Advanced Statistical Methods Hw7

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Problem 9.3

Redraw Figure 9.2, changing the "knot" location from 11 to 12.

Solution

First, we will check case Arm_A of the NCOG. In the book, n = number at risk(patients), y = number of deaths, l = lost to followup, h = hazard rate y/n; \hat{S} = life table survival esimate. Next, we assume that $y_i \stackrel{indep}{\sim} B(n_i, h_i) \quad \forall i = 1, 2, ..., 47$. We will use a generalized linear model. Let $\mu_i = E(y_i) = n_i h_i \quad \forall i = 1, 2, ..., 47$. The pdf of y_i is

$$f(y_i) = \binom{n_i}{y_i} h_i^{y_i} (1 - h_i)^{n_i - y_i} = exp(y_i log \frac{h_i}{1 - h_i} + n_i log (1 - h_i) + log \binom{n_i}{y_i})$$

$$= exp(y_i log \frac{\mu_i}{n_i - \mu_i} + n_i log (\frac{n_i - \mu_i}{n_i}) + log \binom{n_i}{y_i})$$

$$= exp(y_i \theta_i - n_i log (1 + e^{\theta_i}) + log \binom{n_i}{y_i}) \quad \text{where } \theta_i = log \frac{\mu_i}{n_i - \mu_i}$$

Define $b(\theta_i) = n_i log(1+e^{\theta_i})$, $a(\phi) = 1$, $g(\mu_i) = \theta_i = log \frac{\mu_i}{n_i - \mu_i} = \lambda_i = x_i^T \alpha$ where $x_i = (x_{i1}, x_{i2}, x_{i3}, x_{i4}) = (1, i, (i-12)^2_, (i-12)^3_)^T$, $\alpha = (\alpha_1, \alpha_2, \alpha_3, \alpha_4)^T$ and we can express $\mu_i = n_i \frac{e^{\theta_i}}{1+e^{\theta_i}}$. By using this form, calculate log likelihood function $l(\alpha)$.

$$l(\alpha) = \sum_{i=1}^{47} (y_i \theta_i - b(\theta_i) + log \binom{n_i}{y_i})$$
$$= \sum_{i=1}^{47} (y_i x_i^T \alpha - n_i log (1 + e^{x_i^T \alpha}) + log \binom{n_i}{y_i})$$

Let $S(\alpha)$ be score function.

$$S(\alpha_{j}) = \frac{\partial S}{\partial \alpha_{j}}$$

$$= \sum_{i=1}^{47} (y_{i}x_{ij} - n_{i} \frac{e^{x_{i}^{T}\alpha}}{1 + e^{x_{i}^{T}\alpha}}x_{ij})$$

