

Package ‘campsismod’

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Type Package

Title Generic Implementation of a PK/PD Model

Version 1.3.0

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 and write pharmacometric models from and to files, including a JSON-based interface to import Campsis models defined using a formal JSON schema distributed with the package. Models can be adapted further on the fly in the R environment using an intuitive API to add, modify or delete equations, ordinary differential equations (ODEs), model parameters or compartment properties (such as infusion duration or rate, bioavailability and initial values). The package also provides export facilities for use with the simulation packages ‘rxode2’ and ‘mrgsolve’. The package itself is licensed under the GPL (≥ 3); the JSON schema file shipped in inst/extdata is licensed separately under the Creative Commons Attribution 4.0 International (CC BY 4.0). This package is designed and intended to be used with the 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/>,
<https://calvagone.github.io/campsismod.doc/>

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

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 'check.R' 'json_element.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.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' 'parameter.R' 'parameters.R' 'code_record.R'
 'code_records.R' 'model_parser.R' 'campsis_model.R'
 'omega_block.R' 'omega_blocks.R'
 'parameter_uncertainty_utils.R' 'replication_settings.R'
 'replicated_campsis_model.R' 'model_add_suffix.R'
 'rxode_model.R' 'rxode_conversion.R' 'mrgsolve_model.R'
 'mrgsolve_conversion.R' 'json_interface.R'

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add	<i>Add element to list.</i>
-----	-----------------------------

Description

Add element to list.

Usage

```
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'
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)

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

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

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

## S4 method for signature 'omega_blocks,parameters'
add(object, x)
```

Arguments

object	list object
x	element to add
...	extra arguments, unused by this generic list
pos	position where x needs to be added in list

Value

modified list object

addRSE	<i>Add relative standard error (RSE) to the specified parameter.</i>
--------	--

Description

Add relative standard error (RSE) to the specified parameter.

Usage

```
addRSE(object, parameter, value, ...)  
  
## S4 method for signature 'parameters,parameter,numeric'  
addRSE(object, parameter, value, ...)  
  
## S4 method for signature 'campsis_model,parameter,numeric'  
addRSE(object, parameter, value, ...)
```

Arguments

object	model or parameters object
parameter	parameter object (Theta, Omega or Sigma)
value	RSE value, in percent
...	extra arguments, unused

Value

updated object

addSuffix	<i>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.</i>
-----------	--

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	<i>As data frame method.</i>
---------------	------------------------------

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.

Usage

```
assertSingleCharacterString(x)
```

Arguments

x	single character string
---	-------------------------

Value

no return value

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

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

AutoReplicationSettings	<i>Create auto replication settings.</i>
-------------------------	--

Description

By default, all model parameters are sampled from a multivariate normal distribution, whose characteristics are specified by the variance-covariance matrix. OMEGAs and SIGMAs can be sampled from scaled inverse chi-squared or Wishart distributions by setting the `wishart` argument to `TRUE`. In that case, THETAs are still sampled from a multivariate normal distribution, while OMEGAs and SIGMAs are sampled from scaled inverse chi-squared (univariate OMEGA/SIGMA distribution) and Wishart (block of OMEGAs/SIGMAs) distribution, respectively. When `wishart` is set to `TRUE`, the degrees of freedom of the distribution must be specified, respectively, `odf` for the OMEGAs and `sdf` for the SIGMAs.

Usage

```

AutoReplicationSettings(
  wishart = FALSE,
  odf = NA,
  sdf = NA,
  checkMinMax = TRUE,
  checkPosDef = FALSE,
  quiet = NA
)

```

Arguments

wishart	logical, sample OMEGAs and SIGMAs from scaled inverse chi-squared (univariate OMEGA distribution) or Wishart distribution (block of OMEGAs)
odf	the degrees of freedom for the scaled inverse chi-squared/Wishart distribution with regards to the OMEGAs, single integer value (the same degrees of freedom for all OMEGA blocks) or integer vector (one value per OMEGA block)
sdf	the degrees of freedom for the scaled inverse chi-squared/Wishart distribution with regards to the SIGMAs, single integer value (the same degrees of freedom for all SIGMA blocks) or integer vector (one value per SIGMA block)
checkMinMax	logical, check for min/max values when sampling the parameters, default is TRUE
checkPosDef	logical, check for positive definiteness when sampling the OMEGA/SIGMA parameters from the variance-covariance matrix (i.e. when wishart=FALSE), default is FALSE (requires extra time)
quiet	logical, suppress info messages, default is NA. By default, messages will be printed out when the success rate of sampling the parameters is below 95%.

