

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 % Mon Jan 18 13:11:12 2021

	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

```
library(readr)
noStrategy_data <- read_csv("data/Normal_data.csv")
print(xtable(data.frame(noStrategy_data), digits=c(0,0,0,0),
  caption = "Distribution of the population"),
  caption.placement="top")
```

% latex table generated in R 3.6.3 by xtable 1.8-4 package % Mon Jan 18 13:11:12 2021

```
population_data <- readr::read_csv("data/Normal3Stra_data.csv")
population_data <- data.frame(population_data)
print(xtable(data.frame(population_data), digits=c(0,0,0,0,0,0,0),
  caption = "Distribution of the population under different strategies"), caption.placement="top")
```

% latex table generated in R 3.6.3 by xtable 1.8-4 package % Mon Jan 18 13:11:12 2021

Table 4: Distribution of the population

	index	sex	num
1	40	male	229
2	45	male	444
3	50	male	422
4	55	male	410
5	60	male	322
6	65	male	160
7	70	male	116
8	40	female	498
9	45	female	856
10	50	female	822
11	55	female	842
12	60	female	519
13	65	female	394
14	70	female	187

Table 5: Distribution of the population under different strategies

	index	sex	strategy	low	medium	high
1	40	male	strategy1	159	8	62
2	45	male	strategy1	173	64	207
3	50	male	strategy1	188	63	171
4	55	male	strategy1	200	89	121
5	60	male	strategy1	129	89	104
6	65	male	strategy1	71	42	47
7	70	male	strategy1	48	28	40
8	40	female	strategy1	444	6	48
9	45	female	strategy1	738	18	100
10	50	female	strategy1	677	20	125
11	55	female	strategy1	440	217	185
12	60	female	strategy1	216	164	139
13	65	female	strategy1	128	136	130
14	70	female	strategy1	65	55	67
15	40	male	strategy2	163	50	16
16	45	male	strategy2	212	168	64
17	50	male	strategy2	106	231	85
18	55	male	strategy2	35	210	165
19	60	male	strategy2	5	81	236
20	65	male	strategy2	1	15	144
21	70	male	strategy2	0	3	113
22	40	female	strategy2	478	17	3
23	45	female	strategy2	734	108	14
24	50	female	strategy2	537	238	47
25	55	female	strategy2	277	433	132
26	60	female	strategy2	44	282	193
27	65	female	strategy2	4	104	286
28	70	female	strategy2	0	23	164
29	40	male	strategy3	0	0	0
30	45	male	strategy3	0	0	0
31	50	male	strategy3	106	231	85
32	55	male	strategy3	35	210	165
33	60	male	strategy3	5	81	236
34	65	male	strategy3	1	15	144
35	70	male	strategy3	0	3	113
36	40	female	strategy3	0	0	0
37	45	female	strategy3	0	0	0
38	50	female	strategy3	537	238	47
39	55	female	strategy3	277	433	132
40	60	female	strategy3	44	282	193
41	65	female	strategy3	4	104	286
42	70	female	strategy3	0	23	164

```

## General setup
source("../function/transform_func.R")
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)

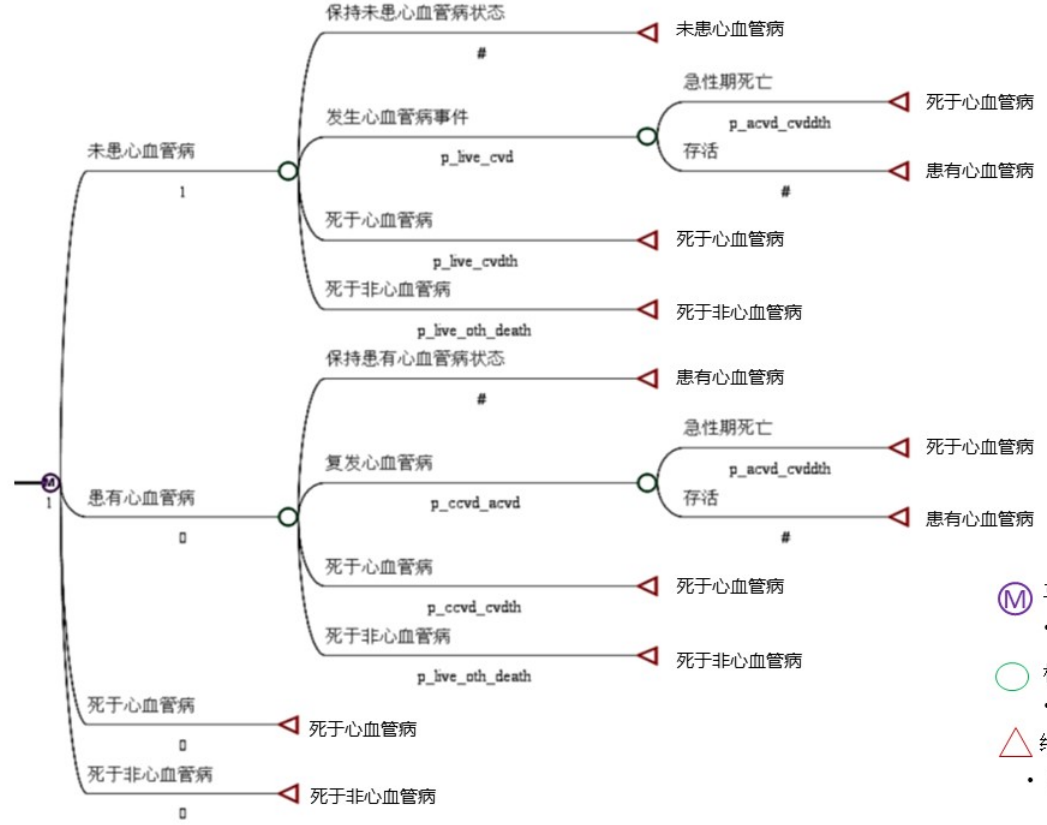
HR_cvdhistory_cvd <- 1.37
HR_cvdhistory_cvdth <- 3.12
HR_high_live_cvdth <- 1.17

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))

# 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

