

Package ‘icmstate’

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Description Allows for the non-parametric estimation of transition intensities in interval-censored multi-state models using the approach of Gomon and Putter (2024) <[doi:10.48550/arXiv.2409.07176](https://doi.org/10.48550/arXiv.2409.07176)> or Gu et al. (2023) <[doi:10.1093/biomet/asad073](https://doi.org/10.1093/biomet/asad073)>.

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icmstate-package	<i>icmstate</i>
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Description

Non-parametric estimation of transition intensities in interval-censored multi-state models

Details

Allows for the estimation of transition intensities in interval-censored multi-state models using the approach of Gomon and Putter (2024) (Multinomial likelihood) or Gu et al. (2023) (Poisson likelihood).

Author(s)

Maintainer: Daniel Gomon <dgstatsoft@gmail.com> [aut, cre]
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References

- Y. Gu, D. Zeng, G. Heiss, and D. Y. Lin, Maximum likelihood estimation for semiparametric regression models with interval-censored multistate data, *Biometrika*, Nov. 2023, doi:10.1093/biomet/asad073
- D. Gomon and H. Putter, Non-parametric estimation of transition intensities in interval censored Markov multi-state models without loops, *arXiv*, 2024, doi:10.48550/arXiv.2409.07176

ageqb	<i>Check if event time is larger/equal than other event time</i>
-------	--

Description

Function which takes as input a vector *a* with event times and a vector *b* with event times and checks whether each entry in *a* is larger or equal than the entries in *b*.

Usage

ageqb(*a*, *b*)

Arguments

<i>a</i>	Vector of event times
<i>b</i>	Vector of event times

Value

Matrix of size (length(*a*) * length(*b*)) with binary values indicating whether the event times in *a* are larger than the event times in *b*

agreaterb	<i>Check if event time is larger than other event time</i>
-----------	--

Description

Function which takes as input a vector *a* with event times and a vector *b* with event times and checks whether each entry in *a* is larger than the entries in *b*.

Usage

agreaterb(*a*, *b*)

Arguments

<i>a</i>	Vector of event times
<i>b</i>	Vector of event times

Value

Matrix of size $(\text{length}(a) * \text{length}(b))$ with binary values indicating whether the event times in a are larger than the event times in b

ainB	<i>Check if event time is contained within half-open interval</i>
------	---

Description

Function which takes as input a vector a with event times and a 2 column matrix B representing half-open intervals $(l, R]$ and checks whether each event time is contained in each half-open interval.

Usage

```
ainB(a, B)
```

Arguments

a	Vector of event times
B	Two column matrix containing intervals

Value

Matrix of size $(\text{length}(a) * \text{nrow}(B))$ with binary values indicating whether the event times in a are contained in the intervals of B

Aintersectb	<i>Check if half-open intervals intersect with event times</i>
-------------	--

Description

Function which takes as input a 2 column matrix of half-open intervals and a vector of event times and returns the event times that intersect with the half-open intervals.

Usage

```
Aintersectb(A, b, A.left.open = FALSE)
```

Arguments

A	Two column matrix containing intervals
b	Vector of event times
$A.left.open$	Are the intervals in A open on the left side? Default = FALSE.

Value

Numeric vector of event times from b that intersect with A .

Alargerb	<i>Check if closed interval is contained in half-open infinite interval</i>
----------	---

Description

Function which takes as input a matrix with 2 columns and a vector indicating left points of intervals [b, Infinity) and checks whether each interval in the matrix is contained within the corresponding interval derived from b.

Usage

```
Alargerb(A, b)
```

Arguments

A	Two column matrix containing intervals to be checked for being contained in b
b	Vector indicating left point in corresponding [b, Infinity) interval

Value

Matrix of size (nrow(A) * length(b)) with binary values indicating whether the intervals in A are contained in the ones induced by b

AsubsetB	<i>Check if closed interval is contained in other closed interval</i>
----------	---

Description

Function which takes as input two matrices with 2 columns each and checks whether each interval in the first matrix is contained within each interval in the second matrix.

Usage

```
AsubsetB(A, B, B.left.open = FALSE, B.right.open = FALSE)
```

Arguments

A	Two column matrix containing intervals to be checked for being contained in B
B	Two column matrix containing intervals possibly overlapping the intervals in A
B.left.open	Are the intervals in B left-open?
B.right.open	Are the intervals in B right-open?

Value

Matrix of size (nrow(A) * nrow(B)) with binary values indicating whether the intervals in A are contained in B

`direct_from_observed_intervals`*Translate observed transition intervals into direct transition intervals*

Description

Given observed transition intervals, determine the "worst" (least informative) possible direct transition intervals that could have occurred to form this sample.

Usage

```
direct_from_observed_intervals(observed_intervals, tmat, gd)
```

Arguments

`observed_intervals`

Output from [get_trans_intervals](#).

`tmat`

A transition matrix as created by `transMat`

`gd`

A `data.frame` with the following named columns

`id`: Subject identifier;

`state`: State at which the subject is observed at time;

`time`: Time at which the subject is observed;

The true transition time between states is then interval censored between the times.

Value

A `data.frame` with the following named columns

`entry_time`: Time of entry into "from" state;

`time_from`: Last time subject(`id`) was seen in state "from";

`time_to`: First time subject(`id`) was seen in state "to";

`from`: State from which a transition was observed;

`to`: State to which the transition was observed;

`id`: Subject identifier;

For right-censored observations, `entry_time` denotes the first time seen in the censored state, `time_from` the last time seen in the censored state, `time_to` is `Inf`, from the censored state and `to` is `NA`.

estimate_support_msm *Estimate the support of a general Markov interval-censored Multi-state model without loops.*

Description

Given a realisation of a multi-state model, estimate the support of the different transitions possible in that MSM. The estimation is performed by viewing each possible state in a competing risks setting and applying the result of Hudgens (2001) to determine the support and left-truncation intervals and Hudgens (2005) to check whether a solution is possible.

