PH 716 Applied Survival Analysis

Part V: Cox Proportional Hazards Model

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Assumptions for Cox proportional hazards (PH) model

- Observed $\widetilde{T}_i = \widetilde{t}_i$ and $\Delta_i = \delta_i$ (event indicator)
- T_i are independent across i, given x_{i1}, \ldots, x_{ip}
- The independent and non-informative censoring
- $\lambda_{T_i}(t) = \lambda(t \mid x_{i1}, \dots, x_{ip}) = \lambda_0(t) \exp(\sum_{j=1}^p x_{ij}\beta_j)$, or equiv. $\ln \lambda_{T_i}(t) = \ln \lambda_0(t) + \sum_{j=1}^p x_{ij}\beta_j$
 - $-\lambda_0(t)$ (the baseline hazard): obtained when all covariates are zeros and left unspecified
 - * A semi-parametric generalized linear model: nonparmetric baseline hazard + paramatric
 - Proportional hazards: the HR between any two individuals, say $\lambda_{T_{i_1}}(t)/\lambda_{T_{i_2}}(t)=\exp(\sum_{j=1}^p x_{i_1j}\beta_j-\sum_{j=1}^p x_{i_2j}\beta_j)$, is constant over time No intercept β_0

 - Interpretation of β_i : exp(β_i) is the HR associated with one-unit change of the jth covariate, fixing everything else

Weibull regression as a special case of PH models

- Recall the Weibull regression: $\ln T_i = \beta_0 + \sum_{j=1}^p x_{ij}\beta_j + \sigma\varepsilon_i$ with $\varepsilon_i \stackrel{\text{iid}}{\sim} F_{\varepsilon_i}(\epsilon) = 1 \exp(-\exp\epsilon)$
 - $-S_{T_i}(t) = \exp[-\{t/\exp(\beta_0 + \sum_{j=1}^p x_{ij}\beta_j)\}^{1/\sigma}] \Rightarrow \lambda_{T_i}(t) = (1/\sigma)t^{1/\sigma 1}\exp\{(-\beta_0 \sum_{j=1}^p x_{ij}\beta_j)/\sigma\}$
- $\lambda_{T_i}(t) = \lambda_0(t) \exp(\sum_{j=1}^p x_{ij}\beta_j^*)$ if $\lambda_0(t) = (1/\sigma)t^{1/\sigma-1} \exp(-\beta_0/\sigma)$ and $\beta_j^* = -\beta_j/\sigma$, $j = 1, \dots, p$
- The only continuous-time model that is both a PH and an AFT model

Partial likelihood (assuming no tied failure time)

- The observed-data likelihood $L(\beta, \lambda_0) = \prod_i \lambda_{T_i}(\tilde{t}_i)^{\delta_i} S_{T_i}(\tilde{t}_i)$ relying on both $\beta = [\beta_1, \dots, \beta_j]^{\top}$ and unspecified $\lambda_0(\cdot)$
- Further assumptions
 - K and only K distinct, ordered failure times, say $t_1 < \cdots < t_K$
 - No tied failure time: for each k, there is one and only one individual, say subject i_k , who fails at t_k
 - Risk set $\mathcal{R}(t) = \{i : \widetilde{T}_i \geq t\}$: the set of individuals who are known to survive just prior to time t
- Rephrase $L(\beta, \lambda_0)$:

$$L(\boldsymbol{\beta}, \lambda_0) = \prod_{i=1}^n \lambda_{T_i}(\tilde{t}_i)^{\delta_i} S_{T_i}(\tilde{t}_i) = \prod_{i=1}^n \left\{ \frac{\lambda_{T_i}(\tilde{t}_i)}{\sum_{\ell \in \mathcal{R}(\tilde{t}_i)} \lambda_{T_\ell}(\tilde{t}_i)} \right\}^{\delta_i} \times \left\{ \sum_{\ell \in \mathcal{R}(\tilde{t}_i)} \lambda_{T_\ell}(\tilde{t}_i) \right\}^{\delta_i} \times S_{T_i}(\tilde{t}_i)$$