Value

replication settings

auto_replication_settings-class

Auto replication settings class.

Description

Auto replication settings class.

Slots

wishart logical, sample OMEGAs and SIGMAs from scaled inverse chi-squared or Wishart distributions

odf the degrees of freedom for the scaled inverse chi-squared/Wishart distribution with regards to the OMEGAs, integer vector

sdf the degrees of freedom for the scaled inverse chi-squared/Wishart distribution with regards to the SIGMAs, integer vector

quiet logical, suppress info messages

max_iterations number of iterations maximum to sample the parameters

max_chunk_size maximum number of rows to sample at once, default value will be the number of replicates, unless specified.

check_min_max logical, check for min/max values when sampling the parameters

check_pos_def logical, check for positive definiteness when sampling the OMEGA/SIGMA parameters

wishart_correction logical, FALSE is default, see <https://github.com/metrumresearchgroup/simpar/issues/11>

Bioavailability

Create a bioavailability for the specified compartment.

Description

Create a bioavailability for the specified compartment.

Usage

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

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

campsis_model-class	Campsis model class.
---------------------	----------------------

Description

Campsis model class.

Slots

model a list of code records
parameters model parameters
compartments model compartments

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	<i>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)</i>
-------------------	---

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	<i>Create a new comment.</i>
---------	------------------------------

Description

Create a new comment.

Usage

Comment(x)

Arguments

x comment, single character string

Value

a comment

comment-class	<i>Comment class. A statement starting with #.</i>
---------------	--

Description

Comment class. A statement starting with #.

Compartment	<i>Create a compartment.</i>
-------------	------------------------------

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	<i>Compartment class.</i>
-------------------	---------------------------

Description

Compartment class.

Slots

name	compartment name (without prefix)
index	compartment index

Compartments	<i>Create a list of compartments</i>
--------------	--------------------------------------

Description

Create a list of compartments

Usage

Compartments()

Value

an empty list of compartments

compartments-class	<i>Compartments class.</i>
--------------------	----------------------------

Description

Compartments class.

Slots

properties compartment properties of the compartments defined in this class

compartment_bioavailability-class	<i>Compartment bioavailability class.</i>
-----------------------------------	---

Description

Compartment bioavailability class.

compartment_infusion_duration-class	<i>Compartment infusion duration class.</i>
-------------------------------------	---

Description

Compartment infusion duration class.

compartment_infusion_rate-class	<i>Compartment infusion rate class.</i>
---------------------------------	---

Description

Compartment infusion rate class.

compartment_initial_condition-class
<i>Compartment initial condition class.</i>

Description

Compartment initial condition class.

compartment_lag_time-class
<i>Compartment lag time class.</i>

Description

Compartment lag time class.

compartment_properties-class
<i>Compartment properties class.</i>

Description

Compartment properties class.

compartment_property-class
<i>Compartment property class.</i>

Description

Compartment property class.

Slots

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

default	<i>Get default element from list.</i>
---------	---------------------------------------

Description

Get default element from list.

Usage

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

Arguments

object	list object
...	additional arguments

Value

the default element from list

delete	<i>Delete an element from this list.</i>
--------	--

Description

Delete an element from this list.

Usage

```
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)

```

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

Description

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

duration_record-class	<i>(Infusion)-duration record class.</i>
-----------------------	--

Description

(Infusion)-duration record class.

Equation	<i>Create a new equation.</i>
----------	-------------------------------

Description

Create a new equation.

Usage

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

Arguments

- lhs left-hand side variable corresponding to the assigned variable name
- rhs right-hand side expression corresponding to a formula
- comment comment if any, single character string

Value

an equation

equation-class	<i>Equation class. Any statement in the form $A = B$.</i>
----------------	--

Description

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

Slots

- lhs left-hand side expression
- rhs right-hand side expression

ErrorRecord	<i>Create ERROR code record.</i>
-------------	----------------------------------

Description

Create ERROR code record.

