# Model B: Estimation Results

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Estimation results of <b>Model B</b> , specified by the following input:	
<pre>q &lt;01 # transition matrix Q &lt;- rbind( c(0, q, 0, q),</pre>	
# misclassification matrix  E <- rbind( c( 0,  0,  0,  0),	
<pre># 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</pre>	

```
"Severe - Dead" # q34
)
```

#### Load environmet

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

### 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
                                                                         FALSE
5121 50402431
                 1 1 91.41136 FALSE 16 94.82272
                                                     92.33402
                                                                         FALSE
                                                              12
                2 1 91.41136 FALSE 16 94.82272
5122 50402431
                                                     93.34702
                                                                         FALSE
5123 50402431
                3 1 91.41136 FALSE 16 94.82272
                                                     94.34634
                                                                         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
                                                              FALSE
                                                                     19
                                                                               1
                    1 91.41136 FALSE 16 92.33402
5121 50402431
                                                              FALSE
                                                                               0
                 1
                                                     3
                                                                     12
                 2 1 91.41136 FALSE 16 93.34702
                                                                               0
5122 50402431
                                                     3
                                                              FALSE
                                                                     5
5123 50402431
                3 1 91.41136 FALSE 16 94.34634
                                                     3
                                                              FALSE
                                                                      0
                                                                               0
             NA 1 91.41136 FALSE 16 94.82272
                                                  4
51201 50402431
                                                              FALSE
                                                                     NA
                                                                               0
```

### Remove cases

```
#### 1) Remove observations with missing age
# Initial number of observations with missing age :
sum(is.na(ds_ms$age))
[1] 1
ds_clean <- ds_ms %>%
 dplyr::filter(!is.na(age))
# Resultant number of observations with missing age
sum(is.na(ds_clean$age))
[1] 0
#### 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 \times 2
   n_data_points n_people
           <int>
                     <int>
                       119
1
               1
2
               2
                       205
3
               3
                       184
4
               4
                       180
               5
                       190
5
6
               6
                       104
7
               7
                       108
8
               8
                       113
9
               9
                       127
10
              10
                       116
                       110
11
              11
12
              12
                       71
                        21
13
              13
14
              14
                        14
15
              15
                        13
                        17
16
              16
              17
                         3
17
# 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</pre>
# How many subjects to be removed from the data set:
length(remove_ids)
[1] 119
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 \times 2
   n_data_points n_people
           <int>
                    <int>
                       205
1
               2
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
              17
16
                        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"]</pre>
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
1
    0-9 years
               0
                2
                     6
2
    0-9 years
3
    0-9 years
                    10
                3
4
    0-9 years
                    17
                4
5
    0-9 years
              5
                    20
6
    0-9 years
                    48
7
    0-9 years
               7
                    27
    0-9 years
               8 178
8
    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
    >11 years 15 554
15
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
    >11 years 21 207
    >11 years 22
22
                   61
    >11 years 23
24
    >11 years 24
                   26
25
    >11 years 25
                   11
26
    >11 years 28
                   21
Frequencies of categorized education :
# A tibble: 3 \times 2
     educatF
      <fctr> <int>
```

386

392

# Age diagnostic

3 >11 years 9479

1 0-9 years

2 10-11 years

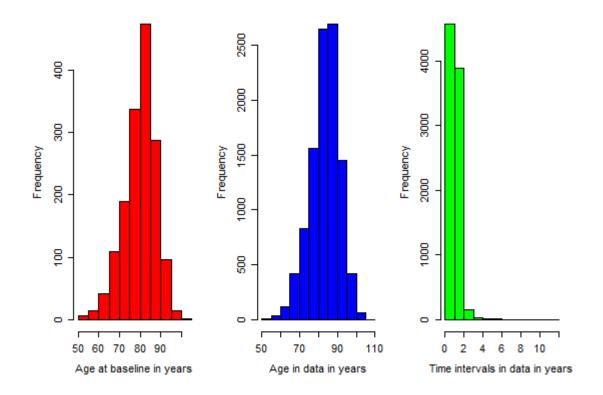
```
Minimum interval length: 0.00273785
```

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	firstobs	fu_year	age	state
1	90544686 7	.696783	0	12	1	>11 years	1	0	7.696783	1
2	90544686 7	.696783	0	12	1	>11 years	0	1	8.682409	1

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

Subject count: 1572

#### State table:

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

The inital values for estimation :  $0.76 \ 0.18 \ 0.06 \ 0$ 

# **Specifications**

### Fitting functions

