Model B : Estimation Results

Contents

Estimation results of **Model B**, specified by the following input:

```
q <- .01
# transition matrix
Q <- rbind( c(0, q, 0, q),
            c(q, 0, q, q),
            c(0, 0, 0, q),
            c(0, 0, 0, 0))
# misclassification matrix
E <- rbind( c( 0,  0,  0, 0),
            c( 0,  0, .1, 0),
            c( 0,  0,  0, 0),
            c( 0,  0,  0, 0) )
# transition names
qnames = c(
  "Healthy - Mild",    # q12
  # "Healthy - Severe", # q13
  "Healthy - Dead",  # q14
  "Mild - Healthy",  # q21
  "Mild - Severe",   # q23
  "Mild - Dead",     # q24
  # "Severe - Healthy",# q31
  # "Severe - Mild",   # q32
  "Severe - Dead"    # q34
)
```

Load environmet

```
 Save fitted models here :
[1] "./data/shared/derived/models/model-b-mod-2/"
```

Load data

```
Before ms encoding:
           id fu_year died   age_bl  male edu age_death age_at_visit mmse presumed_alive
5120 50402431       0    1 91.41136 FALSE  16  94.82272     91.41136   19          FALSE
5121 50402431       1    1 91.41136 FALSE  16  94.82272     92.33402   12          FALSE
5122 50402431       2    1 91.41136 FALSE  16  94.82272     93.34702    5          FALSE
5123 50402431       3    1 91.41136 FALSE  16  94.82272     94.34634    0          FALSE

After ms encoding
            id fu_year died   age_bl  male edu      age state presumed_alive mmse firstobs
5120  50402431       0    1 91.41136 FALSE  16 91.41136     3          FALSE   19        1
5121  50402431       1    1 91.41136 FALSE  16 92.33402     3          FALSE   12        0
5122  50402431       2    1 91.41136 FALSE  16 93.34702     3          FALSE    5        0
5123  50402431       3    1 91.41136 FALSE  16 94.34634     3          FALSE    0        0
51201 50402431      NA    1 91.41136 FALSE  16 94.82272     4          FALSE   NA        0
```

Remove cases

```r
#### 1) Remove observations with missing age
# Initial number of observations with missing age :
sum(is.na(ds_ms$age))
```

```
[1] 1
```

```r
ds_clean <- ds_ms %>%
  dplyr::filter(!is.na(age))
# Resultant number of observations with missing age
sum(is.na(ds_clean$age))
```

```
[1] 0
```

```r
#### 3) Remove subjects with only ONE observed data point
# Initial number of subjects who have *n* observed data points
ds_clean %>%
  dplyr::group_by(id) %>%
  dplyr::summarize(n_data_points = n()) %>%
  dplyr::group_by(n_data_points) %>%
  dplyr::summarize(n_people=n()) %>%
  print()
```

```
# A tibble: 17 × 2
   n_data_points n_people
           <int>    <int>
1              1      119
```

```
2                2      205
3                3      184
4                4      180
5                5      190
6                6      104
7                7      108
8                8      113
9                9      127
10              10      116
11              11      110
12              12       71
13              13       21
14              14       14
15              15       13
16              16       17
17              17        3
```

```r
# Determine which ids have only a single observation
remove_ids <- ds_clean %>%
  dplyr::group_by(id) %>%
  dplyr::summarize(n_data_points = n()) %>%
  dplyr::arrange(n_data_points) %>%
  dplyr::filter(n_data_points==1) %>%
  dplyr::select(id)
remove_ids <- remove_ids$id
# How many subjects to be removed from the data set:
length(remove_ids)
```

```
[1] 119
```

```r
ds_clean <- ds_clean %>%
  dplyr::filter(!(id %in% remove_ids))
# Resultant number of subjects who have *n* observed data points
ds_clean %>%
  dplyr::group_by(id) %>%
  dplyr::summarize(n_data_points = n()) %>%
  dplyr::group_by(n_data_points) %>%
  dplyr::summarize(n_people=n()) %>%
  print()
```

```
# A tibble: 16 × 2
   n_data_points n_people
           <int>    <int>
1              2      205
2              3      184
3              4      180
4              5      190
5              6      104
6              7      108
7              8      113
8              9      127
9             10      116
10            11      110
11            12       71
12            13       21
```

```
13             14       14
14             15       13
15             16       17
16             17        3
```

```
#### 3) Remove subjects with IMS at the first observation
# Initial view of subjects with intermediate missing state at first observation:
ids_firstobs_ims <- ds_clean %>%
  dplyr::filter(firstobs == TRUE & state == -1) %>%
  dplyr::select(id) %>% print()
```

```
        id
1 80333458
2 90214403
3 90447310
4 91804757
```

```
ids_firstobs_ims <- ids_firstobs_ims[,"id"]
ds_clean <- ds_clean %>%
  dplyr::filter(!id %in% ids_firstobs_ims)
# Resultant view of subjects with intermediate missing state at first observation:
ds_clean %>%
  dplyr::filter(firstobs == TRUE & state == -1) %>%
  dplyr::select(id) %>% print()
```

```
[1] id
<0 rows> (or 0-length row.names)
```

