Report for the Markov model (cohort state-transition model)

Results from the paper

These two tables are from the result part of the paper by Yaqin Si.

```r
strategy_names <- c("strategy1", "strategy2", "strategy3")
# QALY
QALY <- data.frame("est" = c(498,691,654),
                   "LB" = c(103,233,105),
                   "UB" = c(894,194,1108))
rownames(QALY) <- strategy_names
# Prevent CVD events
num_CVD <- data.frame("est" = c(298,374,346),
                   "LB" = c(155,181,154),
                   "UB" = c(441,567,538))
rownames(num_CVD) <- strategy_names
```

Table 1: Increased QALY with no screening

	est	LB	UB
strategy1	498	103	894
strategy2	691	233	194
strategy3	654	105	1108

Table 2: Prevent CVD events

	est	LB	UB
strategy1	298	155	441
strategy2	374	181	567
strategy3	346	154	538

Part I. General population (without CVD)

Markov model

```
library(readr)
rate_data <- read_csv("data/ghdx_data.csv")
print(xtable(data.frame(rate_data),digits=c(0,0,0,6,6,6),
      caption = "Data from Global Health Data Exchange"),
      caption.placement="top")
```

% latex table generated in R 3.6.3 by xtable 1.8-4 package % Sat Jan 16 01:08:09 2021

Table 3: Data from Global Health Data Exchange

	index	sex	incidence	death_CVD	death_nonCVD
1	40	male	0.003888	0.000819	0.002494
2	45	male	0.006729	0.001340	0.003399
3	50	male	0.010564	0.002302	0.004951
4	55	male	0.015291	0.003665	0.007282
5	60	male	0.022078	0.006404	0.011159
6	65	male	0.030980	0.011155	0.016946
7	70	male	0.043589	0.019978	0.026305
8	40	female	0.004545	0.000351	0.001137
9	45	female	0.007094	0.000643	0.001620
10	50	female	0.010133	0.001206	0.002475
11	55	female	0.013734	0.002014	0.003705
12	60	female	0.018272	0.003872	0.005850
13	65	female	0.023744	0.006996	0.009060
14	70	female	0.033907	0.013398	0.014907

```
## General setup
source("./function/transform_func.R")
# rate_data <- rate_data[1:7,]
n_t <- 10   # time horizon, number of cycles
# S1: live; S2: cvd; S3: cvdth; S4: oth_death
v_names_states <- c("S1", "S2", "S3", "S4")
n_states    <- length(v_names_states)   # number of health states
v_names_str <- c("Strategy0","Strategy1", "Strategy2", "Strategy3") # store the strategy names
n_str       <- length(v_names_str)      # number of strategies

# Health utilities
out_cvd_free <- 1   # utility when being S1
out_cvd <- 0.9   # utility when being S2
out_dth <-  0   # utility when being S3 and S4 together
out_trans_to_cvd <- -0.038    # TODO

uti_values <- c(out_cvd_free, out_cvd, out_dth, out_dth)

HR_cvdhistory_cvd <-    1.37
HR_cvdhistory_cvdth <- 3.12
HR_high_live_cvdth <-   1.17
```

