

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.

```
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

Data and parameters

```
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 00:45:23 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

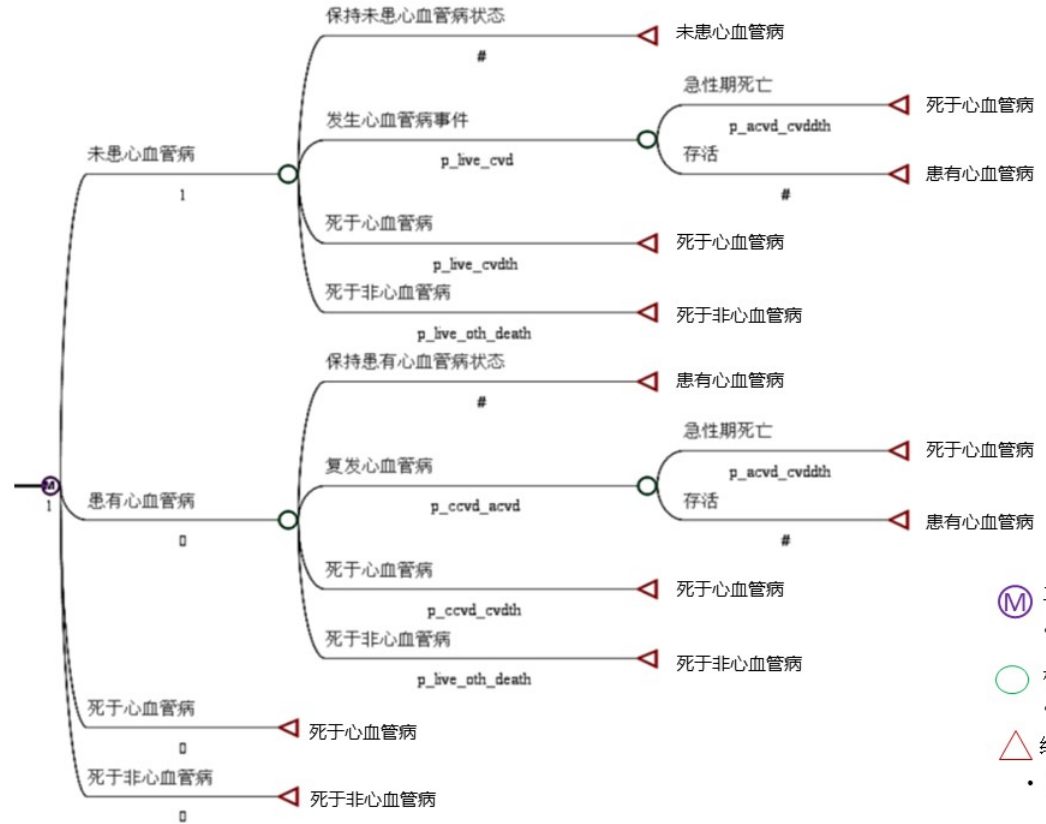
p_live_oth_death <- rate_to_prob(r=rate_data$death_nonCVD, t = 1)
p_live_cvd <- rate_to_prob(r=rate_data$incidence, t=1)
```

```

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

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

Thus,

$$P4 = 1 - P1 - P2 - P3$$

$$P1 = p_live_cvd * (1 - p_acvd_cvdth)$$

$$P2 = p_live_cvdth + p_live_cvd * p_acvd_cvdth$$

$$P3 = p_live_oth_death$$

$$P6 = 1 - (p_ccvd_cvdth + p_ccvd_acvd * p_acvd_cvdth) - p_live_oth_death$$

$$P5 = p_ccvd_cvdth + p_ccvd_acvd * p_acvd_cvdth$$

Strategy 0 (a male 40-45)

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
# is the constructed transition matrix in 10 cycles
# depends on the specific population (age and gender)
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 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000
##
## , , 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 0.000000000
## S4 0.0000000 0.000000000 0.000000e+00 1.000000000

```

```
##
## , , 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]
}
m_M
```

```
##          S1          S2          S3          S4
## 0 1.0000000 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 0.9228083 0.047369591 7.927563e-04 0.029029397
```

This matrix is the trace matrix of the specific population (male, 40-45) during these 10 cycles. The whole cohort starts in $S1$ state and transitions to the rest of the states over time.

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

```
# calculation of the per CVD prevented events
```

```
CVD_prevented <- sum(m_M[,1]*p_live_cvd[1])
```

```
CVD_prevented
```

```
## [1] 0.04118741
```

Strategy 1 (a male 40-45)