$$= \sum_{i=1}^{47} (y_{i} - \mu_{i})x_{ij} = 0 \quad \forall j = 1, 2, 3, 4$$

```
We will find the mle of \alpha_i satisfying S(\alpha_i) = 0. But, we cannot find the exact solution. So we will use the
  Iteratively Rewighted least square algorithm method.
  Let g(y_i) \approx z_i = g(\mu_i) + g'(\mu_i)(y_i - \mu_i) = \lambda_i + \frac{d\lambda_i}{d\mu_i}(y_i - \mu_i) with var(z_i) = \frac{var(y_i)}{\left(\frac{d\mu_i}{d\lambda_i}\right)^2}. Then, g'(\mu_i) = \frac{n_i}{\mu_i(n_i - \mu_i)}
  and define D = diag(\frac{\partial \mu_i}{\partial \lambda_i}) = diag(\frac{\mu_i(n_i - \mu_i)}{n_i}) and V = diag(var(y_i)) = diag(\mu_i(\frac{n_i - \mu_i}{n_i})).
  The IRLS algorithm works as follows.
Step1 Define the kth vector value \alpha_{(k)}.
Step2 By using \alpha_{(k)}, Calculate \lambda_{(k)}, \mu_{(k)}, z_{(k)}, D_{(k)}, V_{(k)}.
Step3 Calculate \alpha_{(k+1)} = (X^T W_{(k)} X)^{-1} X^T W_{(k)} z_{(k)}.
Step4 Continue above process until the \alpha_{(k)} converges.
  Actually, we can simplify W=DV^{-1}D=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})diag(\frac{n_i}{\mu_i(n_i-\mu_i)})diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(n_i-\mu_i)}{n_i})=diag(\frac{\mu_i(
  D. So, we can find the numerical solution of the mle \alpha.
  library(dplyr)
  ##
  ## Attaching package: 'dplyr'
  ## The following objects are masked from 'package:stats':
  ##
  ##
                           filter, lag
  ## The following objects are masked from 'package:base':
  ##
  ##
                           intersect, setdiff, setequal, union
  library(ggplot2)
  NCOG data <- read.csv("https://web.stanford.edu/~hastie/CASI files/DATA/ncog.txt", sep = " ")
   #Separate A and B
  Arm_A <- subset(NCOG_data, subset = arm == "A")</pre>
  Arm_B <- subset(NCOG_data, subset = arm == "B")</pre>
   ## harzard function of Arm A
  num_A = nrow(Arm_A)
  Km_A <- matrix(0, 47, 4)</pre>
   copy_A = Arm_A
   #make the 47 * 4 matrix
  for(i in 1:47){
         Km_A[i,1] = nrow(copy_A)
```

inter_A = copy_A %% filter(t > 30.4*(i-1) & t <= 30.4*i)

Km_A[i, 2] <- length(which(inter_A\$d == 1))
Km_A[i, 3] <- length(which(inter_A\$d == 0))</pre>

 $x_a[i,] \leftarrow c(1, i, (i-12)^2, (i-12)^3)$

Km_A[i, 4] <- Km_A[i, 2] / Km_A[i,1]
copy_A = copy_A %>% filter(t > 30.4*i)

 $x_a \leftarrow matrix(0, 47, 4)$

for(i in 1:47){
 if(i <= 11){

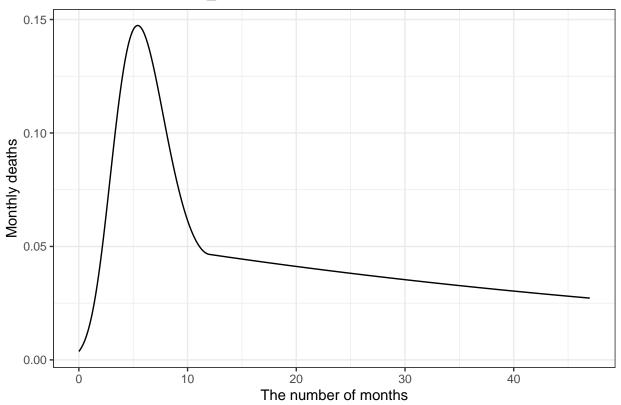
```
}
  else{
    x_a[i,1:2] \leftarrow c(1, i)
  }
}
#number of patients
n_a = Km_A[,1]
#number of deaths
y_a = Km_A[,2]
## Iteratively Rewighted least square(IRLS)
# initial value of alpha
alpha_0 = c(-1, -0.01, 0.1, 0.01)
alpha = matrix(0, 1001, 4)
alpha[1,] = alpha_0
#iterate 1000 times
for(i in 1:1000){
  lambda = x_a %*% alpha[i,]
  \# mu_k = n * exp(lambda_k)/(1 + exp(lambda_k))
  mu = n_a * exp(lambda) / (1 + exp(lambda))
  \# z_k = lambda_k + n / (mu_k * (n - mu_k)) * (y - mu_k)
  z = lambda + (n_a / (mu * (n_a - mu))) * (y_a - mu)
  \# D_k = diag(mu_k(n - mu_k) / n)
  D = diag(as.numeric(mu*(n_a - mu)/n_a))
  \# V_k = diag(mu_k (1 - mu_k/n))
  V = diag(as.numeric(mu*(1 - mu/n_a)))
  # W_k = D %*% solve(V) %*% D
  W = D
  \# \ alpha_(k+1) = (X^t \ W_k \ X)^(-1) \ X^t \ W_k \ Z_k
  alpha[i+1, ] = solve((t(x_a) %*% W %*% x_a)) %*% t(x_a) %*% W %*% z
alpha_hat_a = alpha[1001,]
#The numerical solution of mle
alpha_hat_a
```

