Package 'campsismod'

February 16, 2024

Type Package

Title Generic Implementation of a PK/PD Model

Version 1.1.1

Description A generic, easy-to-use and expandable implementation of a pharmacokinetic (PK) / pharmacodynamic (PD) model based on the S4 class system. This package allows the user to read/write a pharmacometric model from/to files and adapt it further on the fly in the R environment. For this purpose, this package provides an intuitive API to add, modify or delete equations, ordinary differential equations (ODE's), model parameters or compartment properties (like infusion duration or rate, bioavailability and initial values). Finally, this package also provides a useful export of the model for use with simulation packages 'rxode2' and 'mrgsolve'. This package is designed and intended to be used with package 'campsis', a PK/PD simulation platform built on top of 'rxode2' and 'mrgsolve'.

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URL https://github.com/Calvagone/campsismod,
 https://calvagone.github.io/

BugReports https://github.com/Calvagone/campsismod/issues

Depends R (>= 4.0.0)

Imports assertthat, dplyr, magrittr, methods, plyr, purrr, readr, tibble, utils

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Collate 'global.R' 'data.R' 'utilities.R' 'special_operators.R'
 'check.R' 'generic.R' 'generic_element_list.R'
 'generic_element_position.R' 'generic_list.R' 'pattern.R'
 'model_statement.R' 'model_statements.R'
 'model_unknown_statement.R' 'model_comment.R'
 'model_line_break.R' 'model_equation.R' 'model_ode.R'
 'model_if_statement.R' 'compartment_property.R'
 'compartment_properties.R' 'compartment_bioavailability.R'
 'compartment_lag_time.R' 'compartment_infusion_duration.R'
 'compartment_infusion_rate.R' 'compartment_initial_condition.R'
 'compartments.R' 'parameters.R' 'code_record.R'
 'code_records.R' 'model_parser.R' 'campsis_model.R'
 'model_add_suffix.R' 'rxode_model.R' 'rxode_conversion.R'
 'mrgsolve_model.R' 'mrgsolve_conversion.R'

NeedsCompilation no

Author Nicolas Luyckx [aut, cre]

Maintainer Nicolas Luyckx <nicolas.luyckx@calvagone.com>

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add

Add element to list.

Description

Add element to list.

```
add(object, x, ...)
## S4 method for signature 'pmx_list,pmx_element'
add(object, x, pos = NULL)

## S4 method for signature 'pmx_list,pmx_list'
add(object, x)

## S4 method for signature 'pmx_list,list'
add(object, x)

## S4 method for signature 'compartments,compartment_property'
add(object, x)

## S4 method for signature 'compartments,compartments'
```

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```
add(object, x)
## S4 method for signature 'parameters, single_array_parameter'
add(object, x)
## S4 method for signature 'parameters,double_array_parameter'
add(object, x)
## S4 method for signature 'parameters, parameters'
add(object, x)
## S4 method for signature 'code_record, model_statement'
add(object, x, pos = NULL)
## S4 method for signature 'code_record,code_record'
add(object, x)
## S4 method for signature 'code_records, code_records'
add(object, x)
## S4 method for signature 'code_records,model_statement'
add(object, x, pos = NULL)
## S4 method for signature 'campsis_model,compartment_property'
add(object, x)
## S4 method for signature 'campsis_model,parameter'
add(object, x)
## S4 method for signature 'campsis_model,code_record'
add(object, x)
## S4 method for signature 'campsis_model,model_statement'
add(object, x, pos = NULL)
## S4 method for signature 'campsis_model,campsis_model'
add(object, x)
```

Arguments

pos

object list object

x element to add

... extra arguments, unused by this generic list

position where x needs to be added in list

Value

modified list object

addSuffix 7

addSuffix	Generic function to add a suffix to various objects like parameters, code records, compartment names or a model (all previous objects at the same time). This makes it an extremely powerful function to
	combine 2 models or more (using function 'add'), that have similar equation, parameter or compartment names.

Description

Generic function to add a suffix to various objects like parameters, code records, compartment names or a model (all previous objects at the same time). This makes it an extremely powerful function to combine 2 models or more (using function 'add'), that have similar equation, parameter or compartment names.

Usage

```
addSuffix(object, suffix, separator = NULL, ...)
## S4 method for signature 'parameters,character,character'
addSuffix(object, suffix, separator = NULL, ...)
## S4 method for signature 'code_records,character,character'
addSuffix(object, suffix, separator = NULL, ...)
## S4 method for signature 'code_record,character,character'
addSuffix(object, suffix, separator = NULL, ...)
## S4 method for signature 'compartments,character,character'
addSuffix(object, suffix, separator = NULL, ...)
## S4 method for signature 'campsis_model,character,character'
addSuffix(object, suffix, separator = NULL, ...)
```

Arguments

object	generic object
suffix	suffix to be appended, single character value
separator	separator to use before the suffix, default is the underscore
	extra arguments like 'model' if the changes need to be reflected in the model

Value

updated object of the same class as the provided object, unless 'model' was specified, in that case the model is returned

as.data.frame

As data frame method.

Description

As data frame method.

Usage

```
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
## S4 method for signature 'theta,character,logical'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
## S4 method for signature 'omega,character,logical'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
## S4 method for signature 'sigma,character,logical'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

```
x generic object
row.names row names
optional optional
... extra arguments
```

Value

data frame

```
assertSingleCharacterString
```

Assert the given character vector is a single character string.