```

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 0.00000000
## 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]
}
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.

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

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

```
# calculation of the per CVD prevented events
CVD_prevented <- matrix(NA,nrow=14,ncol=1)

for(i in 1:14){
  CVD_prevented[i] <- sum(m_M[,1]*p_live_cvd[i])
}
CVD_prevented
```

```
##           [,1]
## [1,] 0.04118741
## [2,] 0.07118236
## [3,] 0.11153694
## [4,] 0.16106529
## [5,] 0.23176968
## [6,] 0.32378282
## [7,] 0.45271856
## [8,] 0.04813152
## [9,] 0.07502982
## [10,] 0.10700937
## [11,] 0.14477728
## [12,] 0.19217932
## [13,] 0.24905220
## [14,] 0.35385848
```

```
strategy3_noscren_CVD <- matrix(CVD_prevented[c(1,2,8,9)],ncol=2,nrow=2)
colnames(strategy3_noscren_CVD) <- c("male","female")
rownames(strategy3_noscren_CVD) <- c("40","45")
```

```
result_strategy0 <- matrix(NA,nrow=1,ncol=1)
colnames(result_strategy0) <- c("strategy0")

result_strategy0 <- sum(noStrategy_data$num * as.numeric(CVD_prevented))
result_strategy0
```

```
## [1] 895.191
```

This is the CVD events for the general population.

Table 6: 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

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_1 <- sum(m_M[,1]*p_live_cvd_1[1])
CVD_prevented_1
```

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

```
##          S1          S2          S3          S4
## 0  1.0000000 0.000000000 0.000000e+00 0.000000000
## 1  0.9938059 0.003703149 9.068984e-08 0.002490893
```

```
## 2 0.9876501 0.007363817 1.050033e-05 0.004975580
## 3 0.9815325 0.010982369 3.111054e-05 0.007454053
## 4 0.9754527 0.014559170 6.180395e-05 0.009926301
## 5 0.9694106 0.018094580 1.024642e-04 0.012392314
## 6 0.9599167 0.024154631 1.854979e-04 0.015743147
## 7 0.9505158 0.030105633 2.962545e-04 0.019082327
## 8 0.9412069 0.035949049 4.342354e-04 0.022409801
## 9 0.9319892 0.041686325 5.989483e-04 0.025725516
## 10 0.9228618 0.047318892 7.899076e-04 0.029029421
```

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

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

