msmtools

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Contents

1 Introduction

Package **msmtools** is an `R` package whose main goal is to facilitate the workflow with longitudinal datasets which need to be analyzed in the context of multi-state models. In particular, `msmtools` acts as the `msm` package companion.

1.1 Longitudinal Dataset

Everytime we observe a given subject multiple times, we come up with a longitudinal dataset. This means that measures are repeated n times in a sequence which, in general, may not be equal for all the subjects. Moreover, a longitudinal dataset could be viewed as a multilevel dataset: a first level is given by the subject, and a second level is given by the single observation carried out on that subject. A very common case of longitudinal dataset deals with hospital admissions. A patient, our subject, can have a series of entries which correspond to hospital admissions. Each hospital admission is recorded in a single row of the dataset. Let's consider a simplified version of the `hosp` dataset which comes with `msmtools` package and represents synthetic hospital admissions for 10 patients. For a detailed description of the dataset, please run `?hosp`. For demonstration purposes, we extract only the first 2 patients, reducing the `hosp` dataset to a test sample of 17 rows per 8 variables as you can see below.

```r
data( hosp )
hosp[ 1:17, .( subj, adm_number, gender, age, label_2,
               dateIN, dateOUT, dateCENS ) ]
##     subj adm_number gender age label_2     dateIN    dateOUT   dateCENS
##  1:    1          1      F  83    dead 2008-11-30 2008-12-12 2011-04-28
##  2:    1          2      F  83    dead 2009-01-26 2009-02-16 2011-04-28
##  3:    1          3      F  83    dead 2009-05-13 2009-05-15 2011-04-28
##  4:    1          4      F  83    dead 2009-05-20 2009-05-25 2011-04-28
##  5:    1          5      F  83    dead 2009-06-12 2009-06-16 2011-04-28
##  6:    1          6      F  83    dead 2009-06-20 2009-06-25 2011-04-28
##  7:    1          7      F  83    dead 2009-07-17 2009-07-22 2011-04-28
##  8:    1          8      F  84    dead 2010-04-15 2010-04-20 2011-04-28
##  9:    1          9      F  84    dead 2010-10-11 2010-10-14 2011-04-28
## 10:    1         10      F  85    dead 2011-01-14 2011-01-17 2011-04-28
## 11:    1         11      F  85    dead 2011-04-27 2011-04-28 2011-04-28
## 12:    2          1      F  99   alive 2007-09-17 2007-09-27 2012-12-31
## 13:    2          2      F 100   alive 2009-04-09 2009-04-17 2012-12-31
## 14:    2          3      F 103   alive 2012-04-16 2012-04-20 2012-12-31
## 15:    2          4      F 103   alive 2012-04-24 2012-05-19 2012-12-31
## 16:    2          5      F 103   alive 2012-05-20 2012-05-25 2012-12-31
## 17:    2          6      F 103   alive 2012-08-19 2012-08-21 2012-12-31
```

So, these two patients are 'observed' 11 and 6 times through years, respectively.

These data format are very common when dealing with observational studies, or with chronic disease monitoring and with hospital admissions recording. In general, they are a well stabilized system to collect information.

