Package ‘multilevelTools’

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acfByID ... Estimate the autocorrelation by unit (ID)

Description

This function estimates the autocorrelation over time in a time series by a higher level unit, given by ID.

Usage

acfByID(
  xvar,
  timevar,
  idvar,
  data,
  lag.max = 10L,
  na.function = c("na.approx", "na.spline", "na.locf"),
  ...
)

Arguments

xvar A character string giving the variable name of the variable to calculate autocorrelations on.

timevar A character string giving the variable name of the time variable.
idvar  A character string giving the variable name of the ID variable. Can be missing if only one time series provided, in which case one will be created.

data  A data.table containing the variables used in the formula. This is a required argument. If a data.frame, it will silently coerce to a data.table. If not a data.table or data.frame, it will attempt to coerce, with a message.

lag.max  An integer of the maximum lag to estimate. Must be equal to or greater than the number of observations for all IDs in the dataset.

na.function  A character string giving the name of the function to use to address any missing data. Functions come from the zoo package, and must be one of: “na.approx”, “na.spline”, “na.locf”.

...  Additional arguments passed to zoo.

Value
A data.table of the estimated autocorrelations by ID and lag

Examples

## example 1
dat <- data.table::data.table(
  x = sin(1:30),
  time = 1:30,
  id = 1)
acfByID("x", "time", "id", data = dat)

## example 2
dat2 <- data.table::data.table(
  x = c(sin(1:30), sin((1:30)/10)),
  time = c(1:30, 1:30),
  id = rep(1:2, each = 30))
dat2$x[4] <- NA
res <- acfByID("x", "time", "id", data = dat2, na.function = "na.approx")
ggplot2::ggplot(res, ggpplot2::aes(factor(Lag), AutoCorrelation)) +
ggpplot2::geom_boxplot()

## clean up
rm(dat, dat2, res)
Usage

```r
## S3 method for class 'modelTest.merMod'
APAStyler(
  object,
  format = list(FixedEffects = c("%s%s [%s, %s]"), RandomEffects = c("%s", "%s [%s, %s]"), EffectSizes = c("%s/%s, %s")),
  digits = 2,
  pcontrol = list(digits = 3, stars = TRUE, includeP = FALSE, includeSign = FALSE, dropLeadingZero = TRUE),
  ...
)
```

Arguments

- `object` A list of one (or more) models estimated from lmer
- `format` A list giving the formatting style to be used for the fixed effects, random effects, and effect sizes. For the random effects, must be two options, one for when the random effects do not have confidence intervals and one when the random effects do have confidence intervals.
- `digits` A numeric value indicating the number of digits to print. This is still in early implementation stages and currently does not change all parts of the output (which default to 2 decimals per APA style).
- `pcontrol` A list controlling how p values are formatted.
- `...` Additional arguments passed to `confint`. Notably `nsim` and `boot.type` if the bootstrap method is used.

Value

A data table of character data

Examples

```r
library(JWileymisc)
data(sleepstudy, package = "lme4")

m1 <- lme4::lmer(Reaction ~ Days + (1 + Days | Subject),
  data = sleepstudy)
m2 <- lme4::lmer(Reaction ~ Days + I(Days^2) + (1 + Days | Subject),
  data = sleepstudy)

testm1 <- modelTest(m1)
testm2 <- modelTest(m2)

APAStyler(testm1)
APAStyler(list(Linear = testm1, Quadratic = testm2))
APAStyler(testm1,
  format = list(
    FixedEffects = "%s, %s (%s, %s)"
  ),
  ...
)
```
iccMixed

Intraclass Correlation Coefficient (ICC) from Mixed Models

Description

This function estimates the ICC from mixed effects models estimated using \texttt{lme4}.