```
estimate multistate <- function(</pre>
 model_name
  ,ds
                        # data object
  ,Q
                        # Q-matrix of transitions
  ,E
                        # misspecification matrix
                        # names of the rows in the Q matrix
  ,qnames
  ,cov_names
                        # string with covariate names
  covariates_ <- as.formula(paste0("~",cov_names))</pre>
  model <- msm(
   formula
                  = state ~ age,
                 = id,
   subject
   data
                  = ds,
                  = FALSE,
   center
  qmatrix
                 = Q,
```

## Support functions

```
get_crude_Q <- function(ds, Q, cov_names){</pre>
  formula_ <- as.formula(paste0("state ~ ",cov_names))</pre>
  Q_crude <- crudeinits.msm(
    formula = formula_,
    subject = id,
    qmatrix = Q,
    data = ds,
                 = c(-1,-2),
    censor
    censor.states = list(c(1,2,3), c(1,2,3))
 )
 return(Q_crude)
}
msm_summary <- function(model){</pre>
cat("\n-2loglik =", model$minus2loglik,"\n")
cat("Convergence code =", model$opt$convergence,"\n")
    <- model$opt$par</pre>
p.se <- sqrt(diag(solve(1/2*model$opt$hessian)))</pre>
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)
}
```

#### Model

```
c(0, 0, 0, 0)
# misclassification matrix
E \leftarrow 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
```

#### msm options

```
digits = 2
method_ = "BFGS"
                      # alternatively, if does not converge "Nedler-Mead"
                     # additional model constraints
constraint_ = NULL
                      # fixed parameters
fixedpars_ = NULL
initprobs_ = initial_probabilities
# 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]
[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
# estimate_multistate("mB1", ds, Q_crude, E, qnames,cov_names = "age")
# (Q_crude <- get_crude_Q(ds, Q, "age + age_bl"))
# estimate_multistate("mB2", ds, Q_crude, E, qnames,cov_names = "age + age_bl")
\# (Q\_crude \leftarrow get\_crude\_Q(ds, Q, "age + age\_bl + male"))
# estimate_multistate("mB3", ds, Q_crude, E, qnames,cov_names = "age + age_bl + male")
# (Q_crude <- get_crude_Q(ds, Q, "age + age_bl + male + educat"))</pre>
# estimate_multistate("mB4", ds, Q_crude, E, qnames,cov_names = "age + age_bl + male + educat")
# assemble the list object with the results of msm estimation
models <- list()</pre>
models[["age"]][["msm"]] <- readRDS(paste0(pathSaveFolder,'mB1.rds'))</pre>
models[["age_bl"]][["msm"]] <- readRDS(paste0(pathSaveFolder,'mB2.rds'))</pre>
models[["male"]][["msm"]] <- readRDS(paste0(pathSaveFolder, 'mB3.rds'))</pre>
models[["educat"]][["msm"]] <- readRDS(paste0(pathSaveFolder, 'mB4.rds'))</pre>
```

### elect options

