Package 'LambertW'

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Type Package

Title Probabilistic Models to Analyze and Gaussianize Heavy-Tailed,
Skewed Data

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Description Lambert W x F distributions are a generalized framework to analyze
skewed, heavy-tailed data. It is based on an input/output system, where the
output random variable (RV) Y is a non-linearly transformed version of an input
RV X ~ F with similar properties as X, but slightly skewed (heavy-tailed).
The transformed RV Y has a Lambert W x F distribution. This package contains
functions to model and analyze skewed, heavy-tailed data the Lambert Way:
simulate random samples, estimate parameters, compute quantiles, and plot/
print results nicely. Probably the most important function is 'Gaussianize',
which works similarly to 'scale', but actually makes the data Gaussian.
A do-it-yourself toolkit allows users to define their own Lambert W x
'MyFavoriteDistribution' and use it in their analysis right away.

Depends MASS, ggplot2,

Imports lamW (>= 1.3.0), stats, graphics, grDevices, RColorBrewer,
reshape2, Rcpp (>= 1.0.4), methods

Suggests boot, Rsolnp, nortest, numDeriv, testthat, data.table,
moments, knitr, vars,

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R **topics documented:**

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LambertW-package   *R package for Lambert W$\times$ F distributions*

Description

This package is based on notation, definitions, and results of Goerg (2011, 2015, 2016). I will not include these references in the description of each single function.

Lambert W$\times$ F distributions are a general framework to model and transform skewed, heavy-tailed data. Lambert W$\times$ F random variables (RV) are based on an input/ouput system with input RV $X \sim F_X(x \mid \boldsymbol{\beta})$ and output Y, which is a non-linearly transformed version of X – with similar properties to X, but slightly skewed and/or heavy-tailed. Then Y has a 'Lambert W $\times F_X$' distribution - see References.

get_distnames lists all implemented Lambert W $\times$ F distributions in this package. If you want to generate a skewed/heavy-tailed version of a distribution that is not implemented, you can use the do-it-yourself modular toolkit (create_LambertW_input and create_LambertW_output). It allows users to quickly implement their own Lambert W x 'MyFavoriteDistribution' and use it in their analysis right away.

This package contains several functions to analyze skewed and heavy-tailed data: simulate random samples (rLambertW), evaluate pdf and cdf (dLambertW and pLambertW), estimate parameters (IGMM and MLE_LambertW), compute quantiles (qLambertW), and plot/print results nicely (plot.LambertW_fit, print.LambertW_fit, summary.LambertW_fit).

Probably the most useful function is Gaussianize, which works similarly to scale, but makes your data Gaussian (not just centers and scales it, but also makes it symmetric and removes excess kurtosis).

If you use this package in your work please cite it (citation("LambertW")). You can also send me an implementation of your 'Lambert W $\times$ YourFavoriteDistribution' to add to the **LambertW** package (and I will reference your work introducing your 'Lambert W $\times$ YourFavoriteDistribution' here.)

Feel free to contact me for comments, suggestions, code improvements, implementation of new input distributions, bug reports, etc.

Author(s)

Author and maintainer: Georg M. Goerg (im (at) gmge.org)

References

Goerg, G.M. (2011). "Lambert W Random Variables - A New Family of Generalized Skewed Distributions with Applications to Risk Estimation". Annals of Applied Statistics, 5 (3), 2197-2230. (http://arxiv.org/abs/0912.4554).

Goerg, G.M. (2015). "The Lambert Way to Gaussianize heavy-tailed data with the inverse of Tukey's h transformation as a special case". The Scientific World Journal: Probability and Statistics with Applications in Finance and Economics. Available at http://www.hindawi.com/journals/tswj/aa/909231/.

Goerg, G.M. (2016). "Rebuttal of the "Letter to the Editor of Annals of Applied Statistics" on Lambert W x F distributions and the IGMM algorithm". Available on arxiv.

Examples

```
# Replicate parts of the analysis in Goerg (2011)
data(AA)
y <- AA[AA$sex=="f", "bmi"]
test_normality(y)

fit.gmm <- IGMM(y, type = "s")
summary(fit.gmm)  # gamma is significant and positive
plot(fit.gmm)

# Compare empirical to theoretical moments (given parameter estimates)
moments.theory <-
 mLambertW(theta = list(beta = fit.gmm$tau[c("mu_x", "sigma_x")],
                        gamma = fit.gmm$tau["gamma"]),
          distname = "normal")
TAB <- rbind(unlist(moments.theory),
             c(mean(y), sd(y), skewness(y), kurtosis(y)))
rownames(TAB) <- c("Theoretical (IGMM)", "Empirical")
TAB

x <- get_input(y, fit.gmm$tau)
test_normality(x) # input is normal -> fit a Lambert W x Gaussian by MLE

fit.ml <- MLE_LambertW(y, type = "s", distname = "normal", hessian = TRUE)
summary(fit.ml)
plot(fit.ml)
```

---

analyze_convergence   *Analyze convergence of Lambert W estimators*

Description

Analyzes the feasibility of a Lambert W x F distribution for a given dataset based on bootstrapping. In particular it checks whether parameter estimates support the hypothesis that the data indeed follows a Lambert W x F distribution with finite mean and variance of the input distribution, which is an implicit assumption of Lambert W x F random variables in Goerg (2011).

See Goerg (2016) for an alternative definition that does not rely on fnite second order moments (set use.mean.variance = FALSE to use that type of Lambert W $\times$ F distributions).

Usage

```
analyze_convergence(
  LambertW_fit,
  sample.sizes = round(seq(0.2, 1, length = 5) * length(LambertW_fit$data)),
  ...
)

## S3 method for class 'convergence_LambertW_fit'
summary(object, type = c("basic", "norm", "perc", "bca"), ...)

## S3 method for class 'convergence_LambertW_fit'
plot(x, ...)
```

Arguments

LambertW_fit, object, x

                an object of class "LambertW_fit" with an IGMM or MLE_LambertW estimate.

sample.sizes   sample sizes for several steps of the convergence analysis. By default, one of them equals the length of the original data, which leads to improved plots (see plot.convergence_LambertW_fit); it is not necessary, though.

...   additional arguments passed to bootstrap or boot.ci in **boot** package.

type   type of confidence interval from bootstrap estimates. Passes this argument along to boot.ci. However, contrary to the type argument in boot.ci, the summary function can only take one of c("basic","norm","perc","bca"). See boot.ci for details.

Details

Stehlik and Hermann (2015) show that when researchers use the IGMM algorithm outlined in Goerg (2011) erroneously on data that does not have finite input variance (and hence mean), the algorithm estimates do not converge.

In practice, researchers should of course first check if a given model is appropriate for their data-generating process. Since original Lambert W x F distributions assume that mean and variance are finite, it is not a given that for a specific dataset the Lambert W x F setting makes sense.

The bootstrap analysis reverses Stehlik and Hermann's argument and checks whether the IGMM estimates $\{\hat{\tau}^{(n)}\}_n$ converge for increasing (bootstrapped) sample size n: if they do, then modeling the data with a Lambert W x F distribution is appropriate; if estimates do not converge, then this indicates that the input data is too heavy tailed for a classic skewed location-scale Lambert W x F framework. In this case, take a look at (double-)heavy tailed Lambert W x F distributions (type = 'hh') or unrestricted location-scale Lambert W x F distributions (use.mean.variance = FALSE). For details see Goerg (2016).

References

Stehlik and Hermann (2015). "Letter to the Editor". Ann. Appl. Stat. 9 2051. doi:10.1214/15-AOAS864 – http://projecteuclid.org/euclid.aoas/1453994190

Examples

```
## Not run:

sim.data <- list("Lambert W x Gaussian" =
                    rLambertW(n = 100, distname = "normal",
                              theta = list(gamma = 0.1, beta = c(1, 2))),
                 "Cauchy" = rcauchy(n = 100))
# do not use lapply() as it does not work well with match.call() in
# bootstrap()
igmm.ests <- list()
conv.analyses <- list()
for (nn in names(sim.data)) {
  igmm.ests[[nn]] <- IGMM(sim.data[[nn]], type = "s")
  conv.analyses[[nn]] <- analyze_convergence(igmm.ests[[nn]])
}
plot.lists <- lapply(conv.analyses, plot)
for (nn in names(plot.lists)) {
  plot.lists[[nn]] <- lapply(plot.lists[[nn]], "+", ggtitle(nn))
}

require(gridExtra)
for (jj in seq_along(plot.lists[[1]])) {
  grid.arrange(plot.lists[[1]][[jj]], plot.lists[[2]][[jj]], ncol = 2)
}

## End(Not run)
```

---

beta-utils   *Utilities for parameter vector beta of the input distribution*

Description

The parameter $\boldsymbol{\beta}$ specifies the input distribution $X \sim F_X(x \mid \boldsymbol{\beta})$.

beta2tau converts $\boldsymbol{\beta}$ to the transformation vector $\tau = (\mu_x, \sigma_x, \gamma = 0, \alpha = 1, \delta = 0)$, which defines the Lambert W $\times$ F random variable mapping from X to Y (see [tau-utils](#)). Parameters μ_x and σ_x of X in general depend on $\boldsymbol{\beta}$ (and may not even exist for use.mean.variance = TRUE; in this case beta2tau will throw an error).

check_beta checks if $\boldsymbol{\beta}$ defines a valid distribution, e.g., for normal distribution 'sigma' must be positive.

estimate_beta estimates $\boldsymbol{\beta}$ for a given F_X using MLE or methods of moments. Closed form solutions are used if they exist; otherwise the MLE is obtained numerically using [fitdistr](#).

get_beta_names returns (typical) names for each component of $\boldsymbol{\beta}$.

Depending on the distribution $\boldsymbol{\beta}$ has different length and names: e.g., for a "normal" distribution beta is of length 2 ("mu", "sigma"); for an "exp"onential distribution beta is a scalar (rate "lambda").

Usage

```
beta2tau(beta, distname, use.mean.variance = TRUE)

check_beta(beta, distname)

estimate_beta(x, distname)

get_beta_names(distname)
```

Arguments

beta   numeric; vector $\boldsymbol{\beta}$ of the input distribution; specifications as they are for the
                R implementation of this distribution. For example, if `distname = "exp"`, then
                `beta = 2` means that the rate of the exponential distribution equals 2; if `distname
                = "normal"` then `beta = c(1,2)` means that the mean and standard deviation are
                1 and 2, respectively.

distname   character; name of input distribution; see `get_distnames`.

use.mean.variance

                logical; if TRUE it uses mean and variance implied by $\boldsymbol{\beta}$ to do the transformation
                (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with
                location and scale parameter.

x   a numeric vector of real values (the *input* data).

Details

`estimate_beta` does not do any data transformation as part of the Lambert W$\times$ F input/output
framework. For an initial estimate of θ for Lambert W$\times$ F distributions see `get_initial_theta`
and `get_initial_tau`.

A quick initial estimate of θ is obtained by first finding the (approximate) input $\widehat{x}_{\widehat{\theta}}$ by `IGMM`, and
then getting the MLE of $\boldsymbol{\beta}$ for this input data $\widehat{x}_{\widehat{\theta}} \sim F_X(x \mid \boldsymbol{\beta})$ (usually using `fitdistr`).

Value

`beta2tau` returns a numeric vector, which is $\tau = \tau(\boldsymbol{\beta})$ implied by `beta` and `distname`.

`check_beta` throws an error if $\boldsymbol{\beta}$ is not appropriate for the given distribution; e.g., if it has too many
values or if they are not within proper bounds (e.g., `beta['sigma']` of a `"normal"` distribution
must be positive).

`estimate_beta` returns a named vector with estimates for $\boldsymbol{\beta}$ given x.

`get_beta_names` returns a vector of characters.

See Also

`tau-utils`, `theta-utils`

Examples

```
# By default: delta = gamma = 0 and alpha = 1
beta2tau(c(1, 1), distname = "normal")
## Not run:
  beta2tau(c(1, 4, 1), distname = "t")

## End(Not run)
beta2tau(c(1, 4, 1), distname = "t", use.mean.variance = FALSE)
beta2tau(c(1, 4, 3), distname = "t") # no problem


## Not run:
check_beta(beta = c(1, 1, -1), distname = "normal")

## End(Not run)


set.seed(124)
xx <- rnorm(100)^2
estimate_beta(xx, "exp")
estimate_beta(xx, "chisq")
```

---

bootstrap   *Bootstrap Lambert W x F estimates*

Description

Analyzes the Lambert W x F for a given dataset based on bootstrapping. Depends on the **boot**
package and returns a "boot" object.

Usage

```
bootstrap(object, ...)

## S3 method for class 'LambertW_fit'
bootstrap(object, sample.size = length(object$data), R = 100, ...)
```

Arguments

object	an object of class "LambertW_fit"; usually output of [IGMM](#) or [MLE_LambertW](#).
...	additional arguments passed to [boot](#).
sample.size	sample size of the bootstrap. By default, equal to the original data length.
R	number of replicates for the bootstrap. See [boot](#) for details.

Value

An object of class "boot" representing the bootstrap analysis of $\hat{\theta}$ (or $\hat{\tau}$) of an Lambert W x F
estimator (LambertW_fit).

