

Package ‘bild’

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Description Performs logistic regression for binary longitudinal data, allowing for serial dependence among observations from a given individual and a random intercept term. Estimation is via maximization of the exact likelihood of a suitably defined model. Missing values and unbalanced data are allowed, with some restrictions.

M. Helena Goncalves et al. (2012) <[DOI:10.18637/jss.v046.i09](https://doi.org/10.18637/jss.v046.i09)>.

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Author M. Helena Goncalves [aut, cre] (ORCID: <<https://orcid.org/0000-0002-6990-7239>>),
M. Salome Cabral [aut],

Adelchi Azzalini [aut],
 R. Piessens [ctb] (Author of Fortran-77 subroutines from Quadpack),
 E. de Doncker [ctb] (Author of Fortran-77 subroutines from Quadpack)

Maintainer M. Helena Goncalves <mhgoncal@ualg.pt>

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 bild-package

bild: A Package for Binary Longitudinal Data

Description

Performs logistic regression for binary longitudinal data, allowing for serial dependence among observations from a given individual and a random intercept term. Estimation is via maximization of the exact likelihood of a suitably defined model. Missing values and unbalanced data are allowed, with some restrictions. M. Helena Goncalves et al. (2012) [doi: 10.18637/jss.v046.i09](https://doi.org/10.18637/jss.v046.i09).

Author(s)

Maintainer: M. Helena Goncalves <mhgoncal@ualg.pt> ([ORCID](#))

Authors:

- M. Salome Cabral
- Adelchi Azzalini

Other contributors:

- R. Piessens (Author of Fortran-77 subroutines from Quadpack) [contributor]
- E. de Doncker (Author of Fortran-77 subroutines from Quadpack) [contributor]

 airpollution

Airpollution dataset

Description

This example is a subset of data from the Six Cities study, a longitudinal study of the health effects of air pollution (Ware, J. H. et al., 1984).

Usage

```
airpollution
```

Format

A data frame with 128 observations on the following 5 variables:

`id` identifies the number of the individual profile, containing 32 individual profiles.
`wheeze` a numeric vector that identifies the wheezing status (1="yes", 0="no").
`age` a numeric vector corresponding to the age in years since the child's 9th birthday.
`smoking` a factor that identifies if the mother smokes (1="smoke", 0="no smoke").
`counts` a numeric vector corresponding to the replications of each individual profile.

Details

The data set presented by Fitzmaurice and Laird (1993) contains complete records on 537 children from Steubenville, Ohio. The repeated binary response is the wheezing status of a child. Maternal smoking status was determined in the first interview and treated as a time-independent covariate.

Source

Fitzmaurice, G. M. and Laird, N. M. (1993). A Likelihood-Based Method for analyzing Longitudinal Binary Response. *Biometrika*, 80, 141-51.

Examples

```
data(airpollution)
str(airpollution)

# Dependence="MC2"
air2 <- bild(wheeze~age+smoking, data=airpollution, time="age",
            aggregate=smoking, dependence="MC2")
summary(air2)
getAIC(air2)
getLogLik(air2)

# Base graphics diagnostics
plot(air2)

# ggplot2-based diagnostics
library(ggplot2)
autoplot(air2, which = 1) # Residuals vs Fitted values
autoplot(air2, which = 2) # Standardized Residuals vs Time
autoplot(air2, which = 5) # Estimated Parametric Profiles

# Multi-panel diagnostic plots using patchwork
library(patchwork)
(autoplot(air2, which = 5) + autoplot(air2, which = 2)) /
  (autoplot(air2, which = 1) + autoplot(air2, which = 3))

# Dependence="MC2R"
air2r <- bild(wheeze~age+smoking, data=airpollution, time="age",
            aggregate=smoking, dependence="MC2R")
summary(air2r)

# Compare base plot with autoplot for individual profiles
plot(air2r, which=6, subSET=smoking=="0", main="smoking==0", ident=TRUE)
autoplot(air2r, which=6, subSET=smoking=="0", ident=TRUE)
```

anova,bild-method	<i>Analysis of Deviance for 'bild' objects</i>
-------------------	--

Description

Computes an analysis of deviance table for two or more fitted model objects of class `build`.

