

Package ‘hesim’

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Type Package

Title Health Economic Simulation Modeling and Decision Analysis

Version 0.5.0

Description A modular and computationally efficient R package for parameterizing, simulating, and analyzing health economic simulation models. The package supports cohort discrete time state transition models (Briggs et al. 1998) <doi:10.2165/00019053-199813040-00003>, N-state partitioned survival models (Glasziou et al. 1990) <doi:10.1002/sim.4780091106>, and individual-level continuous time state transition models (Siebert et al. 2012) <doi:10.1016/j.jval.2012.06.014>, encompassing both Markov (time-homogeneous and time-inhomogeneous) and semi-Markov processes. Decision uncertainty from a cost-effectiveness analysis is quantified with standard graphical and tabular summaries of a probabilistic sensitivity analysis (Claxton et al. 2005, Barton et al. 2008) <doi:10.1002/hec.985>, <doi:10.1111/j.1524-4733.2008.00358.x>. Use of C++ and data.table make individual-patient simulation, probabilistic sensitivity analysis, and incorporation of patient heterogeneity fast.

URL <https://hesim-dev.github.io/hesim/>,
<https://github.com/hesim-dev/hesim>

BugReports <https://github.com/hesim-dev/hesim/issues>

License GPL-3

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apply_rr	<i>Apply relative risks to transition probability matrices</i>
----------	--

Description

Elements of transition probability matrices are multiplied by relative risks and the transition probability matrices are adjusted so that rows sum to 1. Operations are vectorized and each relative risk is multiplied by every transition matrix (stored in 3-dimensional arrays).

Usage

```
apply_rr(x, rr, index, complement = NULL)
```

Arguments

x	A 3-dimensional array where each slice is a square transition probability matrix.
rr	A 2-dimensional tabular object such as a matrix or data frame where each column is a vector of relative risks to apply to each transition matrix in x.
index	The indices of the transition probability matrices that rr is applied to. Should either be a matrix where the first column denotes a transition probability matrix row and the second column denotes a transition probability matrix column or a list where each element is a vector of length 2 with the first element denoting a transition probability matrix row and the second column denoting a transition probability matrix column.
complement	Denotes indices of transition probability matrices that are "complements" (i.e., computed as 1 less the sum of all other elements in that row). Should be in the same format as index. There can be at most one complementary column in each row of a transition probability matrix. If NULL, then the diagonals are assumed to be the complements.

Details

This function is useful for applying relative treatment effects measured using relative risks to an existing transition probability matrix. For example, a transition probability matrix for the reference treatment strategy may exist or have been estimated from the data. Relative risks estimated from a meta-analysis or network meta-analysis can then be applied to the reference transition probability matrix. If the number of rows in rr exceeds x, then the arrays in x are recycled to the number of rows in rr, which facilitates the application of relative risks from multiple treatment strategies to a reference treatment.

Value

A 3-dimensional array where each slice contains matrices of the same dimension as each matrix in `x` and the number of slices is equal to the number of rows in `rr`.

Examples

```
p_12 <- c(.7, .5)
p_23 <- c(.1, .2)
x <- as_array3(tpmatrix(
  C, p_12, .1,
  0, C,    p_23,
  0, 0,    1
))

# There are the same number of relative risk rows and transition probability matrices
rr_12 <- runif(2, .8, 1)
rr_13 <- runif(2, .9, 1)
rr <- cbind(rr_12, rr_13)
apply_rr(x, rr,
  index = list(c(1, 2), c(1, 3)),
  complement = list(c(1, 1), c(2, 2)))

# There are more relative risk rows than transition probability matrices
rr_12 <- runif(4, .8, 1)
rr_13 <- runif(4, .9, 1)
rr <- cbind(rr_12, rr_13)
apply_rr(x, rr,
  index = list(c(1, 2), c(1, 3)),
  complement = list(c(1, 1), c(2, 2)))
```

```
as.data.table.tparams_transprobs
  Coerce to data.table
```

Description

Creates a `data.table` that combines the transition probability matrices and ID columns from a [tparams_transprobs](#) object. This is often useful for debugging.

Usage

```
## S3 method for class 'tparams_transprobs'
as.data.table(x)
```

Arguments

`x` A [tparams_transprobs](#) object.

Value

A `data.table` with one row for each transition probability matrix.

See Also

[tparams_transprobs](#)

as_array3

Convert between 2D tabular objects and 3D arrays

Description

Convert a 2-dimensional tabular object where each row stores a flattened square matrix to a 3-dimensional array of square matrices and vice versa. This allows multiple transition matrices to be stored as either tabular objects (e.g., matrices, data frames, etc) or as arrays.

Usage

```
as_array3(x)
```

```
as_tbl2(x, output = c("data.table", "data.frame", "matrix", "tpmatrix"))
```

Arguments

x	For <code>as_array3()</code> a 2-dimensional tabular object where each row stores a flattened square matrix ordered rowwise. Reasonable classes are <code>matrix</code> , <code>data.frame</code> , <code>data.table</code> , and <code>tpmatrix</code> . For <code>as_tbl2()</code> a 3-dimensional array where each slice is a square matrix.
output	The class of the object returned by the function. Either a <code>data.table</code> , <code>data.frame</code> , <code>matrix</code> , or <code>tpmatrix</code> .

Value

For `as_array3()` a 3-dimensional array of square matrices; for `as_tbl2()` a 2-dimensional tabular object as specified by `output`.

See Also

[tpmatrix](#)

Examples

```

p_12 <- c(.7, .6)
pmat <- tpmatrix(
  C, p_12,
  0, 1
)
pmat

as_array3(pmat)
as_array3(as.matrix(pmat))
as_tbl2(as_array3(pmat))

```

as_pfs_os

*Convert multi-state data to PFS and OS data***Description**

Convert a multi-state dataset with irreversible transitions containing 3 health states to a dataset with one row per patient and progression-free survival (PFS) and overall survival (OS) time-to-event outcomes.

Usage

```

as_pfs_os(
  data,
  patient_vars,
  status = "status",
  time_stop = "time_stop",
  transition = "transition_id"
)

```

Arguments

<code>data</code>	A multi-state dataset.
<code>patient_vars</code>	Character vector of the names of patient specific variables.
<code>status</code>	Character string with the name of the status variable (1 = event, 0 = censored).
<code>time_stop</code>	Character string with the name of the stopping time variable (i.e., time patient transitions from state r to state s).
<code>transition</code>	Character string with the name of the variable identifying a transition. The transition variable should be integer valued with values 1, 2, and 3 for the Stable -> Progression, Stable -> Death, and Progression -> Death transitions, respectively.

Value

A `data.table` with one row per patient containing each variable in `patient_vars` as well as a time variable and status indicator for both PFS (`pfs_status`, `pfs_time`) and OS (`os_time`, `os_status`).

Examples

```
as_pfs_os(onc3, patient_vars = c("patient_id", "strategy_name", "female", "age"))
```

autoplot.stateprobs *Plot state probabilities*

Description

Quickly plot state probabilities stored in a [stateprobs](#) object.

Usage

```
## S3 method for class 'stateprobs'
autoplot(
  object,
  labels = NULL,
  ci = FALSE,
  prob = 0.95,
  ci_style = c("ribbon", "line"),
  geom_alpha = 0.3,
  ...
)
```

Arguments

object	A stateprobs object.
labels	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by get_labels() for an example.
ci	A logical value indicating whether confidence intervals should be plotted. Default is FALSE.
prob	A numeric scalar in the interval (0,1) giving the confidence interval. Default is 0.95 for a 95 percent interval.
ci_style	Style to use for the confidence interval if ci = TRUE. If "line", then dashed lines are used; if "ribbon", then shaded confidence bands are plotted using <code>ggplot2::geom_ribbon()</code> .
geom_alpha	The opacity for the shaded confidence bands when ci_style = "ribbon". This is the value of the value of the alpha aesthetic passed to <code>ggplot2::geom_ribbon()</code> .
...	Further arguments passed to and from methods. Currently unused.

Value

A ggplot object.

Note

If there are multiple patients/groups, then state probabilities are averaged across patients/groups (using the weights in `patient_wt` if available) prior to plotting.

See Also

[Psm](#) for an example.

autoplot.survival *Plot survival curves*

Description

Quickly plot survival curves stored in a [survival](#) object.

Usage

```
## S3 method for class 'survival'
autoplot(
  object,
  labels = NULL,
  ci = FALSE,
  prob = 0.95,
  ci_style = c("ribbon", "line"),
  geom_alpha = 0.3,
  ...
)
```

Arguments

<code>object</code>	A survival object.
<code>labels</code>	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by get_labels() for an example.
<code>ci</code>	A logical value indicating whether confidence intervals should be plotted. Default is FALSE.
<code>prob</code>	A numeric scalar in the interval (0,1) giving the confidence interval. Default is 0.95 for a 95 percent interval.
<code>ci_style</code>	Style to use for the confidence interval if <code>ci = TRUE</code> . If "line", then dashed lines are used; if "ribbon", then shaded confidence bands are plotted using <code>ggplot2::geom_ribbon()</code> .
<code>geom_alpha</code>	The opacity for the shaded confidence bands when <code>ci_style = "ribbon"</code> . This is the value of the value of the alpha aesthetic passed to <code>ggplot2::geom_ribbon()</code> .
<code>...</code>	Further arguments passed to and from methods. Currently unused.

Value

A ggplot object.

Note

If there are multiple patients, then survival probabilities are averaged across patients (using the weights in `patient_wt` if available) prior to plotting.

See Also

[Psm](#) for an example.

 bootstrap

Bootstrap a statistical model

Description

`bootstrap` is a generic function for generating bootstrap replicates of the parameters of a fitted statistical model.

Usage

```
bootstrap(object, B, ...)
```

```
## S3 method for class 'partsurvfit'
```

```
bootstrap(object, B, max_errors = 0, silent = FALSE, ...)
```

Arguments

<code>object</code>	A statistical model.
<code>B</code>	Number of bootstrap replications.
<code>...</code>	Further arguments passed to or from other methods. Currently unused.
<code>max_errors</code>	Maximum number of errors that are allowed when fitting statistical models during the bootstrap procedure. This argument may be useful if, for instance, the model fails to converge during some bootstrap replications. Default is 0.
<code>silent</code>	Logical indicating whether error messages should be suppressed. Passed to the <code>silent</code> argument of <code>try()</code> .

Value

Sampled values of the parameters.

ce *A cost-effectiveness object*

Description

An object that summarizes simulated measures of clinical effectiveness and costs from a simulation model for use in a cost-effectiveness analysis.

Format

A list containing two elements:

- costs Total (discounted) costs by category.
- qalys (Discounted) quality-adjusted life-years.

Costs

The costs data.table contains the following columns:

category The cost category.

dr The discount rate.

sample A randomly sampled parameter set from the probabilistic sensitivity analysis (PSA)

strategy_id The treatment strategy ID.

grp_id An optional column denoting a subgroup. If not included, it is assumed that a single subgroup is being analyzed.

costs Costs.

Quality-adjusted life-years

The qalys data.table contains the following columns:

dr The discount rate.

sample A randomly sampled parameter set from the probabilistic sensitivity analysis (PSA)

strategy_id The treatment strategy ID.

grp_id An optional column denoting a subgroup. If not included, it is assumed that a single subgroup is being analyzed.

qalys Quality-adjusted life-years

 cea

Cost-effectiveness analysis

Description

Conduct cost-effectiveness analysis (CEA) given output of an economic model; that is, summarize a probabilistic sensitivity analysis (PSA), possibly by subgroup.

- `cea()` computes the probability that each treatment is most cost-effective, output for a cost-effectiveness acceptability frontier, the expected value of perfect information, and the net monetary benefit for each treatment.
- `cea_pw()` conducts pairwise CEA by comparing strategies to a comparator. Computed quantities include the incremental cost-effectiveness ratio, the incremental net monetary benefit, output for a cost-effectiveness plane, and output for a cost-effectiveness acceptability curve.

Usage

```
cea(x, ...)
```

```
cea_pw(x, ...)
```

```
## Default S3 method:
```

```
cea(x, k = seq(0, 2e+05, 500), sample, strategy, grp = NULL, e, c, ...)
```

```
## Default S3 method:
```

```
cea_pw(
  x,
  k = seq(0, 2e+05, 500),
  comparator,
  sample,
  strategy,
  grp = NULL,
  e,
  c,
  ...
)
```

```
## S3 method for class 'ce'
```

```
cea(x, k = seq(0, 2e+05, 500), dr_qalys, dr_costs, ...)
```

```
## S3 method for class 'ce'
```

```
cea_pw(x, k = seq(0, 2e+05, 500), comparator, dr_qalys, dr_costs, ...)
```

Arguments

`x` An object of simulation output characterizing the probability distribution of clinical effectiveness and costs. If the default method is used, then `x` must be

	a <code>data.frame</code> or <code>data.table</code> containing columns of mean costs and clinical effectiveness where each row denotes a randomly sampled parameter set and treatment strategy.
<code>...</code>	Further arguments passed to or from other methods. Currently unused.
<code>k</code>	Vector of willingness to pay values.
<code>sample</code>	Character name of column from <code>x</code> denoting a randomly sampled parameter set.
<code>strategy</code>	Character name of column from <code>x</code> denoting treatment strategy.
<code>grp</code>	Character name of column from <code>x</code> denoting subgroup. If <code>NULL</code> , then it is assumed that there is only one group.
<code>e</code>	Character name of column from <code>x</code> denoting clinical effectiveness.
<code>c</code>	Character name of column from <code>x</code> denoting costs.
<code>comparator</code>	Name of the comparator strategy in <code>x</code> .
<code>dr_qalys</code>	Discount rate for quality-adjusted life-years (QALYs).
<code>dr_costs</code>	Discount rate for costs.

Value

`cea()` returns a list of four `data.table` elements.

summary A `data.table` of the mean, 2.5% quantile, and 97.5% quantile by strategy and group for clinical effectiveness and costs.

mce The probability that each strategy is the most effective treatment for each group for the range of specified willingness to pay values. In addition, the column `best` denotes the optimal strategy (i.e., the strategy with the highest expected net monetary benefit), which can be used to plot the cost-effectiveness acceptability frontier (CEAF).

evpi The expected value of perfect information (EVPI) by group for the range of specified willingness to pay values. The EVPI is computed by subtracting the expected net monetary benefit given current information (i.e., the strategy with the highest expected net monetary benefit) from the expected net monetary benefit given perfect information.

nmb The mean, 2.5% quantile, and 97.5% quantile of net monetary benefits for the range of specified willingness to pay values.

`cea_pw` also returns a list of four `data.table` elements:

summary A `data.table` of the mean, 2.5% quantile, and 97.5% quantile by strategy and group for incremental clinical effectiveness and costs.

delta Incremental effectiveness and incremental cost for each simulated parameter set by strategy and group. Can be used to plot a cost-effectiveness plane.

ceac Values needed to plot a cost-effectiveness acceptability curve by group. The CEAC plots the probability that each strategy is more cost-effective than the comparator for the specified willingness to pay values.

inmb The mean, 2.5% quantile, and 97.5% quantile of incremental net monetary benefits for the range of specified willingness to pay values.

Examples

```

library("data.table")
library("ggplot2")
theme_set(theme_bw())

# Simulation output
n_samples <- 30

sim <- data.table(sample = rep(seq(n_samples), 4),
                  c = c(rlnorm(n_samples, 5, .1), rlnorm(n_samples, 5, .1),
                        rlnorm(n_samples, 11, .1), rlnorm(n_samples, 11, .1)),
                  e = c(rnorm(n_samples, 8, .2), rnorm(n_samples, 8.5, .1),
                        rnorm(n_samples, 11, .6), rnorm(n_samples, 11.5, .6)),
                  strategy_id = rep(1:2, each = n_samples * 2),
                  grp_id = rep(rep(1:2, each = n_samples), 2)
)

# Cost-effectiveness analysis
cea_out <- cea(sim, k = seq(0, 200000, 500), sample = "sample",
              strategy = "strategy_id", grp = "grp_id",
              e = "e", c = "c")
names(cea_out)

## Some sample output
## The probability that each strategy is the most cost-effective
## in each group with a willingness to pay of 20,000
cea_out$mce[k == 20000]

# Pairwise cost-effectiveness analysis
cea_pw_out <- cea_pw(sim, k = seq(0, 200000, 500), comparator = 1,
                    sample = "sample", strategy = "strategy_id",
                    grp = "grp_id", e = "e", c = "c")
names(cea_pw_out)

## Some sample output
## The cost-effectiveness acceptability curve
head(cea_pw_out$ceac[k >= 20000])

# Summarize the incremental cost-effectiveness ratio
labs <- list(strategy_id = c("Strategy 1" = 1, "Strategy 2" = 2),
             grp_id = c("Group 1" = 1, "Group 2" = 2))
format(icer(cea_pw_out, labels = labs))

# Plots
plot_ceplane(cea_pw_out, label = labs)
plot_ceac(cea_out, label = labs)
plot_ceac(cea_pw_out, label = labs)
plot_ceaf(cea_out, label = labs)
plot_evpi(cea_out, label = labs)

```

check_edata	<i>Check data argument for create_input_mats</i>
-------------	--

Description

Check that data argument for create_input_mats exists and that it is of the correct type.

Usage

```
check_edata(data)
```

Arguments

data An object of class "expanded_hesim_data" returned by the function [expand_hesim_data](#).

Value

If all tests passed, returns nothing; otherwise, throws an exception.

CohortDtstm	<i>Cohort discrete time state transition model</i>
-------------	--

Description

Simulate outcomes from a cohort discrete time state transition model.

Format

An [R6::R6Class](#) object.

Public fields

trans_model The model for health state transitions. Must be an object of class [CohortDtstmTrans](#).

utility_model The model for health state utility. Must be an object of class [StateVals](#).

cost_models The models used to predict costs by health state. Must be a list of objects of class [StateVals](#), where each element of the list represents a different cost category.

stateprobs_ An object of class [stateprobs](#) simulated using \$sim_stateprobs().

qalys_ An object of class [qalys](#) simulated using \$sim_qalys().

costs_ An object of class [costs](#) simulated using \$sim_costs().

Methods

Public methods:

- [CohortDtstm\\$new\(\)](#)
- [CohortDtstm\\$sim_stateprobs\(\)](#)
- [CohortDtstm\\$sim_qalys\(\)](#)
- [CohortDtstm\\$sim_costs\(\)](#)
- [CohortDtstm\\$summarize\(\)](#)
- [CohortDtstm\\$clone\(\)](#)

Method `new()`: Create a new CohortDtstm object.

Usage:

```
CohortDtstm$new(trans_model = NULL, utility_model = NULL, cost_models = NULL)
```

Arguments:

`trans_model` The `trans_model` field.

`utility_model` The `utility_model` field.