Examples

```
## Not run:
yy <- rLambertW(n = 1000, theta = list(delta = c(0.1), beta = c(2, 1)),
                distname = "normal")
mod.igmm <- IGMM(yy, type = "h")
boot.est <- bootstrap(mod.igmm, R = 100)
# use summary and plot from 'boot' pkg
plot(boot.est, 3)
summary(boot.est)

## End(Not run)
```

common-arguments	*Common arguments for several functions*

Description

Reference list of most common function arguments in this package.

Arguments

y	a numeric vector of real values (the observed data).
distname	character; name of input distribution; see `get_distnames`.
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
theta	list; a (possibly incomplete) list of parameters alpha, beta, gamma, delta. `complete_theta` fills in default values for missing entries.
beta	numeric vector (deprecated); parameter β of the input distribution. See `check_beta` on how to specify beta for each distribution.
gamma	scalar (deprecated); skewness parameter; default: 0.
delta	scalar or vector (length 2) (deprecated); heavy-tail parameter(s); default: 0.
alpha	scalar or vector (length 2) (deprecated); heavy tail exponent(s); default: 1.
tau	named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see `complete_tau` for details.
return.u	logical; if TRUE, it returns the standardized input that corresponds to U, which is the zero-mean and/or unit-variance version of input $X \sim F_X$.
use.mean.variance	logical; if TRUE it uses mean and variance implied by β to do the transformation (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with location and scale parameter.

---

datasets   *Datasets*

Description

Collection of datasets in this package.

The Australian athletes dataset (AA) were collected in a study of how data on various characteristics of the blood varied with sport body size and sex of the athlete.

The SolarFlares data are $12,773$ observations of peak gamma-ray intensity of solar flares recorded from Feb, 1980 - Dec, 1989. It was analyzed for power-law properties in Clauset et al. (2009) and comes originally from Dennis et al. (1991). Thanks to the authors for giving permission to include the dataset in this package.

Format

AA is a data.frame with 13 columns and 202 rows. See ais dataset in the **DAAG** package for details.

Source

AA was the basis for the analyses that are reported in Telford and Cunningham (1991).

Resources on the SolarFlares dataset can be found at:

http://tuvalu.santafe.edu/~aaronc/powerlaws/data.htm

http://adsabs.harvard.edu/abs/1991chxb.book.....D

See also References.

References

Telford, R.D. and Cunningham, R.B. 1991. Sex, sport and body-size dependency of hematology in highly trained athletes. Medicine and Science in Sports and Exercise 23: 788-794.

Dennis, B. R.; Orwig, L. E.; Kennard, G. S.; Labow, G. J.; Schwartz, R. A.; Shaver, A. R.; Tolbert, A. K. (1991). "The Complete Hard X Ray Burst Spectrometer Event List, 1980-1989." NASA Technical Memorandum 4332.

Clauset, A., C. R. Shalizi, and M. E. J. Newman (2009). "Power-law distributions in empirical data". SIAM Review 51, 661-703 (2009). See also http://tuvalu.santafe.edu/~aaronc/powerlaws/.

| delta_01 | *Input parameters to get zero mean, unit variance output given delta* |

Description

Computes the input mean $\mu_x(\delta)$ and standard deviation $\sigma_x(\delta)$ for input $X \sim F(x \mid \boldsymbol{\beta})$ such that the resulting heavy-tail Lambert W x F RV Y with δ has zero-mean and unit-variance. So far works only for Gaussian input and scalar δ.

The function works for any output mean and standard deviation, but default values are $\mu_y = 0$ and $\sigma_y = 1$ since they are the most useful, e.g., to generate a standardized Lambert W white noise sequence.

Usage

```
delta_01(delta, mu.y = 0, sigma.y = 1, distname = "normal")
```

Arguments

delta	scalar; heavy-tail parameter.
mu.y	output mean; default: 0.
sigma.y	output standard deviation; default: 1.
distname	string; distribution name. Currently this function only supports "normal".

Value

5-dimensional vector $(\mu_x(\delta), \sigma_x(\delta), 0, \delta, 1)$, where $\gamma = 0$ and $\alpha = 1$ are set for the sake of compatiblity with other functions.

Examples

```
delta_01(0) # for delta = 0, input == output, therefore (0,1,0,0,1)
# delta > 0 (heavy-tails):
#   Y is symmetric for all delta:
#   mean = 0; however, sd must be smaller
delta_01(0.1)
delta_01(1/3)  # only moments up to order 2 exist
delta_01(1)  # neither mean nor variance exist, thus NA
```

---

delta_GMM   *Estimate delta*

Description

This function minimizes the Euclidean distance between the sample kurtosis of the back-transformed data $W_\delta(z)$ and a user-specified target kurtosis as a function of δ (see References). Only an iterative application of this function will give a good estimate of δ (see `IGMM`).

Usage

```
delta_GMM(
  z,
  type = c("h", "hh"),
  kurtosis.x = 3,
  skewness.x = 0,
  delta.init = delta_Taylor(z),
  tol = .Machine$double.eps^0.25,
  not.negative = FALSE,
  optim.fct = c("nlm", "optimize"),
  lower = -1,
  upper = 3
)
```

Arguments

z	a numeric vector of data values.
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
kurtosis.x	theoretical kurtosis of the input X; default: 3 (e.g., for $X \sim$ Gaussian).
skewness.x	theoretical skewness of the input X. Only used if type = "hh"; default: 0 (e.g., for $X \sim$ symmetric).
delta.init	starting value for optimization; default: `delta_Taylor`.
tol	a positive scalar; tolerance level for terminating the iterative algorithm; default: `.Machine$double.eps^0.25`.
not.negative	logical; if TRUE the estimate for δ is restricted to the non-negative reals. Default: FALSE.
optim.fct	which R optimization function should be used. Either `'optimize'` (only for type = 'h' and if not.negative = FALSE) or `'nlm'`. Performance-wise there is no big difference.
lower, upper	lower and upper bound for optimization if optim.fct = 'optimize' and not.negative = FALSE. Default: -1 and 3 (this covers most real-world heavy-tail scenarios).

Value

A list with two elements:

delta   optimal δ for data z,

iterations   number of iterations (NA for `'optimize'`).

See Also

[gamma_GMM](#) for the skewed version of this function; [IGMM](#) to estimate all parameters jointly.

Examples

```
# very heavy-tailed (like a Cauchy)
y <- rLambertW(n = 1000, theta = list(beta = c(1, 2), delta = 1),
               distname = "normal")
delta_GMM(y) # after the first iteration
```

---

delta_Taylor   *Estimate of delta by Taylor approximation*

Description

Computes an initial estimate of δ based on the Taylor approximation of the kurtosis of Lambert W $\times$ Gaussian RVs. See Details for the formula.

This is the initial estimate for [IGMM](#) and [delta_GMM](#).

Usage

```
delta_Taylor(y, kurtosis.y = kurtosis(y), distname = "normal")
```

Arguments

y   a numeric vector of data values.

kurtosis.y   kurtosis of y; default: empirical kurtosis of data y.

distname   string; name of the distribution. Currently only supports "normal".

Details

The second order Taylor approximation of the theoretical kurtosis of a heavy tail Lambert W x Gaussian RV around $\delta = 0$ equals

$$\gamma_2(\delta) = 3 + 12\delta + 66\delta^2 + \mathcal{O}(\delta^3).$$

Ignoring higher order terms, using the empirical estimate on the left hand side, and solving for δ yields (positive root)

$$\widehat{\delta}_{Taylor} = \frac{1}{66} \cdot \left(\sqrt{66\widehat{\gamma}_2(\mathbf{y}) - 162} - 6 \right),$$

where $\widehat{\gamma}_2(\mathbf{y})$ is the empirical kurtosis of $\mathbf{y}$.

Since the kurtosis is finite only for $\delta < 1/4$, `delta_Taylor` upper-bounds the returned estimate by 0.25.

Value

scalar; estimated δ.

See Also

`IGMM` to estimate all parameters jointly.

Examples

```
set.seed(2)
# a little heavy-tailed (kurtosis does exist)
y <- rLambertW(n = 1000, theta = list(beta = c(0, 1), delta = 0.2),
               distname = "normal")
# good initial estimate since true delta=0.2 close to 0, and
# empirical kurtosis well-defined.
delta_Taylor(y)
delta_GMM(y) # iterative estimate

y <- rLambertW(n = 1000, theta = list(beta = c(0, 1), delta = 1),
               distname = "normal") # very heavy-tailed (like a Cauchy)
delta_Taylor(y) # bounded by 1/4 (as otherwise kurtosis does not exist)
delta_GMM(y) # iterative estimate
```

---

deprecated-functions   *List of deprecated functions*

Description

These functions have been deprecated in v0.5 of **LambertW** mostly for sake of following R style guides with respect to naming of functions. This means that all deprecated functions here have an analogous function with a similar – more style consistent – name. See also the `NEWS` file.

Deprecated functions still work as expected, but they print out a warning suggesting to use the new function (name).

Usage

```
beta_names(...)

bounds_theta(...)

d1W_1(z, W.z = W(z, branch = -1))

p_1(...)

params2theta(...)

skewness_test(...)

starting_theta(...)

support(...)

normfit(...)

theta2params(...)

vec.norm(...)

W_1(z)

W_gamma_1(z, gamma)

H(...)
```

Arguments

...	arguments passed to deprecated functions.
z, W.z	see deriv_W
gamma	see W_gamma.

---

distname-utils   *Utilities for distributions supported in this package*

Description

The Lambert $W \times F$ framework can take any (continuous) random variable with distribution F and make it skewed (type = "s"), heavy tailed (type = "h"), or both (type = "hh").

In principle, this works for any F. Of course, this package implements only a finite number of distributions, which can be specified with the distname argument. Most functions in this package, however, also allow you to pass your own distribution and parameters and create a Lambert $W \times F$ version of it.

check_distname checks if the distribution specified by the distname argument is implemented in this package.

get_distname_family determines whether a distribution is a location, scale, or location-scale family. It also returns whether the distribution is supported on non-negative values only.

get_distnames lists all currently implemented distributions F_X.

Usage

```
check_distname(distname)

get_distname_family(distname)

get_distnames()
```

Arguments

distname   character; name of input distribution; see [get_distnames](#).

Value

check_distname returns (invisible) that the distribution is implemented, or throws an error otherwise.

get_distname_family returns a list with

location   logical; if TRUE, the distribution is a location family,

scale   logical; if TRUE, the distribution is a scale family.

is.non.negative

                logical; if TRUE, the distribution has support only for the non-negative reals (this is usually the case when location = FALSE and scale = TRUE)

get_distnames returns a vector of strings in alphabetical order. It lists all supported distributions. Each string can be passed as the distname argument to several functions in this package.

See Also

[create_LambertW_input](#), [create_LambertW_output](#).

Examples

```
check_distname("normal")
## Not run:
check_distname("my_great_distribution")

## End(Not run)

get_distname_family("normal")
```

---

gamma_01	*Input parameters to get a zero mean, unit variance output for a given gamma*

Description

Computes the input mean $\mu_x(\gamma)$ and standard deviation $\sigma_x(\gamma)$ for input $X \sim F(x \mid \boldsymbol{\beta})$ such that the resulting skewed Lambert W x F RV Y with γ has zero-mean and unit-variance. So far works only for Gaussian input and scalar γ.

The function works for any output mean and standard deviation, but $\mu_y = 0$ and $\sigma_y = 1$ are set as default as they are the most useful, e.g., to generate a standardized Lambert W white noise sequence.

Usage

```
gamma_01(gamma, mu.y = 0, sigma.y = 1, distname = "normal")
```

Arguments

gamma	skewness parameter
mu.y	output mean; default: 0.
sigma.y	output standard deviation; default: 1.
distname	string; name of distribution. Currently only supports "normal".

Value

A 5-dimensional vector $(\mu_x(\gamma), \sigma_x(\gamma), \gamma, 0, 1)$, where $\delta = 0$ and $\alpha = 1$ are set for the sake of compatiblity with other functions.

Examples

```
gamma_01(0) # for gamma = 0, input == output, therefore (0,1,0,0,1)
# input mean must be slightly negative to get a zero-mean output
gamma_01(0.1) # gamma = 0.1 means it is positively skewed
gamma_01(1)
```

---

gamma_GMM   *Estimate gamma*

Description

This function minimizes the Euclidean distance between the theoretical skewness of a skewed Lambert W x Gaussian random variable and the sample skewness of the back-transformed data $W_\gamma(z)$ as a function of γ (see References). Only an interative application of this function will give a good estimate of γ (see `IGMM`).

Usage

```
gamma_GMM(
  z,
  skewness.x = 0,
  gamma.init = gamma_Taylor(z),
  robust = FALSE,
  tol = .Machine$double.eps^0.25,
  not.negative = FALSE,
  optim.fct = c("optimize", "nlminb")
)
```

Arguments

z	a numeric vector of data values.
skewness.x	theoretical skewness of the input X; default: `0`.
gamma.init	starting value for γ; default: `gamma_Taylor`.
robust	logical; if TRUE, robust measure of asymmetry (`medcouple_estimator`) will be used; default: FALSE.
tol	a positive scalar; tolerance level for terminating the iterative algorithm; default: `.Machine$double.eps^0.25`.
not.negative	logical; if TRUE, the estimate for γ is restricted to non-negative reals, which is useful for scale-family Lambert W$\times$ F random variables. Default: FALSE.
optim.fct	string; which R optimization function should be used. By default it uses `optimize` which is about 8-10x faster than `nlminb`.

Value

A list with two elements:

gamma	scalar; optimal γ,
iterations	number of iterations (NA for `"optimize"`).

