

R codes for "Competing risks regression models with covariates-adjusted censoring weight under the generalized case-cohort design"

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There are three R functions including weight functions, beta estimations, and variance estimations for competing risks regression under generalized case-cohort studies.

```
###weight functions
find.weightcc = function(gamma, disease, v, delta, choice = 1, eta) {
  weightcc = c()
  if (choice == 1) { #weight function for single case-cohort study
    for (i in unique(v)) {
      num = sum(gamma[v == i] * (1 - (disease[v == i] == 1)))
      deno = sum((1 - (disease[v == i] == 1)))
      deno = deno * Tq / F387.9701Tf60.0550Td[(f)]TJ/F537.9701Tf10.150Td[(q)]TJ/F327.9701Tf6.4810Td[(.)-323(e)-152(s)-152(t)-695]
    }
    gelse {
      q.est = numq / denoq
      weightcc[v==i] = (1 - (disease[v==i] == 1)) * gamma[v==i] / alpha.est +
        (disease[v==i]==1) * (gamma[v==i] + (1 - gamma[v==i]) * (eta[v==i] == 1)) /
        (alpha.est + (1 - alpha.est) * q.est)
    }
  }
  gelse if (choice == 3) { # efficient weight function for multiple case-cohort studies

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for (i in unique(v)) f
  num = sum(gamma[v == i] (1 - delta[v == i]))
  deno = sum(1 - delta[v == i])
  deno = deno + (deno == 0)
  alpha.est = num / deno
  alpha.est = alpha.est + (alpha.est == 0)

  denoq1 = sum(gamma[v==i] == 0 &disease[v==i] == 1)
  numq1 = sum(eta[v==i] == 1)
  if (denoq1 == 0) f q1.est = 1
  gelse f
  q1.est = numq1 / denoq1 g

  denoq2 = sum(gamma[v==i] == 0 &disease[v==i] == 2)
  numq2 = sum(eta[v==i] == 2)
  if (denoq2 == 0) f q2.est = 1
  gelse f
  q2.est = numq2 / denoq2 g
  weightcc[v==i] = (disease[v==i] != 0) gamma[v==i] + (disease[v==i] == 0)
    gamma[v==i] / alpha.est +(eta[v==i] == 1) / q1.est +(eta[v==i] == 2) / q2.est
  g
gelse if (choice ==5) f #optimal weight function for multiple case-cohort studies
for (i in unique(v)) f
  deno = sum(disease[v==i] == 0)
  num = sum(gamma[v==i] == 1 &disease[v==i] == 0)
  alpha.est = num / deno
  denoq1 = sum(gamma[v==i] == 0 & disease[v==i] == 1)
  numq1 = sum(eta[v==i] == 1)
  if (denoq1 == 0) f q1.est = 1
  gelse f
  q1.est = numq1 / denoq1 g
  denoq2 = sum(gamma[v==i] == 0 & disease[v==i] == 2)
  numq2 = sum(eta[v==i] == 2)
  if (denoq2 == 0) f q2.est = 1
  gelse f
  q2.est = numq2 / denoq2 g

  weightcc[v==i] = (disease[v==i] ==1)
    gamma[v==i] (1/(alpha.est+(1-alpha.est) q1.est)) +
    (disease[v==i] ==2) gamma[v==i] (1/(alpha.est+(1-alpha.est) q2.est)) +
    (disease[v==i] == 0) gamma[v==i] / alpha.est +
    (eta[v==i] == 1) (1/(alpha.est+(1-alpha.est) q1.est)) +
    (eta[v==i] == 2) (1/(alpha.est+(1-alpha.est) q2.est))
  g
g
return(weightcc)
g
###beta estimation function
# choice: weight functions for case-cohort studies
# 1: weight function for single case-cohort study
# 2: optimal weight function for single case-cohort study
# alpha.est + eta.v==i if i=1

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#           2: covariate-unadjusted weights
# data
# time: observed time
# delta: failure indicator
# disease: cause types (1: cause 1, 2: cause 2, 0: censored)
# z: covariate
# gamma: subcohort indicator
# v: stratum variable
# eta: case indicator
beta.est = function(data, beta = 0, delta0 = 3, choice = 1, choice.c=1) f

n = nrow(data)
time = data[, 2]
delta = data[, 3]
disease = data[, 4]
z = data$Z
gamma = data$gamma
v = data$v
eta = data$eta
npop = n
fail = time[!(disease == 0)]
L = length(fail)
gg1 = (matrix(rep(time, L), npop, L) <
matrix(rep(t(fail), each = npop), npop, L))  1
gg1[disease != 1, ] = 0
gg2 = matrix(1, npop, L)

for (i in 1:npop) f
  if (delta[i] == 0) f
    for (j in 1:L) f
      if (time[i] < fail[j])
        gg2[i, j] = 0
  g
g
Yr = gg2 - gg1
weight.cc = find.weightcc(gamma, disease, v, delta, choice=choice, eta)
Gcweight = list()
faili <- time[disease == 1]
Li <- length(faili)
censor<-1-delta
if (choice.c == 1) f ##COX estimates for censoring distribution
  for (i in unique(v)) f
    i.name = paste(i)
    data.cc<-data.frame(time[v == i], censor[v == i], z[v == i], weight.cc[v == i] )
    data.cc1<-data.cc[data.cc$weight.cc >0,]
    colnames(data.cc1) <- c("time", "censor", "z", "weight.cc")
    ss <- Surv(data.cc1$time, data.cc1$censor)
    fit.cox<-survival::coxph(ss ~ z, weight= weight.cc, data=data.cc1)
    Gc.0 = survfit(fit.cox, newdata=data.frame(z=0))
    Gc.1 = survfit(fit.cox, newdata=data.frame(z=1))

    kmest.0 = stepfun(Gc.0$time, c(1,Gc.0$surv))
    kmest.1 = stepfun(Gc.1$time, c(1,Gc.1$surv))

    gg3 = (matrix(rep(time, Li), npop, Li) >= matrix(rep(t(faili), each=npop), npop, Li))
    foo.0 = matrix(rep(t(kmest.0(faili)), each=npop), npop, Li)
    /(matrix(rep(kmest.0(time), Li), npop, Li))

