

# Assignment 8

(1) (a)  $f_T(x) = \frac{d}{dt} F_T(x) = \frac{d}{dt} P(T \leq t)$   
 $= \frac{d}{dt} P(\varepsilon e^{\beta_0 + \beta_1 x} \leq t)$   
 $= \frac{d}{dt} P(\varepsilon \leq t e^{-\beta_0 - \beta_1 x})$   
 $= \frac{d}{dt} F_\varepsilon(t e^{-\beta_0 - \beta_1 x})$   
 $= f_\varepsilon(t e^{-\beta_0 - \beta_1 x}) \cdot e^{-\beta_0 - \beta_1 x}$   
 $= \frac{1}{e^{\beta_0 + \beta_1 x}} e^{-t e^{-\beta_0 - \beta_1 x}}$  for  $t \geq 0$  and zero otherwise

(b) Because  $\lambda = \frac{1}{\beta_0 + \beta_1 x} e^{-\beta_0 - \beta_1 x}$

(i)  $E(x) = \frac{1}{\beta_0 + \beta_1 x} e^{\beta_0 + \beta_1 x}$

(ii) Median  $(t) = (\log 2) \frac{1}{\beta_0 + \beta_1 x} e^{\beta_0 + \beta_1 x}$

(iii)  $S(x) = e^{-\lambda x} = e^{-t e^{-\beta_0 - \beta_1 x}}$

(c)  $h(x) = \frac{f(x)}{S(x)} = \frac{\lambda e^{-\lambda x}}{e^{-\lambda x}} = \lambda = \frac{1}{\beta_0 + \beta_1 x}$

(c)  $\beta_0 + \beta_1(x+1) = (\beta_0 + \beta_1 x) + \beta_1 = \beta_0 + \beta_1 x + \beta_1$

$$(2) (a) \varepsilon \sim \text{exp}(1), W = \varepsilon^\sigma$$

$$\begin{aligned} f_W(w) &= \frac{d}{dw} F_W(w) = \frac{d}{dw} P(W \leq w) \\ &= \frac{d}{dw} P(\varepsilon^\sigma \leq w) = \frac{d}{dw} P(\varepsilon \leq w^{1/\sigma}) \\ &= \frac{d}{dw} F_\varepsilon(w^{1/\sigma}) = f_\varepsilon(w^{1/\sigma}) \frac{1}{\sigma} w^{1/\sigma - 1} \\ &= \begin{cases} \frac{1}{\sigma} e^{-w^{1/\sigma}} w^{1/\sigma - 1} & \text{for } w > 0 \\ 0 & \text{otherwise} \end{cases} \end{aligned}$$

~~(b)~~

(b) with  $\alpha = \frac{1}{\sigma}$ , density is

$$\alpha e^{-w^\alpha} w^{\alpha-1}, \text{ so } \lambda = 1$$

Formula sheet

(3)  $f_w(w) = \alpha \lambda (\lambda w)^{\alpha-1} e^{-(\lambda w)^\alpha} I(w \geq 0)$

$T = cW$

$f_T(t) = \frac{d}{dt} P(cW \leq t) = \frac{d}{dt} P(W \leq t/c)$   
 $= \frac{d}{dt} F_w(\frac{1}{c}t) = f_w(\frac{1}{c}t) \cdot \frac{1}{c}$

$= \frac{1}{c} \alpha \lambda (\lambda \frac{1}{c}t)^{\alpha-1} e^{-(\lambda \frac{1}{c}t)^\alpha} I(\frac{1}{c}t \geq 0)$   
 $= \alpha (\frac{\lambda}{c}) (\frac{\lambda}{c}t)^{\alpha-1} e^{-(\frac{\lambda}{c}t)^\alpha} I(t \geq 0)$

Weibull  $(\alpha', \lambda')$ ,  $\alpha' = \alpha$ ,  $\lambda' = \frac{\lambda}{c}$

(4) (a)  $t_i \sim \text{Weibull}$ , with  $\alpha = \frac{1}{c}$ ,  $\lambda = \frac{1}{\beta_0 + \beta_1 x_1 + \dots + \beta_{p-1} x_{p-1}}$

(b) 
$$\frac{e^{\beta_0 + \beta_1 x_1 + \dots + \beta_k (x_k + \beta_0) + \dots + \beta_{p-1} x_{p-1}}}{e^{\beta_0 + \beta_1 x_1 + \dots + \beta_k x_k + \dots + \beta_{p-1} x_{p-1}}} = e^{c \beta_k}$$