Usage

ErrorRecord(code = character())

Arguments

- code code record

Value

an ERROR code record

error_record-class	<i>Error record class.</i>
--------------------	----------------------------

Description

Error record class.

export	<i>Export function.</i>
--------	-------------------------

Description

Export function.

Usage

```
export(object, dest, ...)  
  
## S4 method for signature 'campsis_model,character'  
export(object, dest, ...)  
  
## S4 method for signature 'replicated_campsis_model,campsis_model'  
export(object, dest = CampsisModel(), index, ...)  
  
## 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))
```

Arguments

object	generic object
dest	destination
...	optional arguments
index	index of the replicated Campsis model to export
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

exportToJson	<i>Export the given object to a JSON object, ready to be written to files.</i>
--------------	--

Description

Export the given object to a JSON object, ready to be written to files.

Usage

```
exportToJson(object, ...)

## S4 method for signature 'theta'
exportToJson(object, ...)

## S4 method for signature 'omega'
exportToJson(object, ...)

## S4 method for signature 'sigma'
exportToJson(object, ...)

## S4 method for signature 'parameters'
exportToJson(object, ...)

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

Arguments

object	any object
...	extra arguments, unused

Value

the loaded S4 object

export_type-class	<i>Export type class.</i>
-------------------	---------------------------

Description

Export type class.

extractLhs	<i>Extract left-hand-side expression.</i>
------------	---

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	<i>Extract right-hand-side expression.</i>
------------	--

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)

```
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	<i>Fix omega matrix for SAME OMEGA parameters that have NA values due to imperfections in Pharmpy import.</i>
----------	---

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.

getByIndex	Get element by index.
------------	-----------------------

Description

Get element by index.

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	<i>Get an element from a list by name. Never return more than 1 element.</i>
-----------	--

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

getCampsismodOption	<i>Get Campsismod option logic.</i>
---------------------	-------------------------------------

Description

Get Campsismod option logic.

Usage

```
getCampsismodOption(name, default)
```

Arguments

name	option to search
default	default value if option not found

Value

option value

getCompartmentIndex	<i>Get the compartment index for the specified compartment name.</i>
---------------------	--

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	<i>Get element name.</i>
---------	--------------------------

Description

Get element name.

Usage

```
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)
```

```
## 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)
```

```
## 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)

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

Arguments

x element to know the name

Value

the name of this element

getNameInModel	<i>Get the name of the given parameter in the Campsis model.</i>
----------------	--

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

x element to know the name

Value

the name of this parameter

getNames	<i>Get element names from list.</i>
----------	-------------------------------------

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	<i>Get NONMEM name.</i>
---------------	-------------------------

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

Value

the NONMEM name associated with this object

getOmegaBlock	<i>Get the right block of OMEGA's.</i>
---------------	--

Description

Get the right block of OMEGA's.

Usage

```
getOmegaBlock(object, x)

## S4 method for signature 'omega_blocks,double_array_parameter'
getOmegaBlock(object, x)
```

Arguments

object list of OMEGA blocks
x omega param

Value

the corresponding OMEGA block or NULL if not found

getOmegaIndexes	<i>Get the indexes of the omegas.</i>
-----------------	---------------------------------------

Description

Get the indexes of the omegas.

Usage

```
getOmegaIndexes(object)

## S4 method for signature 'omega_block'
getOmegaIndexes(object)
```

Arguments

object omega block

Value

a list of integers

getPrefix	<i>Get prefix.</i>
-----------	--------------------

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

getRecordDelimiter	<i>Get record delimiter.</i>
--------------------	------------------------------

Description

Get record delimiter.

Usage

```
getRecordDelimiter(line)
```

Arguments

line	any line, single character value
------	----------------------------------

Value

the record delimiter between brackets

getRecordName	<i>Get record name.</i>
---------------	-------------------------

Description

Get record name.

Usage

```
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)
```

Arguments

object generic object

Value

the name of the record

getUncertainty	<i>Get uncertainty on the parameters.</i>
----------------	---

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

getVarCov	<i>Get variance-covariance matrix.</i>
-----------	--

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	<i>Check if string contains Campsis-style comments.</i>
------------	---

Description

Check if string contains Campsis-style comments.

Usage

