Package ‘ABCp2’

February 19, 2015

Type Package
Title Approximate Bayesian Computational model for estimating P2
Version 1.1
Date 2013-01-02
Author M. Catherine Duryea, Andrew D. Kern, Robert M. Cox, and Ryan Calsbeek
Maintainer M. Catherine Duryea <duryea@dartmouth.edu>
Description This package 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
License GPL-2
NeedsCompilation no
Repository CRAN
Date/Publication 2013-07-23 23:26:52

R topics documented:

ABC_P2_gamma ......................................................... 2
ABC_P2_norm .......................................................... 3
ABC_P2_pois ............................................................ 4
fit_dist_gamma .......................................................... 5
fit_dist_norm ........................................................... 6
fit_dist_pois ............................................................ 7
fungus ................................................................. 8
newt ................................................................. 9
rove ................................................................. 10
soap ................................................................. 10

Index 12
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

\[
\text{ABC}_P2\_\text{gamma}(n, \text{ObsMean}, S_{\text{Lo}}, S_{\text{Hi}}, R_{\text{Lo}}, R_{\text{Hi}}, \text{delta}, \text{iter})
\]

Arguments

- \(n\) number of observations.
- \(\text{ObsMean}\) the observed mean number of offspring sired by the second male.
- \(S_{\text{Lo}}\) minimum shape value for the distribution.
- \(S_{\text{Hi}}\) maximum shape value for the distribution.
- \(R_{\text{Lo}}\) minimum rate value for the distribution.
- \(R_{\text{Hi}}\) maximum rate value for the distribution.
- \(\text{delta}\) maximum allowed difference between the estimated mean and observed mean number of offspring produced by the second male.
- \(\text{iter}\) number of iterations used to build the posterior.

Value

- \(\text{posterior}\) Posterior distribution of P2 values.
- \(\text{Shape}\) Vector of values for the shape parameter.
- \(\text{Rate}\) Vector of values for the rate parameter.

Author(s)

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

Examples

\[
\begin{align*}
\text{#Fit the Shape and Rate hyperpriors to a distribution of offspring.}
\end{align*}
\]

data(fungus)
fit_dist_gamma(fungus$Total\_Offspring)

\[
\begin{align*}
\text{#Use hyperpriors and priors calculated from the data to estimate P2.}
\text{#Plot the saved distributions for the Shape and Rate parameters.}
\text{#Adjust, if necessary.}
\end{align*}
\]
ABC Extimation 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 hyperpriors 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
fit_dist_gamma

**Examples**

```r
# 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**

- `estimate` Shape and rate parameters estimated from the supplied distribution.
- `sd` Standard deviation of the shape and rate estimates.
- `vcov` Variance/covariance matrix of the shape and rate estimates.
- `loglik` the log-likelihood of the shape and rate 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_gamma` Vector of values generated from a special case of the gamma distribution.
fit_dist_norm

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

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


Examples

# Fit fungus beetle data to the normal distribution and test goodness of fit.
data(fungus)
fit_dist_norm(fungus$Total_Offspring)
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.
P_2_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.
P_2_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


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**

```r
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**


**Examples**

```r
#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**

```r
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**


**Examples**

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

*Topic $\textasciitilde kwd1$
  ABC_P2_gamma, 2
  ABC_P2_norm, 3
  ABC_P2_pois, 4
  fit_dist_gamma, 5
  fit_dist_norm, 6
  fit_dist_pois, 7

*Topic $\textasciitilde kwd2$
  ABC_P2_gamma, 2
  ABC_P2_norm, 3
  ABC_P2_pois, 4
  fit_dist_gamma, 5
  fit_dist_norm, 6
  fit_dist_pois, 7

*Topic datasets
  fungus, 8
  newt, 9
  rove, 10
  soap, 10
  
  ABC_P2_gamma, 2
  ABC_P2_norm, 3
  ABC_P2_pois, 4

  fit_dist_gamma, 5
  fit_dist_norm, 6
  fit_dist_pois, 7
  fungus, 8

  newt, 9
  
  rove, 10
  soap, 10