sim\_results\_create\_Cstat\_tables.Rmd

Alex Pate

28/03/2022

[1] "/mnt/bmh01-rds/mrc-multi-outcome"

##   
## 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

## Loading required package: boot

##   
## Attaching package: 'boot'

## The following object is masked from 'package:survival':  
##   
## aml

## Loading required package: MASS

##   
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':  
##   
## select

## Loading required package: survC1

## Loading required package: doBy

##   
## Attaching package: 'doBy'

## The following object is masked from 'package:dplyr':  
##   
## order\_by

##   
## Attaching package: 'frailtypack'

## The following object is masked from 'package:survival':  
##   
## cluster

## Loading required package: mgcv

## Loading required package: nlme

##   
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':  
##   
## collapse

## This is mgcv 1.8-38. For overview type 'help("mgcv-package")'.

##   
## This is GJRM 0.2-5.1.  
## For overview type 'help("GJRM-package")'.

## Loading required package: lattice

##   
## Attaching package: 'lattice'

## The following object is masked from 'package:boot':  
##   
## melanoma

## Loading required package: Formula

## Loading required package: ggplot2

##   
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:dplyr':  
##   
## src, summarize

## The following objects are masked from 'package:base':  
##   
## format.pval, units

## Loading required package: SparseM

##   
## Attaching package: 'SparseM'

## The following object is masked from 'package:base':  
##   
## backsolve

##   
## Attaching package: 'table1'

## The following objects are masked from 'package:Hmisc':  
##   
## label, label<-, units

## The following objects are masked from 'package:base':  
##   
## units, units<-

##   
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':  
##   
## smiths

## Loading required package: StanHeaders

## rstan (Version 2.21.3, GitRev: 2e1f913d3ca3)

## For execution on a local, multicore CPU with excess RAM we recommend calling  
## options(mc.cores = parallel::detectCores()).  
## To avoid recompilation of unchanged Stan programs, we recommend calling  
## rstan\_options(auto\_write = TRUE)

##   
## Attaching package: 'rstan'

## The following object is masked from 'package:tidyr':  
##   
## extract

##   
## Attaching package: 'mice'

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

## The following objects are masked from 'package:base':  
##   
## cbind, rbind

## Loading required package: foreach

## Loading required package: iterators

## Loading required package: parallel

|  |  |  |  |
| --- | --- | --- | --- |
|  | development | validation | Overall |
|  | (N=100000) | (N=100000) | (N=200000) |
| Age |  |  |  |
| Mean (SD) | 69.3 (± 5.75) | 69.3 (± 5.73) | 69.3 (± 5.74) |
| gender |  |  |  |
| 0 | 47089 (47.1%) | 47628 (47.6%) | 94717 (47.4%) |
| 1 | 52911 (52.9%) | 52372 (52.4%) | 105283 (52.6%) |
| BMI |  |  |  |
| Mean (SD) | 27.3 (± 5.25) | 27.3 (± 5.26) | 27.3 (± 5.26) |
| Cholesterol/HDL ratio |  |  |  |
| Mean (SD) | 3.79 (± 1.17) | 3.79 (± 1.17) | 3.79 (± 1.17) |
| Ethnicity |  |  |  |
| White | 93319 (93.3%) | 93456 (93.5%) | 186775 (93.4%) |
| Mixed race | 450 (0.450%) | 419 (0.419%) | 869 (0.435%) |
| South asian | 3423 (3.42%) | 3257 (3.26%) | 6680 (3.34%) |
| Black | 2087 (2.09%) | 2157 (2.16%) | 4244 (2.12%) |
| Chinese and other | 721 (0.721%) | 711 (0.711%) | 1432 (0.716%) |
| Other | 0 (0%) | 0 (0%) | 0 (0%) |
| SBP |  |  |  |
| Mean (SD) | 139 (± 17.8) | 139 (± 17.8) | 139 (± 17.8) |
| Smoking status |  |  |  |
| Never | 36098 (36.1%) | 35933 (35.9%) | 72031 (36.0%) |
| Ex | 35854 (35.9%) | 35852 (35.9%) | 71706 (35.9%) |
| Current | 28048 (28.0%) | 28215 (28.2%) | 56263 (28.1%) |
| IMD |  |  |  |
| 1 (most deprived) | 24786 (24.8%) | 24654 (24.7%) | 49440 (24.7%) |
| 2 | 22587 (22.6%) | 22277 (22.3%) | 44864 (22.4%) |
| 3 | 20095 (20.1%) | 20408 (20.4%) | 40503 (20.3%) |
| 4 | 17587 (17.6%) | 17295 (17.3%) | 34882 (17.4%) |
| 5 (least deprived) | 14945 (14.9%) | 15366 (15.4%) | 30311 (15.2%) |

|  |  |  |
| --- | --- | --- |
|  | development | validation |
| Diab\_t2.n.at.risk | 89211.00 | 89236.00 |
| Diab\_t2.time.at.risk | 248673105.00 | 248217658.00 |
| Diab\_t2.number.events | 7441.00 | 7512.00 |
| Diab\_t2.rate | 10.93 | 11.05 |
| HF.n.at.risk | 97219.00 | 97225.00 |
| HF.time.at.risk | 275713488.00 | 275489603.00 |
| HF.number.events | 6597.00 | 6450.00 |
| HF.rate | 8.74 | 8.55 |
| CHD\_MI.n.at.risk | 89008.00 | 88974.00 |
| CHD\_MI.time.at.risk | 242660815.00 | 242941571.00 |
| CHD\_MI.number.events | 8324.00 | 8203.00 |
| CHD\_MI.rate | 12.53 | 12.33 |
| Stroke\_TIA.n.at.risk | 94845.00 | 94736.00 |
| Stroke\_TIA.time.at.risk | 266075602.00 | 265233191.00 |
| Stroke\_TIA.number.events | 7362.00 | 7478.00 |
| Stroke\_TIA.rate | 10.11 | 10.30 |