

Package ‘TukeyGH77’

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Type Package

Title Tukey g-&-h Distribution

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Description Functions for density, cumulative density, quantile and simulation of Tukey g-and-h (1977) distributions. The quantile-based transformation (Hoaglin 1985 [doi:10.1002/9781118150702.ch11](https://doi.org/10.1002/9781118150702.ch11)) and its reverse transformation, as well as the letter-value based estimates (Hoaglin 1985), are also provided.

License GPL-2

Depends R (>= 4.4.0)

Imports rstpm2, stats

Suggests fitdistrplus

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Contents

TukeyGH77-package	2
letterValue	2
TukeyGH	4

Index	6
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TukeyGH77-package *Tukey g-&-h Distribution*

Description

Density, cumulative density, quantile and simulation of the 4-parameter Tukey (1977) *g*-&-*h* distributions. The quantile-based transformation (Hoaglin 1985) and its reverse transformation, as well as the letter-value based estimates (Hoaglin 1985), are also provided.

Value

Returned values of individual functions are documented separately.

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References

Tukey, J.W. (1977): Modern Techniques in Data Analysis. In: NSF-sponsored Regional Research Conference at Southeastern Massachusetts University, North Dartmouth, MA.

Hoaglin, D.C. (1985): Summarizing shape numerically: The *g*-and-*h* distributions. Exploring data tables, trends, and shapes, pp. 461–513. John Wiley & Sons, Ltd, New York. doi:[10.1002/9781118150702.ch11](https://doi.org/10.1002/9781118150702.ch11)

letterValue *Letter-Value Estimation of Tukey g-&-h Distribution*

Description

Letter-value based estimation (Hoaglin, 1985) of Tukey *g*-, *h*- and *g*-&-*h* distribution. All equation numbers mentioned below refer to Hoaglin (1985).

Usage

```
letterValue(
  x,
  g_ = seq.int(from = 0.15, to = 0.25, by = 0.005),
  h_ = seq.int(from = 0.15, to = 0.35, by = 0.005),
  halfSpread = c("both", "lower", "upper"),
  ...
)
```

Arguments

<code>x</code>	double vector , one-dimensional observations
<code>g_</code>	double vector , probabilities used for estimating g parameter. Or, use <code>g_ = FALSE</code> to implement the constraint $g = 0$ (i.e., an h -distribution is estimated).
<code>h_</code>	double vector , probabilities used for estimating h parameter. Or, use <code>h_ = FALSE</code> to implement the constraint $h = 0$ (i.e., a g -distribution is estimated).
<code>halfSpread</code>	character scalar, either to use 'both' for half-spreads (default), 'lower' for half-spread, or 'upper' for half-spread.
<code>...</code>	additional parameters, currently not in use

Details

Unexported function `letterV_g()` estimates parameter g using equation (10) for g -distribution and the equivalent equation (31) for g -&- h distribution.

Unexported function `letterV_B()` estimates parameter B for Tukey g -distribution (i.e., $g \neq 0$, $h = 0$), using equation (8a) and (8b).

Unexported function `letterV_Bh_g()` estimates parameters B and h when $g \neq 0$, using equation (33).

Unexported function `letterV_Bh()` estimates parameters B and h for Tukey h -distribution, i.e., when $g = 0$ and $h \neq 0$, using equation (26a), (26b) and (27).

Function `letterValue()` plays a similar role as `fitdistrplus:::start.arg.default`, thus extends `fitdistrplus:::fitdist` for estimating Tukey g -&- h distributions.

Value

Function `letterValue()` returns a 'letterValue' object, which is **double vector** of estimates $(\hat{A}, \hat{B}, \hat{g}, \hat{h})$ for a Tukey g -&- h distribution.

Note

Parameter `g_` and `h_` does not have to be truly unique; i.e., **all.equal** elements are allowed.