• Take the partial likelihood (i.e., the first term of the above $L(\beta, \lambda_0)$)

$$pL(\boldsymbol{\beta}) = \prod_{i=1}^n \left\{ \frac{\lambda_{T_i}(\tilde{t}_i)}{\sum_{k \in \mathcal{R}(\tilde{t}_i)} \lambda_{T_k}(\tilde{t}_i)} \right\}^{\delta_i} = \prod_{i=1}^n \left\{ \frac{\exp(\sum_{j=1}^p x_{ij}\beta_j)}{\sum_{\ell \in \mathcal{R}(\tilde{t}_i)} \exp(\sum_{j=1}^p x_{\ell j}\beta_j)} \right\}^{\delta_i} = \prod_{k=1}^K \frac{\exp(\sum_{j=1}^p x_{ikj}\beta_j)}{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^p x_{\ell j}\beta_j)}$$

as a surrogate of $L(\beta, \lambda_0)$ in estimating β

- Cox (1972) argued that $pL(\beta)$ contained almost all the information about β
- Extensive evidence, both theoretical and numerical, supported this argument in the past few
- decades $\frac{\exp(\sum_{j=1}^p x_{i_k j} \beta_j)}{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^p x_{\ell j} \beta_j)}$: the probability of selecting a particular person (here subject i_k) from the risk set at time t_k
- Log-partial likelihood

$$p\ell(\beta) = \ln pL(\beta) = \sum_{k=1}^{K} \left\{ \sum_{j=1}^{p} x_{kj} \beta_j - \ln \sum_{\ell \in \mathcal{R}(t_k)} \exp \left(\sum_{j=1}^{p} x_{\ell j} \beta_j \right) \right\}$$

Ex. 5.1 The calculation of partial likelihood

\overline{i}	\tilde{t}_i	δ_i	x_i
1	9	1	4
2	8	0	5
3	6	1	7
4	10	1	3

• Follow the following definition (without reordering failure times) and fill in the table

$$pL(\boldsymbol{\beta}) = \prod_{i=1}^{n} \left\{ \frac{\exp(\sum_{j=1}^{p} x_{ij} \beta_{j})}{\sum_{\ell \in \mathcal{R}(\tilde{t}_{i})} \exp(\sum_{j=1}^{p} x_{\ell j} \beta_{j})} \right\}^{\delta_{i}}$$

i	$ ilde{t}_i$	δ_i	x_i	$\mathcal{R}(ilde{t}_i)$	$\left\{\frac{\exp(x_i\beta)}{\sum_{\ell\in\mathcal{R}(\tilde{t}_i)}\exp(x_\ell\beta)}\right\}^{\delta_i}$
1	9	1	4		
2	8	0	5		
3	6	1	7		
4	10	1	3		

Ex. 5.2 The calculation of partial likelihood: comparison of two groups

• Covariate x_i indicating the group label

i	$ ilde{t}_i$	δ_i	x_i	$\mathcal{R}(\tilde{t}_i)$	$\frac{\exp(x_i\beta)}{\sum_{\ell\in\mathcal{R}(\tilde{t}_i)}\exp(x_\ell\beta)}$
1	4	0	0		
2	7	1	0		
3	8	0	0		
4	9	1	0		

i	$ ilde{t}_i$	δ_i	x_i	$\mathcal{R}(ilde{t}_i)$	$\frac{\exp(x_i\beta)}{\sum_{\ell\in\mathcal{R}(\tilde{t}_i)}\exp(x_\ell\beta)}$
5	10	0	0		
6	3	1	1		
7	5	1	1		
8	5	0	1		
9	6	1	1		
10	8	0	1		

```
library(survival)
data = data.frame(
   tte = c(4,7,8,9,10,3,5,5,6,8),
   delta = c(0,1,0,1,0,1,1,0,1,0),
   x = c(0,0,0,0,0,1,1,1,1,1)
)
fit = coxph(Surv(tte,delta)~x, data = data)
summary(fit)
```

- $\exp(\beta)$ is the hazard ratio of group = 1 against group = 0, fixing covariates other than (if any). It implies that one jumps from group = 0 to group = 1 the hazard would be inflated by $(\exp(\beta) 1) \times 100\%$.
- Is there any difference between the survival of the two groups? There are at least four *p*-values. Which one shall we refer to?
- What are meanings of other digits in the output?
- What if there are more covariates?

Ex. 5.3. Leukemia data (with tied event/failure times)

```
survival::leukemia
```

Partial likelihood (Cox's modification)

- Assumptions
 - K and only K distinct, ordered failure times, say $t_1 < \cdots < t_K$
 - $-d_k$ failures at time t_k : there are d_k individuals, say subject $i_{k,1},\ldots,i_{k,d_k}$, who fail at t_k
- Accordingly

$$pL(\boldsymbol{\beta}) = \prod_{k=1}^{K} \frac{\prod_{i \in \{i_{k,1}, \dots, i_{k,d_k}\}} \exp(\sum_{j} x_{ij} \beta_j)}{\sum_{D(d_k) \subset \mathcal{R}(t_k)} \prod_{i \in D(d_k)} \exp(\sum_{j} x_{ij} \beta_j)}$$

- $-D(d_k) \subset \mathcal{R}(t_k)$: a subset of $\mathcal{R}(t_k)$ containing d_k subjects, i.e., a set of d_k individuals who are at risk at t_k
- Labeled as exact by survival::coxph