`cost_models` The `cost_models` field.

Returns: A new CohortDtstm object.

Method `sim_stateprobs()`: Simulate health state probabilities using `CohortDtstmTrans$sim_stateprobs()`.

Usage:

```
CohortDtstm$sim_stateprobs(n_cycles)
```

Arguments:

`n_cycles` The number of model cycles to simulate the model for.

Returns: An instance of `self` with simulated output of class `stateprobs` stored in `stateprobs_`.

Method `sim_qalys()`: Simulate quality-adjusted life-years (QALYs) as a function of `stateprobs_` and `utility_model`. See `vignette("expected-values")` for details.

Usage:

```
CohortDtstm$sim_qalys(
  dr = 0.03,
  integrate_method = c("trapez", "riemann_left", "riemann_right"),
  lys = TRUE
)
```

Arguments:

`dr` Discount rate.

`integrate_method` Method used to integrate state values when computing (QALYs).

`lys` If TRUE, then life-years are simulated in addition to QALYs.

Returns: An instance of `self` with simulated output of class `qalys` stored in `qalys_`.

Method `sim_costs()`: Simulate costs as a function of `stateprobs_` and `cost_models`. See `vignette("expected-values")` for details.

Usage:


```
CohortDtstm$sim_costs(
  dr = 0.03,
  integrate_method = c("trapez", "riemann_left", "riemann_right")
)
```

Arguments:

dr Discount rate.

integrate_method Method used to integrate state values when computing costs.

Returns: An instance of self with simulated output of class `costs` stored in `costs_`.

Method `summarize()`: Summarize costs and QALYs so that cost-effectiveness analysis can be performed. See `summarize_ce()`.

Usage:

```
CohortDtstm$summarize(by_grp = FALSE)
```

Arguments:

by_grp If TRUE, then costs and QALYs are computed by subgroup. If FALSE, then costs and QALYs are aggregated across all patients (and subgroups).

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
CohortDtstm$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[create_CohortDtstm\(\)](#), [CohortDtstmTrans](#), [create_CohortDtstmTrans\(\)](#), [vignette\("markov-cohort"\)](#), [vignette\("markov-inhomogeneous-cohort"\)](#), [vignette\("mlogit"\)](#),

Examples

```
library("data.table")
library("ggplot2")
theme_set(theme_bw())
set.seed(102)

# NOTE: This example replicates the "Simple Markov cohort model" vignette
# using a different approach (i.e., one that is not based on non-standard
# evaluation). The non-standard evaluation based approach does (more or less)
# what is done here under the hood.

# (0) Model setup
hesim_dat <- hesim_data(
  strategies = data.table(
    strategy_id = 1:2,
    strategy_name = c("Monotherapy", "Combination therapy")
  ),
  patients <- data.table(patient_id = 1),
  states = data.table(
```

```

    state_id = 1:3,
    state_name = c("State A", "State B", "State C")
  )
)
n_states <- nrow(hesim_dat$states) + 1
labs <- get_labels(hesim_dat)

# (1) Parameters
n_samples <- 10 # Number of samples for PSA

## Transition matrix
### Input data (one transition matrix for each parameter sample,
###           treatment strategy, patient, and time interval)
p_id <- tpmatrix_id(expand(hesim_dat, times = c(0, 2)), n_samples)
N <- nrow(p_id)

### Transition matrices (one for each row in p_id)
p <- array(NA, dim = c(n_states, n_states, nrow(p_id)))

#### Baseline risk
trans_mono <- rbind(
  c(1251, 350, 116, 17),
  c(0, 731, 512, 15),
  c(0, 0, 1312, 437),
  c(0, 0, 0, 469)
)
mono_ind <- which(p_id$strategy_id == 1 | p_id$time_id == 2)
p[, , mono_ind] <- rdirichlet_mat(n = 2, trans_mono)

#### Apply relative risks
combo_ind <- setdiff(1:nrow(p_id), mono_ind)
lrr_se <- (log(.710) - log(.365))/(2 * qnorm(.975))
rr <- rlnorm(n_samples, meanlog = log(.509), sdlog = lrr_se)
rr_indices <- list( # Indices of transition matrix to apply RR to
  c(1, 2), c(1, 3), c(1, 4),
  c(2, 3), c(2, 4),
  c(3, 4)
)
rr_mat <- matrix(rr, nrow = n_samples, ncol = length(rr_indices))
p[, , combo_ind] <- apply_rr(p[, , mono_ind],
  rr = rr_mat,
  index = rr_indices)
tp <- tparams_transprobs(p, p_id)

## Utility
utility_tbl <- stateval_tbl(
  data.table(
    state_id = 1:3,
    est = c(1, 1, 1)
  ),
  dist = "fixed"
)

```

```

## Costs
drugcost_tbl <- stateval_tbl(
  data.table(
    strategy_id = c(1, 1, 2, 2),
    time_start = c(0, 2, 0, 2),
    est = c(2278, 2278, 2278 + 2086.50, 2278)
  ),
  dist = "fixed"
)

dmedcost_tbl <- stateval_tbl(
  data.table(
    state_id = 1:3,
    mean = c(A = 1701, B = 1774, C = 6948),
    se = c(A = 1701, B = 1774, C = 6948)
  ),
  dist = "gamma"
)

cmedcost_tbl <- stateval_tbl(
  data.table(
    state_id = 1:3,
    mean = c(A = 1055, B = 1278, C = 2059),
    se = c(A = 1055, B = 1278, C = 2059)
  ),
  dist = "gamma"
)

# (2) Simulation
## Constructing the economic model
### Transition probabilities
transmod <- CohortDtstmTrans$new(params = tp)

### Utility
utilitymod <- create_StateVals(utility_tbl,
                              hesim_data = hesim_dat,
                              n = n_samples)

### Costs
drugcostmod <- create_StateVals(drugcost_tbl,
                              hesim_data = hesim_dat,
                              n = n_samples)
dmedcostmod <- create_StateVals(dmedcost_tbl,
                              hesim_data = hesim_dat,
                              n = n_samples)
cmedcostmod <- create_StateVals(cmedcost_tbl,
                              hesim_data = hesim_dat,
                              n = n_samples)
costmods <- list(drug = drugcostmod,
                direct_medical = dmedcostmod,
                community_medical = cmedcostmod)

### Economic model

```

```
econmod <- CohortDtstm$new(trans_model = transmod,
                          utility_model = utilitymod,
                          cost_models = costmods)

## Simulating outcomes
econmod$sim_stateprobs(n_cycles = 20)
autoplot(econmod$stateprobs_, ci = TRUE, ci_style = "ribbon",
         labels = labs)
econmod$sim_qalys(dr = 0, integrate_method = "riemann_right")
econmod$sim_costs(dr = 0.06, integrate_method = "riemann_right")

# (3) Decision analysis
ce_sim <- econmod$summarize()
wtp <- seq(0, 25000, 500)
cea_pw_out <- cea_pw(ce_sim, comparator = 1, dr_qalys = 0, dr_costs = .06,
                   k = wtp)
format(icer(cea_pw_out))
```

CohortDtstmTrans

Transitions for a cohort discrete time state transition model

Description

Simulate health state transitions in a cohort discrete time state transition model.

Format

An [R6::R6Class](#) object.

Public fields

`params` Parameters for simulating health state transitions. Supports objects of class [tparams_transprobs](#) or [params_mlogit](#).

`input_data` An object of class [input_mats](#).

`cycle_length` The length of a model cycle in terms of years. The default is 1 meaning that model cycles are 1 year long.

Active bindings

`start_stateprobs` A non-negative vector with length equal to the number of health states containing the probability that the cohort is in each health state at the start of the simulation. For example, if there were three states and the cohort began the simulation in state 1, then `start_stateprobs = c(1, 0, 0)`. Automatically normalized to sum to 1. If NULL, then a vector with the first element equal to 1 and all remaining elements equal to 0.

`trans_mat` A transition matrix describing the states and transitions in a discrete-time multi-state model. Only required if the model is parameterized using multinomial logistic regression. The (i,j) element represents a transition from state i to state j . Each possible transition from row i should be based on a separate multinomial logistic regression and ordered from 0 to $K - 1$ where K is the number of possible transitions. Transitions that are not possible should be NA, and the reference category for each row should be 0.

Methods

Public methods:

- [CohortDtstmTrans\\$new\(\)](#)
- [CohortDtstmTrans\\$sim_stateprobs\(\)](#)
- [CohortDtstmTrans\\$clone\(\)](#)

Method `new()`: Create a new `CohortDtstmTrans` object.

Usage:

```
CohortDtstmTrans$new(  
  params,  
  input_data = NULL,  
  trans_mat = NULL,  
  start_stateprobs = NULL,  
  cycle_length = 1  
)
```

Arguments:

`params` The `params` field.

`input_data` The `input_data` field.

`trans_mat` The `trans_mat` field.

`start_stateprobs` The `start_stateprobs` field.

`cycle_length` The `cycle_length` field.

Returns: A new `CohortDtstmTrans` object.

Method `sim_stateprobs()`: Simulate probability of being in each health state during each model cycle.

Usage:

```
CohortDtstmTrans$sim_stateprobs(n_cycles)
```

Arguments:

`n_cycles` The number of model cycles to simulate the model for.

Returns: An object of class [stateprobs](#).

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
CohortDtstmTrans$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

[create_CohortDtstmTrans\(\)](#), [CohortDtstm](#)

Examples

```

library("msm")
library("data.table")
set.seed(101)

# Model setup
strategies <- data.table(
  strategy_id = c(1, 2, 3),
  strategy_name = c("SOC", "New 1", "New 2")
)
patients <- data.table(patient_id = 1:2)
hesim_dat <- hesim_data(
  strategies = strategies,
  patients = patients
)

# Fit multi-state model with panel data via msm
qinit <- rbind(
  c(0, 0.28163, 0.01239),
  c(0, 0, 0.10204),
  c(0, 0, 0)
)
fit <- msm(state_id ~ time, subject = patient_id,
  data = onc3p[patient_id %in% sample(patient_id, 100)],
  covariates = list("1-2" =~ strategy_name),
  qmatrix = qinit)

# Simulation model
transmod_data <- expand(hesim_dat)
transmod <- create_CohortDtstmTrans(fit,
  input_data = transmod_data,
  cycle_length = 1/2,
  fixedpars = 2,
  n = 2)
transmod$sim_stateprobs(n_cycles = 2)

```

costs

Costs object

Description

An object of class `costs` returned from methods `$sim_costs()` in model classes that store simulated costs.

Components

A `costs` object inherits from `data.table` and contains the following columns:

sample A random sample from the PSA.

strategy_id The treatment strategy ID.

patient_id The patient ID.

state_id The health state ID.

dr The rate used to discount costs.

category The cost category (e.g., drug costs, medical costs, etc).

costs The simulated cost values.

create_CohortDtstm *Create CohortDtstm object*

Description

A generic function for creating an object of class [CohortDtstm](#).

Usage

```
create_CohortDtstm(object, ...)

## S3 method for class 'model_def'
create_CohortDtstm(
  object,
  input_data,
  cost_args = NULL,
  utility_args = NULL,
  ...
)
```

Arguments

object	An object of the appropriate class.
...	Further arguments passed to <code>CohortDtstmTrans\$new()</code> in CohortDtstmTrans .
input_data	An object of class expanded_hesim_data .
cost_args	A list of further arguments passed to <code>StateVals\$new()</code> in StateVals when initiating cost models.
utility_args	A list of further arguments passed to <code>StateVals\$new()</code> in StateVals when initiating the utility model.

 create_CohortDtstmTrans

Create CohortDtstmTrans object

Description

A generic function for creating an object of class CohortDtstmTrans.

Usage

```
create_CohortDtstmTrans(object, ...)

## S3 method for class 'multinom_list'
create_CohortDtstmTrans(
  object,
  input_data,
  trans_mat,
  n = 1000,
  uncertainty = c("normal", "none"),
  ...
)

## S3 method for class 'msm'
create_CohortDtstmTrans(
  object,
  input_data,
  cycle_length,
  n = 1000,
  uncertainty = c("normal", "none"),
  ...
)
```

Arguments

object	An object of the appropriate class.
...	Further arguments passed to or from other methods. Currently unused.
input_data	An object of class <code>expanded_hesim_data</code> returned by expand.hesim_data()
trans_mat	A transition matrix describing the states and transitions in a discrete-time multi-state model. See CohortDtstmTrans .
n	Number of random observations of the parameters to draw.
uncertainty	Method determining how parameter uncertainty should be handled. See documentation in create_params() .
cycle_length	The length of a model cycle in terms of years. The default is 1 meaning that model cycles are 1 year long.

See Also[CohortDtstmTrans](#)

`create_IndivCtstmTrans`*Create IndivCtstmTrans object*

Description

A generic function for creating an object of class [IndivCtstmTrans](#).

Usage

```
create_IndivCtstmTrans(object, ...)  
  
## S3 method for class 'flexsurvreg_list'  
create_IndivCtstmTrans(  
  object,  
  input_data,  
  trans_mat,  
  clock = c("reset", "forward"),  
  n = 1000,  
  uncertainty = c("normal", "none"),  
  ...  
)  
  
## S3 method for class 'flexsurvreg'  
create_IndivCtstmTrans(  
  object,  
  input_data,  
  trans_mat,  
  clock = c("reset", "forward"),  
  n = 1000,  
  uncertainty = c("normal", "none"),  
  ...  
)  
  
## S3 method for class 'params_surv'  
create_IndivCtstmTrans(  
  object,  
  input_data,  
  trans_mat,  
  clock = c("reset", "forward", "mix"),  
  reset_states = NULL,  
  ...  
)
```

```
## S3 method for class 'params_surv_list'
create_IndivCtstmTrans(
  object,
  input_data,
  trans_mat,
  clock = c("reset", "forward", "mix"),
  reset_states = NULL,
  ...
)
```

Arguments

object	A fitted survival model or the parameters of a survival model.
...	Further arguments passed to <code>IndivCtstmTrans\$new()</code> in IndivCtstmTrans .
input_data	An object of class <code>expanded_hesim_data</code> returned by expand.hesim_data .
trans_mat	The transition matrix describing the states and transitions in a multi-state model in the format from the mstate package. See IndivCtstmTrans .
clock	"reset" for a clock-reset model, "forward" for a clock-forward model, and "mix" for a mixture of clock-reset and clock-forward models. See the field <code>clock</code> in IndivCtstmTrans .
n	Number of random observations of the parameters to draw.
uncertainty	Method determining how parameter uncertainty should be handled. See documentation in create_params() .
reset_states	A vector denoting the states in which time resets. See the field <code>reset_states</code> in IndivCtstmTrans .

Value

Returns an [R6Class](#) object of class [IndivCtstmTrans](#).

See Also

[IndivCtstmTrans](#)

create_lines_dt	<i>Create a data table of treatment lines</i>
-----------------	---

Description

Convert a list of treatment lines for multiple treatment strategies to a data table.

Usage

```
create_lines_dt(strategy_list, strategy_ids = NULL)
```

Arguments

- strategy_list** A list where each element is a treatment strategy consisting of a vector of treatments.
- strategy_ids** A numeric vector denoting the numeric id of each strategy in `strategy_list`.

Value

Returns a data.table in tidy format with three columns:

strategy_id Treatment strategy ids.

line Line of therapy.

treatment_id Treatment ID for treatment used at a given line of therapy within a treatment strategy.

Examples

```
strategies <- list(c(1, 2, 3),
                  c(1, 2))
create_lines_dt(strategies)
```

create_params

Create a parameter object from a fitted model

Description

`create_params` is a generic function for creating an object containing parameters from a fitted statistical model. If `uncertainty != "none"`, then random samples from suitable probability distributions are returned.

Usage

```
create_params(object, ...)

## S3 method for class 'lm'
create_params(object, n = 1000, uncertainty = c("normal", "none"), ...)

## S3 method for class 'flexsurvreg'
create_params(object, n = 1000, uncertainty = c("normal", "none"), ...)

## S3 method for class 'multinom'
create_params(object, n = 1000, uncertainty = c("normal", "none"), ...)

## S3 method for class 'multinom_list'
create_params(object, n = 1000, uncertainty = c("normal", "none"), ...)

## S3 method for class 'flexsurvreg_list'
create_params(object, n = 1000, uncertainty = c("normal", "none"), ...)
```

```
## S3 method for class 'partsurvfit'
create_params(
  object,
  n = 1000,
  uncertainty = c("normal", "bootstrap", "none"),
  ...
)
```

Arguments

object	A statistical model to randomly sample parameters from.
...	Further arguments passed to or from other methods. Only used when object is of class <code>partsurvfit</code> , in which case the arguments are passed to <code>bootstrap.parsurvfit()</code> .
n	Number of random observations to draw. Not used if <code>uncertainty = "none"</code> .
uncertainty	Method determining how parameter uncertainty should be handled. If <code>"normal"</code> , then parameters are randomly drawn from their multivariate normal distribution. If <code>"bootstrap"</code> , then parameters are bootstrapped using <code>bootstrap</code> . If <code>"none"</code> , then only point estimates are returned.

Value

An object prefixed by `params_`. Mapping between `create_params` and the classes of the returned objects are:

- `create_params.lm` -> `params_lm`
- `create_params.multinom` -> `params_mlogit`
- `create_params.multinom_list` -> `params_mlogit_list`
- `create_params.flexsurvreg` -> `params_surv`
- `create_params.flexsurvreg_list` -> `params_surv_list`
- `create_params.parsurvfit` -> `params_surv_list`

Examples

```
# create_params.lm
fit <- stats::lm(costs ~ female, data = psm4_exdata$costs$medical)
n <- 5
params_lm <- create_params(fit, n = n)
head(params_lm$coefs)
head(params_lm$sigma)

# create_params.flexsurvreg
library("flexsurv")
fit <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1,
                             data = ovarian, dist = "weibull")
n <- 5
params_surv_wei <- create_params(fit, n = n)
print(params_surv_wei$dist)
head(params_surv_wei$coefs)
```

create_PsmCurves *Create PsmCurves object*

Description

create_PsmCurves is a function for creating an object of class [PsmCurves](#).

Usage

```
create_PsmCurves(object, ...)

## S3 method for class 'flexsurvreg_list'
create_PsmCurves(
  object,
  input_data,
  n = 1000,
  uncertainty = c("normal", "bootstrap", "none"),
  est_data = NULL,
  ...
)

## S3 method for class 'params_surv_list'
create_PsmCurves(object, input_data, ...)
```

Arguments

object	Fitted survival models.
...	Further arguments passed to or from other methods. Passed to create_params.partsurvfit() when object is of class flexsurvreg_list .
input_data	An object of class expanded_hesim_data returned by expand.hesim_data . Must be expanded by the data tables "strategies" and "patients".
n	Number of random observations of the parameters to draw.
uncertainty	Method determining how parameter uncertainty should be handled. See documentation in create_params() .
est_data	A <code>data.table</code> or <code>data.frame</code> of estimation data used to fit survival models during bootstrap replications.