Description

Assert the given character vector is a single character string.

```
assertSingleCharacterString(x)
```

autoDetectNONMEM 9

Arguments

x single character string

Value

no return value

autoDetectNONMEM

Auto-detect special variables from NONMEM as compartment properties. Bioavailabilities, infusion durations/rates and lag times will be automatically detected.

Description

Auto-detect special variables from NONMEM as compartment properties. Bioavailabilities, infusion durations/rates and lag times will be automatically detected.

Usage

```
autoDetectNONMEM(object, ...)
## S4 method for signature 'campsis_model'
autoDetectNONMEM(object, ...)
```

Arguments

object object that has NONMEM special variables to be identified extra arguments, unused

Value

updated object

Bioavailability

Create a bioavailability for the specified compartment.

Description

Create a bioavailability for the specified compartment.

```
Bioavailability(compartment, rhs = "")
```

10 campsis_model-class

Arguments

compartment compartment index

rhs right-hand side part of the equation

Value

a bioavailability property

CampsisModel

Create a new CAMPSIS model.

Description

Create a new CAMPSIS model.

Usage

CampsisModel()

Value

a CAMPSIS model, empty

 ${\tt campsis_model-class}$

CAMPSIS model class.

Description

CAMPSIS model class.

Slots

```
model a list of code records

parameters model parameters

compartments model compartments
```

CodeRecords 11

CodeRecords

Create a list of code records.

Description

Create a list of code records.

Usage

CodeRecords()

Value

an empty list of code records

code_record-class

Code record class. See this code record as an abstract class. 2 implementations are possible: - properties record (lag, duration, rate & bioavailability properties) - statements record (main, ode & error records)

Description

Code record class. See this code record as an abstract class. 2 implementations are possible: - properties record (lag, duration, rate & bioavailability properties) - statements record (main, ode & error records)

Slots

comment a comment, single character value statements model statements

Comment

Create a new comment.

Description

Create a new comment.

Usage

Comment(x)

12 compartment-class

Arguments

Х

comment, single character string

Value

a comment

comment-class

Comment class. A statement starting with #.

Description

Comment class. A statement starting with #.

Compartment

Create a compartment.

Description

Create a compartment.

Usage

```
Compartment(index, name = NA)
```

Arguments

index

compartment index

name

compartment name (without prefix)

Value

an empty list of compartments

compartment-class

Compartment class.

Description

Compartment class.

Slots

```
name compartment name (without prefix) index compartment index
```

Compartments 13

 ${\tt Compartments}$

Create a list of compartments

Description

Create a list of compartments

Usage

Compartments()

Value

an empty list of compartments

compartments-class

Compartments class.

Description

Compartments class.

Slots

properties compartment properties of the compartments defined in this class

 ${\tt compartment_bioavailability-class}$

Compartment bioavailability class.

Description

Compartment bioavailability class.

 ${\tt compartment_infusion_duration-class}$

Compartment infusion duration class.

Description

Compartment infusion duration class.

compartment_infusion_rate-class

Compartment infusion rate class.

Description

Compartment infusion rate class.

 ${\tt compartment_initial_condition-class}$

Compartment initial condition class.

Description

Compartment initial condition class.

 ${\tt compartment_lag_time_class}$

Compartment lag time class.

Description

Compartment lag time class.

compartment_properties-class

Compartment properties class.

Description

Compartment properties class.

```
compartment_property-class
```

Compartment property class.

Description

Compartment property class.

Slots

```
compartment related compartment index rhs right-hand side formula comment comment if any, single character string
```

default

Get default element from list.

Description

Get default element from list.

Usage

```
default(object, ...)
```

Arguments

object list object

... additional arguments

Value

the default element from list

16 delete

delete

Delete an element from this list.

Description

Delete an element from this list.

```
delete(object, x)
## S4 method for signature 'pmx_list,pmx_element'
delete(object, x)
## S4 method for signature 'pmx_list,integer'
delete(object, x)
## S4 method for signature 'compartments, compartment_property'
delete(object, x)
## S4 method for signature 'parameters,single_array_parameter'
delete(object, x)
## S4 method for signature 'parameters, double_array_parameter'
delete(object, x)
## S4 method for signature 'statements_record,model_statement'
delete(object, x)
## S4 method for signature 'statements_record,integer'
delete(object, x)
## S4 method for signature 'code_records,model_statement'
delete(object, x)
## S4 method for signature 'campsis_model,compartment_property'
delete(object, x)
## S4 method for signature 'campsis_model,parameter'
delete(object, x)
## S4 method for signature 'campsis_model,code_record'
delete(object, x)
## S4 method for signature 'campsis_model,model_statement'
delete(object, x)
```

disable 17

Arguments

object list object

x element to delete or element index

Value

the updated list

disable

Disable.

Description

Disable.

Usage

```
disable(object, x, ...)
## S4 method for signature 'parameters,character'
disable(object, x, ...)
## S4 method for signature 'campsis_model,character'
disable(object, x, ...)
```

Arguments

object generic object

x what needs to be disabled

... extra arguments needed for disabling

Value

object with some disabled features

```
double_array_parameter-class
```

Double-array parameter class. This parameter has 2 indexes. It can thus be used to define correlations between parameters.

Description

Double-array parameter class. This parameter has 2 indexes. It can thus be used to define correlations between parameters.

18 equation-class

duration_record-class (Infusion)-duration record class.

Description

(Infusion)-duration record class.

Equation

Create a new equation.