Categorize covariates

```
 How education was categorized:

       educatF edu    n
1    0-9 years   0    4
2    0-9 years   2    6
3    0-9 years   3   10
4    0-9 years   4   17
5    0-9 years   5   20
6    0-9 years   6   48
7    0-9 years   7   27
8    0-9 years   8  178
9    0-9 years   9   76
10 10-11 years  10  167
11 10-11 years  11  225
12   >11 years  12 2400
13   >11 years  13  862
14   >11 years  14 1199
15   >11 years  15  554
16   >11 years  16 2132
17   >11 years  17  486
18   >11 years  18  942
19   >11 years  19  255
20   >11 years  20  286
```

```
21   >11 years  21  207
22   >11 years  22   61
23   >11 years  23   37
24   >11 years  24   26
25   >11 years  25   11
26   >11 years  28   21
```

```
 Frequencies of categorized education :
```

```
# A tibble: 3 × 2
      educatF     n
       <fctr> <int>
1   0-9 years   386
2 10-11 years   392
3   >11 years  9479
```

```
 Create dummy variables for testing effects of education:
```

```
  -1    0    1 <NA>
 386  392 9479    0
```

```
        0    1
  -1  386    0
  0     0  392
  1  9479    0
```

```
        0    1
  -1  386    0
  0   392    0
  1     0 9479
```

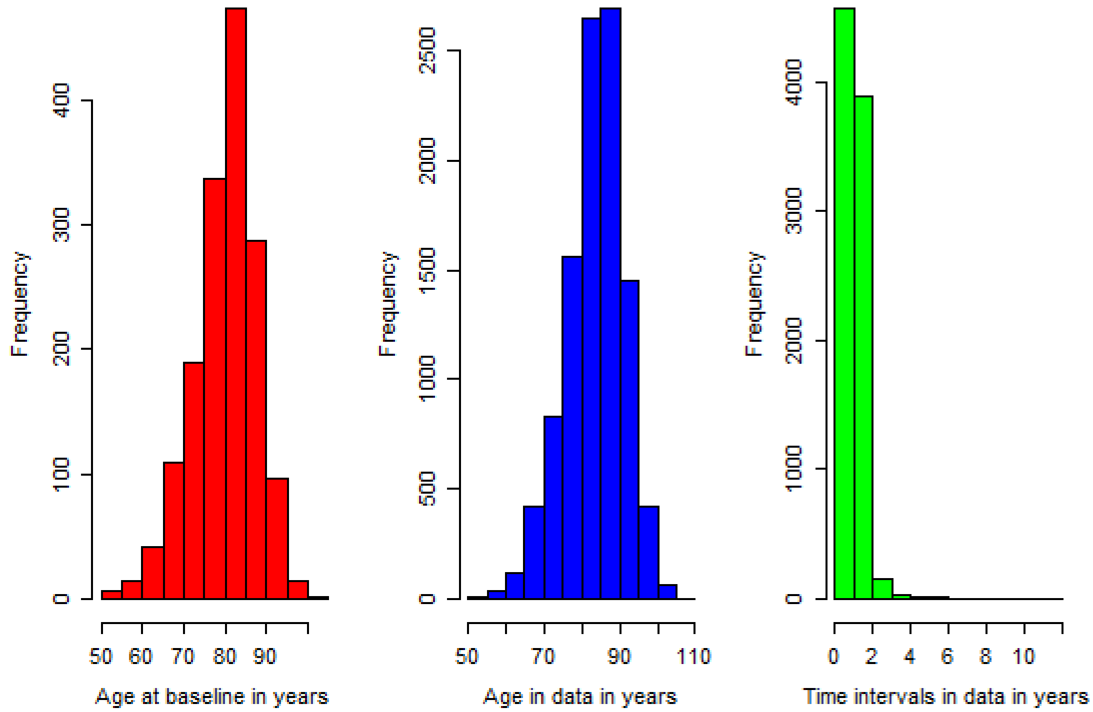
Age diagnostic

```
 Minimum interval length :  0.00273785
```

```
 Maximum interval length :  11.86858
```

```
Time intervals between observations within individuals:
   0%   25%   50%   75%  100%
 0.00  0.96  1.00  1.03 11.87
```

```
 Graphs of age distribution :
```