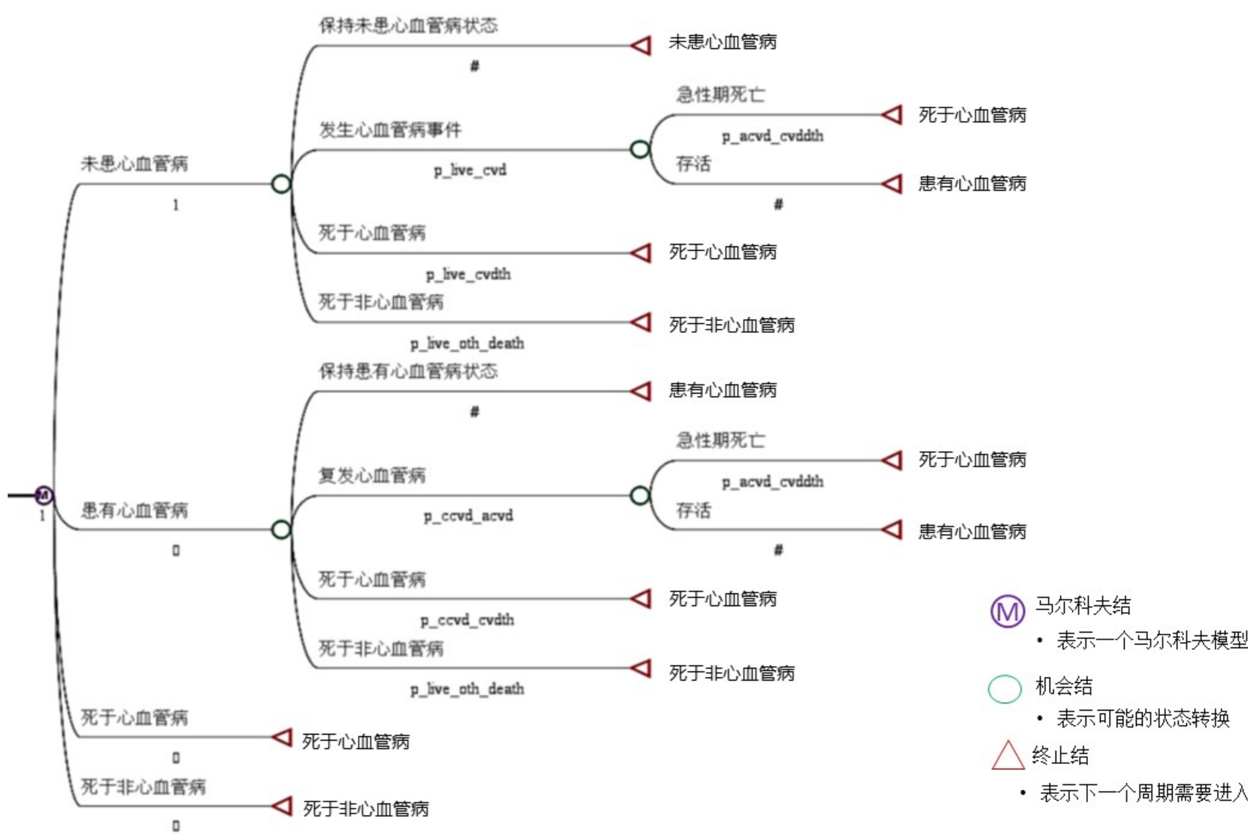
```
p_live_oth_death <- rate_to_prob(r=rate_data$death_nonCVD,t = 1)
p_live_cvd <- rate_to_prob(r=rate_data$incidence, t=1)
p_live_cvdth <- rate_to_prob(r=rate_data$death_CVD, t=1)
# transition probability from S2 to S3
p_ccvd_acvd <- rate_to_prob(rate_data$incidence*HR_cvdhistory_cvd, t=1)
p_ccvd_cvdth <- rate_to_prob(rate_data$death_CVD*HR_cvdhistory_cvdth,t=1)
set.seed(100)
p_acvd_cvdth <- rep(runif(1,min=0.02,max=0.1),length=length(p_live_cvd))
```

Component 1: A transition probability matrix P_t

状态转换概率矩阵

状态	未患心血管病	患有心血管病	死于心血管病	死于非心血管病
未患心血管病	P4	P1	P2	P3
患有心血管病		P6	P5	P3

$$P_t = \begin{Bmatrix} p_{[1,1,t]} & p_{[1,2,t]} & p_{[1,3,t]} & p_{[1,4,t]} \\ p_{[2,1,t]} & p_{[2,2,t]} & p_{[2,3,t]} & p_{[2,4,t]} \\ p_{[3,1,t]} & p_{[3,2,t]} & p_{[3,3,t]} & p_{[3,4,t]} \\ p_{[4,1,t]} & p_{[4,2,t]} & p_{[4,3,t]} & p_{[4,4,t]} \end{Bmatrix}$$



Thus,

$P4 = 1 - P1 - P2 - P3$

$P1 = p\_live\_cvd * (1 - p\_acvd\_cvdth)$

$P2 = p\_live\_cvdth + p\_live\_cvd * p\_acvd\_cvdth$

$P3 = p\_live\_oth\_death$

$P6 = 1 - (p\_ccvd\_cvdth + p\_ccvd\_acvd * p\_acvd\_cvdth) - p\_live\_oth\_death$

