simulation

Intro

This doc reproduces the simulation results of the article provided by Hanneh and Gerko.

Full reproducible script

```
library(Hmisc)
```

```
Loading required package: lattice
```

```
Loading required package: survival
```

```
Warning: package 'survival' was built under R version 4.2.3
```

```
Loading required package: Formula
```

```
Loading required package: ggplot2
```

```

Attaching package: 'Hmisc'
```

```
The following objects are masked from 'package:base':

    format.pval, units
```

```
library(mice)
```

```
Warning: package 'mice' was built under R version 4.2.3


Attaching package: 'mice'

The following object is masked from 'package:stats':

    filter

The following objects are masked from 'package:base':

    cbind, rbind
```

```
library(tidyverse)
```

```
Warning: package 'tidyverse' was built under R version 4.2.3

Warning: package 'tibble' was built under R version 4.2.3

-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.0     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v lubridate 1.9.2     v tibble    3.2.1
v purrr     1.0.1     v tidyr     1.3.0

-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter()    masks mice::filter(), stats::filter()
x dplyr::lag()       masks stats::lag()
x dplyr::src()       masks Hmisc::src()
x dplyr::summarize() masks Hmisc::summarize()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to beco
```

```
d1 <- sasxport.get("../data/DEMO_I.xpt")
```

```
Processing SAS dataset DEMO_I    ..
```

```
d2 <- sasxport.get("../data/BPX_I.xpt")
```

```
Processing SAS dataset BPX_I     ..
```

```
d3 <- sasxport.get("../data/BMX_I.xpt")
```

```
Processing SAS dataset BMX_I     ..
```

```
d4 <- sasxport.get("../data/GHB_I.xpt")
```

```
Processing SAS dataset GHB_I     ..
```

```
d5 <- sasxport.get("../data/TCHOL_I.xpt")
```

```
Processing SAS dataset TCHOL_I   ..
```

```
d1.t <- subset(d1,select=c("seqn","riagendr","ridageyr"))
d2.t <- subset(d2,select=c("seqn","bpxsy1"))
d3.t <- subset(d3,select=c("seqn","bmxbmi"))
d4.t <- subset(d4,select=c("seqn","lbxgh"))
d5.t <- subset(d5,select=c("seqn","lbdtcsi"))
d <- merge(d1.t,d2.t)
d <- merge(d,d3.t)
d <- merge(d,d4.t)
d <- merge(d,d5.t)
# ================================================================
# rename variables:
# RIAGENDR - Gender
# RIDAGEYR - Age in years at screening
# BPXSY1 - Systolic: Blood pres (1st rdg) mm Hg
# BMXBMI - Body Mass Index (kg/m**2)
# LBDTCSI - Total Cholesterol (mmol/L)
# LBXGH - Glycohemoglobin (%)
d$age <- d$ridageyr
d$sex <- d$riagendr
d$bp <- d$bpxsy1
```

```r
d$bmi <- d$bmxbmi
d$HbA1C <- d$lbxgh
d$chol <- d$lbdtcsi
d$age[d$age<18] <- NA
# ========================================================================
# select complete cases:
dc <- cc(subset(d,select=c("age","sex","bmi","HbA1C","bp")))
# analysis:
summary(lm(bp ~ HbA1C + age + as.factor(sex), data=dc))
```

```
Call:
lm(formula = bp ~ HbA1C + age + as.factor(sex), data = dc)

Residuals:
Systolic: Blood pres (1st rdg) mm Hg
    Min      1Q  Median      3Q     Max
-49.887 -10.509  -1.378   8.491 107.583

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     98.75149    1.21418  81.332  < 2e-16 ***
HbA1C            1.12638    0.20291   5.551 2.98e-08 ***
age              0.44486    0.01284  34.648  < 2e-16 ***
as.factor(sex)2 -3.24792    0.45164  -7.191 7.34e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 16.1 on 5088 degrees of freedom