Value

Returns an R6Class object of class [PsmCurves](#).

See Also

[PsmCurves](#)

create_StateVals *Create a StateVals object*

Description

create_StateVals() is a generic function for creating an object of class [StateVals](#) from a fitted statistical model or a [stateval_tbl](#) object.

Usage

```
create_StateVals(object, ...)

## S3 method for class 'lm'
create_StateVals(
  object,
  input_data = NULL,
  n = 1000,
  uncertainty = c("normal", "none"),
  ...
)

## S3 method for class 'stateval_tbl'
create_StateVals(object, hesim_data = NULL, n = 1000, ...)
```

Arguments

object	A model object of the appropriate class.
...	Further arguments (time_reset and method) passed to StateVals\$new() .
input_data	An object of class expanded_hesim_data . Must be expanded by treatment strategies, patients, and health states.
n	Number of random observations of the parameters to draw when parameters are fit using a statistical model.
uncertainty	Method determining how parameter uncertainty should be handled. See documentation in create_params() .
hesim_data	A hesim_data object. Only required when object is of class stateval_tbl . See "details".

Details

If object is a [stateval_tbl](#), then a [hesim_data](#) object is used to specify treatment strategies, patients, and/or health states not included as columns in the table, or, to match patients in the table to groups. Not required if the table includes one row for each treatment strategy, patient, and health state combination. Patients are matched to groups by specifying both a `patient_id` and a `grp_var` column in the `patients` table.

Value

A [StateVals](#) object.

See Also

[StateVals](#), [stateval_tbl\(\)](#)

create_trans_dt	<i>Create a data table of health state transitions</i>
-----------------	--

Description

Create a data table of health state transitions from a transition matrix describing the states and transitions in a multi-state model suitable for use with [hesim_data](#).

Usage

```
create_trans_dt(trans_mat)
```

Arguments

trans_mat A transition matrix in the format from the [mstate](#) package. See [IndivCtstmTrans](#).

Value

Returns a [data.table](#) in tidy format with three columns:

transition_id Health state transition ID.

from The starting health state.

to The health state that will be transitions to.

Examples

```
tmat <- rbind(c(NA, 1, 2),
              c(NA, NA, 3),
              c(NA, NA, NA))
create_trans_dt(tmat)
```

CtstmTrans

An R6 base class for continuous time state transition models

Description

Contains methods that can be used to summarize both individual- and cohort-level continuous time state transition models. That is, this class is relevant for both Markov and semi-Markov multi-state models and does not depend on the methodology used for prediction of state probabilities.

Format

An [R6: :R6Class](#) object.

Methods

Public methods:

- [CtstmTrans\\$hazard\(\)](#)
- [CtstmTrans\\$cumhazard\(\)](#)
- [CtstmTrans\\$clone\(\)](#)

Method [hazard\(\)](#): Predict the hazard functions for each health state transition.

Usage:

```
CtstmTrans$hazard(t)
```

Arguments:

t A numeric vector of times.

Returns: A `data.table` with columns `transition_id`, `sample`, `strategy_id`, `grp_id`, `t`, and `hazard`.

Method [cumhazard\(\)](#): Predict the cumulative hazard functions for each health state transition.

Usage:

```
CtstmTrans$cumhazard(t)
```

Arguments:

t A numeric vector of times.

Returns: A `data.table` with columns `transition_id`, `sample`, `strategy_id`, `grp_id`, `t`, and `cumhazard`.

Method [clone\(\)](#): The objects of this class are cloneable with this method.

Usage:

```
CtstmTrans$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[create_IndivCtstmTrans\(\)](#), [IndivCtstmTrans](#)

define_model	<i>Define and evaluate model expression</i>
--------------	---

Description

A model expression is defined by specifying random number generation functions for a probabilistic sensitivity analysis (PSA) and transformations of the sampled parameters as a function of `input_data`. The unevaluated expressions are evaluated with `eval_model()` and used to generate the model inputs needed to create an economic model.

Usage

```
define_model(tparams_def, rng_def, params = NULL, n_states = NULL)
```

```
eval_model(x, input_data)
```

Arguments

<code>tparams_def</code>	A <code>tparams_def</code> object or a list of <code>tparams_def</code> objects. A list might be considered if time intervals specified with the <code>times</code> argument in <code>define_tparams()</code> vary across parameters. Parameters for a transition probability matrix (<code>tpmatrix</code>), utilities (<code>utility</code>), and/or cost categories (<code>costs</code>) are returned as a named list (see <code>define_tparams()</code> for more details).
<code>rng_def</code>	A <code>rng_def</code> object used to randomly draw samples of the parameters from suitable probability distributions.
<code>params</code>	A list containing the values of parameters for random number generation.
<code>n_states</code>	The number of health states (inclusive of all health states including the the death state) in the model. If <code>tpmatrix</code> is an element returned by <code>tparams_def</code> , then it will be equal to the number of states in the transition probability matrix; otherwise it must be specified as an argument.
<code>x</code>	An object of class <code>model_def</code> created with <code>define_model()</code> .
<code>input_data</code>	An object of class <code>expanded_hesim_data</code> expanded by patients and treatment strategies.

Details

`eval_model()` evaluates the expressions in an object of class `model_def` returned by `define_model()` and is, in turn, used within functions that instantiate economic models (e.g., `create_CohortDtstm()`). The direct output of `eval_model()` can also be useful for understanding and debugging model definitions, but it is not used directly for simulation.

Economic models are constructed as a function of input data and parameters:

1. *Input data*: Objects of class `expanded_hesim_data` consisting of the treatment strategies and patient population.

2. *Parameters*: The underlying parameter estimates from the literature are first stored in a list (params argument). Random number generation is then used to sample the parameters from suitable probability distributions for the PSA (rng_def argument). Finally, the sampled parameters are transformed as a function of the input data into values (e.g., elements of a transition probability matrix) used for the simulation (tparams_def argument). The params argument can be omitted if the underlying parameters values are defined inside a define_rng() block.

Value

define_model() returns an object of class model_def, which is a list containing the arguments to the function. eval_model() returns a list containing ID variables identifying parameter samples, treatment strategies, patient cohorts, and time intervals; the values of parameters of the transition probability matrix, utilities, and/or cost categories; the number of health states; and the number of random number generation samples for the PSA.

See Also

[define_tparams\(\)](#), [define_rng\(\)](#)

Examples

```
# Data
library("data.table")
strategies <- data.table(strategy_id = 1:2,
                         strategy_name = c("Monotherapy", "Combination therapy"))
patients <- data.table(patient_id = 1)
hesim_dat <- hesim_data(strategies = strategies,
                      patients = patients)
data <- expand(hesim_dat)

# Define the model
rng_def <- define_rng({
  alpha <- matrix(c(1251, 350, 116, 17,
                  0, 731, 512, 15,
                  0, 0, 1312, 437,
                  0, 0, 0, 469),
                nrow = 4, byrow = TRUE)
  rownames(alpha) <- colnames(alpha) <- c("A", "B", "C", "D")
  lrr_mean <- log(.509)
  lrr_se <- (log(.710) - log(.365))/(2 * qnorm(.975))
  list(
    p_mono = dirichlet_rng(alpha),
    rr_comb = lognormal_rng(lrr_mean, lrr_se),
    u = 1,
    c_zido = 2278,
    c_lam = 2086.50,
    c_med = gamma_rng(mean = c(A = 2756, B = 3052, C = 9007),
                      sd = c(A = 2756, B = 3052, C = 9007))
  )
}, n = 2)
```

```

tparams_def <- define_tparams({
  rr = ifelse(strategy_name == "Monotherapy", 1, rr_comb)
  list(
    tpmatrix = tpmatrix(
      C, p_mono$A_B * rr, p_mono$A_C * rr, p_mono$A_D * rr,
      0, C, p_mono$B_C * rr, p_mono$B_D * rr,
      0, 0, C, p_mono$C_D * rr,
      0, 0, 0, 1),
    utility = u,
    costs = list(
      drug = ifelse(strategy_name == "Monotherapy",
                    c_zido, c_zido + c_lam),
      medical = c_med
    )
  )
})

model_def <- define_model(
  tparams_def = tparams_def,
  rng_def = rng_def)

# Evaluate the model expression to generate model inputs
# This can be useful for understanding the output of a model expression
eval_model(model_def, data)

# Create an economic model with a factory function
econmod <- create_CohortDtstm(model_def, data)

```

define_rng

Define and evaluate random number generation expressions

Description

Random number generation expressions are used to randomly sample model parameters from suitable distributions for probabilistic sensitivity analysis. These functions are typically used when evaluating an object of class `model_def` defined using `define_model()`.

Usage

```

define_rng(expr, n = 1, ...)

eval_rng(x, params = NULL, check = FALSE)

```

Arguments

`expr` An expression used to randomly draw variates for each parameter of interest in the model. **Braces** should be used so that the result of the last expression within the braces is evaluated. The expression must return a list where each


```

    outptcost = outptcost_mean, # No column names because
                          # outptcost_mean has none.
    aecost = gamma_rng(mean = aecost_mean, # Explicit naming of columns
                      sd = aecost_mean,
                      names = aecost_colnames)
  )
}, n = 2, aecost_colnames = c("A", "B", "C")) # Add aecost_colnames to environment
eval_rng(x = rng_def, params)

```

define_tparams

*Define and evaluate transformed parameter expressions***Description**

Transformed parameter expressions are used to transform the parameter values sampled with `eval_rng()` as a function of input data (treatment strategies and patients) and time intervals. These functions are used when evaluating an object of class `model_def` defined using `define_model()`. The transformed parameters are ultimately converted into `tparams` objects and used to simulate outcomes with an economic model.

Usage

```
define_tparams(expr, times = NULL, ...)
```

```
eval_tparams(x, input_data, rng_params)
```

Arguments

<code>expr</code>	Expressions used to transform parameters. As with <code>define_rng()</code> , braces should be used so that the result of the last expression within the braces is evaluated. The expression must return a named list with the following possible elements: <ul style="list-style-type: none"> • <i>tpmatrix</i>: The transition probability matrix used to simulate transition probabilities in the economic model. This should either be the output of <code>tpmatrix()</code> or a 3-dimensional array as in <code>tparams_transprobs()</code>. • <i>utility</i>: The utility values to attach to states and used to simulate quality-adjusted life-years in the economic model. Either a vector (in which case utility is the same in each health state) or a <code>data.table</code>/<code>data.frame</code>/<code>matrix</code> with a column for each (non-death) health state. • <i>costs</i>: A named list of costs for each category used to simulate costs in the economic model. Each element of the list must be in the same format as <i>utility</i>.
<code>times</code>	Distinct times denoting the stopping time of time intervals.
<code>...</code>	Additional arguments to pass to the environment used to evaluate <code>expr</code> .
<code>x</code>	An object of class <code>tparams_def</code> .
<code>input_data</code>	An object of class <code>expanded_hesim_data</code> (as in <code>eval_model()</code>) expanded by the distinct times in <code>times</code> .
<code>rng_params</code>	Random samples of the parameters returned by <code>eval_rng()</code> .

Details

`define_tparams()` is evaluated when creating economic models as a function of `model_def` objects defined with `define_model()`. Operations are "vectorized" in the sense that they are performed for each unique combination of `input_data` and `params`. `expr` is evaluated in an environment including each variable from `input_data`, all elements of `rng_params`, and a variable `time` containing the values from `times`. The `time` variable can be used to create models where parameters vary as a function of time. `eval_tparams()` is not exported and is only meant for use within `eval_model()`.

Value

`define_tparams()` returns an object of class `tparams_def`, which is a list containing the unevaluated "transformation" expressions passed to `expr`, `times`, and any additional arguments passed to `eval_tparams()`. `eval_tparams()` evaluates the `tparams_def` object and should return a list of transformed parameter objects.

See Also

[define_model\(\)](#), [define_rng\(\)](#)

disprog

Disease progression object

Description

An object of class `disprog` returned from methods `$sim_disease()` in model classes. It contains simulated trajectories through a multi-state model.

Components

A `disprog` object inherits from `data.table` and contains the following columns:

sample A random sample from the PSA.

strategy_id The treatment strategy ID.

patient_id The patient ID.

from The health state ID transitioned from.

to The health state ID transitioned to.

final An indicator equal to 1 if a patient is in their final health state during the simulation and 0 otherwise.

time_start The time at the start of the interval.

time_stop The time at the end of the interval.

See Also

[IndivCtstm](#), [IndivCtstmTrans](#)

expand.hesim_data	<i>Expand hesim_data</i>
-------------------	--------------------------

Description

Create a data table in long format from all combinations of specified tables from an object of class [hesim_data](#) and optionally time intervals. See "Details" for an explanation of how the expansion is done.

Usage

```
## S3 method for class 'hesim_data'  
expand(object, by = c("strategies", "patients"), times = NULL)
```

Arguments

object	An object of class <code>hesim_data</code> .
by	A character vector of the names of the data tables in <code>hesim_data</code> to expand by.
times	Either a numeric vector of distinct times denoting the start of time intervals or a time_intervals object.

Details

This function is similar to [expand.grid\(\)](#), but works for data frames or data tables. Specifically, it creates a `data.table` from all combinations of the supplied tables in `object` and optionally the start of times intervals in `times`. The supplied tables are determined using the `by` argument. The resulting dataset is sorted by prioritizing ID variables as follows: (i) `strategy_id`, (ii) `patient_id`, (iii) the health-related ID variable (either `state_id` or `transition_id`, and (iv) the time intervals from `times`.

Value

An object of class `expanded_hesim_data`, which is a `data.table` with an `"id_vars"` attribute containing the names of the ID variables in the data table and, if `times` is not `NULL`, a `time_intervals` object derived from `times`.

Examples

```
strategies <- data.frame(strategy_id = c(1, 2))  
patients <- data.frame(patient_id = seq(1, 3), age = c(65, 50, 75),  
  gender = c("Female", "Female", "Male"))  
states <- data.frame(state_id = seq(1, 3),  
  state_var = c(2, 1, 9))  
hesim_dat <- hesim_data(strategies = strategies,  
  patients = patients,  
  states = states)  
expand(hesim_dat, by = c("strategies", "patients"))  
expand(hesim_dat, by = c("strategies", "patients"),  
  times = c(0, 2, 10))
```

expmat	<i>Matrix exponential</i>
--------	---------------------------

Description

This is a wrapper around `msm::MatrixExp()` that computes the exponential of multiple square matrices.

Usage

```
expmat(x, t = 1, ...)
```

Arguments

x	An array of matrices.
t	An optional scaling factor for x.
...	Arguments to pass to <code>msm::MatrixExp()</code> .

Details

This function is most useful when exponentiating transition intensity matrices to produce transition probability matrices. To create transition probability matrices for discrete time state transition models with annual cycles, set `t=1`. An array of matrices is returned which can be used to create the value element of a `tparams_transprobs` object. See `qmatrix()` for an example.

Value

Returns an array of exponentiated matrices. If `length(t) > 1`, then `length(t)` arrays are returned for each element in x.

See Also

`qmatrix.msm()`, `qmatrix.data.table()`

fast_rgengamma	<i>Random generation for generalized gamma distribution</i>
----------------	---

Description

Draw random samples from a generalized gamma distribution using the parameterization from `flexsurv`. Written in C++ for speed. Equivalent to `flexsurv::rgengamma`.

Usage

```
fast_rgengamma(n, mu = 0, sigma = 1, Q)
```


Arguments

n	Number of random observations to draw.
mu	Vector of location parameters. and columns correspond to rates during specified time intervals.
sigma	Vector of scale parameters as described in flexsurv.
Q	Vector of shape parameters.

Value

A vector of random samples from the generalized gamma distribution. The length of the sample is determined by n. The numerical arguments other than n are recycled so that the number of samples is equal to n.

Examples

```
n <- 1000
m <- 2 ; s <- 1.7; q <- 1
ptm <- proc.time()
r1 <- fast_rgengamma(n, mu = m, sigma = s, Q = q)
proc.time() - ptm
ptm <- proc.time()
library("flexsurv")
r2 <- flexsurv::rgengamma(n, mu = m, sigma = s, Q = q)
proc.time() - ptm
summary(r1)
summary(r2)
```

flexsurvreg_list	<i>List of flexsurvreg objects</i>
------------------	------------------------------------

Description

Combine [flexsurvreg](#) objects into a list.

Usage

```
flexsurvreg_list(...)
```

Arguments

... Objects of class [flexsurvreg](#), which can be named.

Value

An object of class flexsurvreg_list.

Examples

```
library("flexsurv")
fit1 <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1, data = ovarian, dist = "weibull")
fit2 <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1, data = ovarian, dist = "exp")
fsreg_list <- flexsurvreg_list(wei = fit1, exp = fit2)
class(fsreg_list)
```

get_labels

*Get value labels***Description**

Get value labels for the ID variables in a `hesim_data` object and create a list of named vectors that can be passed to formatting and plotting functions. This lets users create nice labels for treatment strategies, subgroups, health states, and/or transitions when presenting results.

Usage

```
get_labels(
  object,
  strategy = "strategy_name",
  grp = "grp_name",
  state = "state_name",
  transition = "transition_name",
  death_label = "Death"
)
```

Arguments

<code>object</code>	An object of class <code>hesim_data</code> created with <code>hesim_data()</code> .
<code>strategy</code>	The name of the column in the <code>strategy</code> element of <code>object</code> containing labels for <code>strategy_id</code> .
<code>grp</code>	The name of the column in the <code>patient</code> element of <code>object</code> containing labels for <code>grp_id</code> .
<code>state</code>	The name of the column in the <code>state</code> element of <code>object</code> containing labels for <code>state_id</code> .
<code>transition</code>	The name of the column in the <code>transition</code> element of <code>object</code> containing labels for <code>transition_id</code> .
<code>death_label</code>	The label to use for the death health state. By default a label named "Death" will be concatenated to the labels for the non-death health states. The death state can be omitted from labels for the health states by setting <code>death_label = NULL</code> .

Value

A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the ID variables.

See Also

`hesim_data()`, `set_labels()`

Examples

```
library("data.table")
strategies <- data.table(
  strategy_id = c(1, 2),
  strategy_name = c("Strategy 1", "Strategy 2")
)
patients <- data.table(
  patient_id = seq(1, 4),
  age = c(50, 55, 60, 65),
  grp_id = c(1, 1, 2, 2),
  grp_name = rep(c("Age 50-59", "Age 60-69"), each = 2)
)
states <- data.table(
  state_id = seq(1, 2),
  state_name = c("State 1", "State 2")
)
hesim_dat <- hesim_data(
  strategies = strategies,
  patients = patients,
  states = states
)
labs <- get_labels(hesim_dat)
labs