```

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foo.1 = matrix(rep(t(kmest.1(faili)), each=npop), npop, Li)
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S12 = t(z2expz) %%
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for (j in 1:n) f
  if (time[i] < time[j])
    rt[i, j] = 0
g
g
Yrt = rt - Nrt
phit = find.weightcc(gamma
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foo = matrix(rep(t(kmest(time[v == i])), each = n), n-1, n) / fff
foo[gg3] = 1
Gcweight[[i.name]] = foo
g
g
wY.all = Yrt

dNr.all = (do.call(cbind, replicate(n, time, simplify = FALSE))
== do.call(rbind, replicate(n, time, simplify = FALSE))) 1
dNr.all[disease != 1, ] = 0
wdN.all = dNr.all

p = 1
SI = 0
SI0 = list()
Ec = list()

for (i in unique(v)) f
  i.name <- paste(i)
  dis1 = (disease[disease == 1]) 1
  v1 = (v[disease == 1]) 1
  n1 = sum(v == i)
  expz <- exp(z[v == i] beta)
  zexpz <- expz z [v == i]
  temp0 <- colSums(expz (phit[v == i] wY.all[v == i, ] Gcweight[[i.name]]))
  SI0[[i.name]] <- temp0 + (temp0 == 0)
  SI1 <- colSums(zexpz (phit[v == i] wY.all[v == i, ] Gcweight[[i.name]]))
  z2expz = expz z[v == i] z[v == i]
  SI2 = colSums(z2expz (phit[v == i] wY.all[v == i, ] Gcweight[[i.name]]))
  SI1overSI0hat <- SI1 / SI0[[i.name]]
  SI2overSI0hat = SI2 / SI0[[i.name]]
  Ec[[i.name]] = SI1overSI0hat

  ipart1 = do.call(rbind, replicate(n1, SI2overSI0hat, simplify = F))
  wdN.all[v == i, ] Gcweight[[i.name]] phit[v == i]
  lpartIhat = sum(ipart1)

