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## Assignment 9

①  $T \sim LN(\mu, \sigma^2) \Leftrightarrow Z = \log T \sim N(0, 1)$

$$Y = e^\mu T^{\sigma^2} = e^\mu (e^Z)^{\sigma^2} = e^\mu e^{\sigma^2 Z}$$

$$= \exp\{ \sigma Z + \mu \} = \exp\{ X \} \text{ where}$$

$$X = \sigma Z + \mu \sim N(\mu, \sigma^2)$$

Now  $\log e^X = X \sim N(\mu, \sigma^2)$ , so

$$e^X = e^\mu T^{\sigma^2} \sim LN(\mu, \sigma^2)$$

OR one could work with densities, but this is easier.

② Let  $T \sim LN(\mu, \sigma^2)$ .  $m$  is the median of  $T$  iff  $\frac{1}{2} = P(T \leq m) = P(\log T \leq \log m)$

$$= P(X \leq \log m) \text{ where } X \sim N(\mu, \sigma^2)$$

The median of  $X$  is  $\mu$ , so

$$\mu = \log m \iff m = e^\mu$$

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③  ~~$T \sim N(\mu, \sigma^2)$~~ , so

$\log T = X \sim N(\mu, \sigma^2)$   ~~$\log T = X \Leftrightarrow T = e^X$~~

$$E(T) = E(e^X) = E(e^{xt}) = M_x(t)$$

$$M_x(t) = e^{\mu t + \frac{1}{2} \sigma^2 t^2}, \quad |_{t=1}$$

So

$$E(T) = e^{\mu + \frac{1}{2} \sigma^2}$$

✓

④  $t_i = e^{x_i^\top \beta} \varepsilon_i^c$  where  $\varepsilon_i \sim LN(0, 1)$

Take log to get normal regression model.

$$\begin{aligned} & \frac{e^{\beta_0 + \beta_1 x_1 + \dots + \beta_k (x_k + c) + \dots + \beta_{p-1} x_{p-1} + \frac{1}{2} \sigma^2}}{e^{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \dots + \beta_{p-1} x_{p-1} + \frac{1}{2} \sigma^2}} \\ &= \frac{e^{\beta_0} e^{\beta_1 x_1} \dots e^{\beta_k (x_k + c)} \dots e^{\beta_{p-1} x_{p-1}} e^{\frac{1}{2} \sigma^2}}{e^{\beta_0} e^{\beta_1 x_1} \dots e^{\beta_k x_k} \dots e^{\beta_{p-1} x_{p-1}} e^{\frac{1}{2} \sigma^2}} \\ &= \frac{e^{\beta_0 x_k} e^{c \beta_k}}{e^{\beta_0 x_k}} = e^{c \beta_k} \end{aligned}$$

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$$\begin{aligned}
 ⑥ \quad & S(t) = P(T > t) = 1 - F_T(t) \\
 & = 1 - P(T \leq t) = 1 - P(e^X \leq t) \\
 & \quad \text{where } X \sim N(x^\top \beta, \sigma^2) \\
 & = 1 - P(X \leq \log t) = 1 - P\left(\frac{X - x^\top \beta}{\sigma} \leq \frac{\log t - x^\top \beta}{\sigma}\right) \\
 & = 1 - P(Z \leq \frac{\log t - x^\top \beta}{\sigma}) \quad \text{where } Z \sim N(0, 1) \\
 & = 1 - \Phi\left(\frac{\log t - x^\top \beta}{\sigma}\right)
 \end{aligned}$$

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⑦ Using the delta method,

$$g(\theta) = a_1 \theta_1 + a_2 \theta_2 + \dots + a_k \theta_k, = a^T \theta$$

$$\dot{g}(\theta) = (a_1, a_2, \dots, a_k) = a^T, \text{ so}$$

by delta,

$$g(\hat{\theta}_n) = a^T \hat{\theta}_n \sim N(a^T \theta, a^T V_n a)$$

⑧  $\theta = (\beta_0, \beta_1, \dots, \beta_{p-1}, \sigma)$

⑨ (a)  $\widehat{x_{n+1}^T \beta} = x_{n+1}^T \hat{\beta}_n = \hat{y}_{n+1} \sim N(x_{n+1}^T \beta, \sigma^2)$