$P5 = p\_ccvd\_cvdth + p\_ccvd\_acvd * p\_acvd\_cvdth$

In what follows, an example for the groups of male patients, aging from 40 to 45 is illustrated.

```
###################### Construct state-transition models for Strategy1 #####################
#### Create transition arrays ####
a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd[1]*(1-p_acvd_cvdth[1]) +
                               p_live_cvdth[1]*p_live_cvd[1]*p_acvd_cvdth[1] +
                               p_live_oth_death[1])
a_P["S1", "S2", 1:5]  <- p_live_cvd[1]*(1-p_acvd_cvdth[1])
a_P["S1", "S3", 1:5]   <- p_live_cvdth[1]*p_live_cvd[1]*p_acvd_cvdth[1]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[1]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[1]-
  (p_ccvd_cvdth[1]+p_ccvd_acvd[1]*p_acvd_cvdth[1])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[1]+
  p_ccvd_acvd[1]*p_acvd_cvdth[1]
a_P["S2", "S4", 1:5] <- p_live_oth_death[1]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd[1+1]*(1-p_acvd_cvdth[1+1])+
                               p_live_cvdth[1+1]*p_live_cvd[1+1]*p_acvd_cvdth[1+1] +
                               p_live_oth_death[1+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd[1+1]*(1-p_acvd_cvdth[1+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth[1+1]*p_live_cvd[1+1]*p_acvd_cvdth[1+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[1+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[1+1]-
  (p_ccvd_cvdth[1+1]+p_ccvd_acvd[1+1]*p_acvd_cvdth[1+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[1+1]+p_ccvd_acvd[1+1]*p_acvd_cvdth[1+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[1+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
a_P
```

```
## , , 1
##
##            S1          S2           S3          S4
## S1 0.9938017 0.003707301 1.417524e-07 0.002490893
## S2 0.0000000 0.994720043 2.789064e-03 0.002490893
```

```
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 2
##
##           S1          S2           S3          S4
## S1 0.9938017 0.003707301 1.417524e-07 0.002490893
## S2 0.0000000 0.994720043 2.789064e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 3
##
##           S1          S2           S3          S4
## S1 0.9938017 0.003707301 1.417524e-07 0.002490893
## S2 0.0000000 0.994720043 2.789064e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 4
##
##           S1          S2           S3          S4
## S1 0.9938017 0.003707301 1.417524e-07 0.002490893
## S2 0.0000000 0.994720043 2.789064e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 5
##
##           S1          S2           S3          S4
## S1 0.9938017 0.003707301 1.417524e-07 0.002490893
## S2 0.0000000 0.994720043 2.789064e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 6
##
##           S1          S2           S3         S4
## S1 0.9901992 0.006407162 4.007247e-07 0.00339323
## S2 0.0000000 0.992025236 4.581534e-03 0.00339323
## S3 0.0000000 0.000000000 1.000000e+00 0.00000000
## S4 0.0000000 0.000000000 0.000000e+00 1.00000000
##
## , , 7
##
##           S1          S2           S3         S4
## S1 0.9901992 0.006407162 4.007247e-07 0.00339323
## S2 0.0000000 0.992025236 4.581534e-03 0.00339323
## S3 0.0000000 0.000000000 1.000000e+00 0.00000000
## S4 0.0000000 0.000000000 0.000000e+00 1.00000000
##
## , , 8
##
##           S1          S2           S3         S4
```

```
## S1 0.9901992 0.006407162 4.007247e-07 0.00339323
## S2 0.0000000 0.992025236 4.581534e-03 0.00339323
## S3 0.0000000 0.000000000 1.000000e+00 0.00000000
## S4 0.0000000 0.000000000 0.000000e+00 1.00000000
##
## , , 9
##
##           S1          S2           S3         S4
## S1 0.9901992 0.006407162 4.007247e-07 0.00339323
## S2 0.0000000 0.992025236 4.581534e-03 0.00339323
## S3 0.0000000 0.000000000 1.000000e+00 0.00000000
## S4 0.0000000 0.000000000 0.000000e+00 1.00000000
##
## , , 10
##
##           S1          S2           S3         S4
## S1 0.9901992 0.006407162 4.007247e-07 0.00339323
## S2 0.0000000 0.992025236 4.581534e-03 0.00339323
## S3 0.0000000 0.000000000 1.000000e+00 0.00000000
## S4 0.0000000 0.000000000 0.000000e+00 1.00000000
```

Component 2: The cohort trace matrix M

```
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
# TODO: half-cycle correction
corr_matrix <- matrix(1,nrow = 11,ncol = 4)
corr_matrix[1,] <- rep(0.5,4)
corr_matrix[11,] <- rep(0.5,4)
corr_matrix
```

```
##       [,1] [,2] [,3] [,4]
##  [1,]  0.5  0.5  0.5  0.5
##  [2,]  1.0  1.0  1.0  1.0
##  [3,]  1.0  1.0  1.0  1.0
##  [4,]  1.0  1.0  1.0  1.0
##  [5,]  1.0  1.0  1.0  1.0
##  [6,]  1.0  1.0  1.0  1.0
##  [7,]  1.0  1.0  1.0  1.0
##  [8,]  1.0  1.0  1.0  1.0
##  [9,]  1.0  1.0  1.0  1.0
## [10,]  1.0  1.0  1.0  1.0
## [11,]  0.5  0.5  0.5  0.5
```

```
m_M_corr <- m_M*corr_matrix
m_M_corr
```

```
##           S1          S2           S3          S4
## 0  0.5000000 0.000000000 0.000000e+00 0.000000000
## 1  0.9938017 0.003707301 1.417524e-07 0.002490893
## 2  0.9876417 0.007372048 1.062253e-05 0.004975580
## 3  0.9815200 0.010994609 3.132364e-05 0.007454053
## 4  0.9754362 0.014575348 6.212744e-05 0.009926300
## 5  0.9693901 0.018114626 1.029173e-04 0.012392312
## 6  0.9598894 0.024181206 1.862985e-04 0.015743143
## 7  0.9504817 0.030138534 2.974702e-04 0.019082321
## 8  0.9411662 0.035988076 4.359318e-04 0.022409791
## 9  0.9319420 0.041731284 6.011895e-04 0.025725500
## 10 0.4614041 0.023684796 3.963781e-04 0.014514699
```

