

Poisson GLM, Cox PH, & degrees of freedom

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March 7, 2019

1 Introduction

We discuss connections between the Cox proportional hazards model and Poisson generalized linear models as described in Whitehead (1980). We fit comparable models to a sample dataset using `coxph()`, `glm()`, `phmm()`, and `glmer()` and explore similarities.

2 A simple Cox PH example

2.1 Generate data

We generate proportional hazards mixed model data.

```
options(width=75)
library(phmm)

## Loading required package: survival
## Loading required package: lattice
## Loading required package: Matrix

n <- 50      # total sample size
nclust <- 5  # number of clusters
clusters <- rep(1:nclust, each=n/nclust)
beta0 <- c(1,2)
set.seed(13)

Z <- cbind(Z1=sample(0:1,n,replace=TRUE),
           Z2=sample(0:1,n,replace=TRUE),
           Z3=sample(0:1,n,replace=TRUE))
b <- cbind(rep(rnorm(nclust), each=n/nclust),
           rep(rnorm(nclust), each=n/nclust))
Wb <- matrix(0,n,2)
for( j in 1:2) Wb[,j] <- Z[,j]*b[,j]
Wb <- apply(Wb,1,sum)
T <- -log(runif(n,0,1))*exp(-Z[,c('Z1','Z2')]*beta0-Wb)
C <- runif(n,0,1)
time <- ifelse(T<C,T,C)
event <- ifelse(T <= C,1,0)
sum(event)
```

```
## [1] 31

phmmd <- data.frame(Z)
phmmd$cluster <- clusters
phmmd$time <- time
phmmd$event <- event
```

2.2 Fit the Cox PH model

```
fit.ph <- coxph(Surv(time, event) ~ Z1 + Z2,
  phmmd, method="breslow", x=TRUE, y=TRUE)

summary(fit.ph)

## Call:
## coxph(formula = Surv(time, event) ~ Z1 + Z2, data = phmmd, x = TRUE,
##       y = TRUE, method = "breslow")
##
## n= 50, number of events= 31
##
##      coef exp(coef) se(coef)      z Pr(>|z|)
## Z1 0.8549   2.3513   0.3918 2.182 0.02909 *
## Z2 1.0888   2.9708   0.3684 2.955 0.00312 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      exp(coef) exp(-coef) lower .95 upper .95
## Z1      2.351      0.4253   1.091   5.067
## Z2      2.971      0.3366   1.443   6.116
##
## Concordance= 0.71 (se = 0.048 )
## Rsquare= 0.237 (max possible= 0.984 )
## Likelihood ratio test= 13.55 on 2 df,  p=0.001
## Wald test               = 13.52 on 2 df,  p=0.001
## Score (logrank) test = 14.63 on 2 df,  p=7e-04
```

Next we create data to fit an auxiliary Poisson model as described in Whitehead (1980) using the `pseudoPoisPHMM()` function provided in the `phmm` package. This function also extracts the linear predictors as estimated from the Cox PH model so that we can calculate likelihoods and degrees of freedom.

2.3 Likelihood and degrees of freedom for Poisson GLM from Cox PH parameters

```
ppd <- as.data.frame(as.matrix(pseudoPoisPHMM(fit.ph)))

# pois likelihood
poisl <- c()
eventtimes <- sort(phmmd$time[phmmd$event == 1])
for(h in 1:length(eventtimes)){
  js <- ppd$time == eventtimes[h] & ppd$m >= 1 # j star
  j <- ppd$time == eventtimes[h]
  if(sum(js) > 1) stop("tied event times")
}
```

```

poisl <- c(poisl,
  ppd[js, "N"]*exp(-1)*exp(ppd[js, "linear.predictors"])/
  sum(ppd[j, "N"]*exp(ppd[j, "linear.predictors"])))
}

```

Poisson likelihood:

```

(coxph.pois.loglik = sum(log(poisl)))
## [1] -66.5633
coxph.pois.loglik - fit.ph$loglik[2]
## [1] 29.40801