```
alive states \leftarrow c(1,2,3)
ds_alive <- ds[ds$state %in% alive_states,]</pre>
fixedpars <- fixedpars_</pre>
age_min <- 0
age max <- 35
age_bl <- 0
male <- 0
educat <- 0
replication_n <- 1000
time_scale <- "years"</pre>
grid_par <- .5</pre>
# turn this chunk OFF when printing the report
# for(model in names(models) ){
  # determine covariate list
#
   if(model_=="age"){covar_list
                                   = list(age=age_min)}
  if(model_=="age_bl"){covar_list = list(age=age_min, age_bl=age_bl)}
  if(model_=="male"){covar_list = list(age=age_min, age_bl=age_bl, male=male)}
  if(model_=="educat"){covar_list = list(age=age_min, age_bl=age_bl, male=male, educat=educat)}
#
  # compute LE
  models[[model_]][["LE"]] <- elect(</pre>
#
#
    model
                    = models[[model_]][["msm"]], # fitted msm model
#
    b.covariates = covar_list, # list with specified covarites values
#
    statedistdata = ds_alive, # data for distribution of living states
#
    time.scale.msm = time_scale, # time scale in multi-state model ("years", ...)
    h
                     = grid_par, # grid parameter for integration
#
#
                     = age_max, # assumed maximum age in years
     age.max
     S
#
                     = replication_n # number of simulation cycles
#
    \label{eq:condels} \textit{\# models[[model_]][["LE"]] <- models[["msm"]][[model_]]}
#
# }
# #save models estimated by elect() in a external object for faster access in the future
# saveRDS(models, pasteO(pathSaveFolder, "models.rds"))
models <- readRDS(paste0(pathSaveFolder, "models.rds"))</pre>
# inspect created object
lapply(models, names)
$age
[1] "msm" "LE"
$age_bl
[1] "msm" "LE"
$male
[1] "msm" "LE"
$educat
[1] "msm" "LE"
```

```
$edu
[1] "msm" "LE"
```

#### Model results

#### age

#### summary

```
-2loglik = 15059.61
Convergence code = 0
          p se Wald ChiSq Pr>ChiSq
qbase -2.12 0.07
                     865.97
                                 0.00
qbase -4.13 0.17
                     558.14
                                 0.00
                     12.28
                                 0.00
qbase -0.29 0.08
qbase -2.19 0.15
                  199.54
                                 0.00
qbase -3.06 0.35
                     78.06
                                 0.00
qcov 0.08 0.01 134.20
qcov 0.08 0.01 160.84
qcov -0.02 0.01
                                 0.00
                                0.00
                                0.00
                                0.01
                     23.01
                                0.00
qcov
      0.05 0.01
qcov 0.06 0.02
                      6.34
                                0.01
qcov 0.07 0.01
                     33.05
                                0.00
      -2.15 0.09
                     589.75
                                0.00
initp -1.33 0.06
                     433.56
                                 0.00
initp -2.85 0.13
                     480.86
                                 0.00
```

#### solution

of replacement length

```
Call:
msm(formula = state ~ age, subject = id, data = ds, qmatrix = Q, ematrix = E, covariates = covariat
Maximum likelihood estimates
Baselines are with covariates set to 0
Transition intensities with hazard ratios for each covariate
                 Baseline
State 1 - State 1 -0.13609 (-0.15443,-0.11992)
State 1 - State 2 0.11996 (0.10416, 0.13816) 1.0814 (1.0684,1.0946)
State 1 - State 4 0.01613 (0.01145, 0.02271) 1.0869 (1.0559,1.1187)
State 2 - State 1 0.74949 (0.63785, 0.88065) 0.9802 (0.9662,0.9944)
State 2 - State 2 -0.90846 (-1.04359,-0.79082)
State 2 - State 3 0.11212 (0.08276, 0.15189) 1.0560 (1.0328,1.0798)
State 2 - State 4 0.04685 (0.02376, 0.09239) 1.0615 (1.0133,1.1119)
State 3 - State 3 -0.11946 (-0.17114,-0.08339)
State 3 - State 4 0.11946 (0.08339, 0.17114) 1.0674 (1.0439,1.0914)
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i
```

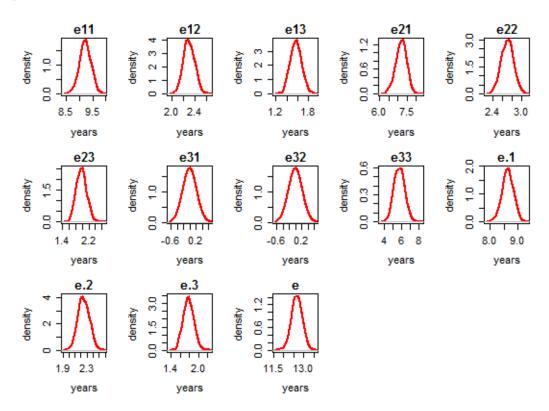
```
Misclassification probabilities
                   Baseline
Obs State 2 | State 2 0
Obs State 3 | State 2 0.1041 (0.08898,0.1215)
Initial state occupancy probabilities
         Estimate
                      LCL
State 1 0.75681606 0.73449835 0.77726093
State 2 0.19930412 0.17966161 0.22057570
State 3 0.04387982 0.03430043 0.05598259
State 4 0.00000000 0.00000000 0.00000000
-2 * log-likelihood: 15059.61
[Note, to obtain old print format, use "printold.msm"]
ELECT summary
_____
ELECT summary
_____
Covariates values in the multi-state model:
age
Covariates in the state-distribution model:
Life expectancies: Using simulation with 1000 replications
Point estimates, and mean, SEs, and quantiles from simulation:
          mn se 0.025q 0.5q 0.975q
     pnt
e11 9.26 9.23 0.22 8.78 9.24
                                9.64
e12 2.33 2.31 0.10 2.12 2.30
                                2.49
e13 1.58 1.57 0.10 1.38 1.57
                                1.77
e21 7.23 7.20 0.30 6.55 7.21
                                7.73
e22 2.74 2.71 0.13 2.45 2.71
                                2.95
e23 2.00 1.99 0.15 1.71 1.99
                                2.30
e31 0.00 0.00 0.00 0.00 0.00
                                0.00
e32 0.00 0.00 0.00 0.00 0.00
                                0.00
e33 5.75 5.76 0.62 4.62 5.75
                                6.98
e.1 8.67 8.64 0.21 8.21 8.65
                                9.04
e.2 2.27 2.25 0.09 2.07 2.24
                                2.44
e.3 1.79 1.79 0.11 1.57 1.79
                                2.01
```

e 12.73 12.68 0.27 12.16 12.68 13.18

of replacement length

Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i

#### plots



### age at baseline

# summary