Table 4: Incidence rate

Item		CVD incidence(HR)	CVD cause-specific mortality (HR)
Strategy 1	Low risk	0.63	1
	Medium risk	1.56	1
	High risk	1.6	1.7
Strategy 2	Low risk	0.43	1
	Medium risk	0.97	1
	High risk	2.06	1.7
Strategy 3	Low risk	0.63	1
	Medium risk	1.09	1
	High risk	2.11	1.7
Intervention	Weight control	0.93	0.93
	Smoke cession	0.85	0.72
	Salt reduction	0.81	0.66
Medication	Statin and antihypertensive	0.7	0.82

```
HR_l_stg1   <- 0.63
HR_m_stg1   <- 1.56
HR_h_stg1   <- 1.6

HR_l_stg2   <- 0.43
HR_m_stg2   <- 0.97
HR_h_stg2   <- 2.06

HR_l_stg3   <- 0.45
HR_m_stg3   <- 1.09
HR_h_stg3   <- 2.11
# lifestyle intervention for medium risk and above
HR_smk_cvd  <-  0.85
HR_smk_cvdth    <-  0.72
HR_salt_cvd <-  0.81
HR_salt_cvdth   <-  0.66
HR_wtc_cvd  <-  0.93
HR_wtc_dth  <-  0.93
# treatment intervention for high risk (additional)
HR_hpt_lip_cvd   <-  0.7
HR_hpt_lip_cvdth <- 0.82
```

Calculation of the QALY under the Strategy 1

An example for a male patient aged 40-45 years old under low level after screening

```
p_live_cvd_l <- ProbFactor(p_live_cvd,HR_l_stg1)
p_live_cvd_m <- ProbFactor(p_live_cvd,HR_m_stg1*
                             HR_smk_cvd*HR_salt_cvd*HR_wtc_cvd)  # lifestyle intervention
p_live_cvd_h <- ProbFactor(p_live_cvd,HR_h_stg1*
                             HR_smk_cvdth*HR_salt_cvdth*HR_wtc_dth*     # lifestyle intervention
                             HR_hpt_lip_cvdth)    # treatment intervention
```

```r
# transition probability to death
p_live_cvdth_l <- ProbFactor(p_live_cvdth,1)     # equal
p_live_cvdth_m <- ProbFactor(p_live_cvdth,1*
                               HR_smk_cvd*HR_salt_cvd*HR_wtc_cvd)  # lifestyle intervention
p_live_cvdth_h <- ProbFactor(p_live_cvdth,1.7*
                               HR_smk_cvdth*HR_salt_cvdth*HR_wtc_dth* # lifestyle intervention
                               HR_hpt_lip_cvdth) # treatment intervention
# again get cvd
p_ccvd_acvd <- ProbFactor(p_live_cvd,HR_cvdhistory_cvd)
p_ccvd_cvdth <- ProbFactor(p_live_cvdth,HR_cvdhistory_cvdth)
```

状态转换概率矩阵

状态	未患心血管病	患有心血管病	死于心血管病	死于非心血管病
未患心血管病	P4	P1	P2	P3
患有心血管病		P6	P5	P3

Thus, we take the example of individuals in the low level

$\underline{P4} = 1 - P1 - P2 - P3$

$\underline{P1} = p\_live\_cvd\_l * (1 - p\_acvd\_cvdth)$

$\underline{P2} = p\_live\_cvdth\_l + p\_live\_cvd\_l * p\_acvd\_cvdth$

$P3 = p\_live\_oth\_death$

$P6 = 1 - (p\_ccvd\_cvdth + p\_ccvd\_acvd * p\_acvd\_cvdth) - p\_live\_oth\_death$

