

Package: nlmixr2extra (via r-universe)

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Title Nonlinear Mixed Effects Models in Population PK/PD, Extra Support Functions

Version 3.0.0

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Description Fit and compare nonlinear mixed-effects models in differential equations with flexible dosing information commonly seen in pharmacokinetics and pharmacodynamics (Almquist, Leander, and Jirstrand 2015 <[doi:10.1007/s10928-015-9409-1](https://doi.org/10.1007/s10928-015-9409-1)>). Differential equation solving is by compiled C code provided in the 'rxode2' package (Wang, Hallow, and James 2015 <[doi:10.1002/psp4.12052](https://doi.org/10.1002/psp4.12052)>). This package is for support functions like preconditioned fits <[doi:10.1208/s12248-016-9866-5](https://doi.org/10.1208/s12248-016-9866-5)>, bootstrap and stepwise covariate selection.

Depends R (>= 4.0)

License GPL (>= 3)

URL <https://nlmixr2.github.io/nlmixr2extra/>,
<https://github.com/nlmixr2/nlmixr2extra/>

BugReports <https://github.com/nlmixr2/nlmixr2extra/issues/>

Imports checkmate, cli (>= 3.4.0), crayon, data.table, digest, dplyr, ggplot2, ggtext, knitr, lotri, methods, nlme, nlmixr2est (>= 2.1.1), Rcpp, rxode2 (>= 2.0.10), stats, symengine, utils

Suggests brms, nlmixr2data, testthat (>= 3.0.0), withr, devtools

LinkingTo Rcpp, RcppArmadillo

Biarch true

Config/testthat/edition 3

Encoding UTF-8

NeedsCompilation yes

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

LazyData true

Repository <https://nlmixr2.r-universe.dev>

RemoteUrl <https://github.com/nlmixr2/nlmixr2extra>

RemoteRef HEAD

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adaptiveLassoCoefficients

Return Adaptive lasso coefficients after finding optimal t

Description

Return Adaptive lasso coefficients after finding optimal t

Usage

```
adaptiveLassoCoefficients(
  fit,
  varsVec,
  covarsVec,
  catvarsVec,
  constraint = 1e-08,
  stratVar = NULL,
  ...
)
```

Arguments

<code>fit</code>	nlmixr2 fit.
<code>varsVec</code>	character vector of variables that need to be added
<code>covarsVec</code>	character vector of covariates that need to be added
<code>catvarsVec</code>	character vector of categorical covariates that need to be added
<code>constraint</code>	theta cutoff. below cutoff then the theta will be fixed to zero.
<code>stratVar</code>	A variable to stratify on for cross-validation.
<code>...</code>	Other parameters to be passed to <code>optimalTvalueLasso</code>

Value

return data frame of final lasso coefficients

Author(s)

Vishal Sarsani

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}
```

```

}

d <- nlmixr2data::theo_sd
d$SEX <-0
d$SEX[d$ID<=6] <-1

fit <-
  nlmixr2(
    one.cmt, d,
    est = "saem",
    control = list(print = 0)
  )
varsVec <- c("ka","cl","v")
covarsVec <- c("WT")
catvarsVec <- c("SEX")

# Adaptive Lasso coefficients:

lassoDf <- adaptivelassoCoefficients(fit, varsVec, covarsVec, catvarsVec)

## End(Not run)

```

addCatCovariates	<i>Make dummy variable cols and updated covarsVec</i>
------------------	---

Description

Make dummy variable cols and updated covarsVec

Usage

```
addCatCovariates(data, covarsVec, catcovarsVec)
```

Arguments

data	data frame used in the analysis
covarsVec	character vector of covariates that need to be added
catcovarsVec	character vector of categorical covariates that need to be added

Value

return updated Data along with the updated covarsVec

Author(s)

Vishal Sarsani

addorremoveCovariate *Add covariate*

Description

Add covariate

Usage

