Package 'nlive'

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Type Package

Title Automated Estimation of Sigmoidal and Piecewise Linear Mixed Models

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Description Estimation of relatively complex nonlinear mixed-effects models, including the Sigmoidal Mixed Model and the Piecewise Linear Mixed Model with abrupt or smooth transition, through a single intuitive line of code and with automated generation of starting values.

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URL <https://github.com/MaudeWagner/nlive>

BugReports <https://github.com/MaudeWagner/nlive/issues>

Encoding UTF-8

LazyLoad yes

LazyData yes

RoxygenNote 7.2.3

Depends R (>= 2.10)

Repository CRAN

Imports dplyr, nlraa, sqldf, ggplot2, graphics, lcmm, saemix, Rmisc, sitar, stats, knitr, fastDummies

Suggests rmarkdown, MASS, survival, testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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R **topics documented:**

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dataCog   *Made-up longitudinal data on global cognition before death*

Description

The dataCog contains 1200 individuals with one line per visit. Repeated measures of global cognition (cognition) were collected over a maximum period of 30 years. Information on the age at death is also provided (ageDeath, ageDeath90).

Format

A data frame with 11867 observations over 1200 subjects and 5 variables:

ID subject identification number

time the retrospective (negative) time before death (in years)

cognition composite score of global cognition

ageDeath age at death (in years)

ageDeath90 age at death centered by the mean

Examples

```
summary(dataCog)
```

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nlive   *Automated Estimation of Sigmoidal and Piecewise Linear Mixed Mod-*
                         els

Description

The nlive() function allows to fit a Sigmoidal Mixed Model with 4 parameters, a Piecewise Linear
Mixed Model with abrupt change, or a Piecewise Linear Mixed Model with a smooth polynomial
transition in the context of longitudinal Gaussian outcomes. This function was designed to be intu-
itive enough to the less sophisticated users, while using recent developments such as the stochastic
approximation expectation-maximization (SAEM) algorithm for efficient estimation. It was de-
signed to optimize the initial values of the main parameters and help interpretation of the output by
providing different features such as annotated outputs and graphs.

Usage

```
nlive(
  model,
  dataset,
  ID,
  outcome,
  time,
  predictor.all = NULL,
  predictor.par1 = NULL,
  predictor.par2 = NULL,
  predictor.par3 = NULL,
  predictor.par4 = NULL,
  start = NULL,
  plot.xlabel = NULL,
  plot.ylabel = NULL,
  traj.marg = FALSE,
  traj.marg.group = NULL,
  spag.plot.title = NULL,
  traj.marg.title = NULL,
  traj.marg.group.title = NULL,
  traj.marg.group.val = NULL
)
```

Arguments

model	indicator of the model to fit (1=Sigmoidal Mixed Model, 2=Piecewise Mixed Model with abrupt change, 3=Piecewise Mixed Model with smooth transition)
dataset	data frame containing the variables ID, outcome, time, predictor.all, and predictor.par1 to predictor.par4.
ID	name of the variable representing the grouping structure specified with " (e.g., "ID" representing the unique identifier of participants).

