Package ‘jointNmix’

October 13, 2022

Type Package
Title Joint N-Mixture Models for Site-Associated Species
Version 1.0
Date 2016-10-04
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Depends R (>= 3.0.0), methods, graphics, stats
Description
   Fits univariate and joint N-mixture models for data on two unmarked site-associated species. Includes functions to estimate latent abundances through empirical Bayes methods.
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
Date/Publication 2016-11-12 00:38:21

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jointNmix-package

**Description**

Fits univariate and joint N-mixture models for data on two unmarked site-associated species. Includes functions to estimate latent abundances through empirical Bayes methods.

**Details**

The DESCRIPTION file:

- **Package**: jointNmix
- **Type**: Package
- **Title**: Joint N-Mixture Models for Site-Associated Species
- **Version**: 1.0
- **Date**: 2016-10-04
- **Author**: Rafael de Andrade Moral [aut, cre], Clarice Garcia Borges Demetrio [aut], John Hinde [aut]
- **Maintainer**: Rafael de Andrade Moral <rafael_moral@yahoo.com.br>
- **Depends**: R (>= 3.0.0), methods, graphics, stats
- **Description**: Fits univariate and joint N-mixture models for data on two unmarked site-associated species. Includes functions to estimate latent abundances through empirical Bayes methods.
- **License**: GPL (>=2)

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- dneymanA: The Neyman-A probability function
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- fitted.uniNmix: Methods for univariate Nmix objects
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- jointNmix-package: Joint N-Mixture Models for Site-Associated Species
- plot.uniNmix: Plot Methods for Nmix objects

**Author(s)**

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Maintainer: Rafael de Andrade Moral <rafael_moral@yahoo.com.br>
References


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Get empirical Bayes predictions of the latent abundances

Description
Computes the conditional abundance distribution given the data and model estimates

Usage
```r
getranef.uniNmix(obj, distr = FALSE)
getranef.jointNmix(obj, distr = FALSE)
```

Arguments
- `obj`: fitted model object
- `distr`: logical. If `TRUE`, returns the matrix of conditional probabilities. If `FALSE`, returns the expected values of the conditional distributions, i.e. the abundance estimates

Details
These functions return the empirical Bayes estimates of the latent abundances from univariate and joint N-mixture models, as described by Royle (2004) and Moral et al. (submitted), respectively.

Author(s)
Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

References

See Also
Nmix, jointNmix
corrcov-jointNmix  Extract correlations and covariances

Description

Extract estimated correlations and covariances between observed abundances for joint N-mixture models

Usage

getcorr.jointNmix(obj)
getcov.jointNmix(obj)

Arguments

obj  fitted model object

Details

The correlations under each specification of the latent abundance distributions are displayed in Moral et al. (submitted)’s Table 1. The covariances are derived as Supplementary information.

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

References


See Also

jointNmix

dneymanA  The Neyman-A probability function

Description

Computes the probability function of the Neyman-A distribution

Usage

dneymanA(x, lambda1, lambda2, K, log = FALSE)
Arguments

- **x**: vector of values
- **lambda1, lambda2**: parameters of the distribution
- **K**: truncation value for the infinite summation
- **log**: logical. If TRUE, the logarithm of the probabilities is returned

Details

The Neyman-A distribution has probability function

\[
ed^{-\lambda_1} \frac{\lambda_1 x}{x!} \sum_{k=0}^{\infty} \frac{(\lambda_1 e^{-\lambda_2})^k k^x}{k!}
\]

and is an overdispersion model. The summation is truncated to K.

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

Examples

```r
x <- 0:10
dneymanA(x, lambda1 = 2, lambda2 = 1.5, K = 50)
```

### jointNmix

**Joint N-mixture models**

Description

Fits joint N-mixture models for site-associated species

Usage

```r
jointNmix(sp1, sp2, start, method = "BFGS", K, mixture = c("P", "P"),
Xp1, Xp2, Xl1, Xl2, Xpsi, includepsi = TRUE)
```

Arguments

- **sp1**: observation matrix for species 1
- **sp2**: observation matrix for species 2
- **start**: initial values for the optimization process
- **method**: optimization method passed to `optim`. Defaults to "BFGS"
- **K**: truncation number of the infinite summations in the log-likelihood. Defaults to `max(sp1, sp2) + 100`
mixture  two-character vector for latent abundance distributions. "P" for Poisson and "NB" for negative binomial. Defaults to c("P", "P")

