Package ‘MPS’

January 20, 2025

Type Package

Title Estimating Through the Maximum Product Spacing Approach

Version 2.3.1

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Description Developed for computing the probability density function, computing the cumulative distribution function, computing the quantile function, random generation, drawing q-q plot, and estimating the parameters of 24 G-family of statistical distributions via the maximum product spacing approach introduced in <`https://www.jstor.org/stable/2345411`>. The set of families contains: beta G distribution, beta exponential G distribution, beta extended G distribution, exponentiated G distribution, exponentiated exponential Poisson G distribution, exponentiated generalized G distribution, exponentiated Kumaraswamy G distribution, gamma type I G distribution, gamma type II G distribution, gamma uniform G distribution, gamma-X generated of log-logistic family of G distribution, gamma-X family of modified beta exponential G distribution, geometric exponential Poisson G distribution, generalized beta G distribution, generalized transmuted G distribution, Kumaraswamy G distribution, log gamma type I G distribution, log gamma type II G distribution, Marshall Olkin G distribution, Marshall Olkin Kumaraswamy G distribution, modified beta G distribution, odd log-logistic G distribution, truncated-exponential skew-symmetric G distribution, and Weibull G distribution.

License GPL (>= 2)

Encoding UTF-8

Depends R(>= 3.1)

NeedsCompilation no

Repository CRAN

Date/Publication 2019-10-04 20:00:02 UTC

Contents

`MPS-package` *Developed for computing pdf, cdf, quantile, random generation, drawing q-q plot, and estimating the parameters of 24 G-family of statistical distributions.*

Description

Developed for computing the probability density function, computing the cumulative distribution function, computing the quantile function, random generation, and estimating the parameters of 24 G-family of statistical distributions via the maximum product spacing approach introduced in <https://www.jstor.org/stable/2345411>. These families are: beta G distribution due to Eugene et al. (2002), beta exponential G distribution due to Alzaatreh et al. (2013), beta extended G distribution due to Alzaatreh et al. (2013), exponentiated G distribution due to Gupta et al. (1998), exponentiated Kumaraswamy G distribution due to Lemonte et al. (2013), exponentiated exponential Poisson G distribution due to Ristic and Nadarajah (2014), exponentiated generalized G distribution due to Cordeiro et al. (2013), gamma type I G distribution due to Zografos and Balakrishnan (2009), gamma type II G distribution due to Ristic and Balakrishnan (2012), gamma uniform G distribution due to Torabi and Montazeri (2012), gamma-X generated of log-logistic family of G distribution due to Alzaatreh et al. (2013), gamma-X family of modified beta exponential G distribution due to Alzaatreh et al. (2013), geometric exponential Poisson G distribution due to Nadarajah et al. (2013), generalized beta G distribution due to Alexander et al. (2012), generalized transmuted G distribution due to Merovci et al. (2017), Kumaraswamy G distribution due to Cordeiro and Castro (2011), log gamma type I G distribution due to Amini et al. (2013), log gamma type II G distribution due to Amini et al. (2013), Marshall-Olkin G distribution due to Marshall and Olkin (1997), Marshall-Olkin Kumaraswamy G distribution due to Roshini and Thobias (2017), modified beta G distribution due to Nadarajah et al. (2013), odd log-logistic G distribution due to Gauss et al. (2017), truncated-exponential skew-symmetric G distribution due to Nadarajah et al. (2014), and Weibull G distribution due to Alzaatreh et al. (2013).

Details

Package: MPS

Type: Package

Version: 2.3.1

Date: 2019-09-04

License: GPL(>=2)

Author(s)

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`betaexpg` *beta exponential G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the beta exponential `G` distribution. The General form for the probability density function (pdf) of the beta exponential `G` distribution due to Alzaatreh et al. (2013) is given by

$$f(x,\Theta) = \frac{d\, g(x-\mu,\theta)\left[1-\left(1-G(x-\mu,\theta)\right)^{d}\right]^{b-1}\left(1-G(x-\mu,\theta)\right)^{ad-1}}{B(a,b)},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the beta exponential `G` distribution is given by

$$F(x,\Theta) = 1-\frac{\int_{0}^{\left(1-G(x-\mu,\theta)\right)^{d}} y^{a-1}(1-y)^{b-1}dy}{B(a,b)}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a, b, d, \theta, \mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dbetaexpg(mydata, g, param, location = TRUE, log=FALSE)
pbetaexpg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qbetaexpg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rbetaexpg(n, g, param, location = TRUE)
qqbetaexpg(mydata, g, location ="TRUE", method)
mpsbetaexpg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alzaatreh, A., Lee, C., and Famoye, F. (2013). A new method for generating families of continuous distributions, *Metron*, 71, 63-79.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dbetaexpg(mydata, "weibull", c(1,1,1,2,2,3))
pbetaexpg(mydata, "weibull", c(1,1,1,2,2,3))
qbetaexpg(runif(100), "weibull", c(1,1,1,2,2,3))
rbetaexpg(100, "weibull", c(1,1,1,2,2,3))
qqbetaexpg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsbetaexpg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`betag` *beta G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the beta `G` distribution. General form for the probability density function (pdf) of beta `G` distribution due to Eugene et al. (2002) is given by

$$f(x,\Theta)=\frac{g(x-\mu,\theta)\left(G(x-\mu,\theta)\right)^{a-1}\left(1-G(x-\mu,\theta)\right)^{b-1}}{B(a,b)},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is `g`. The general form for the cumulative distribution function (cdf) of the beta `G` distribution is given by