See Also

`delta_GMM` for the heavy-tail version of this function; `medcouple_estimator` for a robust measure of asymmetry; `IGMM` for an iterative method to estimate all parameters jointly.

Examples

```
# highly skewed
y <- rLambertW(n = 1000, theta = list(beta = c(1, 2), gamma = 0.5),
               distname = "normal")
gamma_GMM(y, optim.fct = "nlminb")
gamma_GMM(y)
```

---

gamma_Taylor   *Estimate gamma by Taylor approximation*

Description

Computes an initial estimate of γ based on the Taylor approximation of the skewness of Lambert W $\times$ Gaussian RVs around $\gamma = 0$. See Details for the formula.

This is the initial estimate for `IGMM` and `gamma_GMM`.

Usage

```
gamma_Taylor(y, skewness.y = skewness(y), skewness.x = 0, degree = 3)
```

Arguments

y	a numeric vector of data values.
skewness.y	skewness of y; default: empirical skewness of data y.
skewness.x	skewness for input X; default: 0 (symmetric input).
degree	degree of the Taylor approximation; in Goerg (2011) it just uses the first order approximation ($6 \cdot \gamma$); a much better approximation is the third order ($6 \cdot \gamma + 8 \cdot \gamma^3$). By default it uses the better degree = 3 approximation.

Details

The first order Taylor approximation of the theoretical skewness γ_1 (not to be confused with the skewness parameter γ) of a Lambert W x Gaussian random variable around $\gamma = 0$ equals

$$\gamma_1(\gamma) = 6\gamma + \mathcal{O}(\gamma^3).$$

Ignoring higher order terms, using the empirical estimate on the left hand side, and solving γ yields a first order Taylor approximation estimate of γ as

$$\widehat{\gamma}_{Taylor}^{(1)} = \frac{1}{6}\widehat{\gamma}_1(\mathbf{y}),$$

where $\widehat{\gamma}_1(\mathbf{y})$ is the empirical skewness of the data $\mathbf{y}$.

As the Taylor approximation is only good in a neighborhood of $\gamma = 0$, the output of gamma_Taylor is restricted to the interval $(-0.5, 0.5)$.

The solution of the third order Taylor approximation

$$\gamma_1(\gamma) = 6\gamma + 8\gamma^3 + \mathcal{O}(\gamma^5),$$

is also supported. See code for the solution to this third order polynomial.

Value

Scalar; estimate of γ.

See Also

IGMM to estimate all parameters jointly.

Examples

```
set.seed(2)
# a little skewness
yy <- rLambertW(n = 1000, theta = list(beta = c(0, 1), gamma = 0.1),
                distname = "normal")
# Taylor estimate is good because true gamma = 0.1 close to 0
gamma_Taylor(yy)

# very highly negatively skewed
yy <- rLambertW(n = 1000, theta = list(beta = c(0, 1), gamma = -0.75),
                distname = "normal")
# Taylor estimate is bad since gamma = -0.75 is far from 0;
# and gamma = -0.5 is the lower bound by default.
gamma_Taylor(yy)
```

Gaussianize *Gaussianize matrix-like objects*

Description

Gaussianize is probably the most useful function in this package. It works the same way as scale, but instead of just centering and scaling the data, it actually *Gaussianizes* the data (works well for unimodal data). See Goerg (2011, 2016) and Examples.

Important: For multivariate input X it performs a column-wise Gaussianization (by simply calling apply(X, 2, Gaussianize)), which is only a marginal Gaussianization. This does *not* mean (and is in general definitely not the case) that the transformed data is then jointly Gaussian.

By default Gaussianize returns the $X \sim N(\mu_x, \sigma_x^2)$ input, not the zero-mean, unit-variance $U \sim N(0, 1)$ input. Use return.u = TRUE to obtain U.

Usage

```
Gaussianize(
  data = NULL,
  type = c("h", "hh", "s"),
  method = c("IGMM", "MLE"),
  return.tau.mat = FALSE,
  inverse = FALSE,
  tau.mat = NULL,
  verbose = FALSE,
  return.u = FALSE,
  input.u = NULL
)
```

Arguments

data	a numeric matrix-like object; either the data that should be Gaussianized; or the data that should "DeGaussianized" (`inverse = TRUE`), i.e., converted back to the original space.
type	what type of non-normality: symmetric heavy-tails `"h"` (default), skewed heavy-tails `"hh"`, or just skewed `"s"`.
method	what estimator should be used: `"MLE"` or `"IGMM"`. `"IGMM"` gives exactly Gaussian characteristics (kurtosis $\equiv 3$ for `"h"` or skewness $\equiv 0$ for `"s"`), `"MLE"` comes close to this. Default: `"IGMM"` since it is much faster than `"MLE"`.
return.tau.mat	logical; if TRUE it also returns the estimated τ parameters as a matrix (same number of columns as data). This matrix can then be used to Gaussianize new data with pre-estimated τ. It can also be used to "DeGaussianize" data by passing it as an argument (`tau.mat`) to `Gaussianize()` and set `inverse = TRUE`.
inverse	logical; if TRUE it performs the inverse transformation using `tau.mat` to "DeGaussianize" the data back to the original space again.
tau.mat	instead of estimating τ from the data you can pass it as a matrix (usually obtained via `Gaussianize(...,return.tau.mat = TRUE)`). If `inverse = TRUE` it uses this tau matrix to "DeGaussianize" the data again. This is useful to back-transform new data in the Gaussianized space, e.g., predictions or fits, back to the original space.
verbose	logical; if TRUE, it prints out progress information in the console. Default: FALSE.
return.u	logical; if TRUE it returns the zero-mean, unit variance Gaussian input. If FALSE (default) it returns the input X.
input.u	optional; if you used `return.u = TRUE` in a previous step, and now you want to convert the data back to original space, then you have to pass it as `input.u`. If you pass numeric data as data, `Gaussianize` assumes that data is the input corresponding to X, not U.

Value

numeric matrix-like object with same dimension/size as input data. If inverse = FALSE it is the Gaussianize matrix / vector; if TRUE it is the "DeGaussianized" matrix / vector.

The numeric parameters of mean, scale, and skewness/heavy-tail parameters that were used in the Gaussianizing transformation are returned as attributes of the output matrix: `'Gaussianized:mu'`, `'Gaussianized:sigma'`, and for

type = "h":	`'Gaussianized:delta'` & `'Gaussianized:alpha'`,
type = "hh":	`'Gaussianized:delta_l'` and `'Gaussianized:delta_r'` & `'Gaussianized:alpha_l'` and `'Gaussianized:alpha_r'`,
type = "s":	`'Gaussianized:gamma'`.

They can also be returned as a separate matrix using return.tau.mat = TRUE. In this case Gaussianize returns a list with elements:

input	Gaussianized input data x (or u if return.u = TRUE),
tau.mat	matrix with τ estimates that we used to get x; has same number of columns as x, and 3, 5, or 6 rows (depending on type='s', 'h', or 'hh').

Examples

```
# Univariate example
set.seed(20)
y1 <- rcauchy(n = 100)
out <- Gaussianize(y1, return.tau.mat = TRUE)
x1 <- get_input(y1, c(out$tau.mat[, 1]))  # same as out$input
test_normality(out$input) # Gaussianized a Cauchy!

kStartFrom <- 20
y.cum.avg <- (cumsum(y1)/seq_along(y1))[-seq_len(kStartFrom)]
x.cum.avg <- (cumsum(x1)/seq_along(x1))[-seq_len(kStartFrom)]

plot(c((kStartFrom + 1): length(y1)), y.cum.avg, type="l" , lwd = 2,
     main="CLT in practice", xlab = "n",
     ylab="Cumulative sample average",
     ylim = range(y.cum.avg, x.cum.avg))
lines(c((kStartFrom+1): length(y1)), x.cum.avg, col=2, lwd=2)
abline(h = 0)
grid()
legend("bottomright", c("Cauchy", "Gaussianize"), col = c(1, 2),
       box.lty = 0, lwd = 2, lty = 1)

plot(x1, y1, xlab="Gaussian-like input", ylab = "Cauchy - output")
grid()
## Not run:
# multivariate example
y2 <- 0.5 * y1 + rnorm(length(y1))
YY <- cbind(y1, y2)
plot(YY)
```

```
XX <- Gaussianize(YY, type = "hh")
plot(XX)

out <- Gaussianize(YY, type = "h", return.tau.mat = TRUE,
                    verbose = TRUE, method = "IGMM")

plot(out$input)
out$tau.mat

YY.hat <- Gaussianize(data = out$input, tau.mat = out$tau.mat,
                      inverse = TRUE)
plot(YY.hat[, 1], YY[, 1])

## End(Not run)
```

---

get_gamma_bounds *Get bounds for gamma*

Description

get_gamma_bounds returns lower and upper bounds for γ, so that the observed data range falls within the theoretical bounds of the support of the distribution. This is only important for location family input.

Usage

```
get_gamma_bounds(y, tau)
```

Arguments

y	a numeric vector of real values (the observed data).
tau	named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see complete_tau for details.

Details

Skewed Lambert $W \times F$ distributions have parameter-dependent support for location family input. Thus the parameter γ must be bounded such that the observed data is within the theoretical support of the distribution. This theoretical bounds are determined by the Lambert W function (W), which has only real-valued solutions for $z \geq -1/\exp(1)$. Thus, W_gamma has real-valued solutions only for $z \geq -1/\exp(1)\gamma$ These lower and upper bounds are determined by minimum and maxiumum of the normalized data $\mathbf{z} = (\mathbf{y} - \mu_x)/\sigma_x$.

Value

get_gamma_bounds returns a vector of length 2 with "lower" and "upper" bounds of γ given the range of y.

---

get_input   *Back-transform Y to X*

Description

get_input back-transforms the observed data y to the (approximate) input data x_τ using the transformation vector $\tau = (\mu_x(\boldsymbol{\beta}), \sigma_x(\boldsymbol{\beta}), \gamma, \alpha, \delta)$.

Note that get.input should be deprecated; however, since it was explicitly referenced in Goerg (2011) I keep it here for future reference. New code should use get_input exclusively.

Usage

```
get_input(y, tau, return.u = FALSE)

get.input(...)
```

Arguments

y	a numeric vector of data values or an object of class LambertW_fit.
tau	named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see complete_tau for details.
return.u	should the normalized input be returned; default: FALSE.
...	arguments passed to get_input.

Value

The (approximated) input data vector $\widehat{x}_\tau$.

For gamma != 0 it uses the principal branch solution W_gamma(z, branch = 0) to get a unique input.

For gamma = 0 the back-transformation is bijective (for any $\delta \geq 0, \alpha \geq 0$).

If return.u = TRUE, then it returns a list with 2 vectors

u	centered and normalized input $\widehat{u}_\theta$,
x	input data $\widehat{x}_\theta$.

See Also

get_output

Examples

```
set.seed(12)
# unskew very skewed data
y <- rLambertW(n = 1000, theta = list(beta = c(0, 1), gamma = 0.3),
               distname = "normal")
test_normality(y)
```

```
fit.gmm <- IGMM(y, type="s")

x <- get_input(y, fit.gmm$tau)
# the same as
x <- get_input(fit.gmm)
test_normality(x) # symmetric Gaussian
```

---

get_output   *Transform input X to output Y*

Description

get_output transforms the input x to the observed data y given the transformation vector $\tau = (\mu_x(\boldsymbol{\beta}), \sigma_x(\boldsymbol{\beta}), \gamma, \alpha, \delta)$.

This is the inverse of [get_input](#).

Usage

```
get_output(x, tau, return.z = FALSE)
```

Arguments

x   a numeric vector of data values.

tau   named vector τ which defines the variable transformation. Must have at least
                'mu_x' and 'sigma_x' element; see [complete_tau](#) for details.

return.z   should the shifted and scaled output also be returned? Default: FALSE.

Value

A numeric object of same size/dimension as input x.

If return.z = TRUE, then it returns a list with 2 vectors

z   shifted and scaled input z,

y   transformed output data y, which has a Lambert W $\times$ F distribution.

See Also

[get_input](#); [Gaussianize](#) with argument inverse = TRUE.

---

get_support   *Computes support for skewed Lambert W x F distributions*

Description

If the input $X \sim F$ has support on the entire real line $(-\infty, \infty)$, then the skewed Lambert W $\times$ F distribution has truncated support $[a, b]$, $a, b \in R \cup \pm\infty$ depending on β and (the sign of) γ.

For scale-families no truncation occurs.

Usage

```
get_support(tau, is.non.negative = FALSE, input.bounds = c(-Inf, Inf))
```

Arguments

tau
: named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see [complete_tau](#) for details.

is.non.negative
: logical; by default it is set to TRUE if the distribution is not a location but a scale family.

input.bounds
: interval; the bounds of the input distribution. If is.non.negative = FALSE, then it will adjust it to c(0,Inf); also useful for bounded input distributions, such as "unif".

Details

Half-open interval on the real line (if $\gamma \neq 0$) for input with support on the entire real line. For $\gamma = 0$ the support of Y is the same as for X. Heavy-tail Lambert W RVs are not affected by truncated support (for $\delta \geq 0$); thus support is c(lower = -Inf, upper = Inf).

Value

A vector of length 2 with names 'lower' and 'upper'.