5

(a)  $E(x_i) = e^{x_i^T \beta} \Gamma(1 + \sigma)$

(b)  $e^{x_i^T \beta} \times (\log z)^\sigma = \frac{(\log z)^{1/\sigma}}{\lambda} = \text{Median}$

(c)  $S(x_i) = e^{-(\lambda x_i)^\alpha}$   
 $= \text{Exp}\left\{ \frac{x_i^{1/\sigma}}{e^{x_i^T \beta}} \right\}$

(d)  $h(x) = \frac{f(x)}{S(x)} = \frac{\alpha \lambda (\lambda x)^{\alpha-1} e^{-(\lambda x)^\alpha}}{e^{-(\lambda x)^\alpha}}$   
 $= \alpha \lambda (\lambda x)^{\alpha-1} = \frac{1}{\sigma} e^{-\frac{1}{\sigma} x^T \beta} \times x^{1/\sigma - 1}$

Agrees with formula sheet

(e)  $e^{-\beta \epsilon / \sigma}$   
nois

6  $\frac{h_1(t)}{h_2(t)} = \frac{\frac{1}{\sigma} e^{-\frac{1}{\sigma} x_1^T \beta} \times t^{1/\sigma - 1}}{\frac{1}{\sigma} e^{-\frac{1}{\sigma} x_2^T \beta} \times t^{1/\sigma - 1}}$

Does not depend on t. Proportional hazards (Proportion the same for every t).

(7) (a)  $x_i = e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 c_1 + \beta_4 c_2 + \beta_5 c_3} \times \epsilon_i^\sigma$

(b)

	$c_1$	$c_2$	$c_3$	$E(x_i) = e^{x^T \beta} \Gamma(1 + \sigma)$
Squamous	1	0	0	$e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2} e^{\beta_3} \Gamma(1 + \sigma)$
Small cell	0	1	0	$e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2} e^{\beta_4} \Gamma(1 + \sigma)$
Adeno	0	0	1	$e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2} e^{\beta_5} \Gamma(1 + \sigma)$
Large cell	0	0	0	$e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2} \Gamma(1 + \sigma)$

(c)  $E(x_i) = e^{\beta_0 + \beta_5 + 45\beta_1 + 6\beta_2} \Gamma(1 + \sigma)$

(d) (i)  $\theta = (\beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \sigma)$

(ii)  $g(\theta) = e^{x^T \beta} \Gamma(1 + \sigma) = e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 c_1 + \beta_4 c_2 + \beta_5 c_3} \times \Gamma(1 + \sigma)$

$g'(\theta) = \left( \frac{\partial g}{\partial \beta_0}, \frac{\partial g}{\partial \beta_1}, \dots, \frac{\partial g}{\partial \beta_5}, \frac{\partial g}{\partial \sigma} \right)$

$= (e^{x^T \beta} \cdot 1 \cdot \Gamma(1 + \sigma), e^{x^T \beta} \cdot x_1 \cdot \Gamma(1 + \sigma), x_2 e^{x^T \beta} \Gamma(1 + \sigma), c_1 e^{x^T \beta} \Gamma(1 + \sigma), c_2 e^{x^T \beta} \Gamma(1 + \sigma), c_3 e^{x^T \beta} \Gamma(1 + \sigma), e^{x^T \beta} \Gamma'(1 + \sigma))$

(7e)  $e^{\beta_4}$

(f)  $e^{\beta_3 - \beta_5}$  . No.

(g)  $H_0: \beta_3 = \beta_4 = \beta_5 = 0$

(h) i. Reduced model is  $t_i = e^{\beta_0 + \beta_1 x_1 + \beta_2 x_2} \times \epsilon_i$

ii)  $H_0: L \quad B = 0$

$$\begin{pmatrix} 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \beta_5 \\ \epsilon \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}$$

(i)  $H_0: \beta_1 = 0$  (age controlling for others)

(j)  $H_0: \beta_4 = 0$  (Large versus small)

(k)  $H_0: \beta_3 = \beta_5$  (Squamous vs Adeno)

R version 4.2.3 (2023-03-15) -- "Shortstop Beagle"  
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Platform: x86\_64-apple-darwin17.0 (64-bit)