$P5 = p\_ccvd\_cvdth + p\_ccvd\_acvd * p\_acvd\_cvdth$

We say that the screening strategy will have an influence on the first line of the transition matrix.

```r
###################### Construct state-transition models for Strategy1 #####################
#### Create transition arrays ####
a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_l[1]*(1-p_acvd_cvdth[1]) +
                               p_live_cvdth_l[1]*p_live_cvd_l[1]*p_acvd_cvdth[1] +
                               p_live_oth_death[1])

a_P["S1", "S2", 1:5]  <- p_live_cvd_l[1]*(1-p_acvd_cvdth[1])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_l[1]*p_live_cvd_l[1]*p_acvd_cvdth[1]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[1]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[1]-
  (p_ccvd_cvdth[1]+p_ccvd_acvd[1]*p_acvd_cvdth[1])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[1]+
  p_ccvd_acvd[1]*p_acvd_cvdth[1]
a_P["S2", "S4", 1:5] <- p_live_oth_death[1]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1
```

```
## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_l[1+1]*(1-p_acvd_cvdth[1+1])+
                               p_live_cvdth_l[1+1]*p_live_cvd_l[1+1]*p_acvd_cvdth[1+1] +
                               p_live_oth_death[1+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_l[1+1]*(1-p_acvd_cvdth[1+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_l[1+1]*p_live_cvd_l[1+1]*p_acvd_cvdth[1+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[1+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[1+1]-
  (p_ccvd_cvdth[1+1]+p_ccvd_acvd[1+1]*p_acvd_cvdth[1+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[1+1]+p_ccvd_acvd[1+1]*p_acvd_cvdth[1+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[1+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
a_P
```

```
## , , 1
##
##           S1          S2           S3          S4
## S1 0.9951701 0.002338958 8.943242e-08 0.002490893
## S2 0.0000000 0.994722422 2.786685e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 2
##
##           S1          S2           S3          S4
## S1 0.9951701 0.002338958 8.943242e-08 0.002490893
## S2 0.0000000 0.994722422 2.786685e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 3
##
##           S1          S2           S3          S4
## S1 0.9951701 0.002338958 8.943242e-08 0.002490893
## S2 0.0000000 0.994722422 2.786685e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 4
##
##           S1          S2           S3          S4
## S1 0.9951701 0.002338958 8.943242e-08 0.002490893
## S2 0.0000000 0.994722422 2.786685e-03 0.002490893
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 5
##
##           S1          S2           S3          S4
## S1 0.9951701 0.002338958 8.943242e-08 0.002490893
## S2 0.0000000 0.994722422 2.786685e-03 0.002490893
```

```
## S3 0.0000000 0.000000000 1.000000e+00 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 6
##
##          S1          S2           S3         S4
## S1 0.99256 0.004046553 2.530846e-07 0.00339323
## S2 0.00000 0.992031641 4.575129e-03 0.00339323
## S3 0.00000 0.000000000 1.000000e+00 0.00000000
## S4 0.00000 0.000000000 0.000000e+00 1.00000000
##
## , , 7
##
##          S1          S2           S3         S4
## S1 0.99256 0.004046553 2.530846e-07 0.00339323
## S2 0.00000 0.992031641 4.575129e-03 0.00339323
## S3 0.00000 0.000000000 1.000000e+00 0.00000000
## S4 0.00000 0.000000000 0.000000e+00 1.00000000
##
## , , 8
##
##          S1          S2           S3         S4
## S1 0.99256 0.004046553 2.530846e-07 0.00339323
## S2 0.00000 0.992031641 4.575129e-03 0.00339323
## S3 0.00000 0.000000000 1.000000e+00 0.00000000
## S4 0.00000 0.000000000 0.000000e+00 1.00000000
##
## , , 9
##
##          S1          S2           S3         S4
## S1 0.99256 0.004046553 2.530846e-07 0.00339323
## S2 0.00000 0.992031641 4.575129e-03 0.00339323
## S3 0.00000 0.000000000 1.000000e+00 0.00000000
## S4 0.00000 0.000000000 0.000000e+00 1.00000000
##
## , , 10
##
##          S1          S2           S3         S4
## S1 0.99256 0.004046553 2.530846e-07 0.00339323
## S2 0.00000 0.992031641 4.575129e-03 0.00339323
## S3 0.00000 0.000000000 1.000000e+00 0.00000000
## S4 0.00000 0.000000000 0.000000e+00 1.00000000
```

```r
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
```

```
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_l <- sum(m_M_corr*mat)  # is the calculated QALY for the assumed patient under low level
print(m_M_corr*mat)
```

```
##           S1          S2 S3 S4
## 0  0.5000000 0.000000000  0  0
## 1  0.9951701 0.002105062  0  0
## 2  0.9903634 0.004188847  0  0
## 3  0.9855801 0.006251516  0  0
## 4  0.9808198 0.008293230  0  0
## 5  0.9760825 0.010314149  0  0
## 6  0.9688204 0.013786754  0  0
## 7  0.9616123 0.017205242  0  0
## 8  0.9544579 0.020570238  0  0
## 9  0.9473567 0.023882365  0  0
## 10 0.4701542 0.013571119  0  0
```