where  $\hat{\beta}_n \sim N(\beta, C_n)$   $x_{n+1}^T C_n x_{n+1}$

(b)

so  $Z = \frac{\hat{y}_{n+1} - x_{n+1}^T \beta}{\sqrt{x_{n+1}^T C_n x_{n+1}}} \sim N(0, 1)$ , and

$$1 - \alpha \approx P(-z_{\alpha/2} < Z < z_{\alpha/2}) = P\left(-z_{\alpha/2} < \frac{\hat{y}_{n+1} - x_{n+1}^T \beta}{\sqrt{x_{n+1}^T C_n x_{n+1}}} < z_{\alpha/2}\right)$$

$$= P\left\{ -z_{\alpha/2} \sqrt{x_{n+1}^T C_n x_{n+1}} < x_{n+1}^T \hat{\beta} < z_{\alpha/2} \sqrt{x_{n+1}^T C_n x_{n+1}} \right\}$$

(10) From QM  $\hat{y}_{n+1} \sim N(x_{n+1}^T \beta, \sigma^2 + x_{n+1}^T C_n x_{n+1})$

(11)  $E(y_{n+1} - \hat{y}_{n+1}) = E(y_{n+1}) - E(\hat{y}_{n+1}) \approx x_{n+1}^T \beta$

(12)  $\text{Var}(y_{n+1} - \hat{y}_{n+1}) \stackrel{\text{iid}}{=} \text{Var}(y_{n+1}) + \text{Var}(\hat{y}_{n+1}) - x_{n+1}^T \beta = 0$

$\hat{y}_{n+1} \sim N(0, \sigma^2 + x_{n+1}^T C_n x_{n+1})$

Linear combination of normals is normal.

$y_{n+1} - \hat{y}_{n+1} \sim N(0, \sigma^2 + x_{n+1}^T C_n x_{n+1})$

(13) SE of  $y_{n+1} - \hat{y}_{n+1} = \sqrt{\sigma^2 + x_{n+1}^T C_n x_{n+1}}$

(14)  $Z_n = \frac{y_{n+1} - \hat{y}_{n+1}}{\text{SE}} \sim N(0, 1)$

(15)  $0.95 \approx P(-1.96 < Z_n < 1.96)$

$$= P(\hat{y}_{n+1} - 1.96 * \text{SE} < y_{n+1} < \hat{y}_{n+1} + 1.96 * \text{SE})$$

(15) (a)  $d_i = e^{\beta_0 + \beta_1 x + \beta_2 d_1 + \beta_3 d_2 + \beta_4 d_3} \times \varepsilon_i$ ,  $\varepsilon_i \sim LN(0, 1)$

(b) Median Length of Marriage

	$d_1$	$d_2$	$d_3$	
A	1	0	0	$e^{\beta_0 + \beta_1 x} e^{\beta_2}$
B	0	1	0	$e^{\beta_0 + \beta_1 x} e^{\beta_3}$
C	0	0	1	$e^{\beta_0 + \beta_1 x} e^{\beta_4}$
None	0	0	0	$e^{\beta_0 + \beta_1 x}$

(c)  $e^{\beta_0 + \beta_3 + 75\beta_1}$

(d) (i)  $\Theta = (\beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \sigma)$  I am parameterizing by  $\sigma$ ,  
not  $\sigma^2$

(ii) Estimated value =  $g(\Theta) = e^{\beta_0 + \beta_1 x + \beta_2 d_1 + \beta_3 d_2 + \beta_4 d_3 + \frac{1}{2}\sigma^2}$   
 $= e^{x\beta_1 + \frac{1}{2}\sigma^2}$

$$= e^{x\beta_1} (1, x, d_1, d_2, d_3, \sigma) \cdot e^{\frac{1}{2}\sigma^2}$$

(e)  $e^{\beta_2}$

(f)  $e^{\beta_3 - \beta_4}$

(g)  $H_0: \beta_2 = \beta_3 = \beta_4 = 0$

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(14th) (i) Reduced model is

$$x_i = e^{\beta_0 + \beta_1 x_i} \times \epsilon_i^G$$

(ii)

$$\begin{pmatrix} 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \epsilon_i^G \end{pmatrix} = \begin{pmatrix} h \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

