

**Code and documentation for the simulation setup described in  
"Plasmode simulation for the evaluation of pharmacoepidemiologic  
methods in complex healthcare databases"**

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```
hdSimSetup <- function(x, idVar, outcomeVar, timeVar, treatVar,
                      form, effectRR = 1, MM = 1, nsim = 500,
                      size = nrow(x), eventRate = 0.05) {
# x = dataset on which sims are based
# idVar = name of id variable
# outcomeVar = name of outcome variable
# timeVar = name of the follow-up time variable
# treatVar = name of treatment variable
# form = RHS of formula used for outcome simulation - should look like
# "~ C1 + C2 + ...". Can include anything allowed by coxph.
# effectRR = the desired treatment effect relative risk
# MM = multiplier of confounder effects on outcome on
# the log-scale
# nsim = number of desired outcome vectors
# size = desired size of simulated cohort studies (i.e., # of individuals)
# eventRate = desired average event rate -- default is the event
# rate observed in the base dataset

  n <- nrow(x)

  sidx <- sapply(c(idVar, outcomeVar, timeVar, treatVar),
                function(v) which(names(x) == v))
  names(x)[sidx] <- c("ID", "OUTCOME", "TIME", "TREAT")
  y1 <- Surv(x$TIME, x$OUTCOME)
  y2 <- Surv(x$TIME, !x$OUTCOME)
  form1 <- as.formula(paste("y1 ~", form))
  form2 <- as.formula(paste("y2 ~", form))

# estimate survival and censoring models
  smod <- coxph(form1, x = TRUE, data = x)
  fit <- survfit(smod)
  s0 <- fit$surv      # survival curve for average patient
  ts <- fit$time
  nts <- length(ts)
  cm0d <- coxph(form2, data = x)
  fit <- survfit(cm0d)
  c0 <- fit$surv      # censoring curve for average patient

# find event rate in base cohort (if everyone was followed to end of study)
  Xb <- as.vector(smod$x %*% coef(smod))
  mx <- colMeans(smod$x)
  xb0 <- mx %*% coef(smod)
  s0end <- min(s0)
  if(is.null(eventRate)) eventRate <- 1-mean(s0end^exp(Xb - xb0))

# find delta value needed to get approximate desired event rate under new
# parameters
  bnew <- replace(MM*coef(smod), names(coef(smod)) == "TREAT", log(effectRR))
  Xbnew <- as.vector(smod$x %*% bnew)
  sXend <- s0end^(exp(Xb - xb0))
```

```

fn <- function(d) mean(sXend^d) - (1 - eventRate)
delta <- uniroot(fn, lower = 0, upper = 20)$root

# setup n X nts matrix of individual survival and censoring curves under new
# parameters
Sx <- matrix(unlist(lapply(s0, function(s) s^(delta*exp(Xbnew - xb0)))),
             nrow = n)
Xbnew <- as.vector(smod$x %*% coef(cmod))
xb0 <- mx %*% coef(cmod)
Cx <- matrix(unlist(lapply(c0, function(s) s^(delta*exp(Xbnew - xb0)))),
             nrow = n)

#### sample and simulate
ids <- tnew <- ynew <- data.frame(matrix(nrow = size, ncol = nsim))
for(sim in 1:nsim) {
  idxs <- sample(n, size, replace = TRUE)
  ids[,sim] <- x$ID[idxs]

  # event time
  u <- runif(size, 0, 1)
  # the first time survival drops below u
  w <- apply(Sx[idxs,] < u, 1, function(x) which(x)[1])
  stime <- ts[w]
  # for any individuals with survival that never drops below u,
  # replace with arbitrary time beyond last observed event/censoring time
  w <- Sx[idxs,nts] > u
  stime[w] <- max(ts) + 1

  # censoring time
  u <- runif(size, 0, 1)
  # the first time censor-free survival drops below u
  w <- apply(Cx[idxs,] < u, 1, function(x) which(x)[1])
  ctime <- ts[w]
  # for any individuals with censor-free survival that never drops below u,
  # replace with hard censor time at last observed event/censoring time
  w <- Cx[idxs,nts] > u
  ctime[w] <- max(ts)

  # put it together
  tnew[,sim] <- pmin(stime, ctime)
  names(tnew) <- paste("TIME", 1:nsim, sep = "")
  ynew[,sim] <- stime == tnew[,sim]
  names(ynew) <- paste("EVENT", 1:nsim, sep = "")
}

names(ids) <- paste("ID", 1:nsim, sep = "")
names(tnew) <- paste("TIME", 1:nsim, sep = "")
names(ynew) <- paste("EVENT", 1:nsim, sep = "")

data.frame(ids, ynew, tnew)
}

```