Examples

```
get_support(c(mu_x = 0, sigma_x = 1, gamma = 0)) # as gamma = 0
# truncated on the left since gamma > 0
get_support(c(mu_x = 0, sigma_x = 1, gamma = 0.1))

# no truncation for heavy tail(s)
get_support(c(mu_x = 0, sigma_x = 1, delta = 0.1))
```

G_delta_alpha | *Heavy tail transformation for Lambert W random variables*

Description

Heavy-tail Lambert W RV transformation: $G_{\delta,\alpha}(u) = u \exp(\frac{\delta}{2}(u^2)^\alpha)$. Reduces to Tukey's h distribution for $\alpha = 1$ (`G_delta`) and Gaussian input.

Usage

```
G_delta_alpha(u, delta = 0, alpha = 1)

G_delta(u, delta = 0)

G_2delta_2alpha(u, delta = c(0, 0), alpha = c(1, 1))
```

Arguments

u	a numeric vector of real values.
delta	heavy tail parameter; default delta = 0, which implies G_delta_alpha(u) = u.
alpha	exponent in $(u^2)^\alpha$; default alpha = 1 (Tukey's h).

Value

numeric; same dimension/size as u.

H_gamma | *H transformation with gamma*

Description

Skewed Lambert W× F RV transformation: $H_\gamma(u) = u \exp(\gamma u)$.

Usage

```
H_gamma(u, gamma = 0)
```

Arguments

u	a numeric vector of real values.
gamma	skewness parameter; default gamma = 0, which implies H_gamma(u) = u.

Value

numeric; same dimension/size as u

See Also

xexp

IGMM   *Iterative Generalized Method of Moments – IGMM*

Description

An iterative method of moments estimator to find this $\tau = (\mu_x, \sigma_x, \gamma)$ for `type = 's'` ($\tau = (\mu_x, \sigma_x, \delta)$ for `type = 'h'` or $\tau = (\mu_x, \sigma_x, \delta_l, \delta_r)$ for `type = "hh"`) which minimizes the distance between the sample and theoretical skewness (or kurtosis) of x and X.

This algorithm is only well-defined for data with finite mean and variance input X. See analyze_convergence and references therein for details.

Usage

```
IGMM(
  y,
  type = c("h", "hh", "s"),
  skewness.x = 0,
  kurtosis.x = 3,
  tau.init = get_initial_tau(y, type),
  robust = FALSE,
  tol = .Machine$double.eps^0.25,
  location.family = TRUE,
  not.negative = NULL,
  max.iter = 100,
  delta.lower = -1,
  delta.upper = 3
)
```

Arguments

y	a numeric vector of real values.
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
skewness.x	theoretical skewness of input X; default 0 (symmetric distribution).
kurtosis.x	theoretical kurtosis of input X; default 3 (Normal distribution reference).
tau.init	starting values for IGMM algorithm; default: get_initial_tau. See also gamma_Taylor and delta_Taylor.
robust	logical; only used for `type = "s"`. If TRUE a robust estimate of asymmetry is used (see medcouple_estimator); default: FALSE.
tol	a positive scalar specifiying the tolerance level for terminating the iterative algorithm. Default: `.Machine$double.eps^0.25`

location.family

> logical; tell the algorithm whether the underlying input should have a location family distribution (for example, Gaussian input); default: TRUE. If FALSE (e.g., for "exp"onential input), then tau['mu_x'] = 0 throughout the optimization.

not.negative
> logical; if TRUE, the estimate for γ or δ is restricted to non-negative reals. If it is set to NULL (default) then it will be set internally to TRUE for heavy-tail(s) Lambert W× F distributions (type = "h" or "hh"). For skewed Lambert W× F (type = "s") it will be set to FALSE, unless it is not a location-scale family (see [get_distname_family](#)).

max.iter
> maximum number of iterations; default: 100.

delta.lower, delta.upper
> lower and upper bound for [delta_GMM](#) optimization. By default: −1 and 3 which covers most real-world heavy-tail scenarios.

Details

For algorithm details see the References.

Value

A list of class LambertW_fit:

tol	see Arguments
data	data y
n	number of observations
type	see Arguments
tau.init	starting values for τ
tau	IGMM estimate for τ
tau.trace	entire iteration trace of $\tau^{(k)}$, $k = 0, ..., K$, where K <= max.iter.
sub.iterations	number of iterations only performed in GMM algorithm to find optimal γ (or δ)
iterations	number of iterations to update μ_x and σ_x. See References for detals.
hessian	Hessian matrix (obtained from simulations; see References)
call	function call
skewness.x, kurtosis.x	see Arguments
distname	a character string describing distribution characteristics given the target theoretical skewness/kurtosis for the input. Same information as skewness.x and kurtosis.x but human-readable.
location.family	see Arguments
message	message from the optimization method. What kind of convergence?
method	estimation method; here: "IGMM"

Author(s)

Georg M. Goerg

See Also

delta_GMM, gamma_GMM, analyze_convergence

Examples

```
# estimate tau for the skewed version of a Normal
y <- rLambertW(n = 1000, theta = list(beta = c(2, 1), gamma = 0.2),
               distname = "normal")
fity <- IGMM(y, type = "s")
fity
summary(fity)
plot(fity)

# estimate tau for the skewed version of an exponential
y <- rLambertW(n = 1000, theta = list(beta = 1, gamma = 0.5),
               distname = "exp")
fity <- IGMM(y, type = "s", skewness.x = 2, location.family = FALSE)
fity
summary(fity)
plot(fity)

# estimate theta for the heavy-tailed version of a Normal = Tukey's h
y <- rLambertW(n = 500, theta = list(beta = c(2, 1), delta = 0.2),
               distname = "normal")
system.time(
fity <- IGMM(y, type = "h")
)
fity
summary(fity)
plot(fity)
```

---

ks.test.t   *One-sample Kolmogorov-Smirnov test for student-t distribution*

Description

Performs a two-sided KS test for $H_0 : X \sim t_\nu$ with c, scale s, and degrees of freedom ν. If parameters are not specified, the MLE given the data will be used (see fitdistr).

For estimated parameters of the t-distribution the p-values are incorrect and should be adjusted. See ks.test and the references therein (Durbin (1973)). As a more practical approach consider bootstrapping and estimating the p-value empirically.

Usage

```
ks.test.t(x, param = NULL)
```

Arguments

x	a numeric vector of data values.
param	3-dimensional named vector (`'location'`,`'scale'`,`'df'`) which parametrizes the student t distribution. Default: `param = NULL`, in which case it will be estimated from x.

Value

A list of class `"htest"` containing:

statistic	the value of the Kolomogorv-Smirnov statistic.
p.value	the p-value for the test.
alternative	a character string describing the alternative hypothesis.
method	the character string "One-sample Kolomogorov-Smirnov test student-t" plus rounded parameter values.
data.name	a character string giving the name(s) of the data.

See Also

[fitdistr](), [ks.test]()

Examples

```
set.seed(1021)
beta.true <- c(location = 0, scale = 1, df = 4)
xx <- rt(n = 1000, df = beta.true['df'])
ks.test.t(xx)
ks.test.t(xx, beta.true)
```

---

kurtosis	*Skewness and kurtosis*

Description

kurtosis estimates the fourth central, normalized moment from data.

skewness estimates the third central, normalized moment from data.

Usage

```
kurtosis(x)

skewness(x)
```

Arguments

x	a numeric vector.

See Also

Corresponding functions in the **moments** package.

LambertW-toolkit   *Do-it-yourself toolkit for Lambert W$\times$ F distribution*

Description

IMPORTANT: This toolkit functionality is still under active development; function names, arguments, return values, etc. may change.

This do-it-yourself Lambert W$\times$ F toolkit implements the flexible input/output framework of Lambert W $\times$ F random variables (see References). Using a modular approach, it allows users to create their own Lambert W $\times$ 'MyFavoriteDistribution' RVs. See Details below.

If the distribution you inted to use is not already implemented ([get_distnames](#)), then you can create it:

create input: use [create_LambertW_input](#) with your favorite distribution,

create output: pass it as an input argument to [create_LambertW_output](#),

use output: use Rs standard functionality for distributions such as random number generation (rY), pdf (dY) and cdf (pY), quantile function (qY), etc. for this newly generated Lambert W $\times$ 'MyFavoriteDistribution'.

create_LambertW_output converts the input LambertW_input representing random variable $X \sim F_X$ to the Lambert W $\times F_X$ output.

Usage

```
create_LambertW_input(
  distname = NULL,
  beta,
  input.u = list(beta2tau = NULL, d = NULL, p = NULL, r = NULL, q = NULL, distname =
    "MyFavoriteDistribution", is.non.negative = FALSE)
)

create_LambertW_output(
  LambertW.input = NULL,
  theta = NULL,
  distname = LambertW.input$distname
)
```

Arguments

distname   character; name of input distribution; see [get_distnames](#).

beta   numeric vector (deprecated); parameter β of the input distribution. See [check_beta](#) on how to specify beta for each distribution.

input.u	optional; users can make their own 'Lambert W x F' distribution by supplying the necessary functions. See Description for details.
LambertW.input	an object of class LambertW_input
theta	list; a (possibly incomplete) list of parameters alpha, beta, gamma, delta. [complete_theta](#) fills in default values for missing entries.

Details

[create_LambertW_output](#) takes an object of class LambertW_input and creates a class LambertW_output for standard distributions as well as the user-defined distribution. This LambertW_output represents the RV Y $\sim$ Lambert W $\times$ 'MyFavoriteDistribution' with all its properties and R functionality, such as random number generation (rY), pdf (dY) and cdf (pY), etc.

create_LambertW_input allows users to define their own Lambert W $\times$ F distribution by supplying the necessary functions about the input random variable U and $\boldsymbol{\beta}$. Here U is the zero mean and/or unit variance version of $X \sim F_X(x \mid \boldsymbol{\beta})$ (see References).

The argument input.u must be a list containing all of the following:

beta2tau R function of (beta): converts $\boldsymbol{\beta}$ to τ for the user defined distribution

distname optional; users can specify the name of their input distribution. By default it's called "MyFavoriteDistribution". The distribution name will be used in plots and summaries of the Lambert W $\times$ F input (and output) object.

is.non.negative logical; users should specify whether the distribution is for non-negative random variables or not. This will help for plotting and theoretical quantile computation.

d R function of (u,beta): probability density function (pdf) of U,

p R function of (u,beta): cumulative distribution function (cdf) of U,

q R function of (p,beta): quantile function of U,

r R function (n,beta): random number generator for U,

Value

create_LambertW_output returns a list of class LambertW_output with values that are (for the most part) functions themselves (see Examples):

d	pdf of Y $\sim$ Lambert W $\times$ 'MyFavoriteDistribution',
p	cdf of Y,
q	quantile function for Y,
r	random number generator for Y,
distname	character string with the name of the new distribution. Format: "Lambert W x 'MyFavoriteDistribution'",
beta, theta	see Arguments,
distname.with.beta	
	name of the new distribution including the parameter beta. Format: "Lambert W x 'MyFavoriteDistribution'(beta)".

Author(s)

Georg M. Goerg

Examples

```
# create a Gaussian N(1, 2) input
Gauss.input <- create_LambertW_input("normal", beta = c(1, 2))

# create a heavy-tailed version of a normal
# gamma = 0, alpha = 1 are set by default; beta comes from input
params <- list(delta = c(0.3))
LW.Gauss <- create_LambertW_output(LambertW.input = Gauss.input,
                                   theta = params)
LW.Gauss

op <- par(no.readonly = TRUE)
par(mfrow = c(2, 1), mar = c(3, 3, 2, 1))
curve(LW.Gauss$d(x, params), -7, 10, col = "red")
# parameter will get detected automatically from the input
curve(LW.Gauss$d(x), -7, 10, col = "blue") # same in blue;

# compare to the input case (i.e. set delta = 0)
params.0 <- params
params.0$delta <- 0

# to evaluate the RV at a different parameter value,
# it is necessary to pass the new parameter
curve(LW.Gauss$d(x, params.0), -7, 10, add = TRUE, col = 1) #' par(op)

curve(LW.Gauss$p(x, params), -7, 10, col = "red")
curve(LW.Gauss$p(x, params.0), -7, 10, add = TRUE, col = 1)

test_normality(LW.Gauss$r(n = 100), add.legend = FALSE)

## generate a positively skewed version of a shifted, scaled t_3
t.input <- create_LambertW_input("t", beta = c(2, 1, 3))
t.input
params <- list(gamma = 0.05) # skew it
LW.t <- create_LambertW_output(LambertW.input = t.input, theta = params)
LW.t

plot(t.input$d, -7, 11, col = 1)
plot(LW.t$d, -7, 11, col = 2, add = TRUE)
abline(v = t.input$beta["location"], lty = 2)

# draw samples from the skewed t_3
yy <- LW.t$r(n = 100)
test_normality(yy)

### create a skewed exponential distribution
exp.input <- create_LambertW_input("exp", beta = 1)
```

```
plot(exp.input)
params <- list(gamma = 0.2)
LW.exp <- create_LambertW_output(exp.input, theta = params)
plot(LW.exp)

# create a heavy-tail exponential distribution
params <- list(delta = 0.2)
LW.exp <- create_LambertW_output(exp.input, theta = params)
plot(LW.exp)

# create a skewed chi-square distribution with 5 df
chi.input <- create_LambertW_input("chisq", beta = 5)
plot(chi.input)
params <- list(gamma = sqrt(2)*0.2)
LW.chi <- create_LambertW_output(chi.input, theta = params)
plot(LW.chi)


# a demo on how a user-defined U input needs to look like
user.tmp <- list(d = function(u, beta) dnorm(u),
                 r = function(n, beta) rnorm(n),
                 p = function(u, beta) pnorm(u),
                 q = function(p, beta) qnorm(p),
                 beta2tau = function(beta) {
                   c(mu_x = beta[1], sigma_x = beta[2],
                     gamma = 0, alpha = 1, delta = 0)
                   },
                 distname = "MyNormal",
                 is.non.negative = FALSE)
my.input <- create_LambertW_input(input.u = user.tmp, beta = c(0, 1))
my.input
plot(my.input)
```

LambertW-utils *Utilities for Lambert W× F Random Variables*

Description

Density, distribution, quantile function and random number generation for a Lambert W $\times F_X(x \mid \boldsymbol{\beta})$ random variable with parameter $\theta = (\alpha, \boldsymbol{\beta}, \gamma, \delta)$.