```
-2loglik = 15026.84
Convergence code = 0
              se Wald ChiSq Pr>ChiSq
          р
qbase -2.02 0.08
                      679.18
                                 0.00
                                 0.00
qbase -4.25 0.20
                      447.08
qbase -0.19 0.09
                        4.94
                                 0.03
qbase -2.25 0.16
                      196.77
                                 0.00
                                 0.00
qbase -3.10 0.34
                      81.39
qbase -2.22 0.19
                      132.69
                                 0.00
                                 0.01
qcov
       0.04 0.01
                        6.96
       0.12 0.03
                       13.74
                                 0.00
qcov
                                 0.00
     -0.07 0.02
                       16.64
qcov
qcov
       0.08 0.02
                       12.07
                                 0.00
       0.11 0.04
                        6.46
                                 0.01
qcov
qcov
       0.09 0.02
                       20.14
                                 0.00
       0.05 0.01
                       13.09
                                 0.00
qcov
     -0.04 0.03
                        1.47
                                 0.23
qcov
                                 0.00
       0.06 0.02
                       10.64
qcov
     -0.03 0.02
                        1.49
                                 0.22
qcov
                                 0.13
     -0.07 0.05
                        2.30
qcov
qcov -0.04 0.02
                        2.65
                                 0.10
```

