

# Package ‘campsis’

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**Type** Package

**Title** Generic PK/PD Simulation Platform CAMPSIS

**Version** 1.3.0

**Description** A generic, easy-to-use and intuitive pharmacokinetic/pharmacodynamic (PK/PD) simulation platform based on R packages 'rxode2', 'RxODE' and 'mrgsolve'. CAMPSIS provides an abstraction layer over the underlying processes of writing a PK/PD model, assembling a custom dataset and running a simulation. CAMPSIS has a strong dependency to the R package 'campsismod', which allows to read/write a model from/to files and adapt it further on the fly in the R environment. Package 'campsis' allows the user to assemble a dataset in an intuitive manner. Once the user's dataset is ready, the package is in charge of preparing the simulation, calling 'rxode2', 'RxODE' or 'mrgsolve' (at the user's choice) and returning the results, for the given model, dataset and desired simulation settings.

**License** GPL (>= 3)

**URL** <https://github.com/Calvagone/campsis>, <https://calvagone.github.io/>

**BugReports** <https://github.com/Calvagone/campsis/issues>

**Depends** campsismod, R (>= 4.0.0)

**Imports** assertthat, digest, dplyr, ggplot2, MASS, methods, plyr, progress, purrr, rlang, stats, tibble, tidyverse

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**Collate** 'global.R' 'utilities.R' 'check.R' 'generic.R' 'seed.R'  
'distribution.R' 'dataset\_config.R' 'time\_entry.R' 'occasion.R'  
'occasions.R' 'treatment\_ivov.R' 'treatment\_ivovs.R'  
'dose\_adaptation.R' 'dose\_adaptations.R' 'treatment\_entry.R'

```
'treatment.R' 'observations.R' 'observations_set.R'
'covariate.R' 'covariates.R' 'bootstrap.R' 'protocol.R' 'arm.R'
'arms.R' 'event.R' 'events.R' 'scenario.R' 'scenarios.R'
'simulation_engine.R' 'dataset.R' 'parameter_uncertainty.R'
'event_logic.R' 'simulation_progress.R' 'dataset_summary.R'
'simulate_preprocess.R' 'simulate.R' 'results_processing.R'
'default_plot.R'
```

**NeedsCompilation** no

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## R topics documented:

applyCompartmentCharacteristics . . . . .	4
Arm . . . . .	5
arm-class . . . . .	5
arms-class . . . . .	6
Bolus . . . . .	6
bolus-class . . . . .	7
Bootstrap . . . . .	7
bootstrap-class . . . . .	8
BootstrapDistribution . . . . .	8
bootstrap_distribution-class . . . . .	9
ConstantDistribution . . . . .	9
constant_distribution-class . . . . .	9
Covariate . . . . .	10
covariate-class . . . . .	10
covariates-class . . . . .	10
Dataset . . . . .	11
dataset-class . . . . .	11
DataSetConfig . . . . .	12
dataset_config-class . . . . .	12
DiscreteDistribution . . . . .	13
distribution-class . . . . .	13
DoseAdaptation . . . . .	13
dose_adaptation-class . . . . .	14
dose_adaptations-class . . . . .	14
dosingOnly . . . . .	14
EtaDistribution . . . . .	15
Event . . . . .	15
event-class . . . . .	16
EventCovariate . . . . .	16
Events . . . . .	17
events-class . . . . .	17

event_covariate-class . . . . .	17
FixedDistribution . . . . .	18
fixed_covariate-class . . . . .	18
fixed_distribution-class . . . . .	18
FunctionDistribution . . . . .	19
function_distribution-class . . . . .	19
generateIIV . . . . .	20
getCovariates . . . . .	20
getEventCovariates . . . . .	21
getFixedCovariates . . . . .	21
getIOVs . . . . .	22
getOccasions . . . . .	23
getSeedForDatasetExport . . . . .	23
getSeedForIteration . . . . .	24
getSeedForParametersSampling . . . . .	24
getTimes . . . . .	25
getTimeVaryingCovariates . . . . .	26
Infusion . . . . .	26
infusion-class . . . . .	27
IOV . . . . .	28
length,arm-method . . . . .	28
length,dataset-method . . . . .	29
LogNormalDistribution . . . . .	29
mrgsolve_engine-class . . . . .	30
NormalDistribution . . . . .	30
Observations . . . . .	30
observations-class . . . . .	31
observations_set-class . . . . .	31
obsOnly . . . . .	31
Occasion . . . . .	32
occasion-class . . . . .	32
occasions-class . . . . .	32
ParameterDistribution . . . . .	33
PI . . . . .	33
protocol-class . . . . .	34
retrieveParameterValue . . . . .	34
rxode_engine-class . . . . .	34
sample . . . . .	35
Scenario . . . . .	36
scenario-class . . . . .	36
Scenarios . . . . .	37
scenarios-class . . . . .	37
setLabel . . . . .	37
setSubjects . . . . .	38
shadedPlot . . . . .	38
simulate . . . . .	39
SimulationProgress . . . . .	43
simulation_engine-class . . . . .	43

simulation_progress-class . . . . .	44
spaghettiPlot . . . . .	44
TimeVaryingCovariate . . . . .	45
time_varying_covariate-class . . . . .	45
treatment-class . . . . .	45
treatment iov-class . . . . .	46
treatment iovs-class . . . . .	46
undefined_distribution-class . . . . .	46
UniformDistribution . . . . .	47
VPC . . . . .	47
vpcPlot . . . . .	48

<b>Index</b>	<b>49</b>
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## **applyCompartmentCharacteristics**

*Apply compartment characteristics from model. In practice, only compartment infusion duration needs to be applied.*

---

### **Description**

Apply compartment characteristics from model. In practice, only compartment infusion duration needs to be applied.

