

Package ‘discrimARTs’

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Description ‘discrimARTs’ discriminates with explicit confidence the alternative reproductive tactics (ARTs) in dimorphic systems with bimodal traits by computing the maximum likelihood estimate of a mixture of distributions of a measured ARTs trait. Supported distributions include a mixture of 2 normal distributions and a mixture of 2 facing gamma distributions.

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discrimARTs

*Discriminate Alternative Reproductive Tactics (ARTs) of Morphological Dimorphisms Using Likelihood Mixture Models***Description**

Algorithm discriminates with explicit confidence the alternative reproductive tactics (ARTs) in dimorphic mating systems with bimodal trait size distributions such as in the male horn polyphenisms in beetles. The bimodal distribution is parameterized by normal mixture distributions or facing gamma mixture distribution models. Likelihood of the alternative tactics for a given trait size is computed from the mixture models. Algorithm computes MLE of distribution parameters and the morph ratio.

Details

In Rowland & Qualls (2005) and in diverse unpublished data we have found that in the male-dimorphic ornaments of beetles which express gamma distributions the trait of the smaller, usually subordinate male is almost always skewed right and that the trait size distribution of the larger, usually dominant male is almost always skewed left. Unfortunately, previously available gamma mixture models are designed to fit data in which the long tails (skewness) of both gamma distributions extend to the right toward larger values. Therefore, this package is specifically and uniquely designed to fit the mixture of facing gamma distributions, where the trait distribution of the smaller male is skewed right; and the trait size distribution of the larger male is skewed left.

The package user supplies a vector of sample measurements that represent a dimorphic trait; initial parameter values for each of two probability density functions (pdf); and the mixture probability (morph ratio) of the morph with the larger trait sizes. For the normal pdfs each distribution has mean and standard deviation parameters. For the facing gamma pdfs each distribution has shape and scaling parameters: The left gamma distribution is $Y1 = LB + \theta_1 * X1$; and the right gamma distribution is $Y2 = UB - \theta_2 * X2$. In the latter expression LB and UB are the lower and upper bounds of trait sizes; $X1 \sim \text{Gamma}(\alpha_1, 1)$; $X2 \sim \text{Gamma}(\alpha_2, 1)$; alpha is the shape parameter and theta is the scaling parameter. The mean trait size of the first gamma pdf is $LB + \alpha_1 * \theta_1$ and the mean of the facing gamma pdf is $UB - \alpha_2 * \theta_2$. LB may be chosen equal to the smallest trait size in the sample minus a small amount often computed such as 1/2% or 1% or more of the range of sample trait sizes; UB is chosen as the largest trait size in the sample plus a small amount.

The sample column vector and the initial parameter values must represent a mixture of two distributions with adequately separated means, usually by at least two standard deviations. Random sampling of a dimorphic trait and reasonable choices of initial values are also assumptions of this model.

Author(s)

Rowland JM, Qualls CR, Gunning C.

References

Cite the following paper:

Rowland JM, Qualls CR. Likelihood models for discriminating alternative phenotypes in morphologically dimorphic species. *Evolutionary Ecology Research* 7: 421-434 (2005).

See Also

[mix.mle](#), [mix.loglik](#), [x_gideon](#), [o_taurus](#), [mix.synthetic](#)

mix.loglik	<i>Compute the log likelihood of input data given a parameter vector and a list of 2 distribution functions.</i>
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Description

This is the main function to compute the negative $2 \times$ log likelihood function of parameters given data.

This function is not intended to be called directly by users, but can be useful to test user-specified mixture distributions passed to `mix.mle`.

Usage

```
mix.loglik(.pars, .input, .distlist, do.sum = TRUE)
```

Arguments

.pars	<p>A list of the following 5 parameters:</p> <ul style="list-style-type: none"> • mix.prob Probability of second distribution • dist1.par1 Lower distribution: mean for normal, shape for gamma • dist1.par2 Lower distribution: SD for normal, scale for gamma • dist2.par1 Upper distribution: mean for normal, shape for gamma • dist2.par2 Upper distribution: SD for normal, scale for gamma
.input	Vector of (numeric) trait observations.
.distlist	List of 2 distribution density functions. The first is the lower or leftmost distribution; the second is the upper or rightmost.
do.sum	By default, return sum of likelihoods. Set to FALSE for testing.