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[Workspace restored from /Users/brunner/.RData]  
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```
> # Assignment 8, Question 8
>
> rm(list=ls()); # options(scipen=999)
> # install.packages("survival",dependencies=TRUE) # Only need to do this once
> library(survival) # Do this every time
> # help(cancer)
> head(cancer)
  inst time status age sex ph.ecog ph.karno pat.karno meal.cal wt.loss
1    3  306      2  74  1         1         90         100       1175      NA
2    3  455      2  68  1         0         90          90       1225      15
3    3 1010      1  56  1         0         90          90         NA      15
4    5  210      2  57  1         1         90          60       1150      11
5    1  883      2  60  1         0        100          90         NA       0
6   12 1022      1  74  1         1         50          80         513       0
> round( cor(cancer[,2:10],use='pairwise.complete.obs'), 3)
      time status  age  sex ph.ecog ph.karno pat.karno meal.cal wt.loss
time   1.000 -0.171 -0.078 0.130 -0.201  0.133  0.184  0.074  0.009
status -0.171  1.000  0.150 -0.243  0.233 -0.182 -0.172 -0.024  0.035
age    -0.078  0.150  1.000 -0.122  0.193 -0.203 -0.126 -0.231  0.038
sex     0.130 -0.243 -0.122  1.000 -0.021  0.011  0.046 -0.168 -0.129
ph.ecog -0.201  0.233  0.193 -0.021  1.000 -0.807 -0.511 -0.099  0.188
ph.karno 0.133 -0.182 -0.203  0.011 -0.807  1.000  0.520  0.042 -0.175
pat.karno 0.184 -0.172 -0.126  0.046 -0.511  0.520  1.000  0.166 -0.172
meal.cal 0.074  0.024 -0.231 -0.168 -0.099  0.042  0.166  1.000 -0.103
wt.loss 0.009  0.035  0.038 -0.129  0.188 -0.175 -0.172 -0.103  1.000
>
> # Fix up variables
```

```

> Cancer = within(cancer,{
+ status=status-1 # Now status = delta
+ sex = sex-1      # So 0=M, 1=F
+ stime = Surv(time,status)
+ })
> summary(Cancer)

```

inst	time	status	age	sex
Min. : 1.00	Min. : 5.0	Min. : 0.0000	Min. : 39.00	Min. : 0.0000
1st Qu.: 3.00	1st Qu.: 166.8	1st Qu.: 0.0000	1st Qu.: 56.00	1st Qu.: 0.0000
Median : 11.00	Median : 255.5	Median : 1.0000	Median : 63.00	Median : 0.0000
Mean : 11.09	Mean : 305.2	Mean : 0.7237	Mean : 62.45	Mean : 0.3947
3rd Qu.: 16.00	3rd Qu.: 396.5	3rd Qu.: 1.0000	3rd Qu.: 69.00	3rd Qu.: 1.0000
Max. : 33.00	Max. : 1022.0	Max. : 1.0000	Max. : 82.00	Max. : 1.0000
NA's : 1				

  

ph.ecog	ph.karno	pat.karno	meal.cal
Min. : 0.0000	Min. : 50.00	Min. : 30.00	Min. : 96.0
1st Qu.: 0.0000	1st Qu.: 75.00	1st Qu.: 70.00	1st Qu.: 635.0
Median : 1.0000	Median : 80.00	Median : 80.00	Median : 975.0
Mean : 0.9515	Mean : 81.94	Mean : 79.96	Mean : 928.8
3rd Qu.: 1.0000	3rd Qu.: 90.00	3rd Qu.: 90.00	3rd Qu.: 1150.0
Max. : 3.0000	Max. : 100.00	Max. : 100.00	Max. : 2600.0
NA's : 1	NA's : 1	NA's : 3	NA's : 47

  

wt.loss	stime.time	stime.status
Min. : -24.000	Min. : 5.0000	Min. : 0.0000000
1st Qu.: 0.000	1st Qu.: 166.7500	1st Qu.: 0.0000000
Median : 7.000	Median : 255.5000	Median : 1.0000000
Mean : 9.832	Mean : 305.2325	Mean : 0.7236842
3rd Qu.: 15.750	3rd Qu.: 396.5000	3rd Qu.: 1.0000000
Max. : 68.000	Max. : 1022.0000	Max. : 1.0000000
NA's : 14		