Following the usual R dqpr family of functions (e.g., rnorm, dnorm, ...) the Lambert W× F utility functions work as expected: dLambertW evaluates the pdf at y, pLambertW evaluates the cdf at y, qLambertW is the quantile function, and rLambertW generates random samples from a Lambert W $\times F_X(x \mid \boldsymbol{\beta})$ distribution.

mLambertW computes the first 4 central/standardized moments of a Lambert W $\times$ F. Works only for Gaussian distribution.

qqLambertW computes and plots the sample quantiles of the data y versus the theoretical Lambert W $\times F$ theoretical quantiles given θ.

Usage

```
dLambertW(
  y,
  distname = NULL,
  theta = NULL,
  beta = NULL,
  gamma = 0,
  delta = 0,
  alpha = 1,
  input.u = NULL,
  tau = NULL,
  use.mean.variance = TRUE,
  log = FALSE
)

mLambertW(
  theta = NULL,
  distname = c("normal"),
  beta,
  gamma = 0,
  delta = 0,
  alpha = 1
)

pLambertW(
  q,
  distname,
  theta = NULL,
  beta = NULL,
  gamma = 0,
  delta = 0,
  alpha = 1,
  input.u = NULL,
  tau = NULL,
  log = FALSE,
  lower.tail = FALSE,
  use.mean.variance = TRUE
)

qLambertW(
  p,
  distname = NULL,
  theta = NULL,
  beta = NULL,
  gamma = 0,
  delta = 0,
  alpha = 1,
  input.u = NULL,
```

```
    tau = NULL,
    is.non.negative = FALSE,
    use.mean.variance = TRUE
)

qqLambertW(
    y,
    distname,
    theta = NULL,
    beta = NULL,
    gamma = 0,
    delta = 0,
    alpha = 1,
    plot.it = TRUE,
    use.mean.variance = TRUE,
    ...
)

rLambertW(
    n,
    distname,
    theta = NULL,
    beta = NULL,
    gamma = 0,
    delta = 0,
    alpha = 1,
    return.x = FALSE,
    input.u = NULL,
    tau = NULL,
    use.mean.variance = TRUE
)
```

Arguments

y, q	vector of quantiles.
distname	character; name of input distribution; see [get_distnames]().
theta	list; a (possibly incomplete) list of parameters alpha, beta, gamma, delta. [complete_theta]() fills in default values for missing entries.
beta	numeric vector (deprecated); parameter β of the input distribution. See [check_beta]() on how to specify beta for each distribution.
gamma	scalar (deprecated); skewness parameter; default: 0.
delta	scalar or vector (length 2) (deprecated); heavy-tail parameter(s); default: 0.
alpha	scalar or vector (length 2) (deprecated); heavy tail exponent(s); default: 1.
input.u	users can supply their own version of U (either a vector of simulated values or a function defining the pdf/cdf/quanitle function of U); default: NULL. If not NULL, tau must be specified as well.

tau   optional; if input.u = TRUE, then tau must be specified. Note that β is still
                          taken from theta, but "mu_x", "sigma_x", and the other parameters (α, γ, δ)
                          are all taken from tau. This is usually only used by the create_LambertW_output
                          function; users usually don't need to supply this argument directly.

use.mean.variance
                          logical; if TRUE it uses mean and variance implied by β to do the transformation
                          (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with
                          location and scale parameter.

log   logical; if TRUE, probabilities p are given as log(p).

lower.tail   logical; if TRUE (default), probabilities are $P(X \leq x)$ otherwise, $P(X > x)$.

p   vector of probability levels

is.non.negative
                          logical; by default it is set to TRUE if the distribution is not a location but a scale
                          family.

plot.it   logical; should the result be plotted? Default: TRUE.

...   further arguments passed to or from other methods.

n   number of observations

return.x   logical; if TRUE not only the simulated Lambert W$\times$ F sample y, but also the
                          corresponding simulated input x will be returned. Default FALSE. **Note:** if TRUE
                          then rLambertW does not return a vector of length n, but a list of two vectors
                          (each of length n).

Details

All functions here have an optional input.u argument where users can supply their own version
corresponding to zero-mean, unit variance input U. This function usually depends on the input
parameter β; e.g., users can pass their own density function dmydist <-function(u,beta) {...}
as dLambertW(...,input.u = dmydist). dLambertW will then use this function to evaluate the pdf
of the Lambert W x 'mydist' distribution.

Important: Make sure that all input.u in dLambertW, pLambertW, ... are supplied correctly and
return correct values – there are no unit-tests or sanity checks for user-defined functions.

See the references for the analytic expressions of the pdf and cdf. For "h" or "hh" types and for
scale-families of type = "s" quantiles can be computed analytically. For location (-scale) families
of type = "s" quantiles need to be computed numerically.

Value

mLambertW returns a list with the 4 theoretical (central/standardized) moments of Y implied by θ
and distname (currrently, this only works for distname = "normal"):

mean   mean,

sd   standard deviation,

skewness   skewness,

kurtosis   kurtosis (not excess kurtosis, i.e., 3 for a Gaussian).

rLambertW returns a vector of length n. If return.input = TRUE, then it returns a list of two vectors (each of length n):

x   simulated input,

y   Lambert W random sample (transformed from x - see References and [get_output](#)).

qqLambertW returns a list of 2 vectors (analogous to qqnorm):

x   theoretical quantiles (sorted),

y   empirical quantiles (sorted).

Examples

```
###############################
######### mLambertW ###########
mLambertW(theta = list(beta = c(0, 1), gamma = 0.1))
mLambertW(theta = list(beta = c(1, 1), gamma = 0.1)) # mean shifted by 1
mLambertW(theta = list(beta = c(0, 1), gamma = 0)) # N(0, 1)

###############################
######### rLambertW ###########
set.seed(1)
# same as rnorm(1000)
x <- rLambertW(n=100, theta = list(beta=c(0, 1)), distname = "normal")
skewness(x) # very small skewness
medcouple_estimator(x) # also close to zero

y <- rLambertW(n=100, theta = list(beta = c(1, 3), gamma = 0.1),
               distname = "normal")
skewness(y) # high positive skewness (in theory equal to 3.70)
medcouple_estimator(y) # also the robust measure gives a high value

op <- par(no.readonly=TRUE)
par(mfrow = c(2, 2), mar = c(2, 4, 3, 1))
plot(x)
hist(x, prob=TRUE, 15)
lines(density(x))

plot(y)
hist(y, prob=TRUE, 15)
lines(density(y))
par(op)
###############################
######### dLambertW ###########
beta.s <- c(0, 1)
gamma.s <- 0.1

# x11(width=10, height=5)
par(mfrow = c(1, 2), mar = c(3, 3, 3, 1))
curve(dLambertW(x, theta = list(beta = beta.s, gamma = gamma.s),
                distname = "normal"),
      -3.5, 5, ylab = "",  main="Density function")
```

```
plot(dnorm, -3.5, 5, add = TRUE, lty = 2)
legend("topright" , c("Lambert W x Gaussian" , "Gaussian"), lty = 1:2)
abline(h=0)

###############################
######### pLambertW ###########

curve(pLambertW(x, theta = list(beta = beta.s, gamma = gamma.s),
                distname = "normal"),
      -3.5, 3.5, ylab = "", main = "Distribution function")
plot(pnorm, -3.5,3.5, add = TRUE, lty = 2)
legend("topleft" , c("Lambert W x Gaussian" , "Gaussian"), lty = 1:2)
par(op)

######## Animation
## Not run:
gamma.v <- seq(-0.15, 0.15, length = 31) # typical, empirical range of gamma
b <- get_support(gamma_01(min(gamma.v)))[2]*1.1
a <- get_support(gamma_01(max(gamma.v)))[1]*1.1

for (ii in seq_along(gamma.v)) {
  curve(dLambertW(x, beta = gamma_01(gamma.v[ii])[c("mu_x", "sigma_x")],
                  gamma = gamma.v[ii], distname="normal"),
        a, b, ylab="", lty = 2, col = 2, lwd = 2, main = "pdf",
        ylim = c(0, 0.45))
  plot(dnorm, a, b, add = TRUE, lty = 1, lwd = 2)
  legend("topright" , c("Lambert W x Gaussian" , "Gaussian"),
         lty = 2:1, lwd = 2, col = 2:1)
  abline(h=0)
  legend("topleft", cex = 1.3,
         c(as.expression(bquote(gamma == .(round(gamma.v[ii],3))))))
Sys.sleep(0.04)
}

## End(Not run)

###############################
######### qLambertW ###########

p.v <- c(0.01, 0.05, 0.5, 0.9, 0.95,0.99)
qnorm(p.v)
# same as above except for rounding errors
qLambertW(p.v, theta = list(beta = c(0, 1), gamma = 0), distname = "normal")
# positively skewed data -> quantiles are higher
qLambertW(p.v, theta = list(beta = c(0, 1), gamma = 0.1),
          distname = "normal")

###############################
######### qqLambertW ###########
## Not run:
y <- rLambertW(n=500, distname="normal",
               theta = list(beta = c(0,1), gamma = 0.1))
```

```
layout(matrix(1:2, ncol = 2))
qqnorm(y)
qqline(y)
qqLambertW(y, theta = list(beta = c(0, 1), gamma = 0.1),
           distname = "normal")

## End(Not run)
```

LambertW_fit-methods   *Methods for Lambert W× F estimates*

Description

S3 methods (print, plot, summary, etc.) for LambertW_fit class returned by the MLE_LambertW or IGMM estimators.

plot.LambertW_fit plots a (1) histogram, (2) empirical density of the data y. These are compared (3) to the theoretical $F_X(x \mid \widehat{\beta})$ and (4) Lambert $W \times F_X(y \mid \widehat{\beta})$ densities.

print.LambertW_fit prints only very basic information about $\widehat{\theta}$ (to prevent an overload of data/information in the console when executing an estimator).

print.summary.LambertW_fit tries to be smart about formatting the coefficients, standard errors, etc. and also displays "significance stars" (like in the output of summary.lm).

summary.LambertW_fit computes some auxiliary results from the estimate such as standard errors, theoretical support (only for type="s"), skewness tests (only for type="hh"), etc. See print.summary.LambertW_fit for print out in the console.

Usage

```
## S3 method for class 'LambertW_fit'
plot(x, xlim = NULL, show.qqplot = FALSE, ...)

## S3 method for class 'LambertW_fit'
print(x, ...)

## S3 method for class 'summary.LambertW_fit'
print(x, ...)

## S3 method for class 'LambertW_fit'
summary(object, ...)
```

Arguments

x, object	object of class LambertW_fit
xlim	lower and upper limit of x-axis for cdf and pdf plots.
show.qqplot	should a Lambert $W \times$ F QQ plot be displayed? Default: FALSE.
...	further arguments passed to or from other methods.

Value

summary returns a list of class `summary.LambertW_fit` containing

`call`	function call
`coefmat`	matrix with 4 columns: $\widehat{\theta}$, its standard errors, t-statistic, and two-sided p-values
`distname`	see Arguments
`n`	number of observations
`data`	original data (y)
`input`	back-transformed input data
`support`	support of output random variable Y
`data.range`	empirical data range
`method`	estimation method
`hessian`	Hessian at the optimum. Numerically obtained for `method` = `"MLE"`; for `method` = `"IGMM"` a diagonal-matrix approximation from covariance matrix obtained by simulations for $n = 1000$ samples in Goerg (2011).
`p_m1, p_m1n`	Probability that one (or n) observation were caused by input from the non-principal branch (see `p_m1`); only for type = `"s"`.
`symmetry.p.value`	
	p-value from Wald test of identical left and right tail parameters (see `test_symmetry`); only for type = `"hh"`.

Examples

```
# See ?LambertW-package
```

LambertW_input_output-methods

Methods for Lambert W input and output objects

Description

S3 methods for Lambert W input and output objects (created by `create_LambertW_input` and `create_LambertW_output`).

`plot.LambertW_input` plots the theoretical (1) pdf and (2) cdf of the input $X \sim F_X(x \mid \boldsymbol{\beta})$.

`plot.LambertW_output` plots the theoretical (1) pdf and (2) cdf of the output RV $Y \sim$ Lambert W $\times F_X(x \mid \boldsymbol{\beta})$. It overlays the plot with the pdf and cdf of the input RV $X \sim F_X(x \mid \boldsymbol{\beta})$ (setting $\gamma = \delta = 0, \alpha = 1$).

`print.LambertW_input` prints an overview of the input object.

`print.LambertW_output` prints an overview of the output object.