(14th)  $H_0: \beta_2 = 0$ (j)  $H_0: \beta_2 = \beta_3$

```
R version 4.2.3 (2023-03-15) -- "Shortstop Beagle"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin17.0 (64-bit)
```

```
R is free software and comes with ABSOLUTELY NO WARRANTY.
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Type 'license()' or 'licence()' for distribution details.
```

```
Natural language support but running in an English locale
```

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R is a collaborative project with many contributors.
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'citation()' on how to cite R or R packages in publications.
```

```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

```
[R.app GUI 1.79 (8198) x86_64-apple-darwin17.0]
```

```
[Workspace restored from /Users/brunner/.RData]
[History restored from /Users/brunner/.Rapp.history]
```

```
> # Assignment 9, Question 15
>
> rm(list=ls()); options(scipen=999)
> # install.packages("survival",dependencies=TRUE) # Only need to do this once
> library(survival) # Do this every time
>
> # (a)
> ColonCancer = read.table("https://www.utstat.toronto.edu/brunner/data/legal/
ColonCancer.data.txt")
>
> head(ColonCancer); dim(ColonCancer)
      rx sex age nodes status time
2 Lev+5FU 1 43     5     1 968
4 Lev+5FU 1 63     1     0 3087
6 Obs    0 71     7     1 542
8 Lev+5FU 0 66     6     1 245
10 Obs   1 69    22     1 523
12 Lev+5FU 0 57     9     1 904
[1] 929   6
> # Make Obs the reference category for rx
> ColonCancer = within(ColonCancer,{
+ rx = factor(rx)
+ contrasts(rx) = contr.treatment(3,base=3)
+ colnames(contrasts(rx)) = c("Lev","Lev+5FU")
+ })
> summary(ColonCancer)
      rx          sex           age         nodes        status      
Lev    :310  Min.   :0.000  Min.   :18.00  Min.   : 0.00  Min.   :0.0000  
Lev+5FU:304  1st Qu.:0.000  1st Qu.:53.00  1st Qu.: 1.00  1st Qu.:0.0000  
Obs    :315  Median :1.000  Median :61.00  Median : 2.00  Median :1.0000
```

```

Mean    :0.521   Mean    :59.75   Mean    : 3.66   Mean    :0.5038
3rd Qu.:1.000  3rd Qu.:69.00   3rd Qu.: 5.00   3rd Qu.:1.0000
Max.    :1.000  Max.    :85.00   Max.    :33.00   Max.    :1.0000
                                         NA's    :18

time
Min.    : 8
1st Qu.:370
Median :1548
Mean   :1405
3rd Qu.:2289
Max.   :3329

>
>
> # (b)
> # Full model
> full = survreg(Surv(time,status) ~ rx + sex + age + nodes,
+                  dist="lognormal", data=ColonCancer)
> summary(full)

Call:
survreg(formula = Surv(time, status) ~ rx + sex + age + nodes,
        data = ColonCancer, dist = "lognormal")
            Value Std. Error      z          p
(Intercept) 7.47451  0.37240 20.07 < 0.0000000000000002
rxLev       0.03024  0.15991  0.19      0.85
rxLev+5FU   0.75633  0.16838  4.49     0.0000071
sex         0.18520  0.13517  1.37      0.17
age         0.00487  0.00563  0.87      0.39
nodes      -0.15335  0.01804 -8.50 < 0.0000000000000002
Log(scale)  0.60148  0.03711 16.21 < 0.0000000000000002

Scale= 1.82

Log Normal distribution
Loglik(model)= -3933  Loglik(intercept only)= -3983.6
Chisq= 101.24 on 5 degrees of freedom, p= 0.00000000000000029
Number of Newton-Raphson Iterations: 3
n=911 (18 observations deleted due to missingness)

> # Something is going on. At least one variable matters.
>
> # (c)
> exp(0.75633) # Comparing Lev+5FU to nothing.
[1] 2.130443
>
> # (d) See z-test.
> # (e) See z-test.
>
> # (f)
> # LR test of rx
> norx = update(full, . ~ . - rx)
> # summary(norx) # n is correct
> anova(norx,full)