outcome	name of the time-varying variable representing the longitudinal outcome specified with " (e.g., "outcome").
time	name of the variable representing the timescale specified with " (e.g., "time"), which can be negative or positive.
predictor.all	optional vector indicating the name of the variable(s) that the four main parameters of the model of interest will be adjusted to (e.g. predictor.all=c("X1","X2")). Default to NULL.
predictor.par1	optional vector indicating the name of the variable(s) that the first main parameter of the model of interest will be adjusted to (e.g. predictor.all=c("X1","X2")). For model 1, the first parameter = last level. For models 2 and 3, first parameter = intercept. Default to NULL.
predictor.par2	optional vector indicating the name of the variable(s) that the second main parameter of the model of interest will be adjusted to (e.g. predictor.all=c("X1","X2")). For model 1, the second parameter = initial level. For models 2 and 3, second parameter = slope before the change-point. Default to NULL.
predictor.par3	optional vector indicating the name of the variable(s) that the third main parameter of the model of interest will be adjusted to (e.g. predictor.all=c("X1","X2"). For model 1, the third parameter = midpoint. For models 2 and 3, third parameter = slope after the change-point. Default to NULL.
predictor.par4	optional vector indicating the name of the variable(s) that the fourth main parameter of the model of interest will be adjusted to (e.g. predictor.all=c("X1","X2")). For model 1, the fourth parameter is the Hill slope. For models 2 and 3, the fourth parameter is the changepoint. Default to NULL.
start	optional vector to override the specification of the four initial values for the main parameters. For model 1, the values must be included in the following order: last level, initial level, midpoint, Hill slope. For models 2 and 3, the values must be included in the following order: intercept, slope before the changepoint, slope after the changepoint, changepoint. Default to NULL.
plot.xlabel	optional text for the title of the x-axis of all plots
plot.ylabel	optional text for the title of the y-axis of all plots
traj.marg	optional logical indicating if the marginal estimated trajectory should be plotted for the most common profile of covariates, if any. Default to FALSE.
traj.marg.group	
	optional name of the grouping variable listed in one of the predictor arguments to plot and contrast the estimated marginal trajectories between two specific groups, specified with " (e.g., traj.marg.group="X1"). If the variable is binary, the trajectories are contrasted between the two groups of interest. If the variable is continuous, the 10th and 90th percentile values will automatically be considered. The default value is NULL.
spag.plot.title	
	optional text for the title of the spaghetti plot
traj.marg.title	
	optional text for the title of the marginal estimated trajectory
traj.marg.group.title	
	optional text for the title of the marginal estimated trajectories contrasted between groups

```
traj.marg.group.val
```

optional vector that can be used when *traj.marg.group* receives a quantitative variable and that allows to manually specify two percentile values to be considered for contrasting the traj.marg.group. The two values must be between 0 and 1 (e.g., traj.marg.group.val=c(0.2,0.8); for percentiles 20th and 80th). Default to 10th and 90th percentiles (i.e., traj.marg.group.val=c(0.1,0.9)).

Details

CAUTIONS REGARDING THE USE OF THE FUNCTION

traj.marg: if "TRUE", this argument automatically plots the estimated marginal trajectories of the longitudinal outcome for the most common profile of covariates, if any (i.e., ref "1" for binary variables and mean values for continuous variables). Thus, users must ensure that continuous variables are centered on the mean.

Value

An object of class SaemixObject (from the existing *saemix* R package) containing the results of the fit of the data by the non-linear mixed *model* of interest. The *nlive* function automatically provides (i) a spaghetti plot of the observed outcome for 70 randomly selected statistical units in the dataset and (ii) the standard *saemix* output, including the fixed effects estimates, the variance of random effects, and Likelihood of the fitted *model*. The outputs are printed on the terminal and the numerical and graphical outputs are stored in a directory.

Author(s)

Maude Wagner, Ana W. Capuano, Emmanuelle Comets

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References

Capuano AW, Wagner M. nlive: an R package to facilitate the application of the sigmoidal and random changepoint mixed models. BMC Medical Research Methodology. 2023;23(1):257. van den Hout A, Muniz-Terrera G, Matthews F. Smooth random change point models. Statistics in Medicine. 2011;30(6):599-610. Comets E, Lavenu A, Lavielle MM. Parameter estimation in non-linear mixed effect models using saemix, an R implementation of the SAEM algorithm. Journal of Statistical Software. 2017;80(3):1-41.