Usage

\texttt{iccMixed(dv, id, data, family = c("gaussian", "binomial"))}

Arguments

dv \hspace{1cm} \text{A character string giving the variable name of the dependent variable.}

id \hspace{1cm} \text{A character vector of length one or more giving the ID variable(s). Can be more than one.}

data \hspace{1cm} \text{A data.table containing the variables used in the formula. This is a required argument. If a data.frame, it will silently coerce to a data.table. If not a data.table or data.frame, it will attempt to coerce, with a message.}

family \hspace{1cm} \text{A character vector giving the family to use for the model. Currently only supports "gaussian" or "binomial".}
Mean decomposition of a variable by group(s)

Description

This function decomposes a variable in a long data set by grouping factors, such as by ID. If multiple grouping factors are listed, the decomposition is in order from left to right. Residuals from the lowest level are returned.

Usage

meanDecompose(formula, data)

Arguments

formula A formula of the variables to be used in the analysis. Should have the form: variable ~ groupingfactors.
data A data table or data frame containing the variables used in the formula. This is a required argument.

Value

A list of data tables with the means or residuals
meanDeviations

Examples

meanDecompose(mpg ~ vs, data = mtcars)
meanDecompose(mpg ~ vs + cyl, data = mtcars)

## Example plotting the results
tmp <- meanDecompose(Sepal.Length ~ Species, data = iris)
do.call(cowplot::plot_grid, c(lapply(names(tmp), function(x) {
    plot(JWileymisc::testDistribution(tmp[[x]]$X), plot = FALSE, varlab = x)$Density
})), ncol = 1))
rm(tmp)

meanDeviations

Function to calculate the mean and deviations from mean

Description

Tiny helper function to calculate the mean and deviations from the mean, both returned as a list. Works nicely with data.table to calculate a between and within variable.

Usage

meanDeviations(x, na.rm = TRUE)

Arguments

x
A vector, appropriate for the mean function.

na.rm
A logical, whether to remove missing or not. Defaults to TRUE.

Value

A list of the mean (first element) and deviations from the mean (second element).

Examples

## simple example showing what it does
meanDeviations(1:10)

## example use case, applied to a data.table
library(data.table)
d <- as.data.table(iris)
d[, c("BSepal.Length", "WSepal.Length") := meanDeviations(Sepal.Length),
    by = Species]
str(d)
rm(d)
Description

This function provides fit statistics and effect sizes for model comparisons. The models must be nested.

Usage

```r
## S3 method for class 'merMod'
modelCompare(model1, model2, ...)
```

Arguments

- `model1`: A model estimated by `lmer`.
- `model2`: A model estimated by `lmer`.
- `...`: Additional arguments, not currently used but included to match generic.

Value

A data table with the fit indices for each model and comparing models to each other.

References


Examples

```r
library(JWileymisc)
data(aces_daily, package = "JWileymisc")
m1 <- lme4::lmer(PosAff ~ STRESS + (1 + STRESS | UserID),
                 data = aces_daily)
m2 <- lme4::lmer(PosAff ~ STRESS + (1 | UserID),
                 data = aces_daily)
m3 <- lme4::lmer(PosAff ~ STRESS + Female + (1 | UserID),
                 data = aces_daily)
modelCompare(m1, m2)
modelCompare(m2, m3)
rm(m1, m2, m3)
```
modelDiagnostics.lme  

modelDiagnostics method for lme objects

Description

This function creates a number of diagnostics for lme models.

Usage

## S3 method for class 'lme'
modelDiagnostics(
  object,
  ev.perc = 0.001,
  robust = FALSE,
  distr = "normal",
  standardized = TRUE,
  ...
)

Arguments

  object  A fitted model object of class lme.
  ev.perc  A real number between 0 and 1 indicating the proportion of the theoretical distribution beyond which values are considered extreme values (possible outliers). Defaults to .001.
  robust  Whether to use robust mean and standard deviation estimates for normal distribution
  distr  A character string given the assumed distribution. Passed on to testDistribution. Defaults to “normal”.
  standardized  A logical whether to use standardized pearson residuals. Defaults to TRUE generally where possible but may depend on method.
  ...  Additional arguments, not currently used.

Value

A logical (is.modelDiagnostics) or a modelDiagnostics object (list) for as.modelDiagnostics and modelDiagnostics.