Usage

```
estimate_support_msm(gd, tmat)
```

Arguments

gd	A data.frame with the following named columns id: Subject identifier; state: State at which the subject is observed at time; time: Time at which the subject is observed; The true transition time between states is then interval censored between the times.
tmat	A transition matrix as created by transMat

Value

TODO

References

Michael G. Hudgens, On Nonparametric Maximum Likelihood Estimation with Interval Censoring and Left Truncation, *Journal of the Royal Statistical Society Series B: Statistical Methodology*, Volume 67, Issue 4, September 2005, Pages 573-587, doi:[10.1111/j.14679868.2005.00516.x](https://doi.org/10.1111/j.14679868.2005.00516.x)

M. G. Hudgens, G. A. Satten, and I. M. Longini, Nonparametric Maximum Likelihood Estimation for Competing Risks Survival Data Subject to Interval Censoring and Truncation, *Biometrics*, vol. 57, no. 1, Pages 74-80, March 2001, doi:[10.1111/j.0006341x.2001.00074.x](https://doi.org/10.1111/j.0006341x.2001.00074.x)

evalstep	<i>Sample from a markov chain multi state model with exactly observed transition times</i>
----------	--

Description

Given a markov chain multi state model with exactly observed transition times, sample from this chain at the observation times, giving interval censored observations (panel data).

Usage

```
evalstep(time, stepf, newtime, subst = -Inf, to.data.frame = FALSE)
```

Arguments

time	Times at which a transition occurs
stepf	States at which the chain is in at times
newtime	Observation times of the chain, to create observed states
subst	State to return if observation time is before first transition time. Default = -Inf.
to.data.frame	Should the result be returned as a data.frame?

Value

A numeric vector or data.frame (if to.data.frame = TRUE) containing either the observed states or the named columns newtime and res, representing the observation times and observed states.

Author(s)

Hein Putter

Examples

```
obs_states <- evalstep(time = seq(0, 20, 2), stepf = sample(1:9, 11, replace = TRUE),
                      newtime = c(-1, 1, 7, 9, 19))
obs_states
```

get_trans_intervals *Get transition intervals from specified data*

Description

Given a sample from a multi-state model, summarize the transitions that have been observed.

Usage

```
get_trans_intervals(gd, tmat)
```

Arguments

gd A data.frame with the following named columns
id: Subject identifier;
state: State at which the subject is observed at time;
time: Time at which the subject is observed;
The true transition time between states is then interval censored between the times.

tmat A transition matrix as created by transMat

Value

A data.frame with the following named columns

entry_time: Time of entry into "from" state;
time_from: Last time subject(id) was seen in state "from";
time_to: First time subject(id) was seen in state "to";
from: State from which a transition was observed;
to: State to which the transition was observed;
id: Subject identifier;

For right-censored observations, entry_time denotes the first time seen in the censored state, time_from the last time seen in the censored state, time_to is Inf, from the censored state and to is NA.

graphfromIntervals *Construct Graph from censoring/truncation intervals*

Description

Given intervals, construct a graph containing vertices representing these intervals and edges between the vertices if the intervals intersect. See Hudgens (2005).

Usage

```
graphfromIntervals(intervals)
```

Arguments

`intervals` A data.frame with 3 columns containing half-open intervals (left open, right closed) and an indicator whether the interval results from a censored transition or truncation: #

 L: Left side of interval;
 R: Right side of interval;
 cens: Indicator whether interval resulted from censoring or truncation (1 = censoring, 0 = truncation);

Note that the truncation intervals need to be in the form (N, Inf] with N a numeric value.

Value

Returns an 'igraph' object containing the graph with vertices representing the intervals and edges between the vertices if the intervals intersect. The vertices will be named accordingly, starting with a 'T' when representing a truncation interval and 'C' when representing a censoring interval.

References

Michael G. Hudgens, On Nonparametric Maximum Likelihood Estimation with Interval Censoring and Left Truncation, Journal of the Royal Statistical Society Series B: Statistical Methodology, Volume 67, Issue 4, September 2005, Pages 573-587, [doi:10.1111/j.14679868.2005.00516.x](https://doi.org/10.1111/j.14679868.2005.00516.x)

interpol_msfit *Given a msfit object, linearly interpolate the cumulative hazard taking into account the support sets for msfit objects.*

Description

After using this function, use probtrans to get interpolated transition probabilities.

Usage

```
interpol_msfit(msfit, times)
```

Arguments

```
msfit      A msfit object.
times     Times at which to interpolate the msfit object.
```

Value

An msfit object containing the interpolated hazards

Examples

```
library(mstate)
tmat <- trans.illdeath()
times <- seq(0, 5, 0.1)
ms_fit <- list(Haz = data.frame(time = rep(times, 3),
                                Haz = c(replicate(3, cumsum(runif(length(times), 0, 0.02)))),
                                trans = rep(1:3, each = length(times))),
              trans = tmat)
class(ms_fit) <- "msfit"

ms_fit_interpolated <- interpol_msfit(ms_fit, seq(0, 5, 0.01))
```

msm_frydman	<i>Determine NPMLE for Multi State illness death Markov model using Frydman (1995)</i>
-------------	--

Description

Determine NPMLE for Multi State illness death Markov model using Frydman (1995)

Usage

```
msm_frydman(data, tol = 1e-08)
```

Arguments

```
data      A data.frame containing the columns named:
delta: Did a transition from 1 -> 2 occur? (binary: 0 = no, 1 = yes); In the
        left-truncated case, delta = 2 indicates initially observed in state 2.
Delta: Was the transition to state 3 observed? (binary: 0 = no, 1 = yes);
L: Left timepoint of interval censored transition to state 2 (numeric);
R: Right timepoint of interval censored transition to state 2 (numeric);
time: Time of event (transition to 3) or right-censoring in state 2 (numeric);
```

trunc: (optional) Left-truncation time (numeric); Only used for entries with $\delta = 2$.

tol Tolerance of the EM algorithm. Algorithm will stop when the absolute difference between current mass estimates and new estimates is smaller than the tolerance