```

>
> # (a)
>
> self = survreg(stime ~ pat.karno, dist='weibull', data=Cancer)
> summary(self)

```

Call:

```
survreg(formula = stime ~ pat.karno, data = Cancer, dist = "weibull")
```

	Value	Std. Error	z	p
(Intercept)	4.88007	0.31860	15.32	< 2e-16
pat.karno	0.01451	0.00399	3.63	0.00028
Log(scale)	-0.30890	0.06234	-4.95	7.2e-07

Scale= 0.734

Weibull distribution

Loglik(model)= -1127.9 Loglik(intercept only)= -1134.2

Chisq= 12.45 on 1 degrees of freedom, p= 0.00042

Number of Newton-Raphson Iterations: 5

n=225 (3 observations deleted due to missingness)



```

>
> # (b)
>
> full = survreg(stime ~ age + sex + ph.ecog + ph.karno + pat.karno + meal.cal +
wt.loss, dist='weibull', data=Cancer)
> summary(full)

```

Call:

```

survreg(formula = stime ~ age + sex + ph.ecog + ph.karno + pat.karno +
meal.cal + wt.loss, data = Cancer, dist = "weibull")

```

	Value	Std. Error	z	p
(Intercept)	7.38e+00	1.05e+00	7.03	2.1e-12
age	-6.42e-03	7.95e-03	-0.81	0.41983
sex	3.87e-01	1.41e-01	2.75	0.00593
ph.ecog	-5.21e-01	1.53e-01	-3.42	0.00063
ph.karno	-1.64e-02	7.54e-03	-2.17	0.02984
pat.karno	8.60e-03	5.53e-03	1.56	0.11979
meal.cal	-1.25e-05	1.78e-04	-0.07	0.94416
wt.loss	9.42e-03	5.32e-03	1.77	0.07631
Log(scale)	-3.63e-01	7.21e-02	-5.03	4.8e-07

Scale= 0.695

Weibull distribution

Loglik(model)= -833.4 Loglik(intercept only)= -847.6

Chisq= 28.48 on 7 degrees of freedom, p= 0.00018

Number of Newton-Raphson Iterations: 5

n=168 (60 observations deleted due to missingness)

```

>
> # (c)
>
> nodiet = survreg(stime ~ age + sex + ph.ecog + ph.karno + pat.karno,
dist='weibull', data=Cancer) # Dropping meal.cal and wt.loss
> anova(nodiet,full) # LR test

```

	Terms	Resid.	Df
1	age + sex + ph.ecog + ph.karno + pat.karno		216
2	age + sex + ph.ecog + ph.karno + pat.karno + meal.cal + wt.loss		159

  

	-2*LL	Test	Df	Deviance	Pr(>Chi)
1	2209.472	NA	NA	NA	NA
2	1666.763	=	57	542.709	2.301935e-80

```

> # Compare Wald test
> source("http://www.utstat.toronto.edu/~brunner/Rfunctions/Wtest.txt")
> # source("Wtest.txt") # Local copy
> Vnfull = vcov(full)
> Tnfull = full$coefficients; Tnfull = c(Tnfull,log(full$scale))
> L1 = rbind(c(0,0,0,0,0,0,1,0,0),
+           c(0,0,0,0,0,0,0,1,0) )
> Wtest(L=L1, Tn=Tnfull, Vn=Vnfull)
      W      df  p-value
3.1462651 2.0000000 0.2073945

```

```
>
> # (d)
>
> summary(nodiet)
```

Call:

```
survreg(formula = stime ~ age + sex + ph.ecog + ph.karno + pat.karno,
        data = Cancer, dist = "weibull")
```

	Value	Std. Error	z	p
(Intercept)	7.17935	0.88444	8.12	4.8e-16
age	-0.00764	0.00672	-1.14	0.2555
sex	0.39973	0.12155	3.29	0.0010
ph.ecog	-0.41366	0.13040	-3.17	0.0015
ph.karno	-0.01228	0.00684	-1.80	0.0725
pat.karno	0.00738	0.00484	1.52	0.1276
Log(scale)	-0.34464	0.06245	-5.52	3.4e-08

Scale= 0.708

Weibull distribution

Loglik(model)= -1104.7 Loglik(intercept only)= -1121.3

Chisq= 33.17 on 5 degrees of freedom, p= 3.5e-06

Number of Newton-Raphson Iterations: 5

n=223 (5 observations deleted due to missingness)