# Pass to set_labels()
d <- data.table(strategy_id = c(1, 1, 2, 2),
                grp_id = c(1, 2, 1, 2))
set_labels(d, labs, new_name = c("strategy_name", "grp_name"))
d
```

Description

To learn more about hesim visit the [website](#).

 hesim_data

Data for health economic simulation modeling

Description

A list of tables required for health economic simulation modeling. Each table must either be a `data.frame` or `data.table`. All ID variables within each table must be numeric vectors of integers.

Usage

```
hesim_data(strategies, patients, states = NULL, transitions = NULL)
```

Arguments

strategies	A table of treatment strategies. Must contain the column <code>strategy_id</code> denoting a unique strategy. Other columns are variables describing the characteristics of a treatment strategy.
patients	A table of patients. Must contain the column <code>patient_id</code> denoting a unique patient. The number of rows should be equal to the number of patients in the model. The table may also include columns for <code>grp_id</code> for subgroups and <code>patient_wt</code> specifying the weight to apply to each patient (within a subgroup). If <code>grp_id</code> is <code>NULL</code> , then it is assumed that there is only one subgroup. If <code>patient_wt</code> is <code>NULL</code> , then each patient is given the same weight. Weights cannot be used in individual-level models because each patient should be weighted equally; that is, weights can only be specified in cohort models. Weights within subgroups are normalized to sum to one. Other columns are variables describing the characteristics of a patient.
states	A table of health states. Must contain the column <code>state_id</code> , which denotes a unique health state. The number of rows should be equal to the number of health states in the model. Other columns can describe the characteristics of a health state.
transitions	A table of health state transitions. Must contain the column <code>transition_id</code> , which denotes a unique transition; <code>from</code> , which denotes the starting health state; and <code>to</code> which denotes the state that will be transitioned to.

Value

Returns an object of class `hesim_data`, which is a list of data tables for health economic simulation modeling.

See Also

[expand.hesim_data\(\)](#), [get_labels\(\)](#)

Examples

```

strategies <- data.frame(strategy_id = c(1, 2))
patients <- data.frame(patient_id = seq(1, 3), age = c(65, 50, 75),
                       gender = c("Female", "Female", "Male"))
states <- data.frame(state_id = seq(1, 3),
                    state_var = c(2, 1, 9))
hesim_dat <- hesim_data(strategies = strategies,
                      patients = patients,
                      states = states)

```

hesim_survdists *List of survival distributions*

Description

List of additional distributions for parametric survival analysis that are not contained in [flexsurv](#). Can be used to fit models with [flexsurv::flexsurvreg\(\)](#). Same format as [flexsurv::flexsurv.dists](#).

Usage

```
hesim_survdists
```

Format

A list with the following elements:

name Name of the probability distribution.

pars Vector of strings naming the parameters of the distribution. These must be the same names as the arguments of the density and probability functions.

location Name of the location parameter.

transforms List of R functions which transform the range of values taken by each parameter onto the real line. For example, `c(log, log)` for a distribution with two positive parameters.

inv.transforms List of R functions defining the corresponding inverse transformations. Note these must be lists, even for single parameter distributions they should be supplied as, e.g. `c(exp)` or `list(exp)`.

inits A function of the observed survival times `t` (including right-censoring times, and using the halfway point for interval-censored times) which returns a vector of reasonable initial values for maximum likelihood estimation of each parameter. For example, `function(t){ c(1, mean(t)) }` will always initialize the first of two parameters at 1, and the second (a scale parameter, for instance) at the mean of `t`.

icea *Individualized cost-effectiveness analysis*

Description

These functions are deprecated, use `cea()` and `cea_pw()` instead.

Usage

```
icea(x, ...)
```

```
icea_pw(x, ...)
```

Arguments

x	An object of simulation output characterizing the probability distribution of clinical effectiveness and costs. ^{?ic}
...	Further arguments passed to or from other methods.

icer *Incremental cost-effectiveness ratio*

Description

Generate a tidy table of incremental cost-effectiveness ratios (ICERs) given output from `cea_pw()` with `icer()` and format for pretty printing with `format.icer()`.

Usage

```
icer(x, prob = 0.95, k = 50000, labels = NULL, ...)
```

```
## S3 method for class 'icer'
format(
  x,
  digits_qalys = 2,
  digits_costs = 0,
  pivot_from = "strategy",
  drop_grp = TRUE,
  pretty_names = TRUE,
  ...
)
```

Arguments

<code>x</code>	An object of class <code>cea_pw</code> returned by <code>cea_pw()</code> .
<code>prob</code>	A numeric scalar in the interval (0,1) giving the confidence interval. Default is 0.95 for a 95 percent interval.
<code>k</code>	Willingness to pay per quality-adjusted life-year.
<code>labels</code>	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by <code>get_labels()</code> for an example.
<code>...</code>	Further arguments passed to and from methods. Currently unused.
<code>digits_qalys</code>	Number of digits to use to report QALYs.
<code>digits_costs</code>	Number of digits to use to report costs.
<code>pivot_from</code>	Character vector denoting a column or columns used to "widen" the data. Should either be "strategy", "grp", "outcome", or some combination of the three. There will be one column for each value of the variables in <code>pivot_from</code> . Default is to widen so there is a column for each treatment strategy. Set to NULL if you do not want to widen the table.
<code>drop_grp</code>	If TRUE, then the group column will be removed if there is only one subgroup; other it will be kept. If FALSE, then the <code>grp</code> column is never removed.
<code>pretty_names</code>	Logical. If TRUE, then the columns <code>strategy</code> , <code>grp</code> , <code>outcome</code> , and <code>value</code> are renamed (if they exist) to <code>Strategy</code> , <code>Group</code> , <code>Outcome</code> , and <code>Value</code> .

Details

Note that `icer()` will report negative ICERs; however, `format()` will correctly note whether a treatment strategy is dominated by or dominates the reference treatment.

Value

`icer()` returns an object of class `icer` that is a tidy data table with the following columns:

strategy The treatment strategy.

grp The subgroup.

outcome The outcome metric.

estimate The point estimate computed as the average across the PSA samples.

lower The lower limit of the confidence interval.

upper The upper limit of the confidence interval.

`format.icer()` formats the table according to the arguments passed.

See Also

[cea_pw\(\)](#)

icer_tbl

*ICER table***Description**

Generate a table of incremental cost-effectiveness ratios given output from `cea_pw()`.

Usage

```
icer_tbl(
  x,
  k = 50000,
  cri = TRUE,
  prob = 0.95,
  digits_qalys = 2,
  digits_costs = 0,
  output = c("matrix", "data.table"),
  rownames = NULL,
  colnames = NULL,
  drop = TRUE
)
```

Arguments

<code>x</code>	An object of class <code>cea_pw</code> returned by <code>cea_pw()</code> .
<code>k</code>	Willingness to pay.
<code>cri</code>	If TRUE, credible intervals are computed; otherwise they are not.
<code>prob</code>	A numeric scalar in the interval (0,1) giving the credible interval. Default is 0.95 for a 95 percent credible interval.
<code>digits_qalys</code>	Number of digits to use to report QALYs.
<code>digits_costs</code>	Number of digits to use to report costs.
<code>output</code>	Should output be a <code>data.table</code> or a list of matrices for each group.
<code>rownames</code>	Row names for matrices when <code>output = "matrix"</code> .
<code>colnames</code>	Column names for matrices when <code>output = "matrix"</code> .
<code>drop</code>	If TRUE, then the result is coerced to the lowest possible dimension. Relevant if <code>output = "matrix"</code> and there is one group, in which case a single matrix will be returned if <code>drop = TRUE</code> and a list of length 1 will be returned if <code>drop = FALSE</code> .

Value

If `output = "matrix"`, then a list of matrices (or a matrix if `drop = TRUE`) reporting incremental cost-effectiveness ratios (ICERs) by group. Specifically, each matrix contains five rows for: (i) incremental quality-adjusted life-years (QALYs), (ii) incremental costs, (iii) the incremental net

monetary benefit (NMB), (iv) the ICER, and (v) a conclusion stating whether each strategy is cost-effective relative to a comparator. The number of columns is equal to the number of strategies (including the comparator).

If `output = "data.table"`, then the results are reported as a `data.table`, with one row for each strategy and group combination.

See Also

[cea_pw\(\)](#)

<code>id_attributes</code>	<i>Attributes for ID variables</i>
----------------------------	------------------------------------

Description

Stores metadata related to the ID variables used to index [input_mats](#) and [transformed parameter objects](#) already predicted from covariates.

Usage

```
id_attributes(
  strategy_id,
  n_strategies,
  patient_id,
  n_patients,
  state_id = NULL,
  n_states = NULL,
  transition_id = NULL,
  n_transitions = NULL,
  time_id = NULL,
  time_intervals = NULL,
  n_times = NULL,
  sample = NULL,
  n_samples = NULL,
  grp_id = NULL,
  patient_wt = NULL
)
```

Arguments

<code>strategy_id</code>	A numeric vector of integers denoting the treatment strategy.
<code>n_strategies</code>	A scalar denoting the number of unique treatment strategies.
<code>patient_id</code>	A numeric vector of integers denoting the patient.
<code>n_patients</code>	A scalar denoting the number of unique patients.
<code>state_id</code>	A numeric vector of integers denoting the health state.

n_states	A scalar denoting the number of unique health states.
transition_id	A numeric vector denoting the health state transition. This is only used for state transition models.
n_transitions	A scalar denoting the number of unique transitions.
time_id	A numeric vector of integers denoting a unique time interval.
time_intervals	A data.table denoting unique time intervals. Must contain the columns time_id, time_start, and time_stop. time_start is the starting time of an interval and time_stop is the stopping time of an interval. Following the survival package, time intervals are closed on the right and open on the left (except in the final interval where time_stop is equal to infinity).
n_times	A scalar denoting the number of time intervals. Equal to the number of rows in time_intervals.
sample	A numeric vector of integer denoting the sample from the posterior distribution of the parameters.
n_samples	A scalar denoting the number of samples.
grp_id	An optional numeric vector of integers denoting the subgroup.
patient_wt	An optional numeric vector denoting the weight to apply to each patient within a subgroup.

Details

When using the ID variables to index [input_mats](#), sorting order should be the same as specified in [expand.hesim_data\(\)](#); that is, observations must be sorted by: (i) strategy_id, (ii) patient_id, and (iii) the health-related ID variable (either state_id or transition_id). When using ID variables to index transformed parameter objects and sample is used for indexing, then observations must be sorted by: (i) sample, (ii) strategy_id, (iii) patient_id, and (iv) the health-related ID variable.

See Also

[hesim_data\(\)](#), [expand.hesim_data\(\)](#), [input_mats](#)

incr_effect

Incremental treatment effect

Description

Computes incremental effect for all treatment strategies on outcome variables from a probabilistic sensitivity analysis relative to a comparator.

Usage

```
incr_effect(x, comparator, sample, strategy, grp = NULL, outcomes)
```

Arguments

x	A data.frame or data.table containing simulation output with information on outcome variables for each randomly sampled parameter set from a PSA. Each row should denote a randomly sampled parameter set and treatment strategy.
comparator	The comparator strategy. If the strategy column is a character variable, then must be a character; if the strategy column is an integer variable, then must be an integer.
sample	Character name of column denoting a randomly sampled parameter set.
strategy	Character name of column denoting treatment strategy.
grp	Character name of column denoting subgroup. If NULL, then it is assumed that there is only one group.
outcomes	Name of columns to compute incremental changes for.

Value

A data.table containing the differences in the values of each variable specified in outcomes between each treatment strategy and the comparator.

Examples

```
# simulation output
n_samples <- 100
sim <- data.frame(sample = rep(seq(n_samples), 4),
  c = c(rlnorm(n_samples, 5, .1), rlnorm(n_samples, 5, .1),
    rlnorm(n_samples, 11, .1), rlnorm(n_samples, 11, .1)),
  e = c(rnorm(n_samples, 8, .2), rnorm(n_samples, 8.5, .1),
    rnorm(n_samples, 11, .6), rnorm(n_samples, 11.5, .6)),
  strategy = rep(paste0("Strategy ", seq(1, 2)),
    each = n_samples * 2),
  grp = rep(rep(c("Group 1", "Group 2"),
    each = n_samples), 2)
)
# calculate incremental effect of Strategy 2 relative to Strategy 1 by group
ie <- incr_effect(sim, comparator = "Strategy 1", sample = "sample",
  strategy = "strategy", grp = "grp", outcomes = c("c", "e"))
head(ie)
```

Description

Simulate outcomes from an individual-level continuous time state transition model (CTSTM) from a fitted multi-state model. The class supports "clock-reset" (i.e., semi-Markov), "clock-forward" (i.e., Markov), and mixtures of clock-reset and clock-forward models as described in [IndivCtstmTrans](#).

Format

An `R6::R6Class` object.

Public fields

`trans_model` The model for health state transitions. Must be an object of class `IndivCtstmTrans`.

`utility_model` The model for health state utility. Must be an object of class `StateVals`.

`cost_models` The models used to predict costs by health state. Must be a list of objects of class `StateVals`, where each element of the list represents a different cost category.

`disprog_` An object of class `disprog`.

`stateprobs_` An object of class `stateprobs` simulated using `$sim_stateprobs()`.

`qalys_` An object of class `qalys` simulated using `$sim_qalys()`.

`costs_` An object of class `costs` simulated using `$sim_costs()`.

Methods**Public methods:**

- `IndivCtstm$new()`
- `IndivCtstm$sim_disease()`
- `IndivCtstm$sim_stateprobs()`
- `IndivCtstm$sim_qalys()`
- `IndivCtstm$sim_costs()`
- `IndivCtstm$summarize()`
- `IndivCtstm$clone()`

Method `new()`: Create a new `IndivCtstm` object.

Usage:

```
IndivCtstm$new(trans_model = NULL, utility_model = NULL, cost_models = NULL)
```

Arguments:

`trans_model` The `trans_model` field.

`utility_model` The `utility_model` field.

`cost_models` The `cost_models` field.

Returns: A new `IndivCtstm` object.

Method `sim_disease()`: Simulate disease progression (i.e., individual trajectories through a multi-state model) using `IndivCtstmTrans$sim_disease()`.

Usage:

```
IndivCtstm$sim_disease(max_t = 100, max_age = 100, progress = NULL)
```

Arguments:

`max_t` A scalar or vector denoting the length of time to simulate the model. If a vector, must be equal to the number of simulated patients.

`max_age` A scalar or vector denoting the maximum age to simulate each patient until. If a vector, must be equal to the number of simulated patients.

`progress` An integer, specifying the PSA iteration (i.e., sample) that should be printed every `progress` PSA iterations. For example, if `progress = 2`, then every second PSA iteration is printed. Default is `NULL`, in which case no output is printed.

Returns: An instance of `self` with simulated output stored in `disprog_`.

Method `sim_stateprobs()`: Simulate health state probabilities as a function of time using the simulation output stored in `disprog`.

Usage:

```
IndivCtstm$sim_stateprobs(t)
```

Arguments:

`t` A numeric vector of times.

Returns: An instance of `self` with simulated output of class `stateprobs` stored in `stateprobs_`.

Method `sim_qalys()`: Simulate quality-adjusted life-years (QALYs) as a function of `disprog_` and `utility_model`. See `vignette("expected-values")` for details.

Usage:

```
IndivCtstm$sim_qalys(
  dr = 0.03,
  type = c("predict", "random"),
  lys = TRUE,
  by_patient = FALSE
)
```

Arguments:

`dr` Discount rate.

`type` "predict" for mean values or "random" for random samples as in `$sim()` in `StateVals`.

`lys` If `TRUE`, then life-years are simulated in addition to QALYs.

`by_patient` If `TRUE`, then QALYs are computed at the patient level. If `FALSE`, then QALYs are averaged across patients by health state.

Returns: An instance of `self` with simulated output of class `qalys` stored in `qalys_`.

Method `sim_costs()`: Simulate costs as a function of `disprog_` and `cost_models`. See `vignette("expected-values")` for details.

Usage:

```
IndivCtstm$sim_costs(
  dr = 0.03,
  type = c("predict", "random"),
  by_patient = FALSE,
  max_t = Inf
)
```

Arguments:

`dr` Discount rate.

`type` "predict" for mean values or "random" for random samples as in `$sim()` in `StateVals`.

`by_patient` If `TRUE`, then QALYs are computed at the patient level. If `FALSE`, then QALYs are averaged across patients by health state.

`max_t` Maximum time duration to compute costs once a patient has entered a (new) health state. By default, equal to `Inf`, so that costs are computed over the entire duration that a patient is in a given health state. If time varies by each cost category, then time can also be passed as a numeric vector of length equal to the number of cost categories (e.g., `c(1, 2, Inf, 3)` for a model with four cost categories).

Returns: An instance of `self` with simulated output of class `costs` stored in `costs_`.

Method `summarize()`: Summarize costs and QALYs so that cost-effectiveness analysis can be performed. See `summarize_ce()`.

Usage:

```
IndivCtstm$summarize(by_grp = FALSE)
```

Arguments:

`by_grp` If `TRUE`, then costs and QALYs are computed by subgroup. If `FALSE`, then costs and QALYs are aggregated across all patients (and subgroups).

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
IndivCtstm$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

[create_IndivCtstmTrans\(\)](#), [IndivCtstmTrans](#)

Examples

```
library("flexsurv")

# Treatment strategies, target population, and model structure
strategies <- data.frame(strategy_id = c(1, 2))
patients <- data.frame(patient_id = seq(1, 3),
  age = c(45, 50, 60),
  female = c(0, 0, 1))
states <- data.frame(state_id = c(1, 2))
hesim_dat <- hesim_data(strategies = strategies,
  patients = patients,
  states = states)

# Parameter estimation
## Multi-state model
tmat <- rbind(c(NA, 1, 2),
  c(3, NA, 4),
  c(NA, NA, NA))
fits <- vector(length = max(tmat, na.rm = TRUE), mode = "list")
surv_dat <- data.frame(mstate3_exdata$transitions)
for (i in 1:length(fits)){
  fits[[i]] <- flexsurvreg(Surv(years, status) ~ factor(strategy_id),
    data = surv_dat,
```

```

subset = (trans == i),
dist = "weibull")
}
fits <- flexsurvreg_list(fits)

## Utility
utility_tbl <- stateval_tbl(data.frame(state_id = states$state_id,
                                     mean = mstate3_exdata$utility$mean,
                                     se = mstate3_exdata$utility$se),
                           dist = "beta")