Estimation prep

```
Number of subjects with intermediate missing state (-1) :  104

Number of subjects with right censored state (-2) :  46

Number of subjects with either IMS or RC state(s) :  149

Number of subjects with both IMS and RC state(s) :  1

Centering decisions :

The variable `age` is centered at : 75

The variable `age_bl` is centered at : 75


The following dataset will be passed to msm call (view for one person):

        id   age_bl male edu educat    educatF edu_low_med edu_low_high firstobs fu_year        age stat
1  90544686 7.696783    0  12      1 >11 years           0            1        1       0  7.696783
2  90544686 7.696783    0  12      1 >11 years           0            1        0       1  8.682409
```

```
3  90544686 7.696783    0  12      1 >11 years           0             1        0       2  9.731006      1
4  90544686 7.696783    0  12      1 >11 years           0             1        0       3 10.689254      1
5  90544686 7.696783    0  12      1 >11 years           0             1        0       4 11.691307      1
6  90544686 7.696783    0  12      1 >11 years           0             1        0       5 12.709788      1
7  90544686 7.696783    0  12      1 >11 years           0             1        0       6 13.665298      1
8  90544686 7.696783    0  12      1 >11 years           0             1        0       7 14.678303      2
9  90544686 7.696783    0  12      1 >11 years           0             1        0       8 15.680356      1
10 90544686 7.696783    0  12      1 >11 years           0             1        0       9 16.709788      1
```

```
 Subject count :  1572

 Frequency of states at baseline
```

```
# A tibble: 3 × 3
  state count   pct
  <dbl> <int> <dbl>
1     1  1189  0.76
2     2   281  0.18
3     3   102  0.06
```

```
 State table:
```

```
    to
from   -2   -1    1    2    3    4
  -2   32    0    0    0    0    0
  -1    0   25   27   13   26   47
  1    32   59 4855  715  120  251
  2     8   20  534  478  256  146
  3     6   34   24   96  649  232
```

```
 The inital values for estimation :  0.76 0.18 0.06 0
```

Specifications

Fitting functions

```
estimate_multistate <- function(
  model_name
  ,ds                    # data object
  ,Q                     # Q-matrix of transitions
  ,E                     # misspecification matrix
  ,qnames                # names of the rows in the Q matrix
  ,cf                    # string with covariate names for forward transitions
  ,cb                    # string with covariate names for backward transitions
  ,cd                    # string with covariate names for death transitions
){
  cov_forward  <- as.formula(paste0("~",cf))
  cov_backward <- as.formula(paste0("~",cb))
  cov_death    <- as.formula(paste0("~",cd))
  # covariates_ <- as.formula(paste0("~",cov_names))
  covariates_    = list(
```

```
    "1-2"       = cov_forward,
    "2-3"       = cov_forward,
    "2-1"       = cov_backward,
    "1-4"       = cov_death,
    "2-4"       = cov_death,
    "3-4"       = cov_death
  )
  model <- msm(
    formula       = state ~ age,
    subject       = id,
    data          = ds,
    center        = FALSE,
    qmatrix       = Q,
    ematrix       = E,
    death         = TRUE,
    covariates    = covariates_,
    censor        = c(-1,-2),
    censor.states = list(c(1,2,3), c(1,2,3)),
    method        = method_,
    constraint    = constraint_,
    fixedpars     = fixedpars_,
    initprobs     = initprobs_,
    est.initprobs = TRUE,
    control       = list(trace=0,REPORT=1,maxit=1000,fnscale=10000)
  )
  # model <- paste0("test", covariates_)
  saveRDS(model, paste0(pathSaveFolder,model_name,".rds"))
  return(model)
}
```