1.2 Enhancing the Longitudinal Structure with `augment()`

Why the standard longitudinal structure is not enough if a multi-state model has to be run? A first observation could be that we are not able to infer anything about the state in which a given subject (i.e. patient) is at a particular point in time (i.e. hospital admission). The function `augment()` comes into play for this reason: to take advantage of the longitudinal structure in order to extract usable information to fuel a multi-state model. `augment()` takes a longitudinal dataset with exact starting and ending times and reshape it to produce an *augmented* version. For instance, if you apply `augment()` to the dataset above, you get what follows:

```r
hosp_augmented = augment( data = hosp, data_key = subj,
                          n_events = adm_number, pattern = label_3,
                          t_start = dateIN, t_end = dateOUT,
                          t_cens = dateCENS, verbose = FALSE )
## Warning in augment(data = hosp, data_key = subj, n_events = adm_number, :
```

```
## no t_death has been passed. Assuming that dateCENS contains both censoring
## and death time
```

```
hosp_augmented[ 1:35, .( subj, adm_number, gender, age, label_2,
                         augmented, status, n_status ) ]
##     subj adm_number gender age label_2  augmented status n_status
##  1:    1          1      F  83    dead 2008-11-30     IN     1 IN
##  2:    1          1      F  83    dead 2008-12-12    OUT    1 OUT
##  3:    1          2      F  83    dead 2009-01-26     IN     2 IN
##  4:    1          2      F  83    dead 2009-02-16    OUT    2 OUT
##  5:    1          3      F  83    dead 2009-05-13     IN     3 IN
##  6:    1          3      F  83    dead 2009-05-15    OUT    3 OUT
##  7:    1          4      F  83    dead 2009-05-20     IN     4 IN
##  8:    1          4      F  83    dead 2009-05-25    OUT    4 OUT
##  9:    1          5      F  83    dead 2009-06-12     IN     5 IN
## 10:    1          5      F  83    dead 2009-06-16    OUT    5 OUT
## 11:    1          6      F  83    dead 2009-06-20     IN     6 IN
## 12:    1          6      F  83    dead 2009-06-25    OUT    6 OUT
## 13:    1          7      F  83    dead 2009-07-17     IN     7 IN
## 14:    1          7      F  83    dead 2009-07-22    OUT    7 OUT
## 15:    1          8      F  84    dead 2010-04-15     IN     8 IN
## 16:    1          8      F  84    dead 2010-04-20    OUT    8 OUT
## 17:    1          9      F  84    dead 2010-10-11     IN     9 IN
## 18:    1          9      F  84    dead 2010-10-14    OUT    9 OUT
## 19:    1         10      F  85    dead 2011-01-14     IN    10 IN
## 20:    1         10      F  85    dead 2011-01-17    OUT   10 OUT
## 21:    1         11      F  85    dead 2011-04-27     IN    11 IN
## 22:    1         11      F  85    dead 2011-04-28   DEAD      DEAD
## 23:    2          1      F  99   alive 2007-09-17     IN     1 IN
## 24:    2          1      F  99   alive 2007-09-27    OUT    1 OUT
## 25:    2          2      F 100   alive 2009-04-09     IN     2 IN
## 26:    2          2      F 100   alive 2009-04-17    OUT    2 OUT
## 27:    2          3      F 103   alive 2012-04-16     IN     3 IN
## 28:    2          3      F 103   alive 2012-04-20    OUT    3 OUT
## 29:    2          4      F 103   alive 2012-04-24     IN     4 IN
## 30:    2          4      F 103   alive 2012-05-19    OUT    4 OUT
## 31:    2          5      F 103   alive 2012-05-20     IN     5 IN
## 32:    2          5      F 103   alive 2012-05-25    OUT    5 OUT
## 33:    2          6      F 103   alive 2012-08-19     IN     6 IN
## 34:    2          6      F 103   alive 2012-08-21    OUT    6 OUT
## 35:    2          6      F 103   alive 2012-08-21    OUT    6 OUT
##     subj adm_number gender age label_2  augmented status n_status
```

Despite the fact that not the same variables have been reported because of layout concerns, two things come up at first sight. In the first place, the number of rows is more than doubled. We now have 35 observations against the initial 17. In the second place, new variables have been created. We will describe them in a minute.

Given the complexity of the data, which can be very high, building a subject specific status flag which marks a its condition at given time steps, could be tricky and computationally intensive. At the end of the study, so at the censoring time, a subject, in general, can be alive, dead inside a given transition if death occurs within `t_start` and `t_end`, or outside a given transition if death occurs otherwise. After n events, the corresponding flag sequence is given by $2n + 1$ for subjects alive and dead outside the transition, while it is just $2n$ for subjects who died inside of it. Let us consider an individual with 3 events. His/her status combinations will be as follows:

- **ALIVE**: IN-OUT | IN-OUT | IN-OUT | OUT
- **DEAD OUT**: IN-OUT | IN-OUT | IN-OUT | DEAD
- **DEAD IN**: IN-OUT | IN-OUT | IN-DEAD.

This operation produces a dataset in the augmented long format which allows to neatly model transitions between the given states.

From now on, we refer to each row as a transition for which we define a state in which the subject lies. `augment()` automatically creates 4 new variables (if argument `more_status` is missing):

- *augmented*: the new timing variable for the process when looking at transitions. If `t_augmented` is missing, then `augment()` creates *augmented* by default. *augmented*. The function looks directly to `t_start` and `t_end` to build it and thus it inherits their class. In particular, if `t_start` is a date format, then `augment()` computes a new variable cast as integer and names it *augmented_int*. If `t_start` is a difftime format, then `augment()` computes a new variable cast as a numeric and names it *augmented_num*;
- *status*: a status flag which looks at `state`. `augment()` automatically checks whether argument `pattern` has 2 or 3 unique values and computes the correct structure of a given subject. The variable is cast as character;
- *status_num*: the corresponding integer version of *status*;
- *n_status*: a mix of *status* and *status_num* cast as character. *status_num* comes into play when a model on the progression of the process is intended.

1.2.1 Working correctly with `augment()`

The main and only aim of `augment()` is data wrangling. When dealing with complex structure as longitudinal data are, it is really important to introduce some rules which help the user to not fail when using the function. Here we discuss some of these rules which are mandatory in order to get a correct workflow with `augment()`.