```
##           S1           S2           S3           S4
## 0 1.0000000 0.000000000 0.000000e+00 0.000000000
## 1 0.9953560 0.002153078 5.073306e-08 0.002490893
## 2 0.9907335 0.004284794 6.101180e-06 0.004975580
## 3 0.9861325 0.006395307 1.809181e-05 0.007454064
## 4 0.9815529 0.008484775 3.596355e-05 0.009926344
## 5 0.9769946 0.010553356 5.965774e-05 0.012392422
## 6 0.9700395 0.014109055 1.080810e-04 0.015743399
## 7 0.9631339 0.017610510 1.727711e-04 0.019082841
## 8 0.9562774 0.021058338 2.534798e-04 0.022410733
## 9 0.9494698 0.024453148 3.499617e-04 0.025727058
## 10 0.9427107 0.027795546 4.619744e-04 0.029031802
```

```
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 7: prevented CVD (a male patient aged 40-45)

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

When compared what we calculated before, the number of CVD events under Strategy 0 is 0.0411874, 0.0711824, 0.1115369, 0.1610653, 0.2317697, 0.3237828, 0.4527186, 0.0481315, 0.0750298, 0.1070094, 0.1447773, 0.1921793, 0.2490522, 0.3538585, we may conclude that screening could help to prevent the CVD events under all three risk groups in the specific age and gender group.

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]
  }
  m_M
  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_m[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_m[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_m[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_m[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_l[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_l[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_l[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_l[14])

CVD_prevented_l <- as.numeric(CVD_prevented_l)
CVD_prevented_m <- as.numeric(CVD_prevented_m)
CVD_prevented_h <- as.numeric(CVD_prevented_h)

```



```

res <- data.frame(cbind("index"=rate_data$index,
                        "sex"=rate_data$sex,
                        "low"=CVD_prevented_l,
                        "medium"=CVD_prevented_m,
                        "high"=CVD_prevented_h
                        ))
print(xtable(res,digits=c(0,0,0,3,3,3),
  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 % Mon Jan 18 13:11:13 2021

	index	sex	low	medium	high
1	40	male	0.0261971333996861	0.0411423157671217	0.0241418741114777
2	45	male	0.0446662026698032	0.069704932825595	0.0411977580213452
3	50	male	0.0686498212143506	0.106257977576601	0.0633906156178216
4	55	male	0.0964812671663052	0.147811865408869	0.0892169300114954
5	60	male	0.133402396456711	0.201558970142265	0.123598398830557
6	65	male	0.176118520190639	0.261464892450898	0.163583856805719
7	70	male	0.233163576957691	0.339852915513992	0.217135761953413
8	40	female	0.0307923491079538	0.0482983309128298	0.0283814498112105
9	45	female	0.0475251300830973	0.074134262095425	0.0438372600085826
10	50	female	0.0669000278544402	0.103683369229555	0.0617637548542279
11	55	female	0.0889574275344238	0.136816575540527	0.0822147922467317
12	60	female	0.115254496192866	0.175615094116597	0.106657199033764
13	65	female	0.144039065274721	0.216807377740607	0.1335248314275
14	70	female	0.18161177556816	0.265636503674557	0.169046209493589

```

# loop for 3 strategies
pop_dat <- data.frame(cbind(population_data$low,
                             population_data$medium,
                             population_data$high))
cvd_dat <- data.frame(cbind(as.numeric(res$low),
                             as.numeric(res$medium),
                             as.numeric(res$high)))
result <- matrix(NA,nrow=1,ncol=3)
colnames(result) <- c("strategy1","strategy2","strategy3")

for(i in 1:3){ # strategy: strategy1 strategy2 strategy3
  for (x in 1:14){ # gender and age
    for (y in 1:3) { # risk: low medium high
      perstr <- sum(pop_dat[x*i,y] * cvd_dat[x,y])
    }
  }
  result[i] <- perstr
}

# for strategy3, there is no screening for patients aged from 40-50
strategy3_noscreen <- cbind(c(229,444),c(498,856))
colnames(strategy3_noscreen) <- c("male","female")
rownames(strategy3_noscreen) <- c("40","45")
strategy3_noscreen

```

```
##      male female
## 40  229    498
## 45  444    856
```

```
strategy3_noscren_CVD
```

```
##          male      female
## 40 0.04118741 0.04813152
## 45 0.07118236 0.07502982
```

```
result[3] <- result[3] + sum(strategy3_noscren*strategy3_noscren_CVD)
result
```

```
##      strategy1 strategy2 strategy3
## [1,]        871       2132 2261.232
```

This is the result for the CVD events under 3 different strategies