### **Usage**

```
applyCompartmentCharacteristics(table, properties)
```

### **Arguments**

table	current dataset
properties	compartment properties from model

### **Value**

updated dataset

---

Arm	<i>Create a treatment arm.</i>
-----	--------------------------------

---

## Description

Create a treatment arm.

## Usage

```
Arm(id = as.integer(NA), subjects = 1, label = as.character(NA))
```

## Arguments

id	unique identifier for this arm (available through dataset), integer. If NA (default), this identifier is auto-incremented.
subjects	number of subjects in arm, integer
label	arm label, single character string. If set, this label will be output in the ARM column of CAMPSIS instead of the identifier.

## Value

an arm

---

arm-class	<i>Arm class.</i>
-----------	-------------------

---

## Description

Arm class.

## Slots

id	arm unique ID, integer
subjects	number of subjects in arm, integer
label	arm label, single character string
protocol	protocol
covariates	covariates
bootstrap	covariates to be bootstrapped

---

<code>arms-class</code>	<i>Arms class.</i>
-------------------------	--------------------

---

### Description

Arms class.

---

<code>Bolus</code>	<i>Create one or several bolus(es).</i>
--------------------	---

---

### Description

Create one or several bolus(es).

### Usage

```
Bolus(
  time,
  amount,
  compartment = NA,
  f = NULL,
  lag = NULL,
  ii = NULL,
  addl = NULL
)
```

### Arguments

<code>time</code>	treatment time(s), numeric value or vector. First treatment time if used together with <code>ii</code> and <code>addl</code> .
<code>amount</code>	amount to give as bolus, single numeric value
<code>compartment</code>	compartment index, single integer value
<code>f</code>	fraction of dose amount, distribution
<code>lag</code>	dose lag time, distribution
<code>ii</code>	interdose interval, requires argument 'time' to be a single numeric value
<code>addl</code>	number of additional doses, requires argument 'time' to be a single integer value

### Value

a single bolus or a list of boluses

---

bolus-class	<i>Bolus class.</i>
-------------	---------------------

---

### Description

Bolus class.

---

Bootstrap	<i>Create a bootstrap object.</i>
-----------	-----------------------------------

---

### Description

Create a bootstrap object.

### Usage

```
Bootstrap(  
  data,  
  id = "BS_ID",  
  replacement = FALSE,  
  random = FALSE,  
  export_id = FALSE  
)
```

### Arguments

data	data frame to be bootstrapped. It must have a unique identifier column named according to the specified argument 'id' (default value is 'BS_ID'). Other columns are covariates to bootstrap. They must all be numeric. Whatever the configuration of the bootstrap, these covariates are always read row by row and belong to a same individual.
id	unique identifier column name in data
replacement	values can be reused or not when drawn, logical
random	values are drawn randomly, logical
export_id	tell CAMPSIS if the identifier 'BS_ID' must be output or not, logical

### Value

a bootstrap object

**bootstrap-class**      *Bootstrap class.*

## Description

Bootstrap class.

## Slots

**data** data frame to be bootstrapped. Column 'BS\_ID' is mandatory and corresponds to the original row ID from the bootstrap. It must be numeric and unique. Other columns are covariates to be bootstrapped (row by row).

**replacement** values can be reused or not, logical

**random** values are drawn randomly, logical

**export\_id** tell CAMPSIS if 'BS\_ID' must be exported into the dataset, logical

**BootstrapDistribution** *Create a bootstrap distribution. During function sampling, CAMPSIS will generate values depending on the given data and arguments.*

## Description

Create a bootstrap distribution. During function sampling, CAMPSIS will generate values depending on the given data and arguments.

## Usage

```
BootstrapDistribution(data, replacement = FALSE, random = FALSE)
```

## Arguments

<b>data</b>	values to draw, numeric vector
<b>replacement</b>	values can be reused or not, logical
<b>random</b>	values are drawn randomly, logical

## Value

a bootstrap distribution

---

**bootstrap\_distribution-class**

*Bootstrap distribution class.*

---

**Description**

Bootstrap distribution class.

**Slots**

`data` values to draw, numeric vector  
`replacement` values can be reused or not, logical  
`random` values are drawn randomly, logical

---

`ConstantDistribution` *Create a constant distribution. Its value will be constant across all generated samples.*

---

**Description**

Create a constant distribution. Its value will be constant across all generated samples.

**Usage**

`ConstantDistribution(value)`

**Arguments**

`value` covariate value, single numeric value

**Value**

a constant distribution (same value for all samples)

---

**constant\_distribution-class**

*Constant distribution class.*

---

**Description**

Constant distribution class.

**Slots**

`value` covariate value, single numeric value

---

Covariate	<i>Create a non time-varying (fixed) covariate.</i>
-----------	---

---

**Description**

Create a non time-varying (fixed) covariate.

**Usage**

```
Covariate(name, distribution)
```

**Arguments**

name	covariate name, single character value
distribution	covariate distribution

**Value**

a fixed covariate

---

covariate-class	<i>Covariate class.</i>
-----------------	-------------------------

---

**Description**

Covariate class.

**Slots**

name	covariate name, single character value
distribution	covariate distribution

---

covariates-class	<i>Covariates class.</i>
------------------	--------------------------

---

**Description**

Covariates class.

---

Dataset	<i>Create a dataset.</i>
---------	--------------------------

---

**Description**

Create a dataset.

**Usage**

```
Dataset(subjects = NULL)
```

**Arguments**

subjects	number of subjects in the default arm
----------	---------------------------------------

**Value**

a dataset

---

dataset-class	<i>Dataset class.</i>
---------------	-----------------------

---

**Description**

Dataset class.

