

# Package: gems (via r-universe)

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**Type** Package

**Title** Generalized Multistate Simulation Model

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**Author** Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**Maintainer** Luisa Salazar Vizcaya <luisapaola.salazarvizcaya@insel.ch>

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**Suggests** muhaz

**Description** Simulate and analyze multistate models with general hazard functions. gems provides functionality for the preparation of hazard functions and parameters, simulation from a general multistate model and predicting future events. The multistate model is not required to be a Markov model and may take the history of previous events into account. In the basic version, it allows to simulate from transition-specific hazard function, whose parameters are multivariable normally distributed.

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ArtCohort	<i>Class "ArtCohort"</i>
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## Description

Is a S4 class for the artificial cohort generated by `simulateCohort`.

## Usage

```
## S4 method for signature 'ArtCohort,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ArtCohort'
update(object, newsize, addbaseline = matrix(NA, nrow =
  newsize - object@size), newInitialStates = rep(1, newsize - object@size))

## S4 method for signature 'ArtCohort'
head(x, ...)

## S4 method for signature 'ArtCohort'
tail(x, ...)

## S4 method for signature 'ArtCohort'
summary(object)
```

## Arguments

<code>x, object</code>	an <code>ArtCohort</code>
<code>i, j, drop</code>	same as for <code>data.frame</code>
<code>...</code>	passed on to <code>data.frame</code> method
<code>newsize</code>	size of the updated cohort
<code>addbaseline</code>	baseline for new part of cohort
<code>newInitialStates</code>	initial states for new part of cohort

**Slots**

states.number Object of class "numeric": number of states  
 size Object of class "numeric": cohort size  
 baseline Object of class "matrix": baseline matrix  
 follow.up Object of class "numeric": maximum follow-up time  
 parameters Object of class "transition.structure": input parameters  
 parametersCovariances Object of class "transition.structure": input covariance matrices  
 timeToTransition Object of class "matrix": input timeToTransition matrix. logical components  
 transitionFunctions Object of class "transition.structure": input hazard functions  
 time.to.state Object of class "data.frame": entry times for each patient into each of the states

**Objects from the Class**

Objects are created by calls to the function `simulateCohort`.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**See Also**

[simulateCohort](#), [transition.structure](#), [transitionProbabilities](#), [cumulativeIncidence](#)

**Examples**

```
showClass("ArtCohort")
```

---

cumulativeIncidence    *transition probabilities*

---

**Description**

Calculates the cumulative incidence and prediction intervals after first state

**Usage**

```
cumulativeIncidence(object, times, M = 100, stateNames = paste("State",
  as.list(1:dim(cohorts)[1])))
```

**Arguments**

object	either the output of <a href="#">simulateCohort</a> or the matrix with the probabilities slot of that output.
times	a time vector.
M	number of groups for calculating confidence intervals.
stateNames	a list with the names of states.

**Value**

an object of class "PosteriorProbabilities", containing the statenames, timepoints and the cumulative incidence with pointwise prediction intervals over time.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**References**

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

**See Also**

[PosteriorProbabilities](#), [ArtCohort](#), [simulateCohort](#)

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gems

*gems: Generalized Multistate Simulation Model*

---

**Description**

Simulate and analyze multistate models with general hazard functions. gems provides functionality for the preparation of hazard functions and parameters, simulation from a general multistate model and predicting future events. The multistate model is not required to be a Markov model and may take the history of previous events into account. In the basic version, it allows to simulate from transition-specific hazard function, whose parameters are multivariable normally distributed.

**References**

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

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generateHazardMatrix

*generate template for transition functions*

---

**Description**

This function simplifies generating the matrix of transition functions.

**Usage**

```
generateHazardMatrix(statesNumber)
```

**Arguments**

statesNumber    the number of states to be considered.

**Value**

a transition.structure of dimension  $N \times N$ , where  $N$  is the number of states and with value "impossible" for all potential transitions.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**References**

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

**See Also**

[transition.structure](#), [simulateCohort](#)

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generateParameterCovarianceMatrix

*generate a template for parameter covariances*

---

**Description**

This function simplifies generating the matrix of parameter covariances from a matrix of mean parameters.

**Usage**

```
generateParameterCovarianceMatrix(mu)
```

**Arguments**

mu                    a transition.structure of dimension  $N \times N$ , whose components list the mean values for the parameters in the transitionFunction.

**Value**

a transition.structure of dimension  $N \times N$  of covariance matrices for the parameters.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

## References

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

## See Also

[transition.structure](#), [generateParameterMatrix](#), [simulateCohort](#)

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generateParameterMatrix

*generate a template for mean parameters*

---

## Description

This function simplifies generating the matrix of mean parameters from a matrix of transition functions.

## Usage

```
generateParameterMatrix(hf)
```

## Arguments

hf                    a `transition.structure` of dimension  $N \times N$ , where  $N$  is the number of states.