There are some arguments which are fundamental. They are `pattern` and `state`. `pattern` must contains the condition of a given subject at the end of the study. That is, how the subject is found at the censoring time. Because this peculiar structure is very common when dealing with hospital admission, the algorithm of `augment()` takes this framework as a reference. So, what does this mean? `pattern` can be either an integer, a factor or a character. Suppose we have it as an integer. `augment()` accepts only a pattern variable which have 2 or 3 unique values (i.e. running `length( unique( pattern ) )` must return 2 or 3). Now, suppose we provide a variable with 3 unique values. They must be 0, 1, and 3, nothing different than that. The coding for this is as follows:

1. Case 1. *integer*:
   - `pattern = 0`: subject is alive at the censoring time;
   - `pattern = 1`: subject is dead during a transition;
   - `pattern = 2`: subject is dead out of a transition.
2. Case 2. *factor*:
   - `pattern = 'alive'`: this is the first level of the factor and corresponds to `pattern = 0` when integer;
   - `pattern = 'dead in'`: this is the second level of the factor and corresponds to `pattern = 1` when integer;
   - `pattern = 'dead out'`: this is the third level of the factor and corresponds to `pattern = 2` when integer;
3. Case 3. *character*:
   - the unique values must be in alphabetial order to resemble the pattern of the integer and factor case.

Everything else to what described above will inevitably produce wrong behaviour of `augment()` with and uncorrect results.

The second important argument is `state`. This is passed as a list and contains the status flags which will be used to compute all the status variables for the process. The length of `state` is 3, no less, no more and comes with a default given by: `state = list( 'IN', 'OUT', 'DEAD' )`. The order is important here too. The status flags must be passed such that the first one (`'IN`) represents the first state (in `hosp`, being inside a hospital), the second one represents the second state (in `hosp`, being outside a hospital), and the third one represents the absorbing state (in `hosp`, being dead inside or outside a hospital). As you can tell, this peculiar structure is typical of hospital admissions, where a patient can enter a hospital, can be discharged from it, or can die. As we have already see, the `'DEAD'` status is reached no matter if the subject has died inside or outside a transition (i.e. in our case, inside or outside the hospital). One can change the flags in `state`, but they must be exactly 3. One may need a higher level of complexity when specifying the states of subjects. This will be discussed in the next section where `state` acts as the main indicator of states.

1.3 What if a more complex status structure is needed?

`augment()` by default takes a very simple status structure given by 3 different values. In general, this is enough to define a multi-state model. But what if we need a more complex structure. Let's consider again the dataset `hosp` for the 3rd, 4th, 5th, and 6th patient with the following variables:

```
hosp[ 18:28, .( subj, adm_number, rehab, it, rehab_it,
                dateIN, dateOUT, dateCENS ) ]
##     subj adm_number rehab it rehab_it     dateIN    dateOUT   dateCENS
##  1:    3          1     0  0       df 2012-09-18 2012-09-27 2012-12-31
##  2:    3          2     0  1       it 2012-11-28 2012-12-15 2012-12-31
##  3:    3          3     1  0    rehab 2012-12-18 2012-12-28 2012-12-31
##  4:    4          1     0  0       df 2008-08-13 2008-09-20 2012-12-31
##  5:    4          2     0  0       df 2012-03-18 2012-03-19 2012-12-31
##  6:    4          3     0  1       it 2012-07-02 2012-07-20 2012-12-31
##  7:    5          1     0  0       df 2006-02-09 2006-02-25 2008-04-16
##  8:    6          1     0  0       df 2009-03-05 2009-03-16 2010-12-19
##  9:    6          2     0  0       df 2009-07-06 2009-07-20 2010-12-19
## 10:    6          3     0  0       df 2010-11-17 2010-11-23 2010-12-19
## 11:    6          4     0  0       df 2010-12-05 2010-12-19 2010-12-19
```

