# 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 |

# Parameters

```
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
HR_cvdhistory_cvd <-    1.37
HR_cvdhistory_cvdth <-  3.12

HR_high_live_cvdth <-   1.17
```

# Markov model

## Model input

```
library(readr)
rate_data <- read_csv("data/ghdx_data.csv")
xtable(data.frame(rate_data),digits=c(0,0,0,6,6,6))
```

% latex table generated in R 3.6.3 by xtable 1.8-4 package % Fri Dec 18 14:55:53 2020

```
## 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("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
```

| | 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 |

```
out_trans_to_cvd <- -0.038    # TODO


p_live_oth_death <- rate_to_prob(r=rate_data$rate_death_nonCVD,t = n_t)
p_live_cvd <- rate_to_prob(r=rate_data$rate_incidence_CVD,t = n_t)
p_live_cvdth <- rate_to_prob(r=rate_data$rate_death_CVD,t = n_t)


# 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)
p_live_cvdth_m <- ProbFactor(p_live_cvdth,1.7)
p_live_cvdth_h <- ProbFactor(p_live_cvdth,1)
# transition probability from S2 to S3
p_ccvd_acvd <- ProbFactor(p_live_cvd,HR_cvdhistory_cvd)
p_ccvd_cvdth <- ProbFactor(p_live_cvdth,HR_cvdhistory_cvdth)
```

| Item | | CVD incidence | CVD cause-specific mortality |
|---|---|---|---|
| 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 | | |

## The component of a Markov model: A transition probability matrix, $P_t$

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

```
###################### 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)))
### Fill in array
## From S1
# a_P["S1", "S1", ]   <- 0
a_P["S1", "S2", ]  <- p_live_cvd_l[1:10]
a_P["S1", "S3", ]   <- p_live_cvdth_l[1:10]
# a_P["S1", "S4", ]   <- 0

## From S2
a_P["S2", "S2", ] <- p_ccvd_acvd[1:10]
a_P["S2", "S3", ] <- p_ccvd_cvdth[1:10]
# a_P["S2", "S4", ]  <- p_ccvd_cvdth[1:10]
```