Table 5: QALY for the calculation of utility values (a male patient aged 40-45)

Stratification	QALY
Low risk	9.8505857
Medium risk	9.8421437
High risk	9.8517456

Health utilities of Strategy1

To calculate the require QALY for both male and female patients under different ages, construct a vector to and run a loop save the calculated result

```
QALY_h <- matrix(NA,nrow=14,ncol=1)
# i specify the group of male patients (age)
for(i in 1:6){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
               dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_h[i]*(1-p_acvd_cvdth[i]) +
                              p_live_cvdth_h[i]*p_live_cvd_h[i]*p_acvd_cvdth[i] +
                              p_live_oth_death[i])

a_P["S1", "S2", 1:5]  <- p_live_cvd_h[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_h[i]*p_live_cvd_h[i]*p_acvd_cvdth[i]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_h[i+1]*(1-p_acvd_cvdth[i+1])+
                              p_live_cvdth_h[i+1]*p_live_cvd_h[i+1]*p_acvd_cvdth[i+1] +
                              p_live_oth_death[i+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_h[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_h[i+1]*p_live_cvd_h[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
```

```
  mat[j,] <- uti_values
}
QALY_h[i] <- sum(m_M_corr*mat)
}

# the group of the male patients aged 70-75
a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_h[7]*(1-p_acvd_cvdth[7]) +
                               p_live_cvdth_h[7]*p_live_cvd_h[7]*p_acvd_cvdth[7] +
                               p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_h[7]*(1-p_acvd_cvdth[7])
a_P["S1", "S3", 1:10]   <- p_live_cvdth_h[7]*p_live_cvd_h[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_h[7] <- sum(m_M_corr*mat)
#-------------------------------------------------------------------------------------
# i specify the group of female patients (age)
for(i in 8:13){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_h[i]*(1-p_acvd_cvdth[i]) +
                               p_live_cvdth_h[i]*p_live_cvd_h[i]*p_acvd_cvdth[i] +
                               p_live_oth_death[i])

a_P["S1", "S2", 1:5]  <- p_live_cvd_h[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_h[i]*p_live_cvd_h[i]*p_acvd_cvdth[i]
```

```
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_h[i+1]*(1-p_acvd_cvdth[i+1])+
                               p_live_cvdth_h[i+1]*p_live_cvd_h[i+1]*p_acvd_cvdth[i+1] +
                               p_live_oth_death[i+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_h[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_h[i+1]*p_live_cvd_h[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_h[i] <- sum(m_M_corr*mat)
}

a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_h[7]*(1-p_acvd_cvdth[7]) +
                               p_live_cvdth_h[7]*p_live_cvd_h[7]*p_acvd_cvdth[7] +
                               p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_h[7]*(1-p_acvd_cvdth[7])
a_P["S1", "S3", 1:10]   <- p_live_cvdth_h[7]*p_live_cvd_h[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
```

```
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_h[14] <- sum(m_M_corr*mat)
```

```
QALY_m <- matrix(NA,nrow=14,ncol=1)
# i specify the group of male patients (age)
for(i in 1:6){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
               dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_m[i]*(1-p_acvd_cvdth[i]) +
                              p_live_cvdth_m[i]*p_live_cvd_m[i]*p_acvd_cvdth[i] +
                              p_live_oth_death[i])

a_P["S1", "S2", 1:5]  <- p_live_cvd_m[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_m[i]*p_live_cvd_m[i]*p_acvd_cvdth[i]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_m[i+1]*(1-p_acvd_cvdth[i+1])+
                              p_live_cvdth_m[i+1]*p_live_cvd_m[i+1]*p_acvd_cvdth[i+1] +
                              p_live_oth_death[i+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_m[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_m[i+1]*p_live_cvd_m[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
```

```
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:9){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_m[i] <- sum(m_M_corr*mat)
}

# the group of the male patients aged 70-75
a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_m[7]*(1-p_acvd_cvdth[7]) +
                               p_live_cvdth_m[7]*p_live_cvd_m[7]*p_acvd_cvdth[7] +
                               p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_m[7]*(1-p_acvd_cvdth[7])
a_P["S1", "S3", 1:10]   <- p_live_cvdth_m[7]*p_live_cvd_m[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
```

```
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_m[7] <- sum(m_M_corr*mat)
#-------------------------------------------------------------------------------
# i specify the group of female patients (age)
for(i in 8:13){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
               dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_m[i]*(1-p_acvd_cvdth[i]) +
                              p_live_cvdth_m[i]*p_live_cvd_m[i]*p_acvd_cvdth[i] +
                              p_live_oth_death[i])

a_P["S1", "S2", 1:5]  <- p_live_cvd_m[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_m[i]*p_live_cvd_m[i]*p_acvd_cvdth[i]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_m[i+1]*(1-p_acvd_cvdth[i+1])+
                              p_live_cvdth_m[i+1]*p_live_cvd_m[i+1]*p_acvd_cvdth[i+1] +