Xp1  model matrix for detection probabilities of species 1

Xp2  model matrix for detection probabilities of species 2

Xl1  model matrix for abundance of species 1

Xl2  model matrix for linking parameter of species 2

Xpsi model matrix for abundance of species 2

includepsi logical. If FALSE, psi is not estimated and set to zero

Details

The function fits a bivariate extension to Royle’s (2004) N-mixture model to data on the abundance of two species collected at R sites over T time occasions. The model for observation on site i at time t for species 1 can be specified as

\[ Y_{1it} | N_{1i} \sim Bin(N_{1i}, p_{1it}) \]

\[ N_{1i} \text{ account distribution with mean } \lambda_{1i}. \]

The model for species 2 is

\[ Y_{2it} | N_{1i}, N_{2i} \sim Bin(N_{2i}, p_{2it}) \]

\[ N_{2i} | N_{1i} \text{ account distribution with mean } \psi + \lambda_{2i} N_{1i}. \]

Here, users may define a Poisson or negative binomial distribution for the latent abundances \( N_{1i} \) and \( N_{2i} \).

Value

An object of class `jointNmix` and `Nmix`, for which many methods are available (see `methods(class = "jointNmix")` and `methods(class = "Nmix")`)

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

References


See Also

Nmix
Examples

```r
## simulating data with poisson latent abundances
R <- 10 # sites
T <- 10 # time occasions
lambda1 <- 5
psi <- 3
p1 <- .3
p2 <- .6
lambda2 <- .5
set.seed(1234); N1 <- rpois(R, lambda1)
set.seed(1234); N2 <- rpois(R, psi + lambda2*N1)
y1 <- y2 <- matrix(0, ncol=T, nrow=R)
set.seed(1234); for(i in 1:R) y1[,i] <- rbinom(T, N1, p1)
set.seed(1234); for(i in 1:R) y2[,i] <- rbinom(T, N2, p2)

Xp <- cbind(rep(1, R*T))
Xl <- cbind(rep(1, R))

## Not run:
## fitting the Poisson-Poisson joint N-mixture model
fitpp <- jointNmix(y1, y2, Xp1=Xp, Xp2=Xp, Xl1=Xl, Xl2=Xl, mixture=c("P","P"), K=30)

## fitting the negbin-Poisson joint N-mixture model
fitnbp <- jointNmix(y1, y2, Xp1=Xp, Xp2=Xp, Xl1=Xl, Xl2=Xl, mixture=c("NB","P"), K=30)

## likelihood-ratio test between P-P and NB-P models
anova(fitpp, fitnbp)

## comparing using AIC
lapply(list(fitpp, fitnbp), AIC)

## conditional posterior probability functions for abundances
plot(fitpp, posterior = TRUE)

## estimated abundances vs. true abundances
data.frame(getranef.jointNmix(fitpp), N1, N2)

## End(Not run)
```

Description

Fitted values, residual extraction, simulation and print method for joint N-mixture models

Usage

```r
## S3 method for class 'jointNmix'
```

jointNmix-methods

fitted(object, ...)  
## S3 method for class 'jointNmix'
print(x, round = TRUE, ...)
## S3 method for class 'jointNmix'
residuals(object, type = c("ordinary", "standardized"), ...)
## S3 method for class 'jointNmix'
simulate(object, ...)

Arguments

- object: fitted model object
- x: fitted model object
- round: logical. Round the estimates?
- type: type of residuals to be returned. May be ordinary or standardized
- ...: not used

Details

fitted.uniNmix prints the fitted values for the model fit; residuals.uniNmix returns the ordinary ( \[ r_i^o = y_i - \hat{\mu}_i \] ) or standardized ( \[ r_i^s = \frac{y_i - \hat{\mu}_i}{\text{Var}(Y_i)} \] ) residuals; simulate.uniNmix simulates one sample from the fitted model.

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

References


See Also

Nmix jointNmix
Nmix

Univariate N-mixture models

Description

Fits univariate N-mixture models

Usage

Nmix(sp1, start, method = "BFGS", K, mixture, Xp, Xl)

Arguments

- **sp1**: observation matrix for the species
- **start**: initial values for the optimization process
- **method**: optimization method passed to `optim`. Defaults to "BFGS"
- **K**: truncation number of the infinite summations in the log-likelihood. Defaults to `max(sp1, sp2) + 100`
- **mixture**: latent abundance distribution specification. "P" for Poisson, "NB" for negative binomial and "NeymanA" for Neyman-A distributions are available. Defaults to "P"
- **Xp**: model matrix for detection probabilities
- **Xl**: model matrix for abundance parameter

Details

The function fits Royle's (2004) N-mixture model to data on species abundance collected at R sites over T time occasions. The model for observation on site i at time t can be specified as

\[ Y_{it} | N_i \sim Bin(N_i, p_{it}) \]

Here, users may define a Poisson, negative binomial or Neyman-A distributions for the latent abundances N_i.