Usage

```
## S4 method for signature 'build'
anova(object, ..., test = TRUE, correct = FALSE)
```

Arguments

<code>object</code>	An object of class <code>build</code> .
<code>...</code>	Additional objects of class <code>build</code> .
<code>test</code>	Logical. If TRUE, the likelihood ratio test is performed. Default is TRUE.
<code>correct</code>	Logical. If TRUE, a correction for the likelihood ratio test is applied (e.g., for mixture models). Default is FALSE.

Details

Setting `correct = TRUE` is used to test the presence of a random intercept term; the solution proposed by Self and Liang (1987) is adopted for the p-value.

Note

The comparison between two models by `anova` will only be valid if they are fitted to the same dataset.

References

Self, Steven G. and Liang, Kung-Yee (1987). Asymptotic properties of maximum likelihood estimators and likelihood ratio tests under nonstandard conditions. *Journal of the American Statistical Association*, 82, 605-610.

Examples

```
data(locust)
loc1 <- bild::bild(move~(time+I(time^2))*feed*sex, data=locust, dependence="MC1")
loc2 <- bild::bild(move~(time+I(time^2))*feed, data=locust, dependence="MC1")
anova(loc1, loc2)

data(muscatine)
muscatine$time1 <- c(-1, 0, 1)
musc1 <- bild::bild(obese~time1, data=muscatine, time="time1", dependence="MC1")
musc1r <- bild::bild(obese~time1, data=muscatine, time="time1", dependence="MC1R")
anova(musc1, musc1r, correct=TRUE)
```

autoplot.bild

Autoplot Method for bild Objects using ggplot2

Description

Generates ggplot2-based diagnostic and profile plots for a fitted bild longitudinal model object.

Usage

```
## S3 method for class 'bild'
autoplot(object, which = 5, add.unadjusted = FALSE, subSET, ident = FALSE, ...)
```

Arguments

object	A fitted model object of class bild.
which	A numeric value from 1 to 6 specifying the plot type.
add.unadjusted	Logical.
subSET	An optional logical expression to subset individuals in plot 6.
ident	Logical.
...	Further arguments passed.

Value

A ggplot object.

Examples

```
library(ggplot2)
library(patchwork)
library(bild)
data(airpollution)

air1R <- bild::bild(wheeze ~ age + smoking, data = airpollution, time = "age",
  aggregate = smoking, dependence = "MC1R")

# Single diagnostic plot (Standardized Residuals vs Time)
autoplot(air1R, which = 2)

# Multi-panel diagnostic plots using patchwork
(autoplot(air1R, which = 5) + autoplot(air1R, which = 2)) /
  (autoplot(air1R, which = 1) + autoplot(air1R, which = 3))

# Individual mean profiles for the smoker group
autoplot(air1R, which = 6, subSET = smoking == "1", ident = TRUE)
```

bild	<i>Fit of Parametric Models for Binary Longitudinal Data via Likelihood Method</i>
------	--

Description

Performs the fit of parametric models via likelihood method. Serial dependence and random intercept are allowed according to the stochastic model chosen. Missing values and unbalanced data are automatically accounted for computing the likelihood function.

Usage

```
bild(
  formula = formula(data),
  data,
  time,
  id,
  subSET,
  aggregate = FALSE,
  start = NULL,
  trace = FALSE,
  dependence = "ind",
  method = "BFGS",
  control = bildControl(),
  integrate = bildIntegrate()
)
```

Arguments

formula	a description of the model to be fitted of the form response ~ predictors.
data	a data frame containing the variables in the formula.
time	a string that matches the name of the time variable in data.
id	a string that matches the name of the id variable in data.
subSET	an optional expression indicating a subset of the rows of data to be used.
aggregate	a string that permits the user to identify the factor to be used in plot methods.
start	a vector of initial values for the nuisance parameters.
trace	logical; if TRUE, details of the nonlinear optimization are printed.
dependence	a character string stating which dependence structure to use: "ind", "MC1", "MC2", "indR", "MC1R", "MC2R". Default is "ind".
method	the optimization method used by optim . Default is "BFGS".
control	a list of control parameters for optim .
integrate	a list of algorithmic constants for numerical integration (Fortran-77/QUADPACK).

Details

The underlying methodology builds a logistic regression model for the probability that the response variable takes value 1 as a function of the covariates, taking into account that successive observations from the same individual cannot be assumed to be independent.

Value

An object of class `bild`.