**Slots**

arms a list of treatment arms

config dataset configuration for export

iiv data frame containing the inter-individual variability (all ETAS) for the export

---

DatasetConfig	<i>Create a dataset configuration. This configuration allows CAMPSIS to know which are the default depot and observed compartments.</i>
---------------	---

---

**Description**

Create a dataset configuration. This configuration allows CAMPSIS to know which are the default depot and observed compartments.

**Usage**

```
DatasetConfig(
  defDepotCmt = 1,
  defObsCmt = 1,
  exportTSLD = FALSE,
  exportTDOS = FALSE
)
```

**Arguments**

defDepotCmt	default depot compartment, integer
defObsCmt	default observation compartment, integer
exportTSLD	export column TSLD (time since last dose), logical
exportTDOS	export column TDOS (time of last dose), logical

**Value**

a dataset configuration

---

dataset\_config-class    *Dataset configuration class.*

---

**Description**

Dataset configuration class.

**Slots**

def_depot_cmt	default depot compartment, integer
def_obs_cmt	default observation compartment, integer
export_tsld	export column TSLD, logical
export_tdos	export column TDOS, logical

---

DiscreteDistribution *Discrete distribution.*

---

**Description**

Discrete distribution.

**Usage**

```
DiscreteDistribution(x, prob, replace = TRUE)
```

**Arguments**

x	vector of one or more integers from which to choose
prob	a vector of probability weights for obtaining the elements of the vector being sampled
replace	should sampling be with replacement, default is TRUE

**Value**

a discrete distribution

---

distribution-class *Distribution class. See this class as an interface.*

---

**Description**

Distribution class. See this class as an interface.

---

DoseAdaptation *Create a dose adaptation.*

---

**Description**

Create a dose adaptation.

**Usage**

```
DoseAdaptation(formula, compartments = integer(0))
```

**Arguments**

formula	formula to apply, single character string, e.g. "AMT*WT"
compartments	compartment numbers where the formula needs to be applied, integer vector. Default is integer(0) (formula applied on all compartments)

**Value**

a fixed covariate

---

**dose\_adaptation-class** *Dose adaptation class.*

---

**Description**

Dose adaptation class.

**Slots**

**formula** formula to apply, single character string, e.g. "AMT\*WT"

**compartments** compartment numbers where the formula needs to be applied

---

**dose\_adaptations-class**  
*Dose adaptations class.*

---

**Description**

Dose adaptations class.

---

**dosingOnly** *Filter CAMPSIS output on dosing rows.*

---

**Description**

Filter CAMPSIS output on dosing rows.

**Usage**

`dosingOnly(x)`

**Arguments**

**x** data frame, CAMPSIS output

**Value**

a data frame with the dosing rows

---

EtaDistribution	<i>Create an ETA distribution. The resulting distribution is a normal distribution, with mean=0 and sd=sqrt(OMEGA).</i>
-----------------	---

---

**Description**

Create an ETA distribution. The resulting distribution is a normal distribution, with mean=0 and sd=sqrt(OMEGA).

**Usage**

```
EtaDistribution(model, omega)
```

**Arguments**

model	model
omega	corresponding THETA name, character

**Value**

an ETA distribution

---

Event	<i>Create an interruption event.</i>
-------	--------------------------------------

---

**Description**

Create an interruption event.

**Usage**

```
Event(name = NULL, times, fun, debug = FALSE)
```

**Arguments**

name	event name, character value
times	interruption times, numeric vector
fun	event function to apply at each interruption
debug	output the variables that were changed through this event

**Value**

an event definition

---

event-class	<i>Event class.</i>
-------------	---------------------

---

## Description

Event class.

## Slots

name event name, character value  
times interruption times, numeric vector  
fun event function to apply at each interruption  
debug output the variables that were changed through this event

---

EventCovariate	<i>Create an event covariate. These covariates can be modified further in interruption events.</i>
----------------	--

---

## Description

Create an event covariate. These covariates can be modified further in interruption events.

## Usage

```
EventCovariate(name, distribution)
```

## Arguments

name	covariate name, character
distribution	covariate distribution at time 0

## Value

a time-varying covariate

---

Events

*Create a list of interruption events.*

---

### Description

Create a list of interruption events.

### Usage

`Events()`

### Value

a events object

---

events-class

*Events class.*

---

### Description

Events class.

---

event\_covariate-class

*Event covariate class.*

---

### Description

Event covariate class.

---

**FixedDistribution**      *Create a fixed distribution. Each sample will be assigned a fixed value coming from vector 'values'.*

---

**Description**

Create a fixed distribution. Each sample will be assigned a fixed value coming from vector 'values'.

**Usage**

```
FixedDistribution(values)
```

**Arguments**

values            covariate values, numeric vector (1 value per sample)

**Value**

a fixed distribution (1 value per sample)

---

**fixed\_covariate-class**    *Fixed covariate class.*

---

**Description**

Fixed covariate class.

---

**fixed\_distribution-class**      *Fixed distribution class.*

---

**Description**

Fixed distribution class.

**Slots**

values covariate values, numeric vector (1 value per sample)

---

**FunctionDistribution** *Create a function distribution. During distribution sampling, the provided function will be responsible for generating values for each sample. If first argument of this function is not the size (n), please tell which argument corresponds to the size 'n' (e.g. list(size="n")).*

---

## Description

Create a function distribution. During distribution sampling, the provided function will be responsible for generating values for each sample. If first argument of this function is not the size (n), please tell which argument corresponds to the size 'n' (e.g. list(size="n")).

## Usage

```
FunctionDistribution(fun, args)
```

## Arguments

fun	function name, character (e.g. 'rnorm')
args	list of arguments (e.g list(mean=70, sd=10))

## Value

a function distribution

---

**function\_distribution-class**  
*Function distribution class.*

---

## Description

Function distribution class.

## Slots

fun	function name, character (e.g. 'rnorm')
args	list of arguments (e.g list(mean=70, sd=10))

`generateIIV`*Generate IIV.***Description**

Generate IIV.