See Also

nlive.smm, nlive.pmma, nlive.pmms

Examples

```
#### Fitting a sigmoidal mixed model - with no covariate
## Not run:
head(dataCog)
requireNamespace('nlraa')
smm.fit = nlive(model=1, dataset=dataCog, ID="ID", outcome="cognition", time="time")
```

```
## End(Not run)

#### plot(smm.fit): diagnostic plots to assess the goodness-of-fit of smm.fit
#### psi(smm.fit): estimates of individual parameters

#### Fitting a piecewise mixed model with abrupt change - with no covariate
## Not run:
pmm.abrupt.fit = nlive(model=2, dataset=dataCog, ID="ID", outcome="cognition", time="time")

## End(Not run)
#### plot(pmm.abrupt.fit): diagnostic plots to assess the goodness-of-fit of pmm.abrupt.fit
#### psi(pmm.abrupt.fit): estimates of individual parameters


#### Fitting a piecewise mixed model with smooth change - with all parameters
#### adjusted for ageDeath90. Here, the nlive() function will also provide a
#### plot of the estimated marginal trajectory in the whole study sample.
## Not run:
pmm.smooth.fit = nlive(model=3, dataset=dataCog, ID="ID", outcome="cognition", time="time",
predictor.all = c("ageDeath90"), traj.marg = TRUE)

## End(Not run)
#### plot(pmm.smooth.fit): diagnostic plots to assess the goodness-of-fit of the model
#### psi(pmm.smooth.fit): estimates of individual parameters
```

---

nlive.inspect   *Generation of key plots for a longitudinal variable of interest*

Description

The nlive.inspect() function allows to generate basic graphs to describe the longitudinal observed measures of a variable of interest in the dataset

Usage

```
nlive.inspect(
  dataset,
  ID,
  variable,
  time,
  plot.xlabel = NULL,
  plot.ylabel = NULL,
  spag.plot.title = NULL
)
```

Arguments

dataset	data frame containing the ID, variable, and time.
ID	name of the variable representing the grouping structure specified with " (e.g., "ID" representing the unique identifier of participants).
variable	name of the time-varying variable of interest specified with " (e.g., "variable").
time	name of the variable representing the timescale specified with " (e.g., "time"). Can be negative or positive.
plot.xlabel	optional text for the title of the x-axis of all plots.
plot.ylabel	optional text for the title of the y-axis of all plots.
spag.plot.title	
	optional text for the title of the spaghetti plot.

Value

The *nlive.inspect* function automatically provides (i) an histogram of all the repeated measures of the variable available over time, (ii) a spaghetti plot of the longitudinal observed variable for 70 randomly selected statistical units, (iii) repeated boxplots of the longitudinal observed variable for each time unit. The outputs are printed on the terminal and the numerical and graphical outputs are stored in a directory

Author(s)

Maude Wagner, Ana W. Capuano, Emmanuelle Comets

<maude_wagner@rush.edu>

References

Capuano AW, Wagner M. nlive: an R package to facilitate the application of the sigmoidal and random changepoint mixed models. BMC Medical Research Methodology. 2023;23(1):257. Hadley Wickham (2016). ggplot2: elegant graphics for data analysis. Springer.

Examples

```
## Not run:
nlive.inspect(dataset=dataCog, ID="ID", variable="cognition", time="time")

## End(Not run)
```

---

nlive.pmma   *Automated Estimation of the Piecewise Linear Mixed Model with*
                                    Abrupt Change

Description

The nlive.pmma() function allows to fit a Piecewise Linear Mixed Models with abrupt change in the
context of longitudinal Gaussian outcomes. This function was designed to be intuitive enough to
the less sophisticated users, while using recent developments such as the stochastic approximation
expectation-maximization (SAEM) algorithm for efficient estimation. It was designed to optimize
the initial values of the main parameters and help interpretation of the output by providing different
features such as annotated outputs and graphs.

