

# Package ‘nmixgof’

October 13, 2022

**Title** Goodness of Fit Checks for Binomial N-Mixture Models

**Version** 0.1.0

**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](https://doi.org/10.1101/194340)>.

**Depends** R (>= 3.3.0)

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**LinkingTo** Rcpp

**Imports** Rcpp, unmarked

**RoxygenNote** 6.0.1

**URL** <https://github.com/jknape/nmixgof>

**BugReports** <https://github.com/jknape/nmixgof/issues>

**NeedsCompilation** yes

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chat	<i>Overdispersion metrics for binomial N-mixture models.</i>
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### 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 <code>unmarkedFit</code> from a model fitted using <code>pcount</code> .
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")
```

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nmixgof	<i>Goodness of fit checks for binomial N-mixture models</i>
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### 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 Knappe et al. (2018) and at <https://www.biorxiv.org/content/early/2017/09/27/194340>.

### References

Knappe et al. 2018. Sensitivity of binomial N-mixture models to overdispersion: the importance of assessing model fit. *Methods in Ecology and Evolution*, in press.

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residcov	<i>Plot residuals against covariates</i>
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**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 <code>unmarkedFit</code> from a model fitted using <code>pcount</code> .
...	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)
```

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residfit	<i>Plot residuals against fitted values</i>
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**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 <code>pcount</code> .
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")
```

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residqq	<i>Qq plot of randomized quantile residuals against standard normal quantiles</i>
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**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 <code>unmarkedFit</code> from a model fitted using <code>pcount</code> .
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 <code>qqnorm</code> .

**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")
```

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rqresiduals	<i>Randomized quantile residuals for binomial N-mixture models.</i>
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**Description**

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

**Usage**

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

**Arguments**

umFit	An object of class <code>unmarkedFit</code> from a model fitted using <code>pcount</code> .
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))
```

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shoveler	<i>Northern shoveler data</i>
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**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 in press. ([BioRxiv](#))

**Examples**

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

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