**Usage**

```
generateIIV(omega, n)
```

**Arguments**

<code>omega</code>	omega matrix
<code>n</code>	number of subjects

**Value**

IIV data frame

`getCovariates`*Get all covariates (fixed / time-varying / event covariates).***Description**

Get all covariates (fixed / time-varying / event covariates).

**Usage**

```
getCovariates(object)

## S4 method for signature 'covariates'
getCovariates(object)

## S4 method for signature 'arm'
getCovariates(object)

## S4 method for signature 'arms'
getCovariates(object)

## S4 method for signature 'dataset'
getCovariates(object)
```

**Arguments**

<code>object</code>	any object
---------------------	------------

**Value**

all covariates from object

---

getEventCovariates     *Get all event-related covariates.*

---

**Description**

Get all event-related covariates.

**Usage**

```
getEventCovariates(object)

## S4 method for signature 'covariates'
getEventCovariates(object)

## S4 method for signature 'arm'
getEventCovariates(object)

## S4 method for signature 'arms'
getEventCovariates(object)

## S4 method for signature 'dataset'
getEventCovariates(object)
```

**Arguments**

object        any object

**Value**

all event-related covariates from object

---

getFixedCovariates     *Get all fixed covariates.*

---

**Description**

Get all fixed covariates.

**Usage**

```
getFixedCovariates(object)

## S4 method for signature 'covariates'
getFixedCovariates(object)

## S4 method for signature 'arm'
getFixedCovariates(object)

## S4 method for signature 'arms'
getFixedCovariates(object)

## S4 method for signature 'dataset'
getFixedCovariates(object)
```

**Arguments**

object            any object

**Value**

all fixed covariates from object

**getIOVs**

*Get all IOV objects.*

**Description**

Get all IOV objects.

**Usage**

```
getIOVs(object)

## S4 method for signature 'arm'
getIOVs(object)

## S4 method for signature 'arms'
getIOVs(object)

## S4 method for signature 'dataset'
getIOVs(object)
```

**Arguments**

object            any object

**Value**

all IOV's from object

---

getOccurrences

*Get all occasions.*

---

**Description**

Get all occasions.

**Usage**

```
getOccurrences(object)

## S4 method for signature 'arm'
getOccurrences(object)

## S4 method for signature 'arms'
getOccurrences(object)

## S4 method for signature 'dataset'
getOccurrences(object)
```

**Arguments**

object            any object

**Value**

all occasions from object

---

getSeedForDatasetExport

*Get seed for dataset export.*

---

**Description**

Get seed for dataset export.

**Usage**

```
getSeedForDatasetExport(seed, replicate, iterations)
```

**Arguments**

<code>seed</code>	original seed
<code>replicate</code>	the current replicate number
<code>iterations</code>	total number of iterations

**Value**

the seed value used to export the dataset

`getSeedForIteration`     *Get seed for iteration.*

**Description**

Get seed for iteration.

**Usage**

```
getSeedForIteration(seed, replicate, iterations, iteration)
```

**Arguments**

<code>seed</code>	original seed
<code>replicate</code>	the current replicate number
<code>iterations</code>	total number of iterations
<code>iteration</code>	current iteration number

**Value**

the seed value to be used for the given replicate number and iteration

`getSeedForParametersSampling`  
*Get seed for parameter uncertainty sampling.*

**Description**

Get seed for parameter uncertainty sampling.

**Usage**

```
getSeedForParametersSampling(seed)
```

**Arguments**

seed original seed

**Value**

the seed value used to sample parameter uncertainty

---

getTimes *Get all distinct times for the specified object.*

---

**Description**

Get all distinct times for the specified object.

**Usage**

```
getTimes(object)

## S4 method for signature 'observations_set'
getTimes(object)

## S4 method for signature 'arm'
getTimes(object)

## S4 method for signature 'arms'
getTimes(object)

## S4 method for signature 'events'
getTimes(object)

## S4 method for signature 'dataset'
getTimes(object)
```

**Arguments**

object any object

**Value**

numeric vector with all unique times, sorted

---

```
getTimeVaryingCovariates  
Get all time-varying covariates.
```

---

## Description

Get all time-varying covariates.

## Usage

```
getTimeVaryingCovariates(object)  
  
## S4 method for signature 'covariates'  
getTimeVaryingCovariates(object)  
  
## S4 method for signature 'arm'  
getTimeVaryingCovariates(object)  
  
## S4 method for signature 'arms'  
getTimeVaryingCovariates(object)  
  
## S4 method for signature 'dataset'  
getTimeVaryingCovariates(object)
```

## Arguments

object            any object

## Value

all time-varying covariates from object

---

```
Infusion            Create one or several infusion(s).
```

---

## Description

Create one or several infusion(s).

**Usage**

```
Infusion(
  time,
  amount,
  compartment = NA,
  f = NULL,
  lag = NULL,
  duration = NULL,
  rate = NULL,
  ii = NULL,
  addl = NULL
)
```

**Arguments**

time	treatment time(s), numeric value or vector. First treatment time if used together with ii and addl.
amount	total amount to infuse, numeric
compartment	compartment index, integer
f	fraction of infusion amount, distribution
lag	infusion lag time, distribution
duration	infusion duration, distribution
rate	infusion rate, distribution
ii	interdose interval, requires argument 'time' to be a single numeric value
addl	number of additional doses, requires argument 'time' to be a single integer value

**Value**

a single infusion or a list of infusions.

infusion-class

*Infusion class.*

**Description**

Infusion class.

**Slots**

duration infusion duration, distribution  
rate infusion rate, distribution

IOV	<i>Define inter-occasion variability (IOV) into the dataset. A new variable of name 'colname' will be output into the dataset and will vary at each dose number according to the given distribution.</i>
-----	--

**Description**

Define inter-occasion variability (IOV) into the dataset. A new variable of name 'colname' will be output into the dataset and will vary at each dose number according to the given distribution.