## Value

a `transition.structure` of dimension  $N \times N$ , whose components are lists of the right length for the parameters in the corresponding hazard function hf.

## Author(s)

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

## References

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

## See Also

[transition.structure](#), [simulateCohort](#)

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 PosteriorProbabilities

*Class "PosteriorProbabilities"*


---

### Description

This S4 class summarizes the posterior probabilities over time for objects of class "ArtCohort"

### Usage

```
## S4 method for signature 'PosteriorProbabilities,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'PosteriorProbabilities'
plot(x, ci = FALSE, main = paste(x@type,
  "after starting in State", x@states[1], "at time 0"),
  states = 1:dim(x@probabilities)[2], lwd = c(2, 2), col = c("blue",
  "green3"), lty = c(1, 2), xlab = "Time", ylab = "Probability", ...)

## S4 method for signature 'PosteriorProbabilities'
head(x, ...)

## S4 method for signature 'PosteriorProbabilities'
tail(x, ...)
```

### Arguments

x	the PosteriorProbabilities object
i, j, drop	same as for a "data.frame"
...	arguments passed on to main method
ci	should confidence intervals be displayed
main, xlab, ylab	same as any plot
states	which states to display
lwd, col, lty	vectors of length 2, with first component for the point estimate and second component for the confidence interval

### Slots

states Object of class "character": names of states  
 times Object of class "numeric": time points at which probabilities are evaluated  
 probabilities Object of class "matrix": posterior Probabilities to be in each state at each time  
 lower Object of class "matrix": lower prediction bound to be in each state at each time  
 upper Object of class "matrix": upper prediction bound to be in each state at each time  
 type Object of class "character": describes type of probability

**Objects from the Class**

Objects are created by calls to the function `simulateCohort`.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**See Also**

[transitionProbabilities](#), [cumulativeIncidence](#), [ArtCohort](#)

**Examples**

```
showClass("PosteriorProbabilities")
```

---

<code>simulateCohort</code>	<i>Simulate cohort</i>
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---

**Description**

Simulates a cohort of patients from a set of functions associated to each possible transition in a multistate model. The multistate model is not required to be a Markov model and may take the history of previous events into account. In the basic version, it allows to simulate from transition-specific hazard function, whose parameters are multivariable normally distributed. For each state, all transition-specific hazard functions and their parameters need to be specified. For simulating one transition, all possible event times are simulated and the minimum is chosen. Then simulation continues from the corresponding state until an absorbing state of time to is reached.

**Usage**

```
simulateCohort(transitionFunctions, parameters, cohortSize = 1000,
  parameterCovariances = FALSE, timeToTransition = array(FALSE, dim =
  dim(transitionFunctions@list.matrix)), baseline = matrix(NA, nrow =
  cohortSize), initialState = rep(1, cohortSize),
  absorbing = transitionFunctions@states.number, to = 100,
  report.every = 100, sampler.steps = 1000)
```

**Arguments**

<code>transitionFunctions</code>	a transition.structure of dimension $N \times N$ that contains the hazard functions
<code>parameters</code>	a transition.structure of dimension $N \times N$ that contains the parameters
<code>cohortSize</code>	a numeric indicating the number of patients to be simulated.



parameterCovariances	a transition.structure of dimension $N \times N$ of covariance matrices for the parameters.
timeToTransition	a logical matrix; TRUE for all transitions whose transitionFunction is specified as the time until transition instead of as a hazard function or as a character.
baseline	a matrix or data.frame of dimension $cohortSize \times M$ with $M$ baseline characteristics of subjects to be simulated.
initialState	a numeric of length cohortSize with the initial state for each subject simulated.
absorbing	a numeric containing all absorbing states.
to	final time of the simulation.
report.every	a numeric to check progress of simulation.
sampler.steps	a numeric indicating number of steps for discretization of hazard functions

### Details

The transitionFunctions contains hazard functions or time to event function associated to each possible transition. The elements of this list can be either expressed as an explicit R function or as a character ("impossible", "Weibull", "multWeibull", "exponential") in order to express impossible transitions or parametric forms for the distributions of time to event. If the functions should depend on time, baseline characteristics or be *history-dependent*, the function arguments  $t$ ,  $bl$  or  $history$  can be used. Time  $t$  refers to the time since entry into the current state. For the time since the initial state, use  $t + \text{sum}(\text{history})$ .

The components of the parameters argument list the mean values for the parameters in the transitionFunction. If the corresponding transitionFunction is a function, the parameters should appear in the same order as in the function, leaving out  $t$ ,  $bl$  and  $history$ . If the corresponding transitionFunction is the character "Weibull", the first argument is the shape and the second one the scale. If the corresponding transitionFunction is the character "multWeibull", specify weights, shapes, scales in this order.