```
hasComment(x)
```

Arguments

x character vector

Value

logical value

hasOffDiagonalOmegas	<i>Has off-diagonal omegas.</i>
----------------------	---------------------------------

Description

Has off-diagonal omegas.

Usage

```
hasOffDiagonalOmegas(object)

## S4 method for signature 'omega_block'
hasOffDiagonalOmegas(object)
```

Arguments

object	omega block
--------	-------------

Value

TRUE or FALSE

IfStatement	<i>Create a new IF-statement.</i>
-------------	-----------------------------------

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	comment if any, single character string

Value

an IF-statement

if_statement-class	<i>If-statement class. Any statement in the form if (condition) A = B.</i>
--------------------	--

Description

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

Slots

condition IF statement condition
equation any equation or ODE

indexOf	<i>Get the index of an element in list.</i>
---------	---

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	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

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

x	character vector
---	------------------

Value

logical value

isDiag	<i>Is diagonal.</i>
--------	---------------------

Description

Is diagonal.

Usage

```
isDiag(object)
```

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

Arguments

object	generic object
--------	----------------

Value

logical value

isEmptyLine	<i>Check if string is an empty line.</i>
-------------	--

Description

Check if string is an empty line.

Usage

```
isEmptyLine(x)
```

Arguments

x	character vector
---	------------------

Value

logical value

isEquation	<i>Say if line in record is an equation not.</i>
------------	--

Description

Say if line in record is an equation not.

Usage

isEquation(x)

Arguments

x character value

Value

logical value

isIfStatement	<i>Say if line in record is an IF-statement.</i>
---------------	--

Description

Say if line in record is an IF-statement.

Usage

isIfStatement(x)

Arguments

x character value

Value

logical value

`isMatrixPositiveDefinite`*Is matrix positive definite. Same check as mvtnorm does.*

Description

Is matrix positive definite. Same check as mvtnorm does.

Usage

```
isMatrixPositiveDefinite(matrix, tol = 1e-06)
```

Arguments

<code>matrix</code>	matrix to check
<code>tol</code>	tolerance when checking the eigenvalues

`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

<code>x</code>	character vector
----------------	------------------

Value

logical vector

isRecordDelimiter	<i>Is record delimiter. A record delimiter is any line starting with [...].</i>
-------------------	---

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

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

`JSONElement`*Instantiate a JSON element.*

Description

Instantiate a JSON element.

Usage

```
JSONElement(x)
```

Arguments

<code>x</code>	JSON object representation in R
----------------	---------------------------------

Value

JSON element

`jsonToOffDiagParameter`*Convert JSON correlation parameter (OMEGA or SIGMA) into a Campsis parameter.*

Description

Convert JSON correlation parameter (OMEGA or SIGMA) into a Campsis parameter.

Usage

```
jsonToOffDiagParameter(json, diag_names)
```

Arguments

<code>json</code>	JSON data
<code>diag_names</code>	parameter names on the diagonal, character vector

Value

the corresponding Campsis parameter

jsonToParameter	<i>JSON to Campsis parameter.</i>
-----------------	-----------------------------------

Description

JSON to Campsis parameter.

Usage

```
jsonToParameter(x, index = NULL, index2 = NULL)
```

Arguments

- | | |
|--------|---|
| x | JSON data |
| index | parameter index to add |
| index2 | second parameter index to add for OMEGAs and SIGMAs |

Value

Campsis parameter

json_element-class	<i>JSON element class.</i>
--------------------	----------------------------

Description

JSON element class.

LagTime	<i>Create a lag time for the specified compartment.</i>
---------	---

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	<i>Lag record class.</i>
------------------	--------------------------

Description

Lag record class.

LineBreak	<i>Create a new line break.</i>
-----------	---------------------------------

Description

Create a new line break.

Usage

LineBreak()

Value

a line break

line_break-class	<i>Line-break class. A linebreak in the model.</i>
------------------	--

Description

Line-break class. A linebreak in the model.

loadFromJSON	<i>Fill-in S4 object from the JSON content.</i>
--------------	---

Description

Fill-in S4 object from the JSON content.

Usage

```
loadFromJSON(object, json)