As you can see, we have two variables which take into account the type of hospital admission. *rehab* marks a rehabilitation admission while *it* marks an intensive therapy one. They are both binary and integer variables, so one can compose them to get something which is informative and, at the same time, usable in the context of 'making a status'. We then created the variable *rehab_it* which marks all the information in one place and it is a character. You can pass *rehab_it* to the argument `more_status` to tell `augment()` to add these information into a new structure. Now, it is important to remember that `augment()` introduces some rules when you require to compute a more complex status structure. As you can see from the dataset, many values of *rehab_it* are set to `df`. This stands for 'default' and when `augment()` finds it, it just compute the default status you already passed to argument state (i.e. in this case, it can be 'IN', 'OUT', or 'DEAD'). The argument `more_status` always looks for the value `df`, hence whenever you need to specify a default transition make sure to label it with this value. So, if we run `augment()` on this sample, we obtain the following:

```
hosp_augmented = augment( data = hosp, data_key = subj,
                          n_events = adm_number, pattern = label_2,
                          t_start = dateIN, t_end = dateOUT,
                          t_cens = dateCENS, more_status = rehab_it,
                          verbose = FALSE )
## Warning in augment(data = hosp, data_key = subj, n_events = adm_number, :
## no t_death has been passed. Assuming that dateCENS contains both censoring
## and death time
```

```
hosp_augmented[ 36:60, .( subj, adm_number, rehab_it,
                          augmented, status, status_exp, n_status_exp ) ]
##     subj adm_number rehab_it  augmented status status_exp n_status_exp
##  1:    3          1       df 2012-09-18     IN      df_IN       1 df_IN
##  2:    3          1       df 2012-09-27    OUT     df_OUT      1 df_OUT
##  3:    3          2       it 2012-11-28     IN      it_IN       2 it_IN
##  4:    3          2       it 2012-12-15    OUT     it_OUT      2 it_OUT
##  5:    3          3    rehab 2012-12-18     IN   rehab_IN    3 rehab_IN
##  6:    3          3    rehab 2012-12-28    OUT  rehab_OUT   3 rehab_OUT
##  7:    3          3    rehab 2012-12-28    OUT  rehab_OUT   3 rehab_OUT
##  8:    4          1       df 2008-08-13     IN      df_IN       1 df_IN
##  9:    4          1       df 2008-09-20    OUT     df_OUT      1 df_OUT
## 10:    4          2       df 2012-03-18     IN      df_IN       2 df_IN
## 11:    4          2       df 2012-03-19    OUT     df_OUT      2 df_OUT
## 12:    4          3       it 2012-07-02     IN      it_IN       3 it_IN
## 13:    4          3       it 2012-07-20    OUT     it_OUT      3 it_OUT
## 14:    4          3       it 2012-07-20    OUT     it_OUT      3 it_OUT
## 15:    5          1       df 2006-02-09     IN      df_IN       1 df_IN
## 16:    5          1       df 2006-02-25    OUT     df_OUT      1 df_OUT
## 17:    5          1       df 2008-04-16   DEAD       DEAD         DEAD
## 18:    6          1       df 2009-03-05     IN      df_IN       1 df_IN
## 19:    6          1       df 2009-03-16    OUT     df_OUT      1 df_OUT
## 20:    6          2       df 2009-07-06     IN      df_IN       2 df_IN
## 21:    6          2       df 2009-07-20    OUT     df_OUT      2 df_OUT
## 22:    6          3       df 2010-11-17     IN      df_IN       3 df_IN
## 23:    6          3       df 2010-11-23    OUT     df_OUT      3 df_OUT
## 24:    6          4       df 2010-12-05     IN      df_IN       4 df_IN
## 25:    6          4       df 2010-12-19   DEAD       DEAD         DEAD
##     subj adm_number rehab_it  augmented status status_exp n_status_exp
```

Beside the usual status variables, of which we reported only status, `augment()` computed two more:

- *status_exp*: is the direct expansion of status and the variable you passed to `more_status`, which in this case is *rehab_it*. The function composes them by pasting a '_' in between. This is the main reason why it is worth to build a character variable if you know you need to fuel it in as an indicator of a more complex status structure;
- *n_status_exp*: similar to what has been done before, `augment()` mixes information coming from the current expandend status and the number of admission to give you the time evolution of the process.

2 Graphical Assessment of a Multi-state Model

msmtools has been mainly developed to easily manage and work with longitudinal datasets which need to be restructured in order to get msm to work properly.

However, **msmtools** comes with two more functions which try to address graphically and in a very efficient way the problem of the Goodness-of-Fit (Gof) for a multi-state model. When dealing with this type of models, GoF is always a tough quest. Furthermore, up to now, no formal statistical tests are defined when a multi-state model is computed within an exact time framework.

2.1 Comparing fitted and empirical survival with `survplot()`

One of the most common graphical method to assess whether a multi-state model is behaving the way we expect, is to compare the empirical survival with the fitted one. `survplot()` helps out doing this and few more things. The function is a wrapper of the already known `plot.survfit.msm()` from the package **msm**.

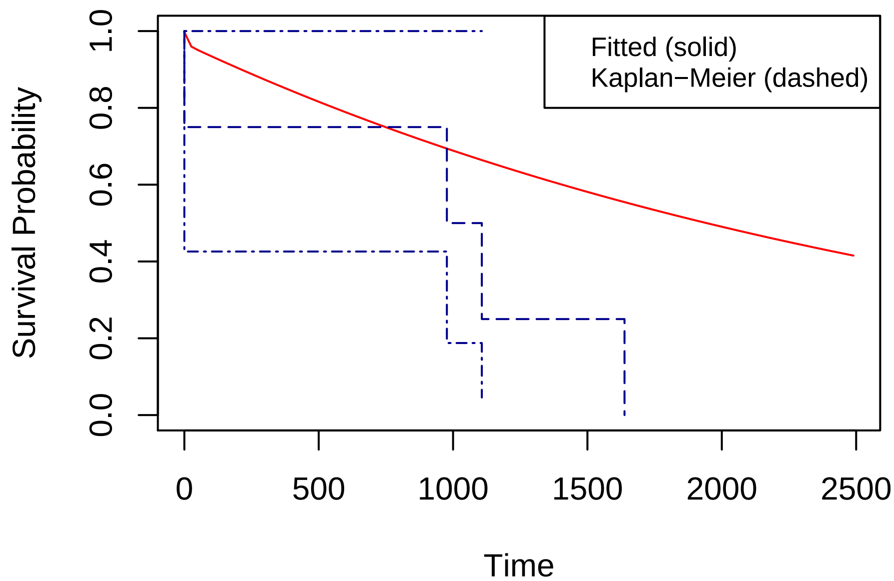
Suppose we ran a multi-state model on dataset hosp with the following code:

```
hosp_augmented = augment( data = hosp, data_key = subj,
                          n_events = adm_number, pattern = label_2,
                          t_start = dateIN, t_end = dateOUT,
                          t_cens = dateCENS, verbose = FALSE )
## Warning in augment(data = hosp, data_key = subj, n_events = adm_number, :
## no t_death has been passed. Assuming that dateCENS contains both censoring
## and death time

# let's define the initial transition matrix for our model
Qmat = matrix( data = 0, nrow = 3, ncol = 3, byrow = TRUE )
Qmat[ 1, 1:3 ] = 1
Qmat[ 2, 1:3 ] = 1
colnames( Qmat ) = c( 'IN', 'OUT', 'DEAD' )
rownames( Qmat ) = c( 'IN', 'OUT', 'DEAD' )
Qmat
##      IN OUT DEAD
## IN    1   1    1
## OUT   1   1    1
## DEAD  0   0    0

# attaching the msm package and running the model using
# gender and age as covariates
library( msm )
msm_model = msm( status_num ~ augmented_int,
                 subject = subj, data = hosp_augmented,
```

```
                  covariates = ~ gender + age,
                  exacttimes = TRUE, gen.inits = TRUE,
                  qmatrix = Qmat, method = 'BFGS',
                  control = list( fnscale = 6e+05, trace = 0,
                                  REPORT = 1, maxit = 10000 ) )
```

