Advanced Data Analysis HW6

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1.

A random variable T is said to have a Weibull distribution is its survival function is give by $S(t) = e(\alpha t)\beta$ where $\alpha > 0$ and $\beta > 0$.

(a)

Find the density, $f_T(t)$ of T

Answer:

$$f_T(t) = -\frac{dS(t)}{dt} = (\beta\alpha^{\beta}t^{\beta-1})e^{-(\alpha t)^{\beta}}$$

(b)

Find the hazard function $\lambda(t)$ of T

Answer:

$$\lambda(t) = \frac{f(t)}{S(t)} = \beta\alpha^{\beta}t^{\beta-1}$$

(c)

Show that

$$log(-log(S(t))) = \beta log(\alpha) + \beta log(t)$$

Based on this, describe a graphical method for checking whether or not the data is from a Weibull distribution.

Answer:

$$\begin{aligned} log(-log(S(t))) &= log((\alpha t)^{\beta}) \\ &= \beta log(\alpha t) \\ &= \beta log(\alpha) + \beta log(t) \end{aligned}$$

Here we get a graphical method for checking whether or not the data is from a Weibull distribution: By plotting all the $(log(t), log(-log(S(t))))$, the points from the same Weibull distribution should lie in a straight line.

(d)

Consider the following data

$$143, 164, 188, 188, 190, 192, 206, 209, 213, 216, 220, 227, 230, 234, 246, 265, 304$$