Description

Create a new equation.

Usage

```
Equation(lhs, rhs = "", comment = as.character(NA))
```

Arguments

1hs left-hand side variable corresponding to the assigned variable name

rhs right-hand side expression corresponding to a formula

comment if any, single character string

Value

an equation

equation-class

Equation class. Any statement in the form A = B.

Description

Equation class. Any statement in the form A = B.

Slots

1hs left-hand side expression rhs right-hand side expression

ErrorRecord 19

ErrorRecord

Create ERROR code record.

Description

Create ERROR code record.

Usage

```
ErrorRecord(code = character())
```

Arguments

code

code record

Value

an ERROR code record

error_record-class

Error record class.

Description

Error record class.

export

Export function.

Description

Export function.

```
export(object, dest, ...)
## S4 method for signature 'campsis_model,character'
export(object, dest, ...)
## S4 method for signature 'campsis_model,rxode_type'
export(object, dest, ...)
## S4 method for signature 'campsis_model,mrgsolve_type'
export(object, dest, outvars = NULL, extra_params = character(0))
```

20 extractLhs

Arguments

object generic object dest destination

... optional arguments

outvars additional variables to capture

extra_params extra parameter names to be added. By default, they will be assigned a zero

value.

Value

specific object depending on given destination

export_type-class

Export type class.

Description

Export type class.

extractLhs

Extract left-hand-side expression.

Description

Extract left-hand-side expression.

Usage

```
extractLhs(x, split = "=")
```

Arguments

x character value

split character where to split

Value

left-hand-side expression, not trimmed

extractRhs 21

extractRhs

Extract right-hand-side expression.

Description

Extract right-hand-side expression.

Usage

```
extractRhs(x, split = "=")
```

Arguments

x character value

split character where to split

Value

right-hand side expression

extractTextBetweenBrackets

Extract text between brackets.

Description

Extract text between brackets.

Usage

```
extractTextBetweenBrackets(x)
```

Arguments

x character value

Value

text between brackets (trimmed)

22 find

find

Find an element in list.

Description

Find an element in list.

Usage

```
find(object, x)
## S4 method for signature 'pmx_list,pmx_element'
find(object, x)
## S4 method for signature 'compartments, compartment_property'
find(object, x)
## S4 method for signature 'statements_record,model_statement'
find(object, x)
## S4 method for signature 'code_records,model_statement'
find(object, x)
## S4 method for signature 'campsis_model,compartment'
find(object, x)
## S4 method for signature 'campsis_model,compartment_property'
find(object, x)
## S4 method for signature 'campsis_model,parameter'
find(object, x)
## S4 method for signature 'campsis_model,code_record'
find(object, x)
## S4 method for signature 'campsis_model,model_statement'
find(object, x)
```

Arguments

object list object
x element to find, only key slots need to be filled in

Value

the element from the list that has same name as x, or NULL if no element was found

fixOmega 23

fixOmega	Fix omega matrix for SAME OMEGA parameters that have NA values due to imperfections in Pharmpy import.
	aue to imperfections in Pharmpy import.

Description

Fix omega matrix for SAME OMEGA parameters that have NA values due to imperfections in Pharmpy import.

Usage

```
fixOmega(object)
## S4 method for signature 'parameters'
fixOmega(object)
```

Arguments

object

generic object

Value

the parameter that matches

f_record-class

Bioavailability record class.

Description

Bioavailability record class.

 ${\tt getByIndex}$

Get element by index.

Description

Get element by index.

24 getByName

Usage

```
getByIndex(object, x)

## S4 method for signature 'pmx_list,integer'
getByIndex(object, x)

## S4 method for signature 'pmx_list,numeric'
getByIndex(object, x)

## S4 method for signature 'compartment_properties,compartment_property'
getByIndex(object, x)

## S4 method for signature 'parameters,parameter'
getByIndex(object, x)
```

Arguments

object list object x element index

Value

element from the list whose index matches with provided index

getByName

Get an element from a list by name. Never return more than 1 element.

Description

Get an element from a list by name. Never return more than 1 element.

Usage

```
getByName(object, name)
## S4 method for signature 'pmx_list,character'
getByName(object, name)
```

Arguments

object list object

name element name to search for

Value

the element that was found or NULL if no element was found with the same name

getCompartmentIndex 25

 ${\tt getCompartmentIndex}$

Get the compartment index for the specified compartment name.

Description

Get the compartment index for the specified compartment name.

Usage

```
getCompartmentIndex(object, name)
## S4 method for signature 'compartments,character'
getCompartmentIndex(object, name)
## S4 method for signature 'campsis_model,character'
getCompartmentIndex(object, name)
```

Arguments

object

generic object that contains compartments information

name

compartment name

Value

the corresponding compartment index

getName

Get element name.

