Package: jointNmix (via r-universe)

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Type Package

Title Joint N-Mixture Models for Site-Associated Species

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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)

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`jointNmix-package` *Joint N-Mixture Models for Site-Associated Species*

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
Authors@R:	c(person("Rafael", "de Andrade Moral", role = c("aut", "cre"), email = "rafael_moral@yahoo.com.br"), person
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 function
License:	GPL (>=2)

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Author(s)

Rafael de Andrade Moral [aut, cre], Clarice Garcia Borges Demetrio [aut], John Hinde [aut]

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References

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

`abundance-prediction` *Get empirical Bayes predictions of the latent abundances*

Description

Computes the conditional abundance distribution given the data and model estimates

Usage

```
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 returnt 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

Royle, J.A. (2004) Models for estimating population size from spatially replicated counts. Biometrics 60:108-105.

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

See Also

`Nmix` `jointNmix`

`corr-cov-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

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

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

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

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

```
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

```
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

$$Y_{1it}|N_{1i}\ Bin(N_{1i}, p_{1it})$$

$$N_{1i}\ acountdistributionwithmean\lambda_{1i}.$$

The model for species 2 is

$$Y_{2it}|N_{1i}, N_{2i}\ Bin(N_{2i}, p_{2it})$$

$$N_{2i}|N_{1i}\ acountdistributionwithmean\psi + \lambda_{2i}N_{1i}.$$

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

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

See Also

`Nmix`

Examples

```
## 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)
```

`jointNmix-methods` *Methods for joint Nmix objects*

Description

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

Usage

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

```
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, 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

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

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

$$Y_{it}|N_i\ Bin(N_i, p_{it})$$

$$N_i\ acountdistributionwithmean\lambda_i.$$

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

References

Royle, J.A. (2004) Models for estimating population size from spatially replicated counts. Biometrics 60:108-105.

See Also

`jointNmix`

Examples

```
## 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)
```

Nmix-methods *Methods for Nmix objects*

Description

AIC, anova, coef, and logLik methods for univariate and joint N-mixture models

Usage

```
## 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

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

`plot-methods-Nmix` *Plot Methods for Nmix objects*

Description

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

Usage

```
## 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

Moral, R.A., Hinde, J., Demétrio, C.G.B., Reigada, C. and Godoy, W.A.C. (submitted) Models for jointly estimating abundance of two unmarked site-associated species subject to imperfect detection.

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 (

$$r_i^o = y_i - \hat{\mu}_i$$

) 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

See Also

`Nmix` `jointNmix`

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