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Title Estimating Through the Maximum Product Spacing Approach

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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.

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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

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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

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

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

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

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

```

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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.

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

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

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

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

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 $\Theta = (a, b, \theta, \mu)$ 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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.

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))
rexp(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)
rexp(g, n, g, param, location = TRUE)
qqexpgg(mydata, g, location = TRUE, method)
mpsexpgg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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)
rexpumg(n, g, param, location = TRUE)
qqexpkumg(mydata, g, location = TRUE, method)
mpsexpkumg(mydata, g, location = TRUE, method, sig.level)
```

Arguments

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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))
rexpkm(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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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
dggammag2(mydata, "weibull", c(1,2,2,3))
pgammag2(mydata, "weibull", c(1,2,2,3))
qggammag2(runif(100), "weibull", c(1,2,2,3))
rgammag2(100, "weibull", c(1,2,2,3))
qqggammag2(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

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

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 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

```

dgbetaexp(mydata, g, param, location = TRUE, log=FALSE)
pgmbetaexp(mydata, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
qgmbetaexp(p, g, param, location = TRUE, log.p = FALSE, lower.tail = TRUE)
rgmbetaexp(n, g, param, location = TRUE)
qqgmbetaexp(mydata, g, location = TRUE, method)
mpsgmbetaexp(mydata, g, location = TRUE, method, sig.level)

```

Arguments

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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
dgbetaexp(mydata, "weibull", c(1,1,2,2,3))
pgbetaexp(mydata, "weibull", c(1,1,2,2,3))
qgbetaexp(runif(100), "weibull", c(1,1,2,2,3))
rgbetaexp(100, "weibull", c(1,1,2,2,3))
qqgbetaexp(mydata, "weibull", TRUE, "Nelder-Mead")
mpsgbetaexp(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

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

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 is given by

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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 family 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 family of G distribution. General form for the probability density function (pdf) of gamma-X generated of the log-logistic-X family of G distribution due to Alzaatreh et al. (2013) is given by

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

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 family of G distribution is given by

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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)
qlloggammag1(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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for $1-p$.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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., MirMostafaei, 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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., MirMostafaei, 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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 $\Theta = (a, \theta, \mu)$ 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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 $\Theta = (a, b, d, \theta, \mu)$ 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, d, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

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

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 $\Theta = (a, b, \theta, \mu)$ 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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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

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

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

<code>g</code>	The name of family's pdf including: "birnbaum-saunders", "burrxii", "chisq", "chen", "exp", "f", "frechet", "gamma", "gompertz", "lfr", "log-normal", "log-logistic", "lomax", "rayleigh", and "weibull".
<code>p</code>	a vector of value(s) between 0 and 1 at which the quantile needs to be computed.
<code>n</code>	number of realizations to be generated.
<code>mydata</code>	Vector of observations.
<code>param</code>	parameter vector $\Theta = (a, b, \theta, \mu)$
<code>location</code>	If FALSE, then the location parameter will be omitted.
<code>log</code>	If TRUE, then log(pdf) is returned.
<code>log.p</code>	If TRUE, then log(cdf) is returned and quantile is computed for $\exp(-p)$.
<code>lower.tail</code>	If FALSE, then 1-cdf is returned and quantile is computed for 1-p.
<code>method</code>	The used method for maximizing the sum of log-spacing function. It will be "BFGS", "CG", "L-BFGS-B", "Nelder-Mead", or "SANN".
<code>sig.level</code>	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 $m(\pi^2/6-1)-0.5-1/(6m)$, respectively, with $m=n+1$, see Cheng and Stephens (1989). So, a hypothesis testing 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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