We now have a multi-state model for which we can carry out some graphical inspections. So, we want a simple comparison between the fitted survival curve and the empirical one, computed using the Kaplan-Meier estimator. The code is as follows:

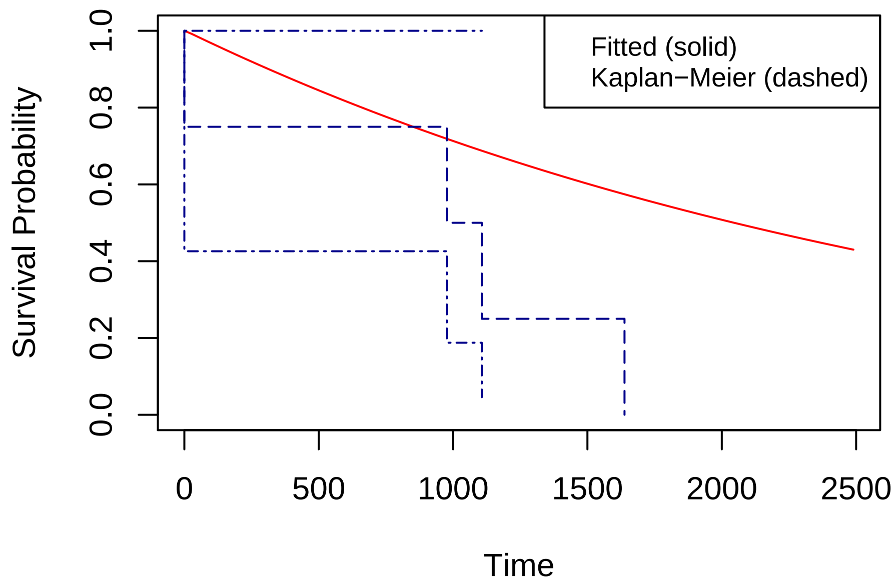
```
survplot( msm_model, km = TRUE, ci = 'none',
          verbose = FALSE, devnew = FALSE )
```



With no surprises, the plot is not so satistying due to the really small dataset we provided.

Now, `survplot()` takes several parameters, many of them come with a default value. For instance, the figureabove has been computed for a transition (IN - DEAD). We can pass to argument `from` any starting state we want. If `to` is missing, `survplot()` will check what is the higher value in the corresponding `msm` object and grabs it. Of course, you are free to compute any survival you want, given the transition is allowed in the initial transition matrix `Qmat`. Let's plot the survival comparison for the transition (OUT - DEAD):

```
survplot( msm_model, km = TRUE, from = 2, ci = 'none',
          verbose = FALSE, devnew = FALSE )
```