References

Azzalini, A. (1994). Logistic regression for autocorrelated data with application to repeated measures. *Biometrika*, 81, 767-775. Goncalves, M. H., Cabral, M. S., and Azzalini, A. (2012). The R Package `bild` for the Analysis of Binary Longitudinal Data. *Journal of Statistical Software*, 46(9), 1-17.

Examples

```
# Example with airpollution data
data(airpollution)
air2r <- bild(wheeze~age+smoking, data=airpollution, trace=TRUE,
             time="age", aggregate=smoking, dependence="MC2R")
summary(air2r)
```

`bild-class`

Class "bild" for Results of a Maximum Likelihood Estimation

Description

This class encapsulates results of a maximum likelihood procedure and is usually created as the result of a call to `bild`.

Slots

`coefficients` Matrix. Estimated parameters.
`se` Matrix. Standard errors of estimated parameters.
`covariance` Matrix. Covariance of estimated parameters.
`correlation` Matrix. Correlation of estimated parameters.
`log.likelihood` Numeric. The value of the log likelihood.
`message` Integer. Information returned by the optimizer.
`n.cases` Numeric. Number of individual profiles used in the optimization.
`ni.cases` Numeric. Number of individual profiles in the dataset.
`aic` Numeric. The Akaike information criterion.

`residuals` Numeric. The residuals of estimated parameters.
`s.residuals` Numeric. The residuals summed over the individual profile.
`ind.probability` Numeric. The transition probabilities.
`prob.matrix` Matrix. The matrix of transition probabilities.
`Fitted` Numeric. The fitted values for the estimated parameters.
`bi.estimate` Matrix. The estimated values for the individual random effects.
`Fitted.av` Numeric. The average fitted values.
`Time` Numeric. Vector of time points.
`model.matrix` Matrix. The model matrix.
`y.matrix` Matrix. The matrix of response values.
`subset.data` Data.frame. The data subset if considered.
`y.av` Numeric. The average of the response value over an individual profile.
`f.value` Factor. Indicates the aggregation factor if present.
`call` Language. The call to "bild".

See Also

[bild-class, show](#)

<code>bildControl</code>	<i>Auxiliary for Controlling "bild" Fitting</i>
--------------------------	---

Description

Auxiliary function as user interface for bild fitting.

Usage

```
bildControl(maxit = 100, abstol = 1e-06, reltol = 1e-06)
```

Arguments

<code>maxit</code>	maximum number of iterations.
<code>abstol</code>	absolute convergence tolerance.
<code>reltol</code>	relative convergence tolerance.

Details

See R documentation of [optim](#) for details of standard default values for the remaining options not considered in `bildControl`.

Value

A list with the arguments as components.

See Also

[bild-class](#), [optim](#)

`bildIntegrate`

Auxiliary for Controlling "bild" Fitting

Description

Auxiliary function as user interface for bild fitting to set integration constants used in numerical integration.

Usage

```

bildIntegrate(
  li = -4,
  ls = 4,
  epsabs = .Machine$double.eps^0.25,
  epsrel = .Machine$double.eps^0.25,
  limit = 100,
  key = 6,
  lig = -4,
  lsg = 4
)

```

Arguments

<code>li</code>	lower limit of integration for the log-likelihood.
<code>ls</code>	upper limit of integration for the log-likelihood.
<code>epsabs</code>	absolute accuracy requested.
<code>epsrel</code>	relative accuracy requested.
<code>limit</code>	integer that gives an upperbound on the number of subintervals.
<code>key</code>	integer from 1 to 6 for choice of local integration rule (Gauss-Kronrod).
<code>lig</code>	lower limit of integration for the gradient.
<code>lsg</code>	upper limit of integration for the gradient.

Details

`bildIntegrate` returns a list of constants used to compute integrals based on a Fortran-77 subroutine `dqage` from the QUADPACK package.

The numerical integration is performed over the interval $(li * \sigma, ls * \sigma)$, where $\sigma = \exp(\omega)/2$. If integration produces errors or NaNs in the information matrix, users should adjust `li`, `ls`, `lig`, or `lsg`.

For datasets with a high number of time points (> 30), it is recommended to set integration limits to smaller values than the default.

Value

A list with the arguments as components.