```
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
```

```
# 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

$$P4 = 1 - P1 - P2 - P3$$

$$P1 = p_live_cvd_l * (1 - p_acvd_cvdth)$$

$$P2 = p_live_cvdth_l + p_live_cvd_l * p_acvd_cvdth$$

$$P3 = p_live_oth_death$$

$$P6 = 1 - (p_ccvd_cvdth + p_ccvd_acvd * p_acvd_cvdth) - p_live_oth_death$$

$$P5 = p_ccvd_cvdth + p_ccvd_acvd * p_acvd_cvdth$$

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

```
##### 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
```

```
## 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
```

```
##          S1          S2          S3          S4
## 0 1.0000000 0.000000000 0.000000e+00 0.000000000
## 1 0.9951701 0.002338958 8.943242e-08 0.002490893
## 2 0.9903634 0.004654274 6.696371e-06 0.004975580
## 3 0.9855801 0.006946129 1.975494e-05 0.007454063
## 4 0.9808198 0.009214701 3.919975e-05 0.009926339
## 5 0.9760825 0.011460165 6.496594e-05 0.012392408
## 6 0.9688204 0.015318616 1.176447e-04 0.015743367
## 7 0.9616123 0.019116935 1.879745e-04 0.019082777
## 8 0.9544579 0.022855820 2.756803e-04 0.022410617
## 9 0.9473567 0.026535961 3.804902e-04 0.025726867
## 10 0.9403083 0.030158042 5.021354e-04 0.029031509
```

This matrix is the trace matrix of the specific population (male, 40-45) during these 10 cycles under Strategy1. The whole cohort starts in $S1$ state and transitions to the rest of the states over time.

```
CVD_prevented_l <- sum(m_M[,1]*p_live_cvd_l[1])
CVD_prevented_l
```

```
## [1] 0.02619713
```

```
CVD_prevented_m <- sum(m_M[,1]*p_live_cvd_m[1])
CVD_prevented_m
```

```
## [1] 0.04114232
```

```
CVD_prevented_h <- sum(m_M[,1]*p_live_cvd_h[1])
CVD_prevented_h
```

```
## [1] 0.02414187
```

We perform the same procedure for all risk levels: low, medium and high, and then obtain the following tables for the health benefit results.

Table 5: prevented CVD (a male patient aged 40-45)

Stratification	perverted CVD events
Low risk	0.0261971
Medium risk	0.0411423
High risk	0.0241419

Health benefits of Strategy1

```

CVD_prevented_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]
  }
  CVD_prevented_h[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

# 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]
}
CVD_prevented_h[7] <- sum(m_M[,1]*p_live_cvd_h[7])
#-----
# 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]
}
CVD_prevented_h[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

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]
}
CVD_prevented_h[14] <- sum(m_M[,1]*p_live_cvd_h[14])

```

```

CVD_prevented_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 1:10){
    m_M[t + 1, ] <- m_M[t, ] %*% a_P[, , t]
  }
  CVD_prevented_m[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

# 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]
}
CVD_prevented_m[7] <- sum(m_M[,1]*p_live_cvd_h[7])

#-----
# 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]
}
CVD_prevented_m[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

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]
}
CVD_prevented_m[14] <- sum(m_M[,1]*p_live_cvd_h[14])

CVD_prevented_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]
  }
  CVD_prevented_l[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

# 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]
}
CVD_prevented_l[7] <- sum(m_M[,1]*p_live_cvd_h[7])

#-----
# 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]
}
CVD_prevented_l[i] <- sum(m_M[,1]*p_live_cvd_h[i])
}

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]
}
CVD_prevented_l[14] <- sum(m_M[,1]*p_live_cvd_h[14])

res <- data.frame(cbind("index"=rate_data$index,
  "sex"=rate_data$sex,
  "CVD_prevented_h"=CVD_prevented_h,

```

```

      "CVD_prevented_m"=CVD_prevented_m,
      "CVD_prevented_l"=CVD_prevented_l))

print(xtable(res,digits=c(0,0,0,4,4,4),
  caption = "prevented CVD events 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 00:45:24 2021

	index	sex	V3	V4	V5
1	40	male	0.0241418741114777	0.02392088550814	0.0241152147524632
2	45	male	0.0411977580213452	0.040575837118562	0.0411223796823456
3	50	male	0.0633906156178216	0.0619526626771687	0.063215276181939
4	55	male	0.0892169300114954	0.0863498492167005	0.0888645118763197
5	60	male	0.123598398830557	0.118079980101286	0.1229125728295
6	65	male	0.163583856805719	0.15373856110733	0.162341889585844
7	70	male	0.217135761953413	0.200865719238674	0.215059599394895
8	40	female	0.0283814498112105	0.0280892355621036	0.0283461766530984
9	45	female	0.0438372600085826	0.0431607623198179	0.0437552796109982
10	50	female	0.0617637548542279	0.0604407107161249	0.0616026727975055
11	55	female	0.0822147922467317	0.079874842475357	0.0819282634734733
12	60	female	0.106657199033764	0.102719143091753	0.106171503988571
13	65	female	0.1335248314275	0.1271005371714	0.132723889671539
14	70	female	0.169046209493589	0.156379530248852	0.167429859392378