Package: nmixgof (via r-universe)

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Title Goodness of Fit Checks for Binomial N-Mixture Models

Version 0.1.2

Description Provides residuals and overdispersion metrics to assess the fit of N-mixture models obtained using the package 'unmarked'. Details on the methods are given in Knape et al. (2017) <doi:10.1101/194340>.

Depends R (>= 3.3.0)

License GPL-3

Encoding UTF-8

LazyData true

LinkingTo Rcpp

Imports Rcpp, unmarked

RoxygenNote 7.3.2

URL https://github.com/jknape/nmixgof

BugReports https://github.com/jknape/nmixgof/issues

Config/pak/sysreqs make

Repository https://jknape.r-universe.dev

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`chat` *Overdispersion metrics for binomial N-mixture models.*

Description

Computes various types of overdispersion metrics, based on Pearson residuals, for binomial N-mixture models.

Usage

```
chat(umFit, type = "marginal")
```

Arguments

`umFit`	An object of class unmarkedFit from a model fitted using pcount.
`type`	The type of metric to compute, one of 'marginal', 'site-sum' or 'observation'.

Value

An estimate of overdispersion relative to the fitted model.

Examples

```
library(unmarked)
data(mallard)
fm.mallard <- pcount(~ 1 ~ 1, unmarkedFramePCount(y = mallard.y), K=100)
chat(fm.mallard, "m")
chat(fm.mallard, "s")
chat(fm.mallard, "o")
```

`nmixgof` *Goodness of fit checks for binomial N-mixture models*

Description

The package contains methods to compute overdispersion metrics, randomized quantile residuals, and graphical diagnostics of model fit for binomial N-mixture models fitted using the unmarked package. Details about the checks are given in Knape et al. (2018).

Author(s)

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References

Knape et al. 2018. Sensitivity of binomial N-mixture models to overdispersion: the importance of assessing model fit. Methods in Ecology and Evolution, 9:2102-2114. doi:10.1111/2041210X.13062

See Also

Useful links:

- https://github.com/jknape/nmixgof
- Report bugs at https://github.com/jknape/nmixgof/issues

`residcov` *Plot residuals against covariates*

Description

A convenience function to plot rq residuals against all untransformed numeric covariates. Site-sum randomized quantile residuals are used for site covariates while marginal residuals are used for observation covariates. The same random residual draws are reused for different covariates.

Usage

```
residcov(umFit, ...)
```

Arguments

`umFit`	An object of class unmarkedFit from a model fitted using pcount.
`...`	Plot arguments.

Examples

```
library(unmarked)
umf = unmarkedFramePCount(y = shoveler$y, obsCovs = shoveler$obs, siteCovs = shoveler$site)
fmP = pcount(~scale(date) + scale(reedcover) ~ scale(log(water)) + scale(latitude),
      data = umf, K = 80)
residcov(fmP)
```

residfit *Plot residuals against fitted values*

Description

Plots randomized-quantile residuals for binomial N-mixture models against fitted values.

Usage

```
residfit(umFit, type = "marginal", ...)
```

Arguments

umFit	An object from a model fitted using pcount.
type	The type of randomized quantile residual to plot. One of 'marginal', 'site-sum' or 'observation'.
...	Plot arguments.

Examples

```
library(unmarked)
umf = unmarkedFramePCount(y = shoveler$y, obsCovs = shoveler$obs, siteCovs = shoveler$site)
fmP = pcount(~scale(date) + scale(reedcover) ~ scale(log(water)) + scale(latitude),
      data = umf, K = 80)
residfit(fmP, "marginal")
residfit(fmP, "site-sum")
residfit(fmP, "observation")
```

residqq *Qq plot of randomized quantile residuals against standard normal quantiles*

Description

Qq plot of randomized quantile residuals against standard normal quantiles

Usage

```
residqq(
  umFit,
  type = "site-sum",
  main = "Residual qq plot",
  plotLine = TRUE,
  ...
)
```

Arguments

umFit	An object of class unmarkedFit from a model fitted using pcount.
type	The type of randomized quantile residual to plot. One of 'site-sum' or 'observation'.
main	Plot label.
plotLine	If true, the identity line is added to the plot.
...	Further arguments passed to qqnorm.

Value

A list with x and y coordinates of the qq plot, see qqnorm.

Examples

```
library(unmarked)
umf = unmarkedFramePCount(y = shoveler$y, obsCovs = shoveler$obs, siteCovs = shoveler$site)
fmP = pcount(~scale(date) + scale(reedcover) ~ scale(log(water)) + scale(latitude),
      data = umf, K = 80)
residqq(fmP, "site-sum")
residqq(fmP, "observation")
```

---

rqresiduals *Randomized quantile resiudals for binomial N-mixture models.*

Description

Computes three types of randomized quantile residuals for binomial N-mixture models.

Usage

```
rqresiduals(umFit, type = "marginal")
```

Arguments

umFit	An object of class unmarkedFit from a model fitted using pcount.
type	The type of rq residuals to compute, one of 'marginal', 'site-sum' or 'observation'.

Value

A matrix (if type is 'marginal' or 'site-sum') or vector (for) con.

Examples

```
library(unmarked)
umf = unmarkedFramePCount(y = shoveler$y, obsCovs = shoveler$obs, siteCovs = shoveler$site)
fmP = pcount(~scale(date) + scale(reedcover) ~ scale(log(water)) + scale(latitude),
      data = umf, K = 80)
qqnorm(rqresiduals(fmP, "s"))
qqnorm(rqresiduals(fmP, "o"))
par(mfcol = c(3,4))
invisible(apply(rqresiduals(fmP, "m"), 2, qqnorm))
```

`shoveler` *Northern shoveler data*

Description

Repeated count data of Northern shoveler with covariates, formatted for use with the unmarked package.

Usage

```
shoveler
```

Format

A list with three elements

y A matrix with Northern shoveler counts

site A data frame with site specific covariates

obs A list containing observation specific covariates

References

Knape et al. (2018) Methods in Ecology and Evolution, 9:2102-2114. doi:10.1111/2041210X.13062

Examples

```
library(unmarked)
umf = unmarkedFramePCount(y = shoveler$y, obsCovs = shoveler$obs, siteCovs = shoveler$site)
```

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