sim\_results\_create\_Cstat\_tables.Rmd

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[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

[1] "model.type = C, data.size = 2e+05" [1] "HarC"

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| product.C Index | dual.C Index | clayton.C Index | gumbel.C Index | frank.C Index | normal.C Index | gamma.C Index | msm.C Index |
| 0.69 | 0.69 | 0.69 | 0.69 | 0.69 | 0.69 | 0.69 | 0.69 |

[1] "UnoC"

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| product | dual | clayton | gumbel | frank | normal | gamma | msm |
| 0.55 | 0.57 | 0.55 | 0.55 | 0.55 | 0.55 | 0.55 | 0.55 |