Partial likelihood (Breslow's approximation)

- Keeping the assumptions for the Cox's modification
- Substituting $\{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^p x_{\ell j} \beta_j)\}^{d_k}$ for the denominator of the Cox's modification

$$pL(\boldsymbol{\beta}) = \prod_{k=1}^{K} \frac{\prod_{i \in \{i_{k,1}, \dots, i_{k,d_k}\}} \exp(\sum_{j} x_{ij} \beta_j)}{\{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^{p} x_{\ell j} \beta_j)\}^{d_k}}$$

• Default tie-handling method in SAS

Partial likelihood (Efron's approximation)

- Keeping the assumptions for the Cox's modification
- Substitute $\prod_{m=1}^{d_k} \{ \sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^p x_{\ell j} \beta_j) \frac{m-1}{d_k} \sum_{i \in \{i_{k,1}, \dots, i_{k,d_k}\}} \exp(\sum_j x_{ij} \beta_j) \}$ for the denominator of Cox's modification

$$pL(\beta) = \prod_{k=1}^{K} \frac{\prod_{i \in \{i_{k,1}, \dots, i_{k,d_k}\}} \exp(\sum_{j} x_{ij} \beta_j)}{\prod_{m=1}^{d_k} \{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^{p} x_{\ell j} \beta_j) - \frac{m-1}{d_k} \sum_{i \in \{i_{k,1}, \dots, i_{k,d_k}\}} \exp(\sum_{j} x_{ij} \beta_j)\}}$$

• Default tie-handling method by survival::coxph

Summary of handling ties

- With no ties, all approximation options give exactly the same results
- With only a few ties, all approximations yield pretty much the same results
- With many ties (relative to the number at risk), both of Breslow's and Efron's approximations yield coefficients β that are biased toward 0.
- Computing time of Cox's method is substantially longer than that of approximate methods. But it is not a big issue with today's hardwares.
- The Efron's approximation almost always works better than the Breslow's method, without consuming
 more time.

Revisit Ex. 5.3. Leukemia data (with tied event/failure times)

```
library(survival)
data = survival::leukemia
fit1 = coxph(Surv(time, status)~x, data = data)
fit2 = coxph(Surv(time, status)~x, data = data, ties = 'efron')
fit3 = coxph(Surv(time, status)~x, data = data, ties = 'breslow')
fit4 = coxph(Surv(time, status)~x, data = data, ties = 'exact')
c(coef(fit1), coef(fit2), coef(fit3), coef(fit4))
```

CIs and hypothesis tests for HRs

- Suppose the HR of interest is the one associated with the one-unit increase of the jth covairate, i.e., $\exp(\beta_j)$
- $\operatorname{var}\{\exp(\hat{\beta}_i)\} \approx \exp(2\hat{\beta}_i)\operatorname{var}(\hat{\beta}_i)$ (delta method)
 - Hence $\operatorname{se}(\exp(\hat{\beta}_i)) \approx \exp(\hat{\beta}_i)\operatorname{se}(\hat{\beta}_i)$
- 95% CI for $\exp(\beta_i)$
 - $\exp(\hat{\beta}_j) \pm \Phi^{-1}(.975) \times \sec(\exp(\hat{\beta}_j))$ * $\Phi^{-1}(.975) \ (\approx 1.96)$: the .975 quantile of N(0,1)- $\exp(\hat{\beta}_i \pm \Phi^{-1}(.975) \times \sec(\hat{\beta}_i))$ (preferred; why?)
- Hypothesis test for $H_0: \exp(\beta_i) = 1$ (i.e., $\beta_i = 0$) vs. $H_1:$ otherwise.
 - Wald test statistic: $\hat{\beta}_j/\text{se}(\hat{\beta}_j) \approx N(0,1)$ under H_0 * Equivalent to checking whether $\exp(\hat{\beta}_i \pm \Phi^{-1}(.975) \times \text{se}(\hat{\beta}_i))$ covers 1
- LRT to compare two nested models

```
- Model 1 nested to Model 2  * \text{ Model 1: } \lambda(t \mid x_{i1}, \dots, x_{ip}) = \lambda_0(t) \exp(\sum_{j=1}^p x_{ij}\beta_j) \\ * \text{ Model 2: } \lambda(t \mid x_{i1}, \dots, x_{ip}, x_{i,q+1}, \dots, x_{i,p+q}) = \lambda_0(t) \exp(\sum_{j=1}^{p+q} x_{ij}\beta_j) \\ - H_0 : \text{ Model 1 is correct (i.e., } \beta_{p+1} = \dots = \beta_{p+q} = 0) \text{ vs. } H_1 : \text{ Model 2 is correct } \\ - \text{ Test statistic: } 2(\ln L_{\text{Model2}} - \ln L_{\text{Model1}}) \approx \chi^2(q) \text{ under } H_0
```