Support functions

```
get_crude_Q <- function(ds, Q, cov_names){
  formula_ <- as.formula(paste0("state ~ ",cov_names))
  Q_crude <- crudeinits.msm(
    formula = formula_,
    subject = id,
    qmatrix = Q,
    data = ds,
    censor        = c(-1,-2),
    censor.states = list(c(1,2,3), c(1,2,3))
  )
  return(Q_crude)
}

msm_summary <- function(model){
cat("\n-2loglik =", model$minus2loglik,"\n")
cat("Convergence code =", model$opt$convergence,"\n")
p    <- model$opt$par
p.se <- sqrt(diag(solve(1/2*model$opt$hessian)))
print(cbind(p=round(p,digits),
            se=round(p.se,digits),"Wald ChiSq"=round((p/p.se)^2,digits),
```

```
            "Pr>ChiSq"=round(1-pchisq((p/p.se)^2,df=1),digits)),
      quote=FALSE)
}

msm_details <- function(model){
  # intensity matrix
  cat("\n Intensity matrix : \n")
  print(qmatrix.msm(model))
  # qmatrix.msm(model, covariates = list(male = 0))
  # transition probability matrix
  t_ <- 2
  cat("\n Transition probability matrix for t = ", t_," : \n")
  print(pmatrix.msm(model, t = t_)) # t = time, in original metric
  # misclassification matrix
  cat("\n Misclassification matrix : \n")
  suppressWarnings(print(ematrix.msm(model), warnings=F))
  # hazard ratios
  cat("\n Hazard ratios : \n")
  print(hazard.msm(model))
  # mean sojourn times
  cat("\n Mean sojourn times : \n")
  print(sojourn.msm(model))
  # probability that each state is next
  cat("\n Probability that each state is next : \n")
  suppressWarnings(print(pnext.msm(model)))
  # total length of stay
  cat("\n  Total length of stay : \n")
  print(totlos.msm(model))
  # expected number of visits to the state
  cat("\n Expected number of visits to the state : \n")
  suppressWarnings(print(envisits.msm(model)))
  # ratio of transition intensities
  # qratio.msm(model,ind1 = c(2,1), ind2 = c(1,2))
}
```

Model

```
q <- .01
# transition matrix
Q <- rbind( c(0, q, 0, q),
            c(q, 0, q, q),
            c(0, 0, 0, q),
            c(0, 0, 0, 0))
# misclassification matrix
E <- rbind( c( 0,  0,  0, 0),
            c( 0,  0, .1, 0),
            c( 0,  0,  0, 0),
            c( 0,  0,  0, 0) )
# transition names
qnames = c(
  "Healthy - Mild",   # q12
  # "Healthy - Severe", # q13
```

```r
  "Healthy - Dead",   # q14
  "Mild - Healthy",   # q21
  "Mild - Severe",    # q23
  "Mild - Dead",      # q24
  # "Severe - Healthy",# q31
  # "Severe - Mild",    # q32
  "Severe - Dead"     # q34
)
```

msm options

```r
digits = 2
method_  = "BFGS"     # alternatively, if does not converge "Nedler-Mead"
constraint_ = NULL    # additional model constraints
fixedpars_ = NULL     # fixed parameters
initprobs_ = initial_probabilities
```

```r
# turn this chunk OFF when printing the report
# compile model objects with msm() call
# each model will be saved in the specified folder, namely pathSaveFolder
(Q_crude <- get_crude_Q(ds, Q, "age"))
```

```
           [,1]       [,2]       [,3]       [,4]
[1,] -0.1569916  0.1141470  0.0000000 0.04284465
[2,]  0.3504402 -0.6212645  0.1696731 0.10115125
[3,]  0.0000000  0.0000000 -0.2434208 0.24342081
[4,]  0.0000000  0.0000000  0.0000000 0.00000000
```

```r
# estimate_multistate("mB_mod2_1", ds, Q_crude, E, qnames,
#                     cf = "age + male + edu_low_med + edu_low_high",
#                     cb = "age",
#                     cd = "age + male")
#
# (Q_crude <- get_crude_Q(ds, Q, "age"))
# m2 <- estimate_multistate("mB_mod2_2", ds, Q_crude, E, qnames,
#                     cf = "age + male + edu_low_med + edu_low_high",
#                     cb = "age",
#                     cd = "age + male + edu_low_med + edu_low_high")
#
```