Usage

```
nlive.pmma(
  dataset,
  ID,
  outcome,
  time,
  var.all = NULL,
  var.last.level = NULL,
  var.slope1 = NULL,
  var.slope2 = NULL,
  var.changepoint = NULL,
  start = NULL,
  plot.xlabel = NULL,
  plot.ylabel = NULL,
  traj.marg = FALSE,
  traj.marg.group = NULL,
  traj.marg.title = NULL,
  traj.marg.group.title = NULL,
  traj.marg.group.val = NULL
)
```

Arguments

dataset	data frame containing the variables ID, outcome, time, var.all, and all other var. arguments.
ID	name of the variable representing the grouping structure specified with " (e.g., "ID" representing the unique identifier of participants).
outcome	name of the time-varying variable representing the longitudinal outcome specified with " (e.g., "outcome").
time	name of the variable representing the timescale specified with " (e.g., "time"), which can be negative or positive.

var.all optional vector indicating the name of the variable(s) that the four main parameters of the model will be adjusted to (e.g. var.all=c("X1","X2")). Default to NULL.

var.last.level optional vector indicating the name of the variable(s) that the last level parameter of the model of interest will be adjusted to (e.g. var.last.level=c("X1","X2")). Default to NULL.

var.slope1 optional vector indicating the name of the variable(s) that the slope1 (before changepoint) parameter of the model of interest will be adjusted to (e.g. var.slope1=c("X1","X2"). Default to NULL.

var.slope2 optional vector indicating the name of the variable(s) that the slope2 (after changepoint) parameter of the model of interest will be adjusted to (e.g. var.slope2=c("X1","X2"). Default to NULL.

var.changepoint
optional vector indicating the name of the variable(s) that the changepoint parameter of the model of interest will be adjusted to (e.g. var.changepoint=c("X1","X2")). Default to NULL.

start optional vector to override the specification of the four initial values for the main parameters - values must be included in the following order: intercept, slope before the changepoint, slope after the changepoint, changepoint. Default to NULL.

plot.xlabel optional text for the title of the x-axis of all plots.

plot.ylabel optional text for the title of the y-axis of all plots.

traj.marg optional logical indicating if the marginal estimated trajectory should be plotted for the most common profile of covariates, if any. Default to FALSE.

traj.marg.group
optional name of the grouping variable listed in one of the predictor arguments to plot and contrast the estimated marginal trajectories between two specific groups, specified with " (e.g., traj.marg.group="X1"). If the variable is binary, the trajectories are contrasted between the two groups of interest. If the variable is continuous, the 10th and 90th percentile values will automatically be considered. The default value is NULL.

traj.marg.title
optional text for the title of the marginal estimated trajectory

traj.marg.group.title
optional text for the title of the marginal estimated trajectories contrasted between groups

traj.marg.group.val
optional vector that can be used when *traj.marg.group* receives a quantitative variable and that allows to manually specify two percentile values to be considered for contrasting the traj.marg.group. The two values must be between 0 and 1 (e.g., traj.marg.group.val=c(0.2,0.8); for percentiles 20th and 80th). Default to 10th and 90th percentiles (i.e., traj.marg.group.val=c(0.1,0.9)).

Details

CAUTIONS REGARDING THE USE OF THE FUNCTION

traj.marg: if "TRUE", this argument automatically plots the estimated marginal trajectories of the longitudinal outcome for the most common profile of covariates, if any (i.e., ref "1" for binary variables and mean values for continuous variables). Thus, users must ensure that continuous variables are centered on the mean.

Value

An object of class SaemixObject (from the existing *saemix* R package) containing the results of the fit of the data by the PMM-abrupt. The *nlive.pmma* function automatically provides the standard saemix output, including the fixed effects estimates, the variance of random effects, and Likelihood of the fitted model. The outputs are printed on the terminal and the numerical and graphical outputs are stored in a directory.