```

Poisson degrees of freedom

```

(coxph.pois.df = length(fit.ph$coef) + sum(phmmd$event))
## [1] 33

```

2.4 Fit auxiliary Poisson GLM

We fit an auxiliary Poisson GLM and note that the parameter estimates for z1 and z2 are identical to the coxph() fit, and the likelihood and degrees of freedom are as expected.

```

ppd$t <- as.factor(ppd$time)
fit.glm <- glm(m~-1+t+z1+z2+offset(log(N)),
  ppd, family=poisson)

summary(fit.glm)

##
## Call:
## glm(formula = m ~ -1 + t + z1 + z2 + offset(log(N)), family = poisson,
## data = ppd)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -0.9685 -0.7531 -0.5553 0.4293 1.6823
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## t0.000277233256778163 -5.0494 1.0704 -4.717 2.39e-06 ***
## t0.000285092717793308 -5.0035 1.0679 -4.685 2.79e-06 ***
## t0.000382448373472765 -4.9876 1.0683 -4.669 3.03e-06 ***
## t0.00559427171447325 -4.9388 1.0655 -4.635 3.57e-06 ***
## t0.00764335258097282 -4.8875 1.0625 -4.600 4.22e-06 ***
## t0.00808285780728387 -4.8648 1.0635 -4.574 4.78e-06 ***
## t0.0216256697018544 -4.8013 1.0609 -4.526 6.02e-06 ***
## t0.0219649983261458 -4.7930 1.0622 -4.512 6.41e-06 ***
## t0.0233956453029104 -4.7681 1.0634 -4.484 7.34e-06 ***
## t0.0235837855332384 -4.7069 1.0598 -4.441 8.95e-06 ***
## t0.0237625311885084 -4.6797 1.0612 -4.410 1.03e-05 ***

```

```

## t0.027482795605763      -4.6127      1.0572     -4.363 1.28e-05 ***
## t0.0278642961804028     -4.5890      1.0573     -4.340 1.42e-05 ***
## t0.0316525538364514     -4.5401      1.0576     -4.293 1.76e-05 ***
## t0.0357745779481545     -4.5147      1.0578     -4.268 1.97e-05 ***
## t0.0366185731334857     -4.4351      1.0529     -4.212 2.53e-05 ***
## t0.066999301944422      -4.3869      1.0556     -4.156 3.24e-05 ***
## t0.0742904888064418     -4.3572      1.0557     -4.127 3.67e-05 ***
## t0.09491415021304       -4.2493      1.0513     -4.042 5.30e-05 ***
## t0.125132209250348      -4.2151      1.0513     -4.010 6.08e-05 ***
## t0.132722661166308      -4.1798      1.0513     -3.976 7.01e-05 ***
## t0.140357744467437      -4.0667      1.0439     -3.896 9.79e-05 ***
## t0.163527928343998      -3.9258      1.0448     -3.757 0.000172 ***
## t0.193971448733795      -3.7760      1.0443     -3.616 0.000299 ***
## t0.204887967162952      -3.7054      1.0458     -3.543 0.000396 ***
## t0.227852125295401      -3.6459      1.0457     -3.486 0.000490 ***
## t0.266238317485871      -3.5253      1.0513     -3.353 0.000799 ***
## t0.276177426334698      -3.2951      1.0356     -3.182 0.001464 **
## t0.360993505812205      -3.2039      1.0353     -3.095 0.001970 **
## t0.426697507683412      -2.7934      1.0367     -2.694 0.007051 **
## t0.511995413073629      -1.8487      1.0105     -1.830 0.067323 .
## z1                        0.8549      0.3918      2.182 0.029092 *
## z2                        1.0888      0.3684      2.955 0.003123 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 1743.184  on 121  degrees of freedom
## Residual deviance:   71.127  on   88  degrees of freedom
## AIC: 199.13
##
## Number of Fisher Scoring iterations: 6

cbind(coxph.coef = fit.ph$coef, glm.coef = coef(fit.glm)[c('z1', 'z2')])

##      coxph.coef  glm.coef
## Z1  0.8549497  0.8549497
## Z2  1.0888337  1.0888337

cbind(coxph.pois.loglik, glm.loglik=logLik(fit.glm))

##      coxph.pois.loglik  glm.loglik
## [1,]                -66.5633    -66.5633