## S4 method for signature 'theta,json_element'
loadFromJSON(object, json)

## S4 method for signature 'omega,json_element'
loadFromJSON(object, json)

## S4 method for signature 'sigma,json_element'
loadFromJSON(object, json)

## S4 method for signature 'campsis_model,json_element'
loadFromJSON(object, json)

## S4 method for signature 'campsis_model,character'
loadFromJSON(object, json)
```

Arguments

object	pre-initiated S4 object
json	JSON (usually a list)

Value

the loaded S4 object

MainRecord	<i>Create MAIN code record.</i>
------------	---------------------------------

Description

Create MAIN code record.

Usage

```
MainRecord(code = character())
```

Arguments

code	code record
main_record-class	<i>Main record class.</i>

Description

Main record class.	
ManualReplicationSettings	<i>Create manual replication settings.</i>

Description

Create manual replication settings.	
Usage	
ManualReplicationSettings(data)	

Arguments

data	data frame with 1 row per replicate, must contain a column named 'REPLICATE' with unique integers from 1 to nrow(data), other columns are model parameters to use.
------	--

Details

Use these settings to import custom replicated model parameters.
--

Value

replication settings	
manual_replication_settings-class	<i>Manual replication settings class.</i>

Description

Manual replication settings class.

Slots

replicated_parameters	data frame, 1 row per replicate
-----------------------	---------------------------------

```
mapJSONPropertiesToS4Slots
```

Map JSON properties to S4 slots.

Description

Map JSON properties to S4 slots.

Usage

```
mapJSONPropertiesToS4Slots(object, json, discard_type = TRUE)
```

Arguments

object	S4 object
json	JSON element, json_element class
discard_type	discard JSON property 'type'

Value

a S4 object

```
mapS4SlotsToJSONProperties
```

Map S4 slots to JSON properties.

Description

Map S4 slots to JSON properties.

Usage

```
mapS4SlotsToJSONProperties(
  object,
  add_type = TRUE,
  optional = NULL,
  ignore = NULL
)
```

Arguments

object	S4 object
add_type	add type as a property, TRUE by default
optional	properties that are optional in JSON, character vector
ignore	slots to be ignored

Value

a JSON object ready to be serialised

maxIndex	<i>Max index.</i>
----------	-------------------

Description

Max index.

Usage

```
maxIndex(object)

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

Arguments

object generic object

Value

max index

minIndex	<i>Min index.</i>
----------	-------------------

Description

Min index.

Usage

```
minIndex(object)

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

Arguments

object generic object

Value

min index

ModelStatements	Create an empty list of model statements.
-----------------	---

Description

Create an empty list of model statements.

Usage

ModelStatements()

Value

a model statements object

model_statement-class	Model statement class. Any statement in a code record.
-----------------------	--

Description

Model statement class. Any statement in a code record.

Slots

comment a comment associated to this model statement

model_statements-class	Model statements class. A list of statements.
------------------------	---

Description

Model statements class. A list of statements.

model_suite	<i>Campsis model suite.</i>
-------------	-----------------------------

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/>

move	<i>Move element 'x' from object to a certain place.</i>
------	---

Description

Move element 'x' from object to a certain place.

Usage

```
move(object, x, to, ...)  
  
## S4 method for signature 'code_records,model_statement,pmx_position'  
move(object, x, to, ...)  
  
## S4 method for signature 'code_records,list,pmx_position'  
move(object, x, to, ...)  
  
## S4 method for signature 'code_records,model_statements,pmx_position'  
move(object, x, to, ...)  
  
## S4 method for signature 'code_records,code_record,pmx_position'  
move(object, x, to, ...)  
  
## S4 method for signature 'campsis_model,ANY,pmx_position'  
move(object, x, to, ...)
```

Arguments

object	generic object (e.g. model, code records, etc.)
x	element to move
to	destination (e.g. a position)
...	extra arguments, unused

Value

updated object

mrgsolveBlock	<i>Convert code record for mrgsolve.</i>
---------------	--

Description

Convert code record for mrgsolve.

Usage

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

Arguments

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

Value

translated record for mrgsolve

mrgsolveCapture	<i>Get the CAPTURE block for mrgsolve.</i>
-----------------	--

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	<i>Get the compartment block for mrgsolve.</i>
---------------------	--

Description

Get the compartment block for mrgsolve.

Usage

mrgsolveCompartment(model)

Arguments

model	Campsis model
-------	---------------

Value

character vector, each value is a line

mrgsolveMain	<i>Get the MAIN block for mrgsolve.</i>
--------------	---

Description

Get the MAIN block for mrgsolve.

Usage