Author(s)

Maude Wagner, Ana W. Capuano, Emmanuelle Comets

<maude_wagner@rush.edu>

References

Capuano AW, Wagner M. nlive: an R package to facilitate the application of the sigmoidal and random changepoint mixed models. BMC Medical Research Methodology. 2023;23(1):257. van den Hout A, Muniz-Terrera G, Matthews F. Smooth random change point models. Statistics in Medicine. 2011;30(6):599-610. Comets E, Lavenu A, Lavielle MM. Parameter estimation in nonlinear mixed effect models using saemix, an R implementation of the SAEM algorithm. Journal of Statistical Software. 2017;80(3):1-41.

Examples

```
#### Fitting a piecewise mixed model with abrupt change - with no covariate
## Not run:
head(dataCog)
pmm.abrupt.fit = nlive.pmma(dataset=dataCog, ID="ID", outcome="cognition", time="time")

## End(Not run)
#### plot(pmm.abrupt.fit): diagnostic plots to assess the goodness-of-fit of pmm.abrupt.fit
#### psi(pmm.abrupt.fit): estimates of individual parameters
```

---

nlive.pmms   *Automated Estimation of the Piecewise Linear Mixed Model with Smooth Change*

Description

The nlive.pmms() function allows to fit a Piecewise Linear Mixed Models with smooth change in the context of longitudinal Gaussian outcomes. This function was designed to be intuitive enough to the less sophisticated users, while using recent developments such as the stochastic approximation expectation-maximization (SAEM) algorithm for efficient estimation. It was designed to optimize the initial values of the main parameters and help interpretation of the output by providing different features such as annotated outputs and graphs.

Usage

```
nlive.pmms(
  dataset,
  ID,
  outcome,
  time,
  var.all = NULL,
  var.last.level = NULL,
  var.slope1 = NULL,
  var.slope2 = NULL,
  var.changepoint = NULL,
  start = NULL,
  plot.xlabel = NULL,
  plot.ylabel = NULL,
  traj.marg = FALSE,
  traj.marg.group = NULL,
  traj.marg.title = NULL,
  traj.marg.group.title = NULL,
  traj.marg.group.val = NULL
)
```

Arguments

dataset	data frame containing the variables ID, outcome, time, var.all, and all other var. arguments.
ID	name of the variable representing the grouping structure specified with " (e.g., "ID" representing the unique identifier of participants).
outcome	name of the time-varying variable representing the longitudinal outcome specified with " (e.g., "outcome").
time	name of the variable representing the timescale specified with " (e.g., "time"), which can be negative or positive.
var.all	optional vector indicating the name of the variable(s) that the four main parameters of the model will be adjusted to (e.g. var.all=c("X1","X2")). Default to NULL.
var.last.level	optional vector indicating the name of the variable(s) that the last level parameter of the model of interest will be adjusted to (e.g. var.last.level=c("X1","X2")). Default to NULL.

var.slope1	optional vector indicating the name of the variable(s) that the slope1 (before changepoint) parameter of the model of interest will be adjusted to (e.g. var.slope1=c("X1","X2"). Default to NULL.
var.slope2	optional vector indicating the name of the variable(s) that the slope2 (after change-point) parameter of the model of interest will be adjusted to (e.g. var.slope2=c("X1","X2"). Default to NULL.
var.changepoint	
	optional vector indicating the name of the variable(s) that the changepoint parameter of the model of interest will be adjusted to (e.g. var.changepoint=c("X1","X2")). Default to NULL.
start	optional vector to override the specification of the four initial values for the main parameters - values must be included in the following order: intercept, slope before the changepoint, slope after the changepoint, changepoint. Default to NULL.
plot.xlabel	optional text for the title of the x-axis of all plots
plot.ylabel	optional text for the title of the y-axis of all plots
traj.marg	optional logical indicating if the marginal estimated trajectory should be plotted for the most common profile of covariates, if any. Default to FALSE.
traj.marg.group	
	optional name of the grouping variable listed in one of the predictor arguments to plot and contrast the estimated marginal trajectories between two specific groups, specified with " (e.g., traj.marg.group="X1"). If the variable is binary, the trajectories are contrasted between the two groups of interest. If the variable is continuous, the 10th and 90th percentile values will automatically be considered. The default value is NULL.
traj.marg.title	
	optional text for the title of the marginal estimated trajectory
traj.marg.group.title	
	optional text for the title of the marginal estimated trajectories contrasted between groups
traj.marg.group.val	
	optional vector that can be used when *traj.marg.group* receives a quantitative variable and that allows to manually specify two percentile values to be considered for contrasting the traj.marg.group. The two values must be between 0 and 1 (e.g., traj.marg.group.val=c(0.2,0.8); for percentiles 20th and 80th). Default to 10th and 90th percentiles (i.e., traj.marg.group.val=c(0.1,0.9)).