                              p_live_oth_death[i+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_m[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_m[i+1]*p_live_cvd_m[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
```

```
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_m[i] <- sum(m_M_corr*mat)
}

a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_m[7]*(1-p_acvd_cvdth[7]) +
                              p_live_cvdth_m[7]*p_live_cvd_m[7]*p_acvd_cvdth[7] +
                              p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_m[7]*(1-p_acvd_cvdth[7])
a_P["S1", "S3", 1:10]   <- p_live_cvdth_m[7]*p_live_cvd_m[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_m[14] <- sum(m_M_corr*mat)
```

```
QALY_l <- matrix(NA,nrow=14,ncol=1)
# i specify the group of male patients (age)
for(i in 1:6){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_l[i]*(1-p_acvd_cvdth[i]) +
                              p_live_cvdth_l[i]*p_live_cvd_l[i]*p_acvd_cvdth[i] +
                              p_live_oth_death[i])
```

```
a_P["S1", "S2", 1:5]  <- p_live_cvd_l[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_l[i]*p_live_cvd_l[i]*p_acvd_cvdth[i]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_l[i+1]*(1-p_acvd_cvdth[i+1])+
                               p_live_cvdth_l[i+1]*p_live_cvd_l[i+1]*p_acvd_cvdth[i+1] +
                               p_live_oth_death[i+1])
a_P["S1", "S2", 6:10]  <- p_live_cvd_l[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_l[i+1]*p_live_cvd_l[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_l[i] <- sum(m_M_corr*mat)
}

# the group of the male patients aged 70-75
a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_l[7]*(1-p_acvd_cvdth[7]) +
                               p_live_cvdth_l[7]*p_live_cvd_l[7]*p_acvd_cvdth[7] +
                               p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_l[7]*(1-p_acvd_cvdth[7])
```

```
a_P["S1", "S3", 1:10]   <- p_live_cvdth_l[7]*p_live_cvd_l[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_l[7] <- sum(m_M_corr*mat)
#---------------------------------------------------------------------------------
# i specify the group of female patients (age)
for(i in 8:13){
  a_P <- array(0, dim      = c(n_states, n_states, 10),
               dimnames = list(v_names_states, v_names_states, 1:10))
## From S1, S2, S3, S4
a_P["S1", "S1", 1:5]   <- 1-(p_live_cvd_l[i]*(1-p_acvd_cvdth[i]) +
                              p_live_cvdth_l[i]*p_live_cvd_l[i]*p_acvd_cvdth[i] +
                              p_live_oth_death[i])

a_P["S1", "S2", 1:5]  <- p_live_cvd_l[i]*(1-p_acvd_cvdth[i])
a_P["S1", "S3", 1:5]   <- p_live_cvdth_l[i]*p_live_cvd_l[i]*p_acvd_cvdth[i]
a_P["S1", "S4", 1:5]   <- p_live_oth_death[i]
a_P["S2", "S1", 1:5] <- 0
a_P["S2", "S2", 1:5] <- 1-p_live_oth_death[i]-
  (p_ccvd_cvdth[i]+p_ccvd_acvd[i]*p_acvd_cvdth[i])
a_P["S2", "S3", 1:5] <- p_ccvd_cvdth[i]+
  p_ccvd_acvd[i]*p_acvd_cvdth[i]
a_P["S2", "S4", 1:5] <- p_live_oth_death[i]
a_P["S3", "S3", 1:5] <- 1
a_P["S4", "S4", 1:5] <- 1

## From S1, S2, S3, S4
a_P["S1", "S1", 6:10] <-  1-(p_live_cvd_l[i+1]*(1-p_acvd_cvdth[i+1])+
                              p_live_cvdth_l[i+1]*p_live_cvd_l[i+1]*p_acvd_cvdth[i+1] +
                              p_live_oth_death[i+1])
```

```
a_P["S1", "S2", 6:10]  <- p_live_cvd_l[i+1]*(1-p_acvd_cvdth[i+1])
a_P["S1", "S3", 6:10]  <- p_live_cvdth_l[i+1]*p_live_cvd_l[i+1]*p_acvd_cvdth[i+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[i+1]
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- 1-p_live_oth_death[i+1]-
  (p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1])
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[i+1]+p_ccvd_acvd[i+1]*p_acvd_cvdth[i+1]
a_P["S2", "S4", 6:10] <-  p_live_oth_death[i+1]
a_P["S3", "S3", 6:10] <- 1
a_P["S4", "S4", 6:10] <- 1
## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_l[i] <- sum(m_M_corr*mat)
}

a_P <- array(0, dim      = c(n_states, n_states, 10),
                dimnames = list(v_names_states, v_names_states, 1:10))
a_P["S1", "S1", 1:10]   <- 1-(p_live_cvd_l[7]*(1-p_acvd_cvdth[7]) +
                              p_live_cvdth_l[7]*p_live_cvd_l[7]*p_acvd_cvdth[7] +
                              p_live_oth_death[7])

a_P["S1", "S2", 1:10]  <- p_live_cvd_l[7]*(1-p_acvd_cvdth[7])
a_P["S1", "S3", 1:10]   <- p_live_cvdth_l[7]*p_live_cvd_l[7]*p_acvd_cvdth[7]
a_P["S1", "S4", 1:10]   <- p_live_oth_death[7]
a_P["S2", "S1", 1:10] <- 0
a_P["S2", "S2", 1:10] <- 1-p_live_oth_death[7]-
  (p_ccvd_cvdth[7]+p_ccvd_acvd[7]*p_acvd_cvdth[7])
a_P["S2", "S3", 1:10] <- p_ccvd_cvdth[7]+
  p_ccvd_acvd[7]*p_acvd_cvdth[7]
a_P["S2", "S4", 1:10] <- p_live_oth_death[7]
a_P["S3", "S3", 1:10] <- 1
a_P["S4", "S4", 1:10] <- 1

## Initial state vector: All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)
## Initialize cohort trace for Markov model
m_M <- matrix(0,nrow     = (n_t+1), ncol = n_states,
              dimnames = list(0:(n_t), v_names_states))
m_M[1, ] <- v_s_init
for(t in 1:10){
```

```
  m_M[t + 1, ]       <- m_M[t, ]      %*% a_P[, , t]
}
m_M_corr <- m_M*corr_matrix
# calculation of the QALY
mat <- matrix(NA, nrow=nrow(m_M_corr),ncol = 4)
for (j in 1:nrow(m_M_corr)){
  mat[j,] <- uti_values
}
QALY_l[14] <- sum(m_M_corr*mat)
```

```
print(xtable(data.frame(cbind(rate_data,QALY_h,QALY_m,QALY_l)),digits=c(0,0,0,6,6,6,4,4,4),
      caption = "QALY under the screening of Strategy 1"),
      caption.placement="top")
```