**Usage**

```
IOV(colname, distribution, doseNumbers = NULL)
```

**Arguments**

colname	name of the column that will be output in dataset
distribution	distribution
doseNumbers	dose numbers, if provided, IOV is generated at these doses only. By default, IOV is generated for all doses.

**Value**

an IOV object

length,arm-method	<i>Return the number of subjects contained in this arm.</i>
-------------------	---

**Description**

Return the number of subjects contained in this arm.

**Usage**

```
## S4 method for signature 'arm'
length(x)
```

**Arguments**

x	arm
---	-----

**Value**

a number

---

length,dataset-method *Return the number of subjects contained in this dataset.*

---

**Description**

Return the number of subjects contained in this dataset.

**Usage**

```
## S4 method for signature 'dataset'  
length(x)
```

**Arguments**

x dataset

**Value**

a number

---

LogNormalDistribution *Create a log normal distribution.*

---

**Description**

Create a log normal distribution.

**Usage**

```
LogNormalDistribution(meanlog, sdlog)
```

**Arguments**

meanlog	mean value of distribution in log domain
sdlog	standard deviation of distribution in log domain

**Value**

a log normal distribution

`mrgsolve_engine-class` *mrgsolve engine class.*

### Description

`mrgsolve` engine class.

`NormalDistribution` *Create a normal distribution.*

### Description

Create a normal distribution.

### Usage

```
NormalDistribution(mean, sd)
```

### Arguments

<code>mean</code>	mean value of distribution
<code>sd</code>	standard deviation of distribution

### Value

a normal distribution

`Observations` *Create an observations list. Please note that the provided 'times' will automatically be sorted. Duplicated times will be removed.*

### Description

Create an observations list. Please note that the provided 'times' will automatically be sorted. Duplicated times will be removed.

### Usage

```
Observations(times, compartment = NA)
```

### Arguments

<code>times</code>	observation times, numeric vector
<code>compartment</code>	compartment index, integer

**Value**

an observations list

---

observations-class     *Observations class.*

---

**Description**

Observations class.

**Slots**

times observation times, numeric vector  
compartment compartment index, integer  
dv observed values, numeric vector (FOR EXTERNAL USE)

---

observations\_set-class  
                  *Observations set class.*

---

**Description**

Observations set class.

---

obsOnly                *Filter CAMPSIS output on observation rows.*

---

**Description**

Filter CAMPSIS output on observation rows.

**Usage**

obsOnly(x)

**Arguments**

x                    data frame, CAMPSIS output

**Value**

a data frame with the observation rows

Occasion	<i>Define a new occasion. Occasions are defined by mapping occasion values to dose numbers. A new column will automatically be created in the exported dataset.</i>
----------	---

**Description**

Define a new occasion. Occasions are defined by mapping occasion values to dose numbers. A new column will automatically be created in the exported dataset.

**Usage**

```
Occasion(colname, values, doseNumbers)
```

**Arguments**

colname	name of the column that will be output in dataset
values	the occasion numbers, any integer vector
doseNumbers	the related dose numbers, any integer vector of same length as 'values'

**Value**

occasion object

occasion-class	<i>Occasion class.</i>
----------------	------------------------

**Description**

Occasion class.

**Slots**

colname	single character value representing the column name related to this occasion
values	occasion values, integer vector, same length as dose_numbers
dose_numbers	associated dose numbers, integer vector, same length as values

occasions-class	<i>Occurrences class.</i>
-----------------	---------------------------

**Description**

Occurrences class.

---

**ParameterDistribution** *Create a parameter distribution. The resulting distribution is a log-normal distribution, with meanlog=log(THETA) and sdlog=sqrt(OMEGA).*

---

**Description**

Create a parameter distribution. The resulting distribution is a log-normal distribution, with meanlog=log(THETA) and sdlog=sqrt(OMEGA).

**Usage**

```
ParameterDistribution(model, theta, omega = NULL)
```

**Arguments**

model	model
theta	corresponding THETA name, character
omega	corresponding OMEGA name, character, NULL if not defined

**Value**

a parameter distribution

---

PI	<i>Compute the prediction interval summary over time.</i>
----	---

---

**Description**

Compute the prediction interval summary over time.

**Usage**

```
PI(x, output, scenarios = NULL, level = 0.9, gather = TRUE)
```

**Arguments**

x	data frame
output	variable to show, character value
scenarios	scenarios, character vector, NULL is default
level	PI level, default is 0.9 (90% PI)
gather	FALSE: med, low & up columns, TRUE: metric column

**Value**

a summary table

**protocol-class**      *Protocol class.*

### Description

Protocol class.

**retrieveParameterValue**

*Retrieve the parameter value (standardized) for the specified parameter name.*

### Description

Retrieve the parameter value (standardized) for the specified parameter name.

### Usage

```
retrieveParameterValue(model, paramName, default = NULL, mandatory = FALSE)
```

### Arguments

model	model
paramName	parameter name
default	default value if not found
mandatory	must be in model or not

### Value

the standardized parameter value or the given default value if not found

**rxode\_engine-class**      *RxODE/rxode2 engine class.*

### Description

RxODE/rxode2 engine class.

### Slots

rxode2 logical field to indicate if CAMPSIS should use rxode2 (field set to TRUE) or RxODE (field set to FALSE). Default is TRUE.

---

sample	<i>Sample generic object.</i>
--------	-------------------------------

---

## Description

Sample generic object.

