI()
# creating data and plotting them
dat <- rZINBI(1000, mu=5, sigma=.5, nu=0.1)
r <- barplot(table(dat), col='lightblue')
dat1 <- rZANBI(1000, mu=5, sigma=.5, nu=0.1)
r1 <- barplot(table(dat1), col='lightblue')
```

ZAP

*Zero adjusted poisson distribution for fitting a GAMLSS model***Description**

The function ZAP defines the zero adjusted Poisson distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZAP`, `pZAP`, `qZAP` and `rZAP` define the density, distribution function, quantile function and random generation for the inflated poisson, `ZAP()`, distribution.

Usage

```
ZAP(mu.link = "log", sigma.link = "logit")
dZAP(x, mu = 5, sigma = 0.1, log = FALSE)
pZAP(q, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZAP(p, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZAP(n, mu = 5, sigma = 0.1)
```

Arguments

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

Details

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

Value

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).
- 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, <http://www.jstatsoft.org/v23/i07>.
- Rigby, R. A. and Stasinopoulos D. M. (2010) The gamlss.family distributions, (distributed with this package or see <http://www.gamlss.org/>)
- 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.

See Also

[gamlss.family](#), [P0](#), [ZIP](#), [ZIP2](#), [ZALG](#)

Examples

```
ZAP()
# creating data and plotting them
dat<-rZAP(1000, mu=5, sigma=.1)
r <- barplot(table(dat), col='lightblue')
```

ZIP

Zero inflated poisson distribution for fitting a GAMLSS model

Description

The function ZIP defines the zero inflated Poisson distribution, a two parameter distribution, for a `gamlss.family` object to be used in GAMLSS fitting using the function `gamlss()`. The functions `dZIP`, `pZIP`, `qZIP` and `rZIP` define the density, distribution function, quantile function and random generation for the inflated poisson, `ZIP()`, distribution.

Usage

```
ZIP(mu.link = "log", sigma.link = "logit")
dZIP(x, mu = 5, sigma = 0.1, log = FALSE)
pZIP(q, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
qZIP(p, mu = 5, sigma = 0.1, lower.tail = TRUE, log.p = FALSE)
rZIP(n, mu = 5, sigma = 0.1)
```

Arguments

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

Details

Let $Y = 0$ with probability σ and $Y \sim Po(\mu)$ with probability $(1 - \sigma)$ the Y has a Zero inflated Poisson Distribution given by

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

if ($y=0$)

$$f(y) = (1 - \sigma) \frac{e^{-\mu} \mu^y}{y!}$$

if ($y>0$) for $y = 0, 1, \dots$,

Value

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

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, 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.
- 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 <http://www.gamlss.org/>).

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, <http://www.jstatsoft.org/v23/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.

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 <code>log(p)</code>
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$

Details

Let $Y = 0$ with probability σ and $Y \sim Po(\mu/[1 - \sigma])$ with probability $(1 - \sigma)$ then Y has a Zero inflated Poisson type 2 distribution given by

$$f(y|\mu, \sigma) = \sigma + (1 - \sigma)e^{-\mu/(1-\sigma)} \quad \text{if } y = 0$$

$$f(y|\mu, \sigma) = (1 - \sigma) \frac{e^{-\mu/(1-\sigma)} [\mu/(1 - \sigma)]^y}{y!} \quad \text{if } y = 1, 2, 3, \dots$$

The mean of the distribution in this parameterization is μ .

Value

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

Author(s)

Bob Rigby, Gillian Heller and Mikis Stasinopoulos

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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 $\zeta()$ is the (Reimann) zeta function.

The distribution has mean $\zeta(\mu)/\zeta(\mu+1)$ and variance $\zeta(\mu+1)\zeta(\mu-1) - [\zeta(\mu)]^2/[\zeta(\mu+1)]^2$.

Value

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

Note

Because the zipf distribution has very long tails the `max.value` in the `q` and `r`, may need to increase.

Author(s)

Mikis Stasinopoulos and Bob Rigby

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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.

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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