```
addorremoveCovariate(ui, varName, covariate, add = TRUE)
```

Arguments

ui	compiled rxode2 nlmir2 model or fit
varName	the variable name to which the given covariate is to be added
covariate	the covariate that needs string to be constructed
add	boolean indicating if the covariate needs to be added or removed.

Author(s)

Matthew Fidler, Vishal Sarsani

adjustedlassoCoefficients
Return Adjusted adaptive lasso coefficients after finding optimal t

Description

Return Adjusted adaptive lasso coefficients after finding optimal t

Usage

```
adjustedlassoCoefficients(
  fit,
  varsVec,
  covarsVec,
  catvarsVec,
  constraint = 1e-08,
  stratVar = NULL,
  ...
)
```

Arguments

<code>fit</code>	nlmixr2 fit.
<code>varsVec</code>	character vector of variables that need to be added
<code>covarsVec</code>	character vector of covariates that need to be added
<code>catvarsVec</code>	character vector of categorical covariates that need to be added
<code>constraint</code>	theta cutoff. below cutoff then the theta will be fixed to zero.
<code>stratVar</code>	A variable to stratify on for cross-validation.
<code>...</code>	Other parameters to be passed to <code>optimalTvalueLasso</code>

Value

return data frame of final lasso coefficients

Author(s)

Vishal Sarsani

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

d <- nlmixr2data::theo_sd
d$SEX <- 0
d$SEX[d$ID <= 6] <- 1

fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))
varsVec <- c("ka", "cl", "v")
covarsVec <- c("WT")
catvarsVec <- c("SEX")

# Adaptive Lasso coefficients:
```

```
lassoDf <- adjustedlassoCoefficients(fit,varsVec,covarsVec,catvarsVec)

## End(Not run)
```

backwardSearch	<i>Backward covariate search</i>
----------------	----------------------------------

Description

Backward covariate search

Usage

```
backwardSearch(
  varsVec,
  covarsVec,
  catvarsVec = NULL,
  fitorig,
  fitupdated,
  pVal = 0.01,
  reFitCovars = FALSE,
  outputDir,
  restart = FALSE
)
```

Arguments

varsVec	character vector of variables that need to be added
covarsVec	character vector of covariates that need to be added
catvarsVec	character vector of categorical covariates that need to be added
fitorig	the original 'fit' object before forward search
fitupdated	the updated 'fit' object, if any, after the forward search
pVal	p-value that should be used for selecting covariates in the forward search
reFitCovars	if the covariates should be added before performing backward search - useful for directly performing backward search without forward search; default is FALSE
outputDir	the name of the output directory that stores the covariate search result
restart	a boolean that controls if the search should be restarted; default is FALSE

Value

returns the updated 'fit' object at the end of the backward search and a table of information for all the covariates tested

Author(s)

Vipul Mann, Matthew Fidler, Vishal Sarsani

bootplot	<i>Produce delta objective function for bootstrap</i>
----------	---

Description

Produce delta objective function for bootstrap

Usage

```
bootplot(x, ...)

## S3 method for class 'nlmixr2FitCore'
bootplot(x, ...)
```

Arguments

x	fit object
...	other parameters

Value

Fit traceplot or nothing.

Author(s)

Vipul Mann, Matthew L. Fidler

References

R Niebecker, MO Karlsson. (2013) *Are datasets for NLME models large enough for a bootstrap to provide reliable parameter uncertainty distributions?* PAGE 2013. <https://www.page-meeting.org/?abstract=2899>

bootstrapFit	<i>Bootstrap nlmixr2 fit</i>
--------------	------------------------------

Description

Bootstrap input dataset and rerun the model to get confidence bounds and aggregated parameters

Usage

```
bootstrapFit(
  fit,
  nboot = 200,
  nSampIndiv,
  stratVar,
  stdErrType = c("perc", "sd", "se"),
  ci = 0.95,
  pvalues = NULL,
  restart = FALSE,
  plotHist = FALSE,
  fitName = as.character(substitute(fit))
)
```