and use as an estimate of $S(t(i))$

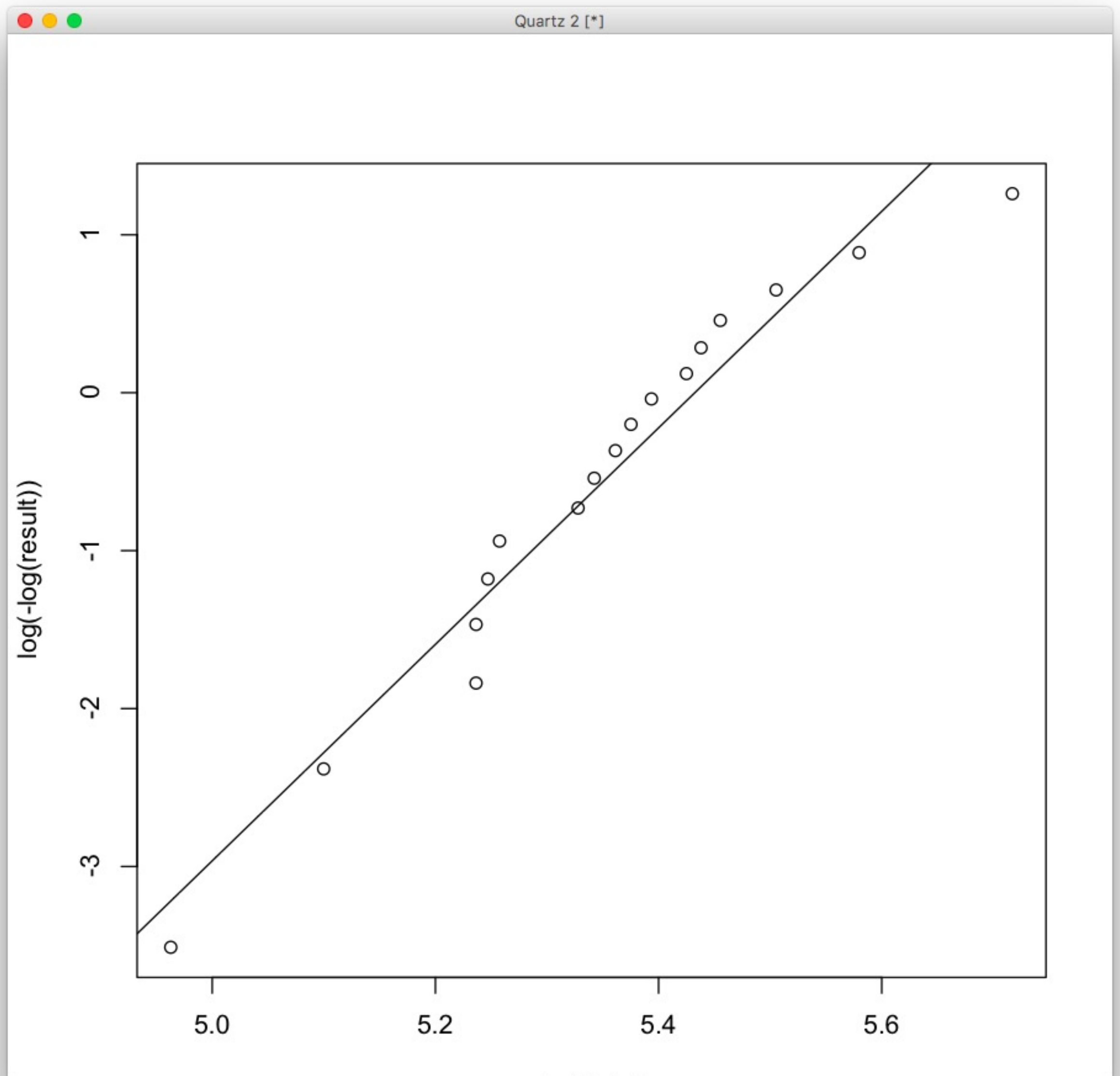
$$S(t(i)) = 1(i - 0.5)/n$$

were $t(i)$ is the ith ordered value and n is the sample size. Use the graphical technique in the previous question to check if a Weibull distribution is appropriate for these data

Answer:

Follow the technique in (c), we plot all the $(log(t_i), log(-log(\hat{S}(t_i)))$ in an axis:

```
data = c(143, 164, 188, 188, 190, 192, 206, 209, 213, 216, 220, 227, 230, 234, 246,
  265, 304)
result = c()
n = length(data)
for (i in 1:17){
  result[i] = 1-(i-0.5)/n
}
plot(log(-log(result))~log(data))
abline(lm(log(-log(result))~log(data)))
```



We can tell from the plot that a Weibull distribution is appropriate for these data.

(e)

Assume that the Weibull distribution is a good fit, use least squares approach to estimate its parameters.

Answer:

```
fit = lm(log(-log(result))~log(data))
abline(fit)
summary(fit)
```

```
 Call:
lm(formula = log(-log(result)) ~ log(data))

Residuals:
     Min       1Q   Median       3Q      Max
-0.68997 -0.12226  0.09174  0.19153  0.30116

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -37.2330     2.1806  -17.07 3.08e-11 ***
log(data)     6.8538     0.4073   16.83 3.80e-11 ***
---
Signif. codes:  0  ***  0.001  **  0.01  *  0.05  .  0.1    1

Residual standard error: 0.2871 on 15 degrees of freedom
Multiple R-squared:  0.9497,  Adjusted R-squared:  0.9463
F-statistic: 283.1 on 1 and 15 DF,  p-value: 3.796e-11
```

Assume that the Weibull distribution is a good fit, by using least squares approach, we have the following estimation for its parameters:

$$\beta = 6.8538$$

$$\alpha = e^{\frac{-37.2330}{\beta}} = 0.0044$$

2.

The data below show survival times in months of patients with Hodgkins disease who were treated with nitrogen mustard. Group A patients received little or no prior therapy whereas Group B patients received heavy prior therapy. Starred are observations are censoring times.

$$\begin{aligned} GroupA :& 1.25, 1.41, 4.98, 5.25, 5.38, 6.92, 8.89, 10.98, 11.18, 13.11, 13.21, 16.33, 19.77, \\ & 21.08, 21.84^*, 22.07, 31.38, 32.61^*, 37.18^*, 42.92 \end{aligned}$$

$$\begin{aligned} GroupB :& 1.05, 2.92, 3.61, 4.20, 4.49, 6.72, 7.31, 9.08, 9.11, 14.49^*, \\ & 16.85, 18.82^*, 26.59^*, 30.26^*, 41.34^* \end{aligned}$$

(a)

Obtain and plot the Kaplan Meier estimates of S_A and S_B, the corresponding survival functions.