Examples

library(JWileymisc)
sleep[1,1] <- NA
m <- nlme::lme(extra ~ group, data = sleep,
  random = ~ 1 | ID, na.action = "na.omit")
```r
modelDiagnostics.merMod

modelDiagnostics method for merMod objects

Description

This function creates a number of diagnostics for merMod models.

Usage

```r
## S3 method for class 'merMod'
modelDiagnostics(
  object,
  ev.perc = 0.001,
  robust = FALSE,
  distr = "normal",
  standardized = TRUE,
  ...
)
``` 

Arguments

- **object**: A fitted model object, either of class merMod from the lme4 package or merModLmerTest from the lmerTest package.
- **ev.perc**: A real number between 0 and 1 indicating the proportion of the theoretical distribution beyond which values are considered extreme values (possible outliers). Defaults to .001.
```
modelPerformance.merMod

robust          Whether to use robust mean and standard deviation estimates for normal distribution
distr           A character string given the assumed distribution. Passed on to testDistribution. Defaults to “normal”.
standardized    A logical whether to use standardized residuals. Defaults to TRUE generally where possible but may depend on method.
...             Additional arguments, not currently used.

Value

A logical (is.modelDiagnostics) or a modelDiagnostics object (list) for as.modelDiagnostics and modelDiagnostics.

Examples

library(JWileymisc)
sleep[,1] <- NA
m <- lme4::lmer(extra ~ group + (1 | ID), data = sleep)

md <- modelDiagnostics(m, ev.perc = .1)
md$extremeValues
class(md)

plot(md)

data(aces_daily, package = "JWileymisc")
m <- lme4::lmer(PosAff ~ STRESS + (1 + STRESS | UserID), data = aces_daily)
md <- modelDiagnostics(m, ev.perc = .1)

# gm1 <- lme4::glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
#                    data = lme4::cbpp, family = binomial)
# modelDiagnostics(gm1) ## should be an error

rm(m, md, sleep)

modelPerformance.merMod

modelPerformance method for merMod objects

Description

For pseudo R2 by cluster, the squared correlation between observed and predicted values for each cluster unit is returned. For the overall model, the marginal and conditional R2 are calculated as described in the references.
Usage

```r
## S3 method for class 'merMod'
modelPerformance(object, ...)
```

Arguments

- `object` A model from `lmer`.
- `...` Additional arguments, not currently used.

Value

A named vector with the marginal and conditional R² values, if `CLUSTER = FALSE`, otherwise, a data table with the pseudo R² for each cluster unit. A list with a `data.table` with the following elements:

- **Model** A character string indicating the model type, here `merMod`
- **Estimator** A character string indicating whether the model was estimated with REML or ML
- **N_Obs** The number of observations
- **N_Groups** A character string indicating the number of unique units in each grouping/clustering variable.
- **AIC** Akaike Information Criterion
- **BIC** Bayesian Information Criterion
- **LL** log likelihood
- **LLDF** log likelihood degrees of freedom
- **Sigma** Residual standard deviation
- **MarginalR2** in sample variance explained by the fixed effects
- **ConditionalR2** in sample variance explained by the fixed and random effects
- **MarginalF2** Cohen’s F² effect size R² / (1 - R²) based off the Marginal R²
- **ConditionalF2** Cohen’s F² effect size R² / (1 - R²) based off the Conditional R²

References


Examples

```r
library(JWileymisc)
data(aces_daily, package = "JWileymisc")
m1 <- lme4::lmer(PosAff ~ 1 + (1 | UserID),
                 data = aces_daily)
modelPerformance(m1)
```
\begin{verbatim}
m1 <- lme4::lmer(PosAff ~ STRESS + (1 + STRESS | UserID),
                 data = aces_daily)
modelPerformance(m1)
rm(m1)
\end{verbatim}

\textbf{modelTest.merMod} estimate detailed results per variable and effect sizes for both fixed and random effects from lmer models

\textbf{Description}
This function extends the current \texttt{drop1} method for \texttt{merMod} class objects from the \texttt{lme4} package. Where the default method to be able to drop both fixed and random effects at once.