Arguments

<code>fit</code>	the nlmixr2 fit object
<code>nboot</code>	an integer giving the number of bootstrapped models to be fit; default value is 200
<code>nSampIndiv</code>	an integer specifying the number of samples in each bootstrapped sample; default is the number of unique subjects in the original dataset
<code>stratVar</code>	Variable in the original dataset to stratify on; This is useful to distinguish between sparse and full sampling and other features you may wish to keep distinct in your bootstrap
<code>stdErrType</code>	This gives the standard error type for the updated standard errors; The current possibilities are: "perc" which gives the standard errors by percentiles (default), "sd" which gives the standard errors by the using the normal approximation of the mean with standard deviation, or "se" which uses the normal approximation with standard errors calculated with nSampIndiv
<code>ci</code>	Confidence interval level to calculate. Default is 0.95 for a 95 percent confidence interval
<code>pvalues</code>	a vector of pvalues indicating the probability of each subject to get selected; default value is NULL implying that probability of each subject is the same
<code>restart</code>	A boolean to try to restart an interrupted or incomplete bootstrap. By default this is FALSE
<code>plotHist</code>	A boolean indicating if a histogram plot to assess how well the bootstrap is doing. By default this is turned off (FALSE)
<code>fitName</code>	is the fit name that is used for the name of the bootstrap files. By default it is the fit provided though it could be something else.

Value

Nothing, called for the side effects; The original fit is updated with the bootstrap confidence bands

Author(s)

Vipul Mann, Matthew Fidler

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- 1; label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

fit <- nlmixr2(one.cmt, nlmixr2data::theo_sd, est = "saem", control = list(print = 0))

withr::with_tempdir({ # Run example in temp dir

  bootstrapFit(fit, nboot = 5, restart = TRUE) # overwrites any of the existing data or model files
  bootstrapFit(fit, nboot = 7) # resumes fitting using the stored data and model files

  # Note this resumes because the total number of bootstrap samples is not 10

  bootstrapFit(fit, nboot=10)

  # Note the bootstrap standard error and variance/covariance matrix is retained.
  # If you wish to switch back you can change the covariance matrix by

  nlmixr2est::setCov(fit, "linFim")

  # And change it back again

  nlmixr2est::setCov(fit, "boot10")

  # This change will affect any simulations with uncertainty in their parameters

  # You may also do a chi-square diagnostic plot check for the bootstrap with
  bootplot(fit)
})

## End(Not run)
```

Description

Build covInfo list from varsVec and covarsVec

Usage

```
buildcovInfo(varsVec, covarsVec)
```

Arguments

varsVec	character vector of variables that need to be added
covarsVec	character vector of covariates that need to be added

Value

covInfo list of covariate info

Author(s)

Vishal Sarsani

buildupatedUI

Build updated from the covariate and variable vector list

Description

Build updated from the covariate and variable vector list

Usage

```
buildupatedUI(ui, varsVec, covarsVec, add = TRUE, indep = FALSE)
```

Arguments

ui	compiled rxode2 nlmir2 model or fit
varsVec	character vector of variables that need to be added
covarsVec	character vector of covariates that need to be added
add	boolean indicating if the covariate needs to be added or removed
indep	a boolean indicating if the covariates should be added independently, or sequentially (append to the previous model). only applicable to adding covariate

Value

updated ui with added covariates

Author(s)

Vishal Sarsani

covarSearchAuto	<i>Stepwise Covariate Model-selection (SCM) method</i>
-----------------	--

Description

Stepwise Covariate Model-selection (SCM) method

Usage

