FRS

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#### ESTIMATING THE 10 YEAR CARDIOVASCULAR DISEASE RISK IN ADULTS ####
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# Originating from the Framingham Risk Study, the model is based on a Cox Proportional Hazard Model

### Required packages ###
library(ggplot2); library(dplyr); library(tidyr)
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##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
### Parameters ###
f_base10_survival = 0.95012 # baseline 10-year survival for females
m_base10_survival = 0.88936 # baseline 10-year survival for males

f_rf <- list(log_age = 2.32888, log_totchol = 1.20904,log_hdl = -0.70833,log_SBP = 2.82263,Smoking = 0.5
m_rf <- list(log_age = 3.06117, log_totchol = 1.12370,log_hdl = -0.93263,log_SBP = 1.99881,Smoking = 0.
betas <- list(f=f_rf,m=m_rf) # nested list of f_rf and m_rf

f_points=data.frame("points"=seq(-3,12),"age_low"=c(NA,NA,NA,30,NA,35,NA,40,45,NA,50,55,60,65,70,75),"ag
m_points=data.frame("points"=seq(-2,15),"age_low"=c(NA,NA,30,NA,35,NA,NA,40,45,NA,50,NA,55,60,65,NA,70,


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# This gets the row where the input (30 in this example) satisfies the condition that it is between the
i=sapply(30, function(p) { which(f_points$age_low <= p & f_points$age_high >= p)})
# Delete all rows except row "i"
keep_df=f_points[-(setdiff(1:16,i)),]
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get_frs = function(gender,age,HDL,TotChol,sbp,smoker,diabetic) {
  list_pts=c() # Initiate list of points
  #### FEMALES ####
  if (gender == 1) {
  ## GET POINTS FROM AGE ##
```

```
  i=sapply(age, function(p) { which(f_points$age_low <= p & f_points$age_high >= p)}); keep_df=f_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM HDL ##
  i=sapply(HDL, function(p) { which(f_points$HDL_low <= p & f_points$HDL_high >= p)}); keep_df=f_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM TOTAL CHOLESTEROL ##
  i=sapply(TotChol, function(p) { which(f_points$TotChol_low <= p & f_points$TotChol_high >= p)}); keep
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM SBP ##
  i=sapply(sbp, function(p) { which(f_points$SBP_low <= p & f_points$SBP_high >= p)}); keep_df=f_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM SMOKER ##
  if (smoker == 2) {list_pts=append(list_pts,0)} else {list_pts=append(list_pts,3)}
  f_smoke <<- 3
  ## GET POINTS FROM DIABETIC ##
  if (diabetic == 2) {list_pts=append(list_pts,0)} else {list_pts=append(list_pts,4)}
  f_diabetic <<- 4
  }
  #### MALES ####
 else {
    ## GET POINTS FROM AGE ##
  i=sapply(age, function(p) { which(m_points$age_low <= p & m_points$age_high >= p)}); keep_df=m_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM HDL ##
  i=sapply(HDL, function(p) { which(m_points$HDL_low <= p & m_points$HDL_high >= p)}); keep_df=m_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM TOTAL CHOLESTEROL ##
  i=sapply(TotChol, function(p) { which(m_points$TotChol_low <= p & m_points$TotChol_high >= p)}); keep
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM SBP ##
  i=sapply(sbp, function(p) { which(m_points$SBP_low <= p & m_points$SBP_high >= p)}); keep_df=m_points
  list_pts=append(list_pts,keep_df[[1]])
  ## GET POINTS FROM SMOKER ##
  if (smoker == 2) {list_pts=append(list_pts,0)} else {list_pts=append(list_pts,4)}
  m_smoke <<- 4
  ## GET POINTS FROM DIABETIC ##
  if (diabetic == 2) {list_pts=append(list_pts,0)} else {list_pts=append(list_pts,3)}
  m_diabetic <<- 3
  }
  return(sum(list_pts))
}

##############################################################################################################
# THE AVERAGES IN THE COX MODEL DEPEND ON OUR PARTICULAR SAMPLE AND THE CHARACTERISTICS OF THAT SAMPLE.

### COX MODEL ESTIMATE ###
# FEMALES
# arg1_f = betas$f$log_age*log(age)+betas$f$log_totchol*log(TotChol)+betas$f$log_hdl*log(HDL)+betas$f$l
# arg2_f = 0 # THE MEAN VALUES HERE #
#
# rho_f = 1-(f_base10_survival^exp(arg1_f - arg2_f))
# # MALES
# arg1_m = betas$m$log_age*log(age)+betas$m$log_totchol*log(TotChol)+betas$m$log_hdl*log(HDL)+betas$m$l
```

```
# arg2_m= 0  # THE MEAN VALUES HERE #
#
# rho_m = 1-(m_base10_survival^exp(arg1_m - arg2_m))
```