## Costs
drugcost_tbl <- stateval_tbl(data.frame(strategy_id = strategies$strategy_id,
                                       est = mstate3_exdata$costs$drugs$costs),
                             dist = "fixed")
medcost_tbl <- stateval_tbl(data.frame(state_id = states$state_id,
                                       mean = mstate3_exdata$costs$medical$mean,
                                       se = mstate3_exdata$costs$medical$se),
                             dist = "gamma")

# Economic model
n_samples = 2

## Construct model
### Transitions
transmod_data <- expand(hesim_dat)
transmod <- create_IndivCtstmTrans(fits, input_data = transmod_data,
                                  trans_mat = tmat,
                                  n = n_samples)

### Utility
utilitymod <- create_StateVals(utility_tbl, n = n_samples, hesim_data = hesim_dat)

### Costs
drugcostmod <- create_StateVals(drugcost_tbl, n = n_samples, hesim_data = hesim_dat)
medcostmod <- create_StateVals(medcost_tbl, n = n_samples, hesim_data = hesim_dat)
costmods <- list(drugs = drugcostmod,
                 medical = medcostmod)

### Combine
ictstm <- IndivCtstm$new(trans_model = transmod,
                        utility_model = utilitymod,
                        cost_models = costmods)

## Simulate outcomes
head(ictstm$sim_disease())$disprog_)
head(ictstm$sim_stateprobs(t = c(0, 5, 10))$stateprobs_[t == 5])
ictstm$sim_qalys(dr = .03)
ictstm$sim_costs(dr = .03)

### Summarize cost-effectiveness
ce <- ictstm$summarize()
head(ce)

```

```
format(summary(ce), pivot_from = "strategy")
```

IndivCtstmTrans	<i>Transitions for an individual-level continuous time state transition model</i>
-----------------	---

Description

Simulate health state transitions in an individual-level continuous time state transition model with parameters that were estimated using a multi-state model.

Format

An [R6::R6Class](#) object.

Super class

[hesim::CtstmTrans](#) -> IndivCtstmTrans

Public fields

`params` An object of class [params_surv](#) or [params_surv_list](#).

`input_data` Input data used to simulate health state transitions by sample from the probabilistic sensitivity analysis (PSA), treatment strategy and patient. Must be an object of class [input_mats](#). If `params` contains parameters from a list of models (i.e., of class [params_surv_list](#)), then `input_data` must contain a unique row for each treatment strategy and patient; if `params` contains parameters from a joint model (i.e., of class [params_surv](#)), then `input_data` must contain a unique row for each treatment strategy, patient, and transition.

`trans_mat` A transition matrix describing the states and transitions in a multi-state model in the format from the [mstate](#) package. See the documentation for the argument "trans" in [mstate::msprep](#).

`start_state` A scalar or vector denoting the starting health state. Default is the first health state. If a vector, must be equal to the number of simulated patients.

`start_age` A scalar or vector denoting the starting age of each patient in the simulation. Default is 38. If a vector, must be equal to the number of simulated patients.

`death_state` The death state in `trans_mat`. Used with `max_age` in `sim_disease` as patients transition to this state upon reaching maximum age. By default, it is set to the final absorbing state (i.e., a row in `trans_mat` with all NAs).

`clock` "reset" for a clock-reset model, "forward" for a clock-forward model, and "mix" for a mixture of clock-reset and clock-forward models. A clock-reset model is a semi-Markov model in which transition rates depend on time since entering a state. A clock-forward model is a Markov model in which transition rates depend on time since entering the initial state. If "mix" is used, then `reset_states` must be specified.

`reset_states` A vector denoting the states in which time resets. Hazard functions are always a function of elapsed time since either the start of the model or from when time was previously reset. Only used if `clock = "mix"`.

Methods**Public methods:**

- [IndivCtstmTrans\\$new\(\)](#)
- [IndivCtstmTrans\\$sim_disease\(\)](#)
- [IndivCtstmTrans\\$sim_stateprobs\(\)](#)
- [IndivCtstmTrans\\$check\(\)](#)
- [IndivCtstmTrans\\$clone\(\)](#)

Method new(): Create a new IndivCtstmTrans object.

Usage:

```
IndivCtstmTrans$new(
  params,
  input_data,
  trans_mat,
  start_state = 1,
  start_age = 38,
  death_state = NULL,
  clock = c("reset", "forward", "mix"),
  reset_states = NULL
)
```

Arguments:

params The params field.
input_data The input_data field.
trans_mat The trans_mat field.
start_state The start_state field.
start_age The start_age field.
death_state The death_state field.
clock The clock field.
reset_states The reset_states field.

Returns: A new IndivCtstmTrans object.

Method sim_disease(): Simulate disease progression (i.e., individual trajectories through a multi-state model using an individual patient simulation).

Usage:

```
IndivCtstmTrans$sim_disease(max_t = 100, max_age = 100, progress = NULL)
```

Arguments:

max_t A scalar or vector denoting the length of time to simulate the model. If a vector, must be equal to the number of simulated patients.
max_age A scalar or vector denoting the maximum age to simulate each patient until. If a vector, must be equal to the number of simulated patients.
progress An integer, specifying the PSA iteration (i.e., sample) that should be printed every progress PSA iterations. For example, if progress = 2, then every second PSA iteration is printed. Default is NULL, in which case no output is printed.

Returns: An object of class `disprog`.

Method `sim_stateprobs()`: Simulate health state probabilities from a `disprog` object.

Usage:

```
IndivCtstmTrans$sim_stateprobs(t, disprog = NULL, ...)
```

Arguments:

`t` A numeric vector of times.

`disprog` A `disprog` object. If `NULL`, then this will be simulated prior to computing state probabilities using `IndivCtstm$sim_disease()`.

`...` Additional arguments to pass to `IndivCtstm$sim_disease()` if `disprog = NULL`.

Returns: An object of class `stateprobs`.

Method `check()`: Input validation for class. Checks that fields are the correct type.

Usage:

```
IndivCtstmTrans$check()
```

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
IndivCtstmTrans$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

[create_IndivCtstmTrans\(\)](#), [IndivCtstm](#)

Examples

```
library("flexsurv")

# Simulation data
strategies <- data.frame(strategy_id = c(1, 2, 3))
patients <- data.frame(patient_id = seq(1, 3),
                       age = c(45, 50, 60),
                       female = c(0, 0, 1))

# Multi-state model with transition specific models
tmat <- rbind(c(NA, 1, 2),
             c(NA, NA, 3),
             c(NA, NA, NA))
fits <- vector(length = max(tmat, na.rm = TRUE), mode = "list")
for (i in 1:length(fits)){
  fits[[i]] <- flexsurvreg(Surv(years, status) ~ 1,
                        data = bosms3[bosms3$trans == i, ],
                        dist = "exp")
}
fits <- flexsurvreg_list(fits)
```

```

# Simulation model
hesim_dat <- hesim_data(strategies = strategies,
                      patients = patients)
fits_data <- expand(hesim_dat)
transmod <- create_IndivCtstmTrans(fits, input_data = fits_data,
                                 trans_mat = tmat,
                                 n = 2)

head(transmod$hazard(c(1, 2, 3)))
head(transmod$cumhazard(c(1, 2, 3)))

## Simulate disease progression and state probabilities together
transmod$sim_stateprobs(t = c(0, 5, 10))[t == 5]

## Simulate disease progression and state probabilities separately
disprog <- transmod$sim_disease(max_t = 10)
transmod$sim_stateprobs(t = c(0, 5, 10), disprog = disprog)[t == 5]

```

input_mats

Input matrices for a statistical model

Description

Create an object of class `input_mats`, which contains inputs matrices for simulating a statistical model. Consists of (i) input matrices, X , and (ii) [metadata](#) used to index each matrix in X . More details are provided under "Details" below.

Usage

```
input_mats(X, ...)
```

Arguments

X	A list of input matrices for predicting the values of each parameter in a statistical model. May also be a list of lists of input matrices when a list of separate models is fit (e.g., with flexsurvreg_list()).
\dots	Arguments to pass to id_attributes() .

Details

Each row of each matrix X is an input vector, x_{hik} , where h denotes a health-related index, i indexes a patient, and k is a treatment strategy. A health-related index is either a health state (e.g., `state_id`) or a transition between health states (e.g., `transition_id`). In some cases, the health-related index h can be suppressed and separate models can be fit for each health index. This is, for instance, the case in a [partitioned survival model](#) where separate models are fit for each survival endpoint.

The rows of the matrices in X must be sorted in a manner consistent with the ID variables as described in [id_attributes\(\)](#).

See Also

[create_input_mats\(\)](#)

Examples

```
strategies <- data.frame(strategy_id = c(1, 2))
patients <- data.frame(patient_id = seq(1, 3),
  age = c(45, 47, 60),
  female = c(1, 0, 0),
  group = factor(c("Good", "Medium", "Poor")))
hesim_dat <- hesim_data(strategies = strategies,
  patients = patients)

dat <- expand(hesim_dat, by = c("strategies", "patients"))
input_mats <- input_mats(X = list(mu = model.matrix(~ age, dat)),
  strategy_id = dat$strategy_id,
  n_strategies = length(unique(dat$strategy_id)),
  patient_id = dat$patient_id,
  n_patients = length(unique(dat$patient_id)))

print(input_mats)
```

mom_beta

Method of moments for beta distribution

Description

Compute the parameters shape1 and shape2 of the beta distribution using method of moments given the mean and standard deviation of the random variable of interest.

Usage

```
mom_beta(mean, sd)
```

Arguments

mean	Mean of the random variable.
sd	Standard deviation of the random variable.

Details

If μ is the mean and σ is the standard deviation of the random variable, then the method of moments estimates of the parameters shape1 = $\alpha > 0$ and shape2 = $\beta > 0$ are:

$$\alpha = \mu \left(\frac{\mu(1-\mu)}{\sigma^2} - 1 \right)$$

and

$$\beta = (1 - \mu) \left(\frac{\mu(1-\mu)}{\sigma^2} - 1 \right)$$

Value

A list containing the parameters shape1 and shape2.

Examples

```
mom_beta(mean = .8, sd = .1)
# The function is vectorized.
mom_beta(mean = c(.6, .8), sd = c(.08, .1))
```

mom_gamma

Method of moments for gamma distribution

Description

Compute the shape and scale (or rate) parameters of the gamma distribution using method of moments for the random variable of interest.

Usage

```
mom_gamma(mean, sd, scale = TRUE)
```

Arguments

mean	Mean of the random variable.
sd	Standard deviation of the random variable.
scale	Logical. If TRUE (default), then the scale parameter is returned; otherwise, the rate parameter is returned.

Details

If μ is the mean and σ is the standard deviation of the random variable, then the method of moments estimates of the parameters shape = $\alpha > 0$ and scale = $\theta > 0$ are:

$$\theta = \frac{\sigma^2}{\mu}$$

and

$$\alpha = \frac{\mu}{\theta}$$

The inverse of the scale parameter, $\beta = 1/\theta$, is the rate parameter.

Value

If scale = TRUE, then a list containing the parameters shape and scale; otherwise, if scale = FALSE, then a list containing the parameters shape and rate.

Examples

```
mom_gamma(mean = 10000, sd = 2000)
# The function is vectorized.
mom_gamma(mean = c(8000, 10000), sd = c(1500, 2000))
```

mstate3_exdata

Example data for a reversible 3-state multi-state model

Description

Example multi-state data for parameterizing a continuous time state transition model. Costs and utility are also included to facilitate cost-effectiveness analysis.

Usage

```
mstate3_exdata
```

Format

A list containing the following elements:

- **transitions** A data frame containing the times at which patient transitions between health states based on the [prothr](#) dataset from the [mstate](#) package.
- **costs** A list of data frames. The first data frame contains summary medical cost estimates and the second data frame contains drug cost data.
- **utility** A data frame of summary utility estimates.

Transitions data

The data frame has the following columns:

strategy_id Treatment strategy identification number.

patient_id Patient identification number.

age Patient age (in years).

female 1 if a patient is female; 0 if male.

from Starting state.

to Receiving state.

trans Transition number.

Tstart Starting time.

Tstop Transition time.

years Elapsed years between Tstart and Tstop.

status Status variable; 1=transition, 0=censored.

Cost data

The cost list contains two data frames. The first data frame contains data on the drug costs associated with each treatment strategy.

strategy_id The treatment strategy identification number.

costs Annualized drug costs.

The second data frame contains summary data on medical costs by health state, and contains the following columns:

state_id The health state identification number.

mean Mean costs.

se Standard error of medical costs.

Utility data

The data frame has the following columns:

state_id The health state identification number.

mean Mean utility

se Standard error of utility

multinom3_exdata	<i>Example data for a 3-state multinomial model</i>
------------------	---

Description

Example discrete time health state transitions data simulated using multinomial logistic regression. Costs and utility are also included to facilitate cost-effectiveness analysis.

Usage

```
multinom3_exdata
```

Format

A list containing the following elements:

- transitions A data frame containing patient transitions between health states at discrete time intervals (i.e., on a yearly basis).
- costs A list of data frames. The first data frame contains drug cost data and the second contains summary medical cost estimates.
- utility A data frame of summary utility estimates.

Transitions data

The data frame has the following columns:

patient_id Patient identification number.

strategy_id Treatment strategy identification number.

strategy_name Treatment strategy name.

age Patient age (in years).

age_cat A factor variable with 3 age groups: (i) age less than 40, (ii) age at least 40 and less than 60, and (iii) age at least 60.

female 1 if a patient is female; 0 if male.

year The year since the start of data collection with the first year equal to 1.

state_from State making a transition from.

state_to State making a transition to.

year_cat Factor variable for year with 3 categories: (i) year 3 and below, (ii) year between 3 and 6, and (iii) year 7 and above.

Cost data

The cost list contains two data frames. The first data frame contains data on the drug costs associated with each treatment strategy.

strategy_id The treatment strategy identification number.

strategy_name The treatment strategy name.

costs Annualized drug costs.

The second data frame contains summary data on medical costs by health state, and contains the following columns:

state_id The health state identification number.

state_name The name of the health state.

mean Mean medical costs.

se Standard error of medical costs.

Utility data

The data frame has the following columns:

state_id The health state identification number.

state_name The name of the health state.

mean Mean utility

se Standard error of utility.

multinom_list	<i>List of multinom objects</i>
---------------	---------------------------------

Description

Combine multinom objects into a list.

Usage

```
multinom_list(...)
```

Arguments

... Objects of class `multinom`, which can be named.

Value

An object of class `multinom_list`.

Examples

```
library("nnet")
library("data.table")
trans_data <- data.table(multinom3_exdata$transitions)
dat_healthy <- trans_data[state_from == "Healthy"]
fit_healthy <- multinom(state_to ~ strategy_name + female + age_cat + year_cat,
  data = dat_healthy)
dat_sick <- trans_data[state_from == "Sick"]
dat_sick$state_to <- droplevels(dat_sick$state_to)
fit_sick <- multinom(state_to ~ strategy_name + female + age_cat + year_cat,
  data = dat_sick)
fits <- multinom_list(healthy = fit_healthy, sick = fit_sick)
class(fits)
```

onc3	<i>Multi-state oncology data for 3-state model</i>
------	--

Description

Simulated 3-state dataset in oncology with three health states (Stable, Progression, and Death) and three possible transitions (Stable -> Progression, Stable -> Death, and Progression -> Death).

Usage

```
onc3
```

Format

A data.table with the following columns:

from Health state making a transition from.

to Health state making a transition to.

strategy_name Standard of care (SOC), new treatment 1 (New 1), or new treatment 2 (New 2).

female 1 if a patient is female; 0 if male.

age Patient age (in years).

patient_id Patient identification number.

time_start Starting time.

time_stop Stopping time.

status Status indicator: 1=transition, 0=censored.

transition_id Integer denoting transition: 1 = Stable -> Progression, 2 = Stable -> Death, 3 = Progression -> Death.

strategy_id Strategy identification number.

time Elapsed years between time_start and time_stop.

See Also

[onc3p](#)

Examples

```
head(onc3)
```

onc3p

Multi-state panel oncology data for 3-state model

Description

The same dataset as [onc3](#) converted into a panel data format in which health states are recorded at a finite series of times.

Usage

```
onc3p
```

Format

A data table with the following columns:

state The name of the health state (Stable, Progression, and Death).

strategy_name Standard of care (SOC), new treatment 1 (New 1), or new treatment 2 (New 2).

female 1 if a patient is female; 0 if male.

age Patient age (in years).

patient_id Patient identification number.

time Time that state was recorded.

strategy_id Strategy identification number.

state_id The health state identification number.

See Also

[onc3](#)

Examples

```
head(onc3p)
```

params

Parameter object

Description

Objects prefixed by "params_" are lists containing the parameters of a statistical model used for simulation modeling. The parameters are used to simulate outcomes as a function of covariates contained in input matrices ([input_mats](#)).

See Also

[tparams](#)

 params_joined_surv_list

Parameters of joined lists of survival models

Description

Create a list containing the parameters of multiple sets of survival models, each joined at specified time points. See [joined](#) for more details.

Usage

```
params_joined_surv_list(..., times)
```

Arguments

`...` Objects of class [params_surv_list](#), which can be named.

`times` A list of sorted numeric vectors, with the length of each list element equal to the number of sets of models.

Value

An object of class `params_joined_surv_list`, which is a list containing two elements:

models A list of [params_surv_list](#), each containing [params_surv](#) objects to be joined.

times Equivalent to the argument `times`.

Examples

```
library("flexsurv")
fit_exp <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1,
                               data = ovarian, dist = "exp")
fit_wei <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1,
                               data = ovarian, dist = "weibull")
fit_lnorm <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1,
                                  data = ovarian, dist = "lognormal")

params_exp <- create_params(fit_exp, n = 2)
params_wei <- create_params(fit_wei, n = 2)
params_lnorm <- create_params(fit_lnorm, n = 2)

params_list1 <- params_surv_list(params_exp, params_wei)
params_list2 <- params_surv_list(params_exp, params_lnorm)
params_joined <- params_joined_surv_list(model1 = params_list1,
                                       model2 = params_list2,
                                       times = list(3, 5))

print(params_joined)
```

`params_lm`*Parameters of a linear model*

Description

Create a list containing the parameters of a fitted linear regression model.

Usage

```
params_lm(coefs, sigma = NULL)
```

Arguments

<code>coefs</code>	Matrix of samples of the coefficients under sampling uncertainty.
<code>sigma</code>	A vector of samples of the standard error of the regression model. Must only be specified if the model is used to randomly simulate values (rather than to predict means).

Details

Fitted linear models are used to predict values, y , as a function of covariates, x ,

$$y = x^T \beta + \epsilon.$$

Predicted means are given by $x^T \hat{\beta}$ where $\hat{\beta}$ is the vector of estimated regression coefficients. Random samples are obtained by sampling the error term from a normal distribution, $\epsilon \sim N(0, \hat{\sigma}^2)$.

Value

An object of class `params_lm`, which is a list containing `coefs`, `sigma`, and `n_samples`. `n_samples` is equal to the number of rows in `coefs`.

Examples