Details

For an illness death model (1 = healthy, 2 = ill, 3 = dead) estimate the NPMLE in the following form:

F12: Cumulative distribution function of 1->2 transition;

F13: Cumulative distribution function of 1->3 transition;

Lambda23: Cumulative intensity of 2->3 transition;

Value

A list with the following entries:

data_idx: A list containing the data used for the fit (matdata), the indices for which group a subject belongs to (GroupX_idx), some computational parameters (see Frydman(1995)) and the unique failure times of the 2->3 and 1->3 transitions respectively in t_n_star and e_k_star;

supportMSM: A list containing all transition intervals in A and the theoretical support intervals in Q_mat;

z_lambda: Computational quantities, see Frydman(1995);

cdf: A list of functions that allow to recover the cdf for the 1->3 (F13) and 1->2 (F12) transition and the cumulative hazard for the 2->3 (Lambda23) transition.;

References

Frydman, H. (1995). Nonparametric Estimation of a Markov 'Illness-Death' Process from Interval-Censored Observations, with Application to Diabetes Survival Data. *Biometrika*, 82(4), 773-789. [doi:10.2307/2337344](https://doi.org/10.2307/2337344)

Examples

```
data <- data.frame(delta = c(0, 0, 1, 1), Delta = c(0, 1, 0, 1),
                  L = c(NA, NA, 1, 1.5), R = c(NA, 3, 2, 3),
                  time = c(4, 5, 6, 7))
```

```
mod_frydman <- msm_frydman(data)
visualise_data(data, mod_frydman)
```

npmsm	<i>NPMLE for general multi-state model with interval censored transitions</i>
-------	---

Description

For a general Markov chain multi-state model with interval censored transitions calculate the NPMLE of the transition intensities. The estimates are returned as an `msfit` object.

Usage

```
npmsm(
  gd,
  tmat,
  method = c("multinomial", "poisson"),
  inits = c("equalprob", "homogeneous", "unif", "beta"),
  beta_params,
  support_manual,
  exact,
  maxit = 100,
  tol = 1e-04,
  conv_crit = c("haz", "prob", "lik"),
  verbose = FALSE,
  manual = FALSE,
  newmet = FALSE,
  include_inf = FALSE,
  checkMLE = TRUE,
  checkMLE_tol = 1e-04,
  prob_tol = tol/10,
  remove_redundant = TRUE,
  remove_bins = FALSE,
  estimateSupport = FALSE,
  init_int = c(0, 0),
  ...
)
```

Arguments

gd	<p>A data.frame with the following named columns</p> <ul style="list-style-type: none"> id: Subject identifier; state: State at which the subject is observed at time; time: Time at which the subject is observed; <p>The true transition time between states is then interval censored between the times.</p>
tmat	A transition matrix as created by transMat

method	Which method should be used for the EM algorithm. Choices are <code>c("multinomial", "poisson")</code> , with multinomial the default. Multinomial will use the EM algorithm described in Gomon and Putter (2024) and Poisson will use the EM algorithm described in Gu et al. (2023).
inits	Which distribution should be used to generate the initial estimates of the intensities in the EM algorithm. One of <code>c("equalprob", "unif", "beta")</code> , with "equalprob" assigning $1/K$ to each intensity, with K the number of distinct observation times (<code>length(unique(gd[, "time"]))</code>). For "unif", each intensity is sampled from the <code>Unif[0,1]</code> distribution and for "beta" each intensity is sampled from the <code>Beta(a, b)</code> distribution. If "beta" is chosen, the argument <code>beta_params</code> must be specified as a vector of length 2 containing the parameters of the beta distribution. Default = "equalprob".
beta_params	A vector of length 2 specifying the beta distribution parameters for initial distribution generation. First entry will be used as <code>shape1</code> and second entry as <code>shape2</code> . See <code>help(rbeta)</code> . Only used if <code>inits = "beta"</code> .
support_manual	Used for specifying a manual support region for the transitions. A list of length the number of transitions in <code>tmat</code> , each list element containing a data frame with 2 named columns <code>L</code> and <code>R</code> indicating the left and right values of the support intervals. When specified, all intensities outside of these intervals will be set to zero for the corresponding transitions. Intensities set to zero cannot be changed by the EM algorithm. Will use <code>inits = "equalprob"</code> .
exact	Numeric vector indicating to which states transitions are observed at exact times. Must coincide with the column number in <code>tmat</code> .
maxit	Maximum number of iterations. Default = 100.
tol	Tolerance of the convergence procedure. A change in the value of <code>conv_crit</code> in an iteration of less than <code>tol</code> will make the procedure stop.
conv_crit	Convergence criterion. Stops procedure when the difference in the chosen quantity between two consecutive iterations is smaller than the tolerance level <code>tol</code> . One of the following: "haz" Stop when change in maximum estimated intensities (<code>hazards</code>) < <code>tol</code> . "prob" Stop when change in estimated probabilities < <code>tol</code> . "lik" Stop when change in observed-data likelihood < <code>tol</code> . Default is "haz". The options "haz" and "lik" can be compared across different methods, but "prob" is dependent on the chosen method. Most conservative (requiring most iterations) is "prob", followed by "haz" and finally "lik".
verbose	Should iteration messages be printed? Default is FALSE
manual	Manually specify starting transition intensities? If TRUE, the transition intensity for each bin for each transition must be entered manually. DO NOT USE for large data sets, and in general it is not advised to use this.
newmet	Should contributions after last observation time also be used in the likelihood? Default is FALSE.
include_inf	Should an additional bin from the largest observed time to infinity be included in the algorithm? Default is FALSE.