See Also

[bild-class](#)

Examples

```
library(bild)
data(locust)
# Example using locust data
Integ <- bildIntegrate(li = -2.5, ls = 2.5, lig = -2.5, lsg = 2.5)
locust2r_feed1 <- bild(move ~ (time + I(time^2)) * sex, data = locust,
                      subSET = feed == "1", aggregate = sex,
                      dependence = "MC2R", integrate = Integ)
```

fitted.bild	<i>Fitted values for 'bild' objects</i>
-------------	---

Description

Fitted values for 'bild' objects

Usage

```
## S4 method for signature 'bild'
fitted(object, ...)
```

Arguments

object	an object of class bild .
...	Additional arguments.

Value

A numeric vector of the fitted values.

See Also

[bild-class](#), [fitted](#)

fixeff	<i>Extract fixed effects estimates</i>
--------	--

Description

Extract fixed effects estimates

Usage

```
## S4 method for signature 'bild'  
fixeff(object)
```

Arguments

object an object of class [bild](#).

Value

A matrix or vector containing the fixed effects estimates.

See Also

[bild-class](#)

getAIC	<i>Extract the Akaike Information Criterion</i>
--------	---

Description

Extract the Akaike Information Criterion

Usage

```
## S4 method for signature 'bild'  
getAIC(object)
```

Arguments

object an object of class [bild](#).

Value

Returns a numeric value corresponding to the AIC of the fitted model.

See Also

[bild-class](#)

getcoef	<i>Extract the coefficient estimates</i>
---------	--

Description

Extract the coefficient estimates

Usage

```
## S4 method for signature 'bild'  
getcoef(object)
```

Arguments

object an object of class [bild](#).

Value

Returns the coefficient estimates of the fitted model (a matrix).

See Also

[bild-class](#)

getLogLik	<i>Extract Log-Likelihood</i>
-----------	-------------------------------

Description

Extract Log-Likelihood

Usage

```
## S4 method for signature 'bild'  
getLogLik(object)
```

Arguments

object an object of class [bild](#).

Value

Returns a numeric value corresponding to the log-Likelihood of the fitted model.

See Also

[bild-class](#)

getVariance	<i>Extract variance estimates of random effects</i>
-------------	---

Description

These functions extract the variance estimate of the random effect ($\sigma^2 = \exp(\omega)$) from an object of class `build`.

Usage

```
## S4 method for signature 'build'
getVariance(object, se = FALSE)
```

Arguments

<code>object</code>	an object of class <code>build</code> .
<code>se</code>	logical; if TRUE, includes the standard error of the variance. If <code>se = TRUE</code> , it also includes the standard error calculated via the Delta method. <code>vareff</code> is a wrapper for <code>getVariance</code> with <code>se = FALSE</code> for backward compatibility.

Value

A data frame containing the variance estimate.

getvcov	<i>Extract variance-covariance matrix</i>
---------	---

Description

Extract variance-covariance matrix

Usage

```
## S4 method for signature 'build'
getvcov(object)
```

Arguments

<code>object</code>	an object of class <code>build</code> .
---------------------	---

Value

Returns a numeric matrix corresponding to the variance-covariance matrix of the fitted model.

See Also

[build-class](#)

glance.bild	<i>Glance at a bild object</i>
-------------	--------------------------------

Description

Glance at a fitted longitudinal model object of class `bild` to extract a single-row summary tibble with key statistics.

Usage

```
## S3 method for class 'bild'
glance(x, ...)
```

Arguments

<code>x</code>	A fitted model object of class <code>bild</code> .
<code>...</code>	Additional arguments. Not used.

Value

A `tibble::tibble` with summary statistics (number of observations, degrees of freedom/parameters, log-likelihood, AIC, and BIC).

Examples

```
library(bild)
library(generics)
data(airpollution)
air1R <- bild::bild(wheeze ~ age + smoking, data = airpollution, time = "age",
  aggregate = smoking, dependence = "MC1R")
glance(air1R)
```

locust	<i>Locust dataset</i>
--------	-----------------------

Description

This data set was presented by MacDonald and Raubenheimer (1995) and analyzes the effect of hunger on locomotory behaviour of 24 locusts (*Locusta migratoria*) observed at 161 time points.

Usage

```
locust
```

Format

A data frame with 3864 observations on the following 5 variables:

`id` a numeric vector that identifies the number of the individual profile.

`move` a numeric vector representing the response variable (1="moving", 0="not moving").

`sex` a factor with levels 1 for "male" and 0 for "female".

`time` a numeric vector that identifies the number of the time points observed.

`feed` a factor with levels 0 "no" and 1 "yes".

