

Package ‘ABCp2’

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Title Approximate Bayesian Computational Model for Estimating P2

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Description Tests the goodness of fit of a distribution of offspring to the Normal, Poisson, and Gamma distribution and estimates the proportional paternity of the second male (P2) based on the best fit distribution.

Depends MASS

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ABC_P2_gamma

*ABC Estimation of P2 for Gamma Distribution***Description**

This function fits offspring data to a special case of the gamma distribution, in which zero values of offspring are excluded and all values are rounded to a whole number, and estimates P2 based on that distribution and the specified priors.

Usage

```
ABC_P2_gamma(n, ObsMean, S_Lo, S_Hi, R_Lo, R_Hi, delta, iter)
```

Arguments

n	number of observations.
ObsMean	the observed mean number of offspring sired by the second male.
S_Lo	minimum shape value for the distribution.
S_Hi	maximum shape value for the distribution.
R_Lo	minimum rate value for the distribution.
R_Hi	maximum rate value for the distribution.
delta	maximum allowed difference between the estimated mean and observed mean number of offspring produced by the second male.
iter	number of iterations used to build the posterior.

Value

posterior	Posterior distribution of P2 values.
Shape	Vector of values for the shape parameter.
Rate	Vector of values for the rate parameter.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```
#Fit the Shape and Rate hyperpriors to a distribution of offspring.

data(fungus)
fit_dist_gamma(fungus$Total_Offspring)

#Use hyperiors and priors calculated from the data to estimate P2.
#Plot the saved distributions for the Shape and Rate parameters.
#Adjust, if necessary.
```

```

fungus_P2<-ABC_P2_gamma(12, 9.9, 1.14, 2.52, 0.06, 0.18, 0.1, 100)
hist(fungus_P2$posterior)
hist(fungus_P2$Shape)
hist(fungus_P2$Rate)

```

ABC_P2_norm

ABC Estimation of P2 for Normal Distribution

Description

This function fits offspring data to a special case of the normal distribution, in which zero and negative values of offspring are excluded, and estimates P2 based on that distribution and the specified priors.

Usage

```
ABC_P2_norm(n, ObsMean, M_Lo, M_Hi, SD_Lo, SD_Hi, delta, iter)
```

Arguments

n	number of observations.
ObsMean	the observed mean number of offspring sired by the second male.
M_Lo	minimum mean value for the distribution.
M_Hi	maximum mean value for the distribution.
SD_Lo	minimum standard deviation value for the distribution.
SD_Hi	maximum standard deviation value for the distribution.
delta	maximum allowed difference between the estimated mean and observed mean number of offspring produced by the second male.
iter	number of iterations used to build the posterior.

Value

posterior	Posterior distribution of P2 values.
Avg	Vector of values for the mean parameter.
Std	Vector of values for the standard deviation parameter.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```
#Fit the Mean and Standard Deviation hyperpriors to a distribution of offspring.

data(fungus)
fit_dist_norm(fungus$Total_Offspring)

#Use hyperiors and priors calculated from the data to estimate P2.
#Plot the saved distributions for the Mean and Standard Deviation parameters.
#Adjust, if necessary.

fungus_P2<-ABC_P2_norm(12, 9.9, 11.35, 17.31, 8.22, 12.44, 0.1, 100)
hist(fungus_P2$posterior)
hist(fungus_P2$Avg)
hist(fungus_P2$Std)
```

ABC_P2_pois

ABC Estimation of P2 for Poisson Distribution

Description

This function fits offspring data to the Poisson distribution and estimates P2 based on that distribution and the specified priors.

Usage

```
ABC_P2_pois(n, ObsMean, L_Lo, L_Hi, delta, iter)
```

Arguments

n	the number of observations.
ObsMean	the observed mean number of offspring sired by the second male.
L_Lo	minimum lambda value for the distribution.
L_Hi	maximum lambda value for the distribution.
delta	maximum allowed difference between the estimated mean and observed mean number of offspring produced by the second male.
iter	number of iterations used to build the posterior.