## Usage

```
sample(object, n, ...)

## S4 method for signature 'constant_distribution,integer'
sample(object, n)

## S4 method for signature 'fixed_distribution,integer'
sample(object, n)

## S4 method for signature 'function_distribution,integer'
sample(object, n)

## S4 method for signature 'bootstrap_distribution,integer'
sample(object, n)

## S4 method for signature 'bolus,integer'
sample(object, n, ...)

## S4 method for signature 'infusion,integer'
sample(object, n, ...)

## S4 method for signature 'observations,integer'
sample(object, n, ...)

## S4 method for signature 'covariate,integer'
sample(object, n)

## S4 method for signature 'bootstrap,integer'
sample(object, n)

## S4 method for signature 'campsis_model,integer'
sample(object, n)
```

## Arguments

object	generic object
n	number of samples required
...	extra arguments

**Value**

sampling result

---

Scenario

*Create an scenario.*

---

**Description**

Create an scenario.

**Usage**

```
Scenario(name = NULL, model = NULL, dataset = NULL)
```

**Arguments**

name	scenario name, single character string
model	either a CAMPSIS model, a function or lambda-style formula
dataset	either a CAMPSIS dataset, a function or lambda-style formula

**Value**

a new scenario

---

scenario-class

*Scenario class.*

---

**Description**

Scenario class.

**Slots**

name	scenario name, single character string
model	either a CAMPSIS model, a function or lambda-style formula
dataset	either a CAMPSIS dataset, a function or lambda-style formula

---

Scenarios	<i>Create a list of scenarios.</i>
-----------	------------------------------------

---

**Description**

Create a list of scenarios.

**Usage**

```
Scenarios()
```

**Value**

a scenarios object

---

scenarios-class	<i>Scenarios class.</i>
-----------------	-------------------------

---

**Description**

Scenarios class.

---

setLabel	<i>Set the label.</i>
----------	-----------------------

---

**Description**

Set the label.

**Usage**

```
setLabel(object, x)

## S4 method for signature 'arm,character'
setLabel(object, x)
```

**Arguments**

object	any object that has a label
x	the new label

**Value**

the updated object

`setSubjects`            *Set the number of subjects.*

### Description

Set the number of subjects.

### Usage

```
setSubjects(object, x)

## S4 method for signature 'arm,integer'
setSubjects(object, x)

## S4 method for signature 'dataset,integer'
setSubjects(object, x)
```

### Arguments

<code>object</code>	any object
<code>x</code>	the new number of subjects

### Value

the updated object

`shadedPlot`            *Shaded plot (or prediction interval plot).*

### Description

Shaded plot (or prediction interval plot).

### Usage

```
shadedPlot(x, output, scenarios = NULL, level = 0.9, alpha = 0.25)
```

### Arguments

<code>x</code>	data frame
<code>output</code>	variable to show
<code>scenarios</code>	scenarios
<code>level</code>	PI level, default is 0.9 (90% PI)
<code>alpha</code>	alpha parameter (transparency) given to geom_ribbon

**Value**

a ggplot object

---

**simulate***Simulate function.*

---

**Description**

Simulate function.

**Usage**

```
simulate(  
  model,  
  dataset,  
  dest = NULL,  
  events = NULL,  
  scenarios = NULL,  
  tablefun = NULL,  
  outvars = NULL,  
  outfun = NULL,  
  seed = NULL,  
  replicates = 1,  
  nocb = NULL,  
  dosing = FALSE,  
  ...  
)  
  
## S4 method for signature  
## 'campsis_model,  
##   dataset,  
##   character,  
##   events,  
##   scenarios,  
##   `function`,  
##   character,  
##   `function`,  
##   integer,  
##   integer,  
##   logical,  
##   logical'  
simulate(  
  model,  
  dataset,  
  dest = NULL,  
  events = NULL,
```

```
scenarios = NULL,
tablefun = NULL,
outvars = NULL,
outfun = NULL,
seed = NULL,
replicates = 1,
nocb = NULL,
dosing = FALSE,
...
)

## S4 method for signature
## 'campsis_model,
##   tbl_df,
##   character,
##   events,
##   scenarios,
##   `function`,
##   character,
##   `function`,
##   integer,
##   integer,
##   logical,
##   logical'
simulate(
  model,
  dataset,
  dest = NULL,
  events = NULL,
  scenarios = NULL,
  tablefun = NULL,
  outvars = NULL,
  outfun = NULL,
  seed = NULL,
  replicates = 1,
  nocb = NULL,
  dosing = FALSE,
  ...
)
## S4 method for signature
## 'campsis_model,
##   data.frame,
##   character,
##   events,
##   scenarios,
##   `function`,
##   character,
```

```
##  `function`,
##  integer,
##  integer,
##  logical,
##  logical'
simulate(
  model,
  dataset,
  dest = NULL,
  events = NULL,
  scenarios = NULL,
  tablefun = NULL,
  outvars = NULL,
  outfun = NULL,
  seed = NULL,
  replicates = 1,
  nocb = NULL,
  dosing = FALSE,
  ...
)

## S4 method for signature
## 'campsis_model,
##   tbl_df,
##   rkode_engine,
##   events,
##   scenarios,
##   `function`,
##   character,
##   `function`,
##   integer,
##   integer,
##   logical,
##   logical'
simulate(
  model,
  dataset,
  dest = NULL,
  events = NULL,
  scenarios = NULL,
  tablefun = NULL,
  outvars = NULL,
  outfun = NULL,
  seed = NULL,
  replicates = 1,
  nocb = NULL,
  dosing = FALSE,
  ...
```

```

)
## S4 method for signature
## 'campsis_model',
##   tbl_df,
##   mrgsolve_engine,
##   events,
##   scenarios,
##   `function`,
##   character,
##   `function`,
##   integer,
##   integer,
##   logical,
##   logical'
simulate(
  model,
  dataset,
  dest = NULL,
  events = NULL,
  scenarios = NULL,
  tablefun = NULL,
  outvars = NULL,
  outfun = NULL,
  seed = NULL,
  replicates = 1,
  nocb = NULL,
  dosing = FALSE,
  ...
)