$$F(x,\Theta)=\frac{\int_0^{G(x-\mu,\theta)} y^{a-1}\left(1-y\right)^{b-1}dy}{B(a,b)}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dbetag(mydata, g, param, location = TRUE, log=FALSE)
pbetag(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qbetag(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rbetag(n, g, param, location = TRUE)
qqbetag(mydata, g, location =TRUE, method)
mpsbetag(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Eugene, N., Lee, C., and Famoye, F. (2002). Beta-normal distribution and its applications, *Communications in Statistics-Theory and Methods*, 31, 497-512.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dbetag(mydata, "weibull", c(1,1,2,2,3))
pbetag(mydata, "weibull", c(1,1,2,2,3))
qbetag(runif(100), "weibull", c(1,1,2,2,3))
rbetag(100, "weibull", c(1,1,2,2,3))
qqbetag(mydata, "weibull", TRUE, "Nelder-Mead")
mpsbetag(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`expexppg` *exponentiated exponential Poisson G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the exponentiated exponential Poisson `G` distribution. The general form for the probability density function (pdf) of the the exponentiated exponential Poisson `G` distribution due to Ristic and Nadarajah (2014) is given by

$$f(x,\Theta)=\frac{a\,b\,g(x-\mu,\theta)(G(x-\mu,\theta))^{a-1}e^{-b(G(x-\mu,\theta))^{a}}}{1-e^{-b}},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the exponentiated exponential Poisson `G` distribution is given by

$$F(x,\Theta)=\frac{1-e^{-b(G(x-\mu,\theta))^{a}}}{1-e^{-b}}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dexpexppg(mydata, g, param, location = TRUE, log=FALSE)
pexpexppg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qexpexppg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rexpexppg(n, g, param, location = TRUE)
qqexpexppg(mydata, g, location = TRUE, method)
mpsexpexppg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

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References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Ristic, M. M. and Nadarajah, S. (2014). A new lifetime distribution, *Journal of Statistical Computation and Simulation*, 84 (1), 135-150.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dexpexppg(mydata, "weibull", c(1,1,2,2,3))
pexpexppg(mydata, "weibull", c(1,1,2,2,3))
qexpexppg(runif(100), "weibull", c(1,1,2,2,3))
rexpexppg(100, "weibull", c(1,1,2,2,3))
qqexpexppg(mydata, "weibull", location = TRUE, "Nelder-Mead")
mpsexpexppg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`expg` *exponentiated G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the exponentiated `G` distribution. General form for the probability density function (pdf) of the exponentiated `G` distribution due to Gupta et al. (1998) is given by

$$f(x, \Theta) = a\, g(x-\mu, \theta)\big(G(x-\mu, \theta)\big)^{a-1},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the exponentiated `G` distribution is given by

$$F(x, \Theta) = \big(G(x-\mu, \theta)\big)^{a}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a, \theta, \mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a is the shape parameter). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dexpg(mydata, g, param, location = TRUE, log=FALSE)
pexpg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qexpg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rexpg(n, g, param, location = TRUE)
qqexpg(mydata, g, location = TRUE, method)
mpsexpg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

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References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Gupta, R. C., Gupta, P. L., and Gupta, R. D. (1998). Modeling failure time data by Lehman alternatives, *Communications in Statistics-Theory and Methods*, 27, 887-904.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dexpg(mydata, "weibull", c(1,2,2,3))
pexpg(mydata, "weibull", c(1,2,2,3))
qexpg(runif(100), "weibull", c(1,2,2,3))
rexpg(100, "weibull", c(1,2,2,3))
qqexpg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsexpg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`expgg` *exponentiated generalized G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the exponentiated generalized `G` distribution. The General form for the probability density function (pdf) of the exponentiated generalized `G` distribution due to Cordeiro et al. (2013) is given by

$$f(x,\Theta) = a\, b\, g(x-\mu,\theta)(1-G(x-\mu,\theta))^{a-1}[1-(1-G(x-\mu,\theta))^{a}]^{b-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is `g`. The general form for the cumulative distribution function (cdf) of the exponentiated generalized `G` distribution is given by

$$F(x,\Theta) = [1-(1-G(x-\mu,\theta))^{a}]^{b}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a, b, \theta, \mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dexpgg(mydata, g, param, location = TRUE, log=FALSE)
pexpgg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qexpgg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rexpgg(n, g, param, location = TRUE)
qqexpgg(mydata, g, location = TRUE, method)
mpsexpgg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Cordeiro, G. M., Ortega, E. M. M., and da Cunha, D. C. C. (2013). The exponentiated generalized class of distributions, *Journal of Data Science*, 11, 1-27.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dexpgg(mydata, "weibull", c(1,1,2,2,3))
pexpgg(mydata, "weibull", c(1,1,2,2,3))
qexpgg(runif(100), "weibull", c(1,1,2,2,3))
rexpgg(100, "weibull", c(1,1,2,2,3))
qqexpgg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsexpgg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`expkumg` *exponentiated Kumaraswamy G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the exponentiated Kumaraswamy `G` distribution. The General form for the probability density function (pdf) of exponentiated Kumaraswamy `G` distribution due to Lemonte et al. (2013) is given by