Note that when using the parameterCovariances argument it is the users responsibility to ensure that the functions are parametrized such that parameters for each transition are multivariate normally distributed and mutually independent.

### Value

an object of class "ArtCohort" with time.to.state slot of dimension  $cohortSize \times N$  with entry times for each patient into each of the states.

### Author(s)

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

### References

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

**See Also**

[generateHazardMatrix](#), [generateParameterMatrix](#), [generateParameterCovarianceMatrix](#), [ArtCohort](#), [transitionProbabilities](#), [cumulativeIncidence](#)

**Examples**

```
# Here is an example model with 3 states and 2 possible transitions.

# number of states in the model
statesNumber <- 3

# cohort size
cohortSize <- 100

# specification of hazard functions
hazardf <- generateHazardMatrix(statesNumber)
hazardf[[1,2]] <- function(t, r1, r2)
{
  ifelse(t<=2, r1 , r2)
}
hazardf[[2,3]] <- "Weibull"

# list of parameters for the hazard functions
mu <- generateParameterMatrix(hazardf)
mu[[1,2]] <- list(0.33, 0.03) # r1, r2
mu[[2,3]] <- list(1,0.84) # shape, scale

# time
maxTime <- 10

# simulate the cohort
cohort <- simulateCohort(
  transitionFunctions = hazardf,
  parameters = mu,
  cohortSize = cohortSize,
  to=maxTime)

# output
head(cohort)

# transition probability
tr <- transitionProbabilities(cohort, times=seq(0,4,.1))
plot(tr, ci=FALSE)

# cumulative incidence
inc <- cumulativeIncidence(cohort, times=seq(0,4,.1))
plot(inc, ci=FALSE, states=c(2,3))
```

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tavi	<i>tavi data set</i>
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### Description

The simulated data set for each patient contains data for kidney injuries, bleeding complications and the combined endpoint of stroke or death. The data was simulated from the original data following the steps described in the package vignette.

### Format

A data frame with 194 observations on the following 7 variables.

**id** a character vector that contains the patient id's

**kidney** a numeric vector; indicator variable that show if an event has occurred

**kidney.dur** a numeric vector; times at which the events occurred or the patients were censored

**bleeding** a numeric vector; indicator variable that show if an event has occurred

**bleeding.dur** a numeric vector; times at which the events occurred or the patients were censored

**death** a numeric vector; indicator variable that show if an event has occurred

**death.dur** a numeric vector; times at which the events occurred or the patients were censored

### References

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. Journal of Statistical Software, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

### Examples

```
head(data(tavi))
```

---

```
transition.structure  Class "transition.structure"
```

---

### Description

This S4 class provides a structure to specify different characteristics of transitions, such as transition functions functions, parameters or parameter covariances.

**Usage**

```
## S4 method for signature 'transition.structure'
x[[i, j, ..., exact = TRUE]]

## S4 replacement method for signature 'transition.structure'
x[[i, j]] <- value

possibleTransitions(object)

## S4 method for signature 'transition.structure'
possibleTransitions(object)

## S4 method for signature 'transition.structure'
print(x)
```

**Arguments**

x, object            the transition.structure  
i, j                    same as for matrix  
exact, value, ...    passed on to list method

**Slots**

states.number Object of class "numeric": number of states  
list.matrix Object of class "matrix": a list with two dimensions, where list element [i,j] correspond to transitions from i to j

**Objects from the Class**

Objects are created by calls to the functions `generateHazardMatrix`, `generateParameterMatrix`, `generateParameterCovarianceMatrix`.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**See Also**

[generateHazardMatrix](#), [generateParameterMatrix](#), [generateParameterCovarianceMatrix](#)

**Examples**

```
showClass("transition.structure")
```

---

transitionProbabilities  
*transition probabilities*

---

**Description**

Calculates the probabilities and prediction intervals after first state

**Usage**

```
transitionProbabilities(object, times, M = 100, stateNames = paste("State",  
  as.list(1:dim(cohorts)[1])))
```

**Arguments**

object	either the output of <a href="#">simulateCohort</a> or the matrix with the probabilities slot of that output.
times	a time vector.
M	number of groups for calculating confidence intervals.
stateNames	a list with the names of states.

**Value**

an object of class "PosteriorProbabilities", containing the statenames, timepoints and the transition probabilities with pointwise prediction intervals over time.

**Author(s)**

Luisa Salazar Vizcaya, Nello Blaser, Thomas Gsponer

**References**

Nello Blaser, Luisa Salazar Vizcaya, Janne Estill, Cindy Zahnd, Bindu Kalesan, Matthias Egger, Olivia Keiser, Thomas Gsponer (2015). gems: An R Package for Simulating from Disease Progression Models. *Journal of Statistical Software*, 64(10), 1-22. URL <http://www.jstatsoft.org/v64/i10/>.

**See Also**

[PosteriorProbabilities](#), [ArtCohort](#), [simulateCohort](#)

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