Model results

model 1

The model was fitted using the following specification of covariates:

```
# Forward transitions:
  "1-2"       = "age + male + edu_low_med + edu_low_high"
  "2-3"       = "age + male + edu_low_med + edu_low_high"
# Backward transitions:
  "2-1"       = "age"
# Death transitions:
```

```
  "1-4"       = "age + male"
  "2-4"       = "age + male"
  "3-4"       = "age + male"
```

summary

```
-2loglik = 15002.66
Convergence code = 0
          p   se Wald ChiSq Pr>ChiSq
qbase -1.66 0.19      77.54     0.00
qbase -4.21 0.18     525.29     0.00
qbase -0.27 0.08      10.87     0.00
qbase -1.98 0.30      42.46     0.00
qbase -3.40 0.42      67.10     0.00
qbase -2.28 0.20     132.11     0.00
qcov   0.08 0.01     157.07     0.00
qcov   0.08 0.01      31.02     0.00
qcov  -0.02 0.01       7.70     0.01
qcov   0.05 0.01      23.00     0.00
qcov   0.06 0.03       6.42     0.01
qcov   0.07 0.01      35.21     0.00
qcov   0.29 0.08      13.10     0.00
qcov   0.42 0.22       3.67     0.06
qcov  -0.18 0.16       1.38     0.24
qcov   0.72 0.28       6.50     0.01
qcov   0.36 0.14       6.65     0.01
qcov  -0.27 0.24       1.32     0.25
qcov  -0.12 0.40       0.10     0.75
qcov  -0.56 0.18       9.90     0.00
qcov  -0.17 0.29       0.33     0.56
p     -2.15 0.09     590.61     0.00
initp -1.33 0.06     432.47     0.00
initp -2.84 0.13     481.41     0.00
```

details

```
 Intensity matrix :
        State 1                      State 2                      State 3
State 1 -0.25700 (-0.27608,-0.23925)  0.22532 ( 0.20772, 0.24440) 0
State 2  0.64404 ( 0.58426, 0.70994) -0.88548 (-0.95896,-0.81763)  0.17435 ( 0.14811, 0.20524)
State 3 0                            0                            -0.19402 (-0.23913,-0.15743)
State 4 0                            0                            0
        State 4
State 1  0.03169 ( 0.02583, 0.03888)
State 2  0.06708 ( 0.04373, 0.10290)
State 3  0.19402 ( 0.15743, 0.23913)
State 4 0

 Transition probability matrix for t =  2  :
          State 1   State 2    State 3   State 4
State 1 0.7224079 0.1683030 0.03522663 0.0740625
```

```
State 2 0.4810716 0.2529645 0.14008255 0.1258814
State 3 0.0000000 0.0000000 0.67838075 0.3216193
State 4 0.0000000 0.0000000 0.00000000 1.0000000

 Misclassification matrix :
       State 1 State 2 State 3                State 4
State 1 1.0000  0       0                      0
State 2 0       0       0.1039 (0.08881,0.1212) 0
State 3 0       0       1.0000                 0
State 4 0       0       0                      1.0000

 Hazard ratios :
$age
                         HR         L         U
State 1 - State 2 1.080777 1.0677267 1.0939862
State 1 - State 4 1.085146 1.0543871 1.1168023
State 2 - State 1 0.979584 0.9654133 0.9939627
State 2 - State 3 1.055787 1.0326212 1.0794722
State 2 - State 4 1.066975 1.0148080 1.1218231
State 3 - State 4 1.071141 1.0470990 1.0957349

$male
                          HR         L        U
State 1 - State 2 1.3383578 1.1429501 1.567174
State 1 - State 4 1.5254411 0.9901823 2.350043
State 2 - State 1 1.0000000 1.0000000 1.000000
State 2 - State 3 0.8325447 0.6129781 1.130759
State 2 - State 4 2.0610765 1.1822137 3.593290
State 3 - State 4 1.4287728 1.0892843 1.874067

$edu_low_med
                          HR         L        U
State 1 - State 2 0.7596424 0.4753863 1.213869
State 1 - State 4 1.0000000 1.0000000 1.000000
State 2 - State 1 1.0000000 1.0000000 1.000000
State 2 - State 3 0.8827809 0.4036470 1.930653
State 2 - State 4 1.0000000 1.0000000 1.000000
State 3 - State 4 1.0000000 1.0000000 1.000000

$edu_low_high
                          HR         L         U
State 1 - State 2 0.5719336 0.4038369 0.8100003
State 1 - State 4 1.0000000 1.0000000 1.0000000
State 2 - State 1 1.0000000 1.0000000 1.0000000
State 2 - State 3 0.8474639 0.4823419 1.4889749
State 2 - State 4 1.0000000 1.0000000 1.0000000
State 3 - State 4 1.0000000 1.0000000 1.0000000


 Mean sojourn times :
       estimates         SE        L        U
State 1  3.890975 0.14215479 3.622098 4.179811
State 2  1.129335 0.04593426 1.042800 1.223050
State 3  5.154020 0.54965949 4.181848 6.352198
```

```
 Probability that each state is next :
        State 1                  State 2                  State 3                  State 4
State 1 0                        0.87670 (0.84783,0.8990) 0                        0.12330 (0.10104,0.15
State 2 0.72734 (0.68784,0.7600) 0                        0.19690 (0.16834,0.2264) 0.07576 (0.04796,0.11
State 3 0                        0                        0                        1.00000 (1.00000,1.00
State 4 0                        0                        0                        0

  Total length of stay :
  State 1   State 2   State 3   State 4
10.738426  2.732486  2.455486       Inf

 Expected number of visits to the state :
  State 1   State 2   State 3   State 4
1.7598289 2.4195539 0.4764214 1.0000000
```