```

## Arguments

<code>model</code>	generic CAMPSIS model
<code>dataset</code>	CAMPSIS dataset or 2-dimensional table
<code>dest</code>	destination simulation engine, default is 'RxODE'
<code>events</code>	interruption events
<code>scenarios</code>	list of scenarios to be simulated
<code>tablefun</code>	function or lambda formula to apply on exported 2-dimensional dataset
<code>outvars</code>	variables to output in resulting dataframe
<code>outfun</code>	function or lambda formula to apply on resulting dataframe after each replicate
<code>seed</code>	seed value
<code>replicates</code>	number of replicates, default is 1
<code>nocb</code>	next-observation carried backward mode (NOCB), default value is TRUE for mrgsolve, FALSE for RxODE
<code>dosing</code>	output dosing information, default is FALSE
<code>...</code>	optional arguments like 'declare' and 'nocbvars'

**Value**

dataframe with all results

---

**SimulationProgress**

*Create a simulation progress object.*

---

**Description**

Create a simulation progress object.

**Usage**

```
SimulationProgress(replicates = 1, scenarios = 1)
```

**Arguments**

replicates	total number of replicates to simulate
scenarios	total number of scenarios to simulate

**Value**

a progress bar

---

**simulation\_engine-class**

*Simulation engine class.*

---

**Description**

Simulation engine class.

**simulation\_progress-class***Simulation progress class.***Description**

Simulation progress class.

**Arguments**

<code>replicates</code>	total number of replicates to simulate
<code>scenarios</code>	total number of scenarios to simulate
<code>iterations</code>	total number of iterations to simulate
<code>slices</code>	total number of slices to simulate
<code>replicate</code>	current replicate number being simulated
<code>scenario</code>	current scenario number being simulated
<code>iteration</code>	current iteration number being simulated
<code>slice</code>	current slice number being simulated

**spaghettiPlot***Spaghetti plot.***Description**

Spaghetti plot.

**Usage**

```
spaghettiPlot(x, output, scenarios = NULL)
```

**Arguments**

<code>x</code>	data frame
<code>output</code>	variable to show
<code>scenarios</code>	scenarios

**Value**

plot

---

TimeVaryingCovariate *Create a time-varying covariate. This covariate will be implemented using EVID=2 rows in the exported dataset and will not use interruption events.*

---

### Description

Create a time-varying covariate. This covariate will be implemented using EVID=2 rows in the exported dataset and will not use interruption events.

### Usage

```
TimeVaryingCovariate(name, table)
```

### Arguments

name	covariate name, character
table	data.frame, must contain the mandatory columns 'TIME' and 'VALUE'. An 'ID' column may also be specified. In that case, ID's between 1 and the max number of subjects in the dataset/arm can be used. All ID's must have a VALUE defined for TIME 0.

### Value

a time-varying covariate

---

time\_varying\_covariate-class  
*Time-varying covariate class.*

---

### Description

Time-varying covariate class.

---

treatment-class      *Treatment class.*

---

### Description

Treatment class.

---

**treatment iov-class**    *Treatment IOV class.*

---

### Description

Treatment IOV class.

### Slots

`colname` name of the column that will be output in dataset

`distribution` distribution

`dose_numbers` associated dose numbers, integer vector, same length as values

---

**treatment\_iobs-class**    *Treatment IOV's class.*

---

### Description

Treatment IOV's class.

---

**undefined\_distribution-class**

*Undefined distribution class. This type of object is automatically created in method `toExplicitDistribution()` when the user does not provide a concrete distribution. This is because S4 objects do not accept NULL values.*

---

### Description

Undefined distribution class. This type of object is automatically created in method `toExplicitDistribution()` when the user does not provide a concrete distribution. This is because S4 objects do not accept NULL values.

---

`UniformDistribution`    *Create an uniform distribution.*

---

**Description**

Create an uniform distribution.

**Usage**

`UniformDistribution(min, max)`

**Arguments**

<code>min</code>	min value
<code>max</code>	max value

**Value**

an uniform distribution

---

`VPC`    *Compute the VPC summary. Input data frame must contain the following columns: - replicate: replicate number - low: low percentile value in replicate (and in scenario if present) - med: median value in replicate (and in scenario if present) - up: up percentile value in replicate (and in scenario if present) - any scenario column*

---

**Description**

Compute the VPC summary. Input data frame must contain the following columns: - replicate: replicate number - low: low percentile value in replicate (and in scenario if present) - med: median value in replicate (and in scenario if present) - up: up percentile value in replicate (and in scenario if present) - any scenario column

**Usage**

`VPC(x, scenarios = NULL, level = 0.9)`

**Arguments**

<code>x</code>	data frame
<code>scenarios</code>	scenarios, character vector, NULL is default
<code>level</code>	PI level, default is 0.9 (90% PI)

**Value**

VPC summary with columns TIME, <scenarios> and all combinations of low, med, up (i.e. low\_low, low\_med, low\_up, etc.)

---

**vpcPlot**

*VPC plot.*

---

**Description**

VPC plot.