checkMLE	Should a check be performed whether the estimate has converged towards a true Maximum Likelihood Estimate? This is done by comparing the reduced gradient to the value of checkMLE_tol. Default is TRUE.
checkMLE_tol	Tolerance for checking whether the estimate has converged to MLE. Whenever an estimated transition intensity is smaller than prob_tol, it is assumed to be zero and its reduced gradient is not considered for determining whether the NPMLE has been reached. Default = 1e-4.
prob_tol	If an estimated probability is smaller than prob_tol, it will be set to zero during estimation. Default value is tol/10.
remove_redundant	Should redundant observations be removed before running the algorithm? An observation is redundant when the same state has been observed more than 3 times consecutively, or if it is a repeat observation of an absorbing state. Default is TRUE.
remove_bins	Should a bin be removed during the algorithm if all estimated intensities are zero for a single bin? Can improve computation speed for large data sets. Note that zero means the estimated intensities are smaller than prob_tol. Default is FALSE.
estimateSupport	Should the support of the transitions be estimated using the result of Hudgens (2005)? Currently produces incorrect support sets - DO NOT USE. Default = FALSE
init_int	A vector of length 2, with the first entry indicating what percentage of mass should be distributed over (second entry) what percentage of all first bins. Default is c(0, 0), in which case the argument is ignored. This argument has no practical uses and only exists for demonstration purposes in the related article.
...	Further arguments to estimate_support_msm

Details

Denote the unique observation times in the data as $0 = \tau_0, \tau_1, \dots, \tau_K$. Let $g, h \in H$ denote the possible states in the model and $X(t)$ the state of the process at time t .

Then this function can be used to estimate the transition intensities $\alpha_{gh}^k = \alpha_{gh}(\tau_k)$.

Having obtained these estimated, it is possible to recover the transition probabilities $P(X(t) = h | X(s) = g)$ for $t > s$ using the [transprob](#) functions.

Value

A list with the following entries:

A: A list of class [msfit](#) containing the cumulative intensities for each transition and the transition matrix used;

Ainit: Initial intensities, in an object of class [msfit](#);

gd: Data used for the estimation procedure;

ll: Log-likelihood value of the procedure at the last iteration;

delta: Change in log-likelihood value at the last iteration;

it: Number of iterations of the procedure;
taus: Unique time points of the data, the cumulative intensity only makes jumps at these time points.;
tmat: The transition matrix used, see [transMat](#);
tmat2: A summary of the transitions in the model, see [to.trans2](#);
ll_history: The log-likelihood value at every iteration of the procedure;
KKT_violated: How often were KKT conditions violated during maximisation of the likelihood? In other words, how often did we hit the optimization boundary during the procedure?;
min_time: The smallest time of an observation in the used data. Note that the smallest time in the data is used as zero reference;
reduced_gradient: The reduced gradient at the last iteration. Rows indicate the transitions and columns the unique observation times;
isMLE: Has the procedure converged to the NPMLE? Checked using `checkMLE_tol`;
langrangemultiplier: The lagrange multipliers at the last iteration;
aghmat: A matrix representation of the transition intensities in A. Rows represent transitions and columns unique observation times;
Ygk: The summed at-risk indicator for all subjects in the data at the last iteration. Rows represent transitions and columns unique observation times;
Dmk: The summed probability of making a transition for all subjects at the last iteration. Rows represent transitions and columns unique observation times;
method: Method used for the optimization procedure;
maxit: Maximum number of allowed iterations;
tol: Tolerance of the convergence procedure;
conv_crit: Convergence criterion of the procedure;
checkMLE: Was the reduced gradient checked at the last iteration to determine convergence?;
checkMLE_tol: The tolerance of the checkMLE procedure;
prob_tol: Tolerance for probabilities to be set to zero;
remove_redundant: Were redundant observations removed before performing the procedure?;

References

- D. Gomon and H. Putter, Non-parametric estimation of transition intensities in interval censored Markov multi-state models without loops, arXiv, 2024, [doi:10.48550/arXiv.2409.07176](https://doi.org/10.48550/arXiv.2409.07176)
- Y. Gu, D. Zeng, G. Heiss, and D. Y. Lin, Maximum likelihood estimation for semiparametric regression models with interval-censored multistate data, *Biometrika*, Nov. 2023, [doi:10.1093/biomet/asad073](https://doi.org/10.1093/biomet/asad073)
- Michael G. Hudgens, On Nonparametric Maximum Likelihood Estimation with Interval Censoring and Left Truncation, *Journal of the Royal Statistical Society Series B: Statistical Methodology*, Volume 67, Issue 4, September 2005, Pages 573-587, [doi:10.1111/j.14679868.2005.00516.x](https://doi.org/10.1111/j.14679868.2005.00516.x)

See Also

[transprob](#) for calculating transition probabilities, [plot.npmsm](#) for plotting the cumulative intensities, [print.npmsm](#) for printing some output summaries, [visualise_msm](#) for visualising data, [msfit](#) for details on the output object.

Examples

```
#Create transition matrix using mstate functionality: illness-death
if(require(mstate)){
  tmat <- mstate::trans.illdeath()
}

#Write a function for evaluation times: observe at 0 and uniform inter-observation times.
eval_times <- function(n_obs, stop_time){
  cumsum( c( 0, runif( n_obs-1, 0, 2*(stop_time-4)/(n_obs-1) ) ) )
}

#Use built_in function to simulate illness-death data
#from Weibull distributions for each transition
sim_dat <- sim_id_weib(n = 50, n_obs = 6, stop_time = 15, eval_times = eval_times,
start_state = "stable", shape = c(0.5, 0.5, 2), scale = c(5, 10, 10/gamma(1.5)))

tmat <- mstate::trans.illdeath()

#Fit the model using method = "multinomial"
mod_fit <- npmsm(gd = sim_dat, tmat = tmat, tol = 1e-2)

#Plot the cumulative intensities for each transition
plot(mod_fit)
```

plot.npmsm

Plot a "npmsm" object

Description

Plot the cumulative intensities of a 'npmsm' objects. A wrapper for [plot.msfit](#) from the [mstate](#) package.

Usage

```
## S3 method for class 'npmsm'
plot(x, ...)
```

Arguments

x An object of class "npmsm"
... Additional arguments to [msfit](#)

Value

A plot will be produced in the plotting window

plot_probtrans	<i>Plot the transition probabilities for a fitted npmsm model</i>
----------------	---

Description

For a fitted npmsm model plot the transition probabilities from a certain state for all possible (direct and indirect) transitions.