Description

Get element name.

```
getName(x)
## S4 method for signature 'unknown_statement'
getName(x)
## S4 method for signature 'comment'
getName(x)
## S4 method for signature 'line_break'
getName(x)
```

26 getName

```
## S4 method for signature 'equation'
getName(x)
## S4 method for signature 'ode'
getName(x)
## S4 method for signature 'if_statement'
getName(x)
## S4 method for signature 'compartment'
getName(x)
## S4 method for signature 'compartment_bioavailability'
getName(x)
## S4 method for signature 'compartment_lag_time'
getName(x)
## S4 method for signature 'compartment_infusion_duration'
getName(x)
## S4 method for signature 'compartment_infusion_rate'
getName(x)
## S4 method for signature 'compartment_initial_condition'
getName(x)
## S4 method for signature 'theta'
getName(x)
## S4 method for signature 'omega'
getName(x)
## S4 method for signature 'sigma'
getName(x)
## S4 method for signature 'main_record'
getName(x)
## S4 method for signature 'ode_record'
getName(x)
## S4 method for signature 'f_record'
getName(x)
## S4 method for signature 'lag_record'
getName(x)
```

getNameInModel 27

```
## S4 method for signature 'duration_record'
getName(x)

## S4 method for signature 'rate_record'
getName(x)

## S4 method for signature 'init_record'
getName(x)

## S4 method for signature 'error_record'
getName(x)
```

Arguments

Χ

element to know the name

Value

the name of this element

getNameInModel

Get the name of the given parameter in the CAMPSIS model.

Description

Get the name of the given parameter in the CAMPSIS model.

Usage

```
getNameInModel(x)
## S4 method for signature 'theta'
getNameInModel(x)
## S4 method for signature 'omega'
getNameInModel(x)
## S4 method for signature 'sigma'
getNameInModel(x)
```

Arguments

Х

element to know the name

Value

the name of this parameter

28 getNONMEMName

getNames

Get element names from list.

Description

Get element names from list.

Usage

```
getNames(object)
## S4 method for signature 'pmx_list'
getNames(object)
```

Arguments

object

list object

Value

character vector with all the element names of this list

getNONMEMName

Get NONMEM name.

Description

Get NONMEM name.

Usage

```
getNONMEMName(object)

## S4 method for signature 'theta'
getNONMEMName(object)

## S4 method for signature 'omega'
getNONMEMName(object)

## S4 method for signature 'sigma'
getNONMEMName(object)
```

Arguments

object

generic object

getPrefix 29

Value

the NONMEM name associated with this object

getPrefix

Get prefix.

Description

Get prefix.

Usage

```
getPrefix(object, ...)
## S4 method for signature 'compartment_bioavailability'
getPrefix(object, ...)
## S4 method for signature 'compartment_lag_time'
getPrefix(object, ...)
## S4 method for signature 'compartment_infusion_duration'
getPrefix(object, ...)
## S4 method for signature 'compartment_infusion_rate'
getPrefix(object, ...)
## S4 method for signature 'compartment_initial_condition'
getPrefix(object, ...)
```

Arguments

```
object generic object
... e.g. dest='mrgsolve'
```

Value

the prefix of this object

30 getRecordName

 ${\tt getRecordDelimiter}$

Get record delimiter.

Description

Get record delimiter.

Usage

```
getRecordDelimiter(line)
```

Arguments

line

any line, single character value

Value

the record delimiter between brackets

getRecordName

Get record name.

Description

Get record name.

```
getRecordName(object)

## S4 method for signature 'compartment_bioavailability'
getRecordName(object)

## S4 method for signature 'compartment_lag_time'
getRecordName(object)

## S4 method for signature 'compartment_infusion_duration'
getRecordName(object)

## S4 method for signature 'compartment_infusion_rate'
getRecordName(object)

## S4 method for signature 'compartment_initial_condition'
getRecordName(object)
```

getUncertainty 31

Arguments

object generic object

Value

the name of the record

getUncertainty

Get uncertainty on the parameters.

Description

Get uncertainty on the parameters.

Usage

```
getUncertainty(object, ...)
## S4 method for signature 'parameter'
getUncertainty(object, varcov, ...)
## S4 method for signature 'parameters'
getUncertainty(object, ...)
## S4 method for signature 'campsis_model'
getUncertainty(object, ...)
```

Arguments

object generic object
... extra arguments

varcov variance covariance matrix

Value

data frame with standard error (se) and relative standard error (rse

32 hasComment

 ${\tt getVarCov}$

Get variance-covariance matrix.

Description

Get variance-covariance matrix.

Usage

```
getVarCov(object)
## S4 method for signature 'parameters'
getVarCov(object)
## S4 method for signature 'campsis_model'
getVarCov(object)
```

Arguments

object

generic object

Value

a variance-covariance matrix (data frame) or NULL if no matrix present

hasComment

Check if string contains CAMPSIS-style comments.

Description

Check if string contains CAMPSIS-style comments.

Usage

```
hasComment(x)
```

Arguments

Χ

character vector

Value

logical value

IfStatement 33

IfStatement

Create a new IF-statement.

Description

Create a new IF-statement.

Usage

```
IfStatement(condition, equation, comment = as.character(NA))
```

Arguments

condition condition, single character string

equation equation if condition is met

comment if any, single character string

Value

an IF-statement

if_statement-class

If-statement class. Any statement in the form if (condition) A = B.

Description

If-statement class. Any statement in the form if (condition) A = B.

Slots

condition IF statement condition equation any equation or ODE

34 InfusionDuration

index0f

Get the index of an element in list.

Description

Get the index of an element in list.

Usage

```
indexOf(object, x)
## S4 method for signature 'pmx_list,pmx_element'
indexOf(object, x)
```

Arguments

object list object

x element to know the index

Value

index of this element

InfusionDuration

Create an infusion duration.

Description

Create an infusion duration.

Usage

```
InfusionDuration(compartment, rhs = "")
```

Arguments

compartment compartment index

rhs right-hand side part of the equation

Value

an infusion duration property

InfusionRate 35

 ${\tt InfusionRate}$

Create an infusion rate.

Description

Create an infusion rate.

