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

2020.12.16

Results from the paper

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

Table 1: Increased QALY with no screening

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

rate_incidence_CVD = col_double(),

Table 2: Prevent CVD events

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

Markov model

```
# parameters TODO
cycle <- 4
factor <- 0.8

# transition probability and related parameters
# calculated by ratetoprob function, based on the incidence of a disease and incidence of a death from
library(readr)
rate_data <- read_csv("data/ghdx_data.csv")

## Parsed with column specification:
## cols(
## Index = col_double(),
## sex = col character(),</pre>
```

```
rate_death_CVD = col_double(),
##
##
    rate_death_nonCVD = col_double()
## )
source("./function/transform_func.R")
p_live_oth_death <- RateToProb(rate=rate_data$rate_death_nonCVD,t=cycle)</pre>
p_live_cvd <- RateToProb(rate=rate_data$rate_incidence_CVD,t = cycle)</pre>
p_live_cvdth <- RateToProb(rate=rate_data$rate_death_CVD,t = cycle)</pre>
# incidence rate of the cohort of 3 levels
p_live_cvd_l <- ProbFactor(p_live_cvd,factor)</pre>
p_live_cvd_m <- ProbFactor(p_live_cvd,factor)</pre>
p_live_cvd_h <- ProbFactor(p_live_cvd,factor)</pre>
# death rate of the cohort of 3 levels
p_live_cvdth_l <- ProbFactor(p_live_cvdth,factor)</pre>
p_live_cvdth_m <- ProbFactor(p_live_cvdth,factor)</pre>
p_live_cvdth_h <- ProbFactor(p_live_cvdth,factor)</pre>
```

Health Status

```
# chi-squared test
# t-test
```

```
HR_1_stg1 <- 0.63

HR_1_stg2 <- 0.43

HR_1_stg3 <- 0.45

HR_m_stg1 <- 1.56

HR_m_stg2 <- 0.97

HR_m_stg3 <- 1.09

HR_h_stg1 <- 1.6

HR_h_stg2 <- 2.06

HR_h_stg3 <- 2.11
```