```
library("MASS")
n <- 2
params <- params_lm(coefs = MASS::mvrnorm(n, mu = c(.5, .6),
                                         Sigma = matrix(c(.05, .01, .01, .05), nrow = 2)),
                  sigma <- rgamma(n, shape = .5, rate = 4))
print(params)
```

params_mlogit	<i>Parameters of a multinomial logit model</i>
---------------	--

Description

Store the parameters of a fitted multinomial logistic regression model. The model is used to predict probabilities of K classes.

Usage

```
params_mlogit(coefs)
```

Arguments

coefs A 3D array of stacked matrices. The number of matrices (i.e., the number of slices in the cube) should be equal to $K - 1$. Each matrix contains samples of the regression coefficients under sampling uncertainty corresponding to a particular class. Rows index parameter samples and columns index coefficients.

Details

Multinomial logit models are used to predict the probability of membership for subject i in each of K classes as a function of covariates:

$$Pr(y_i = c) = \frac{e^{\beta_c x_i}}{\sum_{k=1}^K e^{\beta_k x_i}}$$

Value

An object of class `params_mlogit`, which is a list containing `coefs` and `n_samples`, where `n_samples` is equal to the number of rows in each element of `coefs`.

Examples

```
params <- params_mlogit(coefs = array(
  c(matrix(c(intercept = 0, treatment = log(.75)), nrow = 1),
    matrix(c(intercept = 0, treatment = log(.8)), nrow = 1)),
  dim = c(1, 2, 2)
))
```

params_mlogit_list *Parameters of a list of multinomial logit models*

Description

Create a list containing the parameters of multiple fitted multinomial logit models.

Usage

```
params_mlogit_list(...)
```

Arguments

... Objects of class `params_mlogit`, which can be named.

Value

An object of class `params_mlogit_list`, which is a list containing `params_mlogit` objects.

params_surv *Parameters of a survival model*

Description

Create a list containing the parameters of a single fitted parametric or flexibly parametric survival model.

Usage

```
params_surv(coefs, dist, aux = NULL)
```

Arguments

`coefs` A list of length equal to the number of parameters in the survival distribution. Each element of the list is a matrix of samples of the regression coefficients under sampling uncertainty used to predict a given parameter. All parameters are expressed on the real line (e.g., after log transformation if they are defined as positive).

`dist` Character vector denoting the parametric distribution. See "Details".

`aux` Auxiliary arguments used with splines or fractional polynomials. See "Details".

Details

Survival is modeled as a function of L parameters α_l . Letting $F(t)$ be the cumulative distribution function, survival at time t is given by

$$1 - F(t|\alpha_1(x_1), \dots, \alpha_L(x_L)).$$

The parameters are modeled as a function of covariates, x_l , with an inverse transformation function $g^{-1}()$,

$$\alpha_l = g^{-1}(x_l^T \beta_l).$$

$g^{-1}()$ is typically $\exp()$ if a parameter is strictly positive and the identity function if the parameter space is unrestricted.

The types of distributions that can be specified are:

- `exponential` or `exp` Exponential distribution. `coef` must contain the rate parameter on the log scale and the same parameterization as in `stats::Exponential`.
- `weibull` or `weibull.quiet` Weibull distribution. The first element of `coef` is the shape parameter (on the log scale) and the second element is the scale parameter (also on the log scale). The parameterization is that same as in `stats::Weibull`.
- `weibullPH` Weibull distribution with a proportional hazards parameterization. The first element of `coef` is the shape parameter (on the log scale) and the second element is the scale parameter (also on the log scale). The parameterization is that same as in `flexsurv::WeibullPH`.
- `gamma` Gamma distribution. The first element of `coef` is the shape parameter (on the log scale) and the second element is the rate parameter (also on the log scale). The parameterization is that same as in `stats::GammaDist`.
- `lnorm` Lognormal distribution. The first element of `coef` is the `meanlog` parameter (i.e., the mean of survival on the log scale) and the second element is the `sdlog` parameter (i.e., the standard deviation of survival on the log scale). The parameterization is that same as in `stats::Lognormal`. The coefficients predicting the `meanlog` parameter are untransformed whereas the coefficients predicting the `sdlog` parameter are defined on the log scale.
- `gompertz` Gompertz distribution. The first element of `coef` is the shape parameter and the second element is the rate parameter (on the log scale). The parameterization is that same as in `flexsurv::Gompertz`.
- `llogis` Log-logistic distribution. The first element of `coef` is the shape parameter (on the log scale) and the second element is the scale parameter (also on the log scale). The parameterization is that same as in `flexsurv::Llogis`.
- `gengamma` Generalized gamma distribution. The first element of `coef` is the location parameter μ , the second element is the scale parameter σ (on the log scale), and the third element is the shape parameter Q . The parameterization is that same as in `flexsurv::GenGamma`.
- `survspline` Survival splines. Each element of `coef` is a parameter of the spline model (i.e. `gamma_0`, `gamma_1`, ...) with length equal to the number of knots (including the boundary knots). See below for details on the auxiliary arguments. The parameterization is that same as in `flexsurv::Survspline`.
- `fracpoly` Fractional polynomials. Each element of `coef` is a parameter of the fractional polynomial model (i.e. `gamma_0`, `gamma_1`, ...) with length equal to the number of powers minus 1. See below for details on the auxiliary arguments (i.e., powers).

- `pwexp` Piecewise exponential distribution. Each element of `coef` is rate parameter for a distinct time interval. The times at which the rates change should be specified with the auxiliary argument `time` (see below for more details).
- `fixed` A fixed survival time. Can be used for "non-random" number generation. `coef` should contain a single parameter, `est`, of the fixed survival times.

Auxiliary arguments for spline models should be specified as a list containing the elements:

`knots` A numeric vector of knots.

`scale` The survival outcome to be modeled as a spline function. Options are "log_cumhazard" for the log cumulative hazard; "log_hazard" for the log hazard rate; "log_cumodds" for the log cumulative odds; and "inv_normal" for the inverse normal distribution function.

`timescale` If "log" (the default), then survival is modeled as a spline function of log time; if "identity", then it is modeled as a spline function of time.

Auxiliary arguments for fractional polynomial models should be specified as a list containing the elements:

`powers` A vector of the powers of the fractional polynomial with each element chosen from the following set: -2, -1, -0.5, 0, 0.5, 1, 2, 3.

Auxiliary arguments for piecewise exponential models should be specified as a list containing the element:

`time` A vector equal to the number of rate parameters giving the times at which the rate changes.

Furthermore, when splines (with `scale = "log_hazard"`) or fractional polynomials are used, numerical methods must be used to compute the cumulative hazard and for random number generation. The following additional auxiliary arguments can therefore be specified:

`cumhaz_method` Numerical method used to compute cumulative hazard (i.e., to integrate the hazard function). Always used for fractional polynomials but only used for splines if `scale = "log_hazard"`. Options are "quad" for adaptive quadrature and "riemann" for Riemann sum.

`random_method` Method used to randomly draw from an arbitrary survival function. Options are "invcdf" for the inverse CDF and "discrete" for a discrete time approximation that randomly samples events from a Bernoulli distribution at discrete times.

`step` Step size for computation of cumulative hazard with numerical integration. Only required when using "riemann" to compute the cumulative hazard or using "discrete" for random number generation.

Value

An object of class `params_surv`, which is a list containing `coefs`, `dist`, and `n_samples`. `n_samples` is equal to the number of rows in each element of `coefs`, which must be the same. The list may also contain `aux` if a spline, fractional polynomial, or piecewise exponential model is used.

Examples

```
library("flexsurv")
fit <- flexsurvreg(Surv(futime, fustat) ~ 1, data = ovarian, dist = "weibull")
params <- params_surv(coefs = list(shape = fit$res.t["shape", "est", drop = FALSE],
                                  scale = fit$res.t["scale", "est", drop = FALSE]),
                     dist = fit$dlist$name)
print(params)
```

params_surv_list	<i>Parameters of a list of survival models</i>
------------------	--

Description

Create a list containing the parameters of multiple fitted parametric survival models.

Usage

```
params_surv_list(...)
```

Arguments

... Objects of class [params_surv](#), which can be named.

Value

An object of class `params_surv_list`, which is a list containing [params_surv](#) objects.

Examples

```
library("flexsurv")
fit_wei <- flexsurvreg(Surv(futime, fustat) ~ 1, data = ovarian, dist = "weibull")
params_wei <- create_params(fit_wei, n = 2)

fit_exp <- flexsurvreg(Surv(futime, fustat) ~ 1, data = ovarian, dist = "exp")
params_exp <- create_params(fit_exp, n = 2)

params_list <- params_surv_list(wei = params_wei, exp = params_exp)
print(params_list)
```

plot_ceac

Plot cost-effectiveness acceptability curve

Description

Plot a cost-effectiveness curve from either the output of `cea()` or `cea_pw()` using `ggplot2`. The former compares all treatment strategies simultaneously and uses the probabilistic sensitivity analysis (PSA) to compute the probability that each strategy is the most cost-effective at a given willingness to pay value, while the latter uses the PSA to compute the probability that each treatment is cost-effective relative to a comparator.

Usage

```
plot_ceac(x, ...)

## S3 method for class 'cea_pw'
plot_ceac(x, labels = NULL, ...)

## S3 method for class 'cea'
plot_ceac(x, labels = NULL, ...)
```

Arguments

x	An object of the appropriate class.
...	Further arguments passed to and from methods. Currently unused.
labels	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by <code>get_labels()</code> for an example.

Details

See the `cea()` documentation for an example. If there are multiple subgroups, then a faceted plot is produced with one plot for each subgroup.

plot_ceaf

Plot cost-effectiveness acceptability frontier

Description

Plot a cost-effectiveness acceptability frontier (CEAF) from the output of `cea` using `ggplot2`. The CEAF plots the probability that the optimal treatment strategy (i.e., the strategy with the highest expected net monetary benefit) is cost-effective.

Usage

```
plot_ceaf(x, labels = NULL)
```

Arguments

x A cea object produced by [cea](#).

labels A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by [get_labels\(\)](#) for an example.

Details

See the [cea\(\)](#) documentation for an example. If there are multiple subgroups, then a faceted plot is produced with one plot for each subgroup.

Value

A ggplot object.

plot_ceplane	<i>Plot cost-effectiveness plane</i>
--------------	--------------------------------------

Description

Plot a cost-effectiveness plane from the output of [cea_pw\(\)](#) using [ggplot2](#). Each point is a random draw of incremental costs (y-axis) and incremental QALYs (x-axis) from a probabilistic sensitivity analysis.

Usage

```
plot_ceplane(x, k = 50000, labels = NULL)
```

Arguments

x A cea_pw object produced by [cea_pw\(\)](#).

k Willingness to pay per QALY.

labels A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by [get_labels\(\)](#) for an example.

Details

See the [cea_pw\(\)](#) documentation for an example. If there are multiple subgroups, then a faceted plot is produced with one plot for each subgroup.

Value

A ggplot object.

plot_evpi	<i>Plot expected value of perfect information</i>
-----------	---

Description

Plot the expected value of perfect information (EVPI) from the output of `cea()` using `ggplot2`. Intuitively, the EVPI provides an estimate of the amount that a decision maker would be willing to pay to collect additional data and completely eliminate uncertainty.

Usage

```
plot_evpi(x, labels = NULL)
```

Arguments

<code>x</code>	A cea object produced by <code>cea()</code> .
<code>labels</code>	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by <code>get_labels()</code> for an example.

Details

See the `cea()` documentation for an example. If there are multiple subgroups, then a faceted plot is produced with one plot for each subgroup.

Value

A ggplot object.

Psm	<i>N-state partitioned survival model</i>
-----	---

Description

Simulate outcomes from an N-state partitioned survival model.

Format

An `R6::R6Class` object.

Public fields

- `survival_models` The survival models used to predict survival curves. Must be an object of class `PsmCurves`.
- `utility_model` The model for health state utility. Must be an object of class `StateVals`.
- `cost_models` The models used to predict costs by health state. Must be a list of objects of class `StateVals`, where each element of the list represents a different cost category.
- `n_states` Number of states in the partitioned survival model.
- `t_` A numeric vector of times at which survival curves were predicted. Determined by the argument `t` in `$sim_curves()`.
- `survival_` An object of class `survival` simulated using `sim_survival()`.
- `stateprobs_` An object of class `stateprobs` simulated using `$sim_stateprobs()`.
- `qalys_` An object of class `qalys` simulated using `$sim_qalys()`.
- `costs_` An object of class `costs` simulated using `$sim_costs()`.

Methods**Public methods:**

- `Psm$new()`
- `Psm$sim_survival()`
- `Psm$sim_stateprobs()`
- `Psm$sim_qalys()`
- `Psm$sim_costs()`
- `Psm$summarize()`
- `Psm$clone()`

Method `new()`: Create a new Psm object.

Usage:

```
Psm$new(survival_models, utility_model = NULL, cost_models = NULL)
```

Arguments:

`survival_models` The `survival_models` field.

`utility_model` The `utility_model` field.

`cost_models` The `cost_models` field.

Details: `n_states` is set equal to the number of survival models plus one.

Returns: A new Psm object.

Method `sim_survival()`: Simulate survival curves as a function of time using `PsmCurves$sim_survival()`.

Usage:

```
Psm$sim_survival(t)
```

Arguments:

`t` A numeric vector of times. The first element must be 0.

Returns: An instance of `self` with simulated output from `PsmCurves$sim_survival()` stored in `survival_`.

Method `sim_stateprobs()`: Simulate health state probabilities from `survival_` using a partitioned survival analysis.

Usage:

```
Psm$sim_stateprobs()
```

Returns: An instance of `self` with simulated output of class `stateprobs` stored in `stateprobs_`.

Method `sim_qalys()`: Simulate quality-adjusted life-years (QALYs) as a function of `stateprobs_` and `utility_model`. See `vignette("expected-values")` for details.

Usage:

```
Psm$sim_qalys(
  dr = 0.03,
  integrate_method = c("trapz", "riemann_left", "riemann_right"),
  lys = TRUE
)
```

Arguments:

`dr` Discount rate.

`integrate_method` Method used to integrate state values when computing (QALYs).

`lys` If TRUE, then life-years are simulated in addition to QALYs.

Returns: An instance of `self` with simulated output of class `qalys` stored in `qalys_`.

Method `sim_costs()`: Simulate costs as a function of `stateprobs_` and `cost_models`. See `vignette("expected-values")` for details.

Usage:

```
Psm$sim_costs(
  dr = 0.03,
  integrate_method = c("trapz", "riemann_left", "riemann_right")
)
```

Arguments:

`dr` Discount rate.

`integrate_method` Method used to integrate state values when computing costs.

Returns: An instance of `self` with simulated output of class `costs` stored in `costs_`.

Method `summarize()`: Summarize costs and QALYs so that cost-effectiveness analysis can be performed. See `summarize_ce()`.

Usage:

```
Psm$summarize(by_grp = FALSE)
```

Arguments:

`by_grp` If TRUE, then costs and QALYs are computed by subgroup. If FALSE, then costs and QALYs are aggregated across all patients (and subgroups).

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
Psm$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.


```

utility_tbl <- stateval_tbl(tbl = data.frame(state_id = states$state_id,
                                           min = psm4_exdata$utility$lower,
                                           max = psm4_exdata$utility$upper),
                          dist = "unif")
psm_utility <- create_StateVals(utility_tbl, n = n_samples,
                              hesim_data = hesim_dat)

# Partitioned survival decision model
psm <- Psm$new(survival_models = psm_curves,
              utility_model = psm_utility,
              cost_models = list(medical = psm_costs_medical))
psm$sim_survival(t = seq(0, 5, 1/12))
autoplot(psm$survival_, labels = labs, ci = FALSE, ci_style = "ribbon")
psm$sim_stateprobs()
autoplot(psm$stateprobs_, labels = labs)
psm$sim_costs(dr = .03)
head(psm$costs_)
head(psm$sim_qalys(dr = .03)$qalys_)

```

psm4_exdata

Example data for a 4-state partitioned survival model

Description

A collection of example datasets containing simulated survival, costs, and utility data for a 4-state partitioned survival model.

Usage

```
psm4_exdata
```

Format

A list containing the following elements:

- **Survival** A data frame containing patient information and time to 3 separate survival endpoints.
- **Costs** A list of data frames. The first data frame contains medical cost data and the second data frame contains drug cost data.

Survival data

The survival data frame contains a list of 3 survival curves, each containing the following columns.

female An indicator variable equal to 1 if the patient is female and 0 otherwise.

age The age of the patient in years.

strategy_id The id of the treatment strategy used.

endpoint1_time Follow up time with right censored data to survival endpoint 1.

endpoint1_status A status indicator for survival endpoint 1 equal to 0 if alive and 1 if dead.

endpoint2_time Follow up time with right censored data to survival endpoint 2.

endpoint2_status A status indicator for survival endpoint 2 equal to 0 if alive and 1 if dead.

endpoint3_time Follow up time with right censored data to survival endpoint 3.

endpoint3_status A status indicator for survival endpoint 3 equal to 0 if alive and 1 if dead.

Cost data

The cost list contains two data frames. The first data frame contains data on the medical costs by patient and health state, and contains the following columns:

patient_id An integer denoting the id of the patient.

female An indicator variable equal to 1 if the patient is female and 0 otherwise.

state_name A categorical variable denoting the three possible health states.

costs Annualized medical costs.

The second data frame contains data on the drug costs associated with each treatment strategy.

strategy_id The id of each treatment strategy.

costs Annualized drug costs.

PsmCurves

Partitioned survival curves

Description

Summarize N-1 survival curves for an N-state partitioned survival model.

Format

An [R6::R6Class](#) object.

Public fields

`params` An object of class [params_surv_list](#).

`input_data` An object of class [input_mats](#). Each row in X must be a unique treatment strategy and patient.

Methods

Public methods:

- `PsmCurves$new()`
- `PsmCurves$hazard()`
- `PsmCurves$cumhazard()`
- `PsmCurves$survival()`
- `PsmCurves$rmst()`
- `PsmCurves$quantile()`
- `PsmCurves$check()`
- `PsmCurves$clone()`

Method `new()`: Create a new `PsmCurves` object.

Usage:

```
PsmCurves$new(params, input_data)
```

Arguments:

`params` The `params` field.

`input_data` The `input_data` field.

Returns: A new `PsmCurves` object.

Method `hazard()`: Predict the hazard function for each survival curve as a function of time.

Usage:

```
PsmCurves$hazard(t)
```

Arguments:

`t` A numeric vector of times.

Returns: A `data.table` with columns `sample`, `strategy_id`, `patient_id`, `grp_id`, `curve` (the curve number), `t`, and `hazard`.

Method `cumhazard()`: Predict the cumulative hazard function for each survival curve as a function of time.

Usage:

```
PsmCurves$cumhazard(t)
```

Arguments:

`t` A numeric vector of times.

Returns: A `data.table` with columns `sample`, `strategy_id`, `patient_id`, `grp_id`, `curve`, `t`, and `cumhazard`.

Method `survival()`: Predict survival probabilities for each survival curve as a function of time.

Usage:

```
PsmCurves$survival(t)
```

Arguments:

`t` A numeric vector of times.

Returns: An object of class [survival](#).

Method `rmst()`: Predict the restricted mean survival time up until time points `t` for each survival curve.

Usage:

```
PsmCurves$rmst(t, dr = 0)
```

Arguments:

`t` A numeric vector of times.
`dr` Discount rate.

Returns: A data.table with columns `sample`, `strategy_id`, `patient_id`, `grp_id`, `curve`, `t`, and `rmst`.

Method `quantile()`: Predict quantiles of the survival distribution for each survival curve.

Usage:

```
PsmCurves$quantile(p)
```

Arguments:

`p` A numeric vector of probabilities for computing quantiles.

Returns: A data.table with columns `sample`, `strategy_id`, `patient_id`, `grp_id`, `curve`, `p` and `quantile`.

Method `check()`: Input validation for class. Checks that fields are the correct type.

Usage:

```
PsmCurves$check()
```

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
PsmCurves$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

[Psm](#), [create_PsmCurves\(\)](#)

Examples

```
library("flexsurv")

# Simulation data
dt_strategies <- data.frame(strategy_id = c(1, 2, 3))
dt_patients <- data.frame(patient_id = seq(1, 3),
                          age = c(45, 50, 60),
                          female = c(0, 0, 1))
hesim_dat <- hesim_data(strategies = dt_strategies,
                       patients = dt_patients)
```

```

# Fit survival models
surv_est_data <- psm4_exdata$survival
fit1 <- flexsurv::flexsurvreg(Surv(endpoint1_time, endpoint1_status) ~ age,
                             data = surv_est_data, dist = "exp")
fit2 <- flexsurv::flexsurvreg(Surv(endpoint2_time, endpoint2_status) ~ age,
                             data = surv_est_data, dist = "exp")
fit3 <- flexsurv::flexsurvreg(Surv(endpoint3_time, endpoint3_status) ~ age,
                             data = surv_est_data, dist = "exp")
fits <- flexsurvreg_list(fit1, fit2, fit3)

# Form PsmCurves
surv_input_data <- expand(hesim_dat, by = c("strategies", "patients"))
psm_curves <- create_PsmCurves(fits, input_data = surv_input_data, n = 3,
                               uncertainty = "bootstrap", est_data = surv_est_data)

# Summarize survival curves
head(psm_curves$quantile(p = c(.25, .5, .75)))
head(psm_curves$survival(t = seq(0, 3, by = .1)))
head(psm_curves$rmst(t = c(2, 5)))

```

qalys

Quality-adjusted life-years object

Description

An object of class `qalys` returned from methods `$sim_qalys()` in model classes that store simulated quality-adjusted life-years (QALYs).

Components

A `qalys` object inherits from `data.table` and contains the following columns:

sample A random sample from the PSA.

strategy_id The treatment strategy ID.

patient_id The patient ID.

state_id The health state ID.

dr The rate used to discount QALYs.

category A single category always equal to "qalys".

qalys The simulated values of QALYs.

If the argument `lys = TRUE`, then the `data.table` also contains a column `lys` containing simulated life-years.

qmatrix	<i>Transition intensity matrix</i>
---------	------------------------------------

Description

A generic function for creating transition intensity matrices where elements represent the instantaneous risk of moving between health states.

Usage

```
qmatrix(x, ...)
```

Arguments

x	An R object.
...	Further arguments passed to or from other methods. Currently unused.

qmatrix.matrix	<i>Transition intensity matrix from tabular object</i>
----------------	--

Description

Creates transition intensity matrices where elements represent the instantaneous risk of moving between health states.

Usage

```
## S3 method for class 'matrix'
qmatrix(x, trans_mat, ...)

## S3 method for class 'data.table'
qmatrix(x, trans_mat, ...)

## S3 method for class 'data.frame'
qmatrix(x, trans_mat, ...)
```

Arguments

x	A two-dimensional tabular object containing elements of the transition intensity matrix. A column represents a transition from state r to state s . Each row represents elements of a different transition intensity matrix. See "Details" for more information.
trans_mat	Just as in IndivCtstmTrans , a transition matrix describing the states and transitions in a multi-state model.
...	Further arguments passed to or from other methods. Currently unused.

Details

The object `x` must only contain non-zero and non-diagonal elements of a transition intensity matrix. The diagonal elements are automatically computed as the negative sum of the other rows.

Value

An array of transition intensity matrices with the third dimension equal to the number of rows in `x`.

See Also

[qmatrix.msm\(\)](#)

Examples

```
# 3 state irreversible model
tmat <- rbind(c(NA, 1, 2),
             c(NA, NA, 3),
             c(NA, NA, NA))
q12 <- c(.8, .7)
q13 <- c(.2, .3)
q23 <- c(1.1, 1.2)
q <- data.frame(q12, q13, q23)
qmat <- qmatrix(q, trans_mat = tmat)
print(qmat)

# Matrix exponential of each matrix in array
expmat(qmat)
```

qmatrix.msm

Transition intensity matrix from msm object

Description

Draw transition intensity matrices for a probabilistic sensitivity analysis from a fitted `msm` object.

Usage

```
## S3 method for class 'msm'
qmatrix(x, newdata = NULL, uncertainty = c("normal", "none"), n = 1000, ...)
```

Arguments

<code>x</code>	A <code>msm</code> : <code>msm</code> object.
<code>newdata</code>	A data frame to look for variables with which to predict. A separate transition intensity matrix is predicted based on each row in <code>newdata</code> . Can be <code>NULL</code> if no covariates are included in the fitted <code>msm</code> object.

uncertainty	Method used to draw transition intensity matrices. If "none", then point estimates are used. If "normal", then samples are drawn from the multivariate normal distribution of the regression coefficients.
n	Number of random observations of the parameters to draw.
...	Further arguments passed to or from other methods. Currently unused.

Value

An array of transition intensity matrices with the third dimension equal to the number of rows in newdata.

See Also

qmatrix.matrix()

Examples

```
library("msm")
set.seed(101)
qinit <- rbind(
  c(0, 0.28163, 0.01239),
  c(0, 0, 0.10204),
  c(0, 0, 0)
)
fit <- msm(state_id ~ time, subject = patient_id,
           data = onc3p[patient_id %in% sample(patient_id, 100)],
           covariates = list("1-2" =~ age + strategy_name),
           qmatrix = qinit)
qmatrix(fit, newdata = data.frame(age = 55, strategy_name = "New 1"),
        uncertainty = "none")
qmatrix(fit, newdata = data.frame(age = 55, strategy_name = "New 1"),
        uncertainty = "normal", n = 3)
```

rcat

Random generation for categorical distribution

Description

Draw random samples from a categorical distribution given a matrix of probabilities. rcat is vectorized and written in C++ for speed.

Usage

```
rcat(n, prob)
```

Arguments

n	Number of random observations to draw.
prob	A matrix of probabilities where rows correspond to observations and columns correspond to categories.

Value

A vector of random samples from the categorical distribution. The length of the sample is determined by n. The numerical arguments other than n are recycled so that the number of samples is equal to n.

Examples

```
p <- c(.2, .5, .3)
n <- 10000
pmat <- matrix(rep(p, n), nrow = n, ncol = length(p), byrow = TRUE)

# rcat
set.seed(100)
ptm <- proc.time()
samp1 <- rcat(n, pmat)
proc.time() - ptm
prop.table(table(samp1))

# rmultinom from base R
set.seed(100)
ptm <- proc.time()
samp2 <- t(apply(pmat, 1, rmultinom, n = 1, size = 1))
samp2 <- apply(samp2, 1, function(x) which(x == 1))
proc.time() - ptm
prop.table(table(samp2))
```

rdirichlet_mat

Random generation for multiple Dirichlet distributions

Description

Draw random samples from multiple Dirichlet distributions for use in transition probability matrices.

Usage

```
rdirichlet_mat(
  n,
  alpha,
  output = c("array", "matrix", "data.frame", "data.table")
)
```

Arguments

n	Number of samples to draw.
alpha	A matrix where each row is a separate vector of shape parameters.
output	The class of the object returned by the function. Either an array, matrix, data.frame, or data.table.

Details

This function is meant for representing the distribution of transition probabilities in a transition matrix. The (i,j) element of alpha is a transition from state i to state j. It is vectorized and written in C++ for speed.

Value

If output = "array", then an array of matrices is returned where each row of each matrix is a sample from the Dirichlet distribution. If output results in a two dimensional object (i.e., a matrix, data.frame, or data.table, then each row contains all elements of the sampled matrix from the Dirichlet distribution ordered rowwise; that is, each matrix is flattened. In these cases, the number of rows must be less than or equal to the number of columns.

Examples

```
alpha <- matrix(c(100, 200, 500, 50, 70, 75), ncol = 3, nrow = 2, byrow = TRUE)
samp <- rdirichlet_mat(100, alpha)
print(samp[, , 1:2])
```

rng_distributions *Random number generation distributions*

Description

A collection of functions for randomly generating deviates from probability distributions with [define_rng\(\)](#).

Usage

```
beta_rng(shape1 = 1, shape2 = 1, mean = NULL, sd = NULL, names = NULL)
```

```
dirichlet_rng(alpha, names = NULL)
```

```
fixed(est, names = NULL)
```

```
custom(x, names = NULL)
```

```
gamma_rng(mean, sd, names = NULL)
```

```
lognormal_rng(meanlog, sdlog, names = NULL)
```

```
multi_normal_rng(mu, Sigma, names = NULL, ...)
```

```
normal_rng(mean, sd, names = NULL)
```

```
uniform_rng(min, max, names = NULL)
```

Arguments

shape1, shape2	Non-negative parameters of the Beta distribution.
mean, sd	Mean and standard deviation of the random variable.
names	Names for columns if an object with multiple columns is returned by the function.
alpha	A matrix where each row is a separate vector of shape parameters.
est	A vector of estimates of the variable of interest.
x	A numeric vector, matrix, data.frame, or data.table containing random samples of the variable of interest from a suitable probability distribution. This would typically be a posterior distribution from a Bayesian analysis.
meanlog, sdlog	Mean and standard deviation of the distribution on the log scale.
mu, Sigma	mu is a vector giving the means of the variables and Sigma is a positive-definite symmetric matrix specifying the covariance matrix of the variables.
...	Additional arguments to pass to underlying random number generation functions. See "details".
min, max	Lower and upper limits of the distribution. Must be finite.

Details

These functions are not exported and are meant for use with `define_rng()`. They consequently assume that the number of samples to draw, `n`, is defined in the parent environment. Convenience random number generation functions include:

`beta_rng()` If `mean` and `sd` are both not `NULL`, then parameters of the beta distribution are derived using the methods of moments with `mom_beta()`. Beta variates are generated with `stats::rbeta()`.

`custom()` Use previously sampled values from a custom probability distribution. There are three possibilities: (i) if `n` is equal to the number previously sampled values (say `n_samples`), then `x` is returned as is; (ii) if `n < n_samples`, then samples from `x` are sampled without replacement; and (iii) if `n > n_samples`, then samples from `x` are sampled with replacement and a warning is provided.

`dirichlet_rng()` Dirichlet variates for each row in the matrix are generated with `rdirichlet_mat()`. The sampled values are stored in a `data.table` where there is a column for each element of `alpha` (with elements ordered rowwise).

`fixed()` This function should be used when values of the variable of interest are fixed (i.e., they are known with certainty). If `length(est) > 1`, an `n` by `length(est)` `data.table` is returned meaning that each element of `est` is repeated `n` times; otherwise (if `length(est) == 1`), a vector is returned where `est` is repeated `n` times.

`gamma_rng()` The parameters of the gamma distribution are derived using the methods of moments with `mom_gamma()` and gamma variates are generated with `stats::rgamma()`.

`lognormal_rng()` Lognormal variates are generated with `stats::rlnorm()`.

`multi_normal_rng()` Multivariate normal variates are generated with `MASS::mvrnorm()`.

`normal_rng()` Normal variates are generated with `stats::rnorm()`.

`uniform_rng()` Uniform variates are generated with `stats::runif()`.

Value

Functions either return a vector of length `n` or an `n` by `k` `data.table`. Multivariate distributions always return a `data.table`. If a univariate distribution is used, then a `data.table` is returned if each parameter is specified as a vector with length greater than 1; otherwise, if parameters are scalars, then a vector is returned. In the `data.table` case, `k` is equal to the length of the parameter vectors entered as arguments. For example, if the probability distribution contained mean as an argument and mean were of length 3, then an `n` by 3 matrix would be returned. The length of all parameter vectors must be the same. For instance, if the vector mean were of length 3 then all additional parameters (e.g., `sd`) must also be of length 3.

If a `data.table` is returned by a distribution, then its column names are set according to the following hierarchy:

1. With the `names` argument if it is not `NULL`
2. With the names of the parameter vectors if they are named vectors. If there are multiple parameter vector arguments, then the names of the first parameter vector with non `NULL` names is used. For instance, if `mean` and `sd` are both arguments to a random number generation function and `mean` is a named vector, then the names from the vector `mean` are used.
3. As `v1`, ..., `vk` if the `names` argument is `NULL` and there are no named parameter vectors.

See Also

[define_rng\(\)](#)

rpxexp

Random generation for piecewise exponential distribution

Description

Draw random samples from an exponential distribution with piecewise rates. `rpxexp` is vectorized and written in C++ for speed.

Usage

```
rpxexp(n, rate = 1, time = 0)
```

Arguments

n	Number of random observations to draw.
rate	A matrix of rates where rows correspond to observations and columns correspond to rates during specified time intervals.
time	A vector equal to the number of columns in rate giving the times at which the rate changes

Value

A vector of random samples from the piecewise exponential distribution. The length of the sample is determined by n. The numerical arguments other than n are recycled so that the number of samples is equal to n.

Examples

```
rate <- c(.6, 1.2, 1.3)
n <- 100000
ratemat <- matrix(rep(rate, n/2), nrow = n,
                  ncol = 3, byrow = TRUE)
t <- c(0, 10, 15)
ptm <- proc.time()
samp <- rpwexp(n, ratemat, t)
proc.time() - ptm
summary(samp)
```

 set_labels

Set value labels

Description

Update existing variables or create new ones that replace existing values with more informative labels as in `factor()`. All modifications are performed by reference (see `data.table::set()` for more information about assignment by reference).

Usage

```
set_labels(x, labels, new_names = NULL, as_factor = TRUE)
```

Arguments

x	A data.table.
labels	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by <code>get_labels()</code> for an example.

<code>new_names</code>	A character vector of the same length as <code>labels</code> where each element denotes the name of a new variable to create for the corresponding element in <code>labels</code> . If <code>NULL</code> , then the variables in <code>labels</code> are modified and no new variables are created; otherwise, the existing variables are not modified and new variables are created instead.
<code>as_factor</code>	If <code>TRUE</code> factor variables are created; otherwise character vectors are created.

Value

`x` is modified by reference and returned invisibly.

See Also

[get_labels\(\)](#)

Examples

```
library("data.table")
labs <- list("strategy_id" = c("s1" = 1,
                             "s2" = 2),
            "grp_id" = c("g1" = 1,
                       "g2" = 2))
d1 <- data.table(strategy_id = 1:2, grp_id = 1:2)
d2 <- copy(d1); d3 <- copy(d2)
set_labels(d2, labels = labs)
set_labels(d3, labels = labs, new_names = c("strategy_name", "grp_name"))
d1
d2
d3
```

stateprobs

State probability object

Description

An object of class `stateprobs` returned from methods `$sim_stateprobs()` in model classes.

Components

A `stateprobs` object inherits from `data.table` and contains the following columns:

sample A random sample from the PSA.

strategy_id The treatment strategy ID.

patient_id The patient ID.

grp_id The subgroup ID.

state_id The health state ID.

t The time at which a state probability is computed.

prob The probability of being in a given health state.

When simulating individual-level models, the `patient_id` column is not included as state probabilities are computed by averaging across patients.

StateVals

Model for state values

Description

Simulate values (i.e., utility or costs) associated with health states in a state transition or partitioned survival model.

Public fields

`params` Parameters for simulating state values. Currently supports objects of class `tparams_mean` or `params_lm`.

`input_data` An object of class `input_mats`. Only used for `params_lm` objects.

`method` The method used to simulate costs and quality-adjusted life-years (QALYs) as a function of state values. If `wlos`, then costs and QALYs are simulated by weighting state values by the length of stay in a health state. If `starting`, then state values represent a one-time value that occurs when a patient enters a health state. When `starting` is used in a cohort model, the state values only accrue at time 0; in contrast, in an individual-level model, state values accrue each time a patient enters a new state and are discounted based on time of entrance into that state.

`time_reset` If `FALSE` then time intervals are based on time since the start of the simulation. If `TRUE`, then time intervals reset each time a patient enters a new health state. This is relevant if, for example, costs vary over time within health states. Only used if `method = wlos`.

Methods

Public methods:

- `StateVals$new()`
- `StateVals$sim()`
- `StateVals$check()`
- `StateVals$clone()`

Method `new()`: Create a new `StateVals` object.

Usage:

```
StateVals$new(
  params,
  input_data = NULL,
  method = c("wlos", "starting"),
  time_reset = FALSE
)
```


Arguments:

params The params field.
input_data The input_data field.
method The method field.
time_reset The time_reset field.

Returns: A new StateVals object.

Method sim(): Simulate state values with either predicted means or random samples by treatment strategy, patient, health state, and time t.

Usage:

```
StateVals$sim(t, type = c("predict", "random"))
```

Arguments:

t A numeric vector of times.
type "predict" for mean values or "random" for random samples.

Returns: A data.table of simulated state values with columns for sample, strategy_id, patient_id, state_id, time, and value.

Method check(): Input validation for class. Checks that fields are the correct type.

Usage:

```
StateVals$check()
```

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
StateVals$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

stateval_tbl

Table to store state value parameters

Description

Create a table for storing parameter estimates used to simulate costs or utility in an economic model by treatment strategy, patient, health state, and (optionally) time interval.

Usage