```
p -2.15 0.09
initp -1.33 0.06
                    588.84
                                0.00
                    433.67
                                0.00
                     487.60
initp -2.83 0.13
                                0.00
solution
Call:
msm(formula = state ~ age, subject = id, data = ds, qmatrix = Q, ematrix = E, covariates = covariat
Maximum likelihood estimates
Baselines are with covariates set to 0
Transition intensities with hazard ratios for each covariate
                  Baseline
                                                                       age_bl
State 1 - State 1 -0.14696 (-0.168443,-0.12821)
State 1 - State 2 0.13272 (0.114020, 0.15449) 1.0361 (1.0092,1.0638) 1.0519 (1.0234,1.081)
State 1 - State 4 0.01423 (0.009598, 0.02111) 1.1269 (1.0579,1.2004) 0.9605 (0.8999,1.025)
State 2 - State 1 0.82371 (0.694275, 0.97728) 0.9317 (0.9006,0.9639) 1.0628 (1.0246,1.102)
State 2 - State 2 -0.97424 (-1.130972,-0.83923)
State 2 - State 3 0.10552 (0.077071, 0.14448) 1.0812 (1.0346,1.1299) 0.9720 (0.9287,1.017)
State 2 - State 4 0.04500 (0.022944, 0.08827) 1.1185 (1.0260,1.2194) 0.9332 (0.8534,1.020)
State 3 - State 3 -0.10897 (-0.158895,-0.07473)
State 3 - State 4 0.10897 (0.074732, 0.15889) 1.0985 (1.0544,1.1445) 0.9652 (0.9249,1.007)
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i
of replacement length
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i
of replacement length
Misclassification probabilities
                      Baseline
Obs State 2 | State 2 0
Obs State 3 | State 2 0.1041 (0.08896,0.1215)
Initial state occupancy probabilities
                         LCI.
                                    UCI.
          Estimate
State 1 0.75610249 0.73399586 0.77561052
State 2 0.19930454 0.18017069 0.22017770
State 3 0.04459297 0.03486444 0.05662713
State 4 0.00000000 0.00000000 0.00000000
-2 * log-likelihood: 15026.84
[Note, to obtain old print format, use "printold.msm"]
ELECT summary
```

Covariates values in the multi-state model:

ELECT summary

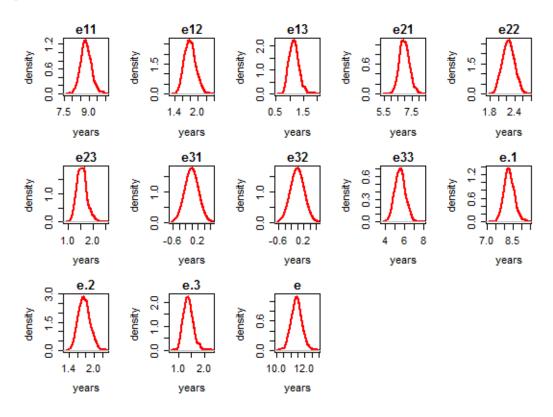
age age\_bl Covariates in the state-distribution model:

Life expectancies: Using simulation with 1000 replications

Point estimates, and mean, SEs, and quantiles from simulation:

	pnt	mn	se	0.025q	0.5q	0.975q	
e11	8.87	8.83	0.32	8.23	8.81	9.50	
e12	1.83	1.80	0.14	1.55	1.79	2.09	
e13	1.17	1.16	0.18	0.87	1.15	1.56	
e21	7.03	6.98	0.35	6.34	6.97	7.76	
e22	2.29	2.25	0.14	1.99	2.25	2.53	
e23	1.58	1.57	0.20	1.22	1.56	2.04	
e31	0.00	0.00	0.00	0.00	0.00	0.00	
e32	0.00	0.00	0.00	0.00	0.00	0.00	
e33	5.58	5.58	0.55	4.54	5.58	6.69	
e.1	8.32	8.28	0.31	7.71	8.26	8.92	
e.2	1.80	1.77	0.13	1.53	1.76	2.04	
e.3	1.39	1.39	0.18	1.08	1.38	1.79	
е	11.51	11.43	0.37	10.75	11.43	12.18	

# $\mathbf{plots}$



#### male

#### summary

```
-2loglik = 14977.86
Convergence code = 0
              se Wald ChiSq Pr>ChiSq
          р
qbase -2.10 0.08
                     667.99
                                0.00
qbase -4.38 0.21
                     437.79
                                0.00
                                0.01
qbase -0.23 0.09
                       5.94
qbase -2.23 0.17
                     179.55
                                0.00
qbase -3.29 0.38
                      74.60
                                0.00
qbase -2.47 0.21
                     132.89
                                0.00
                      6.79
                                0.01
qcov
      0.04 0.01
qcov
      0.13 0.03
                      15.41
                                0.00
                      15.98
                                0.00
qcov -0.07 0.02
                      14.44
                                0.00
qcov
     0.09 0.02
qcov
      0.09 0.05
                      4.06
                                0.04
qcov 0.11 0.02
                      27.79
                                0.00
qcov
     0.05 0.01
                      13.23
                                0.00
qcov -0.05 0.03
                      2.12
                                0.15
qcov
      0.06 0.02
                      10.04
                                0.00
                      2.46
                                0.12
qcov -0.04 0.02
qcov -0.05 0.05
                       0.87
                                0.35
                      5.80
                                0.02
qcov -0.05 0.02
                      13.14
                                0.00
qcov 0.33 0.09
                                0.05
qcov 0.45 0.23
                       3.77
                                0.25
qcov 0.12 0.11
                      1.30
qcov -0.16 0.16
                       1.08
                                0.30
qcov
      0.64 0.28
                       5.13
                                0.02
                                0.00
                       9.23
qcov
     0.43 0.14
                                0.00
     -2.15 0.09
                     589.03
initp -1.33 0.06
                     434.12
                                0.00
initp -2.84 0.13
                     486.43
                                0.00
```

#### solution