Usage

```
InfusionRate(compartment, rhs = "")
```

Arguments

compartment

compartment index

rhs

right-hand side part of the equation

Value

an infusion rate property

InitialCondition

Create an initial condition.

Description

Create an initial condition.

Usage

```
InitialCondition(compartment, rhs = "")
```

Arguments

compartment

compartment index

rhs

right-hand side part of the equation

Value

an initial condition property

isDiag isDiag

init_record-class

Init record class.

Description

Init record class.

isComment

Check if string is a CAMPSIS comment (i.e. not an equation).

Description

Check if string is a CAMPSIS comment (i.e. not an equation).

Usage

```
isComment(x)
```

Arguments

Χ

character vector

Value

logical value

isDiag

Is diagonal.

Description

Is diagonal.

Usage

```
isDiag(object)
## S4 method for signature 'double_array_parameter'
isDiag(object)
```

Arguments

object

generic object

Value

logical value

isEmptyLine 37

 ${\tt isEmptyLine}$

Check if string is an empty line.

Description

Check if string is an empty line.

Usage

```
isEmptyLine(x)
```

Arguments

Х

character vector

Value

logical value

 ${\tt is Equation}$

Say if line in record is an equation not.

Description

Say if line in record is an equation not.

Usage

```
isEquation(x)
```

Arguments

Х

character value

Value

logical value

isODE

isIfStatement

Say if line in record is an IF-statement.

Description

Say if line in record is an IF-statement.

Usage

```
isIfStatement(x)
```

Arguments

Х

character value

Value

logical value

isODE

Say if line(s) in record is/are ODE or not.

Description

Say if line(s) in record is/are ODE or not.

Usage

```
isODE(x)
```

Arguments

Х

character vector

Value

logical vector

isRecordDelimiter 39

isRecordDelimiter

Is record delimiter. A record delimiter is any line starting with [...].

Description

Is record delimiter. A record delimiter is any line starting with [...].

Usage

```
isRecordDelimiter(line)
```

Arguments

line

any line, single character value

Value

a logical value

isStrictRecordDelimiter

Is strict record delimiter. A strict record delimiter is any line starting with [...] and followed by nothing but spaces or a possible comment.

Description

Is strict record delimiter. A strict record delimiter is any line starting with [...] and followed by nothing but spaces or a possible comment.

Usage

```
isStrictRecordDelimiter(line)
```

Arguments

line

any line, single character value

Value

a logical value

40 LineBreak

 ${\tt LagTime}$

Create a lag time for the specified compartment.

Description

Create a lag time for the specified compartment.

Usage

```
LagTime(compartment, rhs = "")
```

Arguments

compartment

compartment index

rhs

right-hand side part of the equation

Value

a lag time property

lag_record-class

Lag record class.

Description

Lag record class.

LineBreak

Create a new line break.

Description

Create a new line break.

Usage

LineBreak()

Value

a line break

line_break-class 41

line_break-class

Line-break class. A linebreak in the model.

Description

Line-break class. A linebreak in the model.

MainRecord

Create MAIN code record.

Description

Create MAIN code record.

Usage

MainRecord(code = character())

Arguments

code

code record

main_record-class

Main record class.

Description

Main record class.

42 minIndex

maxIndex

Max index.

Description

Max index.

Usage

```
maxIndex(object)
## S4 method for signature 'parameters'
maxIndex(object)
```

Arguments

object

generic object

Value

max index

 $\min Index$

Min index.

Description

Min index.

Usage

```
minIndex(object)
## S4 method for signature 'parameters'
minIndex(object)
```

Arguments

object

generic object

Value

min index

ModelStatements 43

ModelStatements

Create an empty list of model statements.

Description

Create an empty list of model statements.

Usage

ModelStatements()

Value

a model statements object

Description

Model statement class. Any statement in a code record.

Slots

comment a comment associated to this model statement

 ${\sf model_statements\text{-}class}$

Model statements class. A list of statements.

Description

Model statements class. A list of statements.

44 mrgsolveBlock

model_suite

CAMPSIS model suite.

Description

A library of models of all kinds, ready to be simulated in Campsis. These model templates are sorted into the following categories: pharmacokinetic (PK), pharmacodynamic (PD), target-mediated drug disposition (TMDD), NONMEM, literature and other (custom models).

Usage

```
model_suite
```

Format

A list with all the models:

pk extensive list of pharmacokinetic (PK) model templates

pd list of pharmacodynamic (PD) model templates, to be plugged into any pharmacokinetic (PK) model

tmdd extensive list of target-mediated drug disposition (TMDD) model templates

nonmem list of model templates translated from standard NONMEM control streams

literature a couple of models coming from the literature

other a couple of custom models

Source

```
https://calvagone.github.io/campsis.doc/
https://www.iconplc.com/solutions/technologies/nonmem/
```

mrgsolveBlock

Convert code record for mrgsolve.

Description

Convert code record for mrgsolve.

Usage

```
mrgsolveBlock(record, init = NULL, capture = FALSE)
```

mrgsolveCapture 45

Arguments

record code record

init name of mrgsolve block capture 'capture' instead of 'double'

Value

translated record for mrgsolve

mrgsolveCapture

Get the CAPTURE block for mrgsolve.

Description

Get the CAPTURE block for mrgsolve.

Usage

```
mrgsolveCapture(outvars, model)
```

Arguments

outvars outvars in method simulate

model CAMPSIS model

Value

CAPTURE block or character(0) if no variable in outvars

mrgsolveCompartment Get the compartment block for mrgsolve.