```
covarSearchAuto(
  fit,
  varsVec,
  covarsVec,
  pVal = list(fwd = 0.05, bck = 0.01),
  catvarsVec = NULL,
  searchType = c("scm", "forward", "backward"),
  restart = FALSE
)
```

Arguments

<code>fit</code>	an nlmixr2 'fit' object
<code>varsVec</code>	a list of candidate variables to which the covariates could be added
<code>covarsVec</code>	a list of candidate covariates that need to be tested
<code>pVal</code>	a named list with names 'fwd' and 'bck' for specifying the p-values for the forward and backward searches, respectively
<code>catvarsVec</code>	character vector of categorical covariates that need to be added
<code>searchType</code>	one of 'scm', 'forward' and 'backward' to specify the covariate search method; default is 'scm'
<code>restart</code>	a boolean that controls if the search should be restarted; default is FALSE

Value

A list summarizing the covariate selection steps and output; This list has the "summaryTable" for the overall summary of the covariate selection as well as "resFwd" for the forward selection method and "resBck" for the backward selection method.

Author(s)

Vipul Mann, Matthew Fidler, Vishal Sarsani

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

fit <- nlmixr2(one.cmt, nlmixr2data::theo_sd, est = "saem", control = list(print = 0))
rxode2::.rxWithWd(tempdir(), {# with temporary directory

auto1 <- covarSearchAuto(fit, varsVec = c("ka", "cl"),
  covarsVec = c("WT"))

})

## Note that this didn't include sex, add it to dataset and restart model

d <- nlmixr2data::theo_sd
d$SEX <- 0
d$SEX[d$ID<=6] <- 1

fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))

# This would restart if for some reason the search crashed:

rxode2::.rxWithWd(tempdir(), {# with temporary directory

auto2 <- covarSearchAuto(fit, varsVec = c("ka", "cl"), covarsVec = c("WT"),
  catvarsVec= c("SEX"), restart = TRUE)

auto3 <- covarSearchAuto(fit, varsVec = c("ka", "cl"), covarsVec = c("WT"),
  catvarsVec= c("SEX"), restart = TRUE,
  searchType = "forward")

})

## End(Not run)
```

fixedControl	<i>Control options for fixed-value likelihood profiling</i>
--------------	---

Description

Control options for fixed-value likelihood profiling

Usage

```
fixedControl()
```

Value

A validated list of control options for fixed-value likelihood profiling

See Also

[profileFixed\(\)](#)

Other Profiling: [llpControl\(\)](#), [profile.nlmixr2FitCore\(\)](#), [profileFixed\(\)](#), [profileLlp\(\)](#), [profileNlmixr2FitCoreRet\(\)](#)

foldgen	<i>Stratified cross-validation fold generator function, inspired from the caret</i>
---------	---

Description

Stratified cross-validation fold generator function, inspired from the caret

Usage

```
foldgen(data, nfold = 5, stratVar = NULL)
```

Arguments

data	data frame used in the analysis
nfold	number of k-fold cross validations. Default is 5
stratVar	Stratification Variable. Default is NULL and ID is used for CV

Value

return data.frame with the fold column attached

Author(s)

Vishal Sarsani, caret

Examples

```
d <- nlmixr2data::theo_sd
d$SEX <-0
d$SEX[d$ID<=6] <-1

covarsVec <- c("WT")

# Stratified cross-validation data with CMT
df1 <- foldgen(d, nfold=5, stratVar="CMT")

# Stratified cross-validation data with ID (individual)
df2 <- foldgen(d, nfold=5, stratVar=NULL)
```

forwardSearch	<i>Forward covariate search</i>
---------------	---------------------------------

Description

Forward covariate search

Usage

```
forwardSearch(
  varsVec,
  covarsVec,
  catvarsVec = NULL,
  fit,
  pVal = 0.05,
  outputDir,
  restart = FALSE
)
```

Arguments

varsVec	character vector of variables that need to be added
covarsVec	character vector of covariates that need to be added
catvarsVec	character vector of categorical covariates that need to be added
fit	an nlmixr2 'fit' object
pVal	p-value that should be used for selecting covariates in the forward search
outputDir	the name of the output directory that stores the covariate search result
restart	a boolean that controls if the search should be restarted; default is FALSE

Value

returns the updated 'fit' object at the end of the forward search and a table of information for all the covariates tested

Author(s)

