Package ‘iccCounts’

Title Intraclass Correlation Coefficient for Count Data
Version 1.0.3
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Depends R (>= 4.0)
Imports glmmTMB, ggplot2, Deriv, gridExtra, VGAM, dplyr
Suggests knitr, rmarkdown
Description Estimates the intraclass correlation coefficient (ICC) for count data to assess repeatability (intra-methods concordance) and concordance (between-method concordance). In the concordance setting, the ICC is equivalent to the concordance correlation coefficient estimated by variance components. The ICC is estimated using the estimates from generalized linear mixed models. The within-subjects distributions considered are: Poisson; Negative Binomial with additive and proportional extradispersion; Zero-Inflated Poisson; and Zero-Inflated Negative Binomial with additive and proportional extradispersion. The statistical methodology used to estimate the ICC with count data can be found in Carrasco (2010) <doi:10.1111/j.1541-0420.2009.01335.x>.

VignetteBuilder knitr
Encoding UTF-8
License GPL (>= 2)
LazyData true
RoxygenNote 7.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2021-07-30 13:00:02 UTC

R topics documented:

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Description
A dataset containing CD34+ count cell data obtained by two methods

Usage
AF

Format
A data frame with 40 rows and 3 variables:
y  CD34+ counts
id  Subject
met  Method

References

DispersionTest
Dispersion test for GLMM

Description
Dispersion test for GLMM

Usage
DispersionTest(x)

Arguments
x  An object of class GOF generated by GOF_check function.
Details

The function prints the dispersion of sample randomized quantile residuals (RQR) and the simulated P-value.

Value

A vector with the sample RQR dispersion and the P-value.

See Also

GOF_check()

Examples

# Poisson model. Repeatability setting.
iccpois<-icc_counts(EPP,y="Social",id="id")
iccpois.gof<-GOF_check(iccpois)
DispersionTest(iccpois.gof)

EPP Sparrow fledglings paternity data

Description

A dataset containing the counts of fledglings a male had in every breeding season

Usage

EPP

Format

A data frame with 193 rows and 3 variables:

- **Social**  Fledglings counts
- **id**  Subject identifier
- **Year**  Breeding season

References

GOF_check

**Goodness of fit for GLMM**

**Description**

Assessment of goodness of fit for GLMM

**Usage**

GOF_check(x, nsim = 100)

**Arguments**

- **x**: An object of class `iccc`.
- **nsim**: Number of simulations to run. Default is set to 100.

**Details**

Randomized quantile residuals are computed for the fitted model. Simulations based on the fitted model are generated and the model is refitted to each simulated dataset. Envelopes for RQR are built as the minimum and maximum RQR from the refitted models. Additionally, a test for dispersion and zero inflation are carried out by comparing the RQR dispersion and the number of zeros from the original model and data to those from the refitted models and simulated data.

**Value**

An object of class `GOF`. A list with the following components:

- `plot_env`: Plot of RQR envelopes with the original RQR.
- `plot_var`: Plot of the simulated RQR dispersion.
- `plot_zi`: Plot of the count of zeros in the simulated datasets.
- `res_var`: Dispersion of RQR from the original sample. Proportion of simulated RQR dispersion that are greater than the original dispersion that can be interpreted as a simulated P-value to check the goodness of fit on dispersion.
- `pval_var`: Proportion of simulated RQR dispersion that are greater than the original dispersion that can be interpreted as a simulated P-value to check the goodness of fit on dispersion.
- `zero_count`: Count of zeros in the original sample.
- `pval_zi`: Proportion of simulated zero count that are greater than that of the original sample. It can be interpreted as a simulated P-value to check the hypothesis of zero-inflation.
Examples

```r
# Poisson model. Repeatability setting.
iccpois <- icc_counts(EPP, y = "Social", id = "id")
GOF_check(iccpois)
# Zero-inflated Poisson model. Repeatability setting
icczip <- icc_counts(EPP, y = "Social", id = "id", fam = "zip")
GOF_check(icczip)
```

**Grimso**

<table>
<thead>
<tr>
<th>Tick counts data</th>
</tr>
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</table>

**Description**

A dataset containing the counts of ticks in Grimsö area

**Usage**

Grimso

**Format**

A data frame with 520 rows and 3 variables:

- **Tot**  Tick counts
- **TransectID**  Subject identifier
- **Round**  Replicate identifier

**References**


**ICC**

*Prints the intraclass correlation coefficient*

**Description**

Prints the intraclass correlation coefficient (ICC)

**Usage**

ICC(x, digits = getOption("digits"))
icc_counts

Intraclass correlation coefficient (ICC) for count data

Description

Estimates the intraclass correlation coefficient (ICC) for count data

Usage

icc_counts(
  data,
  y,
  id,
  met = NULL,
  type = c("rep", "con"),
  fam = c("poisson", "nbinom1", "nbinom2", "zip", "zinb1", "zinb2"),
  conf = 0.95
)

Arguments

x
An object of class iccc
digits
Number of digits to print

Value

A vector with the ICC estimate, its standard error and confidence interval.