Usage

```
plot_probtrans(
  npmsmlist,
  from = NULL,
  to = NULL,
  transitions = NULL,
  landmark,
  interpolate = TRUE,
  facet = TRUE,
  times_interpol = NULL,
  c.legend = TRUE,
  c.names = NULL
)
```

Arguments

npmsmlist	An "npmsm" object or a list containing multiple "npmsm" objects
from	A numeric value indicating the state from which we consider the transition probabilities. Default is NULL, meaning we consider transition probabilities from all states from which a direct transition is possible.
to	A numeric vector indicating to which states we consider the transition probabilities. Only states that can be reached from the "from" state are considered.
transitions	A numeric vector indicating which transitions to consider (plot). Can only be used if "from" is not specified, as it only works for direct transitions.
landmark	A landmark time indicating from which time on survival should be determined. If missing, the smallest between the time in the first "npmsm" object or 0 will be used.
interpolate	Should the cumulative hazard be linearly interpolated before determining transition probabilities? Default is TRUE.
facet	Should the resulting plot be faceted (one panel per transition)? Default is TRUE.
times_interpol	At which times should the cumulative hazard be interpolated? Only necessary to specify if interpolate = TRUE.

- c.legend Should legend be displayed for colour (different entries in npmsm1ist)? Default is TRUE.
- c.names A character vector indicating the names to display in the legend. These names should represent the entries in npmsm1ist.. Default = NULL.

Value

A plot will be produced in the plotting window. When assigning the output to an object, the underlying data frame used for plotting and a 'ggplot' object will be returned in a list.

Examples

```
require(mstate)
require(ggplot2)
#Generate from an illness-death model with exponential transitions with
#rates 1/2, 1/10 and 1 for 10 subjects over a time grid.
gd <- sim_weibmsm(tmat = trans.illdeath(), shape = c(1,1,1),
                 scale = c(2, 10, 1), n_subj = 10, obs_pars = c(2, 0.5, 20),
                 startprobs = c(0.9, 0.1, 0))
#Fit 2 models: 1 with at most 4 iterations and 1 with at most 20
mod1 <- npmsm(gd, trans.illdeath(), maxit = 4)
mod2 <- npmsm(gd, trans.illdeath(), maxit = 20)

#Plot the transition probabilities from state 1, without interpolating
#the cumulative hazard for the npmsm runs with max 4 and 20 iterations.
plot_probtrans(list(mod1, mod2), from = 1, interpolate = FALSE,
               c.names = c("4 iterations", "20 iterations"))
```

plot_surv	<i>Plot the transition specific survival probabilities for a fitted npmsm model</i>
-----------	---

Description

For a fitted npmsm model plot the transition specific survival probabilities. These are given by the product integral of the hazard increments estimated for a single transition. This is equivalent to a Kaplan-Meier estimator ignoring the existence of all other transitions.

Usage

```
plot_surv(npmsm1ist, landmark, support = FALSE, sup_cutoff = 1e-08)
```

Arguments

npmsm	An "npmsm" object or a list containing multiple "npmsm" objects
landmark	A landmark time indicating from which time on survival should be determined. If missing, the smallest time in the first "npmsm" object will be used.
support	Should the support regions be displayed as rectangles?
sup_cutoff	Cutoff to be used for determining the support intervals.

Value

A plot will be produced in the plotting window. When assigning the output to an object, the underlying data frame used for plotting and a 'ggplot' object will be returned in a list.

Examples

```
require(mstate)
require(ggplot2)
#Generate from an illness-death model with exponential transitions with
#rates 1/2, 1/10 and 1 for 10 subjects over a time grid.
gd <- sim_weibmsm(tmat = trans.illdeath(), shape = c(1,1,1),
                 scale = c(2, 10, 1), n_subj = 10, obs_pars = c(2, 0.5, 20),
                 startprobs = c(0.9, 0.1, 0))
mod1 <- npmsm(gd, trans.illdeath(), maxit = 4)
mod2 <- npmsm(gd, trans.illdeath(), maxit = 20)

#Plot the transition specific Kaplan-Meier estimators and their numerically
#determined support sets.
plot_surv(list(mod1, mod2), support = TRUE)
```

```
print.npmsm          Print a "npmsm" object
```

Description

Print some details of a [npmsm](#) fit

Usage

```
## S3 method for class 'npmsm'
print(x, ...)
```

Arguments

x	An object of class "npmsm"
...	Additional arguments to print

Value

A summary of the fitted model will be displayed in the console

probtrans_weib	<i>Determine transition probabilities for a multi-state model with Weibull hazards for the transitions.</i>
----------------	---

Description

Determine transition probabilities for a multi-state model with Weibull hazards for the transitions.

Usage

```
probtrans_weib(transMat, times, shapes, scales, type = c("prodint", "ODE"))
```

Arguments

transMat	A transition matrix as generated by <code>mstate::transMat</code> describing the possible transitions for the multi-state model.
times	The times at which the transition probabilities should be determined. Will always determine the probabilities forward in time starting from <code>min(times)</code> .
shapes	The Weibull shapes corresponding to the numbered transitions in <code>transMat</code> . See <code>?pweibull</code> for more info.
scales	The Weibull scales corresponding to the numbered transitions in <code>transMat</code> . See <code>?pweibull</code> for more info.
type	Should the transition probabilities be determined using product integration "prodint" or by solving the Kolmogorov forward ordinary differential equation "ODE".

Value

An object containing the "true" transition probabilities for the specified Weibull hazards.