Details

Computes maximum likelihood function for either the normal mixture distribution or the facing gamma distribution model for a dimorphic trait.

Value

Numeric: the negative $2 \times$ log likelihood of trait measurement.

References

Rowland JM, Qualls CR. 2005. Likelihood models for discriminating alternative phenotypes in morphologically dimorphic species. *Evolutionary Ecology Research* 7: 421-434.

See Also

[mix.mle](#)

mix.mle	<i>Find maximum likelihood estimate (MLE) of 5 parameters given input vector of observations, initial parameter values, and a method specifying distributions.</i>
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Description

Algorithm computes maximum likelihood estimates of the parameters of either the normal mixture distribution or the facing gamma distribution model for a dimorphic trait.

Usage

```
mix.mle(input, method = "normal", mix.prob = NULL,
        dist1.par1 = NULL, dist1.par2 = NULL,
        dist2.par1 = NULL, dist2.par2 = NULL,
        lower = NULL, upper = NULL, distlist = NULL,
        optim.lower = rep(0, 5), optim.upper = c(1, rep(NA, 4)), ...)
```

Arguments

input	Vector of (numeric) trait observations. Observations should be strictly positive.
method	Either "normal" or "facing.gamma". Initial parameter estimation is implemented for "normal", but is only appropriate when mix.prob is close to 0.5. User supplies initial parameter estimates for the facing gamma mixture distribution.
mix.prob	The initial probability of mixture distributions, specifying the proportion of the upper distribution.
dist1.par1	First parameter of the lower distribution. This specifies the mean for method="normal", and the shape for method="facing.gamma".
dist1.par2	Second parameter of the lower distribution. This specifies the standard deviation for method="normal", and the scale for method="facing.gamma".
dist2.par1	First parameter of the upper distribution, specifying parameters as in dist1.par1.
dist2.par2	Second parameter of the upper distribution, specifying parameters as in dist1.par2.

distlist	<p>Optionally, the user can specify their own list containing a lower and upper distribution (PDF) function.</p> <p>Each density function must take observations and 2 positional parameters, as per dnorm.</p> <p>Distributions taking >2 parameters may be used, but the remaining parameters must be encapsulated as fixed values within the functions.</p> <p>If distlist is specified, then method is set to "user".</p>
lower	<p>For method="facing.gamma", the lower bound may be set to minimum trait size minus 0.5%, 1%, or more of the range of trait sizes.</p> <p>Otherwise ignored.</p>
upper	<p>For method="facing.gamma"; the upper bound may be set to maximum trait size plus 0.5%, 1%, or more of the range of trait sizes.</p> <p>Otherwise ignored.</p>
optim.lower, optim.upper	<p>Numeric vector. lower and upper bounds used by optim, specifying: c(mix.prob, dist1.par1, dist1.par2, dist2.par1, dist2.par2).</p> <p>By default, mix.prob is bounded between 0 and 1, and distribution parameters are bounded from below by 0.</p> <p>optim calls these by position; thus order is significant and names are not needed.</p>
...	<p>Additional arguments are passed to optim. In particular, control=list(trace=5, REPORT=1) displays information about the optimization process.</p>

Details

Computes maximum likelihood estimates of the parameters of either the normal mixture distribution or the facing gamma distribution model for a dimorphic trait.

Value

An object of class discrimARTs, which is a list containing the original input data and parameter values, as well as output from optim.

neglogLik	Numeric. Negative 2 x log likelihood of final optimized parameters.
MLE.est	Named vector containing the final optimized parameter values.

Note

In general, method="normal" is converges well for a range of initial values. method="facing.gamma" requires more care.

References

Rowland JM, Qualls CR. 2005. Likelihood models for discriminating alternative phenotypes in morphologically dimorphic species. *Evolutionary Ecology Research* 7: 421-434.