\textbf{Usage}
\begin{verbatim}
## S3 method for class 'merMod'
modelTest(object, method = c("Wald", "profile", "boot"), control, ...)
\end{verbatim}

\textbf{Arguments}
- \texttt{object} A \texttt{merMod} class object, the fitted result of \texttt{lmer}.
- \texttt{method} A character vector indicating the types of confidence intervals to calculate. One of “Wald”, “profile”, or “boot”.
- \texttt{control} A \texttt{lmerControl()} results used to control how models are estimated when updating.
- ... Additional arguments passed to \texttt{confint}

\textbf{Details}
At the moment, the function is aimed to \texttt{lmer} models and has very few features for \texttt{glmer} or \texttt{nlmer} models. The primary motivation was to provide a way to provide an overall test of whether a variable “matters”. In multilevel data, a variable may be included in both the fixed and random effects. To provide an overall test of whether it matters requires jointly testing the fixed and random effects. This also is needed to provide an overall effect size.

The function works by generating a formula with one specific variable or “term” removed at all levels. A model is then fit on this reduced formula and compared to the full model passed in. This is a complex operation for mixed effects models for several reasons. Firstly, \texttt{R} has no default mechanism for dropping terms from both the fixed and random portions. Secondly, mixed effects models do not accommodate all types of models. For example, if a model includes only a random slope with no random intercept, if the random slope was dropped, there would be no more random effects, and at that point, \texttt{lmer} or \texttt{glmer} will not run the model. It is theoretically possible to instead fit the model using \texttt{lm} or \texttt{glm} but this becomes more complex for certain model comparisons and calculations and is not currently implemented. Marginal and conditional R2 values are calculated for each term, and these are used also to calculate something akin to an f-squared effect size.
This is a new function and it is important to carefully evaluate the results and check that they are accurate and that they are sensible. Check accuracy by viewing the model formulae for each reduced model and checking that those are indeed accurate. In terms of checking whether a result is sensible or not, there is a large literature on the difficulty interpreting main effect tests in the presence of interactions. As it is challenging to detect all interactions, especially ones that are made outside of R formulae, all terms are tested. However, it likely does not make sense to report results from dropping a main effect but keeping the interaction term, so present and interpret these with caution.

Examples

```r
## these examples are slow to run
library(JWileymisc)
m1 <- lme4::lmer(extra ~ group + (1 | ID),
data = sleep, REML=FALSE)
modelTest(m1)

data(aces_daily, package = "JWileymisc")

strictControl <- lme4::lmerControl(optCtrl = list(
  algorithm = "NLOPT_LN_NELDERMEAD",
  xtol_abs = 1e-10,
  ftol_abs = 1e-10))

m1 <- lme4::lmer(NegAff ~ STRESS + (1 + STRESS | UserID),
data = aces_daily,
control = strictControl)
modelTest(m1, method = "profile")

m2 <- lme4::lmer(NegAff ~ STRESS + I(STRESS^2) + (1 + STRESS | UserID),
data = aces_daily, control = strictControl)

## might normally use more bootstraps but keeping low for faster run
modelTest(m2, method = "boot", nsim = 100)
```

---

**nEffective**

Estimate the effective sample size from longitudinal data

---

**Description**

This function estimates the (approximate) effective sample size.

**Usage**

```r
nEffective(n, k, icc, dv, id, data, family = c("gaussian", "binomial")))
```
omegaSEM

**Arguments**

- **n**: The number of unique/indepedent units of observation
- **k**: The (average) number of observations per unit
- **icc**: The estimated ICC. If missing, will estimate (and requires that the family argument be correctly specified).
- **dv**: A character string giving the variable name of the dependent variable.
- **id**: A character vector of length one giving the ID variable.
- **data**: A data.table containing the variables used in the formula. This is a required argument. If a data.frame, it will silently coerce to a data.table. If not a data.table or data.frame, it will attempt to coerce, with a message.
- **family**: A character vector giving the family to use for the model. Currently only supports "gaussian" or "binomial".

**Value**

A data.table including the effective sample size.