Vipul Mann, Matthew Fidler, Vishal Sarsani

horseshoeSummardf

Create Horseshoe summary posterior estimates

Description

Create Horseshoe summary posterior estimates

Usage

```
horseshoeSummardf(fit, covarsVec, ...)
```

Arguments

fit	compiled rxode2 nlmir2 model fit
covarsVec	character vector of covariates that need to be added
...	other parameters passed to brm(): warmup = 1000, iter = 2000, chains = 4, cores = 4, control = list(adapt_delta = 0.99, max_treedepth = 15)

Value

Horse shoe Summary data frame of all covariates

Author(s)

Vishal Sarsani, Christian Bartels

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}
```



```

}

d <- nlmixr2data::theo_sd
fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))
covarsVec <- c("WT")

# Horseshoe summary posterior estimates:

#hsDf <- horseshoeSummardf(fit,covarsVec,cores=2)
#brms sometimes may throw a Error in sink(type = "output")
#Issue Should be fixed by uninstalling and re-installing rstan

## End(Not run)

```

knit_print.nlmixr2FitCore

Extract the equations from an nlmixr2/rxode2 model to produce a 'LaTeX' equation.

Description

Extract the equations from an nlmixr2/rxode2 model to produce a 'LaTeX' equation.

Usage

```

## S3 method for class 'nlmixr2FitCore'
knit_print(x, ..., output = "equations")

## S3 method for class 'rxUi'
knit_print(x, ...)

```

Arguments

x	The model to extract equations from
...	Ignored
output	The type of output to request (currently, just "equations")

lassoCoefficients

Return Final lasso coefficients after finding optimal t

Description

Return Final lasso coefficients after finding optimal t

Usage

```
lassoCoefficients(
  fit,
  varsVec,
  covarsVec,
  catvarsVec,
  constraint = 1e-08,
  stratVar = NULL,
  ...
)
```

Arguments

<code>fit</code>	nlmixr2 fit.
<code>varsVec</code>	character vector of variables that need to be added
<code>covarsVec</code>	character vector of covariates that need to be added
<code>catvarsVec</code>	character vector of categorical covariates that need to be added
<code>constraint</code>	theta cutoff. below cutoff then the theta will be fixed to zero
<code>stratVar</code>	A variable to stratify on for cross-validation
<code>...</code>	Other parameters to be passed to <code>optimalTvalueLasso</code>

Value

return data frame of final lasso coefficients

Author(s)

Vishal Sarsani

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}
```

```

}

d <- nlmixr2data::theo_sd
d$SEX <-0
d$SEX[d$ID<=6] <-1

fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))
varsVec <- c("ka","cl","v")
covarsVec <- c("WT")
catvarsVec <- c("SEX")

# Lasso coefficients:

lassoDf <- lassoCoefficients(fit, varsVec, covarsVec, catvarsVec, constraint=1e-08, stratVar = NULL)

## End(Not run)

```

lassoSummardf	<i>Create Lasso summary posterior estimates</i>
---------------	---

Description

Create Lasso summary posterior estimates

Usage

```
lassoSummardf(fit, covarsVec, ...)
```

Arguments

<code>fit</code>	compiled rxode2 nlmir2 model fit
<code>covarsVec</code>	character vector of covariates that need to be added
<code>...</code>	other parameters passed to <code>brm()</code> : <code>warmup = 1000</code> , <code>iter = 2000</code> , <code>chains = 4</code> , <code>cores = 4</code> , <code>control = list(adapt_delta = 0.99, max_treedepth = 15)</code>

Value

Horse shoe Summary data frame of all covariates

Author(s)

Vishal Sarsani, Christian Bartels

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

d <- nlmixr2data::theo_sd
fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))
covarsVec <- c("WT")

# Horseshoe summary posterior estimates:

#lassoDf <- lassoSummardf(fit,covarsVec,cores=2)
#brms sometimes may throw a Error in sink(type = "output")
#Issue Should be fixed by uninstalling and re-installing rstan