Answer:

For group A, we have:

$y_A(i)$	1.25	1.41	4.98	5.25	5.38	6.92	8.89	10.98	11.18	13.11	13.21	16.33	19.77	21.08	22.07	42.92
$d_A(i)$	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
$N_A(i)$	20	19	18	17	16	15	14	13	12	11	10	9	8	7	5	1

So the Kaplan-Meier estimator of S(t) is:

$$\hat{S}_A(t) = \Pi_{y_A(j) \leq t}(1 - \frac{d_A(j)}{N_A(j)})$$

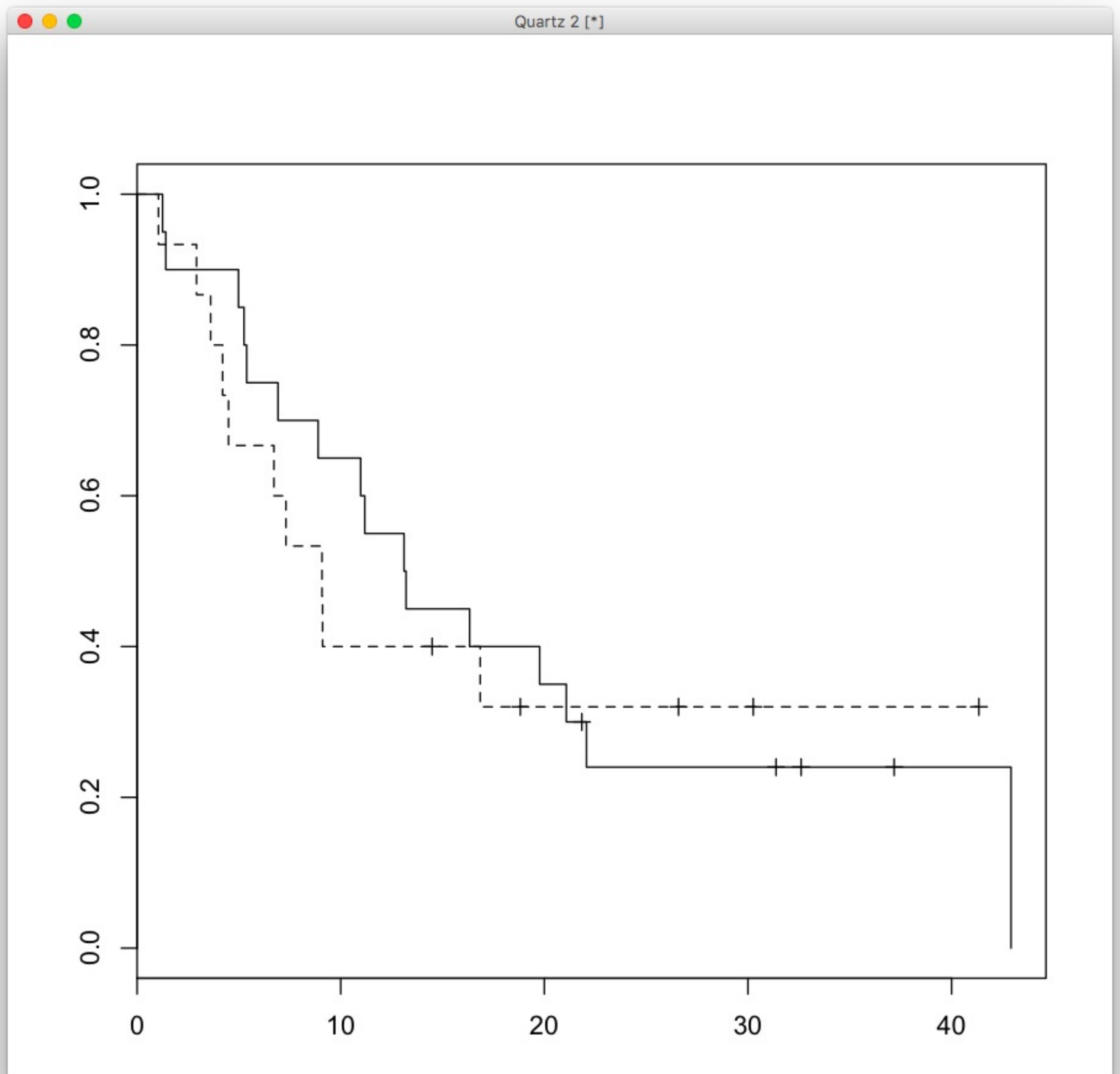
For group B, we have:

$y_B(i)$	1.05	2.92	3.61	4.20	4.49	6.72	7.31	9.08	9.11	16.85
$d_B(i)$	1	1	1	1	1	1	1	1	1	1
$N_B(i)$	15	14	13	12	11	10	9	8	7	5

So the Kaplan-Meier estimator of S(t) is:

$$\hat{S}_B(t) = \Pi_{y_B(j)\leq t}(1 - \frac{d_B(j)}{N_B(j)})$$

```
library(survival)
time = c(1.25, 1.41, 4.98, 5.25, 5.38, 6.92, 8.89, 10.98, 11.18, 13.11, 13.21, 16.33,
    19.77, 21.08, 21.84, 22.07, 31.38, 32.61, 37.18, 42.92, 1.05, 2.92, 3.61, 4.20,
  4.49, 6.72, 7.31, 9.08, 9.11, 14.49, 16.85, 18.82, 26.59, 30.26, 41.34)
status = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1,
    1, 1, 1, 1, 0, 1, 0, 0, 0, 0)
group = c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2)
#data = data.frame(time, status, group)
fit <- survfit(Surv(time,status)~group,type = "kaplan-meier")
plot(fit, lty=1:2 )
```



(b)

Estimate $S_A(10)$ and $S_B(10)$ using a 95% confidence interval.

Answer:

```
> summary(fit)
```

```
Call: survfit(formula = Surv(time, status) ~ group, type = "kaplan-meier")

                group=1
 time n.risk n.event survival std.err lower 95% CI upper 95% CI
 1.25     20       1     0.95  0.0487        0.859        1.000
 1.41     19       1     0.90  0.0671        0.778        1.000
 4.98     18       1     0.85  0.0798        0.707        1.000
 5.25     17       1     0.80  0.0894        0.643        0.996
 5.38     16       1     0.75  0.0968        0.582        0.966
 6.92     15       1     0.70  0.1025        0.525        0.933
 8.89     14       1     0.65  0.1067        0.471        0.897
10.98     13       1     0.60  0.1095        0.420        0.858
11.18     12       1     0.55  0.1112        0.370        0.818
13.11     11       1     0.50  0.1118        0.323        0.775
13.21     10       1     0.45  0.1112        0.277        0.731
16.33      9       1     0.40  0.1095        0.234        0.684
19.77      8       1     0.35  0.1067        0.193        0.636
21.08      7       1     0.30  0.1025        0.154        0.586
22.07      5       1     0.24  0.0980        0.108        0.534
42.92      1       1     0.00     NaN           NA           NA

                group=2
 time n.risk n.event survival std.err lower 95% CI upper 95% CI
 1.05     15       1    0.933  0.0644        0.815        1.000
 2.92     14       1    0.867  0.0878        0.711        1.000
 3.61     13       1    0.800  0.1033        0.621        1.000
 4.20     12       1    0.733  0.1142        0.540        0.995
 4.49     11       1    0.667  0.1217        0.466        0.953
 6.72     10       1    0.600  0.1265        0.397        0.907
 7.31      9       1    0.533  0.1288        0.332        0.856
 9.08      8       1    0.467  0.1288        0.272        0.802
 9.11      7       1    0.400  0.1265        0.215        0.743
16.85      5       1    0.320  0.1239        0.150        0.684
```

According to the output from above,

$$\hat{S}_A(10) = \hat{S}_A(8.89) = 0.65$$

the 95% CI for $\hat{S}_A(10)$ is:

$$(0.471, 0.897)$$

$$\hat{S}_B(10) = \hat{S}_B(9.11) = 0.40$$

the 95% CI for $\hat{S}_B(10)$ is:

$$(0.215, 0.743)$$

(c)

Test H_0 :S_A =S_B against H_a :$S_A \neq S_B$. Use $\alpha = 0.05$.

Answer:

To test the hypothesis, we do the following test in R:

```
> survdiff(Surv(time,status)~group, rho=0)
```

```
  Call:
survdiff(formula = Surv(time, status) ~ group, rho = 0)

         N Observed Expected (O-E)^2/E (O-E)^2/V
group=1 20       16    16.66    0.0261    0.0749
group=2 15       10     9.34    0.0466    0.0749

 Chisq= 0.1  on 1 degrees of freedom, p= 0.784
```

Since the p-value is $0.784 > 0.05$, we cannot reject the Null Hypothesis that $S_A = S_B$.