```

The additional parameter estimates correspond to the estimated log baseline hazard, which we verify using the `basehaz()` function.

```

bh <- basehaz(fit.ph, centered = FALSE)
cbind(
  coxph.bh.step = log(bh$hazard - c(0, bh$hazard[1:(length(bh$hazard)-1)])) [1:5],
  glm.bh.step = coef(fit.glm) [1:5]
)

##      coxph.bh.step  glm.bh.step
## t0.000277233256778163      -5.049378    -5.049378

```

```
## t0.000285092717793308      -5.003546   -5.003546
## t0.000382448373472765      -4.987633   -4.987633
## t0.00559427171447325       -4.938810   -4.938810
## t0.00764335258097282       -4.887479   -4.887479
```

3 Extending to PHMM

3.1 Fit PHMM

```
fit.phmm <- phmm(Surv(time, event) ~ Z1 + Z2 + (Z1 + Z2|cluster),
  phmmd, Gbs = 100, Gbsvar = 1000, VARSTART = 1,
  NINIT = 10, MAXSTEP = 100, CONVERG=90)
summary(fit.phmm)

##
## Proportional Hazards Mixed-Effects Model fit by MCMC-EM
## Model: Surv(time, event) ~ Z1 + Z2 + (Z1 + Z2 | cluster)
## Data: phmmd
## Log-likelihood:
## Conditional      Laplace          RIS
##      -83.43      -122.61      -122.53
##
## Fixed effects: Surv(time, event) ~ Z1 + Z2
## Estimate Std.Error
## Z1  0.8171  0.3888
## Z2  1.5158  0.2903
##
## Random effects: (Z1 + Z2 | cluster)
## Estimated variance-covariance matrix:
##      (Intercept)      Z1      Z2
## (Intercept)      0.1951 0.0000 0.0000
## Z1                0.0000 0.4559 0.0000
## Z2                0.0000 0.0000 0.3465
##
## Number of Observations: 50
## Number of Groups: 5
```

3.2 Likelihood and degrees of freedom for Poisson GLMM from PHMM parameters

```
ppd <- as.data.frame(as.matrix(pseudoPoisPHMM(fit.phmm)))

poisl <- c()
eventtimes <- sort(phmmd$time[phmmd$event == 1])
for(h in 1:length(eventtimes)){
  js <- ppd$time == eventtimes[h] & ppd$m >= 1 # j star
  j <- ppd$time == eventtimes[h]
  if(sum(js) > 1) stop("tied event times")
  poisl <- c(poisl,
    ppd[js, "N"]*exp(-1)*exp(ppd[js, "linear.predictors"])/
    sum(ppd[j, "N"]*exp(ppd[j, "linear.predictors"])))
}
```

```
}
```

Poisson likelihood:

```
phmm.pois.loglik = sum(log(poisl))
phmm.pois.loglik - fit.phmm$loglik[1]

## Conditional
## -10.03456
```

Poisson degrees of freedom

```
# Poisson GLMM degrees of freedom length(unique(x$cluster)) * x$nrandom + x$fixed
traceHat(fit.phmm, "pseudoPois") # + 2*sum(phmmd$event)

## [1] 6.505417
```