See Also

[mix.loglik](#), [optim](#), [x_gideon](#), [o_taurus](#), [mix.synthetic](#)

Examples

```
data(x_gideon)

## Assuming normal, estimate initial conditions from data
fit.default.gideon <- mix.mle(x_gideon$horn)

## Estimation of mixture of normals, explicitly specifying method and parameters
fit.gideon <- mix.mle(x_gideon$horn, method='normal',
  mix.prob=0.5, dist1.par1=100, dist1.par2=10, dist2.par1=300, dist2.par2=10)

## Default printing and plotting methods
print(fit.gideon)

## Compare results
layout(1:2)
plot(fit.gideon)
plot(fit.default.gideon)
```

mix.synthetic

Generate synthetic mixtures for testing of mix.mle.

Description

These functions can be helpful in assessing the convergence of `mix.mle`.

Usage

```
mix.synthetic.normal(N = 200, mix.prob = 0.5, mu1, sd1, mu2, sd2)
mix.synthetic.facing.gamma(N = 200, mix.prob = 0.5, lower, upper,
  shape1, scale1, shape2, scale2)
```

Arguments

N	Number of draws.
mix.prob	Probability of drawing from upper distribution.
lower, upper	Bounds for facing gamma.
shape1, scale1, shape2, scale2	Distribution parameters for facing gammas. Lower = 1, upper = 2.
mu1, sd1, mu2, sd2	Distribution parameters for normals. Lower = 1, upper = 2.

Value

Numeric vector of random deviates from the mixture of distributions.

See Also[mix.loglik](#)**Examples**

```
## Normal: draw samples
normalmix.draws <- mix.synthetic.normal(mix.prob=0.1,
  mu1=10, sd1=2, mu2=20, sd2=2)
## Estimated initial conditions may fail for mix.prob far from 0.5
normalmix.fit <- mix.mle(normalmix.draws)
plot(normalmix.fit)

## Facing gamma: draw samples
gammamix.params <- list(lower = 0.37, upper=4.72, mix.prob=0.55,
  dist1.par1=1.50, dist1.par2=.4, dist2.par1=3.2, dist2.par2=.5)
## simulate synthetic data
gammamix.draws <- with(gammamix.params,
  mix.synthetic.facing.gamma( lower=lower, upper=upper, mix.prob=mix.prob,
    shape1=dist1.par1, scale1=dist1.par2,
    shape2=dist2.par1, scale2=dist2.par2
  )
)
## Fit and return
## Use parameters as initial values
gammamix.fit <- with(gammamix.params,
  mix.mle(gammamix.draws, method='facing.gamma',
    lower=lower, upper=upper, mix.prob=mix.prob,
    dist1.par1=dist1.par1, dist1.par2=dist1.par2,
    dist2.par1=dist2.par1, dist2.par2=dist2.par2
  )
)
plot(gammamix.fit)
```

o_taurus

*Horn measurements of the dung beetle Onthophagus taurus.***Description**

A measured sample of 275 males. Pronotum width (body) and cephalic horn length (horn) were measured in units of mm/100 from digital images using the procedures detailed below. This sample of horn lengths is used to illustrate fitting the mixture of two facing gamma probability distributions.

Usage

data(o_taurus)

Format

A data frame with 275 observations on the following 2 variables.

body Pronotum width (mm/100)

horn Cephalic horn length (mm/100)

Details

Onthophagus taurus:

Collection data for the measured sample of the scarabaeid dung beetle *Onthophagus taurus*:
Cherry Research Farm; North Carolina Department of Agriculture;
North Carolina State University Goldsboro; Wayne Co., NC; UTM: 17S 769433E 3919364N; 3
June 2010;
collected by Lena Guisewite & Wes Watson; dung-baited pitfall traps.

A measured sample of 275 males was selected from the above total sample of 1238.
Pronotum width was measured in ocular micrometer units with an M5Wild stereo microscope out-fitted with a ocular lens graticule and converted to mm/100.
Cephalic horn length was measured as its curvilinear function in standardized units and converted to mm/100 from digital images using the procedures and landmarks indicated in Tomkins, J.L. et al. 2006. Major differences in minor allometries: A reply to Moczek. The American Naturalist 167:612-618.
After conversion to metric scale, all measures were transformed by addition of a small amount of "jitter" to reduce artifacts in bin-sorting due to data stratification caused by the measurement conversion factors. All measures were rounded to the nearest mm/100.