$$f(x,\Theta) = a\,b\,d\,g(x-\mu,\theta)(G(x-\mu,\theta))^{a-1}[1-(G(x-\mu,\theta))^{a}]^{b-1}\Big\{1-[1-(G(x-\mu,\theta))^{a}]^{b}\Big\}^{d-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the exponentiated Kumaraswamy `G` distribution is given by

$$F(x,\Theta) = \Big\{1-[1-(G(x-\mu,\theta))^{a}]^{b}\Big\}^{d}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a,b,d,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dexpkumg(mydata, g, param, location = TRUE, log=FALSE)
pexpkumg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qexpkumg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rexpkumg(n, g, param, location = TRUE)
qqexpkumg(mydata, g, location = TRUE, method)
mpsexpkumg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Lemonte, A. J., Barreto-Souza, W., and Cordeiro, G. M. (2013). The exponentiated Kumaraswamy distribution and its log-transform, *Brazilian Journal of Probability and Statistics*, 27, 31-53.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dexpkumg(mydata, "weibull", c(1,1,1,2,2,3))
pexpkumg(mydata, "weibull", c(1,1,1,2,2,3))
qexpkumg(runif(100), "weibull", c(1,1,1,2,2,3))
rexpkumg(100, "weibull", c(1,1,1,2,2,3))
qqexpkumg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsexpkumg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gammag` *gamma uniform G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the gamma uniform `G` distribution. General form for the probability density function (pdf) of the gamma uniform `G` distribution due to Torabi and Montazeri (2012) is given by

$$f(x,\Theta)=\frac{g(x-\mu,\theta)}{\Gamma(a)\left(1-G(x-\mu,\theta)\right)^2}\left(\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}\right)^{a-1}e^{-\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the gamma uniform `G` distribution is given by

$$F(x,\Theta)=\int_{0}^{\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}}\frac{y^{a-1}e^{-y}}{\Gamma(a)}dy.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a is the shape parameter). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgammag(mydata, g, param, location = TRUE, log=FALSE)
pgammag(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgammag(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgammag(n, g, param, location = TRUE)
qqgammag(mydata, g, location = TRUE, method)
mpsgammag(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Torabi, H. and Montazeri, N. H. (2012). The gamma uniform distribution and its applications, *Kybernetika*, 48, 16-30.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgammag(mydata, "weibull", c(1,2,2,3))
pgammag(mydata, "weibull", c(1,2,2,3))
qgammag(runif(100), "weibull", c(1,2,2,3))
rgammag(100, "weibull", c(1,2,2,3))
qqgammag(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgammag(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gammag1` *gamma uniform type I G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the gamma uniform type I `G` distribution. General form for the probability density function (pdf) of the gamma uniform type I `G` distribution due to Zografos and Balakrishnan (2009) is given by

$$f(x,\Theta) = \frac{g(x-\mu,\theta)}{\Gamma\left(a\right)}[-\log\left(1-G(x-\mu,\theta)\right)]^{a-1},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the gamma uniform type I `G` distribution is given by

$$F(x,\Theta) = \int_{0}^{-\log(1-G(x-\mu,\theta))} \frac{y^{a-1}e^{-y}}{\Gamma(a)}dy.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a is the shape parameter). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgammag1(mydata, g, param, location = TRUE, log=FALSE)
pgammag1(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgammag1(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgammag1(n, g, param, location = TRUE)
qqgammag1(mydata, g, location = TRUE, method)
mpsgammag1(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Zografos, K. and Balakrishnan, N. (2009). On families of beta- and generalized gamma-generated distributions and associated inference, *Statistical Methodology*, 6, 344-362.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgammag1(mydata, "weibull", c(1,2,2,3))
pgammag1(mydata, "weibull", c(1,2,2,3))
qgammag1(runif(100), "weibull", c(1,2,2,3))
rgammag1(100, "weibull", c(1,2,2,3))
qqgammag1(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgammag1(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gammag2` *gamma uniform type II G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the gamma uniform type II `G` distribution . General form for the probability density function (pdf) of the gamma uniform type II `G` distribution due to Ristic and Balakrishnan (2012) is given by

$$f(x,\Theta)=\frac{g(x-\mu,\theta)}{\Gamma\left(a\right)}\left[-\log\left(G(x-\mu,\theta)\right)\right]^{a-1},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the gamma uniform type II `G` distribution is given by

$$F(x,\Theta)=\int_{0}^{-\log(G(x-\mu,\theta))}\frac{y^{a-1}e^{-y}}{\Gamma(a)}dy.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a is the shape parameter). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgammag2(mydata, g, param, location = TRUE, log=FALSE)
pgammag2(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgammag2(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgammag2(n, g, param, location = TRUE)
qqgammag2(mydata, g, location = TRUE, method)
mpsgammag2(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Ristic, M. M. and Balakrishnan, N. (2012). The gamma exponentiated exponential distribution, *Journal of Statistical Computation and Simulation*, 82, 1191-1206.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgammag2(mydata, "weibull", c(1,2,2,3))
pgammag2(mydata, "weibull", c(1,2,2,3))
qgammag2(runif(100), "weibull", c(1,2,2,3))
rgammag2(100, "weibull", c(1,2,2,3))
qqgammag2(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgammag2(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gbetag` *generalized beta G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the generalized beta `G` distribution. General form for the probability density function (pdf) of the generalized beta `G` distribution due to Alexander et al. (2012) is given by