3.3 Fit auxiliary Poisson GLMM

We fit an auxiliary Poisson GLMM, although with a general variance-covariance matrix for the random effects (phmm() only fits models with diagonal variance-covariance matrix).

```
library(lme4)
ppd$t <- as.factor(ppd$time)
fit.lmer <- glmer(m~1+t+z1+z2+
  (z1+z2|cluster)+offset(log(N)),
  data=ppd, family=poisson, nAGQ=0)

summary(fit.lmer)$coef

##              Estimate Std. Error  z value    Pr(>|z|)
## t0.000277233256778163 -5.958010  1.1564660 -5.151911 2.578457e-07
## t0.000285092717793308 -5.812091  1.1439927 -5.080531 3.763812e-07
## t0.000382448373472765 -5.793228  1.1454929 -5.057411 4.249877e-07
## t0.00559427171447325  -5.695820  1.1403300 -4.994887 5.887022e-07
## t0.00764335258097282  -5.587889  1.1353871 -4.921572 8.585188e-07
## t0.00808285780728387  -5.579025  1.1366552 -4.908283 9.187739e-07
## t0.0216256697018544  -5.354631  1.1140436 -4.806482 1.536091e-06
## t0.0219649983261458  -5.351292  1.1147514 -4.800436 1.583210e-06
## t0.0233956453029104  -5.305904  1.1172975 -4.748873 2.045537e-06
## t0.0235837855332384  -5.003952  1.0894229 -4.593214 4.364714e-06
## t0.0237625311885084  -4.939091  1.0914764 -4.525147 6.035353e-06
## t0.027482795605763   -4.909025  1.0906328 -4.501080 6.760915e-06
## t0.0278642961804028  -4.876374  1.0907984 -4.470463 7.805027e-06
## t0.0316525538364514  -4.818245  1.0926035 -4.409875 1.034302e-05
## t0.0357745779481545  -4.766444  1.0943791 -4.355386 1.328324e-05
## t0.0366185731334857  -4.466495  1.0662062 -4.189148 2.800043e-05
## t0.066999301944422   -4.341048  1.0720560 -4.049274 5.137684e-05
## t0.0742904888064418  -4.317349  1.0714179 -4.029566 5.588003e-05
## t0.09491415021304    -4.260289  1.0698365 -3.982187 6.828400e-05
## t0.125132209250348   -4.196863  1.0699310 -3.922555 8.761488e-05
## t0.132722661166308   -4.181387  1.0700511 -3.907652 9.319747e-05
## t0.140357744467437   -4.050659  1.0570046 -3.832206 1.269992e-04
## t0.163527928343998   -3.850829  1.0550657 -3.649848 2.623956e-04
```

```
## t0.193971448733795 -3.567027 1.0528487 -3.387976 7.041032e-04
## t0.204887967162952 -3.445926 1.0538681 -3.269789 1.076278e-03
## t0.227852125295401 -3.386892 1.0531723 -3.215896 1.300380e-03
## t0.266238317485871 -3.255781 1.0602681 -3.070715 2.135471e-03
## t0.276177426334698 -3.082084 1.0473420 -2.942767 3.252930e-03
## t0.360993505812205 -2.859386 1.0472011 -2.730504 6.323764e-03
## t0.426697507683412 -2.392130 1.0413227 -2.297203 2.160717e-02
## t0.511995413073629 -1.634348 1.0219183 -1.599294 1.097553e-01
## z1 0.811712 0.4574939 1.774257 7.602057e-02
## z2 1.609640 0.4527416 3.555317 3.775230e-04
```

```
fit.phmm$coef
```

```
##          Z1          Z2
## 0.8170856 1.5157523
```

```
logLik(fit.lmer)
```

```
## 'log Lik.' -100.9984 (df=39)
```

```
phmm.pois.loglik - logLik(fit.lmer)[1]
```

```
## [1] 7.533638
```

```
cbind(
  phmm.bh.step = log(fit.phmm$lambda)[1:5],
  glm.bh.step = fixef(fit.lmer)[1:5]
)
```

```
##          phmm.bh.step glm.bh.step
## t0.000277233256778163 -5.903387 -5.958010
## t0.000285092717793308 -5.779829 -5.812091
## t0.000382448373472765 -5.756366 -5.793228
## t0.00559427171447325 -5.661413 -5.695820
## t0.00764335258097282 -5.556490 -5.587889
```