Usage

```
## S3 method for class 'LambertW_input'
plot(x, xlim = NULL, ...)

## S3 method for class 'LambertW_output'
plot(x, xlim = NULL, ...)

## S3 method for class 'LambertW_input'
print(x, ...)

## S3 method for class 'LambertW_output'
print(x, ...)
```

Arguments

x	object of class LambertW_input or LambertW_output.
xlim	lower and upper limit of x-axis for cdf and pdf plots. If NULL, it tries to determine good limits based on the family type of the distribution and the quantiles. Most of the times it will show the pdf and cdf from the 0.5% to 99.5% quantile.
...	further arguments passed to or from other methods.

Examples

```
# create a Normal(1, 2) input
Gauss.input <- create_LambertW_input("normal", beta = c(1, 2))
plot(Gauss.input)
# make it a bit heavy tailed (beta in theta comes from Gauss.input)
LW.Gauss <- create_LambertW_output(LambertW.input = Gauss.input,
                                   theta = list(delta = c(0.3)))
LW.Gauss  # print a nice overview in the console
plot(LW.Gauss)

# draw random sample
LW.Gauss$r(n=10)
Gauss.input$r(n=10)
# quantiles
LW.Gauss$q(p=0.6)
Gauss.input$q(p=0.6)
```

---

loglik-LambertW-utils   *Log-Likelihood for Lambert W× F RVs*

Description

Evaluates the log-likelihood for θ given observations y.

`loglik_LambertW` computes the log-likelihood of θ for a Lambert W $\times$ F distribution given observations y.

`loglik_input` computes the log-likelihood of various distributions for the parameter $\boldsymbol{\beta}$ given the data x. This can be used independently of the Lambert W x F framework to compute the log-likelihood of parameters for common distributions.

`loglik_penalty` computes the penalty for transforming the data back to the input (see Goerg 2016). This penalty is independent of the distribution specified by `distname`, but only depends on τ. If `type = "s"` then the penalty term exists if the distribution is non-negative (see `get_distname_family`) and `gamma >= 0`; otherwise, it returns NA.

Usage

```
loglik_LambertW(
  theta,
  y,
  distname,
  type,
  return.negative = FALSE,
  flattened.theta.names = names(theta),
  use.mean.variance = TRUE
)

loglik_input(
  beta,
  x,
  distname,
  dX = NULL,
  log.dX = function(x, beta) log(dX(x, beta))
)

loglik_penalty(tau, y, type = c("h", "hh", "s"), is.non.negative = FALSE)
```

Arguments

theta	list; a (possibly incomplete) list of parameters alpha, beta, gamma, delta. [complete_theta](#) fills in default values for missing entries.
y	a numeric vector of real values (the observed data).
distname	character; name of input distribution; see [get_distnames](#).
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
return.negative	
	logical; if TRUE it returns the negative log-likelihood as a scalar (which is useful for numerical *minimization* algorithms for *maximum* likelihood estimation); otherwise it returns a list of input log-likelihood, penalty, and their sum = full likelihood. Default: FALSE.

flattened.theta.names

> vector of strings with names of flattened theta; this is necessary for optimization functions since they drop the names of a vector, but all functions in this package use names to select elements of (the flattened) theta.

use.mean.variance

> logical; if TRUE it uses mean and variance implied by β to do the transformation (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with location and scale parameter.

beta   numeric vector (deprecated); parameter β of the input distribution. See check_beta on how to specify beta for each distribution.

x   a numeric vector of real values (the *input* data).

dX   optional; density function of x. Common distributions are already built-in (see distname). If you want to supply your own density, you **must** supply a function of (x, beta) and set distname = "user".

log.dX   optional; a function that returns the logarithm of the density function of x. Often – in particular for exponential families – the log of $f_X(x)$ has a simpler form (and is thus faster to evaluate).

tau   named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see complete_tau for details.

is.non.negative

> logical; by default it is set to TRUE if the distribution is not a location but a scale family.

Details

For heavy-tail Lambert W $\times$ F distributions (type = "h" or type = "hh") the log-likelihood decomposes into an input log-likelihood plus a penalty term for transforming the data.

For skewed Lambert W $\times$ F distributions this decomposition only exists for non-negative input RVs (e.g., "exp"onential, "gamma", "f", ...). If negative values are possible ("normal", "t", "unif", "cauchy", ...) then loglik_input and loglik_penalty return NA, but the value of the output log-likelihood will still be returned correctly as loglik.LambertW.

See Goerg (2016) for details on the decomposition of the log-likelihood into a log-likelihood on the input parameters plus a penalty term for transforming the data.

Value

loglik_input and loglik_penalty return a scalar; loglik_LambertW returns a list with 3 values:

loglik.input   loglikelihood of beta given the transformed data,

loglik.penalty penalty for transforming the data,

loglik.LambertW

> total log-likelihood of theta given the observed data; if the former two values exist this is simply their sum.

Examples

```
set.seed(1)
yy <- rLambertW(n = 1000, distname = "normal",
                theta = list(beta = c(0, 1), delta = 0.2))
loglik_penalty(tau = theta2tau(list(beta = c(1, 1), delta = c(0.2, 0.2)),
                               distname = "normal"),
               y = yy, type = "hh")
# For a type = 's' Lambert W x F distribution with location family input
# such a decomposition doesn't exist; thus NA.
loglik_penalty(tau = theta2tau(list(beta = c(1, 1), gamma = 0.03),
                               distname = "normal"),
               is.non.negative = FALSE,
               y = yy, type = "s")
# For scale-family input it does exist
loglik_penalty(tau = theta2tau(list(beta = 1, gamma = 0.01),
                               distname = "exp"),
               is.non.negative = TRUE,
               y = yy, type = "s")

# evaluating the Gaussian log-likelihood
loglik_input(beta = c(0, 1), x = yy, distname = "normal") # built-in version
# or pass your own log pdf function
loglik_input(beta = c(0, 1), x = yy, distname = "user",
             log.dX = function(xx, beta = beta) {
                 dnorm(xx, mean = beta[1], sd = beta[2], log = TRUE)
             })
## Not run:
# you must specify distname = 'user'; otherwise it does not work
loglik_input(beta = c(0, 1), x = yy, distname = "mydist",
             log.dX = function(xx, beta = beta) {
                 dnorm(xx, mean = beta[1], sd = beta[2], log = TRUE)
                 })

## End(Not run)

### loglik_LambertW returns all three values
loglik_LambertW(theta = list(beta = c(1, 1), delta = c(0.09, 0.07)),
                y = yy, type = "hh", distname ="normal")

# can also take a flattend vector; must provide names though for delta
loglik_LambertW(theta = flatten_theta(list(beta = c(1, 1),
                                            delta = c(delta_l = 0.09,
                                                      delta_r = 0.07))),
                y = yy, type = "hh", distname ="normal")
```

---

lp_norm   *lp norm of a vector*

Description

Computes the ℓ^p norm of an n-dimensional (real/complex) vector $\mathbf{x} \in \mathbf{C}^n$

$$||\mathbf{x}||_p = \left(\sum_{i=1}^{n} |x_i|^p \right)^{1/p}, p \in [0, \infty],$$

where $|x_i|$ is the absolute value of x_i. For $p = 2$ this is Euclidean norm; for $p = 1$ it is Manhattan norm. For $p = 0$ it is defined as the number of non-zero elements in $\mathbf{x}$; for $p = \infty$ it is the maximum of the absolute values of $\mathbf{x}$.

The norm of $\mathbf{x}$ equals 0 if and only if $\mathbf{x} = \mathbf{0}$.

Usage

```
lp_norm(x, p = 2)
```

Arguments

x   n-dimensional vector (possibly complex values)

p   which norm? Allowed values $p \geq 0$ including `Inf`. Default: 2 (Euclidean norm).

Value

Non-negative float, the norm of $\mathbf{x}$.

Examples

```
kRealVec <- c(3, 4)
# Pythagoras
lp_norm(kRealVec)
# did not know Manhattan,
lp_norm(kRealVec, p = 1)

# so he just imagined running in circles.
kComplexVec <- exp(1i * runif(20, -pi, pi))
plot(kComplexVec)
sapply(kComplexVec, lp_norm)
```

---

medcouple_estimator   *MedCouple Estimator*

Description

A robust measure of asymmetry. See References for details.

Usage

```
medcouple_estimator(x, seed = sample.int(1e+06, 1))
```

Arguments

x   numeric vector; if length > 3,000, it uses a random subsample (otherwise it takes too long to compute as calculations are of order N^2.)

seed   numeric; seed used for sampling (when `length(x) > 3000`).

Value

float; measures the degree of asymmetry

References

Brys, G., M. Hubert, and A. Struyf (2004). "A robust measure of skewness". Journal of Computational and Graphical Statistics 13 (4), 996 - 1017.

See Also

[test_symmetry](#)

Examples

```
# a simulation
kNumSim <- 100
kNumObs <- 200

################# Gaussian (Symmetric) ####
A <- t(replicate(kNumSim, {xx <- rnorm(kNumObs); c(skewness(xx), medcouple_estimator(xx))}))
########### skewed LambertW x Gaussian ####
tau.s <- gamma_01(0.2) # zero mean, unit variance, but positive skewness
rbind(mLambertW(theta = list(beta = tau.s[c("mu_x", "sigma_x")],
                             gamma = tau.s["gamma"]),
               distname="normal"))
B <- t(replicate(kNumSim,
                 {
                   xx <- rLambertW(n = kNumObs,
                                   theta = list(beta = tau.s[c("mu_x", "sigma_x")],
                                                gamma = tau.s["gamma"]),
```

```
                                     distname="normal")
                      c(skewness(xx), medcouple_estimator(xx))
                  }))

colnames(A) <- colnames(B) <- c("MedCouple", "Pearson Skewness")

layout(matrix(1:4, ncol = 2))
plot(A, main = "Gaussian")
boxplot(A)
abline(h = 0)

plot(B, main = "Skewed Lambert W x Gaussian")
boxplot(B)
abline(h = mLambertW(theta = list(beta = tau.s[c("mu_x", "sigma_x")],
                                  gamma = tau.s["gamma"]),
                     distname="normal")["skewness"])

colMeans(A)
apply(A, 2, sd)

colMeans(B)
apply(B, 2, sd)
```

MLE_LambertW   *Maximum Likelihood Estimation for Lambert W× F distributions*

Description

Maximum Likelihood Estimation (MLE) for Lambert W $\times F$ distributions computes $\widehat{\theta}_{MLE}$.

For type = "s", the skewness parameter γ is estimated and $\delta = 0$ is held fixed; for type = "h" the one-dimensional δ is estimated and $\gamma = 0$ is held fixed; and for type = "hh" the 2-dimensional δ is estimated and $\gamma = 0$ is held fixed.

By default $\alpha = 1$ is fixed for any type. If you want to also estimate α (for type = "h" or "hh") set theta.fixed = list().

Usage

```
MLE_LambertW(
  y,
  distname,
  type = c("h", "s", "hh"),
  theta.fixed = list(alpha = 1),
  use.mean.variance = TRUE,
 theta.init = get_initial_theta(y, distname = distname, type = type, theta.fixed =
    theta.fixed, use.mean.variance = use.mean.variance, method = "IGMM"),
  hessian = TRUE,
  return.estimate.only = FALSE,
```

```
    optim.fct = c("optim", "nlm", "solnp"),
    not.negative = FALSE
)
```

Arguments

y	a numeric vector of real values.
distname	character; name of input distribution; see [get_distnames]().
type	type of Lambert W × F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
theta.fixed	a list of fixed parameters in the optimization; default only alpha = 1.
use.mean.variance	
	logical; if TRUE it uses mean and variance implied by $\boldsymbol{\beta}$ to do the transformation (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with location and scale parameter.
theta.init	a list containing the starting values of $(\alpha, \boldsymbol{\beta}, \gamma, \delta)$ for the numerical optimization; default: see [get_initial_theta]().
hessian	indicator for returning the (numerically obtained) Hessian at the optimum; default: TRUE. If the **numDeriv** package is available it uses numDeriv::hessian(); otherwise stats::optim(...,hessian = TRUE).
return.estimate.only	
	logical; if TRUE, only a named flattened vector of $\widehat{\theta}_{MLE}$ will be returned (only the estimated, non-fixed values). This is useful for simulations where it is usually not necessary to give a nicely organized output, but only the estimated parameter. Default: FALSE.
optim.fct	character; which R optimization function should be used. Either 'optim' (default), 'nlm', or 'solnp' from the **Rsolnp** package (if available). Note that if 'nlm' is used, then not.negative = TRUE will be set automatically.
not.negative	logical; if TRUE, it restricts delta or gamma to the non-negative reals. See [theta2unbounded]() for details.

Value

A list of class LambertW_fit:

data	data y,
loglik	scalar; log-likelihood evaluated at the optimum $\widehat{\theta}_{MLE}$,
theta.init	list; starting values for numerical optimization,
beta	estimated $\boldsymbol{\beta}$ vector of the input distribution via Lambert W MLE (In general this is not exactly identical to $\widehat{\boldsymbol{\beta}}_{MLE}$ for the input data),
theta	list; MLE for θ,
type	see Arguments,
hessian	Hessian matrix; used to calculate standard errors (only if hessian = TRUE, otherwise NULL),
call	function call,

distname	see Arguments,
message	message from the optimization method. What kind of convergence?,
method	estimation method; here `"MLE"`.