Description

Get the compartment block for mrgsolve.

Usage

mrgsolveCompartment(model)

Arguments

model CAMPSIS model

Value

character vector, each value is a line

46 mrgsolveMatrix

mrgsolveMain

Get the MAIN block for mrgsolve.

Description

Get the MAIN block for mrgsolve.

Usage

```
mrgsolveMain(model)
```

Arguments

model

CAMPSIS model

Value

MAIN block

mrgsolveMatrix

Get the OMEGA/SIGMA matrix for mrgsolve.

Description

Get the OMEGA/SIGMA matrix for mrgsolve.

Usage

```
mrgsolveMatrix(model, type = "omega")
```

Arguments

model

CAMPSIS model

type

either omega or sigma

Value

named matrix or character(0) if matrix is empty

mrgsolveOde 47

mrgsolveOde

Get the ODE block for mrgsolve.

Description

Get the ODE block for mrgsolve.

Usage

```
mrgsolveOde(model)
```

Arguments

model

CAMPSIS model

Value

ODE block

mrgsolveParam

Get the parameters block for mrgsolve.

Description

Get the parameters block for mrgsolve.

Usage

```
mrgsolveParam(model, extra_params = character(0))
```

Arguments

model

CAMPSIS model

extra_params

extra parameter names to be added. By default, they will be assigned a zero value.

Value

character vector, 1 parameter per line. First one is header [PARAM].

48 Ode

mrgsolveTable

Get the TABLE block for mrgsolve.

Description

Get the TABLE block for mrgsolve.

Usage

```
mrgsolveTable(model)
```

Arguments

model

CAMPSIS model

Value

TABLE block if at least one line in error record, character(0) otherwise

mrgsolve_type-class

Mrgsolve export type class.

Description

Mrgsolve export type class.

0de

Create a new ordinary differential equation (ODE).

Description

Create a new ordinary differential equation (ODE).

Usage

```
Ode(lhs, rhs = "", comment = as.character(NA))
```

Arguments

1hs left-hand side variable corresponding to derivative name, must start with 'A_'

rhs right-hand side expression corresponding to derivative value

comment if any, single character string

Value

an ODE

ode-class 49

ode-class

ODE class. Any statement in the form $d/dt(A_CMT) = B$.

Description

ODE class. Any statement in the form $d/dt(A_CMT) = B$.

OdeRecord

Create ODE code record.

Description

Create ODE code record.

Usage

```
OdeRecord(code = character())
```

Arguments

code

code record

Value

an ODE code record

ode_record-class

ODE record class.

Description

ODE record class.

Omega Omega

Omega

Create an OMEGA parameter.

Description

Create an OMEGA parameter.

Usage

```
Omega(
  name = NA,
  index = NA,
  index2 = NA,
  value = NA,
  fix = FALSE,
  type = NULL,
  same = NA,
  label = NA,
  comment = NA
```

Arguments

name	parameter name, e.g. CL (prefix OMEGA will be added automatically)
index	parameter index
index2	second parameter index
value	parameter value
fix	parameter was fixed in estimation, logical value
type	variance type: 'var', 'sd', 'covar', 'cor', 'cv' or 'cv%'
same	NA by default, FALSE for first OMEGA followed by 'SAME' OMEGA's, TRUE for 'SAME' OMEGA's
label	parameter label, optional

Value

comment

```
an OMEGA parameter
```

any comment, optional

omega-class 51

omega-class

Omega parameter class.

Description

Omega parameter class.

Slots

same logical value, tell if this omega is the same as the previous one

parameter-class

Parameter class. Any parameter in a pharmacometric model.

Description

Parameter class. Any parameter in a pharmacometric model.

Slots

name parameter name, optional (although recommended)
index parameter index, integer
value parameter value (e.g. the estimated value from a modelling tool)
fix logical value, say if parameter was fixed in the modelling phase
label parameter label, any string
comment any comment on this parameter, any string

Parameters

Create a list of parameters.

Description

Create a list of parameters.

Usage

Parameters()

Value

an empty list of parameters

52 parseIfStatement

parameters-class

Parameters class.

Description

Parameters class.

Slots

varcov associated variance-covariance matrix

parseIfStatement

Parse IF-statement. Assumption: isIfStatement method already called and returned TRUE.

Description

Parse IF-statement. Assumption: isIfStatement method already called and returned TRUE.

Usage

```
parseIfStatement(line, comment = as.character(NA))
```

Arguments

line IF-statement as single character string value, comment omitted

comment any comment, NA by default

Value

an IF statement object

parseStatements 53

parseStatements

Parse statements code and return CAMPSIS statements.

Description

Parse statements code and return CAMPSIS statements.

Usage

```
parseStatements(code)
```

Arguments

code

character vector containing all statements (text form)

Value

a list of CAMPSIS statements

Pattern

Create a pattern.

Description

Create a pattern.

Usage

Pattern(x)

Arguments

Χ

regular expression

Value

a pattern

pattern-class

Pattern class.

Description

Pattern class.

pmx_element-class	PMX element class.
Description	
PMX element class.	
pmx_position-class	PMX position class.
Description	
PMX position class.	
•	
pmx_position_by_eleme	
	PMX position by element class.
Description	
PMX position by eleme	ent class.
pmx_position_by_index	x-class

PMX position by index class.

Description

PMX position by index class.

Position 55

Description

Element position in list.