  E2 = SI1overSI0hat SI1overSI0hat
  ipart2 = do.call(rbind, replicate(n1, E2, simplify = F))
  wdN.all[v == i, ] Gcweight[[i.name]] phit[v == i]
  lpartIIhat = sum(ipart2)

  SI <- SI + (lpartIhat - lpartIIhat)
g
templ = SI
Yt = (do.call(cbind, replicate(n, time, simplify = FALSE))
>= do.call(rbind, replicate(n, time, simplify = FALSE))) 1
Nct = (do.call(cbind, replicate(n, time, simplify = FALSE))
<= do.call(rbind, replicate(n, time, simplify = FALSE))) 1
Nct[disease != 0, ] = 0

var.1 = 0
expz = exp(z beta)
for (i in unique(v)) f
  i.name = paste(i)
  n1 = sum(v == i)
  dlamb10t = colSums(wdN.all[v == i, ] Gcweight[[i.name]] phit[v == i] )

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/ S10[[i.name]]
zminEc = (do.call(cbind, replicate(n, z[v == i], simplify = FALSE)))
- (do.call(rbind, replicate(sum(v == i), Ec[[i.name]], simplify = FALSE)))

wdM = wdN.all[v == i,] Gcweight[[i.name]] - wY.all[v == i,]
Gcweight[[i.name]] expz[v == i] (do.call(rbind, replicate(sum(v == i),
dlamb10t, simplify = FALSE)))
eta11 = rowSums(zminEc wdM)
eta21 = c()
if (choice.c == 1){
WeightedY<- phit[v==i] Yt[v==i,]
gamma.hat<- fit.cox$coef
expg<-exp(z[v==i] gamma.hat)
zexpg<-z[v==i] expg
s0c<- colSums( WeightedY expg)
s0c<- s0c + (s0c==0)
s1c<- colSums( WeightedY zexpg)
ecox <-s1c/s0c
S1overS02hat<- ecox/s0c
zc_min_ec<- (do.call(cbind, replicate(n, z[v==i], simplify = FALSE)))
- (do.call(rbind, replicate(nl, ecox, simplify = FALSE)))
ilc_mat<-vcov(fit.cox)[1]
censor.w<-

```



```

deltaw = do.call(cbind, replicate(n, wlict, simplify = F)) -
do.call(rbind, replicate(nl, wct, simplify = F))
ind = do.call(cbind, replicate(n, time[v == i], simplify = F))
< do.call(rbind, replicate(sum(v == i), time, simplify = F))
eta21 = c(eta21, sum(deltaw zminEc ind wdM))

```

g

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eta.comb = (eta11 + eta21)
eta.comb2 = eta.comb eta.comb
qest1 = sum(eta[v==i]==1)/sum(disease[v==i]==1& gamma[v==i]==0)
alphaest = sum(
[v ==(n)-55(E)-56(c)]TJ7F32 9.9701 Tf 35.227 0 Td [(*)]TJ5.87 7.9701 Tf 5.604 0 Td [(()-270(d)-158(i)-158(s)-158(e)-158(a)-158(s)-158(e) Td [(()-210(v)
32 7.9701 Tf 20.055 0 Td [(())TJ/F53 7.9701 Tf 4.528 0 Td [(r)-43(b)-42(i)-43(n)-43(d)]TJ/F32 7.9701 Tf 26.429 0 Td [(,)-987(r)-178(e)-178(p)-178(l)-179(i)-178(c)-178(a)-178(t)

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Q = wY.all[v == i,] Gcweight[[i.name]] zminEc expz[v == i]
if (choice.c == 1) f
  eta31 = rowSums((1 - delta[v == i]) Q do.call(rbind, replicate(
    sum(v == i), dlamb10t, simplify = FALSE)))
  eta32 = (1 - delta[v == i]) eta21
  eta3 <- eta31 - eta32
else f
  eta3 = rowSums((1 - delta[v == i]) Q do.call(rbind, replicate(
    sum(v == i), dlamb10t, simplify = FALSE)))
g
V331 = sum(eta.comb eta.comb

```