$$f(x,\Theta)=\frac{d\,g(x-\mu,\theta)(G(x-\mu,\theta))^{ad-1}\Big[1-(G(x-\mu,\theta))^{d}\Big]^{b-1}}{B\left(a,b\right)},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the generalized beta `G` distribution is given by

$$F(x,\Theta)=\frac{\int_{0}^{(G(x-\mu,\theta))^{d}}y^{a-1}(1-y)^{b-1}dy}{B(a,b)}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,d,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgbetag(mydata, g, param, location = TRUE, log=FALSE)
pgbetag(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgbetag(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgbetag(n, g, param, location = TRUE)
qqgbetag(mydata, g, location = TRUE, method)
mpsgbetag(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12*m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alexander, C., Cordeiro, G. M., and Ortega, E. M. M. (2012). Generalized beta-generated distributions, *Computational Statistics and Data Analysis*, 56, 1880-1897.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgbetag(mydata, "weibull", c(1,1,1,2,2,3))
pgbetag(mydata, "weibull", c(1,1,1,2,2,3))
qgbetag(runif(100), "weibull", c(1,1,1,2,2,3))
rgbetag(100, "weibull", c(1,1,1,2,2,3))
qqgbetag(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgbetag(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gexppg` *geometric exponential Poisson G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the geometric exponential Poisson `G` distribution. General form for the probability density function (pdf) of the geometric exponential Poisson `G` distribution due to Nadarajah et al. (2013) is given by

$$f(x,\Theta)=\frac{a(1-b)\,g(x-\mu,\theta)\,(1-e^{-a})\,e^{-a+a\,G(x-\mu,\theta)}}{\left(1-e^{-a}-b+be^{-a+a\,G(x-\mu,\theta)}\right)^{2}},$$

where θ is the baseline family parameter vector. Also, a>0, 0<b<1, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the geometric exponential Poisson `G` distribution is given by

$$F(x,\Theta)=\frac{e^{-a+aG(x-\mu,\theta)}-e^{-a}}{1-e^{-a}-b+be^{-a+aG(x-\mu,\theta)}}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgexppg(mydata, g, param, location = TRUE, log=FALSE)
pgexppg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgexppg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgexppg(n, g, param, location = TRUE)
qqgexppg(mydata, g, location = TRUE, method)
mpsgexppg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Nadarajah, S., Cancho, V. G., and Ortega, E. M. M. (2013). The geometric exponential Poisson distribution, *Statistical Methods & Applications*, 22, 355-380.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgexppg(mydata, "weibull", c(1,0.5,2,2,3))
pgexppg(mydata, "weibull", c(1,0.5,2,2,3))
qgexppg(runif(100), "weibull", c(1,0.5,2,2,3))
rgexppg(100, "weibull", c(1,0.5,2,2,3))
qqgexppg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgexppg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gmbetaexpg` *gamma-X family of modified beta exponential G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the gamma-X family of modified beta exponential `G` distribution. The General form for the probability density function (pdf) of the gamma-X family of the modified beta exponential `G` distribution due to Alzaatreh et al. (2013) is given by

$$f(x,\Theta)=abg(x-\mu,\theta)(1-G(x-\mu,\theta))^{-2}e^{-b\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}}\left[1-e^{-b\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}}\right]^{a-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the gamma-X family of modified beta exponential `G` distribution is given by

$$F(x,\Theta)=\left(1-e^{-b\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}}\right)^{a}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgmbetaexpg(mydata, g, param, location = TRUE, log=FALSE)
pgmbetaexpg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgmbetaexpg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgmbetaexpg(n, g, param, location = TRUE)
qqgmbetaexpg(mydata, g, location = TRUE, method)
mpsgmbetaexpg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alzaatreh, A., Lee, C., and Famoye, F. (2013). A new method for generating families of continuous distributions, *Metron*, 71, 63-79.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgmbetaexpg(mydata, "weibull", c(1,1,2,2,3))
pgmbetaexpg(mydata, "weibull", c(1,1,2,2,3))
qgmbetaexpg(runif(100), "weibull", c(1,1,2,2,3))
rgmbetaexpg(100, "weibull", c(1,1,2,2,3))
qqgmbetaexpg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgmbetaexpg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gtransg` *exponentiated exponential Poisson G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the generalized transmuted `G` distribution. The general form for the probability density function (pdf) of the generalized transmuted `G` distribution due to Merovci et al. (2017) is given by

$$f(x,\Theta) = a\, g(x-\mu,\theta)(G(x-\mu,\theta))^{a-1}\left[1+b-2bG(x-\mu,\theta)\right]\left[1+b\left(1-G(x-\mu,\theta)\right)\right]^{a-1},$$

where θ is the baseline family parameter vector. Also, a>0, b<1, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the generalized transmuted `G` distribution distribution is given by

$$F(x,\Theta) = (G(x-\mu,\theta))^{a}[1+b\left(1-G(x-\mu,\theta)\right)]^{a}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgtransg(mydata, g, param, location = TRUE, log=FALSE)
pgtransg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgtransg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgtransg(n, g, param, location = TRUE)
qqgtransg(mydata, g, location = TRUE, method)
mpsgtransg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Merovcia, F., Alizadeh, M., Yousof, H. M., and Hamedani, G. G. (2017). The exponentiated transmuted-G family of distributions: Theory and applications, *Communications in Statistics-Theory and Methods*, 46(21), 10800-10822.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgtransg(mydata, "weibull", c(1,0.5,2,2,3))
pgtransg(mydata, "weibull", c(1,0.5,2,2,3))
qgtransg(runif(100), "weibull", c(1,0.5,2,2,3))
rgtransg(100, "weibull", c(1,0.5,2,2,3))
qqgtransg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgtransg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`gxlogisticg` *gamma-X generated of log-logistic-X familiy of G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the log-logistic-X familiy of `G` distribution. General form for the probability density function (pdf) of gamma-X generated of the log-logistic-X familiy of `G` distribution due to Alzaatreh et al. (2013) is given by