% latex table generated in R 3.6.3 by xtable 1.8-4 package % Sat Jan 16 01:08:10 2021

Table 6: QALY under the screening of Strategy 1

	index	sex	incidence	death_CVD	death_nonCVD	QALY_h	QALY_m	QALY_l
1	40	male	0.003888	0.000819	0.002494	9.8517	9.3594	9.8506
2	45	male	0.006729	0.001340	0.003399	9.7895	9.2982	9.7875
3	50	male	0.010564	0.002302	0.004951	9.6903	9.2011	9.6870
4	55	male	0.015291	0.003665	0.007282	9.5382	9.0535	9.5331
5	60	male	0.022078	0.006404	0.011159	9.2965	8.8168	9.2882
6	65	male	0.030980	0.011155	0.016946	8.9297	8.4546	8.9159
7	70	male	0.043589	0.019978	0.026305	8.5562	8.4069	8.5370
8	40	female	0.004545	0.000351	0.001137	9.9226	9.9121	9.9213
9	45	female	0.007094	0.000643	0.001620	9.8859	9.8697	9.8839
10	50	female	0.010133	0.001206	0.002475	9.8285	9.8052	9.8257
11	55	female	0.013734	0.002014	0.003705	9.7421	9.7086	9.7380
12	60	female	0.018272	0.003872	0.005850	9.6021	9.5529	9.5960
13	65	female	0.023744	0.006996	0.009060	9.3772	9.3006	9.3676
14	70	female	0.033907	0.013398	0.014907	8.5562	8.4069	8.5370