Details

CAUTIONS REGARDING THE USE OF THE FUNCTION

traj.marg: if "TRUE", this argument automatically plots the estimated marginal trajectories of the longitudinal outcome for the most common profile of covariates, if any (i.e., ref "1" for binary variables and mean values for continuous variables). Thus, users must ensure that continuous variables are centered on the mean.

Value

An object of class SaemixObject (from the existing *saemix* R package) containing the results of the fit of the data by the PMM-smooth. The *nlive.pmms* function automatically provides the standard saemix output, including the fixed effects estimates, the variance of random effects, and Likelihood of the fitted model. The outputs are printed on the terminal and the numerical and graphical outputs are stored in a directory.

Author(s)

Maude Wagner, Ana W. Capuano, Emmanuelle Comets

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References

Capuano AW, Wagner M. nlive: an R package to facilitate the application of the sigmoidal and random changepoint mixed models. BMC Medical Research Methodology. 2023;23(1):257. van den Hout A, Muniz-Terrera G, Matthews F. Smooth random change point models. Statistics in Medicine. 2011;30(6):599-610. Comets E, Lavenu A, Lavielle MM. Parameter estimation in nonlinear mixed effect models using saemix, an R implementation of the SAEM algorithm. Journal of Statistical Software. 2017;80(3):1-41.

Examples

```
#### Fitting a piecewise mixed model with abrupt change - with no covariate
## Not run:
head(dataCog)
pmm.smooth.fit = nlive.pmms(dataset=dataCog, ID="ID", outcome="cognition", time="time")

## End(Not run)
#### plot(pmm.smooth.fit): diagnostic plots to assess the goodness-of-fit of pmm.smooth.fit
#### psi(pmm.smooth.fit): estimates of individual parameters
```

---

nlive.smm   *Automated Estimation of the Sigmoidal Mixed Model*

Description

The *nlive.smm()* function allows to fit a Sigmoidal Mixed Model with 4 parameters in the context of longitudinal Gaussian outcomes. This function was designed to be intuitive enough to the less sophisticated users, while using recent developments such as the stochastic approximation expectation-maximization (SAEM) algorithm for efficient estimation. It was designed to optimize the initial values of the main parameters and help interpretation of the output by providing different features such as annotated outputs and graphs.

Usage

```
nlive.smm(
  dataset,
  ID,
  outcome,
  time,
  var.all = NULL,
  var.first.level = NULL,
  var.last.level = NULL,
  var.midpoint = NULL,
  var.Hslope = NULL,
  start = NULL,
  plot.xlabel = NULL,
  plot.ylabel = NULL,
  traj.marg = FALSE,
  traj.marg.group = NULL,
  traj.marg.title = NULL,
  traj.marg.group.title = NULL,
  traj.marg.group.val = NULL
)
```

