Cox regression: Estimation

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Introduction

- In our last lecture, we introduced the Cox partial likelihood; today, we will go over how to solve for $\widehat{\boldsymbol{\beta}}$, the maximum (partial) likelihood estimator
- As in previous models, this will require working out the score vector and Hessian matrix and applying an iterative Newton-Raphson procedure
- On a superficial level this procedure is similar to our other regression models, but the details are quite different: although the observations are independent, we can no longer treat the partial likelihood contributions from each observation in isolation

Partial likelihood; at-risk indicator

- Recall the Cox partial likelihood (PL):

$$L(\boldsymbol{\beta}) = \prod_j \frac{\exp(\mathbf{x}_j^T \boldsymbol{\beta})}{\sum_{k \in R(t_j)} \exp(\mathbf{x}_k^T \boldsymbol{\beta})},$$

  where j indexes the observed failure times and $R(t)$ is the set of observations at risk at time t

- The denominator in the expression above is also sometimes written as

$$\sum_{k=1}^{n} Y_k(t_j) \exp(\mathbf{x}_k^T \boldsymbol{\beta}),$$

  where $Y_i(t)$ is an *at-risk indicator*, equal to 1 if subject i is at risk at time t, and 0 otherwise

Cox PL in terms of individual weights

- As an alternative, it is often convenient to express the likelihood as a product of terms for each individual, as opposed to each failure time
- To simplify the expression, let $w_j = \exp(\mathbf{x}_j^T \boldsymbol{\beta})$; the cox partial likelihood can now be written as

$$L(\boldsymbol{\beta}) = \prod_i \left\{ \frac{w_i}{\sum_{R_i} w_j} \right\}^{d_i}$$

- Expressing the partial likelihood in this way emphasizes the fact that the model assigns weights w_i to the relative likelihood that individual i will fail compared to the other subjects at risk

Comments

- Note that the d_i exponent ensures that only the observations at which a failure is observed contribute to the likelihood
- However, because each subject affects the total hazard $\sum w_j$ over all the failure times at which they are in the risk set, the contribution that subject i makes to the likelihood is not limited to the ith term in the product
- Because this sum will appear many times in our derivations today, I will denote it W_i:

$$W_i = \sum_{R(t_i)} w_j,$$

where W_i represents the total hazard for all subjects at risk for the time at which subject i fails

Failure probabilities

- The relative probability of failure for subject i is given by w_i; let us denote the absolute probability of failure for subject i at time t_j as π_{ij}:

$$\pi_{ij} = Y_i(t_j)\frac{w_i}{W_j}$$

- Note, of course, that this probability is absolute only in the conditional sense, given that a failure occurs at time t_j

Log-likelihood

- The (partial) log-likelihood is therefore

$$\begin{aligned}\ell &= \sum_i d_i \log w_i - \sum_i d_i \log W_i \\ &= \sum_i d_i \eta_i - \sum_i d_i \log W_i\end{aligned}$$

- As we begin to take derivatives, keep in mind that the W_i term contains many η terms in addition to η_i

Score (with respect to $\boldsymbol{\eta}$)

- Solving for $\widehat{\boldsymbol{\beta}}$ involves deriving the score equations and setting them equal to zero
- Let us begin by evaluating the partial derivative of the likelihood with respect to the kth linear predictor:

$$\frac{\partial \ell}{\partial \eta_k} = d_k - \sum_i \pi_{ki} d_i$$

- Thus, we can write the score with respect to the vector of linear predictors as

$$\mathbf{u}(\boldsymbol{\eta}) = \mathbf{d} - \mathbf{P}\mathbf{d},$$

where $\mathbf{P}$ is an $n \times n$ matrix with elements π_{ij}

Score (with respect to β)

- As we have seen before, by the chain rule the score with respect to $\boldsymbol{\beta}$ is therefore

$$\mathbf{u}(\boldsymbol{\beta}) = \mathbf{X}^T(\mathbf{d} - \mathbf{P}\mathbf{d})$$

- Alternatively, we can express the score equations as

$$\sum_j (\mathbf{x}_j - \mathbb{E}_j \mathbf{x}) = \mathbf{0},$$

where $\mathbb{E}_j \mathbf{x} = \sum_i \mathbf{x}_i \pi_{ij}$ can be thought of as the expected value of the covariate vector at the jth failure time given the probability distribution implied by the model

Hessian (with respect to $\boldsymbol{\eta}$)

- The score, of course, is nonlinear in $\boldsymbol{\beta}$, meaning that we will have to apply a Taylor series expansion in order to solve it
- This, in turn, involves finding second derivatives: i.e., the Hessian matrix
- Let us start with the diagonal elements (with respect to the linear predictors):

$$\frac{\partial^2 \ell}{\partial \eta_k^2} = -\sum_i d_i \pi_{ki}(1 - \pi_{ki})$$

- Similarly,

$$\frac{\partial^2 \ell}{\partial \eta_k \partial \eta_j} = \sum_i d_i \pi_{ki} \pi_{ji}$$

Hessian (with respect to β)