Examples

```
# See ?LambertW-package
```

---

p_m1 *Non-principal branch probability*

Description

Computes the probability that (at least) one (out of n) observation(s) of the latent variable U lies in the non-principal branch region. The 'm1' in `p_m1` stands for 'minus 1', i.e, the non-principal branch.

See Goerg (2011) and Details for mathematical derivations.

Usage

```
p_m1(gamma, beta, distname, n = 1, use.mean.variance = TRUE)
```

Arguments

gamma	scalar; skewness parameter.
beta	numeric vector (deprecated); parameter β of the input distribution. See [check_beta](#) on how to specify `beta` for each distribution.
distname	character; name of input distribution; see [get_distnames](#).
n	number of RVs/observations.
use.mean.variance	
	logical; if `TRUE` it uses mean and variance implied by β to do the transformation (Goerg 2011). If `FALSE`, it uses the alternative definition from Goerg (2016) with location and scale parameter.

Details

The probability that one observation of the latent RV U lies in the non-principal region equals at most

$$p_{-1}(\gamma, n = 1) = P\left(U < -\frac{1}{|\gamma|}\right),$$

where U is the zero-mean, unit variance version of the input $X \sim F_X(x \mid \beta)$ – see References.

For N independent RVs $U_1, \ldots, U_N$, the probability that at least one data point came from the non-principal region equals

$$p_{-1}(\gamma, n = N) = P\left(U_i < -\frac{1}{|\gamma|} \text{ for at least one } i\right)$$

This equals (assuming independence)

$$P\left(U_i < -\frac{1}{|\gamma|} \text{ for at least one } i\right) = 1 - P\left(U_i \geq -\frac{1}{|\gamma|}, \forall i\right) = 1 - \prod_{i=1}^{N} P\left(U_i \geq -\frac{1}{|\gamma|}\right)$$

$$= 1 - \prod_{i=1}^{N} (1 - p_{-1}(\gamma, n = 1)) = 1 - (1 - p_{-1}(\gamma, n = 1))^N.$$

For improved numerical stability the cdf of a geometric RV (pgeom) is used to evaluate the last expression. Nevertheless, numerical problems can occur for $|\gamma| < 0.03$ (returns 0 due to rounding errors).

Note that $1 - (1 - p_{-1}(\gamma, n = 1))^N$ reduces to $p_{-1}(\gamma)$ for $N = 1$.

Value

non-negative float; the probability p_{-1} for n observations.

Examples

```
beta.01 <- c(mu = 0, sigma = 1)
# for n=1 observation
p_m1(0, beta = beta.01, distname = "normal") # identical to 0
# in theory != 0; but machine precision too low
p_m1(0.01, beta = beta.01, distname = "normal")
p_m1(0.05, beta = beta.01, distname = "normal") # extremely small
p_m1(0.1, beta = beta.01, distname = "normal") # != 0, but very small
# 1 out of 4 samples is a non-principal input;
p_m1(1.5, beta = beta.01, distname = "normal")
# however, gamma=1.5 is not common in practice

# for n=100 observations
p_m1(0, n=100, beta = beta.01, distname = "normal") # == 0
p_m1(0.1, n=100, beta = beta.01, distname = "normal") # still small
p_m1(0.3, n=100, beta = beta.01, distname = "normal") # a bit more likely
p_m1(1.5, n=100, beta = beta.01, distname = "normal")
# Here we can be almost 100% sure (rounding errors) that at least one
# y_i was caused by an input in the non-principal branch.
```

---

tau-utils	*Utilities for transformation vector tau*

Description

All functions here are for the transformation parameter vector $\tau = (\mu_x, \sigma_x, \gamma, \delta, \alpha)$.

check_tau checks if τ is correctly specified (correct names, non-negativity constraints, etc.)

complete_tau completes missing values so users don't have to specify every element of τ explicitly. 'mu_x' and 'sigma_x' must be specified, but alpha = 1, gamma = 0, and delta = 0 will be set automatically if missing.

get_initial_tau provides starting estimates for τ.

normalize_by_tau shifts and scales data given the tau vector as

$$(data - \mu_x)/\sigma_x.$$

Parameters μ_x and σ_x are not necessarily mean and standard deviation in the τ vector; that depends on the family type and use.mean.variance (for location families they usually are mean and standard deviation if use.mean.variance = TRUE; for scale and non-location non-scale families they are just location/scale parameters for the transformation).

tau2theta converts τ to the parameter list θ (inverse of theta2tau).

tau2type guesses the type ('s', 'h', 'hh') from the names of tau vector; thus make sure tau is named correctly.

Usage

```
check_tau(tau)

complete_tau(tau, type = tau2type(tau))

get_initial_tau(y, type = c("h", "hh", "s"), location.family = TRUE)

normalize_by_tau(data, tau, inverse = FALSE)

tau2theta(tau, beta)

tau2type(tau)
```

Arguments

tau	named vector τ which defines the variable transformation. Must have at least 'mu_x' and 'sigma_x' element; see complete_tau for details.
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
y	a numeric vector of real values (the observed data).

location.family

> logical; if FALSE it sets mu_x to 0 and only estimates sigma_x; if TRUE (default), it estimates mu_x as well.

data

> numeric; a numeric object in R. Usually this is either y or x (or z and u if inverse = TRUE.)

inverse

> logical; if TRUE it applies the inverse transformation $data \cdot \sigma_x + \mu_x$

beta

> numeric vector (deprecated); parameter β of the input distribution. See `check_beta` on how to specify beta for each distribution.

Value

check_tau throws an error if τ does not define a proper transformation.

complete_tau returns a named numeric vector.

get_initial_tau returns a named numeric vector.

tau2theta returns a list with entries `alpha`, `beta`, `gamma`, and `delta`.

tau2type returns a string: either "s", "h", or "hh".

---

test_normality   *Visual and statistical Gaussianity check*

Description

Graphical and statistical check if data is Gaussian (three common Normality tests, QQ-plots, histograms, etc).

test_normality does not show the autocorrelation function (ACF) estimate for lag 0, since it always equals 1. Thus removing it does not lose any information, but greatly improves the y-axis scale for higher order lags (which are usually very small compared to 1).

test_norm is a shortcut for test_normality.

Usage

```
test_normality(
  data,
  show.volatility = FALSE,
  plot = TRUE,
  pch = 1,
  add.legend = TRUE,
  seed = sample(1e+06, 1)
)

test_norm(...)
```

Arguments

`data`	a numeric vector of data values.
`show.volatility`	
	logical; if `TRUE` the squared (centered) data and its ACF are also shown. Useful for time series data to see if squares exhibit dependence (for financial data they typically do); default: `FALSE`.
`plot`	Should visual checks (histogram, densities, qqplot, ACF) be plotted? Default `TRUE`; otherwise only hypothesis test results are returned.
`pch`	a vector of plotting characters or symbols; default pch = 1.
`add.legend`	logical; if `TRUE` (default) a legend is placed in histogram/density plot.
`seed`	optional; if sample size > 5,000, then some normality tests fail to run. In this case it uses a subsample of size 5,000. For reproducibility, the seed can be specified by user. By default it uses a random seed.
`...`	arguments as in `test_normality`.

Value

A list with results of 3 normality tests (each of class `htest`) and the seed used for subsampling:

`anderson.darling`	
	Anderson Darling (if **nortest** package is available),
`shapiro.francia`	
	Shapiro-Francia (if **nortest** package is available),
`shapiro.wilk`	Shapiro-Wilk,
`seed`	seed for subsampling (only used if sample size > 5,000).

References

Thode Jr., H.C. (2002): "Testing for Normality". Marcel Dekker, New York.

See Also

`shapiro.test` in the **stats** package; `ad.test`, `sf.test` in the **nortest** package.

Examples

```
y <- rLambertW(n = 1000, theta = list(beta = c(3, 4), gamma = 0.3),
               distname = "normal")
test_normality(y)

x <- rnorm(n = 1000)
test_normality(x)

# mixture of exponential and normal
test_normality(c(rexp(100), rnorm(100, mean = -5)))
```

---

test_symmetry   *Test symmetry based on Lambert W heavy tail(s)*

Description

Performs a test for the null hypothesis of symmetry, $H_0 : \delta_l = \delta_r$, versus the alternative of asymmetry. This can be done using a Wald test of the linear restriction $H_0 : \delta_l - \delta_r = 0$ or a likelihood ratio test.

By default it uses "Wald" test since this only requires the Hessian of the "hh" Lambert W fit. The "LR" test requires the log-likelihood values for both MLEs (type "h" and "hh") and thus takes longer to compute.

Usage

```
test_symmetry(LambertW.fit, method = c("Wald", "LR"))
```

Arguments

LambertW.fit   an object of class `LambertW_fit` with `type = "hh"` or a numeric vector (observed data). If it is data, then an asymmetric Lambert W × Gaussian distribution (`distname = "normal"`) with two tail parameters ("hh") will be fit to the data internally and then used as the new `LambertW.fit`.

method   test methodology: "Wald" (default) or a likelihood ratio "LR" test

Value

A list of class "htest" containing:

statistic   value of the test statistic,

p.value   p-value for the test,

method   character string describing the test,

data.name   a character string giving the name(s) of the data.

Examples

```
## Not run:
# skewed
yy <- rLambertW(n = 500, theta = list(delta = c(0.1, 0.25), beta = c(2, 1)),
                distname = "normal")
fit.ml <- MLE_LambertW(yy, type = "hh", distname = "normal",
                       hessian = TRUE)
summary(fit.ml)
test_symmetry(fit.ml, "LR")
test_symmetry(fit.ml, "Wald")

# symmetric
```

```
yy <- rLambertW(n = 500, theta = list(delta = c(0.2, 0.2), beta = c(2, 1)),
                distname = "normal")
fit.ml <- MLE_LambertW(yy, type = "hh", distname = "normal")
summary(fit.ml)
test_symmetry(fit.ml, "LR")
test_symmetry(fit.ml, "Wald")

## End(Not run)
```

---

theta-utils   *Utilities for the parameter vector of Lambert W× F distributions*

Description

These functions work with $\boldsymbol{\theta} = (\boldsymbol{\beta}, \gamma, \delta, \alpha)$, which fully parametrizes Lambert W× F distributions.

See Details for more background information on some functions.

check_theta checks if $\theta = (\alpha, \boldsymbol{\beta}, \gamma, \delta)$ describes a well-defined Lambert W distribution.

complete_theta completes missing values in a parameters list so users don't have to specify everything in detail. If not supplied, then alpha = 1, gamma = 0, and delta = 0 will be set by default.

flatten_theta and unflatten_theta convert between the list theta and its vector-style flattened type. The flattened version is required for several optimization routines, since they optimize over multivariate vectors – not lists.

get_initial_theta provides initial estimates for α, $\boldsymbol{\beta}$, γ, and δ, which are then used in maximum likelihood (ML) estimation ([MLE_LambertW](#)).

get_theta_bounds returns lower and upper bounds for θ (necessary for optimization such as [MLE_LambertW](#)).

theta2tau converts θ to the transformation vector $\tau = (\mu_x, \sigma_x, \gamma, \delta, \alpha)$.

theta2unbounded transforms θ from the bounded space to an unrestricted space (by $\log$-transformation on σ_x, δ, and α; note that this restricts $\gamma \geq 0$, $\delta \geq 0$, and $\alpha \geq 0$.).

Usage

```
check_theta(theta, distname)

complete_theta(theta = list(), LambertW.input = NULL)

flatten_theta(theta)

get_initial_theta(
  y,
  distname,
  type = c("h", "hh", "s"),
  theta.fixed = list(alpha = 1),
  method = c("Taylor", "IGMM"),
  use.mean.variance = TRUE
```

```
)

get_theta_bounds(
  distname,
  beta,
  type = c("s", "h", "hh"),
  not.negative = FALSE
)

theta2tau(theta = list(beta = c(0, 1)), distname, use.mean.variance = TRUE)

theta2unbounded(theta, distname, type = c("h", "hh", "s"), inverse = FALSE)

unflatten_theta(theta.flattened, distname, type)
```

Arguments

theta	list; a (possibly incomplete) list of parameters alpha, beta, gamma, delta. [complete_theta](#) fills in default values for missing entries.
distname	character; name of input distribution; see [get_distnames](#).
LambertW.input	optional; if beta is missing in theta, LambertW.input (which has a beta element) must be specified.
y	a numeric vector of real values (the observed data).
type	type of Lambert W $\times$ F distribution: skewed "s"; heavy-tail "h"; or skewed heavy-tail "hh".
theta.fixed	list; fixed parameters for the optimization; default: alpha = 1.
method	character; should a fast "Taylor" (default) approximation be used ([delta_Taylor](#) or [gamma_Taylor](#)) to estimate δ or γ, or should "IGMM" ([IGMM](#)) estimates be used. Use "Taylor" as initial values for [IGMM](#); [IGMM](#) improves upon it and should be used for [MLE_LambertW](#). Do **not** use "IGMM" as initial values for [IGMM](#) – this will run [IGMM](#) twice.
use.mean.variance	
	logical; if TRUE it uses mean and variance implied by β to do the transformation (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with location and scale parameter.
beta	numeric vector (deprecated); parameter β of the input distribution. See [check_beta](#) on how to specify beta for each distribution.
not.negative	logical; if TRUE it sets the lower bounds for alpha and delta to 0. Default: FALSE.
inverse	logical; if TRUE, it transforms the unbounded theta back to the original, bounded space. Default: FALSE.
theta.flattened	
	named vector; flattened version of list theta.