Arguments

`dataset`	data frame containing the variables ID, outcome, time, var.all, and all other var. arguments.
`ID`	name of the variable representing the grouping structure specified with " (e.g., "ID" representing the unique identifier of participants).
`outcome`	name of the time-varying variable representing the longitudinal outcome specified with " (e.g., "outcome").
`time`	name of the variable representing the timescale specified with " (e.g., "time"), which can be negative or positive.
`var.all`	optional vector indicating the name of the variable(s) that the four main parameters of the model will be adjusted to (e.g. var.all=c("X1","X2")). Default to NULL.
`var.first.level`	
	optional vector indicating the name of the variable(s) that the first level parameter of the model will be adjusted to (e.g. var.first.level=c("X1","X2")). Default to NULL.
`var.last.level`	optional vector indicating the name of the variable(s) that the last level parameter of the model of interest will be adjusted to (e.g. var.last.level=c("X1","X2")). Default to NULL.
`var.midpoint`	optional vector indicating the name of the variable(s) that the third main parameter of the model of interest will be adjusted to (e.g. var.midpoint=c("X1","X2"). Default to NULL.
`var.Hslope`	optional vector indicating the name of the variable(s) that the fourth main parameter of the model of interest will be adjusted to (e.g. var.Hslope=c("X1","X2")). Default to NULL.

start	optional vector to override the specification of the four initial values for the main parameters - values must be included in the following order: last level, initial level, midpoint, Hill slope. Default to NULL.
plot.xlabel	optional text for the title of the x-axis of all plots
plot.ylabel	optional text for the title of the y-axis of all plots
traj.marg	optional logical indicating if the marginal estimated trajectory should be plotted for the most common profile of covariates, if any. Default to FALSE.
traj.marg.group	optional name of the grouping variable listed in one of the predictor arguments to plot and contrast the estimated marginal trajectories between two specific groups, specified with " (e.g., traj.marg.group="X1"). If the variable is binary, the trajectories are contrasted between the two groups of interest. If the variable is continuous, the 10th and 90th percentile values will automatically be considered. The default value is NULL.
traj.marg.title	optional text for the title of the marginal estimated trajectory
traj.marg.group.title	optional text for the title of the marginal estimated trajectories contrasted between groups
traj.marg.group.val	optional vector that can be used when *traj.marg.group* receives a quantitative variable and that allows to manually specify two percentile values to be considered for contrasting the traj.marg.group. The two values must be between 0 and 1 (e.g., traj.marg.group.val=c(0.2,0.8); for percentiles 20th and 80th). Default to 10th and 90th percentiles (i.e., traj.marg.group.val=c(0.1,0.9)).

Details

CAUTIONS REGARDING THE USE OF THE FUNCTION

traj.marg: if "TRUE", this argument automatically plots the estimated marginal trajectories of the longitudinal outcome for the most common profile of covariates, if any (i.e., ref "1" for binary variables and mean values for continuous variables). Thus, users must ensure that continuous variables are centered on the mean.

Value

An object of class SaemixObject (from the existing *saemix* R package) containing the results of the fit of the data by the SMM. The *nlive.smm* function automatically provides the standard saemix output, including the fixed effects estimates, the variance of random effects, and Likelihood of the fitted model. The outputs are printed on the terminal and the numerical and graphical outputs are stored in a directory.

Author(s)

Maude Wagner, Ana W. Capuano, Emmanuelle Comets

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References

Capuano AW, Wagner M. nlive: an R package to facilitate the application of the sigmoidal and random changepoint mixed models. BMC Medical Research Methodology. 2023;23(1):257. van den Hout A, Muniz-Terrera G, Matthews F. Smooth random change point models. Statistics in Medicine. 2011;30(6):599-610. Comets E, Lavenu A, Lavielle MM. Parameter estimation in nonlinear mixed effect models using saemix, an R implementation of the SAEM algorithm. Journal of Statistical Software. 2017;80(3):1-41.

Examples

```
#### Fitting a sigmoidal mixed model - with no covariate
## Not run:
head(dataCog)
requireNamespace('nlraa')
smm.fit = nlive.smm(dataset=dataCog, ID="ID", outcome="cognition", time="time")

## End(Not run)
#### plot(smm.fit): diagnostic plots to assess the goodness-of-fit of smm.fit
#### psi(smm.fit): estimates of individual parameters
```

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