- Again, applying the chain rule we obtain the Hessian with respect to $\boldsymbol{\beta}$:

$$\mathbf{H}(\boldsymbol{\beta}) = -\mathbf{X}^T\mathbf{W}\mathbf{X},$$

where $\mathbf{W}$ denotes the (non-diagonal) matrix whose terms are given on the previous slide, with signs reversed (note that $\mathbf{W}$ is unrelated to W_i; my apologies if the notation is confusing)

- Alternatively, one can express the Hessian as

$$-\mathbf{H}(\boldsymbol{\beta}) = \sum_j \sum_k \pi_{kj}(\mathbf{x}_k - \mathbb{E}_j\mathbf{x})(\mathbf{x}_k - \mathbb{E}_j\mathbf{x})^T,$$

where j here indexes the observed failure times

Newton-Raphson algorithm

- As we have seen previously with the exponential and Weibull regression models, the Newton-Raphson algorithm is an effective, efficient iterative procedure that converges to the MLE (usually)
- For Cox regression, the Newton-Raphson update is given by

$$\widehat{\boldsymbol{\beta}}_{(m+1)} = (\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\mathbf{X}^T(\mathbf{d} - \mathbf{P}\mathbf{d}) + \widehat{\boldsymbol{\beta}}_{(m)},$$

  where $\mathbf{W}$ and $\mathbf{P}$ are evaluated at $\widehat{\boldsymbol{\beta}}_{(m)}$, the current value of the regression coefficients

Crude R code

```
for (i in 1:20) {
  eta <- X %*% b
  haz <- as.numeric(exp(eta))   # w[i]
  rsk <- rev(cumsum(rev(haz)))  # W[i]
  P <- outer(haz, rsk, '/')
  P[upper.tri(P)] <- 0
  W <- -P %*% diag(d) %*% t(P)
  diag(W) <- diag(P %*% diag(d) %*% t(1-P))
  b <- solve(t(X)%*%W%*% X) %*% t(X) %*% (d - P%*%d) + b
}
```

The above code assumes that the data has been sorted by time on study, and assumes no ties are present

Comments

- The code on the previous slide is crude for several reasons:
  - It could be faster/more efficient
  - It doesn't check for convergence
  - It can occasionally fail to converge, because it doesn't implement step-halving when needed
- You are tasked with addressing the last two shortcomings on your next homework assignment

Examples: pbc data

Some examples for how well Newton-Raphson works on the `pbc` data:

- Model contains `trt`, `stage`, and `hepato`: Converges in 4 iterations
- Model contains `trt`, `stage`, `hepato`, and `bili`: Fails to converge
- Model contains `trt`, `stage`, `hepato`, and `bili`, but we employ step-halving: Converges in ~ 20 iterations

Conditional step-halving

- The `survival` package, however, can fit the Cox model with `trt`, `stage`, `hepato`, and `bili` in just 6 iterations . . . how does it do that?
- The fundamental tradeoff here is between stability and speed: step-halving slows down convergence (intentionally!), but provides stability
- It would be desirable to use Newton-Raphson as a default, but have some sort of check in place that uses step-halving when problems arise

Likelihood checking

- It turns out that this is fairly straightforward to accomplish
- Let $\widetilde{\boldsymbol{\beta}}$ denote the Newton-Raphson update, and consider the following procedure:
  (1) Calculate $\ell(\widehat{\boldsymbol{\beta}}_{(m)})$
  (2) Calculate $\ell(\widetilde{\boldsymbol{\beta}})$
  (3) If $\ell(\widetilde{\boldsymbol{\beta}}) > \ell(\widehat{\boldsymbol{\beta}}_{(m)})$, then $\widehat{\boldsymbol{\beta}}_{(m+1)} \leftarrow \widetilde{\boldsymbol{\beta}}$; otherwise, $\widehat{\boldsymbol{\beta}}_{(m+1)} \leftarrow \frac{1}{2}\widetilde{\boldsymbol{\beta}} + \frac{1}{2}\widehat{\boldsymbol{\beta}}_{(m)}$
- Using this procedure, we can solve for $\widehat{\boldsymbol{\beta}}$ in 6 iterations, using step-halving only once, on the initial update

Guaranteed convergence?

- The procedure on the previous page almost always works, but is still not *guaranteed* to converge
- The reason is that step halving might not be enough: it is possible that $\ell(\frac{1}{2}\widetilde{\boldsymbol{\beta}} + \frac{1}{2}\widehat{\boldsymbol{\beta}}_{(m)})$ is still smaller than $\ell(\widehat{\boldsymbol{\beta}}_{(m)})$
- To guarantee convergence, we need to iteratively reapply the step-halving: consider $\frac{1}{4}, \frac{1}{8}, \frac{1}{16}, \ldots$ until we reach a step size small enough that the likelihood does, in fact, increase
- Typically, this is not necessary, but this kind of check is necessary to ensure that the likelihood goes up with every iteration, even in pathological cases

Ties

- As a final comment, note that we are ignoring the issue of tied observations, even though there are in fact a few ties in the `pbc` data
- However, unless there are a large number of ties, this is typically a very minor issue:

	trt	stage	hepato	bili
Crude	-0.15530	0.62157	0.34860	0.13358
`survival`	-0.15473	0.62138	0.34854	0.13353

- We will, however, discuss ties more carefully in a future lecture