```
Call:
```

msm(formula = state ~ age, subject = id, data = ds, qmatrix = Q, ematrix = E, covariates = covariat

Maximum likelihood estimates

Baselines are with covariates set to 0

Transition intensities with hazard ratios for each covariate

```
Baseline age age_bl male

State 1 - State 1 -0.13442 (-0.155254,-0.11639)

State 1 - State 2 0.12190 ( 0.103921, 0.14300) 1.0357 (1.0087,1.0635) 1.0523 (1.0238,1.0817) 1.3930 (1

State 1 - State 4 0.01252 ( 0.008307, 0.01887) 1.1332 (1.0646,1.2062) 0.9528 (0.8927,1.0169) 1.5623 (0

State 2 - State 1 0.79683 ( 0.663817, 0.95650) 0.9327 (0.9014,0.9651) 1.0612 (1.0229,1.1009) 1.1290 (0

State 2 - State 2 -0.94185 (-1.104543,-0.80312)

State 2 - State 3 0.10788 ( 0.077894, 0.14942) 1.0892 (1.0422,1.1383) 0.9642 (0.9212,1.0091) 0.8497 (0
```

```
State 2 - State 4 0.03714 (0.017591, 0.07841) 1.0979 (1.0026,1.2024) 0.9558 (0.8692,1.0511) 1.8957 (1
State 3 - State 3 -0.08480 (-0.128998,-0.05574)
State 3 - State 4 0.08480 (0.055742, 0.12900) 1.1198 (1.0737,1.1679) 0.9489 (0.9093,0.9903) 1.5390 (1
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i
of replacement length
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i
of replacement length
Misclassification probabilities
                    Baseline
Obs State 2 | State 2 0
Obs State 3 | State 2 0.1042 (0.08905,0.1216)
Initial state occupancy probabilities
         Estimate
                       LCL
State 1 0.75644307 0.7336018 0.77663358
State 2 0.19914669 0.1799655 0.22019658
State 3 0.04441024 0.0350617 0.05654718
State 4 0.00000000 0.0000000 0.00000000
-2 * log-likelihood: 14977.86
[Note, to obtain old print format, use "printold.msm"]
ELECT summary
______
ELECT summary
Covariates values in the multi-state model:
   age age_bl male
           Ω
Covariates in the state-distribution model:
  age
Life expectancies: Using simulation with 1000 replications
Point estimates, and mean, SEs, and quantiles from simulation:
     pnt
          mn se 0.025q 0.5q 0.975q
e11 9.35 9.29 0.37 8.63 9.28 10.09
e12 1.85 1.81 0.16 1.51 1.80
                                  2.13
e13 1.31 1.29 0.19 0.96 1.28
                                  1.68
e21 7.40 7.31 0.40 6.52 7.31
                                 8.13
e22 2.34 2.30 0.17 1.98 2.29
                                  2.64
e23 1.81 1.80 0.22 1.41 1.78
                                  2.28
e31 0.00 0.00 0.00 0.00 0.00
                                  0.00
e32 0.00 0.00 0.00 0.00 0.00
                                  0.00
e33 6.24 6.26 0.65 5.02 6.22
                                  7.54
```

e.1 8.76 8.70 0.35 8.08 8.69

e.3 1.57 1.55 0.19 1.22 1.54

e.2 1.82 1.78 0.15

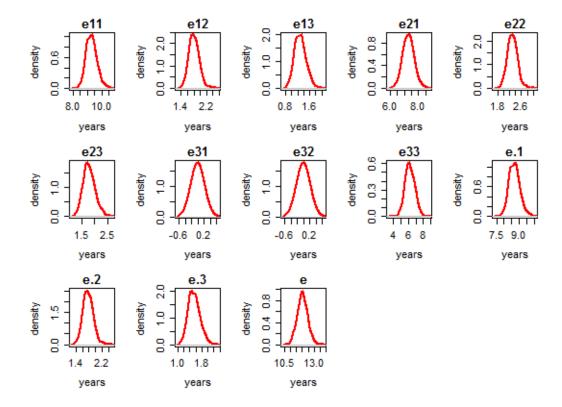
9.47

2.08

1.96

1.50 1.77

# plots



# education

## summary

-2loglik = 14965.72 Convergence code = 0

	_			
	р	se	Wald ChiSq	Pr>ChiSq
qbase	-1.87	0.11	265.81	0.00
qbase	-4.32	0.32	186.83	0.00
qbase	-0.23	0.11	4.07	0.04
qbase	-2.15	0.19	125.35	0.00
qbase	-3.47	0.49	49.52	0.00
qbase	-2.38	0.22	112.26	0.00
qcov	0.04	0.01	6.79	0.01
qcov	0.12	0.03	14.88	0.00
qcov	-0.07	0.02	16.22	0.00
qcov	0.08	0.02	14.06	0.00
qcov	0.10	0.05	4.23	0.04
qcov	0.11	0.02	28.29	0.00
qcov	0.05	0.01	12.34	0.00
qcov	-0.05	0.03	1.87	0.17