$$f(x,\Theta)=\frac{ag(x-\mu,\theta)[-\log\left(1-G(x-\mu,\theta)\right)]^{-a-1}}{\left(1-G(x,\theta)\right)\left\{1+\left[-\log\left(1-G(x,\theta)\right)\right]^{a}\right\}^{2}},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. It should be noted that here we set $W(G(x,\theta))=-log(1-G(x,\theta))$. The general form for the cumulative distribution function (cdf) of the gamma-X generated of log-logistic familiy of `G` distribution is given by

$$F(x,\Theta)=\frac{1}{1+\left[-\log\left(1-G(x,\theta)\right)\right]^{-a}}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a is the shape parameter). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dgxlogisticg(mydata, g, param, location = TRUE, log=FALSE)
pgxlogisticg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgxlogisticg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgxlogisticg(n, g, param, location = TRUE)
qqgxlogisticg(mydata, g, location = TRUE, method)
mpsgxlogisticg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alzaatreh, A., Lee, C., and Famoye, F. (2013). A new method for generating families of continuous distributions, *Metron*, 71, 63-79.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dgxlogisticg(mydata, "weibull", c(1,2,2,3))
pgxlogisticg(mydata, "weibull", c(1,2,2,3))
qgxlogisticg(runif(100), "weibull", c(1,2,2,3))
rgxlogisticg(100, "weibull", c(1,2,2,3))
qqgxlogisticg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgxlogisticg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`kumg` *Kumaraswamy G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the Kumaraswamy `G` distribution. General form for the probability density function (pdf) of the Kumaraswamy `G` distribution due to Cordeiro and Castro (2011) is given by

$$f(x,\Theta) = a\,b\,g(x-\mu,\theta)(G(x-\mu,\theta))^{a-1}[1-(G(x-\mu,\theta))^{a}]^{b-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is `g`. The general form for the cumulative distribution function (cdf) of the Kumaraswamy `G` distribution is given by

$$F(x,\Theta) = 1-[1-(G(x-\mu,\theta))^{a}]^{b}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dkumg(mydata, g, param, location = TRUE, log=FALSE)
pkumg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qkumg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rkumg(n, g, param, location = TRUE)
qqkumg(mydata, g, location = TRUE, method)
mpskumg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Cordeiro, G. M. and Castro, M. (2011). A new family of generalized distributions, *Journal of Statistical Computation and Simulation*, 81, 883-898.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dkumg(mydata, "weibull", c(1,1,2,2,3))
pkumg(mydata, "weibull", c(1,1,2,2,3))
qkumg(runif(100), "weibull", c(1,1,2,2,3))
rkumg(100, "weibull", c(1,1,2,2,3))
qqkumg(mydata, "weibull", TRUE, "Nelder-Mead")
mpskumg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`loggammag1` *log gamma G type I distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the log gamma type I `G` distribution. General form for the probability density function (pdf) of the log gamma type I `G` distribution due to Amini et al. (2013) is given by

$$f(x,\Theta)=\frac{b^a}{\Gamma(a)}g(x-\mu,\theta)[-\log(1-G(x-\mu,\theta))]^{a-1}(1-G(x-\mu,\theta))^{b-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the log gamma type I `G` distribution is given by

$$F(x,\Theta)=\int_0^{-b\log(1-G(x-\mu,\theta))}\frac{y^{a-1}e^{-y}}{\Gamma(a)}dy.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dloggammag1(mydata, g, param, location = TRUE, log=FALSE)
ploggammag1(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qloggammag1(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rloggammag1(n, g, param, location = TRUE)
qqloggammag1(mydata, g, location = TRUE, method)
mpsloggammag1(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Amini, M., MirMostafaee, S. M. T. K., and Ahmadi, J. (2013). Log-gamma-generated families of distributions, *Statistics*, 48 (4), 913-932.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dloggammag1(mydata, "weibull", c(1,1,2,2,3))
ploggammag1(mydata, "weibull", c(1,1,2,2,3))
qloggammag1(runif(100), "weibull", c(1,1,2,2,3))
rloggammag1(100, "weibull", c(1,1,2,2,3))
qqloggammag1(mydata, "weibull", TRUE, "Nelder-Mead")
mpsloggammag1(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`loggammag2` *log gamma G type II distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the log gamma type II `G` distribution. General form for the probability density function (pdf) of the log gamma type II `G` distribution due to Amini et al. (2013) is given by

$$f(x,\Theta) = \frac{b^a}{\Gamma(a)} g(x-\mu,\theta)[-\log(G(x-\mu,\theta))]^{a-1}(G(x-\mu,\theta))^{b-1},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the log gamma type II `G` distribution is given by