**References**


**Examples**

```r
## example where n, k, and icc are estimated from the data
## provided, partly using iccMixed function
nEffective(dv = "mpg", id = "cyl", data = mtcars)

## example where n, k, and icc are known (or being 'set')
## useful for sensitivity analyses
nEffective(n = 60, k = 10, icc = .6)
```

---

omegaSEM  
*Calculate multilevel omega reliability*

**Description**

This function uses multilevel structural equation modelling to calculate between and within reliability using coefficient omega.

**Usage**

```r
omegaSEM(items, id, data, savemodel = FALSE)
```
Arguments

- `items`: A character vector giving the variables that map to the items in the scale. Note that these should be reverse scored prior to running this function.
- `id`: A character string giving the name of the variable that indicates which rows of the dataset belong to the same person or group for the multilevel analysis.
- `data`: A data table or data frame to be used for analysis.
- `savemodel`: A logical value indicating whether the underlying model should be saved and returned. Defaults to `FALSE`.

Value

A list with two elements, the first, “Results” contains the estimates for coefficient omega at the within and between level. The next element, “Fit” contains the entire fitted model from lavaan, if `savemodel = TRUE`.

References


Examples

```r
data(aces_daily, package = "JWileymisc")
omeasureSEM(
  items = c("COPEPrb", "COPEPrc", "COPEExp"),
  id = "UserID",
  data = aces_daily,
  savemodel = FALSE)
```

plot.modelDiagnostics.lme

*Plot Diagnostics for an lme model*

Description

This function creates a number of diagnostic plots from lme models.

Usage

```r
## S3 method for class 'modelDiagnostics.lme'
plot(x, y, plot = TRUE, ask = TRUE, ncol = 1, nrow = 1, ...)
```
Arguments

- **x**: A fitted model object from `lme()`.
- **y**: Included to match the generic. Not used.
- **plot**: A logical value whether or not to plot the results or simply return the graphical objects.
- **ask**: A logical whether to ask before changing plots. Only applies to interactive environments.
- **ncol**: The number of columns to use for plots. Defaults to 1.
- **nrow**: The number of rows to use for plots. Defaults to 1.
- **...**: Included to match the generic. Not used.

Value

- a list including plots of the residuals, residuals versus fitted values, and one list for plots of all random effects

Examples

```
library(JWileymisc)
sleep[1,1] <- NA
m <- nlme::lme(extra ~ group, data = sleep, random = ~ 1 | ID, na.action = "na.omit")
md <- modelDiagnostics(m, ev.perc = .1)
print(md$extremeValues)
plot(md)
data(aces_daily, package = "JWileymisc")
m <- nlme::lme(PosAff ~ STRESS, data = aces_daily,
               random = ~ 1 + STRESS | UserID, na.action = "na.omit")
md <- modelDiagnostics(m, ev.perc = .001)
print(md$extremeValues)
plot(md$modelDiagnostics[[2]][[2]])
plot(md, ncol = 2, nrow = 2)
plot(md, ncol = 2, nrow = 3)
rm(m, md, sleep)
```

Description

This function creates a number of diagnostic plots from Lmer models.
Usage

## S3 method for class 'modelDiagnostics.merMod'

plot(x, y, plot = TRUE, ask = TRUE, ncol = 1, nrow = 1, ...)

Arguments

x A fitted model object from lmer().
y Included to match the generic. Not used.
plot A logical value whether or not to plot the results or simply return the graphical objects.
ask A logical whether to ask before changing plots. Only applies to interactive environments.
ncol The number of columns to use for plots. Defaults to 1.
nrow The number of rows to use for plots. Defaults to 1.
... Included to match the generic. Not used.

Value

a list including plots of the residuals, residuals versus fitted values, and one list for plots of all random effects

Examples

library(JWileymisc)
sleep[1,1] <- NA
m <- lme4::lmer(extra ~ group + (1 | ID), data = sleep)

md <- modelDiagnostics(m, ev.perc = .1)
md$extremeValues

data(aces_daily, package = "JWileymisc")
m <- lme4::lmer(PosAff ~ STRESS + (1 + STRESS | UserID), data = aces_daily)

md <- modelDiagnostics(m, ev.perc = .001)
md$extremeValues
plot(md$modelDiagnostics[[2]][[2]])
plot(md, ncol = 2, nrow = 2)
plot(md, ncol = 2, nrow = 3)
rm(m, md, sleep)
Description

For pseudo R2 by cluster, the squared correlation between observed and predicted values for each cluster unit is returned. For the overall model, the marginal and conditional R2 are calculated as described in the references.