See Also

icc_counts()

Examples

# Poisson model. Repeatability setting.
iccpois<-icc_counts(Grimso,y="Tot",id="TransectID")
ICC(iccpois)

# Negative Binomial with proportional extra-dispersion. Concordance setting
iccnb2<-icc_counts(AF,y="y",id="id",met="met",type="con",fam="nbinom2")
ICC(iccnb2)

# Zero-inflated Poisson model. Repeatability setting
icczip<-icc_counts(EPP,y="Social",id="id",fam="zip")
ICC(icczip)
icc_counts

Arguments

data A data frame containing at least two columns: outcome and subject identifier. In case of estimating the ICC for concordance setting, a third column with the method identifier will be needed.
y Character string indicating the name of the outcome column in the dataset.
id Character string indicating the name of the subjects column in the dataset.
met Character string indicating the name of the methods column in the dataset. Only needed in the concordance setting.
type Character string. It chooses the setting in which the ICC should be estimated. Valid values are: "rep" (default) for repeatability setting; "con" for concordance setting.
fam Character string. The within-subjects pdf to use. Valid options are: "poisson" (default) for Poisson pdf; "nbinom1" for Negative Binomial pdf with additive extradispersion; "nbinom2" for Negative Binomial pdf with proportional extradispersion; "zip" for zero-inflated Poisson pdf; "zinb1" for zero-inflated Negative Binomial nbinom1 pdf; "zinb2" for zero-inflated Negative Binomial nbinom2 pdf;
conf Confidence level for the confidence interval estimation. Default value is set to 95%.

Details

The intraclass correlation coefficient (ICC) is estimated using the variance components of a generalized linear mixed model (GLMM) (Carrasco, 2010).

The GLMM is estimated using the glmmTMB package (Brooks et al. 2017). The ICC standard error is estimated by applying the delta method (Ver Hoef, 2012) using the variance-covariance matrix of parameters involved in the ICC estimate.

The parameters involved in the estimation of the ICC depends on the within-subjects pdf family chosen: the between-subjects variance, the between-methods variability (in case of concordance analysis), and parameters involved in the within-subjects family chosen. In all cases the output includes the overall expectation identified as \( \mu \); the between-subjects variance named as \( BSVar \); the between-methods variability (in case of concordance analysis) named as \( BMVar \).

In the Negative Binomial pdf with additive extradispersion,

\[
Var(y) = \mu \ast (1 + r)
\]

and Negative Binomial pdf with proportional extradispersion

\[
Var(y) = \mu \ast (1 + r \ast \mu^2)
\]

the extra-dispersion parameter \( r \) is included in the output.

For zero-inflated models, the probability of observing an extra zero is included in the output as \( pi \).
Value

An object of class iccc. The output is a list with the following components:

- model. An object of class glmmTMB. The estimated generalized linear mixed model.
- ICC. Estimate of the ICC, its standard error and confidence interval.
- varcomp. Variance components and parameters related to ICC expression.

References


Examples

```r
# Poisson model. Repeatability setting.
iccpois<-icc_counts(Grimso,y="Tot",id="TransectID")

# Negative Binomial with proportional extra-dispersion. Concordance setting
iccnb2<-icc_counts(AF,y="y",id="id",met="met",type="con",fam="nbinom2")

# Zero-inflated Poisson model. Repeatability setting
icczip<-icc_counts(EPP,y="Social",id="id",fam="zip")
```

plot.GOF

Goodness of fit plots

Description

Draws the plots to assess the goodness of fit

Usage

```r
## S3 method for class 'GOF'
plot(x, ..., type = c("all", "envelope", "dispersion", "zeros"))
```

Arguments

- `x` An object of class GOF generated by GOF_check function.
- `...` Ignore dispersion for plot to assess the dispersion; zeros for plot to assess the zero inflation.
- `type` Which plot to draw. Values: all (default); envelope for envelopes of randomized quantile residuals;
VarComp

Value

A vector with the variance components and related parameters

See Also

GOF_check()

Examples

# Poisson model. Repeatability setting.
iccpois<-icc_counts(EPP,y="Social",id="id")
iccpois.gof<-GOF_check(iccpois)
plot(iccpois.gof)
plot(iccpois.gof,type="envelope")
plot(iccpois.gof,type="dispersion")
plot(iccpois.gof,type="zeros")

VarComp

<table>
<thead>
<tr>
<th>VarComp</th>
<th>GLMM variance components</th>
</tr>
</thead>
</table>

Description

Prints the GLMM variance components and related parameters to estimate the intraclass correlation coefficient (ICC)

Usage

VarComp(x, digits =getOption("digits"))

Arguments

x

An object of class icce
digits

Number of digits to print

Value

A vector with the variance components and related parameters

See Also

icc_counts()
### Examples

```r
# Poisson model. Repeatability setting.
iccpois<-icc_counts(Grimso,y="Tot",id="TransectID")
VarComp(iccpois)
# Negative Binomial with proportional extra-dispersion. Concordance setting
iccnb2<-icc_counts(AF,y="y",id="id",met="met",type="con",fam="nbinom2")
VarComp(iccnb2)
# Zero-inflated Poisson model. Repeatability setting
icczip<-icc_counts(EPP,y="Social",id="id",fam="zip")
VarComp(icczip)
```

### Description

Zero-Inflation test for GLMM

### Usage

```r
ZeroTest(x)
```

### Arguments

- `x`: An object of class `GOF` generated by `GOF_check` function.

### Details

The function prints the count of zeros in the sample and the simulated P-value.

### Value

A vector with the zero count and the P-value.

### See Also

- `GOF_check()`

### Examples

```r
# Poisson model. Repeatability setting.
iccpois<-icc_counts(EPP,y="Social",id="id")
iccppois.gof<-GOF_check(iccppois)
ZeroTest(iccppois.gof)
# Zero-inflated Poisson model. Repeatability setting
icczip<-icc_counts(EPP,y="Social",id="id",fam="zip")
icczip.gof<-GOF_check(icczip)
ZeroTest(icczip.gof)
```
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