[1] -2.830345147 -0.015866307 0.082670750 0.008488984

Thus, the numerical mle of α in Arm_A case is $\hat{\alpha} = (-2.8303, -0.01587, 0.08267, 0.0085)^T$. Next, we'll draw the graph of harzard ratio.

```
#harzard ratio
harzard_func <- function(x){</pre>
 h = 1/(1 + \exp(-x\%*\alpha lpha_hat_a))
 return(h)
#cubic linear spline function
spline_func <- function(x){</pre>
 if(x \le 12){
    return(c(1, x, (x-12)^2, (x-12)^3))
 else{
    return(c(1, x, 0, 0))
#range of x
range_xa = seq(0, 47, 0.01)
h_a = rep(0, 4701)
for(i in 1:4701){
 v = spline_func(range_xa[i])
 h_a[i] = harzard_func(v)
harzard_ratio_a = as.data.frame(cbind(range_xa, h_a))
ggplot(data=harzard_ratio_a, aes(x=range_xa, y=h_a)) + geom_line(color='black', lwd=0.5) + ggtitle("har
xlab("The number of months") + ylab("Monthly deaths") +theme_bw()
```

harzard ratio of Arm_A



In the same way as above, the case of Arm_B of the NCOG can also be obtained.

```
## harzard function of Arm_B
num_B = nrow(Arm_B)
Km_B \leftarrow matrix(0, 76, 4)
copy_B = Arm_B
for(i in 1:76){
  Km_B[i,1] = nrow(copy_B)
  inter_B = copy_B \%>% filter(t > 30.4*(i-1) & t <= 30.4*i)
  Km_B[i, 2] <- length(which(inter_B$d == 1))</pre>
  Km_B[i, 3] <- length(which(inter_B$d == 0))</pre>
  Km_B[i, 4] <- Km_B[i, 2] / Km_B[i,1]</pre>
  copy_B = copy_B \%\% filter(t > 30.4*i)
}
x_b \leftarrow matrix(0, 76, 4)
for(i in 1:76){
  if(i <= 11){
    x_b[i,] \leftarrow c(1, i, (i-12)^2, (i-12)^3)
  }
  else{
    x_b[i,1:2] \leftarrow c(1, i)
  }
}
n_b = Km_B[,1]
y_b = Km_B[,2]
## Iteratively Rewighted least square(IRLS)
# initial value of alpha
```

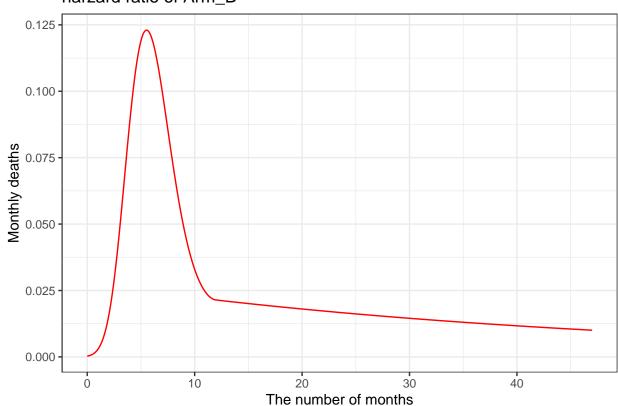
```
alpha_0 = c(1, 0.01, 0.01, 0.01)
alpha = matrix(0, 1001, 4)
alpha[1,] = alpha_0
for(i in 1:1000){
  lambda = x_b %*% alpha[i,]
  \# mu_k = n * exp(lambda_k)/(1 + exp(lambda_k))
 mu = n_b * exp(lambda) / (1 + exp(lambda))
  \# z_k = lambda_k + n / (mu_k * (n - mu_k)) * (y - mu_k)
  z = lambda + (n_b/(mu * (n_b - mu))) * (y_b - mu)
  \# D_k = diag(mu_k(n - mu_k) / n)
  D = diag(as.numeric(mu*(n_b-mu)/n_b))
  \# V_k = diag(mu_k (1 - mu_k/n))
  V = diag(as.numeric(mu*(1 - mu/n_b)))
  # W_k = D %*% solve(V) %*% D
 W = D
  \# \ alpha_(k+1) = (X^t \ W_k \ X)^(-1) \ X^t \ W_k \ Z_k
 alpha[i+1, ] = solve((t(x_b) %*% W %*% x_b)) %*% t(x_b) %*% W %*% z
alpha_hat_b = alpha[1001,]
alpha_hat_b
```