Details

get_initial_theta obtains a quick initial estimate of θ by first finding the (approximate) input $\widehat{\boldsymbol{x}}_{\widehat{\theta}}$ by IGMM, and then estimating $\boldsymbol{\beta}$ for this input data $\widehat{\boldsymbol{x}}_{\widehat{\theta}} \sim F_X(x \mid \boldsymbol{\beta})$ (see estimate_beta).

Converting theta to an unbouded space is especially useful for optimization routines (like nlm), which can be performed over an unconstrained space. The obtained optimum can be converted back to the original space using the inverse transformation (set inverse = TRUE transforms it via $\exp$) – this guarantees that the estimate satisfies non-negativity constraints (if required). The main advantage is that this avoids using optimization routines with boundary constraints – since they are much slower compared to uncostrained optimization.

Value

check_theta throws an error if list theta does not define a proper Lambert W $\times$ F distribution; does nothing otherwise.

complete_theta returns a list containing:

alpha	heavy tail exponent(s),
beta	named vector $\boldsymbol{\beta}$ of the input distribution,
gamma	skewness parameter,
delta	heavy-tail parameter(s).

get_initial_theta returns a list containing:

alpha	heavy tail exponent; default: 1,
beta	named vector $\boldsymbol{\beta}$ of the input distribution; estimated from the recovered input data $\widehat{\mathrm{x}}_{\widehat{\tau}}$,
gamma	skewness parameter; if type is "h" or "hh" gamma = 0; estimated from IGMM,
delta	heavy-tail parameter; estimated from IGMM. If type = "s", then delta = 0.

get_theta_bounds returns a list containing two vectors:

lower	flattened vector of lower bounds for valid θ,
upper	flattened vector of upper bounds for valid θ.

See Also

check_beta

estimate_beta, get_initial_tau

beta2tau

Examples

```
## Not run:
check_theta(theta = list(beta =  c(1, 1, -1)), distname = "t")

## End(Not run)
```

```
check_theta(theta = list(beta =  c(1, 1)), distname = "normal") # ok

params <- list(beta = c(2, 1), delta = 0.3) # alpha and gamma are missing
complete_theta(params) # added default values

params <- list(beta = c(2, 1), delta = 0.3, alpha = c(1, 2))
params <- complete_theta(params)
check_theta(params, distname = 'normal')

###
x <- rnorm(1000)
get_initial_theta(x, distname = "normal", type = "h")
get_initial_theta(x, distname = "normal", type = "s")

# starting values for the skewed version of an exponential
y <- rLambertW(n = 1000, distname = "exp", beta = 2, gamma = 0.1)
get_initial_theta(y, distname = "exp", type = "s")

# starting values for the heavy-tailed version of a Normal = Tukey's h
y <- rLambertW(n = 1000, beta = c(2, 1), distname = "normal", delta = 0.2)
get_initial_theta(y, distname = "normal", type = "h")#'

###
get_theta_bounds(type = "hh", distname = "normal", beta = c(0, 1))

###
theta.restr <- theta2unbounded(list(beta = c(-1, 0.1),
                                     delta = c(0.2, 0.2)),
                               distname = "normal")
theta.restr
# returns again the beta and delta from above
theta2unbounded(theta.restr, inverse = TRUE, distname = "normal")
```

U-utils   *Zero-mean, unit-variance version of standard distributions*

Description

Density, distribution function, quantile function and random number generation for the shifted and scaled U of the (location-)scale family input $X \sim F_X(x \mid \beta)$ - see References.

Since the normalized random variable U is one of the main building blocks of Lambert W $\times$ F distributions, these functions are wrappers used by other functions such as dLambertW or rLambertW.

Usage

```
dU(u, beta, distname, use.mean.variance = TRUE)
```

```
pU(u, beta, distname, use.mean.variance = TRUE)

qU(p, beta, distname, use.mean.variance = TRUE)

rU(n, beta, distname, use.mean.variance = TRUE)
```

Arguments

u	vector of quantiles.
beta	numeric vector (deprecated); parameter β of the input distribution. See `check_beta` on how to specify `beta` for each distribution.
distname	character; name of input distribution; see `get_distnames`.
use.mean.variance	
	logical; if TRUE it uses mean and variance implied by β to do the transformation (Goerg 2011). If FALSE, it uses the alternative definition from Goerg (2016) with location and scale parameter.
p	vector of probability levels
n	number of samples

Value

dU evaluates the pdf at y, pU evaluates the cdf, qU is the quantile function, and rU generates random samples from U.

Examples

```
# a zero-mean, unit variance version of the t_3 distribution.
curve(dU(x, beta = c(1, 1, 3), distname = "t"), -4, 4,
      ylab = "pdf", xlab = "u",
      main = "student-t \n zero-mean, unit variance")
# cdf of unit-variance version of an exp(3) -> just an exp(1)
curve(pU(x, beta = 3, distname = "exp"), 0, 4, ylab = "cdf", xlab = "u",
      main = "Exponential \n unit variance", col = 2, lwd = 2)
curve(pexp(x, rate = 1), 0, 4, add = TRUE, lty = 2)
# all have (empirical) variance 1
var(rU(n = 1000, distname = "chisq", beta = 2))
var(rU(n = 1000, distname = "normal", beta = c(3, 3)))
var(rU(n = 1000, distname = "exp", beta = 1))
var(rU(n = 1000, distname = "unif", beta = c(0, 10)))
```

W   *Lambert W function, its logarithm and derivative*

Description

The Lambert W function $W(z) = u$ is defined as the inverse of (see [xexp](#))

$$u \exp(u) = z,$$

i.e., it satisfies $W(z) \exp(W(z)) = z$.

W evaluates the Lambert W function (W), its first derivative (deriv_W), and its logarithm (log_W). All of them have a principal (branch = 0 (default)) and non-principal branch (branch = -1) solution.

W is a wrapper for `lambert_W0C` and `lambert_Wm1_C` in the **lamW** package.

Usage

```
W(z, branch = 0)

deriv_W(z, branch = 0, W.z = W(z, branch = branch))

log_deriv_W(z, branch = 0, W.z = W(z, branch = branch))

deriv_log_W(z, branch = 0, W.z = W(z, branch = branch))

log_W(z, branch = 0, W.z = W(z, branch = branch))
```

Arguments

z	a numeric vector of real values; note that W(Inf, branch = 0) = Inf.
branch	either 0 or -1 for the principal or non-principal branch solution.
W.z	Lambert W function evaluated at z; see Details below for why this is useful.

Details

Depending on the argument z of $W(z)$ one can distinguish 3 cases:

$z \geq 0$ solution is unique W(z) = W(z, branch = 0);

$-1/e \leq z < 0$ two solutions: the principal (W(z, branch = 0)) and non-principal (W(z, branch = -1)) branch;

$z < -1/e$ no solution exists in the reals.

log_W computes the natural logarithm of $W(z)$. This can be done efficiently since $\log W(z) = \log z - W(z)$. Similarly, the derivative can be expressed as a function of $W(z)$:

$$W'(z) = \frac{1}{(1 + W(z)) \exp(W(z))} = \frac{W(z)}{z(1 + W(z))}.$$

Note that $W'(0) = 1$ and $W'(-1/e) = \infty$.

Moreover, by taking logs on both sides we can even simplify further to

$$\log W'(z) = \log W(z) - \log z - \log(1 + W(z))$$

which, since $\log W(z) = \log z - W(z)$, simplifies to

$$\log W'(z) = -W(z) - \log(1 + W(z)).$$

For this reason it is numerically faster to pass the value of $W(z)$ as an argument to `deriv_W` since `W(z)` often has already been evaluated in a previous step.

Value

numeric; same dimensions/size as `z`.

`W` returns numeric, `Inf` (for `z = Inf`), or `NA` if $z < -1/e$.

Note that `W` handles `NaN` differently to `lambertW0_C` and `lambertWm1_C` in the **lamW** package; it returns `NA`.

References

Corless, R. M., G. H. Gonnet, D. E. G. Hare, D. J. Jeffrey and D. E. Knuth (1996). "On the Lambert W function". *Advances in Computational Mathematics*, pp. 329-359.

See Also

`lambertW0_C` and `lambertWm1_C` in the **lamW** package; `xexp`.

Examples

```
W(-0.25) # "reasonable" input event
W(-0.25, branch = -1) # "extreme" input event

curve(W(x, branch = -1), -1, 2, type = "l", col = 2, lwd = 2)
curve(W(x), -1, 2, type = "l", add = TRUE, lty = 2)
abline(v = - 1 / exp(1))

# For lower values, the principal branch gives the 'wrong' solution;
# the non-principal must be used.
xexp(-10)
W(xexp(-10), branch = 0)
W(xexp(-10), branch = -1)
curve(log(x), 0.1, 5, lty = 2, col = 1, ylab = "")
curve(W(x), 0, 5, add = TRUE, col = "red")
curve(log_W(x), 0.1, 5, add = TRUE, col = "blue")
grid()
legend("bottomright", c("log(x)", "W(x)", "log(W(x))"),
       col = c("black", "red", "blue"), lty = c(2, 1, 1))
```

W_delta   *Inverse transformation for heavy-tail Lambert W RVs*

Description

Inverse transformation `W_delta_alpha` for heavy-tail Lambert W RVs and its derivative. This is the inverse of Tukey's h transformation as a special case of `alpha = 1`.

Usage

```
W_delta(z, delta = 0)

W_delta_alpha(z, delta = 0, alpha = 1)

W_2delta(z, delta = c(0, 1/5))

W_2delta_2alpha(z, delta = c(0, 0), alpha = c(1, 1))

deriv_W_delta(z, delta = 0)

deriv_W_delta_alpha(z, delta = 1, alpha = 1)
```

Arguments

z	a numeric vector of real values.
delta	heavy-tail parameter(s); by default `delta = 0`, which implies `W_delta(z) = z`. If a vector of length 2 is supplied, then `delta[1]` on the left and `delta[2]` on the right (of the center) will be used.
alpha	heavy-tail exponent(s) in $(u^2)^\alpha$; default: `alpha = 1`.

Value

Computes $\text{sgn}(z) \left(\frac{1}{\alpha\delta} W(\alpha\delta(z^2)^\alpha) \right)^{1/2\alpha}$. If z is a vector, so is the output.

Examples

```
G_delta(0)
W_delta(0)

# W_delta is the inverse of G_delta
u.v <- -2:2
W_delta(G_delta(u.v, delta = 0.3), delta = 0.3)

# with alpha too
G_delta_alpha(u.v, delta = 1, alpha = 0.33)
W_delta_alpha(G_delta_alpha(u.v, delta = 1, alpha = 0.33),
              delta = 1, alpha = 0.33) # the inverse
```

W_gamma   *Inverse transformation for skewed Lambert W RVs*

Description

Inverse transformation for skewed Lambert W RVs and its derivative.

Usage

```
W_gamma(z, gamma = 0, branch = 0)

deriv_W_gamma(z, gamma = 0, branch = 0)
```

Arguments

z	a numeric vector of real values; note that `W(Inf, branch = 0) = Inf`.
gamma	skewness parameter; by default `gamma = 0`, which implies `W_gamma(z) = z`.
branch	either `0` or `-1` for the principal or non-principal branch solution.

Details

A skewed Lambert W$\times$ F RV Z (for simplicity assume zero mean, unit variance input) is defined by the transformation (see H_gamma)

$$z = U \exp(\gamma U) =: H_\gamma(U), \quad \gamma \in \mathbf{R},$$

where U is a zero-mean and/or unit-variance version of the distribution F.

The inverse transformation is $W_\gamma(z) := \frac{W(\gamma z)}{\gamma}$, where W is the Lambert W function.

`W_gamma(z, gamma, branch = 0)` (and `W_gamma(z, gamma, branch = -1)`) implement this inverse.

If $\gamma = 0$, then $z = u$ and the inverse also equals the identity.

If $\gamma \neq 0$, the inverse transformation can be computed by

$$W_\gamma(z) = \frac{1}{\gamma} W(\gamma z).$$

Same holds for `W_gamma(z, gamma, branch = -1)`.

The derivative of $W_\gamma(z)$ with respect to z simplifies to

$$\frac{d}{dz} W_\gamma(z) = \frac{1}{\gamma} \cdot W'(\gamma z) \cdot \gamma = W'(\gamma z)$$

`deriv_W_gamma` implements this derivative (for both branches).

Value

numeric; if z is a vector, so is the output.

See Also

H_gamma

---

xexp *Transformation that defines the Lambert W function and its derivative*

Description

The Lambert W function $W(z)$ is the inverse of $u \exp(u) = z$.

In versions $< 0.6.0$ of the package this function was denoted as H. It is now replaced with the more descriptive xexp (and H is deprecated).

Usage

```
xexp(x)

deriv_xexp(x, degree = 1)
```

Arguments

x   a numeric vector of real/complex values.

degree   non-negative integer; degree of the derivative

Details

The n-th derviative of $x \cdot \exp(x)$ is available in closed for as

$$\exp(x) \cdot (x + n).$$

Value

Returns $z = x \exp(x)$ for $x \in C$. If x is a vector/matrix, so is z.

See Also

W

Examples

```
plot(xexp, -5, 0.5, type="l", xlab="u", ylab="z")
grid()
abline(h=0, lty = 2)
abline(v=0, lty = 2)
```

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