## End(Not run)
```

llpControl

Control options for log-likelihood profiling

Description

Control options for log-likelihood profiling

Usage

```
llpControl(
  ofvIncrease = qchisq(0.95, df = 1),
  rseTheta = 30,
  itermax = 10,
  ofvtol = 0.005,
  paramDigits = 3,
  extrapolateExpand = 1.5
)
```

Arguments

ofvIncrease	The targetted change in objective function value (3.84 corresponds to a Chi-squared test with a 95% confidence interval)
rseTheta	The relative standard error (percent) for the model parameters. It can be missing (the default) in which case a default value of 30% will be applied. If given as a single number, it will be applied to all parameters. If given as a named vector of numbers, it will be applied to each named parameter.
itermax	Maximum number of likelihood profiling iterations for each bound estimated
ofvtol	The relative tolerance for the objective function being close enough to the ofvIncrease.
paramDigits	The number of significant digits required for the parameter. When interpolation attempts to get smaller than that number of significant digits, it will stop.
extrapolateExpand	When extrapolating outside the range previously tested, how far should the step occur as a ratio

Value

A validated list of control options for log-likelihood profiling

See Also

[profilellp\(\)](#)

Other Profiling: [fixedControl\(\)](#), [profile.nlmixr2FitCore\(\)](#), [profileFixed\(\)](#), [profilellp\(\)](#), [profileNlmixr2FitCoreRet\(\)](#)

normalizedData	<i>Function to return data of normalized covariates</i>
----------------	---

Description

Function to return data of normalized covariates

Usage

```
normalizedData(data, covarsVec, replace = TRUE)
```

Arguments

data	a dataframe with covariates to normalize
covarsVec	a list of covariate names (parameters) that need to be estimates
replace	replace the original covariate data with normalized data for easier updated model.

Value

data frame with all normalized covariates

Author(s)

Vishal Sarsani

Examples

```
d <- nlmixr2data::theo_sd
d$SEX <-0
d$SEX[d$ID<=6] <-1

covarsVec <- c("WT")

# Normalized covariate (replaced)
df1 <- normalizedData(d,covarsVec,replace=TRUE)

# Normalized covariate (without replacement)
df2 <- normalizedData(d,covarsVec,replace=FALSE)
```

optimUnisampling	<i>Sample from uniform distribution by optim</i>
------------------	--

Description

Sample from uniform distribution by optim

Usage

```
optimUnisampling(xvec, N = 1000, medValue, floorT = TRUE)
```

Arguments

xvec	A vector of min,max values . Ex:c(10,20)
N	Desired number of values
medValue	Desired Median
floorT	boolean indicating whether to round up

Value

Samples with approx desired median.

Author(s)

Vishal Sarsani

Examples

```
# Simulate 1000 creatine clearance values with median of 71.7 within range of c(6.7,140)
creatCl <- optimUnisampling(xvec=c(6.7,140), N=1000, medValue = 71.7, floorT=FALSE)
```

preconditionFit	<i>Linearly re-parameterize the model to be less sensitive to rounding errors</i>
-----------------	---

Description

Linearly re-parameterize the model to be less sensitive to rounding errors

Usage

```
preconditionFit(fit, estType = c("full", "posthoc", "none"), ntry = 10L)
```

Arguments

fit	A nlmixr2 fit to be preconditioned
estType	Once the fit has been linearly reparameterized, should a "full" estimation, "posthoc" estimation or simply a estimation of the covariance matrix "none" before the fit is updated
ntry	number of tries before giving up on a pre-conditioned covariance estimate

Value

A nlmixr2 fit object that was preconditioned to stabilize the variance/covariance calculation

References

Aoki Y, Nordgren R, Hooker AC. Preconditioning of Nonlinear Mixed Effects Models for Stabilisation of Variance-Covariance Matrix Computations. AAPS J. 2016;18(2):505-518. doi:10.1208/s12248-016-9866-5

profile.nlmixr2FitCore	<i>Perform likelihood profiling on nlmixr2 focei fits</i>
------------------------	---

Description

Perform likelihood profiling on nlmixr2 focei fits

Usage