Value

An object of class `uniNmix` and `Nmix`, for which many methods are available (see `methods(class = "uniNmix")` and `methods(class = "Nmix")`)

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde
## simulating data with negative binomial latent abundances
R <- 10 # sites
T <- 10 # time occasions
lambda <- 5 # abundance parameter
p <- .3 # probability of detection
phi <- 1 # dispersion parameter
set.seed(1234); Ni <- rnbinom(R, mu=lambda, size=phi) # latent abundances
y <- matrix(0, ncol=T, nrow=R)
set.seed(1234); for(i in 1:R) y[,i] <- rbinom(T, Ni, p) # observed abundances

## fitting the Poisson N-mixture model
fitp <- Nmix(y, Xp=cbind(rep(1, R*T)), Xl=cbind(rep(1, R)), mixture="P", K=25)

## fitting the negative binomial N-mixture model
fitnb <- Nmix(y, Xp=cbind(rep(1, R*T)), Xl=cbind(rep(1, R)), mixture="NB", K=25)

## fitting the Neyman-A N-mixture model
fitna <- Nmix(y, Xp=cbind(rep(1, R*T)), Xl=cbind(rep(1, R)), mixture="NeymanA", K=25)

## likelihood-ratio test between Poisson and negbin models
anova(fitp, fitnb)

## comparing using AIC
lapply(list(fitp, fitnb, fitna), AIC)

## conditional posterior probability functions for abundances
plot(fitnb, posterior = TRUE)

## estimated abundances vs. true abundances
data.frame(getranef.uniNmix(fitnb), Ni)
## Usage

```r
## S3 method for class 'Nmix'
AIC(object, ...)
## S3 method for class 'Nmix'
anova(object, object2, ...)
## S3 method for class 'Nmix'
coef(object, ...)
## S3 method for class 'Nmix'
logLik(object, ...)
```

### Arguments

- `object`: fitted model object
- `object2`: second model object for the `anova` method
- `...`: not used

### Details

The `AIC.Nmix` method provides the Akaike Information Criterion for the model fit; the `anova.Nmix` method performs a likelihood-ratio test between two nested model fits; the `coef.Nmix` method prints the estimates of the model fit; the `logLik.Nmix` method prints the log-likelihood of the model fit.

### Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

### See Also

- `Nmix`
- `jointNmix`

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## Description

Plots residuals vs. fitted values or the conditional distributions of the abundances for each site

### Usage

```r
## S3 method for class 'uniNmix'
plot(x, posterior = FALSE, layout, sites, restype, ...)
## S3 method for class 'jointNmix'
plot(x, posterior = FALSE, layout, sites, restype, ...)
```
Arguments

x fitted model object
posterior logical. If TRUE, plots the conditional distributions of the abundances. If FALSE, plots residuals vs. fitted values
layout two-number vector indicating the partition of the graphical window in rows and columns, respectively
sites index of sites to plot the conditional distribution of the abundances. If left unspecified, all sites are plotted
restype type of residuals to be plotted. Defaults to "ordinary"
... not used

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

References


See Also

Nmix jointNmix

uniNmix-methods Methods for univariate Nmix objects

Description

Fitted values, residual extraction, simulation and print method for univariate N-mixture models

Usage

## S3 method for class 'uniNmix'
fitted(object, ...)
## S3 method for class 'uniNmix'
print(x, round = TRUE, ...)
## S3 method for class 'uniNmix'
residuals(object, type = c("ordinary", "standardized"), ...)
## S3 method for class 'uniNmix'
simulate(object, ...)
Arguments

- **object, x**: fitted model object
- **round**: logical. Round the estimates?
- **type**: type of residuals to be returned. May be ordinary or standardized
- **...**: not used

Details

- `fitted.uniNmix` prints the fitted values for the model fit; `residuals.uniNmix` returns the ordinary
  \( r^o_i = y_i - \hat{\mu}_i \)
- or standardized \( r^s_i = \frac{y_i - \hat{\mu}_i}{\text{Var}(Y_i)} \)

- `simulate.uniNmix` simulates one sample from the fitted model.

Author(s)

Rafael A. Moral <rafael_moral@yahoo.com.br>, Clarice G. B. Demétrio and John Hinde

See Also

- `Nmix`, `jointNmix`
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