[1] -3.55862953 -0.02194139 0.12619500 0.01316970

Thus, the numerical mle of α in Arm_B case is $\hat{\alpha} = (-3.5586, -0.0219, 0.1262, 0.0132)^T$. Next, we'll draw the graph of harzard ratio.

```
harzard_func <- function(x){
    h = 1/(1 + exp(-x**alpha_hat_b))
    return(h)
}
spline_func <- function(x){
    if(x<= 12){
        return(c(1, x, (x-12)^2, (x-12)^3))
    }
    else{
        return(c(1, x, 0, 0))
    }
}
range_xb = seq(0, 47, 0.01)
h_b = rep(0, 4701)
for(i in 1:4701){
    v = spline_func(range_xb[i])
    h_b[i] = harzard_func(v)
}
harzard_ratio_b = as.data.frame(cbind(range_xb, h_b))</pre>
```

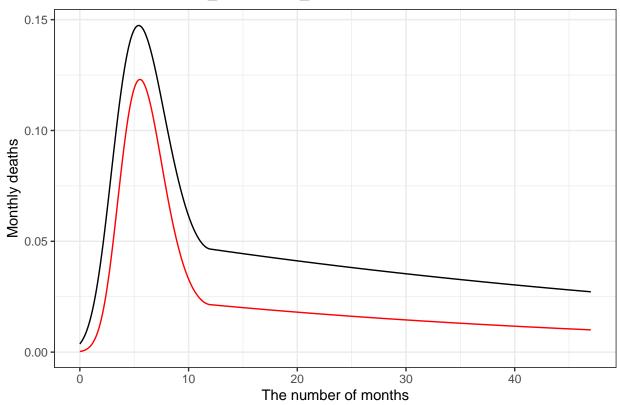
harzard ratio of Arm_B



So we can combine above two graphs.

```
ggplot() + geom_line(data = harzard_ratio_a, aes(x=range_xa, y=h_a), color = "black", lwd = 0.5) +
   theme(legend.position = c(0.9,0.7)) +
   geom_line(data = harzard_ratio_b, aes(x = range_xb, y = h_b), color = 'red', lwd = 0.5) +
   ggtitle("harzard ratio of Arm_A and Arm_B") +
   xlab("The number of months") + ylab("Monthly deaths") +
   theme_bw()
```

harzard ratio of Arm_A and Arm_B



Problem 9.5

Why does the hypergeometric distribution enter into formula (9.24)?

Solution

In the book, the notations mean n_A = the number of at risk in Arm_A, n_d = the number of deaths, n_B = the number of at risk in Arm_B, n_s = the number of survived patients and y = the number of Arm_A deaths. The data of 2 by 2 display of month-6 for NCOG study are observed after the patients died which means we know n_d . Also, we know the number of patient using the treatments Arm_A and Arm_B respectively which means we know n_A and n_B . Therefore, the sum of each columns and rows 2 by 2 contingency table is fixed. So y determines the other three table entires by substraction, so we are not losing any information by focusing on y. This is why the distribution of y follows the hypergeometric distribution.