Examples

```
#Illness-death model
tmat <- mstate::trans.illdeath()
IDM <- probtrans_weib(tmat, seq(0, 15, 0.01), shapes = c(0.5, 0.5, 2),
                     scales = c(5, 10, 10/gamma(1.5)), type = "prodint")
IDM2 <- probtrans_weib(tmat, seq(0, 15, 0.01), shapes = c(0.5, 0.5, 2),
                      scales = c(5, 10, 10/gamma(1.5)), type = "ODE")

plot(IDM)
plot(IDM2)

#Extended illness-death model
tmat <- mstate::transMat(list(c(2, 3), c(4), c(), c()))
IDM <- probtrans_weib(tmat, seq(0, 15, 0.01), shapes = c(0.5, 0.5, 2),
                     scales = c(5, 10, 10/gamma(1.5)), type = "prodint")
```

```
IDM2 <- probtrans_weib(tmat, seq(0, 15, 0.01), shapes = c(0.5, 0.5, 2),
                      scales = c(5, 10, 10/gamma(1.5)), type = "ODE")
plot(IDM)
plot(IDM2)
```

prod_lambda_G_base	<i>Calculate the product of intensities over interval decided by failure times</i>
--------------------	--

Description

This function calculates $\prod_{\lambda} G$ as defined in Frydman (1995), with t_n the failure times. Note that $\text{length}(t_n)$ must be equal to $\text{length}(\text{lambda})$

Usage

```
prod_lambda_G_base(lambda, t_n, Q, A)
```

Arguments

lambda	Intensities of the 2->3 transition
t_n	Unique failure times, same length as lambda
Q	Matrix (2 column) containing support intervals as rows
A	Matrix (2 column) containing censoring intervals as rows

remove_redundant_observations	<i>Remove redundant observations from supplied data frame</i>
-------------------------------	---

Description

Remove redundant observed states from a supplied data frame. Observations are redundant either when we observe an absorbing state multiple times (as we cannot leave an absorbing state), or when a transient state is observed multiple times between transitions (as we cannot have loops, therefore no extra information is provided when we observe a transient state multiple times).

Usage

```
remove_redundant_observations(gd, tmat)
```

Arguments

gd	A data.frame with the following named columns id: Subject identifier; state: State at which the subject is observed at time; time: Time at which the subject is observed; The true transition time between states is then interval censored between the times.
tmat	A transition matrix as created by transMat

Value

A data.frame containing the information contained in the input data.frame gd, but without redundant observations. Depending on whether tmat was specified the function may remove more observations.

Examples

```
#We simulate some data
#Function to generate evaluation times: at 0 and uniform inter-observation
eval_times <- function(n_obs, stop_time){
  cumsum( c( 0,  runif( n_obs-1, 0, 2*(stop_time-4)/(n_obs-1) ) ) )
}

#Simulate illness-death model data with Weibull transitions
sim_dat <- sim_id_weib(n = 20, n_obs = 6, stop_time = 15, eval_times = eval_times,
                      start_state = "stable", shape = c(0.5, 0.5, 2),
                      scale = c(5, 10, 10/gamma(1.5)))

visualise_msm(sim_dat)
require(mstate)
sim_dat_clean <- remove_redundant_observations(sim_dat, trans.illdeath())
visualise_msm(sim_dat_clean)
```

sim_id_weib	<i>Simulate panel data from an illness-death model with Weibull transition hazards</i>
-------------	--

Description

An illness-death model has 3 transitions:

- 1: State 1 (Healthy) to State 2 (Illness);
- 2: State 1 (Healthy) to State 3 (Death);
- 3: State 2 (Illness) to State 3 (Death);

Using this function, it is possible to simulate data from an illness-death model with Weibull transition intensities. Requires the use of an external (self-written) function to generate observation times.

Usage

```
sim_id_weib(
  n,
  n_obs,
  stop_time,
  eval_times,
  start_state = c("stable", "equalprob"),
  shape,
  scale,
  ...
)
```

Arguments

n	Number of subjects to generate paths for.
n_obs	Number of observations in time period for each subject.
stop_time	Largest time at which the model is considered.
eval_times	A function which returns the evaluation times for a subject. Must have as arguments at least n_obs and stop_time.
start_state	In which states can subjects start? Either everyone starts in state 1 ("stable") or equal probability to start in state 1 or 2 ("equalprob").
shape	Vector of shape parameters for the 3 transitions. See rweibull . The first entry will be used for the first transition and so on.
scale	Vector of scale parameters for the 3 transitions. See rweibull The first entry will be used for the first transition and so on.
...	Further parameters to eval_times function.

Details

Taking shape = 1 we get an exponential distribution with rate 1/scale

Value

Panel data in the form of a data.frame with 3 named columns id, time and state. These represent the subject identifier, the observation time and the state at the observation time.

Examples

```
#Function to generate evaluation times: at 0 and uniform inter-observation
eval_times <- function(n_obs, stop_time){
  cumsum( c( 0,  runif( n_obs-1, 0, 2*(stop_time-4)/(n_obs-1) ) ) )
}

#Simulate illness-death model data with Weibull transitions
sim_dat <- sim_id_weib(n = 20, n_obs = 6, stop_time = 15, eval_times = eval_times,
start_state = "stable", shape = c(0.5, 0.5, 2), scale = c(5, 10, 10/gamma(1.5)))
```



```
visualise_msm(sim_dat)
```

sim_weibmsm	<i>Simulate multiple trajectories from an interval-censored multi-state model with Weibull transition intensities</i>
-------------	---

Description

Simulate multiple trajectories from a multi-state model quantified by a transition matrix, with interval-censored transitions and Weibull distributed transition intensities. Allows for Weibull censoring in each of the states.

