Package 'nlmixr2lib'

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Type Package

Version 0.1.0

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, rxode2, nlmixr2est

License GPL (>= 2)

LazyData true

RoxygenNote 7.2.1

VignetteBuilder knitr

URL `https://github.com/nlmixr2/nlmixr2lib`, `https://nlmixr2.github.io/nlmixr2lib/`

Encoding UTF-8

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

Config/testthat/edition 3

NeedsCompilation no

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R topics documented:

`addDirToModelDb` *Add a directory to the modeldb*

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` *Add random effects to a model*

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

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

`addResErr` *Add residual error to a model*

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 `cppropSd`.

Value

The model with residual error modified

Examples

```
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 6 rows and 5 columns

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

description Model description in free from 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

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`modellib` *Get the model from the model library*

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` *Read a model from the nlmixr2 model database*

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)

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