```
0.06 0.02
                     10.14
                               0.00
qcov
                               0.14
qcov -0.03 0.02
                      2.14
qcov -0.05 0.05
                      1.08
                               0.30
qcov -0.05 0.02
                      5.71
                               0.02
qcov 0.33 0.09
                     12.92
                               0.00
qcov 0.49 0.23
                      4.41
                               0.04
                               0.25
qcov 0.12 0.11
                      1.30
qcov -0.14 0.16
                      0.81
                               0.37
qcov
     0.57 0.30
                      3.63
                               0.06
qcov
     0.44 0.14
                      9.66
                               0.00
qcov -0.25 0.09
                      7.31
                               0.01
                      0.11
                               0.74
qcov -0.09 0.27
qcov 0.02 0.11
                      0.03
                               0.87
                      0.56
                               0.45
qcov -0.10 0.14
                      0.33
                               0.56
qcov 0.25 0.44
qcov -0.15 0.12
                      1.39
                               0.24
     -2.15 0.09
                    588.76
                               0.00
initp -1.33 0.06
                    433.80
                               0.00
initp -2.83 0.13
                               0.00
                    486.75
```

#### solution

msm(formula = state ~ age, subject = id, data = ds, qmatrix = Q, ematrix = E, covariates = covariat

Maximum likelihood estimates

Baselines are with covariates set to 0

```
Transition intensities with hazard ratios for each covariate
```

```
Baseline
                                                                      age_bl
                                                                                             male
                                               age
State 1 - State 1 -0.16778 (-0.205801,-0.13679)
State 1 - State 2 0.15445 (0.123388, 0.19334) 1.0360 (1.0088,1.0640) 1.0510 (1.0222,1.0805) 1.3914 (1
State 1 - State 4 0.01333 (0.007177, 0.02476) 1.1327 (1.0632,1.2067) 0.9546 (0.8931,1.0204) 1.6254 (1
State 2 - State 1 0.79401 (0.634537, 0.99357) 0.9317 (0.9001,0.9643) 1.0617 (1.0233,1.1015) 1.1304 (0
State 2 - State 2 -0.94182 (-1.146462,-0.77370)
State 2 - State 3 0.11662 (0.080061, 0.16989) 1.0880 (1.0411,1.1371) 0.9662 (0.9228,1.0117) 0.8667 (0
State 2 - State 4 0.03118 (0.011869, 0.08192) 1.1008 (1.0046,1.2063) 0.9492 (0.8603,1.0472) 1.7758 (0
State 3 - State 3 -0.09296 (-0.144258,-0.05990)
State 3 - State 4 0.09296 (0.059902, 0.14426) 1.1218 (1.0753,1.1703) 0.9490 (0.9091,0.9906) 1.5593 (1
                 educat
State 1 - State 1
State 1 - State 2 0.7751 (0.6445,0.9323)
State 1 - State 4 0.9152 (0.5427,1.5433)
State 2 - State 1 1.0175 (0.8271,1.2518)
```

State 2 - State 2

State 2 - State 3 0.9007 (0.6848,1.1847)

State 2 - State 4 1.2886 (0.5450,3.0466)

State 3 - State 3

State 3 - State 4 0.8635 (0.6765,1.1022)

Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i of replacement length