Multiple R-squared:  0.2305,    Adjusted R-squared:   0.23
F-statistic:   508 on 3 and 5088 DF,  p-value: < 2.2e-16
```

```r
confint(lm(bp ~ HbA1C + age + as.factor(sex), data=dc))
```

```
                    2.5 %      97.5 %
(Intercept)     96.3711755 101.1317982
HbA1C            0.7285836   1.5241825
age              0.4196932   0.4700355
as.factor(sex)2 -4.1333281  -2.3625106
```

```r
summary(lm(bp ~ HbA1C + bmi + age + as.factor(sex), data=dc))
```

```
Call:
lm(formula = bp ~ HbA1C + bmi + age + as.factor(sex), data = dc)

Residuals:
Systolic: Blood pres (1st rdg) mm Hg
    Min      1Q  Median      3Q     Max
-51.068 -10.251  -1.504   8.264 107.410

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     92.65583    1.39320  66.506  < 2e-16 ***
HbA1C            0.75177    0.20596   3.650 0.000265 ***
bmi              0.28632    0.03282   8.724  < 2e-16 ***
age              0.44586    0.01275  34.979  < 2e-16 ***
as.factor(sex)2 -3.63115    0.45049  -8.060  9.4e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 15.98 on 5087 degrees of freedom
Multiple R-squared:  0.2418,    Adjusted R-squared:  0.2412
F-statistic: 405.7 on 4 and 5087 DF,  p-value: < 2.2e-16
```

```r
confint(lm(bp ~ HbA1C + bmi + age + as.factor(sex), data=dc))
```

```
                    2.5 %     97.5 %
(Intercept)     89.9245592 95.3871089
HbA1C            0.3479966  1.1555348
bmi              0.2219815  0.3506673
age              0.4208695  0.4708464
as.factor(sex)2 -4.5143014 -2.7479929
```

```r
# ========================================================================
```

```r
# simulation of measurement error:
#| output: FALSE
ref <- lm(bp ~ HbA1C + bmi + age + as.factor(sex), data=dc)$coef[2]
```

```r
n.sim <- 1e3
perc.me.exp <- seq(0,.5,.1)
perc.me.conf<- seq(0,.5,.1)
scenarios <- expand.grid(perc.me.exp,perc.me.conf)
var.exp <- var(dc$HbA1C)
var.conf <- var(dc$bmi)
n <- dim(dc)[1]
beta.hat <- matrix(ncol=dim(scenarios)[1], nrow=n.sim)
for (k in 1:n.sim){
  print(k)
  set.seed(k)
  for (i in 1:dim(scenarios)[1]){
    var.me.exp <- var.exp*scenarios[i,1]/(1-scenarios[i,1])
    var.me.conf <- var.conf*scenarios[i,2]/(1-scenarios[i,2])
    dc$HbA1C.me <- dc$HbA1C + rnorm(dim(dc)[1], 0, sqrt(var.me.exp) )
    dc$bmi.me <- dc$bmi + rnorm(dim(dc)[1], 0, sqrt(var.me.conf) )
    beta.hat[k,i] <- lm(bp ~ HbA1C.me + age + bmi.me + as.factor(sex), data=dc)$coef[2]
  }}
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```r
# ======================================================================
# create figure:
tot.mat <- cbind(100*scenarios,apply(beta.hat,2,mean))
colnames(tot.mat) <- c("me.exp","me.conf","estimate")
FIGURE <- ggplot(tot.mat, aes(me.exp, me.conf)) +
  geom_tile(color="white",aes(fill = estimate)) +
  geom_text(aes(label = round(estimate, 2))) +
  scale_fill_gradient2(low="#D55E00",mid="white",high = "#56B4E9", midpoint=ref) +
  labs(x=paste("% of total variance of HbA1c due to measurement error"),
       y=paste("% of total variance of BMI due to measurement error")) +
```

```
  coord_equal()+
  scale_y_continuous(breaks=unique(tot.mat[,1]))+
  scale_x_continuous(breaks=unique(tot.mat[,1]))+
  theme(panel.background = element_rect(fill='white', colour='grey'),
        plot.title=element_text(hjust=0),
        axis.ticks=element_blank(),
        axis.title=element_text(size=12),
        axis.text=element_text(size=10),
        legend.title=element_text(size=12),
        legend.text=element_text(size=10))
FIGURE
```