```
>
> # With missing values on the variables that are omitted from the restricted model,
statistics from the restricted model are based on a larger sample size. -2LL, badness
of fit, is a sum of negative terms. There are too many in the -2LL for the restricted
model, so the "badness" seems worse than it is.  $G^2 = -2LL$  for the restricted model
minus  $-2LL$  for the full model is too large, resulting in rejection of  $H_0$  too often.
This is a good example.
```

```
>
> # (e) Make a data frame with no missing values for the full model.
> # help(na.omit)
```

```
>
> dim(Cancer)
[1] 228 11
> Cancer2 = Cancer[,2:11]; dim(Cancer2) # Exclude column 1, institution
[1] 228 10
> Cancer2 = na.omit(Cancer2); dim(Cancer2)
[1] 168 10
```

```
>
>
> # (f)
>
> full2 = survreg(Surv(time,status) ~ age + sex + ph.ecog + ph.karno + pat.karno +
meal.cal + wt.loss, dist='weibull',data=Cancer2)
> nodiet2 = survreg(Surv(time,status) ~ age + sex + ph.ecog + ph.karno + pat.karno,
dist='weibull',data=Cancer2)
> anova(nodiet2,full2)
```

```

                                Terms Resid. Df
1                                age + sex + ph.ecog + ph.karno + pat.karno    161
2 age + sex + ph.ecog + ph.karno + pat.karno + meal.cal + wt.loss          159
-2*LL Test Df Deviance Pr(>Chi)
1 1670.043      NA      NA      NA
2 1666.763      = 2 3.279398 0.1940384
> # Note that update does not get the job done here. I might forget this point.
>
> # (g)
>
> model2 = survreg(stime ~ sex + ph.ecog + ph.karno, dist='weibull', data=Cancer);
summary(model2)

```

Call:

```
survreg(formula = stime ~ sex + ph.ecog + ph.karno, data = Cancer,
        dist = "weibull")
```

	Value	Std. Error	z	p
(Intercept)	7.07575	0.65093	10.87	< 2e-16
sex	0.41141	0.12287	3.35	0.00081
ph.ecog	-0.47729	0.12618	-3.78	0.00016
ph.karno	-0.00906	0.00675	-1.34	0.17983
Log(scale)	-0.32452	0.06207	-5.23	1.7e-07

Scale= 0.723

Weibull distribution

Loglik(model)= -1126.3 Loglik(intercept only)= -1141.1

Chisq= 29.49 on 3 degrees of freedom, p= 1.8e-06

Number of Newton-Raphson Iterations: 5

n=226 (2 observations deleted due to missingness)

```
> model3 = survreg(stime ~ sex + ph.ecog, dist='weibull', data=Cancer);
summary(model3)
```

Call:

```
survreg(formula = stime ~ sex + ph.ecog, data = Cancer, dist = "weibull")
```

	Value	Std. Error	z	p
(Intercept)	6.2210	0.1096	56.74	< 2e-16
sex	0.4014	0.1237	3.24	0.0012
ph.ecog	-0.3557	0.0826	-4.31	1.7e-05
Log(scale)	-0.3133	0.0613	-5.11	3.3e-07

Scale= 0.731

Weibull distribution

Loglik(model)= -1133.1 Loglik(intercept only)= -1147.4

Chisq= 28.73 on 2 degrees of freedom, p= 5.8e-07

Number of Newton-Raphson Iterations: 5

n=227 (1 observation deleted due to missingness)

```
> # model3.5 = survreg(stime ~ sex + ph.ecog + pat.karno, dist='weibull',
```

```

data=Cancer); summary(model3.5)
>
> # (g iv.)
> patient = data.frame(sex=1,ph.ecog=1)
> predlist = predict(model3,newdata=patient,type='quantile',p=0.5,se=TRUE)
> predlist
$fit
      1
402.8872

$se.fit
      1
40.62783

> mhat = predlist$fit; se = predlist$se
> L = mhat - 1.96*se; U = mhat+1.96*se
> c(L,U)
      1      1
323.2567 482.5177
>
> # Note ph.ecog=1 is the mode.
> table(Cancer$ph.ecog)

  0   1   2   3
63 113  50   1
>
>

```