**Usage**

```
vpcPlot(x, scenarios = NULL, level = 0.9, alpha = 0.15)
```

**Arguments**

x	data frame, output of CAMPSIS with replicates
scenarios	scenarios, character vector, NULL is default
level	PI level, default is 0.9 (90% PI)
alpha	alpha parameter (transparency) given to geom_ribbon

**Value**

a ggplot object

# Index

applyCompartmentCharacteristics, 4  
Arm, 5  
arm-class, 5  
arms-class, 6  
  
Bolus, 6  
bolus-class, 7  
Bootstrap, 7  
bootstrap-class, 8  
bootstrap\_distribution-class, 9  
BootstrapDistribution, 8  
  
constant\_distribution-class, 9  
ConstantDistribution, 9  
Covariate, 10  
covariate-class, 10  
covariates-class, 10  
  
Dataset, 11  
dataset-class, 11  
dataset\_config-class, 12  
DatasetConfig, 12  
DiscreteDistribution, 13  
distribution-class, 13  
dose\_adaptation-class, 14  
dose\_adaptations-class, 14  
DoseAdaptation, 13  
dosingOnly, 14  
  
EtaDistribution, 15  
Event, 15  
event-class, 16  
event\_covariate-class, 17  
EventCovariate, 16  
Events, 17  
events-class, 17  
  
fixed\_covariate-class, 18  
fixed\_distribution-class, 18  
FixedDistribution, 18  
function\_distribution-class, 19  
  
FunctionDistribution, 19  
  
generateIIV, 20  
getCovariates, 20  
getCovariates, arm-method  
    (getCovariates), 20  
getCovariates, arms-method  
    (getCovariates), 20  
getCovariates, covariates-method  
    (getCovariates), 20  
getCovariates, dataset-method  
    (getCovariates), 20  
getEventCovariates, 21  
getEventCovariates, arm-method  
    (getEventCovariates), 21  
getEventCovariates, arms-method  
    (getEventCovariates), 21  
getEventCovariates, covariates-method  
    (getEventCovariates), 21  
getEventCovariates, dataset-method  
    (getEventCovariates), 21  
getFixedCovariates, 21  
getFixedCovariates, arm-method  
    (getFixedCovariates), 21  
getFixedCovariates, arms-method  
    (getFixedCovariates), 21  
getFixedCovariates, covariates-method  
    (getFixedCovariates), 21  
getFixedCovariates, dataset-method  
    (getFixedCovariates), 21  
getIOVs, 22  
getIOVs, arm-method (getIOVs), 22  
getIOVs, arms-method (getIOVs), 22  
getIOVs, dataset-method (getIOVs), 22  
getOccasions, 23  
getOccasions, arm-method (getOccasions),  
    23  
getOccasions, arms-method  
    (getOccasions), 23

get0occasions, dataset-method  
     (get0occasions), 23  
 getSeedForDatasetExport, 23  
 getSeedForIteration, 24  
 getSeedForParametersSampling, 24  
 getTimes, 25  
 getTimes, arm-method (getTimes), 25  
 getTimes, arms-method (getTimes), 25  
 getTimes, dataset-method (getTimes), 25  
 getTimes, events-method (getTimes), 25  
 getTimes, observations\_set-method  
     (getTimes), 25  
 getTimeVaryingCovariates, 26  
 getTimeVaryingCovariates, arm-method  
     (getTimeVaryingCovariates), 26  
 getTimeVaryingCovariates, arms-method  
     (getTimeVaryingCovariates), 26  
 getTimeVaryingCovariates, covariates-method  
     (getTimeVaryingCovariates), 26  
 getTimeVaryingCovariates, dataset-method  
     (getTimeVaryingCovariates), 26  
  
 Infusion, 26  
 infusion-class, 27  
 IOV, 28  
  
 length, arm-method, 28  
 length, dataset-method, 29  
 LogNormalDistribution, 29  
  
 mrgsolve\_engine-class, 30  
  
 NormalDistribution, 30  
  
 Observations, 30  
 observations-class, 31  
 observations\_set-class, 31  
 obsOnly, 31  
 Occasion, 32  
 occasion-class, 32  
 occasions-class, 32  
  
 ParameterDistribution, 33  
 PI, 33  
 protocol-class, 34  
  
 retrieveParameterValue, 34  
 rxode\_engine-class, 34  
  
 sample, 35

sample, bolus, integer-method (sample), 35  
 sample, bootstrap, integer-method  
     (sample), 35  
 sample, bootstrap\_distribution, integer-method  
     (sample), 35  
 sample, campsisi\_model, integer-method  
     (sample), 35  
 sample, constant\_distribution, integer-method  
     (sample), 35  
 sample, covariate, integer-method  
     (sample), 35  
 sample, fixed\_distribution, integer-method  
     (sample), 35  
 sample, function\_distribution, integer-method  
     (sample), 35  
 sample, infusion, integer-method  
     (sample), 35  
 sample, observations, integer-method  
     (sample), 35  
 Scenario, 36  
 scenario-class, 36  
 Scenarios, 37  
 scenarios-class, 37  
 setLabel, 37  
 setLabel, arm, character-method  
     setLabel), 37  
 setSubjects, 38  
 setSubjects, arm, integer-method  
     (setSubjects), 38  
 setSubjects, dataset, integer-method  
     (setSubjects), 38  
 shadedPlot, 38  
 simulate, 39  
 simulate, campsisi\_model, data.frame, character, events, scenarios,  
     (simulate), 39  
 simulate, campsisi\_model, dataset, character, events, scenarios,  
     (simulate), 39  
 simulate, campsisi\_model, tbl\_df, character, events, scenarios,  
     (simulate), 39  
 simulate, campsisi\_model, tbl\_df, mrgsolve\_engine, events, scenarios,  
     (simulate), 39  
 simulate, campsisi\_model, tbl\_df, rxode\_engine, events, scenarios,  
     (simulate), 39  
 simulation\_engine-class, 43  
 simulation\_progress-class, 44  
 SimulationProgress, 43  
 spaghettiPlot, 44  
  
 time\_varying\_covariate-class, 45

TimeVaryingCovariate, [45](#)  
treatment-class, [45](#)  
treatment iov-class, [46](#)  
treatment iovs-class, [46](#)  
  
undefined\_distribution-class, [46](#)  
UniformDistribution, [47](#)  
  
VPC, [47](#)  
vpcPlot, [48](#)