model 2

The model was fitted using the following specification of covariates:

```
# Forward transitions:
  "1-2"       = "age + age_bl + male + edu_low_med + edu_low_high"
  "2-3"       = "age + age_bl + male + edu_low_med + edu_low_high"
# Backward transitions:
  "2-1"       = "age + age_bl"
# Death transitions:
  "1-4"       = "age + age_bl + male + edu_low_med + edu_low_high"
  "2-4"       = "age + age_bl + male + edu_low_med + edu_low_high"
  "3-4"       = "age + age_bl + male + edu_low_med + edu_low_high"
```

summary

```
-2loglik = 15001.18
Convergence code = 0
          p   se Wald ChiSq Pr>ChiSq
qbase -1.69 0.19      75.02     0.00
qbase -4.26 0.68      39.60     0.00
qbase -0.28 0.08      11.11     0.00
qbase -1.96 0.31      40.42     0.00
qbase -3.71 0.87      18.20     0.00
qbase -2.18 0.30      52.27     0.00
qcov   0.08 0.01     157.60     0.00
qcov   0.08 0.01      30.52     0.00
qcov  -0.02 0.01       7.49     0.01
qcov   0.05 0.01      22.97     0.00
qcov   0.06 0.03       5.71     0.02
qcov   0.07 0.01      36.01     0.00
qcov   0.29 0.08      12.83     0.00
qcov   0.44 0.22       3.92     0.05
qcov  -0.16 0.16       1.00     0.32
qcov   0.69 0.29       5.49     0.02
qcov   0.38 0.14       7.23     0.01
```

```
qcov  -0.26 0.25       1.07     0.30
qcov   0.31 0.79       0.16     0.69
qcov  -0.12 0.42       0.09     0.77
qcov   0.06 1.18       0.00     0.96
qcov   0.12 0.41       0.08     0.78
qcov  -0.53 0.18       8.20     0.00
qcov   0.03 0.67       0.00     0.97
qcov  -0.20 0.30       0.43     0.51
qcov   0.34 0.88       0.15     0.70
qcov  -0.15 0.27       0.32     0.57
p     -2.16 0.09     590.25     0.00
initp -1.33 0.06     433.05     0.00
initp -2.85 0.13     481.80     0.00
```