Usage

```r
## S3 method for class 'merMod'
R2(object, cluster = FALSE, ...)
```

Arguments

- `object`: A model estimated by `lmer`.
- `cluster`: A logical whether to calculate individual pseudo R2 values by cluster unit (if `TRUE`) or the marginal and conditional R2 for the overall model (if `FALSE`, the default).
- `...`: Added for consistency with generic. Not currently used.

Value

A named vector with the marginal and conditional R2 values, if `CLUSTER = FALSE`, otherwise, a data table with the pseudo R2 for each cluster unit.

References


Examples

```r
library(JWileymisc)
data(aces_daily, package = "JWileymisc")
m1 <- lme4::lmer(PosAff ~ STRESS + (1 + STRESS | UserID),
  data = aces_daily)
R2(m1)
R2(m1, cluster = TRUE)
hist(R2(m1, cluster = TRUE)$R2)
rm(m1)
```
residualDiagnostics.lme

residualDiagnostics methods for lme objects

Description

residualDiagnostics methods for lme objects

Usage

## S3 method for class 'lme'
residualDiagnostics(
  object,
  ev.perc = 0.001,
  robust = FALSE,
  distr = "normal",
  standardized = TRUE,
  ...
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object with class lme.</td>
</tr>
<tr>
<td>ev.perc</td>
<td>The extreme value percentile to use. Defaults to .001.</td>
</tr>
<tr>
<td>robust</td>
<td>A logical value, whether to use robust estimates or not. Defaults to FALSE.</td>
</tr>
<tr>
<td>distr</td>
<td>A character string specifying the assumed distribution. Currently “normal”, but future options may be supported in the future.</td>
</tr>
<tr>
<td>standardized</td>
<td>A logical value whether to use standardized pearson residual values or not. Defaults to TRUE.</td>
</tr>
<tr>
<td>...</td>
<td>Additional arguments. Not currently used.</td>
</tr>
</tbody>
</table>

Value

A logical (is.residualDiagnostics) or a residualDiagnostics object (list) for as.residualDiagnostics and residualDiagnostics.

Examples

```
library(JWileymisc)
sleep[1,1] <- NA
m <- nlme::lme(extra ~ group, data = sleep, random = ~ 1 | ID,
               na.action = na.omit)
residualDiagnostics(m)$Residuals
```
residualDiagnostics.merMod

m <- nlme::lme(hp ~ mpg, data = mtcars, random = ~ 1 | cyl, 
na.action = na.omit) 
residualDiagnostics(m)$Residuals 
rm(m, sleep) 

residualDiagnostics.merMod

residualDiagnostics methods for merMod objects

Description

residualDiagnostics methods for merMod objects

Usage

## S3 method for class 'merMod'
residualDiagnostics(
  object, 
ev.perc = 0.001, 
robust = FALSE, 
distr = "normal", 
standardized = TRUE, 
...
)

Arguments

object An object with class merMod. Currently only lmer() models are supported.
ev.perc The extreme value percentile to use. Defaults to .001.
robust A logical value, whether to use robust estimates or not. Defaults to FALSE.
distr A character string specifying the assumed distribution. Currently "normal", but
may expand in the future if glmer() models are supported.
standardized A logical value whether to use standardized residual values or not. Defaults to 
TRUE.
... Additional arguments. Not currently used.

Value

A logical (is.residualDiagnostics) or a residualDiagnostics object (list) for as.residualDiagnostics 
and residualDiagnostics.
Examples

library(JWileymisc)
sleep[1,1] <- NA
m <- lme4::lmer(extra ~ group + (1 | ID), data = sleep)
residualDiagnostics(m)$Residuals

# gm1 <- lme4::glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
# data = lme4::cbpp, family = binomial)
# residualDiagnostics(gm1) ## should be an error

rm(m, sleep)
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