Source

MacDonald, I. and Raubenheimer, D. (1995). Hidden Markov models and animal behaviour. *Biometrical Journal*, 37, 701-712.

Examples

```
data(locust)
str(locust)

# Dependence="MC2" (Fast computation)
locust2_feed1 <- bild(move ~ (time + I(time^2)) * sex, data = locust,
  subSET = feed == "1", aggregate = sex, dependence = "MC2")
summary(locust2_feed1)

# Base plot diagnostics (Standard)
plot(locust2_feed1, which = 5, ylab = "probability of locomoting",
  main = "Feed=1", add.unadjusted = TRUE)

# ggplot2-based diagnostic plots (New)
library(ggplot2)
# Comparing which=5 with the base plot above
autoplot(locust2_feed1, which = 5)

# Other diagnostic plots
autoplot(locust2_feed1, which = 1)
autoplot(locust2_feed1, which = 2)
```

model.mat

Extract the fixed effects model matrix

Description

Extract the fixed effects model matrix

Usage

```
## S4 method for signature 'bild'
model.mat(object)
```

Arguments

object an object of class `bild`.

Value

Returns the fixed effects model matrix of the fitted model.

See Also

[bild-class](#)

muscatine	<i>Muscatine dataset</i>
-----------	--------------------------

Description

This example is a subset of data from the Muscatine Coronary Risk Factor Study, a longitudinal study of coronary risk factors in school children from Muscatine (Iowa, USA).

Usage

```
muscatine
```

Format

A data frame with 156 observations on the following 5 variables:

`id` identifies the number of the individual profile.

`obese` a numeric vector that identifies the obesity status (1="yes", 0="no").

`sex` a factor with levels 1 for "female" and 0 for "male".

`time` a numeric vector (1,2,3) indicating the observed time points.

`counts` a numeric vector indicating the number of times that each profile is replicated.

Source

Fitzmaurice, G. M., Laird, N. M. and Lipsitz, S. R. (1994). Analyzing incomplete longitudinal binary responses: a likelihood based approach. *Biometrics*, 38, 602-612.

Examples

```
data(muscatine)
str(muscatine)

# we decompose the time effect in orthogonal components
muscatine$time1 <- c(-1, 0, 1)
muscatine$time2 <- c(1, -2, 1)

# second order Markov Chain without random effects
musc2 <- bild(obese~(time1+time2)*sex, data=muscatine,
             time="time1", aggregate=sex, trace=TRUE, dependence="MC2")

summary(musc2)
getAIC(musc2)
getLogLik(musc2)
fitted(musc2)
```

plot-bild-method

Plot Diagnostics for 'bild' Objects (Base Graphics)

Description

Diagnostic and profile plots for a fitted bild longitudinal model object using standard R base graphics. Six plots (selectable by which) are currently available. By default, the first five are provided.

Usage

```
## S4 method for signature 'bild,missing'
plot(
  x,
  y,
  which = c(1:5),
  ylab = NULL,
  main = NULL,
  ask = prod(par("mfcol")) < length(which) && dev.interactive(),
  subSET,
  add.unadjusted = FALSE,
  ident = FALSE,
  caption = c("Residuals vs Fitted", "Residuals vs Time", "ACF residuals",
             "PACF residuals", "Individual mean profiles"),
  cex.caption = 1
)
```

Arguments

<code>x</code>	An object of class <code>build</code> .
<code>y</code>	Not used. Must be missing.
<code>which</code>	If a subset of the plots is required, specify a subset of the numbers 1:6: • 1: A plot of residuals against fitted values. • 2: A plot of standardized residuals against time. • 3: A plot of the autocorrelation function (ACF) of the residuals. • 4: A plot of the partial autocorrelation function (PACF) of the residuals. • 5: A plot for the fitted parametric model. • 6: A plot for the individual mean profile.
<code>ylab</code>	Label to some plots (<code>which=5</code> and <code>6</code>).
<code>main</code>	Title to some plots in addition to the caption (<code>which=5</code> and <code>6</code>).
<code>ask</code>	Logical expression; if TRUE, the user is asked before each plot. Defaults to <code>prod(par("mfcol")) < length(which) && dev.interactive()</code> .
<code>subSET</code>	Logical expression indicating elements to keep in individual mean profile plots: missing values are taken as FALSE. The <code>subSET</code> argument is only for option <code>which=6</code> .
<code>add.unadjusted</code>	Logical expression indicating whether or not to add the unadjusted fit for plot in <code>which=5</code> .
<code>ident</code>	Logical expression indicating whether or not to add the number of the subject to individual mean profile plots. The <code>ident</code> argument is only for option <code>which=6</code> .
<code>caption</code>	Captions to appear above the plots. Defaults to a vector of standard labels.
<code>cex.caption</code>	Controls the font size expansion factor for the caption.