$$F(x,\Theta) = 1 - \int_0^{-b\log(G(x-\mu,\theta))} \frac{y^{a-1}e^{-y}}{\Gamma(a)} dy.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a, b, \theta, \mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dloggammag2(mydata, g, param, location = TRUE, log=FALSE)
ploggammag2(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qloggammag2(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rloggammag2(n, g, param, location = TRUE)
qqloggammag2(mydata, g, location = TRUE, method)
mpsloggammag2(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Amini, M., MirMostafaee, S. M. T. K., and Ahmadi, J. (2013). Log-gamma-generated families of distributions, *Statistics*, 48 (4), 913-932.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dloggammag2(mydata, "weibull", c(1,1,2,2,3))
ploggammag2(mydata, "weibull", c(1,1,2,2,3))
qloggammag2(runif(100), "weibull", c(1,1,2,2,3))
rloggammag2(100, "weibull", c(1,1,2,2,3))
qqloggammag2(mydata, "weibull", TRUE, "Nelder-Mead")
mpsloggammag2(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`mbetag` *modified beta G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the modified beta `G` distribution. General form for the probability density function (pdf) of the modified beta `G` distribution due to Nadarajah et al. (2013) is given by

$$f(x,\Theta)=\frac{d^{a}g(x-\mu,\theta)\big(G(x-\mu,\theta)\big)^{a-1}\big(1-G(x-\mu,\theta)\big)^{b-1}}{B(a,b)[1-(1-d)\,G(x-\mu,\theta)]^{a+b}},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cdf of the modified beta `G` distribution is given by

$$F(x,\Theta)=\frac{\int_{0}^{\frac{d\,G(x-\mu,\theta)}{1-(1-d)G(x-\mu,\theta)}} y^{a-1}(1-y)^{b-1}dy}{B(a,b)}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,d,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dmbetag(mydata, g, param, location = TRUE, log=FALSE)
pmbetag(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qmbetag(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rmbetag(n, g, param, location = TRUE)
qqmbetag(mydata, g, location = TRUE, method)
mpsmbetag(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Nadarajah, S., Teimouri, M., and Shih, S. H. (2014). Modified beta distributions, *Sankhya*, 76 (1), 19-48.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dmbetag(mydata, "weibull", c(1,1,1,2,2,3))
pmbetag(mydata, "weibull", c(1,1,1,2,2,3))
qmbetag(runif(100), "weibull", c(1,1,1,2,2,3))
rmbetag(100, "weibull", c(1,1,1,2,2,3))
qqmbetag(mydata, "weibull", TRUE, "Nelder-Mead")
mpsmbetag(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`mog` *Marshall-Olkin G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the Marshall-Olkin `G` distribution. General form for the probability density function (pdf) of the Marshall-Olkin `G` distribution due to Marshall and Olkin (1997) is given by

$$f(x,\Theta) = \frac{a g(x-\mu,\theta)}{\left[1-(1-a)\left(1-G(x-\mu,\theta)\right)\right]^{2}},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the Marshall-Olkin `G` distribution is given by

$$F(x,\Theta) = 1-\frac{a\left(1-G(x-\mu,\theta)\right)}{\left[1-(1-a)\left(1-G(x-\mu,\theta)\right)\right]}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta = (a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter. Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dmog(mydata, g, param, location = TRUE, log=FALSE)
pmog(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qmog(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rmog(n, g, param, location = TRUE)
qqmog(mydata, g, location = TRUE, method)
mpsmog(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Marshall, A. W. and Olkin, I. (1997). A new method for adding a parameter to a family of distributions with application to the exponential and Weibull families, *Biometrika*, 84, 641-652.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dmog(mydata, "weibull", c(0.5,2,2,3))
pmog(mydata, "weibull", c(0.5,2,2,3))
qmog(runif(100), "weibull", c(0.5,2,2,3))
rmog(100, "weibull", c(0.5,2,2,3))
qqmog(mydata, "weibull", TRUE, "Nelder-Mead")
mpsmog(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`mokumg` *Marshall-Olkin Kumaraswamy G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the Marshall-Olkin Kumaraswamy `G` distribution. General form for the probability density function (pdf) of the Marshall-Olkin Kumaraswamy `G` distribution due to Roshini and Thobias (2017) is given by

$$f(x,\Theta)=\frac{abdg(x-\mu,\theta)(G(x-\mu,\theta))^{a-1}[1-(G(x-\mu,\theta))^{a}]^{b-1}}{\left[1-(1-d)\left[1-(G(x-\mu,\theta))^{a}\right]^{b}\right]^{2}},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the Marshall-Olkin Kumaraswamy `G` distribution is given by

$$F(x,\Theta)=1-\frac{d[1-(G(x-\mu,\theta))^{a}]^{b}}{1-(1-d)\left[1-(G(x-\mu,\theta))^{a}\right]^{b}}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,d,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dmokumg(mydata, g, param, location = TRUE, log=FALSE)
pmokumg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qmokumg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rmokumg(n, g, param, location = TRUE)
qqmokumg(mydata, g, location = TRUE, method)
mpsmokumg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Roshini, G. and Thobias, S. (2017). Marshall-Olkin Kumaraswamy Distribution, *International Mathematical Forum*, 12 (2), 47-69.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dmokumg(mydata, "weibull", c(1,1,1,2,2,3))
pmokumg(mydata, "weibull", c(1,1,1,2,2,3))
qmokumg(runif(100), "weibull", c(1,1,1,2,2,3))
rmokumg(100, "weibull", c(1,1,1,2,2,3))
qqmokumg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsmokumg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`ologlogg` *odd log-logistic G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the odd log-logistic `G` distribution. General form for the probability density function (pdf) of the odd log-logistic `G` distribution due to Gauss et al. (2017) is given by

