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library(rankreg)

a = read.table("c:\\My Teach\\ST745\\bone_transplant.txt")

event.time = a[,3]
delta = a[,4]
allo = 2-a[,1]
hodgkins = a[,2]-1
kscore = a[,5]
wtime = a[,6]
x = as.matrix(cbind(allo,hodgkins,kscore,wtime))
y = log(event.time)

####using rankaft function, without computing the variance of the estimates

> fit1 = rankaft(x,y,delta)

####output from rankaft
> fit1$beta
      xnewallo xnewhodgkins xnewkscore  xnewwtime
betag 0.3055718   -1.549300 0.06074927 0.01443342  ####Gehan type
estimator
betal 0.3522702   -1.494406 0.07495995 0.01066983  ####log-rank
estimator

####using aft.fun function, automatically including computing the variance of the estimates

> fit2 = aft.fun(x,y,delta)

####output from aft.fun
> fit2$beta
      allo  hodgkins      kscore      wtime
betag 0.3055718 -1.549300 0.06074927 0.01443342  ####Gehan estimator
betal 0.3244511 -1.494337 0.07504969 0.01032466  ####log-rank estimator

> sqrt(apply(fit2$betagm,1,var))
[1] 0.540879687 0.646372329 0.011232689 0.007314381  ####standard error
of Gehan estimator
> sqrt(apply(fit2$betalw,1,var))
[1] 0.694427754 0.821533829 0.010118149 0.006615196  ####standard error
of log-rank estimator

> fit2$beta[1,]/sqrt(apply(fit2$betagm,1,var))
      allo  hodgkins      kscore      wtime
0.5649534 -2.3969163  5.4082572  1.9732936  ####z-statistic of Gehan
estimator
> fit2$beta[2,]/sqrt(apply(fit2$betalw,1,var))
      allo  hodgkins      kscore      wtime
0.4672208 -1.8189603  7.4173339  1.5607492  ####z-statistic of log-rank
estimator

> round(10000*2.0*(1-
pnorm(abs(fit2$beta[1,]/sqrt(apply(fit2$betagm,1,var))))))/10000
      allo hodgkins      kscore      wtime

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0.5721    0.0165    0.0000    0.0485 ###p-value of Gehan estimator

> round(10000*2.0*(1-
pnorm(abs(fit2$beta[2,]/sqrt(apply(fit2$betalw,1,var)))))/10000
      allo hodgkins    kscore    wtime
0.6403    0.0689    0.0000    0.1186 ###z-statistic of log-rank
estimator

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