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

2020.12.20

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

Part I. General population (without CVD)

Markov model

```
library(readr)
rate_data <- read_csv("data/ghdx_data.csv")
# male
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 Dec 26 19:10:12 2020

Table 3: Data from Global Health Data Exchange

	Index	sex	rate_incidence_CVD	rate_death_CVD	rate_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
# Utilities: for calculation of QALY
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

p_live_oth_death <- rate_to_prob(r=rate_data$rate_death_nonCVD,t = 1)
p_live_cvd <- rate_to_prob(r=rate_data$rate_incidence_CVD,t = 1)
p_live_cvdth <- rate_to_prob(r=rate_data$rate_death_CVD,t = 1)
# transition probability from S2 to S3
p_ccvd_acvd <- rate_to_prob(rate_data$rate_incidence_CVD*HR_cvdhistory_cvd,t=5)
p_ccvd_cvdth <- rate_to_prob(rate_data$rate_death_CVD*HR_cvdhistory_cvdth,t=5)
```

Component 1: A transition probability matrix P_t

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

For example, the transition matrix for the cohort is:

$$P_1 = \begin{Bmatrix} p_{[1,1,t]} & p\_live\_cvd & p\_live\_cvdth & p\_live\_oth\_death \\ 0 & p\_ccvd\_acvd & p\_ccvd\_cvdth & p\_live\_oth\_death \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{Bmatrix}$$

```
####################### Construct state-transition models for Strategy1 ####################
#### Create transition arrays ####
a_P <- array(0, dim      = c(n_states, n_states, n_t),
             dimnames = list(v_names_states, v_names_states, 0:(n_t - 1)))
## From S1
a_P["S1", "S1", 0:6]   <- (1-(p_live_cvd[1] +
                            p_live_cvdth[1] +
                            p_live_oth_death[1]))
a_P["S1", "S2", 0:6]  <- p_live_cvd[1]
a_P["S1", "S3", 0:6]   <- p_live_cvdth[1]
a_P["S1", "S4", 0:6]   <- p_live_oth_death[1]
## From S2
a_P["S2", "S1", 0:6] <- 0
a_P["S2", "S2", 0:6] <- p_ccvd_acvd[1]
a_P["S2", "S3", 0:6] <- p_ccvd_cvdth[1]
# TODO: cvd people to death of other reasons (P3)
a_P["S2", "S4", 0:6] <- 1 - (p_ccvd_acvd[1] + p_ccvd_cvdth[1])
## From S3
a_P["S3", "S3", 0:6] <- 1
## From S4
a_P["S4", "S4", 0:6] <- 1

# From S1
a_P["S1", "S1", 6:10] <- (1-(p_live_cvd[1+1] +
                            p_live_cvdth[1+1] +
                            p_live_oth_death[1+1]))
a_P["S1", "S2", 6:10]  <- p_live_cvd[1+1]
a_P["S1", "S3", 6:10]  <- p_live_cvdth[1+1]
a_P["S1", "S4", 6:10]  <- p_live_oth_death[1+1]
## From S2
a_P["S2", "S1", 6:10] <- 0
a_P["S2", "S2", 6:10] <- p_ccvd_acvd[1+1]
a_P["S2", "S3", 6:10] <- p_ccvd_cvdth[1+1]
# TODO: cvd people to death of other reasons
# p_live_oth_death != p_cvd _oth_death (P3)
a_P["S2", "S4", 6:10] <- 1 - (p_ccvd_acvd[1+1] + p_ccvd_cvdth[1+1])
## From S3
a_P["S3", "S3", 6:10] <- 1
## From S4
a_P["S4", "S4", 6:10] <- 1
```

Component 2: A cohort trace matrix M

```
#### Run Markov model ####
## Initial state vector
# All starting healthy
v_s_init <- c(state0 = 1, state1 = 0, state2 = 0, state3 = 0)

## Initialize cohort trace for cSTM
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

## Iterative solution of cSTM
for(t in 1:n_t){
  ## Fill in cohort trace
  m_M[t + 1, ]      <- m_M[t, ]      %*% a_P[, , t]
}
plot_trace(m_M)
```

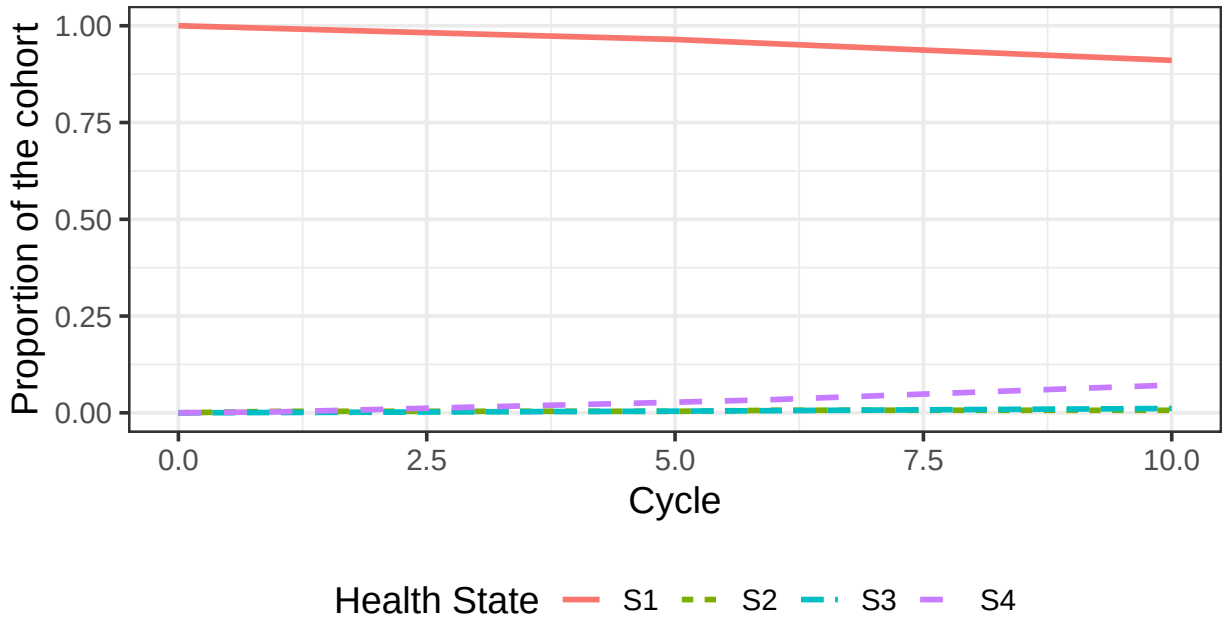

Figure 1: For the group male aging from 40-45

Table 4: Incedence 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		

```
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

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
HR_hpt_lip_cvd  <-  0.7
HR_hpt_lip_cvdth <- 0.82
# transition probability from S1 to S2
p_live_cvd_l <- ProbFactor(p_live_cvd,HR_l_stg1)
p_live_cvd_m <- ProbFactor(p_live_cvd,HR_m_stg1)
p_live_cvd_h <- ProbFactor(p_live_cvd,HR_h_stg1)
# transition probability from S1 to S3
p_live_cvdth_l <- ProbFactor(p_live_cvdth,1)    # equal
# p_live_cvdth_m <- ProbFactor(p_live_cvdth,1.7) # intervention etc.
# p_live_cvdth_h <- ProbFactor(p_live_cvdth,1) # intervention etc.
```