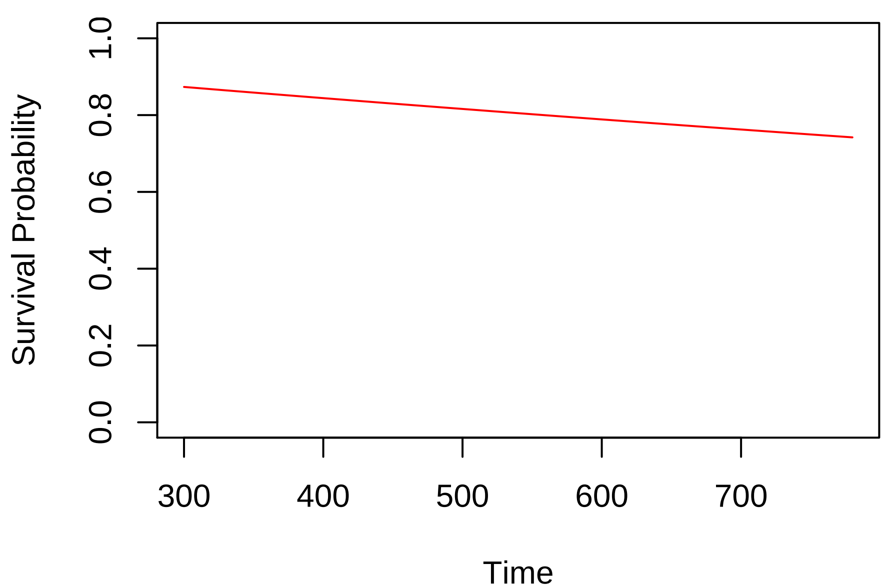
If we do not want to show the Kaplan-Meier, we can pass `km = FALSE`, which is the default.

2.1.1 Setting a custom time sequence

By default `survplot()` computes the fitted survival on a given grid. The number of grid points is given by `grid`. In some cases, one would like to pass a custom time sequence. This can be achieved by passing the argument `times` a numeric vector. Now `grid` is ignored.

Consider our dataset and suppose we want to compute a fitted survival only fo specific points in time. The following code addresses this request.

```
time_seq = seq( 300, 800, by = 30 )
survplot( msm_model, times = time_seq, ci = 'none',
          verbose = FALSE, devnew = FALSE )
```



2.1.2 Obtaining the dataset for the Kaplan-Meier

It is possible to tell `survplot()` to return the associated Kaplan-Meier dataset by setting `return.km = TRUE`. This fastly computes the data through `data.table`. Passing only `km = TRUE` won't return any data, even if they must be computed anyway to plot results.

```
survplot( msm_model, ci = 'none', return.km = TRUE,
          verbose = FALSE, do.plot = FALSE )
##    subject mintime mintime_exact anystate
## 1:       1   15092          1107        1
## 2:       5   13985             0        1
## 3:       6   14962           977        1
## 4:       7   15623          1638        1
```

A preview of the dataset is printed out only if no assignment is done. If you want to store the information in the current environmen, you must assign `survplot()` to an object as follows:

```
# running survplot() and assigning it to an object
km_data = survplot( msm_model, ci = 'none', return.km = TRUE,
                    verbose = FALSE, do.plot = FALSE )

# let's see the dataset
km_data
##    subject mintime mintime_exact anystate
## 1:       1   15092          1107        1
## 2:       5   13985             0        1
## 3:       6   14962           977        1
## 4:       7   15623          1638        1
```

The structure of the data is consistent. `survplot()` always computes a dataset in wide format, as requested by `survfit` with 3 columns:

- *subject*: the ordered subject ID as passed to `msm` function;
- *mintime*: the time at which the event occurred;
- *anystate*: tansition indicator to compute the Kaplan-Meier.

The only modification you might encounter really depends on argument `exacttimes`. This is inherited from `msm` function whose aim was to tell the model that transitions occurred at exact and known times, including deaths. This is the main reason why this argument should always be set the same way you set it in `msm`. In our case, we do have a multi-state model in which transitions are well known and exact as you can see from the `msm` call above. `survplot()` puts `exacttimes = TRUE` by default so we don't have to worry about it. As you can see from the results, `km_data` has another column named *mintime_exact*. This is the relative time for each subject.

2.1.3 Obtaining the dataset for the fitted survival

Similarly to what done for the Kaplan-Meier, it is possible to obtain the data used to compute the fitted survival as well. This can be achieve by setting `return.p = TRUE`. If `times` is passed, then the resulting dataset will have as many rows as the elements in `times`. If `times` is missing, then `survplot()` uses `grid` to know how many time points are requested. Below there is the snippet that addresses what described.

```
survplot( msm_model, ci = 'none', return.p = TRUE,
          verbose = FALSE, do.plot = FALSE )
##       time  probs
## 1:    1.00 0.9957
## 2:   26.14 0.9596
## 3:   51.28 0.9503
## 4:   76.42 0.9422
## 5:  101.56 0.9341
## 6:  126.70 0.9262
```

As before, only the first 6 rows are printed. Saving the data in the current environment follows the same procedure as seen before:

```
# running survplot() and assigning it to an object
fitted_data = survplot( msm_model, ci = 'none', return.p = TRUE,
                        verbose = FALSE, do.plot = FALSE )

# let's see the dataset
fitted_data
##       time  probs
## 1:    1.00 0.9957
## 2:   26.14 0.9596
## 3:   51.28 0.9503
## 4:   76.42 0.9422
## 5:  101.56 0.9341
## 6:  126.70 0.9262
```

The structure of the data is consistent here too. `survplot()` always computes a dataset in wide format with 2 columns:

- *time*: time at which to compute the fitted survival. It can be obtained either by `grid` or by `times` so that the cardinality of the data depends on them;
- *probs*: the corresponding value of the fitted survival.