Usage

```
sim_weibmsm(
  data,
  tmat,
  startprobs,
  exact,
  shape,
  scale,
  censshape,
  censscale,
  n_subj,
  obs_pars,
  true_trajec = FALSE
)
```

Arguments

data	A data.frame or matrix with named columns time and id, representing the observation times and corresponding subject id(entifier).
tmat	A transition matrix as created by transMat , with H rows and H columns indicating the states. The total number of possible transitions will be indicated by M.
startprobs	A numeric vector of length H indicating the probability of each subject to start in any of the possible states. Must sum to 1. By default, all subjects will start in state 1.
exact	A numeric vector indicating which states are exactly observed. The transition time to exact states will be observed at exact times, regardless of the times in obstimes. No exact states if missing.
shape	A numeric vector of length M indicating the shape of the Weibull transition intensity for the corresponding transition in tmat. See help(dweibull) .
scale	A numeric vector of length M indicating the scale of the Weibull transition intensity for the corresponding transition in tmat. See help(dweibull) .

censshape	A numeric vector of length H indicating the Weibull censoring shape in each of the states. If no censoring is required in some states, set corresponding entries to NA. If left missing, no censoring is applied. See details.
censscale	A numeric vector of length H indicating the Weibull censoring scale in each of the states. If no censoring is required in some states, set corresponding entries to NA. If left missing, no censoring is applied. See details.
n_subj	(Optional) Instead of specifying data, specify the number of subjects to generate trajectories for. Requires obs_pars to also be specified.
obs_pars	(Optional) A numeric vector of length 3 specifying what the time is between planned assessments, what the uniform deviation from this time is at the visits and the maximum visit time. Specifying obs_pars = c(2, 0.5, 20) will generate a grid of observation times (0, 2, 4, ..., 20) with a uniform[-0.5, 0.5] random variable added to each observation time, and cut-off at the end-points 0 and 20. The observation times may not overlap, so the first argument must be at least twice as large as the second.
true_trajec	Should the true (right-censored) trajectory be returned for the subjects as well? Default = FALSE.

Details

Taking (cens)shape to be 1 for all transitions, we obtain exponential (censoring)/transitions with rate 1/(cens)scale.

If right-censoring parameters are specified, a right-censoring time is generated in each of the visited states. If the subject is right-censored, we assume the subject is no longer observed at later obstimes. Due to the interval-censored nature of the generation process, it may therefore appear as if the subject was right-censored in an earlier state.

Suppose a subject arrives in state g at time s . If we wish to generate a survival time from that state according to a Weibull intensity in a clock forward model, we can use the inverse transform of the conditional Weibull intensity. More specifically, letting a denote the shape and σ denote the scale, the conditional survival function for $t > s$ is given by

$$S(t|s) = \mathbf{P}(T \geq t | T \geq s) = \exp\left(\left(\frac{s}{\sigma}\right)^a - \left(\frac{t}{\sigma}\right)^a\right)$$

The corresponding cumulative intensity is then given by:

$$A(t|s) = -\log(S(t|s)) = \left(\frac{t}{\sigma}\right)^a - \left(\frac{s}{\sigma}\right)^a$$

And the inverse cumulative intensity is then:

$$A^{-1}(t|s) = \sigma \sqrt[t + \left(\frac{s}{\sigma}\right)^a]{}^a$$

A conditional survival time is then generated by:

$$T|s = A^{-1}(-\log(U)|s)$$

with U a sample from the standard uniform distribution. If we additionally have covariates (or frailties), the $-\log(U)$ above should be replaced by $\frac{-\log(U)}{\exp(\beta X)}$ with β and X the coefficients and covariates respectively.

Value

A matrix with 3 columns time, state and id, indicating the observation time, the corresponding state and subject identifier. If `true_trajec = TRUE`, a list with the matrix described above and a matrix representing the underlying right-censored trajectory.

Examples

```
require(mstate)
require(ggplot2)
#Generate from an illness-death model with exponential transitions with
#rates 1/2, 1/10 and 1 for 10 subjects over a time grid.
gd <- sim_weibmsm(tmat = trans.illdeath(), shape = c(1,1,1),
                 scale = c(2, 10, 1), n_subj = 10, obs_pars = c(2, 0.5, 20),
                 startprobs = c(0.9, 0.1, 0), true_trajec = TRUE)

#Observed trajectories
visualise_msm(gd$observed)
#True trajectories
visualise_msm(gd$true)

#Can supply data-frame with specified observation times
obs_df <- data.frame(time = c(0, 1, 3, 5, 0.5, 6, 9),
                    id = c(1, 1, 1, 1, 2, 2, 2))
gd <- sim_weibmsm(data = obs_df, tmat = trans.illdeath(), shape = c(1, 1, 1),
                 scale = c(2, 10, 1))
visualise_msm(gd)
```

supportHudgens

Determine the support of the NPMLE for interval censored data.

Description

Given censoring/truncation intervals, find the maxcliques and determine the support of the interval censored problem.

Usage

```
supportHudgens(intervals, reduction = TRUE, existence = FALSE)
```

Arguments

`intervals` A data.frame with 3 columns containing half-open intervals (left open, right closed) and an indicator whether the interval results from a censored transition or truncation:

- L: Left side of interval;
- R: Right side of interval;

	<p>cens: Indicator whether interval resulted from interval censoring or left truncation (1 = censoring, 0 = truncation);</p> <p>id: (optional) Identifier for the observation this interval belongs to (numeric/integer). Only required if existence = TRUE;</p> <p>Note that the truncation intervals need to be in the form (N, Inf] with N a numeric value.</p>
reduction	Should the support be reduced using Lemma 3 from Hudgens (2005)? This requires checking an extra condition. Default is TRUE.
existence	Should the existence of the NPMLE be checked using Theorem 1/Lemma 4 from Hudgens (2005)? Requires id to be present in intervals. Default is FALSE.

Value

- **graph:** An igraph object representing the censoring/truncation intervals
- **support:** Support estimated from the censoring intervals
- **dir_graph:** A directed igraph object used to determine whether the NPMLE exists in the presence of left-truncation.
- **exist_mle:** Logical output indicating whether the NPMLE exists.

References

Michael G. Hudgens, On Nonparametric Maximum Likelihood Estimation with Interval Censoring and Left Truncation, *Journal of the Royal Statistical Society Series B: Statistical Methodology*, Volume 67, Issue 4, September 2005, Pages 573-587, [doi:10.1111/j.14679868.2005.00516.x](https://doi.org/10.1111/j.14679868.2005.00516.x)

support_from_direct_intervals

Estimate support of multiple transitions given direct transition intervals

Description

Given only direct transition intervals, determine the support for each transition separately using Hudgens(2001) result. Each state is considered from a competing-risks viewpoint. Hudgens(2005) result is applied to see if the NPMLE for any of the transitions does not exist.