```

```

      Terms Resid. Df   -2*LL Test Df Deviance      Pr(>Chi)
1     sex + age + nodes      906 7891.115      NA      NA      NA
2 rx + sex + age + nodes      904 7865.945 = 2 25.16918 0.000003424373
>
> # Wald test of rx
> betahat = coef(full); betahat
(Intercept)      rxLev    rxLev+5FU       sex       age      nodes
7.474508107 0.030236057 0.756331612 0.185201833 0.004873333 -0.153352960
> V = vcov(full)[(1:6),(1:6)] # Omitting last row and col for log scale.
> round(V,5)
(Intercept)      rxLev    rxLev+5FU       sex       age      nodes
(Intercept) 0.13868 -0.01169 -0.01343 -0.00879 -0.00190 -0.00191
rxLev      -0.01169 0.02557 0.01251 -0.00060 -0.00001 0.00003
rxLev+5FU   -0.01343 0.01251 0.02835 0.00157 0.00001 0.00001
sex        -0.00879 -0.00060 0.00157 0.01827 -0.00002 0.00005
age        -0.00190 -0.00001 0.00001 -0.00002 0.00003 0.00001
nodes     -0.00191 0.00003 0.00001 0.00005 0.00001 0.00033
> Lrx = rbind(c(0,1,0,0,0,0),
+              c(0,0,1,0,0,0))
> colnames(Lrx) = names(coef(full))
> Lrx
(Intercept) rxLev rxLev+5FU sex age nodes
[1,] 0 1 0 0 0 0
[2,] 0 0 1 0 0 0
> source("http://www.utstat.toronto.edu/brunner/Rfunctions/Wtest.txt")
> Wtest(Lrx,betahat,V)
      W          df      p-value
24.767674038180 2.000000000000 0.000004185698
>
> # (g) Levamisole alone versus patients receiving both Levamisole and 5-FU
> # Custom test.
>
> Lqf = cbind(0,1,-1,0,0,0)
> Wtest(Lqf,betahat,V)
      W          df      p-value
18.23931306793 1.000000000000 0.00001948159
>
>
> # (h) See z-test.
> # (i) See z-test.
>
> # (j) Nope.
>
> # (k) Prediction interval based on a model with just treatment and number of nodes.
>
> model2 = survreg(Surv(time,status) ~ rx + nodes, dist="lognormal", data=ColonCancer)
> summary(model2)

```

Call:

```

survreg(formula = Surv(time, status) ~ rx + nodes, data = ColonCancer,
        dist = "lognormal")
      Value Std. Error      z      p
(Intercept) 7.8722      0.1385 56.86 < 0.0000000000000002
rxLev       0.0382      0.1601  0.24      0.81

```

```

rxLev+5FU    0.7409    0.1682  4.41          0.000011
nodes       -0.1556    0.0180 -8.64 < 0.0000000000000002
Log(scale)   0.6032    0.0371 16.25 < 0.0000000000000002

Scale= 1.83

Log Normal distribution
Loglik(model)= -3934.3 Loglik(intercept only)= -3983.6
  Chisq= 98.56 on 3 degrees of freedom, p= 0.00000000000000032
Number of Newton-Raphson Iterations: 3
n=911 (18 observations deleted due to missingness)

>
> new = data.frame(rx="Lev", nodes=6); new
  rx nodes
1 Lev      6
> pred = predict(model2,newdata=new,type='linear',se=TRUE) ; pred
$fit
  1
6.976977

$se.fit
  1
0.1222231

> yhat = pred$fit
> t_hat= exp(yhat)
> t_hat # Prediction = estimated median number of days
  1
1071.674
>
> # Prediction interval
> sigmasqhat = model2$scale^2
> se = sqrt(sigmasqhat+pred$se^2); se
  1
1.832001
> L = yhat - 1.96*se; U = yhat + 1.96*se
> lower95 = exp(L); upper95 = exp(U)
> predint = c(t_hat,lower95,upper95)
> names(predint) = c('t-hat','lower95','upper95')
> predint
  t-hat    lower95    upper95
1071.67380  29.55505 38859.17061
> predint/365
  t-hat    lower95    upper95
2.93609260  0.08097274 106.46348112
>
>
>
>
```