Details

The option `which=5` provides the parametric fitted model if the dependence structure is "ind" (independence), "MC1" (first order Markov Chain) or "MC2" (second order Markov Chain).

When the dependence structure is "indR" (independence with random intercept), "MC1R" (first order Markov Chain with random intercept) or "MC2R" (second order Markov Chain with random intercept), the parametric adjusted fit is provided and the user can set `add.unadjusted=TRUE` to provide the unadjusted fitted curves.

The option `which=6` is used only if the random intercept is present (models ending in "R") and provides the individual mean profile plots.

Value

No return value, called for side effects (generating plots).

Methods

`signature(x="ANY", y="ANY")` Generic function.

`signature(x="build", y="missing")` Plot diagnostics for `build` object.

Examples

```

library(bild)
data(locust)
# It takes a very long time to run
str(locust)

# dependence="MC2R"
Integ <- bild::bildIntegrate(li=-2.5, ls=2.5, lig=-2.5, lsg=2.5)
locust2r_feed1 <- bild::bild(move~(time+I(time^2))*sex, data=locust,
  subSET=feed=="1", aggregate=sex, dependence="MC2R",
  integrate=Integ)

summary(locust2r_feed1)

plot(locust2r_feed1, which=5, ylab="probability of locomoting",
  add.unadjusted=TRUE)

plot(locust2r_feed1, which=6, subSET=sex=="1",
  main="sex==1 & Feed=1", ident=TRUE)

locust2r <- bild::bild(move~(time+I(time^2))*feed, data=locust,
  trace=TRUE, aggregate=feed, dependence="MC2R",
  integrate=Integ)

par(mfrow=c(2,2))
plot(locust2r, which=1)
plot(locust2r, which=2)
plot(locust2r, which=3)
plot(locust2r, which=4)
par(mfrow=c(1,1))

plot(locust2r, which=5, ylab="probability of locomoting",
  main="Feed & Unfeed groups", add.unadjusted=TRUE)

plot(locust2r, which=6, ylab="probability of locomoting",
  main="Fed & Unfed groups", ident=TRUE)

```

predict.bild

Predict Method for bild Objects

Description

Obtains predictions (link, response, or dynamic transition probabilities) from a fitted bild model object for existing or new data structures.

Usage

```
## S3 method for class 'bild'
```

```

predict(
  object,
  newdata = NULL,
  type = c("link", "response", "transition"),
  ...
)

```

Arguments

<code>object</code>	A fitted model object of class <code>bild-class</code> .
<code>newdata</code>	Optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors or probabilities from the original fit are returned.
<code>type</code>	The type of prediction required. Use "link" for the linear predictor scale, "response" for the marginal population probability scale, and "transition" for the dynamic Markov transition probabilities conditional on the recent lag history.
<code>...</code>	Additional arguments passed to or from other methods.

Value

A numeric vector of predicted values or probabilities matching the data rows.

See Also

`bild`, `bild-class`

Examples

```

library(bild)

# First-order Markov dependence (MC1)
data(airpollution)

air1 <- bild(wheeze ~ age + smoking, data = airpollution,
            time = "age", aggregate = smoking, dependence = "MC1")

# Standard marginal response prediction on original data
pred_mar <- predict(air1, type = "response")
head(pred_mar)

# Dynamic transition probabilities on new data (requires y_prev1)
new_data_air <- data.frame(
  age = c(9, 10, 11, 9, 10, 11),
  smoking = factor(c("0", "0", "0", "1", "1", "1")),
  y_prev1 = c(0, 1, 0, 1, 1, 0))

dynamic_pred_air <- predict(air1, newdata = new_data_air, type = "transition")
print(cbind(new_data_air, Prob_Transition = dynamic_pred_air))