```
mrgsolveMain(model)
```

Arguments

model	Campsis model
-------	---------------

Value

MAIN block

mrgsolveMatrix	<i>Get the OMEGA/SIGMA matrix for mrgsolve.</i>
----------------	---

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	<i>Get the ODE block for mrgsolve.</i>
-------------	--

Description

Get the ODE block for mrgsolve.

Usage

mrgsolveOde(model)

Arguments

model Campsis model

Value

ODE block

mrgsolveParam	<i>Get the parameters block for mrgsolve.</i>
---------------	---

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].

mrgsolveTable	<i>Get the TABLE block for mrgsolve.</i>
---------------	--

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	<i>Mrgsolve export type class.</i>
---------------------	------------------------------------

Description

Mrgsolve export type class.

Ode	<i>Create a new ordinary differential equation (ODE).</i>
-----	---

Description

Create a new ordinary differential equation (ODE).

Usage

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

Arguments

lhs	left-hand side variable corresponding to derivative name, must start with 'A_'
rhs	right-hand side expression corresponding to derivative value
comment	comment if any, single character string

Value

an ODE

ode-class	<i>ODE class. Any statement in the form $d/dt(A_CMT) = B$.</i>
-----------	--

Description

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

OdeRecord	<i>Create ODE code record.</i>
-----------	--------------------------------

Description

Create ODE code record.

Usage

OdeRecord(code = character())

Arguments

code code record

Value

an ODE code record

ode_record-class	<i>ODE record class.</i>
------------------	--------------------------

Description

ODE record class.

Omega

Create an OMEGA parameter.

Description

Create an OMEGA parameter.

Usage

```
Omega(
  name = NA,
  index = NA,
  index2 = NA,
  value = NA,
  min = NA,
  max = 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
min	minimum value for this parameter when parameter uncertainty is enabled
max	maximum value for this parameter when parameter uncertainty is enabled
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
comment	any comment, optional

Value

an OMEGA parameter

omega-class	<i>Omega parameter class.</i>
-------------	-------------------------------

Description

Omega parameter class.

Slots

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

OmegaBlock	<i>Create a block of OMEGA's.</i>
------------	-----------------------------------

Description

Create a block of OMEGA's.

Usage

OmegaBlock()

OmegaBlocks	<i>Create a list of OMEGA blocks.</i>
-------------	---------------------------------------

Description

Create a list of OMEGA blocks.

Usage

OmegaBlocks()

parameter-class	<i>Parameter class. Any parameter in a pharmacometric model.</i>
-----------------	--

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)
- min minimum value for this parameter when parameter uncertainty is enabled
- max maximum value for this parameter when parameter uncertainty is enabled
- 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	<i>Create a list of parameters.</i>
------------	-------------------------------------

Description

Create a list of parameters.

Usage

Parameters()

Value

an empty list of parameters

parameters-class	<i>Parameters class.</i>
------------------	--------------------------

Description

Parameters class.

Slots

- varcov associated variance-covariance matrix

parseIfStatement	<i>Parse IF-statement. Assumption: isIfStatement method already called and returned TRUE.</i>
------------------	---

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	<i>Parse statements code and return Campsis statements.</i>
-----------------	---

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	<i>Create a pattern.</i>
---------	--------------------------

Description

Create a pattern.

Usage

Pattern(x)

Arguments

x regular expression

Value

a pattern

pattern-class	<i>Pattern class.</i>
---------------	-----------------------

Description

Pattern class.

pmx_element-class	<i>PMX element class.</i>
-------------------	---------------------------

Description

PMX element class.

pmx_position-class	<i>PMX position class.</i>
--------------------	----------------------------

Description

PMX position class.

pmx_position_by_element-class
<i>PMX position by element class.</i>

Description

PMX position by element class.

pmx_position_by_index-class
<i>PMX position by index class.</i>

Description

PMX position by index class.