To fit a mixture of facing gamma distributions to the horn length distribution, we set a lower bound equal to the minimum horn length minus 1.5% of the range of horn lengths ($LB = 2 - 7 = -5$) and an upper bound equal to maximum horn length plus 0.5% of the range ($UB = 482 + 3 = 485$). Here and occasionally in other samples, there is a technical problem when the minimum trait size is zero or close to zero; the lower gamma probability density function for the minimum horn length x cannot be evaluated at a negative value of $LB + x = -5 + 2 = -3$. A simple solution is to shift the horn length distribution up by at least +3, fit the shifted horn length distribution with the mixture of facing gammas, and then translate the fitted mixture probability density function back to the original scale. Here we shift the horn length sample data up by +8; set $LB = -5 + 8 = 3$ and $UB = 485 + 8 = 493$; and estimate $\theta_1 = 45.6$, $\alpha_1 = 1.48$, $\theta_2 = 62.8$, $\alpha_2 = 1.84$, and mixture probability = 0.62. To translate the fit back to the original scale, one can plot the fitted mixture probability density function versus the original data vector.

Source

Data published for the first time here in.

References

Rowland JM, Qualls CR. 2005. Likelihood models for discriminating alternative phenotypes in morphologically dimorphic species. *Evolutionary Ecology Research* 7: 421-434.

See Also

[mix.mle](#), [x_gideon](#)

Examples

```
data(o_taurus)
## Scatter plot of horn versus body showing trait scaling
plot(o_taurus$horn, o_taurus$body)

## Plot histogram with observations
hist(o_taurus$horn, freq=FALSE)
## To include points on x-axis of histogram
points( o_taurus$horn, rep(0, nrow(o_taurus)))

## use the o_taurus dataset to estimate facing gamma
## Using an offset to shift data away from zero
horn.offset <- 8
taurus.fit <- mix.mle(input=o_taurus$horn+horn.offset, method='facing.gamma',
  mix.prob=0.59, lower=2 + horn.offset - 7, upper=482 + horn.offset + 3,
  dist1.par1=1.37, dist1.par2=52.7, dist2.par1=2.29, dist2.par2=43.8)
## Default printing function shows a subset of the available information
print(taurus.fit)
## Default plotting function shows histogram, raw observations, and the computed distributions,
## along with a legend including estimated values
plot(taurus.fit)
## To exclude legend
plot(taurus.fit, legend=FALSE)
```

x_gideon

Horn measurements of the rhinoceros beetle Xylotrupes gideon.

Description

A measured sample of 177 males. Pronotum width (body) and pronotal horn length (horn) were measured in mm/10 with a slide micrometer.

This sample of horn lengths is used to illustrate fitting the mixture of two normal probability distributions.

Usage

```
data(x_gideon)
```

Format

A data frame with 177 observations on the following 2 variables.

body Pronotum width (mm/10)

horn Pronotal horn length (mm/10)

Details

Xylotrupes gideon:

Collection data for the measured sample of the dynastine rhinoceros beetle *Xylotrupes* gideon: Lampung Province, Sumatra, Indonesia; 1999; collected by Agusyanto Hasan.

A measured sample of 177 males was selected from the above total sample of 193. Pronotum width was measured at its greatest width.

Pronotal horn length was measured from the mid-dorsal point of the posterior margin of the pronotum to the anterior apex of the left line of the pronotal horn.

Source

Rowland, J.M. 2003. Male horn dimorphism, phylogeny and systematics of rhinoceros beetles of the genus *Xylotrupes* (Scarabaeidae: Coleoptera). Aust. J. Zool., 51: 213-258.

References

Rowland JM, Qualls CR. 2005. Likelihood models for discriminating alternative phenotypes in morphologically dimorphic species. Evolutionary Ecology Research 7: 421-434.

See Also

[mix.mle](#), [o_taurus](#)

Examples

```
data(x_gideon)
## Scatter plot of horn versus body showing trait scaling
plot(x_gideon$horn, x_gideon$body)

## Plot histogram with overlaid density plot
hist(x_gideon$horn, freq=FALSE)
points(x_gideon$horn, rep(0, nrow(x_gideon)))

## Estimation of mixture of normals
fit.gideon <- mix.mle(x_gideon$horn, method='normal',
  mix.prob=0.5, dist1.par1=100, dist1.par2=10, dist2.par1=300, dist2.par2=10)

print(fit.gideon)
plot(fit.gideon)
```

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