```

```

# Second-order Markov with random effects (MC2R)
data(muscatine)
muscatine$time1 <- c(-1, 0, 1)
muscatine$time2 <- c(1, -2, 1)

Integ <- bildIntegrate(lig = -3.95, lsg = 3.95)
musc2r <- bild(obese ~ (time1 + time2) * sex, data = muscatine,
              time = "time1", start = c(1, 1, 1), dependence = "MC2R", integrate = Integ)

# Dynamic transition probabilities for second-order model (requires y_prev1 and y_prev2)
new_data_musc <- data.frame(
  time1 = c(0, 1),
  time2 = c(-2, 1),
  sex = factor(c("0", "1")),
  y_prev1 = c(1, 0),
  y_prev2 = c(0, 1))

dynamic_pred_musc <- predict(musc2r, newdata = new_data_musc, type = "transition")
print(cbind(new_data_musc, Prob_Transition = dynamic_pred_musc))

```

randeff

Extract conditional random effects

Description

Extract conditional random effects

Usage

```
## S4 method for signature 'bild'
randeff(object)
```

Arguments

object an object of class `bild`.

Value

A data frame containing the random effects estimates, if the model contains random effects. Otherwise, it issues a warning.

See Also

[bild-class](#)

show,bild-method	<i>Show a 'bild' object</i>
------------------	-----------------------------

Description

show displays a brief summary of a fitted bild model object, including the function call, the number of profiles used in the fit, the number of estimated coefficients, the maximized log-likelihood, and any convergence message.

Usage

```
## S4 method for signature 'bild'  
show(object)
```

Arguments

object An object of class [bild](#).

Value

No return value, called for side effects (printing to the console).

See Also

[bild-class](#)

summary,bild-method	<i>Summary of a 'bild' object</i>
---------------------	-----------------------------------

Description

Summary method for class bild. Computes and prints summary statistics for a fitted bild object.

Usage

```
## S4 method for signature 'bild'  
summary(object, cov = FALSE, cor = FALSE)
```

Arguments

object	an object of class bild .
cov	logical. If TRUE, prints the covariance matrix of coefficients.
cor	logical. If TRUE, prints the correlation matrix of coefficients.

Value

Returns the summary object (invisibly).

See Also

[bild](#), [bild-class](#)

summary.bild-class	Class " <i>summary.bild</i> "
--------------------	-------------------------------

Description

Summary of [bild](#) objects. Extracted from a bild object, it contains values meant for printing by the show method.

Slots

`coefficients` Matrix. Estimated parameters.

`se` Matrix. Standard errors of estimated parameters.

`covariance` Matrix. Covariance of estimated parameters.

`correlation` Matrix. Correlation of estimated parameters.

`log.likelihood` Numeric. The value of the log likelihood.

`message` Integer. Information returned by the optimizer.

`n.cases` Numeric. Number of individual profiles used in the optimization procedure.

`ni.cases` Numeric. Number of individual profiles in the dataset.

`aic` Numeric. The Akaike information criterion.

`call` Language. The call that generated the bild object.

See Also

[bild](#), [show](#)

tidy.bild	<i>Tidy a bild object into a tibble</i>
-----------	---

Description

Tidy a bild object into a tibble

Usage

```
## S3 method for class 'bild'  
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A fitted model object of class bild.
conf.int	Logical. Whether or not to include a confidence interval in the tidied output. Defaults to FALSE.
conf.level	The confidence level to use for the confidence interval if conf.int = TRUE. Defaults to 0.95.
...	Additional arguments. Not used.

Details

For parameters estimated on the log-scale (such as dependence parameters `log.psi1`, `log.psi2`) and the random effect variance parameter `omega`, `tidy.bild` automatically transforms the estimates to their natural scale (`psi1`, `psi2`, `sigma2`) via the exponential function. Consequently, their standard errors are adjusted using the Delta method, and confidence intervals are computed accordingly.

Value

A `tibble::tibble` containing columns: `term`, `estimate`, `std.error`, `statistic`, `p.value`, `conf.low`, `conf.high`.

Examples

```
library(bild)  
library(generics)  
data(airpollution)  
air1R <- bild::bild(wheeze ~ age + smoking, data = airpollution, time = "age",  
  aggregate = smoking, dependence = "MC1R")  
tidy(air1R, conf.int = TRUE)
```

vareff	<i>Extract variance estimates of random effects (wrapper)</i>
--------	---

Description

Extract variance estimates of random effects (wrapper)

Usage

```
## S4 method for signature 'bild'  
vareff(object)
```

Arguments

object an object of class [bild](#).

Value

A data frame containing the variance estimate.

See Also

[getVarVariance](#)

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