Usage

```
support_from_direct_intervals(direct_intervals, tmat)
```

Arguments

direct_intervals Output from [direct_from_observed_intervals](#).

tmat A transition matrix as created by `transMat`

Value

A list containing the estimated support sets for each possible transition in tmat.

support_npmsm	<i>Numerically find the support of the transitions from a converged npmsm algorithm</i>
---------------	---

Description

For each transition in tmat, determine all consecutive bins with non-zero (higher than cutoff) transition intensities. These then determine the numerical support of the transition.

Usage

```
support_npmsm(npmsm, cutoff = 1e-08)
```

Arguments

npmsm	Output from npmsm function or an msfit object.
cutoff	Above which value is a mass in a bin considered to be non-zero? Default = 1e-8. Note that this is independent of bin size, so can be tricky!!

Value

A list containing a list for each transition. Each transition specific list contains the support intervals for that transition in a matrix with 3 named columns L, R and dA, indicating the left/right-endpoints of the support intervals and the change in the estimated intensities over this support interval.

Examples

```
require(mstate)
require(ggplot2)
#Generate from an illness-death model with exponential transitions with
#rates 1/2, 1/10 and 1 for 10 subjects over a time grid.
gd <- sim_weibmsm(tmat = trans.illdeath(), shape = c(1,1,1),
                 scale = c(2, 10, 1), n_subj = 10, obs_pars = c(2, 0.5, 20),
                 startprobs = c(0.9, 0.1, 0))
#Fit 2 models: 1 with at most 4 iterations and 1 with at most 20
mod1 <- npmsm(gd, trans.illdeath(), maxit = 4)

#Determine support numerically:
mod1_supp <- support_npmsm(mod1)
mod1_supp[[1]]
```

`transprob.msm`*Wrapper for the [probtrans](#) function*

Description

For 'msm' objects: determine transition probabilities (as in [probtrans](#)) from an [msm](#) object. Currently only `direction = "forward"` is supported.

For 'npmsm' objects: Determine transition probabilities for an 'npmsm' object using the [probtrans](#) function.

For 'msfit' objects: Wrapper for [probtrans](#)

Usage

```
## S3 method for class 'msm'  
transprob(object, predt, times, ...)
```

```
## S3 method for class 'npmsm'  
transprob(object, ...)
```

```
## S3 method for class 'msfit'  
transprob(object, ...)
```

```
transprob(object, ...)
```

Arguments

<code>object</code>	Object of compatible class
<code>predt</code>	A positive number indicating the prediction time. This is the time at which the prediction is made. If missing, smallest time of <code>times</code> is chosen.
<code>times</code>	A vector of times at which the transition probabilities should be determined.
<code>...</code>	Further arguments to probtrans

Details

Can be used for objects of class 'npmsm', 'msm' and 'msfit'

Value

A [probtrans](#) object containing the estimated transition probabilities.

visualise_data	<i>Visualise data for illness-death model, only applicable to Frydman(1995) setting.</i>
----------------	--

Description

Visualise data for illness-death model, only applicable to Frydman(1995) setting.

Usage

```
visualise_data(data, msmFrydman)
```

Arguments

data	A <code>data.frame</code> containing the columns named: delta: Did a transition from 1 -> 2 occur? (binary: 0 = no, 1 = yes); In the left-truncated case, delta = 2 indicates initially observed in state 2. Delta: Was the transition to state 3 observed? (binary: 0 = no, 1 = yes); L: Left timepoint of interval censored transition to state 2 (numeric); R: Right timepoint of interval censored transition to state 2 (numeric); time: Time of event (transition to 3) or right-censoring in state 2 (numeric); trunc: (optional) Left-truncation time (numeric); Only used for entries with delta = 2.
msmFrydman	A fitted model from msm_frydman

Value

Returns a visualisation of illness-death data, with the transition from healthy to illness interval-censored and the other two transitions observed exactly or right-censored. If `msmFrydman` is specified, the support intervals from the fit are additionally plotted at the top of the data visualisation.

References

Frydman, H. (1995). Nonparametric Estimation of a Markov 'Illness-Death' Process from Interval-Censored Observations, with Application to Diabetes Survival Data. *Biometrika*, 82(4), 773-789. [doi:10.2307/2337344](https://doi.org/10.2307/2337344)

See Also

See [msm_frydman](#) for fitting a model.

Examples

```
data <- data.frame(delta = c(0, 0, 1, 1), Delta = c(0, 1, 0, 1),
                  L = c(NA, NA, 1, 1.5), R = c(NA, 3, 2, 3),
                  time = c(4, 5, 6, 7))

mod_frydman <- msm_frydman(data)
visualise_data(data, mod_frydman)
```

 visualise_msm

Visualise multi-state data

Description

Produce a plot with the y-axis representing subjects in the data and the x-axis representing the time at which states have been observed.

Usage

```
visualise_msm(gd, npmsm, tmat, neat = TRUE, cutoff)
```

Arguments

gd	A data.frame containing the following named columns: id: Identifier of subject; state: state of subject at time; time: time at which subject is observed;
npmsm	Output from npmsm function
tmat	A transition matrix as created by transMat
neat	Boolean indicating whether redundant observations should be removed in the plot. Default is TRUE
cutoff	cutoff value for numerically determining the support using support_npmsm

Value

A plot will be produced in the plotting window.

Examples

```
#Write a function for evaluation times: observe at 0 and uniform inter-observation times.
eval_times <- function(n_obs, stop_time){
  cumsum( c( runif(1, 0, 0.5), runif( n_obs-1, 0, 2*(stop_time-4)/(n_obs-1) ) ) )
}
#Use built_in function to simulate illness-death data
#from Weibull distributions for each transition
sim_dat <- sim_id_weib(n = 50, n_obs = 6, stop_time = 15, eval_times = eval_times,
                    start_state = "stable", shape = c(0.5, 0.5, 2),
```



```
scale = c(5, 10, 10/gamma(1.5))  
  
#Visualise the data  
visualise_msm(sim_dat)
```

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