Package ‘emg’

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Type Package

Title Exponentially Modified Gaussian (EMG) Distribution

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Depends R (>= 1.8.0), stats, stats4, moments

Description Provides basic distribution functions for a mixture model of a Gaussian and exponential distribution.

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LazyLoad yes

NeedsCompilation no

Repository CRAN

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Contents

`emg-package` *Exponentially Modified Gaussian (EMG) Distribution*

Description

Provide basic functions for a mixture of gaussian and exponential distributions.

Details

Package:	emg
Type:	Package
Date:	2012-01-03
License:	GPL 2.0
LazyLoad:	yes

Provides basic distribution functions for the EMG model, pemg, demg, qemg and remg. As well as an MLE estimation routine emg.mle.

Author(s)

Shawn Garbett, Mark Kozdoba, Maintainer: Shawn Garbett <Shawn@Garbett.org>

References

Gladney H.M., B.F. Dowden, J.D. Swalen. Computer-Assisted Gas-Liquid Chromatography. Anal. Chem., 1969, 41(7):883-8.

Golubev A. Exponentially modified Gaussian (EMG) relevance to distributions related to cell proliferation and differentiation. J Theor Biol. 2010 Jan 21;262(2):257-66.

Grushka E. Charaterization of Exponentially Modified Peaks in Chromatography. Anal. Chem., 1972, 44(11):1733-38.

See Also

`EMG` `emg.mle` `Normal` `Exponential`

Examples

```
y <- remg(200)
hist(y, freq=FALSE, ylim=c(0, 0.35), breaks=20)
x <- 1:100/100 * 11 - 3
lines(x, demg(x))
m <- emg.mle(y)
sqrt(diag(m@vcov)) # Show stderr in estimate
ks.test(y, "pemg", 0, 1, 1)
```

`EMG` *The Exponential Modified Gaussian (EMG) Distribution*

Description

Density, distribution function, quantile function and random generation for the EMG distribution with three parameters, mu, sigma, lambda. The distribution is a mixture of an exponential and gaussian (normal) distribution.

Usage

```
demg(x, mu = 0, sigma = 1, lambda = 1, log = FALSE)
pemg(q, mu = 0, sigma = 1, lambda = 1, lower.tail = TRUE, log.p = FALSE)
qemg(p, mu = 0, sigma = 1, lambda = 1, lower.tail = TRUE, log.p = FALSE)
remg(n, mu = 0, sigma = 1, lambda = 1)
```

Arguments

`x, q`	vector of quantiles.
`p`	vector of probabilities.
`n`	number of observations. If `length(n) > 1`, the length is taken to be the number required.
`mu`	mu value, the mean of the normal component. Note: this is not the mean of the distribution. The mean is mu+1/lambda
`sigma`	sigma value, the deviation of the normal component. Note: this is not the deviation of the distribution
`lambda`	lambda value (1/kappa), the rate of the exponential component.
`log, log.p`	logical; if TRUE, probabilities p are given as log(p).
`lower.tail`	logical; if TRUE(default), probabilities are P[X <= x] otherwise, P[X > x].

Details

If `mean` or `sd` are not specified they assume the default values of `0` and `1`, respectively.

The EMG distribution has density

$$f(x) = \frac{1}{2}\lambda e^{\frac{\lambda}{2}(2\mu+\lambda\sigma^2-2x)} erfc((\mu+\lambda\sigma\sigma-x)/(\sqrt{2}\sigma))$$

where μ is the mean of the normal distribution, σ the standard deviation of the normal and λ rate of the exponential. Note μ does not represent the mean of the distribution. The mean is $\mu + 1/\lambda$

Value

`demg` gives the density, `pemg` gives the distribution function, `qemg` gives the quantile function, and `remg` generates random deviates.

References

Golubev. Exponentially modified Gaussian (EMG) relevance to distributions related to cell proliferation and differentiation. J Theor Biol. 2010 Jan 21;262(2):257-66. Epub 2009 Oct 13.

Examples

```
plot(demg, -2, 5)
```

`emg.mle` *Maximum Likelihood estimate of parameters*

Description

Compute the maximum likelihood model for the parameters given a set of observations. Returns a model with estimates for mu, sigma, and lambda.

Usage

```
emg.mle(x, lower=NULL, upper=NULL, start=NULL, ...)
```

Arguments

`x`	vector of observations to estimate parameters for.
`lower`	list of lower bounds for parameters.
`upper`	list of upper bounds for parameters.
`start`	list of starting parameters for search.
`...`	optional parameters to pass to ‘mle‘.

Value

An object of class `mle-class`.

Author(s)

Shawn Garbett

See Also

`EMG` `emg.nllik`

Examples

```
emg.mle(remg(200))

## a example involving fitting
data(pc9_3um_erlotinib)

intermitotic.time <- subset(pc9_3um_erlotinib, end.of.movie=='N' & died=='N')$observed

hist(intermitotic.time, freq=FALSE, main="PC9 in 3um erlotinib", xlab='intermitotic time (hours)')

fit <- emg.mle(intermitotic.time)
pdf <- function(x) demg(x, coef(fit)['mu'], coef(fit)['sigma'], coef(fit)['lambda'])
curve(pdf, from=0, to=170, add=TRUE, col='red')
```

`emg.nllik` *Negative Log Likelihood for EMG*

Description

Negative log likelihood function for EMG

Usage

```
emg.nllik(x, mu, sigma, lambda)
```

Arguments

`x`	vector of observations
`mu`	mu of normal
`sigma`	sigma of normal
`lambda`	lambda of exponential

Value

A single real value of the negative log likelihood that the given parameters explain the observations.

Author(s)

Shawn Garbett

See Also

`emg.mle`

Examples

```
y <- remg(200)
emg.nllik(y, 0, 1, 1)
```

`pc9_3um_erlotinib` *PC9 cancer cell observations with 3 micro-molar erlotinib at time 0.*

Description

PC9 cancer cell observations with 3um erlotinib applied at time 0. Experiment was performed on 2011/9/9 (F07) in the Vito Quaranta laboratory at Vanderbilt University Cancer Biology Center by Darren Tyson. Cells were tracked by nuclear labeling with histone H2B and imaged on a BD Pathway 855 for several days. All numerical values are in hours. Funding was provided by the National Cancer Institute (NCI).

This data set was specifically chosen to give the emg.mle function something difficult to work on.

Usage

```
data(pc9_3um_erlotinib)
```

Value

A data frame of lifespan PC9 observations.

Author(s)

Darren Tyson, Shawn Garbett

Examples

```
data(pc9_3um_erlotinib)
```

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