$$f(x,\Theta)=\frac{a\,b\,d\,g(x-\mu,\theta)(G(x-\mu,\theta))^{a\,d-1}\big[\bar{G}(x-\mu,\theta)\big]^{d-1}}{\Big[(G(x-\mu,\theta))^{d}-\big(\bar{G}(x-\mu,\theta)\big)^{d}\Big]^{a+1}}\left\{1-\left[\frac{(G(x-\mu,\theta))^{d}}{(G(x-\mu,\theta))^{d}-\big(\bar{G}(x-\mu,\theta)\big)^{d}}\right]^{a}\right\}^{b-1},$$

with $\bar{G}(x-\mu,\theta)=1-G(x-\mu,\theta)$ where θ is the baseline family parameter vector. Also, a>0, b>0, d>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is `g`. The general form for the cumulative distribution function (cdf) of the odd log-logistic `G` distribution is given by

$$F(x,\Theta)=1-\left\{1-\left[\frac{(G(x-\mu,\theta))^{d}}{(G(x-\mu,\theta))^{d}-\big(\bar{G}(x-\mu,\theta)\big)^{d}}\right]^{a}\right\}^{b}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,d,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a, b, and d are the first, second, and the third shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dologlogg(mydata, g, param, location = TRUE, log=FALSE)
pologlogg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qologlogg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rologlogg(n, g, param, location = TRUE)
qqologlogg(mydata, g, location = TRUE, method)
mpsologlogg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, d, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Gauss, M. C., Alizadeh, M., Ozel, G., Hosseini, B. Ortega, E. M. M., and Altunc, E. (2017). The generalized odd log-logistic family of distributions: properties, regression models and applications, *Journal of Statistical Computation and Simulation*, 87(5), 908-932.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dologlogg(mydata, "weibull", c(1,1,1,2,2,3))
pologlogg(mydata, "weibull", c(1,1,1,2,2,3))
qologlogg(runif(100), "weibull", c(1,1,1,2,2,3))
rologlogg(100, "weibull", c(1,1,1,2,2,3))
qqologlogg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsologlogg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`texpsg` *truncated-exponential skew-symmetric G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the truncated-exponential skew-symmetric `G` distribution. General form for the probability density function (pdf) of the truncated-exponential skew-symmetric `G` distribution due to Nadarajah et al. (2014) is given by

$$f(x,\Theta)=\frac{a}{1-e^{-a}}g(x-\mu,\theta)e^{-aG(x-\mu,\theta)},$$

where θ is the baseline family parameter vector. Also, a>0 and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the truncated-exponential skew-symmetric `G` distribution is given by

$$F(x,\Theta)=\frac{1-e^{-aG(x-\mu,\theta)}}{1-e^{-a}}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter. Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dtexpsg(mydata, g, param, location = TRUE, log=FALSE)
ptexpsg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qtexpsg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rtexpsg(n, g, param, location = TRUE)
qqtexpsg(mydata, g, location = TRUE, method)
mpstexpsg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Nadarajah, S., Nassiri, V., and Mohammadpour, A. (2014). Truncated-exponential skew-symmetric distributions, *Statistics*, 48 (4), 872-895.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dtexpsg(mydata, "weibull", c(1,2,2,3))
ptexpsg(mydata, "weibull", c(1,2,2,3))
qtexpsg(runif(100), "weibull", c(1,2,2,3))
rtexpsg(100, "weibull", c(1,2,2,3))
qqtexpsg(mydata, "weibull", TRUE,"Nelder-Mead")
mpstexpsg(mydata, "weibull", TRUE,"Nelder-Mead", 0.05)
```

`weibullextg` *T-X*`{log-logistic}` *G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the Weibull extended or T-X`{log-logistic}` `G` distribution. General form for the probability density function (pdf) of the Weibull extended `G` distribution due to Alzaatreh et al. (2013) is given by

$$f(x,\Theta)=\frac{a\,g(x-\mu,\theta)}{b(1-G(x-\mu,\theta))^2}\biggl(\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}\biggr)^{\frac{1}{b}-1}\exp\biggl\{-a\biggl(\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}\biggr)^{\frac{1}{b}}\biggr\},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the Weibull extended `G` distribution is given by

$$F(x,\Theta)=1-\exp\biggl\{-a\biggl(\frac{G(x-\mu,\theta)}{1-G(x-\mu,\theta)}\biggr)^{\frac{1}{b}}\biggr\}.$$

Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dweibullextg(mydata, g, param, location = TRUE, log=FALSE)
pweibullextg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qweibullextg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rweibullextg(n, g, param, location = TRUE)
qqweibullextg(mydata, g, location = TRUE, method)
mpsweibullextg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alzaatreh, A., Lee, C., and Famoye, F. (2013). A new method for generating families of continuous distributions, *Metron*, 71, 63-79.

Examples

```
mydata<-rweibull(100, shape=2, scale=2)+3
dweibullextg(mydata, "weibull", c(1,1,2,2,3))
pweibullextg(mydata, "weibull", c(1,1,2,2,3))
qweibullextg(runif(100), "weibull", c(1,1,2,2,3))
rweibullextg(100, "weibull", c(1,1,2,2,3))
qqweibullextg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsweibullextg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

