

Package ‘nlmixr2lib’

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Type Package

Version 0.2.0

Title A Model Library for 'nlmixr2'

Description A model library for 'nlmixr2'. The models include (and plan to include) pharmacokinetic, pharmacodynamic, and disease models used in pharmacometrics. Where applicable, references for each model are included in the meta-data for each individual model. The package also includes model composition and modification functions to make model updates easier.

Depends R (>= 4.0)

Imports checkmate, cli, methods, nlmixr2est, rxode2 (>= 2.0.12)

License GPL (>= 2)

LazyData true

RoxygenNote 7.2.3

VignetteBuilder knitr

URL <https://github.com/nlmixr2/nlmixr2lib>,
<https://nlmixr2.github.io/nlmixr2lib/>

Encoding UTF-8

Language en-US

Suggests covr, knitr, rmarkdown, testthat (>= 3.0.0)

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addDirToModelDb	<i>Add a directory to the modeldb</i>
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Description

Add a directory to the modeldb

Usage

```
addDirToModelDb(dir, modeldb = data.frame())
```

```
addFileToModelDb(dir, file, modeldb)
```

Arguments

dir	Directory name containing model files
modeldb	The starting modeldb data.frame
file	The file name (without the directory name)

Value

The updated modeldb data.frame

Functions

- addFileToModelDb(): Add a file to the modeldb

addEta	<i>Add random effects to a model</i>
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Description

Add random effects to a model

Usage

```
addEta(model, eta)
```

Arguments

model	The model as a function
eta	vector with the parameters to add random effects (sometimes referred to as inter-individual variability, IIV) on

Value

The model with eta added to the requested parameters

Examples

```
library(rxode2)
readModelDb("PK_1cmt") %>% addEta("ka")
```

addResErr	<i>Add residual error to a model</i>
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Description

Add residual error to a model

Usage

```
addResErr(model, reserr)
```

Arguments

model	The model as a function
reserr	The type or types of residual error (currently "addSd", "propSd", and "lnormSd" are accepted)

Details

For reserr, the parameter will be named with the dependent variable from the model as a prefix. For example, if the dependent variable in the model is cp, the parameter name for propSd will become cpropSd.

Value

The model with residual error modified

Examples

```
library(rxode2)
readModelDb("PK_1cmt") %>% addResErr("addSd")
readModelDb("PK_1cmt") %>% addResErr("lnormSd")
readModelDb("PK_1cmt") %>% addResErr(c("addSd", "propSd"))
```

modeldb

Model library for nlmixr2

Description

This is a data frame of the available models in nlmixr2lib, it is generated with the package. Custom modeldb may be used.

Usage

```
modeldb
```

Format

A data frame with 13 rows and 5 columns

name Model name that can be used to extract the model from the model library

description Model description in free form text; in model itself

parameters A comma separated string listing either the parameter in the model defined by population/individual effects or a population effect parameter

DV The definition of the dependent variable(s)

filename Filename of the model. By default these are installed in the model library and read on demand

modellib	<i>Get the model from the model library</i>
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Description

This function gets a model from the available model library

Usage

```
modellib(name = NULL, eta = NULL, reserr = NULL)
```

Arguments

name	character with the name of the model to load (if NULL, lists all available base models)
eta	vector with the parameters to add random effects (sometimes referred to as inter-individual variability, IIV) on
reserr	The type or types of residual error (currently "addSd", "propSd", and "lnormSd" are accepted)

Details

This is a very first draft just to look at the proof of concept

Value

The function returns a function the model code (or NULL if the model = NULL)

Examples

```
modellib(name="PK_1cmt")
modellib(name="PK_1cmt", eta = c("ka", "vc"), reserr = "addSd")
modellib(name="PK_1cmt", reserr = "addSd")
```

readModelDb	<i>Read a model from the nlmixr2 model database</i>
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Description

Read a model from the nlmixr2 model database

Usage

```
readModelDb(name)
```

Arguments

name The name of the model (must be one of modeldb\$name)

Value

The model as a function

Examples

```
readModelDb("PK_1cmt")
```

searchReplace *Search within a model to replace part of the model*

Description

Search within a model to replace part of the model

Usage

```
searchReplace(object, find, replace)
```

```
searchReplaceHelper(object, find, replace)
```

Arguments

object function specifying the nlmixr2 model

find, replace Character scalars of parts of the model to replace

Value

object with find replaced with replace

Functions

- searchReplaceHelper(): A helper function for searchReplace (not intended for users to use directly)

`updateOncologyXenograftSimeoni2004`*Update an oncology xenograft model based on Simeoni 2004*

Description

Update an oncology xenograft model based on Simeoni 2004

Usage

```
updateOncologyXenograftSimeoni2004(  
  object,  
  ncmt,  
  damagedCmtName = "damagedCells",  
  drugEffectName = "drugEffectCyclingCells",  
  undamagedCmtName = "cyclingCells",  
  tumorVolName = "tumorVol",  
  transitRateName = "damageTransit"  
)
```

Arguments

<code>object</code>	Fitted object or function specifying the model.
<code>ncmt</code>	The desired number of damaged cell compartments
<code>damagedCmtName, undamagedCmtName, tumorVolName</code>	character string names for the compartments for damaged cells, undamaged cells, and the calculated tumor volume (the sum of undamaged and damaged cells)
<code>drugEffectName, transitRateName</code>	character string names of the drug effect and transit rate (as used in the model block)

Value

An updated model with the new number of compartments

Examples

```
library(rxode2)  
readModelDb("oncology_xenograft_simeoni_2004") %>%  
  updateOncologyXenograftSimeoni2004(ncmt = 5)
```

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