Usage

```
Position(x, after = TRUE)
```

Arguments

x either an integer position (useful to add an element in a code record at a specified

position) or an model element (element can be a model statement or a code

record)

after element to be added will be added after x (if after is TRUE) or before x (if after

is FALSE)

Value

a position object

processExtraArg

Process extra arguments.

Description

Process extra arguments.

Usage

```
processExtraArg(args, name, default = NULL, mandatory = FALSE)
```

Arguments

args arguments list

name argument name to retrieve

default value if argument is not present mandatory mandatory argument, logical value

Value

requested argument value

56 read

```
properties_record-class
```

Properties record class.

Description

Properties record class.

rate_record-class

(Infusion)-rate record class.

Description

(Infusion)-rate record class.

read

Generic read method to read data from a file or a folder.

Description

Generic read method to read data from a file or a folder.

Usage

```
read(file, ...)
```

Arguments

file path to the file or folder to be read

... extra arguments

Value

the object representation of the data contained in the file

read.allparameters 57

read.allparameters

Read all parameters files at once.

Description

Read all parameters files at once.

Usage

```
read.allparameters(folder)
```

Arguments

folder

path to folder or path to zipped project

Value

parameters object

read.campsis

Read a CAMPSIS model.

Description

Read a CAMPSIS model.

Usage

```
read.campsis(file)
```

Arguments

file

path to folder

Value

a CAMPSIS model

58 read.parameters

read.model

Read model file.

Description

Read model file.

Usage

```
read.model(file = NULL, text = NULL)
```

Arguments

file path to file 'model.campsis'

text model file as text, character (single or multiple lines)

Value

records object

read.parameters

Read parameters file.

Description

Read parameters file.

Usage

```
read.parameters(file, type)
```

Arguments

file path to CSV file

type parameter type: 'theta', 'omega' or 'sigma'

Value

parameters sub list

read.varcov 59

read.varcov

Read variance-covariance file.

Description

Read variance-covariance file.

Usage

```
read.varcov(file)
```

Arguments

file

path to CSV file

Value

variance-covariance matrix

replace

Replace element by another in list.

Description

Replace element by another in list.

Usage

```
replace(object, x)
## S4 method for signature 'pmx_list,pmx_element'
replace(object, x)
## S4 method for signature 'pmx_list,pmx_list'
replace(object, x)
## S4 method for signature 'pmx_list,list'
replace(object, x)
## S4 method for signature 'compartments,compartment_property'
replace(object, x)
## S4 method for signature 'parameters,single_array_parameter'
replace(object, x)
## S4 method for signature 'parameters,double_array_parameter'
```

60 replaceAll

```
replace(object, x)

## S4 method for signature 'statements_record,model_statement'
replace(object, x)

## S4 method for signature 'code_records,model_statement'
replace(object, x)

## S4 method for signature 'campsis_model,compartment'
replace(object, x)

## S4 method for signature 'campsis_model,compartment_property'
replace(object, x)

## S4 method for signature 'campsis_model,parameter'
replace(object, x)

## S4 method for signature 'campsis_model,code_record'
replace(object, x)

## S4 method for signature 'campsis_model,model_statement'
replace(object, x)
```

Arguments

object list object

x element to replace

Value

list object or an error if the element does not exist in the list

replaceAll

Replace all occurrences in object.

Description

Replace all occurrences in object.

Usage

```
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'character, variable_pattern, character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'character, pattern, character'
```

rxodeCode 61

```
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'model_statement,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'equation, pattern, character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'if_statement,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'compartment_property,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'code_record,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'code_records,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'campsis_model,pattern,character'
replaceAll(object, pattern, replacement, ...)
## S4 method for signature 'campsis_model,character,character'
replaceAll(object, pattern, replacement, ...)
```

Arguments

object generic object (e.g. model, code_record(s), etc.)

pattern pattern to be replaced replacement replacement string extra arguments

Value

the same object with all occurrences replaced

rxodeCode

Get code for RxODE.

Description

Get code for RxODE.

Usage

rxodeCode(model)

62 rxodeParams

Arguments

model

CAMPSIS model

Value

corresponding model code for RxODE

rxodeMatrix

Get the OMEGA/SIGMA matrix for RxODE.

Description

Get the OMEGA/SIGMA matrix for RxODE.

Usage

```
rxodeMatrix(model, type = "omega")
```

Arguments

model

CAMPSIS model

type

either omega or sigma

Value

omega/sigma named matrix

rxodeParams

Get the parameters vector for RxODE.

Description

Get the parameters vector for RxODE.

Usage

rxodeParams(model)

Arguments

model

CAMPSIS model

Value

named vector with THETA values

rxode_type-class 63

rxode_type-class

RxODE export type class.

Description

RxODE export type class.

select

Get a subset of an object.

Description

Get a subset of an object.

Usage

```
select(object, ...)
## S4 method for signature 'data.frame'
select(object, ...)
## S4 method for signature 'compartment_properties'
select(object, ...)
## S4 method for signature 'parameters'
select(object, ...)
```

Arguments

```
object generic object
... arguments to select
```

Value

subset of an object

64 sigma-class

Sigma

Create a SIGMA parameter.

Description

Create a SIGMA parameter.