Of course, you can request `survplot()` to return both the datasets by passing all the parameters. Below you can see the code and the output when no assignment is done and when you save the data into a new object.

```r
# just running survplot()
survplot( msm_model, ci = 'none',
                     return.km = TRUE, return.p = TRUE,
                     verbose = FALSE, do.plot = FALSE )
## $km
##    subject mintime mintime_exact anystate
## 1:       1   15092          1107        1
## 2:       5   13985             0        1
## 3:       6   14962           977        1
## 4:       7   15623          1638        1
##
## $fitted
##      time  probs
## 1:   1.00 0.9957
## 2:  26.14 0.9596
## 3:  51.28 0.9503
## 4:  76.42 0.9422
## 5: 101.56 0.9341
## 6: 126.70 0.9262

# running survplot() and assigning it to an object
all_data = survplot( msm_model, ci = 'none',
                     return.km = TRUE, return.p = TRUE,
                     verbose = FALSE, do.plot = FALSE )

# let's see the dataset
all_data
## $km
##    subject mintime mintime_exact anystate
## 1:       1   15092          1107        1
## 2:       5   13985             0        1
## 3:       6   14962           977        1
## 4:       7   15623          1638        1
##
## $fitted
##      time  probs
## 1:   1.00 0.9957
## 2:  26.14 0.9596
## 3:  51.28 0.9503
## 4:  76.42 0.9422
## 5: 101.56 0.9341
## 6: 126.70 0.9262
```

`all_data` is a list of two elements. If you want to split up the datasets, just use common syntax:

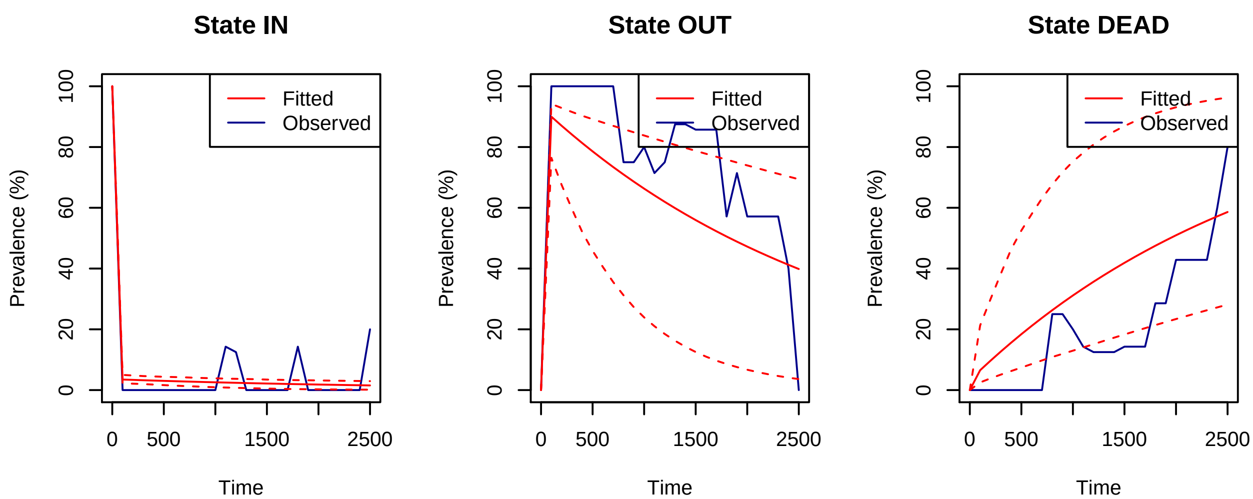
```
# do not extract data using just one [].
# This keeps the class, so it returns a list
km_data_wrong = all_data[ 1 ]
# extracting data using the list way so be careful to use double []
km_data_1 = all_data[[ 1 ]]
# extracting data using the '$' access operator
km_data_2 = all_data$km
identical( km_data_wrong, km_data_1 )
## [1] FALSE
identical( km_data_1, km_data_2 )
## [1] TRUE
km_data_1
##    subject mintime mintime_exact anystate
## 1:       1   15092          1107        1
## 2:       5   13985             0        1
## 3:       6   14962           977        1
## 4:       7   15623          1638        1

fitted_data_1 = all_data[[ 2 ]]
fitted_data_2 = all_data$fitted
identical( fitted_data_1, fitted_data_2 )
## [1] TRUE
fitted_data_1
##      time  probs
## 1:   1.00 0.9957
## 2:  26.14 0.9596
## 3:  51.28 0.9503
## 4:  76.42 0.9422
## 5: 101.56 0.9341
## 6: 126.70 0.9262
```

2.2 Comparing expected and observed prevalences with `prevplot()`

A second graphical tool which helps us in the attempt to understand the goodness of the model is given by comparing the expected and observed prevalences. `prevplot()` is a wrapper of the `plot.prevalence.msm()` function inside the `msm` package but, again, it does more things.