`weibullg` *Weibull G distribution*

Description

Computes the pdf, cdf, quantile, and random numbers, draws the q-q plot, and estimates the parameters of the Weibull `G` distribution. General form for the probability density function (pdf) of the Weibull `G` distribution due to Alzaatreh et al. (2013) is given by

$$f(x,\Theta)=\frac{a}{b^{a}}\frac{g(x-\mu,\theta)}{1-G(x-\mu,\theta)}\left[-\log\left(1-G(x-\mu,\theta)\right)\right]^{a-1}e^{-\left(\frac{-\log(1-G(x-\mu,\theta))}{b}\right)^{a}},$$

where θ is the baseline family parameter vector. Also, a>0, b>0, and μ are the extra parameters induced to the baseline cumulative distribution function (cdf) `G` whose pdf is g. The general form for the cumulative distribution function (cdf) of the Weibull `G` distribution is given by

$$F(x,\Theta)=1-e^{-\left(\frac{-\log(1-G(x-\mu,\theta))}{b}\right)^{a}}.$$

The `weibullg` is the special case (Weibull-`X`) of the Alzaatreh et al. (2013) families of distributions. Here, the baseline `G` refers to the cdf of famous families such as: Birnbaum-Saunders, Burr type XII, Exponential, Chen, Chisquare, F, Frechet, Gamma, Gompertz, Linear failure rate (lfr), Log-normal, Log-logistic, Lomax, Rayleigh, and Weibull. The parameter vector is $\Theta=(a,b,\theta,\mu)$ where θ is the baseline `G` family's parameter space. If θ consists of the shape and scale parameters, the last component of θ is the scale parameter (here, a and b are the first and second shape parameters). Always, the location parameter μ is placed in the last component of Θ.

Usage

```
dweibullg(mydata, g, param, location = TRUE, log=FALSE)
pweibullg(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qweibullg(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rweibullg(n, g, param, location = TRUE)
qqweibullg(mydata, g, location = TRUE, method)
mpsweibullg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

`g`	The name of family's pdf including: "`birnbaum-saunders`", "`burrxii`", "`chisq`", "`chen`", "`exp`", "`f`", "`frechet`", "`gamma`", "`gompetrz`", "`lfr`", "`log-normal`", "`log-logistic`", "`lomax`", "`rayleigh`", and "`weibull`".
`p`	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
`n`	number of realizations to be generated.
`mydata`	Vector of observations.
`param`	parameter vector $\Theta = (a, b, \theta, \mu)$
`location`	If `FALSE`, then the location parameter will be omitted.
`log`	If `TRUE`, then log(pdf) is returned.
`log.p`	If `TRUE`, then log(cdf) is returned and quantile is computed for `exp(-p)`.
`lower.tail`	If `FALSE`, then `1-cdf` is returned and quantile is computed for `1-p`.
`method`	The used method for maximizing the sum of log-spacing function. It will be "`BFGS`", "`CG`", "`L-BFGS-B`", "`Nelder-Mead`", or "`SANN`".
`sig.level`	Significance level for the Chi-square goodness-of-fit test.

Details

It can be shown that the Moran's statistic follows a normal distribution. Also, a chi-square approximation exists for small samples whose mean and variance approximately are m(`log`(m)+0.57722)-0.5-1/(12m) and m(π^2/6-1)-0.5-1/(6m), respectively, with `m=n+1`, see Cheng and Stephens (1989). So, a hypothesis tesing can be constructed based on a sample of `n` independent realizations at the given significance level, indicated in above as `sig.level`.

Value

1. A vector of the same length as `mydata`, giving the pdf values computed at `mydata`.
2. A vector of the same length as `mydata`, giving the cdf values computed at `mydata`.
3. A vector of the same length as `p`, giving the quantile values computed at `p`.
4. A vector of the same length as `n`, giving the random numbers realizations.
5. A sequence of goodness-of-fit statistics such as: Akaike Information Criterion (`AIC`), Consistent Akaike Information Criterion (`CAIC`), Bayesian Information Criterion (`BIC`), Hannan-Quinn information criterion (`HQIC`), Cramer-von Misses statistic (`CM`), Anderson Darling statistic (`AD`), log-likelihood statistic (`log`), and Moran's statistic (`M`). The Kolmogorov-Smirnov (`KS`) test statistic and corresponding `p-value`. The Chi-square test statistic, critical upper tail Chi-square distribution, related `p-value`, and the convergence status.

Author(s)

Mahdi Teimouri

References

Cheng, R. C. H. and Stephens, M. A. (1989). A goodness-of-fit test using Moran's statistic with estimated parameters, *Biometrika*, 76 (2), 385-392.

Alzaatreh, A., Lee, C., and Famoye, F. (2013). A new method for generating families of continuous distributions, *Metron*, 71, 63-79.

Examples

```
mydata<-rweibull(100,shape=2,scale=2)+3
dweibullg(mydata, "weibull", c(1,1,2,2,3))
pweibullg(mydata, "weibull", c(1,1,2,2,3))
qweibullg(runif(100), "weibull", c(1,1,2,2,3))
rweibullg(100, "weibull", c(1,1,2,2,3))
qqweibullg(mydata, "weibull", TRUE, "Nelder-Mead")
mpsweibullg(mydata, "weibull", TRUE, "Nelder-Mead", 0.05)
```

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