Position	<i>Element position in list.</i>
----------	----------------------------------

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	<i>Process extra arguments.</i>
-----------------	---------------------------------

Description

Process extra arguments.

Usage

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

Arguments

args	arguments list
name	argument name to retrieve
default	default value if argument is not present
mandatory	mandatory argument, logical value

Value

requested argument value

processJSONDoubleArrayParameter	<i>Process JSON double array parameter.</i>
---------------------------------	---

Description

Process JSON double array parameter.

Usage

processJSONDoubleArrayParameter(x)

Arguments

x	JSON data, OMEGA or SIGMA parameter
---	-------------------------------------

Value

updated JSON data with updated 'name' field and removed 'name2' field

properties_record-class	<i>Properties record class.</i>
-------------------------	---------------------------------

Description

Properties record class.

rate_record-class	<i>(Infusion)-rate record class.</i>
-------------------	--------------------------------------

Description

(Infusion)-rate record class.

read	<i>Generic read method to read data from a file or a folder.</i>
------	--

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	<i>Read all parameters files at once.</i>
--------------------	---

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	<i>Read a Campsis model.</i>
--------------	------------------------------

Description

Read a Campsis model.

Usage

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

Arguments

file	path to folder (old format) or path to JSON file (new format)
------	---

Value

Campsis model

read.model	<i>Read model file.</i>
------------	-------------------------

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	<i>Read parameters file.</i>
-----------------	------------------------------

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	<i>Read variance-covariance file.</i>
-------------	---------------------------------------

Description

Read variance-covariance file.

Usage

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

Arguments

file	path to CSV file
------	------------------

Value

variance-covariance matrix

replace	<i>Replace element by another in list.</i>
---------	--

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'
```

```

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	<i>Replace all occurrences in object.</i>
------------	---

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'

```

```

replaceAll(object, pattern, replacement, ...)

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

## S4 method for signature 'unknown_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

replicate	<i>Replicate generic object.</i>
-----------	----------------------------------

Description

Replicate generic object.

Usage

```
replicate(object, n, settings = NULL, ...)

## S4 method for signature 'campsis_model,integer,auto_replication_settings'
replicate(object, n, settings)

## S4 method for signature 'campsis_model,integer>manual_replication_settings'
replicate(object, n, settings)
```

Arguments

object	generic object
n	number of replicates required
settings	settings for replication
...	extra arguments

Value

object replicated n times

```
replicated_campsis_model-class
```

Replicated Campsis model class.

Description

Replicated Campsis model class.

```
replication_settings-class
```

Replication settings interface.

Description

Replication settings interface.

rxodeCode	<i>Get code for rxode2</i>
-----------	----------------------------

Description

Get code for rxode2

Usage

```
rxodeCode(model)
```

Arguments

model	Campsis model
-------	---------------

Value

corresponding model code for rxode2

rxodeMatrix	<i>Get the OMEGA/SIGMA matrix for rxode2.</i>
-------------	---

Description

Get the OMEGA/SIGMA matrix for rxode2.

Usage

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

Arguments

model	Campsis model or Campsis parameters
type	either omega or sigma

Value

omega/sigma named matrix

rxodeParams	<i>Get the parameters vector for rxode2.</i>
-------------	--

Description

Get the parameters vector for rxode2.

Usage

```
rxodeParams(model)
```

Arguments

model	Campsis model
-------	---------------

Value

named vector with THETA values

rxode_type-class	<i>RxODE/rxode2 export type class.</i>
------------------	--

Description

RxODE/rxode2 export type class.

select	<i>Get a subset of an object.</i>
--------	-----------------------------------

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

setMinMax

Set the minimum and maximum value on a model parameter.

Description

Set the minimum and maximum value on a model parameter.