Consider the multi-state model we have built above. We can compute the prevalences using `prevalence.msm()` function. This produces a named list which will be used inside `prevplot()`. For instance, running the following code produces a plot of prevalences for each state of the model.

```
# defining the times at which compute the prevalences
t_min = min( hosp_augmented$augmented_int )
t_max = max( hosp_augmented$augmented_int )
steps = 100L

# computing prevalences
prev = prevalence.msm( msm_model, covariates = 'mean', ci = 'normal',
                       times = seq( t_min, t_max, steps ) )

# and plotting them using prevplot()
prevplot( msm_model, prev, ci = TRUE, devnew = F )
```



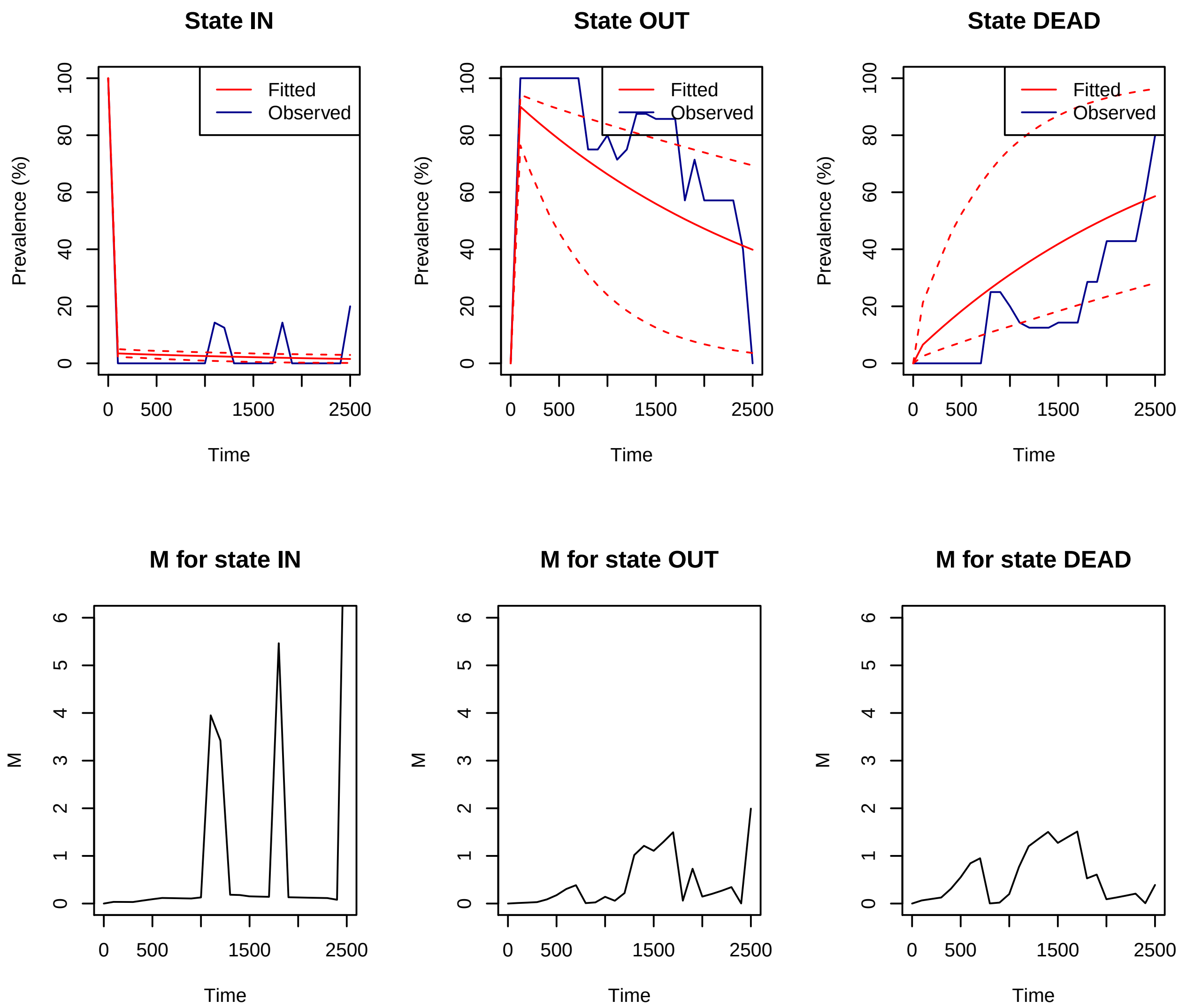
It is mandatory for `prevplot()` to work that a `msm` object and a list compute by `prevalence.msm` are passed.

It is also possibile to plot the following statistic:

$$M^2 = \frac{(O_{is} - E_{is})^2}{E_{is}}$$

which gives an idea of the deviance from the Markov model. This is computed according to Titman and Sharples (2008). The following code addresses this request.

```
prevplot( msm_model, prev, M = TRUE, ci = TRUE, devnew = F )
```


State IN
State OUT
State DEAD
Fitted
Observed
Prevalence (%)
Time
M for state IN
M for state OUT
M for state DEAD
M
0
500
1500
2500