Usage

```
Sigma(
  name = NA,
  index = NA,
  index2 = NA,
  value = NA,
  fix = FALSE,
  type = NULL,
  label = NA,
  comment = NA
)
```

Arguments

name parameter name, e.g. CL (prefix SIGMA will be added automatically)

index parameter index

index2 second parameter index

value parameter value

fix parameter was fixed in estimation, logical value type variance type: 'var', 'sd', 'covar', 'cv' or 'cv%'

label parameter label, optional comment any comment, optional

Value

a SIGMA parameter

sigma-class

Sigma parameter class.

Description

Sigma parameter class.

```
single\_array\_parameter-class
```

Single-array parameter class. This parameter has a single index value.

Description

Single-array parameter class. This parameter has a single index value.

sort

Sort the specified list.

Description

Sort the specified list.

Usage

```
sort(x, decreasing = FALSE, ...)
## S4 method for signature 'compartment_properties'
sort(x, decreasing = FALSE, ...)
## S4 method for signature 'compartments'
sort(x, decreasing = FALSE, ...)
## S4 method for signature 'parameters'
sort(x, decreasing = FALSE, ...)
## S4 method for signature 'code_records'
sort(x, decreasing = FALSE, ...)
## S4 method for signature 'campsis_model'
sort(x, decreasing = FALSE, ...)
```

Arguments

```
x list object
decreasing increasing or decreasing order
... extra arguments
```

Value

same list but ordered

standardise

Standardise.

Description

Standardise.

Usage

```
standardise(object, ...)
## S4 method for signature 'theta'
standardise(object, ...)
## S4 method for signature 'double_array_parameter'
standardise(object, parameters = NULL, ...)
## S4 method for signature 'parameters'
standardise(object, ...)
```

Arguments

object generic object

... extra arguments needed for standardisation

parameters the list of parameters, to be provided only if parameter type is 'cor'

Value

standardised object

```
statements_record-class
```

Statements record class.

Description

Statements record class.

Theta 67

Theta

Create a THETA parameter.

Description

Create a THETA parameter.

Usage

```
Theta(
  name = NA,
  index = NA,
  value = NA,
  fix = FALSE,
  label = NA,
  unit = NA,
  comment = NA
```

Arguments

```
name parameter name, e.g. CL (prefix THETA will be added automatically) index parameter index value parameter value fix parameter was fixed in estimation, logical value label parameter label, optional unit parameter unit, optional any comment any comment, optional
```

Value

a THETA parameter

theta-class

Theta parameter class.

Description

Theta parameter class.

Slots

```
unit parameter unit
```

68 toString

toString

ToString generic method.

Description

ToString generic method.

Usage

```
toString(object, ...)
## S4 method for signature 'unknown_statement'
toString(object, ...)
## S4 method for signature 'comment'
toString(object, ...)
## S4 method for signature 'line_break'
toString(object, ...)
## S4 method for signature 'equation'
toString(object, ...)
## S4 method for signature 'ode'
toString(object, ...)
## S4 method for signature 'if_statement'
toString(object, ...)
## S4 method for signature 'compartment'
toString(object, ...)
## S4 method for signature 'compartment_property'
toString(object, ...)
## S4 method for signature 'compartment_initial_condition'
toString(object, ...)
## S4 method for signature 'mrgsolve_model'
toString(object, ...)
```

Arguments

```
object generic object
... extra arguments needed for toString conversion
```

trim 69

Value

character value/vector

trim

Trim character vector. Remove all leading and trailing spaces.

Description

Trim character vector. Remove all leading and trailing spaces.

Usage

trim(x)

Arguments

Х

character vector

Value

character vector without leading and trailing spaces

UnknownStatement

Create a new ordinary differential equation (ODE).

Description

Create a new ordinary differential equation (ODE).

Usage

```
UnknownStatement(line, comment = as.character(NA))
```

Arguments

line line which was not recognised

comment if any, single character string

Value

an unknown statement

70 VariablePattern

unknown_statement-class

Unknown statement class. Any statement not recognized by campsismod.

Description

Unknown statement class. Any statement not recognized by campsismod.

updateCompartments

Update compartments list from the persisted records. Exported especially for package pmxtran. However, this method should not be called.

Description

Update compartments list from the persisted records. Exported especially for package pmxtran. However, this method should not be called.

Usage

updateCompartments(model)

Arguments

model

CAMPSIS model

Value

an updated CAMPSIS model, with an updated compartments list

VariablePattern

Create a variable pattern.

Description

Create a variable pattern.

Usage

VariablePattern(x)

Arguments

Х

variable name

variable_pattern-class 71

Value

```
a variable pattern
```

```
variable_pattern-class
```

Variable pattern class.

Description

Variable pattern class.

write

Write generic object to files.

Description

Write generic object to files.

Usage

```
write(object, file, ...)
## S4 method for signature 'parameters, character'
write(object, file, ...)
## S4 method for signature 'code_records, character'
write(object, file, ...)
## S4 method for signature 'campsis_model, character'
write(object, file, ...)
```

Arguments

object generic object

file path of the output file or directory

... extra arguments

Value

logical value, TRUE for success, FALSE for failure

72 writeVarcov

writeParameters

Write subset of parameters (theta, omega or sigma).

Description

Write subset of parameters (theta, omega or sigma).

Usage

```
writeParameters(object, file, ...)
```

Arguments

object subset of parameters

file filename

... extra arguments, like defaultDf for empty parameters list

Value

TRUE if success

writeVarcov

Write variance-covariance matrix.

Description

Write variance-covariance matrix.

Usage

```
writeVarcov(object, file)
```

Arguments

object matrix file filename

Value

TRUE if success

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