Usage

```
setMinMax(object, parameter, min, max, ...)

## S4 method for signature 'parameters,parameter,numeric,numeric'
setMinMax(object, parameter, min, max, ...)

## S4 method for signature 'parameters,character,numeric,numeric'
setMinMax(object, parameter, min, max, ...)

## S4 method for signature 'campsis_model,parameter,numeric,numeric'
setMinMax(object, parameter, min, max, ...)

## S4 method for signature 'campsis_model,character,numeric,numeric'
setMinMax(object, parameter, min, max, ...)
```

Arguments

object	model or parameters object
parameter	parameter object (Theta, Omega or Sigma)
min	minimum value for this parameter when parameter uncertainty is enabled
max	maximum value for this parameter when parameter uncertainty is enabled
...	extra arguments, unused

Value

updated object

shiftOmegaIndexes	<i>Shift OMEGA indexes.</i>
-------------------	-----------------------------

Description

Shift OMEGA indexes.

Usage

```
shiftOmegaIndexes(object)

## S4 method for signature 'omega_block'
shiftOmegaIndexes(object)
```

Arguments

object omega block

Value

same block but shifted

Sigma	<i>Create a SIGMA parameter.</i>
-------	----------------------------------

Description

Create a SIGMA parameter.

Usage

```
Sigma(
  name = NA,
  index = NA,
  index2 = NA,
  value = NA,
  min = NA,
  max = 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
min	minimum value for this parameter when parameter uncertainty is enabled
max	maximum value for this parameter when parameter uncertainty is enabled
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	<i>Sigma parameter class.</i>
-------------	-------------------------------

Description

Sigma parameter class.

single_array_parameter-class	<i>Single-array parameter class. This parameter has a single index value.</i>
------------------------------	---

Description

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

sort	<i>Sort the specified list.</i>
------	---------------------------------

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, ...)

## S4 method for signature 'omega_blocks'
sort(x, decreasing = FALSE, ...)
```

Arguments

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

Value

same list but ordered

standardise	<i>Standardise.</i>
-------------	---------------------

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, ...)

## S4 method for signature 'campsis_model'
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	<i>Statements record class.</i>
-------------------------	---------------------------------

Description

Statements record class.

Theta	Create a THETA parameter.
-------	---------------------------

Description

Create a THETA parameter.

Usage

```
Theta(  
  name = NA,  
  index = NA,  
  value = NA,  
  min = NA,  
  max = 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
min	minimum value for this parameter when parameter uncertainty is enabled
max	maximum value for this parameter when parameter uncertainty is enabled
fix	parameter was fixed in estimation, logical value
label	parameter label, optional
unit	parameter unit, optional
comment	any comment, optional

Value

a THETA parameter

theta-class	<i>Theta parameter class.</i>
-------------	-------------------------------

Description

Theta parameter class.

Slots

unit parameter unit

toString	<i>ToString generic method.</i>
----------	---------------------------------

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

Value

character value/vector

trim	<i>Trim character vector. Remove all leading and trailing spaces.</i>
------	---

Description

Trim character vector. Remove all leading and trailing spaces.

Usage

```
trim(x)
```

Arguments

x	character vector
---	------------------

Value

character vector without leading and trailing spaces

UnknownStatement	<i>Create a new ordinary differential equation (ODE).</i>
------------------	---

Description

Create a new ordinary differential equation (ODE).

Usage

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

Arguments

line	line which was not recognised
comment	comment if any, single character string

Value

an unknown statement

unknown_statement-class	<i>Unknown statement class. Any statement not recognized by campsismod.</i>
-------------------------	---

Description

Unknown statement class. Any statement not recognized by campsismod.

updateCompartments	<i>Update compartments list from the persisted records. Exported especially for package campsistrans. However, this method should not be called.</i>
--------------------	--

Description

Update compartments list from the persisted records. Exported especially for package campsistrans. 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

x variable name

Value

a variable pattern

variable_pattern-class	Variable pattern class.
------------------------	-------------------------

Description

Variable pattern class.

write	<i>Write generic object to files.</i>
-------	---------------------------------------

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, ...)

## S4 method for signature 'json_element,character'
write(object, file, digits = 12, ...)
```

Arguments

object	generic object
file	path of the output file or directory
...	extra arguments
digits	significant digits in JSON file, default is 12

Value

logical value, TRUE for success, FALSE for failure

writeParameters	<i>Write subset of parameters (theta, omega or sigma).</i>
-----------------	--

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	<i>Write variance-covariance matrix.</i>
-------------	--

Description

Write variance-covariance matrix.

Usage

writeVarcov(object, file)

Arguments

- object matrix
- file filename

Value

TRUE if success

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