```
stateval_tbl(  
tbl,  
dist = c("norm", "beta", "gamma", "lnorm", "unif", "fixed", "custom"),  
hesim_data = NULL,  
grp_var = NULL  
)
```

Arguments

<code>tbl</code>	A <code>data.frame</code> or <code>data.table</code> for storing parameter values. See "Details" for specifics.
<code>dist</code>	Probability distribution used to sample parameters for a probabilistic sensitivity analysis (PSA).
<code>hesim_data</code>	A <code>hesim_data</code> object. This argument is deprecated and should be passed to <code>create_StateVals.stateval_tbl()</code> instead.
<code>grp_var</code>	The name of the variable used to group patients.

Details

`tbl` is a tabular object containing columns for treatment strategies (`strategy_id`), patients (`patient_id`), health states (`state_id`), and/or the start of time intervals (`time_start`). The table must contain at least one column named `strategy_id`, `patient_id`, or `state_id`, but does not need to contain all of them. Each row denotes a unique treatment strategy, patient, health state, and/or time interval pair. `tbl` may also contain a column with the name specified in `grp_var` (rather than `patient_id`) so that state values are assigned to groups of patients.

`tbl` must also contain columns summarizing the state values for each row, which depend on the probability distribution selected with `dist`. Available distributions include the normal (`norm`), beta (`beta`), gamma (`gamma`), lognormal (`lnorm`), and uniform (`unif`) distributions. In addition, the option `fixed` can be used if estimates are known with certainty and `custom` can be used if parameter values for a PSA have been previously sampled from an arbitrary probability distribution. The columns in `tbl` that must be included, by distribution, are:

norm mean and sd

beta mean and se or shape1 and shape2

gamma mean and se, shape and rate, or shape and scale

lnorm meanlog or sdlog

unif min and max

fixed est

custom sample and value

Note that if `dist = "custom"`, then `tbl` must include a column named `sample` (an integer vector denoting a unique random draw) and `value` (denoting the value of the randomly sampled parameter). In this case, there is a unique row in `tbl` for each random draw (`sample`) and each combination of strategies, patients, health states, and/or time intervals. Again, `tbl` must contain at least one column named `strategy_id`, `patient_id` (or `grp_var`), or `state_id`, but does not need to contain them all.

Value

An object of class `stateval_tbl`, which is a `data.table` of parameter values with attributes for `dist` and `grp_var`.

See Also

[create_StateVals\(\)](#), [StateVals](#)

Examples

```

strategies <- data.frame(strategy_id = c(1, 2))
patients <- data.frame(patient_id = seq(1, 3),
  grp = c(1, 1, 2),
  age = c(45, 50, 60),
  female = c(0, 0, 1))
states <- data.frame(state_id = c(1, 2))
hesim_dat <- hesim_data(strategies = strategies,
  patients = patients,
  states = states)

# Utility varies by health state and patient group
utility_tbl <- stateval_tbl(data.frame(state_id = rep(states$state_id, 2),
  grp = rep(rep(c(1, 2)), each = nrow(states)),
  mean = c(.8, .7, .75, .55),
  se = c(.18, .12, .10, .06)),
  dist = "beta",
  grp_var = "grp")

print(utility_tbl)
utilmod <- create_StateVals(utility_tbl, n = 2, hesim_data = hesim_dat)

# Costs vary by treatment strategy
cost_tbl <- stateval_tbl(data.frame(strategy_id = strategies$strategy_id,
  mean = c(5000, 3000),
  se = c(200, 100)),
  dist = "gamma")

print(cost_tbl)
costmod <- create_StateVals(cost_tbl, n = 2, hesim_data = hesim_dat)

```

summarize_ce

Summarize costs and effectiveness

Description

Summarize costs and quality-adjusted life-years (QALYs) given output simulated from an economic model. The summary output is used to perform cost-effectiveness analysis with [cea\(\)](#) and [cea_pw\(\)](#).

Usage

```
summarize_ce(costs, qalys, by_grp = FALSE)
```

Arguments

costs	Simulated costs by category (objects of class costs).
qalys	Simulated QALYs (objects of class qalys).
by_grp	If TRUE, then costs and QALYs are computed by subgroup. If FALSE, then costs and QALYs are aggregated across all patients (and subgroups).

Details

If mean costs and/or QALYs have already been computed (i.e., an average within a population), then there must be one observation for each discount rate (`dr`), PSA sample (`sample`), treatment strategy (`strategy_id`), and health state (`state_id`). Alternatively, there can be a column denoting a patient (`patient_id`), in which case outcomes will first be averaged across patients. A `grp_id` column can also be used so that outcomes are computed for each subgroup (if `by_grp = TRUE`); otherwise it is assumed that there is only one subgroup.

Value

An object of class `ce`.

summary.ce

Summary method for cost-effectiveness object

Description

Summarize a `ce` object by producing confidence intervals for quality-adjusted life-years (QALYs) and each cost category with `summary.ce()` and format for pretty printing with `format.summary.ce()`.

Usage

```
## S3 method for class 'ce'
summary(object, prob = 0.95, labels = NULL, ...)

## S3 method for class 'summary.ce'
format(
  x,
  digits_qalys = 2,
  digits_costs = 0,
  dr_qalys = NULL,
  dr_costs = NULL,
  pivot_from = "strategy",
  drop_grp = TRUE,
  pretty_names = TRUE,
  ...
)
```

Arguments

<code>object</code>	A <code>ce</code> object.
<code>prob</code>	A numeric scalar in the interval (0,1) giving the confidence interval. Default is 0.95 for a 95 percent interval.
<code>labels</code>	A list of named vectors containing the values and labels of variables. The elements of each vector are the values of a variable and the names are the labels. The names of the list are the names of the variables. See the output returned by <code>get_labels()</code> for an example.

...	Further arguments passed to or from other methods. Currently unused.
x	A <code>summary.ce</code> object.
digits_qalys	Number of digits to use to report QALYs.
digits_costs	Number of digits to use to report costs.
dr_qalys	Discount rate to subset to for quality-adjusted life-years (QALYs).
dr_costs	Discount rate to subset to for costs.
pivot_from	Character vector denoting a column or columns used to "widen" the data. Should either be "strategy", "grp", "outcome", or some combination of the three. There will be one column for each value of the variables in <code>pivot_from</code> . Default is to widen so there is a column for each treatment strategy. Set to NULL if you do not want to widen the table.
drop_grp	If TRUE, then the group column will be removed if there is only one subgroup; other it will be kept. If FALSE, then the <code>grp</code> column is never removed.
pretty_names	Logical. If TRUE, then the columns <code>strategy</code> , <code>grp</code> , <code>outcome</code> , <code>dr</code> , and <code>value</code> are renamed (if they exist) to <code>Strategy</code> , <code>Group</code> , <code>Outcome</code> , <code>Discount rate</code> , and <code>Value</code> .

Details

For an example, see [IndivCtstm](#).

Value

`summary.ce()` returns an object of class `summary.ce` that is a tidy data table with the following columns:

dr The discount rate.

strategy The treatment strategy.

grp The patient subgroup.

type Either "QALYs" or "Costs".

category Category is always "QALYs" when `type == "QALYs"`; otherwise, it is the cost category.

estimate The point estimate computed as the average across the PSA samples.

lower The lower limit of the confidence interval.

upper The upper limit of the confidence interval.

`format.summary.ce()` formats the table according to the arguments passed.

survival	<i>Survival object</i>
----------	------------------------

Description

An object of class `survival` returned from `Psm$sim_survival()` or `PsmCurves$survival()`.

Components

A `survival` object inherits from `data.table` and contains the following columns:

sample A random sample from the PSA.

strategy_id The treatment strategy ID.

patient_id The patient ID.

grp_id The subgroup ID.

curve One of the N-1 survival curves in an N-state partitioned survival model. Each curve corresponds to unique endpoint.

t The time at which a survival probability is computed.

survival The probability of surviving to time `t`.

See Also

[Psm](#), [PsmCurves](#)

surv_quantile	<i>Survival quantiles</i>
---------------	---------------------------

Description

Compute quantiles from survival curves.

Usage

```
surv_quantile(x, probs = 0.5, t, surv_cols, by)
```

Arguments

`x` A `data.table` or `data.frame`.

`probs` A numeric vector of probabilities with values in $[0, 1]$.

`t` A character scalar of the name of the time column.

`surv_cols` A character vector of the names of columns containing survival curves.

`by` A character vector of the names of columns to group by.

tparams	<i>Transformed parameter object</i>
---------	-------------------------------------

Description

Objects prefixed by "tparams_" are lists containing transformed parameters used to simulate outcomes. The parameters have presumably already been transformed as a function of input data and consequently do not need to be used alongside input matrices. In other words, transformed parameters are parameters that have already been predicted as a function of covariates.

See Also

[params](#)

tparams_mean	<i>Predicted means</i>
--------------	------------------------

Description

Create a list containing means predicted from a statistical model.

Usage

```
tparams_mean(value, ...)
```

Arguments

value	Matrix of samples from the distribution of the mean. Columns denote random samples and rows denote means for different observations.
...	Arguments to pass to id_attributes . Each row in value must be a prediction for a strategy_id, patient_id, state_id, and optionally time_id combination.

Value

An object of class tparams_mean, which is a list containing value, n_samples, and the ID attributes passed to [id_attributes](#).

See Also

[tparams](#)

Examples

```
tparams_mean(value = matrix(1:8, nrow = 4),
             strategy_id = rep(1:2, each = 2),
             n_strategies = 2,
             patient_id = rep(1, 4),
             n_patients = 1,
             state_id = rep(1:2, times = 2),
             n_states = 2)
```

```
tparams_transprobs      Transition probabilities
```

Description

Create a list containing predicted transition probabilities at discrete times. Since the transition probabilities have presumably already been predicted based on covariate values, no input data is required for simulation. The class can be instantiated from either an array, a `data.table`, a `data.frame`, or a `tpmatrix`.

Usage

```
tparams_transprobs(object, ...)

## S3 method for class 'array'
tparams_transprobs(
  object,
  tpmatrix_id = NULL,
  times = NULL,
  grp_id = NULL,
  patient_wt = NULL,
  ...
)

## S3 method for class 'data.table'
tparams_transprobs(object, ...)

## S3 method for class 'data.frame'
tparams_transprobs(object, ...)

## S3 method for class 'tpmatrix'
tparams_transprobs(object, tpmatrix_id, ...)
```

Arguments

```
object      An object of the appropriate class.
...         Further arguments passed to or from other methods. Currently unused.
```

<code>tpmatrix_id</code>	An object of class <code>tpmatrix_id</code> (or an equivalent <code>data.table</code> with the same ID columns as returned by <code>tpmatrix_id()</code>).
<code>times</code>	An optional numeric vector of distinct times to pass to <code>time_intervals</code> representing time intervals indexed by the 4th dimension of the array. May either be the start or the end of intervals. This argument is not required if there is only one time interval.
<code>grp_id</code>	An optional numeric vector of integers denoting the subgroups. Must be the same length as the 3rd dimension of the array.
<code>patient_wt</code>	An optional numeric vector denoting the weight to apply to each patient within a subgroup. Must be the same length as the 3rd dimension of the array.

Details

The format of object depends on its class:

array Either a 3D or a 6D array is possible.

- If a 3D array, then each slice is a square transition probability matrix. In this case `tpmatrix_id` is required and each matrix slice corresponds to the same numbered row in `tpmatrix_id`. The number of matrix slices must equal the number of rows in `tpmatrix_id`.
- If a 6D array, then the dimensions of the array should be indexed as follows: 1st (`sample`), 2nd (`strategy_id`), 3rd (`patient_id`), 4th (`time_id`), 5th (rows of transition matrix), and 6th (columns of transition matrix). In other words, an index of `[s, k, i, t]` represents the transition matrix for the `s`th sample, `k`th treatment strategy, `i`th patient, and `t`th time interval.

data.table Must contain the following:

- ID columns for the parameter `sample` (`sample`), treatment strategy (`strategy_id`), and patient (`patient_id`). If the number of time intervals is greater than 1 it must also contain the column `time_start` denoting the starting time of a time interval. A column `patient_wt` may also be used to denote the weight to apply to each patient.
- Columns for each element of the transition probability matrix. They should be prefixed with "prob_" and ordered rowwise. For example, the following columns would be used for a 2x2 transition probability matrix: `prob_1` (1st row, 1st column), `prob_2` (1st row, 2nd column), `prob_3` (2nd row, 1st column), and `prob_4` (2nd row, 2nd column).

data.frame Same as `data.table`.

tpmatrix An object of class `tpmatrix`.

A `tparams_transprobs` object is also instantiated when creating a cohort discrete time state transition model using `define_model()`.

Value

An object of class `tparams_transprobs`, which is a list containing `value` and relevant ID attributes. The element `value` is an array of predicted transition probability matrices from the probability distribution of the underlying statistical model. Each matrix in `value` is a prediction for a `sample`, `strategy_id`, `patient_id`, and optionally `time_id` combination.

See Also

[define_model\(\)](#), [create_CohortDtstm\(\)](#), [tpmatrix\(\)](#)

tpmatrix

Transition probability matrix

Description

`tpmatrix()` both defines and evaluates a transition probability matrix in which elements are expressions. It can be used within `define_tparams()` to create a transition probability matrix or directly to create a `tparams_transprobs()` object. These are, in turn, ultimately used to create a `CohortDtstmTrans` object for simulating health state transitions.

Usage

```
tpmatrix(...)
```

Arguments

... Named values of expressions defining elements of the matrix. Each element of ... should either be a vector or a 2-dimensional tabular object such as a data frame. See "Details" and the examples below.

Details

A `tpmatrix` is a 2-dimensional tabular object that stores flattened square transition probability matrices in each row. Each transition probability matrix is filled rowwise. The complementary probability (equal to 1 minus the sum of the probabilities of all other elements in a row of a transition probability matrix) can be conveniently referred to as `C`. There can only be one complement for each row in a transition probability matrix.

Value

Returns a `tpmatrix` object that inherits from `data.table` where each column is an element of the transition probability matrix with elements ordered rowwise.

See Also

[define_model\(\)](#), [define_tparams\(\)](#), [tpmatrix_id\(\)](#), [tparams_transprobs\(\)](#), [CohortDtstmTrans\(\)](#)

Examples

```
# Pass vectors
p_12 <- c(.7, .6)
tpmatrix(
  C, p_12,
  0, 1
)
```

```
tpmatrix(  
  C, p_12,  
  C, 1  
)  
  
# Pass matrix  
pmat <- matrix(c(.5, .5, .3, .7), byrow = TRUE, ncol = 4)  
tpmatrix(pmat)  
  
# Pass vectors and data frames  
p1 <- data.frame(  
  p_12 = c(.7, .6),  
  p_13 = c(.1, .2)  
)  
  
p2 <- data.frame(  
  p_21 = 0,  
  p_22 = c(.4, .45),  
  p_23 = c(.6, .55)  
)  
  
p3 <- data.frame(  
  p_31 = c(0, 0),  
  p_32 = c(0, 0),  
  p_33 = c(1, 1)  
)  
  
tpmatrix(  
  C, p1,  
  p2,  
  p3  
)
```

tpmatrix_id

Transition probability matrix IDs

Description

Creates ID variables for each row returned by `tpmatrix()`. This function is most conveniently used along with `tpmatrix()` to construct a `tparams_transprobs()` object.

Usage

```
tpmatrix_id(object, n_samples)
```

Arguments

object	An object of class <code>expanded_hesim_data</code> returned by <code>expand.hesim_data()</code> . This dataset must be expanded by treatment strategies, patients, and optionally time intervals.
n_samples	The number of parameters samples used for the probabilistic sensitivity analysis (PSA).

Value

Returns a `tpmatrix_id` object that inherits from `data.table` with the same columns in `object` repeated `n_samples` times. That is, to facilitate creation of a `tparams_transprobs()` object, there is one row for each parameter sample, treatment strategy, patient, and optionally time interval.

See Also

[tpmatrix\(\)](#), [tparams_transprobs\(\)](#), [expand.hesim_data\(\)](#)

Examples

```
strategies <- data.frame(strategy_id = c(1, 2))
patients <- data.frame(patient_id = seq(1, 3), age = c(65, 50, 75),
  gender = c("Female", "Female", "Male"))
hesim_dat <- hesim_data(strategies = strategies,
  patients = patients)
input_data <- expand(hesim_dat, by = c("strategies", "patients"))
tpmatrix_id(input_data, n_samples = 2)
```

<code>tpmatrix_names</code>	<i>Names for elements of a transition probability matrix</i>
-----------------------------	--

Description

Create names for all elements of a transition probability matrix given names for the health states. This is useful for flattening a transition probability matrix (rowwise) into a vector and naming the resulting vector. The name of an element of the flattened vector representing a transition from the *i*th state to the *j*th state is of the form `paste0(prefix, state_i, sep, state_j)`.

Usage

```
tpmatrix_names(states, prefix = "p_", sep = "_")
```

Arguments

states	A character vector of the names of health states in the transition matrix.
prefix	A prefix that precedes the described transitions between states.
sep	A character string to separate the terms representing state <i>i</i> and state <i>j</i> .

Value

A character vector containing a name for each element of the transition probability matrix encompassing all possible transitions.

Examples

```
tpmatrix_names(LETTERS[1:4])
tpmatrix_names(LETTERS[1:4], prefix = "")
tpmatrix_names(LETTERS[1:4], prefix = "", sep = ".")
```

weibullNMA

Parameterization of the Weibull distribution for network meta-analysis

Description

Density, distribution function, hazards, quantile function and random generation for the Weibull distribution when parameterized for network meta-analysis.

Usage

```
dweibullNMA(x, a0, a1 = FALSE, log = FALSE)
pweibullNMA(q, a0, a1, lower.tail = TRUE, log.p = FALSE)
qweibullNMA(p, a0, a1, lower.tail = TRUE, log.p = FALSE)
rweibullNMA(n, a0, a1)
hweibullNMA(n, a0, a1, log = FALSE)
HweibullNMA(n, a0, a1, log = FALSE)
rmst_weibullNMA(t, a0, a1, start = 0)
mean_weibullNMA(a0, a1)
```

Arguments

x, q	Vector of quantiles
a0	Intercept of reparameterization of the Weibull distribution.
a1	Slope of the reparameterization of the Weibull distribution.
log, log.p	logical; if TRUE, probabilities p are given as log(p).
lower.tail	logical; if TRUE (default), probabilities are $P(X \leq x)$, otherwise, $P(X > x)$.
p	Vector of probabilities

n	Number of observations. If <code>length(n) > 1</code> , the length is taken to be the number required.
t	Vector of times for which restricted mean survival time is evaluated.
start	Optional left-truncation time or times. The returned restricted mean survival will be conditional on survival up to this time.

Value

`dweibullNMA` gives the density, `pweibullNMA` gives the distribution function, `qweibullNMA` gives the quantile function, `rweibullNMA` generates random deviates, `HweibullNMA` returns the cumulative hazard and `hweibullNMA` the hazard.

See Also

[dweibull](#)

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