Value

posterior	Posterior distribution of P2 values.
Lambda	Vector of values for the lambda parameter.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```
#Fit the Lambda hyperprior to a distribution of offspring.

data(fungus)
fit_dist_pois(fungus$Total_Offspring)

#Use hyperiors and priors calculated from the data to estimate P2.
#Plot the saved distributions for the Lambda parameter.
#Adjust, if necessary.

fungus_P2<-ABC_P2_pois(12, 9.9, 13.24, 15.42, 0.1, 100)
hist(fungus_P2$posterior)
hist(fungus_P2$Lambda)
```

fit_dist_gamma

Fit Offspring Distribution to the Gamma Distribution

Description

This function fits offspring data to a special case of the gamma distribution, in which zero values of offspring are excluded and all values are rounded to a whole number, and tests the goodness of fit using the chi-squared test.

Usage

```
fit_dist_gamma(dist)
```

Arguments

`dist` a numeric vector of data values for number of offspring per dam.

Value

<code>estimate</code>	Shape and rate parameters estimated from the supplied distribution.
<code>sd</code>	Standard deviation of the shape and rate estimates.
<code>vcov</code>	Variance/covariance matrix of the shape and rate estimates.
<code>loglik</code>	the log-likelihood of the shape and rate estimates.
<code>n</code>	The number of observations.
<code>statistic</code>	The chi-squared test statistic.
<code>parameter</code>	Degrees of freedom for the chi-squared test.
<code>p.value</code>	P-value for the chi-squared test.
<code>data_gamma</code>	Vector of values generated from a special case of the gamma distribution.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```
#Fit the Shape and Rate parameters to a distribution of offspring.
#Test the goodness of fit.

data(fungus)
fungus_fit<-fit_dist_gamma(fungus$Total_Offspring)
fungus_fit$fit_gamma
fungus_fit$chi_gamma
hist(fungus_fit$data_gamma)
```

fit_dist_norm

Fit Offspring Distribution to the Normal Distribution

Description

This function fits offspring data to a special case of the normal distribution, in which zero and negative values of offspring are excluded, and tests the goodness of fit using the chi-squared test.

Usage

```
fit_dist_norm(dist)
```

Arguments

dist a numeric vector of data values for number of offspring per dam.

Value

estimate	Mean and standard deviation parameters estimated from the supplied distribution.
sd	Standard deviation of the mean and standard deviation estimates.
vcov	Variance/covariance matrix of the mean and standard deviation estimates.
loglik	the log-likelihood of the mean and standard deviation estimates.
n	The number of observations.
statistic	The chi-squared test statistic.
parameter	Degrees of freedom for the chi-squared test.
p.value	P-value for the chi-squared test.
data_norm	Vector of values generated from a special case of the normal distribution.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```

#Fit the Mean and Standard Deviation parameters to a distribution of offspring.
#Test the goodness of fit.

data(fungus)
fungus_fit<-fit_dist_norm(fungus$Total_Offspring)
fungus_fit$fit_norm
fungus_fit$chi_norm
fungus_fit$data_norm

```

fit_dist_pois	<i>Fit Offspring Distribution to the Poisson Distribution</i>
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Description

This function fits offspring data to the Poisson distribution, and tests the goodness of fit using the chi-squared test.

Usage

```
fit_dist_pois(dist)
```

Arguments

dist a numeric vector of data values for number of offspring per dam.

Value

estimate	Lambda parameter estimated from the supplied distribution.
sd	Standard deviation of the lambda estimate.
vcov	Variance/covariance matrix of the lambda estimate.
loglik	the log-likelihood of the lambda estimate.
n	The number of observations.
statistic	The chi-squared test statistic.
parameter	Degrees of freedom for the chi-squared test.
p.value	P-value for the chi-squared test.
data_pois	Vector of values generated from the Poisson distribution.

Author(s)

M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek

Examples

```
#Fit the Lambda parameter to a distribution of offspring.  
#Test the goodness of fit.  
  