```
## S3 method for class 'nlmixr2FitCore'
profile(
  fitted,
  ...,
  which = NULL,
  method = c("llp", "fixed"),
  control = list()
)
```

Arguments

fitted	The fit model
...	ignored
which	The parameter names to perform likelihood profiling on (NULL indicates all parameters)
method	Method to use for profiling (see the details)
control	Control arguments for the method

Value

A data.frame with one column named Parameter indicating the parameter being fixed on that row, one column for the OFV indicating the OFV estimated for the model at that step, one column named profileBound indicating the estimated value for the profile likelihood and its step above the minimum profile likelihood value, and columns for each parameter estimate (or fixed) in the model.

Log-likelihood profiling

```
method = "llp"
```

The search will stop when either the OFV is within ofvtol of the desired OFV change or when the parameter is interpolating to more significant digits than specified in paramDigits. The "llp" method uses the profileLlp() function. See its help for more details.

Fixed points

```
method = "fixed"
```

Estimate the OFV for specific fixed values. The "fixed" method uses the profileFixed() function. See its help for more details.

See Also

Other Profiling: [fixedControl\(\)](#), [llpControl\(\)](#), [profileFixed\(\)](#), [profileLlp\(\)](#), [profileNlmixr2FitCoreRet\(\)](#)

Examples

```
## Not run:
# Likelihood profiling takes a long time to run each model multiple times, so
# be aware that running this example may take a few minutes.
oneCmt <- function() {
  ini({
    tka <- log(1.57)
    tcl <- log(2.72)
    tv <- fixed(log(31.5))
    eta.ka ~ 0.6
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl)
```



```

      v <- exp(tv)
      cp <- linCmt()
      cp ~ add(add.sd)
    })
  }

  fit <-
    nlmixr2(
      oneCmt, data = nlmixr2data::theo_sd, est="focei", control = list(print=0)
    )
  # profile all parameters
  profall <- profile(fit)

  # profile a single parameter
  profotka <- profile(fit, which = "tka")

  ## End(Not run)

```

profileFixed	<i>Estimate the objective function values for a model while fixing defined parameter values</i>
--------------	---

Description

Estimate the objective function values for a model while fixing defined parameter values

Usage

```
profileFixed(fitted, which, control = list())
```

```
profileFixedSingle(fitted, which)
```

Arguments

fitted	The fit model
which	A data.frame with column names of parameters to fix and values of the fitted value to fix (one row only).
control	A list passed to fixedControl() (currently unused)

Value

which with a column named OFV added with the objective function value of the fitted estimate fixing the parameters in the other columns

Functions

- profileFixedSingle(): Estimate the objective function value for a model while fixing a single set of defined parameter values (for use in parameter profiling)

See Also

Other Profiling: `fixedControl()`, `llpControl()`, `profile.nlmixr2FitCore()`, `profileLlp()`, `profileNlmixr2FitCoreRet()`

Other Profiling: `fixedControl()`, `llpControl()`, `profile.nlmixr2FitCore()`, `profileLlp()`, `profileNlmixr2FitCoreRet()`

profileLlp

Profile confidence intervals with log-likelihood profiling

Description

Profile confidence intervals with log-likelihood profiling

Usage

```
profileLlp(fitted, which, control)
```

Arguments

fitted	The fit model
which	Either NULL to profile all parameters or a character vector of parameters to estimate
control	A list passed to <code>llpControl()</code>

Value

A data.frame with columns named "Parameter" (the parameter name(s) that were fixed), OFV (the objective function value), and the current estimate for each of the parameters. In addition, if any boundary is found, the OFV increase will be indicated by the absolute value of the "profileBound" column and if that boundary is the upper or lower boundary will be indicated by the "profileBound" column being positive or negative, respectively.

See Also

Other Profiling: `fixedControl()`, `llpControl()`, `profile.nlmixr2FitCore()`, `profileFixed()`, `profileNlmixr2FitCoreRet()`

profileNlmixr2FitCoreRet	<i>Give the output data.frame for a single model for profile.nlmixr2FitCore</i>
--------------------------	---

Description

Give the output data.frame for a single model for profile.nlmixr2FitCore

Usage