details

```
 Intensity matrix :
        State 1                       State 2                       State 3
State 1 -0.25675 (-0.27582,-0.23900)  0.22523 ( 0.20762, 0.24433) 0
State 2  0.64325 ( 0.58349, 0.70914) -0.88436 (-0.95786,-0.81650)  0.17361 ( 0.14726, 0.20467)
State 3 0                             0                             -0.19007 (-0.23563,-0.15332)
State 4 0                             0                             0
        State 4
State 1  0.03152 ( 0.02557, 0.03886)
State 2  0.06750 ( 0.04310, 0.10571)
State 3  0.19007 ( 0.15332, 0.23563)
State 4 0

 Transition probability matrix for t =  2  :
          State 1   State 2    State 3    State 4
State 1 0.7226273 0.1684136 0.03518858 0.07377055
State 2 0.4809945 0.2533314 0.14023226 0.12544192
State 3 0.0000000 0.0000000 0.68376659 0.31623341
State 4 0.0000000 0.0000000 0.00000000 1.00000000

 Misclassification matrix :
        State 1 State 2 State 3                State 4
State 1 1.0000  0       0                      0
State 2 0       0       0.1038 (0.08874,0.1212) 0
State 3 0       0       1.0000                 0
State 4 0       0       0                      1.0000

 Hazard ratios :
$age
                         HR         L         U
State 1 - State 2 1.0810352 1.0679642 1.0942662
State 1 - State 4 1.0851747 1.0541584 1.1171036
State 2 - State 1 0.9798409 0.9656587 0.9942314
State 2 - State 3 1.0562092 1.0328517 1.0800948
State 2 - State 4 1.0669022 1.0117297 1.1250835
State 3 - State 4 1.0732165 1.0487328 1.0982718
```

```
$male
                         HR        L        U
State 1 - State 2 1.3352491 1.139855 1.564137
State 1 - State 4 1.5558672 1.004304 2.410349
State 2 - State 1 1.0000000 1.000000 1.000000
State 2 - State 3 0.8549199 0.628904 1.162162
State 2 - State 4 1.9935253 1.119284 3.550613
State 3 - State 4 1.4556315 1.107118 1.913855

$edu_low_med
                         HR         L         U
State 1 - State 2 0.7746750 0.4779028  1.255739
State 1 - State 4 1.3660242 0.2927307  6.374536
State 2 - State 1 1.0000000 1.0000000  1.000000
State 2 - State 3 0.8851032 0.3914057  2.001524
State 2 - State 4 1.0667119 0.1059017 10.744627
State 3 - State 4 1.1239639 0.5033243  2.509902

$edu_low_high
                         HR         L         U
State 1 - State 2 0.5892899 0.4103330 0.8462946
State 1 - State 4 1.0275460 0.2767308 3.8154442
State 2 - State 1 1.0000000 1.0000000 1.0000000
State 2 - State 3 0.8221826 0.4573361 1.4780909
State 2 - State 4 1.4076005 0.2532502 7.8236442
State 3 - State 4 0.8566714 0.5022316 1.4612500


 Mean sojourn times :
        estimates        SE        L        U
State 1  3.894867 0.1423680 3.625592 4.184142
State 2  1.130764 0.0460590 1.043999 1.224739
State 3  5.261238 0.5767942 4.243947 6.522377

 Probability that each state is next :
        State 1                   State 2                   State 3                   State 4
State 1 0                         0.87723 (0.84986,0.9016) 0                         0.12277 (0.09840,0.15
State 2 0.72737 (0.68919,0.7613) 0                         0.19631 (0.16746,0.2289) 0.07632 (0.04951,0.1
State 3 0                         0                         0                         1.00000 (1.00000,1.00
State 4 0                         0                         0                         0

  Total length of stay :
  State 1   State 2   State 3   State 4
10.761354  2.740683  2.503303       Inf

 Expected number of visits to the state :
  State 1   State 2   State 3   State 4
1.7629577 2.4237453 0.4758011 1.0000000
```

Session Info

```r
sessionInfo()
```

```
R version 3.3.1 (2016-06-21)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 14393)

locale:
[1] LC_COLLATE=English_United States.1252  LC_CTYPE=English_United States.1252    LC_MONETARY=English_Un
[4] LC_NUMERIC=C                           LC_TIME=English_United States.1252

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] msm_1.6.1    magrittr_1.5 nnet_7.3-12  knitr_1.14

loaded via a namespace (and not attached):
 [1] Rcpp_0.12.6        formatR_1.4        nloptr_1.0.4       plyr_1.8.4         tools_3.3.1        dige
 [7] lme4_1.1-12        evaluate_0.9       tibble_1.2         gtable_0.2.0       nlme_3.1-128       latt
[13] mgcv_1.8-14        Matrix_1.2-7.1     DBI_0.5            yaml_2.1.13        parallel_3.3.1     Spar
[19] mvtnorm_1.0-5      expm_0.999-0       dplyr_0.5.0        stringr_1.1.0      MatrixModels_0.4-1 grid
[25] R6_2.1.3           survival_2.39-5    rmarkdown_1.0      minqa_1.2.4        ggplot2_2.1.0      car_
[31] scales_0.4.0       htmltools_0.3.5    splines_3.3.1      MASS_7.3-45        assertthat_0.1     pbkr
[37] testit_0.5         colorspace_1.2-6   quantreg_5.26      stringi_1.1.1      lazyeval_0.2.0     muns
```