```
Warning in res[plabs == "pbase"][unique(states[plabs == "p"])] <- 1/(1 + : number of items to replace i of replacement length
```

Misclassification probabilities

Baseline

Obs State 2 | State 2 0

Obs State 3 | State 2 0.1042 (0.08904,0.1216)

Initial state occupancy probabilities

Estimate LCL UCL

State 1 0.75627049 0.73396526 0.77637390

State 2 0.19927786 0.17984784 0.22039809

State 3 0.04445165 0.03500507 0.05651733

State 4 0.00000000 0.00000000 0.00000000

-2 \* log-likelihood: 14965.72

[Note, to obtain old print format, use "printold.msm"]

#### **ELECT** summary

-----

ELECT summary

-----

Covariates values in the multi-state model:

age age\_bl male educat

0 0 0 0

Covariates in the state-distribution model: age

Life expectancies: Using simulation with 1000 replications

Point estimates, and mean, SEs, and quantiles from simulation:

pnt mn se 0.025q 0.5q 0.975q

e11 8.33 8.24 0.51 7.31 8.22 9.33

e12 2.07 2.02 0.23 1.58 2.01 2.49

e13 1.45 1.43 0.26 1.00 1.41 1.98

e21 6.56 6.46 0.50 5.56 6.43 7.46

e22 2.51 2.45 0.24 1.99 2.44 2.94

e23 1.92 1.90 0.30 1.37 1.87 2.55

e31 0.00 0.00 0.00 0.00 0.00 0.00

e32 0.00 0.00 0.00 0.00 0.00 0.00 e33 5.84 5.84 0.69 4.57 5.83 7.25

e.1 7.80 7.72 0.48 6.85 7.69 8.75

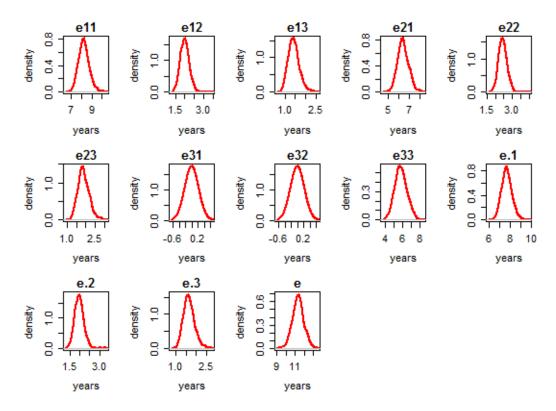
e.2 2.03 1.97 0.22 1.56 1.97 2.43

e.3 1.68 1.66 0.26 1.20 1.64 2.23

e 11.51 11.36 0.60 10.22 11.36 12.55

-----

#### plots



# Session Info

#### 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\_United 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):

Toaded 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	lat <sup>.</sup>
[13] mgcv_1.8-14	Matrix_1.2-7.1	DBI_0.5	yaml_2.1.13	parallel_3.3.1	Spa:
[19] mvtnorm_1.0-5	expm_0.999-0	dplyr_0.5.0	stringr_1.1.0	MatrixModels_0.4-1	gri
[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	pbk:

[37] testit\_0.5 colorspace\_1.2-6 quantreg\_5.26 stringi\_1.1.1 lazyeval\_0.2.0

mun