References

Hoaglin, D.C. (1985). Summarizing Shape Numerically: The g -and- h Distributions. [doi:10.1002/9781118150702.ch11](https://doi.org/10.1002/9781118150702.ch11)

Examples

```
set.seed(77652); x = rGH(n = 1e3L, g = -.3, h = .1)
letterValue(x, g_ = FALSE, h_ = FALSE)
letterValue(x, g_ = FALSE)
letterValue(x, h_ = FALSE)
(m3 = letterValue(x))

library(fitdistrplus)
fit = fitdist(x, distr = 'GH', start = as.list.default(m3))
```

```
plot(fit) # fitdistrplus:::plot.fitdist
```

 TukeyGH

Tukey g-&-h Distribution

Description

Density, distribution function, quantile function and simulation for Tukey *g*-&-*h* distribution with location parameter *A*, scale parameter *B*, skewness *g* and elongation *h*.

Usage

```
dGH(x, A = 0, B = 1, g = 0, h = 0, log = FALSE, ...)
```

```
rGH(n, A = 0, B = 1, g = 0, h = 0)
```

```
qGH(p, A = 0, B = 1, g = 0, h = 0, lower.tail = TRUE, log.p = FALSE)
```

```
pGH(q, A = 0, B = 1, g = 0, h = 0, lower.tail = TRUE, log.p = FALSE, ...)
```

Arguments

<code>x, q</code>	double vector , quantiles
<code>A</code>	double scalar, location parameter $A = 0$ by default
<code>B</code>	double scalar, scale parameter $B > 0$. Default $B = 1$
<code>g</code>	double scalar, skewness parameter $g = 0$ by default (i.e., no skewness)
<code>h</code>	double scalar, elongation parameter $h \geq 0$. Default $h = 0$ (i.e., no elongation)
<code>log, log.p</code>	logical scalar, if TRUE, probabilities p are given as $\log(p)$.
<code>...</code>	other parameters of function <code>vuniroot2()</code>
<code>n</code>	integer scalar, number of observations
<code>p</code>	double vector , probabilities
<code>lower.tail</code>	logical scalar, if TRUE (default), probabilities are $Pr(X \leq x)$ otherwise, $Pr(X > x)$.

Value

Function `dGH()` returns the density and accommodates **vector** arguments *A*, *B*, *g* and *h*. The quantiles *x* can be either **vector** or **matrix**. This function takes about 1/5 time of `gk::dgh`.

Function `pGH()` returns the distribution function, only taking scalar arguments and **vector** quantiles *q*. This function takes about 1/10 time of function `gk::pgh`.

Function `qGH()` returns the quantile function, only taking scalar arguments and **vector** probabilities *p*.

Function `rGH()` generates random deviates, only taking scalar arguments.

Examples

```
(x = c(NA_real_, rGH(n = 5L, g = .3, h = .1)))
dGH(x, g = c(0,.1,.2), h = c(.1,.1,.1))

p0 = seq.int(0, 1, by = .2)
(q0 = qGH(p0, g = .2, h = .1))
range(pGH(q0, g = .2, h = .1) - p0)

q = (-2):3; q[2L] = NA_real_; q
(p1 = pGH(q, g = .3, h = .1))
range(qGH(p1, g = .3, h = .1) - q, na.rm = TRUE)
(p2 = pGH(q, g = .2, h = 0))
range(qGH(p2, g = .2, h = 0) - q, na.rm = TRUE)

curve(dGH(x, g = .3, h = .1), from = -2.5, to = 3.5)
```

Index

`all.equal`, 3

`character`, 3

`dGH (TukeyGH)`, 4

`dGH()`, 4

`double`, 3, 4

`integer`, 4

`letterValue`, 2

`letterValue()`, 3

`logical`, 4

`matrix`, 4

`pGH (TukeyGH)`, 4

`pGH()`, 4

`qGH (TukeyGH)`, 4

`qGH()`, 4

`rGH (TukeyGH)`, 4

`rGH()`, 4

`TukeyGH`, 4

`TukeyGH77 (TukeyGH77-package)`, 2

`TukeyGH77-package`, 2

`vector`, 3, 4

`vunirroot2()`, 4