Ex. 5.4. Nursing home data

- Variables:
 - ID: Patient ID
 - lstay: Length of stay of a resident (in days)
 - age: Age of a resident
 - trt: Nursing home assignment (1: receive treatment, 0: control)
 - gender: Gender (1:male, 0:female)
 - marstat: Marital status (1: married, 0: not married)
 - hlstat: Health status (2: second best, 5: worst)
 - cens: Censoring indicator (1:censored, 0: discharged)

```
options(digits=4)
library(survival)
data = read.csv("NursingHome.csv")
data$event <- 1-data$cens
head(data)
data$trt = factor(data$trt) # not necessary because it is of two levels
data$gender = factor(data$gender) # not necessary because it is of two levels
data$marstat = factor(data$marstat) # not necessary because it is of two levels
data$hlstat = factor(data$hlstat) # necessary because it is of more than two levels
fit1 <- coxph(Surv(lstay, event) ~ trt + age + gender + marstat + hlstat, data=data)
summary(fit1)
# Testing if trt is necessary against the full model
fit2 <- coxph(Surv(lstay, event) ~ age + gender + marstat + hlstat, data=data)
anova(fit1, fit2)
summary(fit2)
# Testing if trt, age and marstat are necessary against the full model
fit3 <- coxph(Surv(lstay, event) ~ gender + hlstat, data=data)
anova(fit1, fit3)
summary(fit3)
```

Estimating the baseline survival function

- Have to maximize the likelihood $L(\beta, \lambda_0)$ instead of the partial likelihood $pL(\beta)$
 - Assuming $\lambda_0(\cdot)$ as piecewise constant between uncensored failure time, Breslow (1972) proved that
 - * $L(\beta, \lambda_0)$ and $pL(\beta)$ share the identical maximizer, say $\hat{\beta}$, with respect to β
 - * The maximizer of $L(\beta, \lambda_0)$ with respect to λ_0 , say $\hat{\lambda}_0$, satisfies that

$$\hat{\Lambda}_0(t) = \sum_{k:t_k < t} \frac{d_k}{\sum_{\ell \in \mathcal{R}(t_k)} \exp(\sum_{j=1}^p x_{\ell j} \hat{\beta}_j)}$$

- · $\hat{\Lambda}_0(t)$: Breslow estimator of the baseline cumulative hazard rate, reducing to the NA estimator (Lecture Note Part II) if all covariates are zeros
- · d_k : # of events at t_k

```
 \begin{array}{c} \cdot \ \mathcal{R}(t_k) \text{: the risk set at } t_k \\ \bullet \ \widehat{S}_{T_i}(t) = \exp\{-\hat{\Lambda}_0(t)\}^{\exp(\sum_{j=1}^p x_{ij}\hat{\beta}_j)} = \widehat{S}_0(t)^{\exp(\sum_{j=1}^p x_{ij}\hat{\beta}_j)} \\ - \ \widehat{S}_0(t) = \exp\{-\hat{\Lambda}_0(t)\} \text{: estimated baseline survival function} \end{array}
```

Ex. 5.4. Revisit the nursing home data

```
options(digits=4)
library(survival)
data.ex54 = read.csv("NursingHome.csv")
data.ex54$event <- 1-data.ex54$cens
data.ex54$marstat = factor(data.ex54$marstat) # not necessary because it is of two levels
data.ex54$hlstat = factor(data.ex54$hlstat) # necessary because it is of more than two levels
fit.ex54 <- coxph(Surv(lstay,event) ~ marstat + hlstat, data=data.ex54)</pre>
## P.S. note the mandatory scaling of covariates in `survival::coxph`
# baseline hazard and survival
baseline <- basehaz(fit.ex54, centered = FALSE)</pre>
names(baseline)[1] = 'cum.haz'
baseline$surv = exp(-baseline$cum.haz)
baseline
# Plot the survival function with given values of covariates
newdata.ex54 <- data.frame(</pre>
 marstat = factor(c(0,0,1,1)),
 hlstat = factor(c(2,5,2,5))
newdata.ex54
cox.predicted.survival <- survfit(fit.ex54, newdata=newdata.ex54)</pre>
plot(
  cox.predicted.survival, lty=1:4, col=1:4, lwd=2,
  xlab="Survival Time", ylab="Estimated Probability"
legend(
  "topright",
  c(
    "Not married, health status second best",
    "Not married, health status worst",
    "Married, health status second best",
    "Married, health status worst"
  ),
  lty=1:4, col=1:4, lwd=2
```