```
profileNlmixr2FitCoreRet(fitted, which, fixedVal)
```

Arguments

fitted	The fit model
which	The parameter names to perform likelihood profiling on (NULL indicates all parameters)
fixedVal	The value that which is fixed to in case the model does not converge.

Value

A data.frame with columns named "Parameter" (the parameter name(s) that were fixed), OFV (the objective function value), and the current estimate for each of the parameters. Omega values are given as their variances and covariances.

See Also

Other Profiling: [fixedControl\(\)](#), [llpControl\(\)](#), [profile.nlmixr2FitCore\(\)](#), [profileFixed\(\)](#), [profileLlp\(\)](#)

regularmodel	<i>Regular lasso model</i>
--------------	----------------------------

Description

Regular lasso model

Usage

```
regularmodel(
  fit,
  varsVec,
  covarsVec,
  catvarsVec,
  constraint = 1e-08,
  lassotype = c("regular", "adaptive", "adjusted"),
  stratVar = NULL,
  ...
)
```

Arguments

fit	nlmixr2 fit.
varsVec	character vector of variables that need to be added
covarsVec	character vector of covariates that need to be added
catvarsVec	character vector of categorical covariates that need to be added
constraint	theta cutoff. below cutoff then the theta will be fixed to zero.
lassotype	must be 'regular', 'adaptive', 'adjusted'
stratVar	A variable to stratify on for cross-validation.
...	Other parameters to be passed to optimalTvaluelasso

Value

return fit of the selected lasso coefficients

Author(s)

Vishal Sarsani

Examples

```
## Not run:
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
  })
}
```

```

        linCmt() ~ add(add.sd)
    })
}

d <- nlmixr2data::theo_sd
d$SEX <- 0
d$SEX[d$ID<=6] <- 1

fit <- nlmixr2(one.cmt, d, est = "saem", control = list(print = 0))
varsVec <- c("ka", "cl", "v")
covarsVec <- c("WT")
catvarsVec <- c("SEX")

# Model fit with regular lasso coefficients:

lassoDf <- regularmodel(fit, varsVec, covarsVec, catvarsVec)
# Model fit with adaptive lasso coefficients:

lassoDf <- regularmodel(fit, varsVec, covarsVec, catvarsVec, lassotype='adaptive')
# Model fit with adaptive-adjusted lasso coefficients:

lassoDf <- regularmodel(fit, varsVec, covarsVec, catvarsVec, lassotype='adjusted')

## End(Not run)

```

theoFitOde

Example single dose Theophylline ODE model

Description

This is a nlmixr2 model that is pre-run so that it can be used in package testing and development. It is regenerated whenever binaries of nlmixr2extra are created. If there is a binary incompatibility between the fit objects, a simple rerun of the installation will fix this nlmixr2 fit object.

Format

A (modified) data frame with 132 rows and 22 columns.

ID Patient identifier

TIME Time (hr)

DV Dependent variable (concentration)

PRED Predictions without any between subject variability

RES Population Residual

WRES Weighted Residuals under the FO assumption

IPRED Individual Predictions

IRES Individual Residuals

IWRES Individual Weighted Residuals

CPRED Conditional Prediction under the FOCE assumption
CRES Conditional Residuals under the FOCE assumption
CWRES Conditional Weighted Residuals under the FOCE assumption
eta.ka Between subject changes for k_a
eta.cl Between subject changes for v
depot amount in the depot compartment
center amount in the central compartment
ka Individual k_a values
cl Individual cl values
v Individual volume of distribution
tad Time after dose
dosenum Dose number

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