data(fungus)  
fungus_fit<-fit_dist_pois(fungus$Total_Offspring)  
fungus_fit$fit_pois  
fungus_fit$chi_pois  
hist(fungus_fit$data_pois)
```

fungus

Sperm Precedence Data from the Fungus Beetle

Description

Offspring counts and proportional paternity by mating order for a breeding experiment of the fungus beetle conducted by JK Conner (1995).

Usage

```
data(fungus)
```

Format

A data frame with 12 observations on the following 4 variables.

Female a numeric vector to identify females.

P2 proportional paternity of the second male.

Total_Offspring total number of offspring for the female.

No_2nd_Male number of offspring sired by the second male.

Source

J. K. Conner (1995) Extreme variability in sperm precedence in the fungus beetle, *Bolitotherus cornutus* (Coleoptera Tenebrionidae), *Ethology Ecology & Evolution* 7, 277-280.

Examples

```
#Fit fungus beetle data to the normal distribution and test goodness of fit.  
data(fungus)  
fit_dist_norm(fungus$Total_Offspring)
```

newt

Sperm Precedence Data from the Rough-Skinned Newt

Description

Offspring counts from two clutches and proportional paternity by mating order for a breeding experiment of the rough-skinned newt conducted by Jones et al., (2002)

Usage

```
data(newt)
```

Format

A data frame with 10 observations on the following 10 variables.

Female a numeric code to identify females.

No_1st_Clutch total offspring in the first clutch.

P2_1 proportional paternity of the second male for the first clutch.

No_2nd_Male_1st_Clutch total offspring sired by the second male from the first clutch.

No_2nd_Clutch total offspring in the second clutch.

P2_2 proportional paternity of the second male for the second clutch.

No_2nd_Male_2nd_Clutch total offspring sired by the second male from the second clutch.

Total_2nd_Male total offspring sired by the second male from both clutches.

Total_Offspring total offspring for both clutches.

Total_P2 total overall proportional paternity of the second male for both clutches.

Source

A. G. Jones, E. M. Adams, and S. J. Arnold (2002) A mechanism of first-male precedence in a vertebrate. *Proceedings of the National Academy of Sciences of the United States of America* **99**, 2078-2081.

Examples

```
#Fit newt data to the Poisson distribution and test goodness of fit.
data(newt)
fit_dist_pois(newt$Total_Offspring)
```

 rove

Sperm Precedence Data from the Rove Beetle

Description

Offspring counts and proportional paternity by mating order for a breeding experiment of the rove beetle conducted by T Benken et al., (1999).

Usage

```
data(rove)
```

Format

A data frame with 17 observations on the following 4 variables.

Female a numeric vector to identify females.

Total_Offspring total number of offspring for the female.

P2 proportional paternity of the second male.

No_2nd_Male number of offspring sired by the second male.

Source

T. Benken, A. Knaak, C. Gack, M. Eberle, and K. Peschke (1999) Variation of sperm precedence in the rove beetle, *Aleochara curtula* (Coleoptera: Staphylinidae), *Behaviour* **136**, 1065-1077.

Examples

```
#Fit rove beetle data to the normal distribution and test goodness of fit.
data(rove)
fit_dist_norm(rove$Total_Offspring)
```

 soap

Sperm Precedence Data from the Soapberry Bug

Description

Offspring counts and proportional paternity by mating order for a breeding experiment of the soapberry bug conducted by SP Carroll (1991).

Usage

```
data(soap)
```

Format

A data frame with 18 observations on the following 4 variables.

Female a numeric vector to identify females.

P2 proportional paternity of the second male.

Total_Offspring total number of offspring for the female.

No_2nd_Male number of offspring sired by the second male.

Source

S. P. Carroll (1991) The adaptive significance of mate guarding in the soapberry bug, *Jadera haematoloma* (Hemiptera: Rhopalidae), *Journal of Insect Behavior*, **4**, 509-530.

Examples

```
#Fit soapberry bug data to the normal distribution and test goodness of fit.  
data(soap)  
fit_dist_norm(soap$Total_Offspring)
```

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