

Lin_ST625_HW7

Frances Lin

2/20/2022

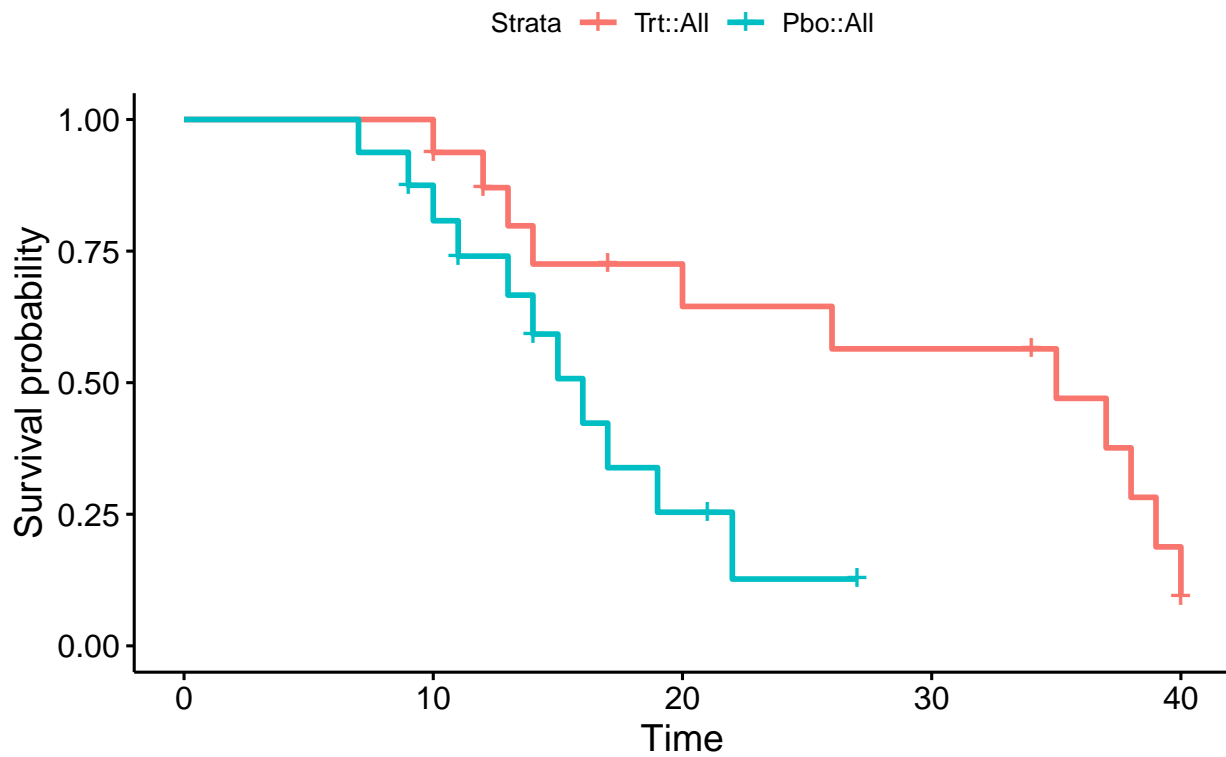
1

Treatment: 10 10+ 12 12+ 13 14 17+ 20 26 34+ 35 37 38 39 40 40+

Placebo: 7 9 9+ 10 11 11+ 13 14 14+ 15 16 17 19 21+ 22 27+

1a

Survival curves of leukemia patients



1b

H_0 : There is no difference between two survival functions.

Log-rank test results:

```
## Call:
## survdiff(formula = Surv(time, status) ~ type, data = Leukemia)
##
##           N Observed Expected (O-E)^2/E (O-E)^2/V
## type=Pbo 16         11      6.56      3.01      5.24
## type=Trt 16         11     15.44      1.28      5.24
##
##  Chisq= 5.2  on 1 degrees of freedom, p= 0.02
```

The treatment has an effect on patient's survival (Chisq= 5.2, p= 0.02).

1c

$H_0: \beta_{typeTrt} = 0.$

Exponential regression test results:

```
##
## Call:
## survreg(formula = Surv(time, status) ~ type, data = Leukemia,
##         dist = "exponential")
##           Value Std. Error      z      p
## (Intercept) 3.062      0.302 10.15 <2e-16
## typeTrt      0.524      0.426  1.23  0.22
##
## Scale fixed at 1
##
## Exponential distribution
## Loglik(model)= -95.1  Loglik(intercept only)= -95.9
##  Chisq= 1.5 on 1 degrees of freedom, p= 0.22
## Number of Newton-Raphson Iterations: 4
## n= 32
```

The treatment has no effect on patient's survival (Chisq= 1.51219, p= 0.2186795).

Wald test test statistics: $\chi^2 = Z^2 = \left(\frac{\beta_{typeTrt}}{SE(\beta_{typeTrt})}\right)^2 =$

```
## [1] 1.51219
```

p-val =

```
## [1] 0.2188051
```

1d

Log-rank test is a rank-based, nonparametric method with few assumptions. On the other hand, exponential regression model is a parametric method. For AFT (accelerated failure time) model like Exponential regression model, we need to assume a distribution on survival time. In the later cases, choices of distribution will affect the results.

In addition, the test statistics of log-rank test depends only on the ranks of the observed times. On the other hand, AFT model models the survival time directly.

2

| Time | Delta | Type |
|------|-------|------|
| 1.5 | 1 | 1 |
| 3.5 | 1 | 1 |
| 4.5 | 1 | 1 |

2a

Weibull regression model results for Group 2 only:

```
##
## Call:
## survreg(formula = Surv(Time, Delta) ~ 1, data = Kidney_2, dist = "weibull")
##           Value Std. Error      z      p
## (Intercept) 5.411      1.024  5.29 1.3e-07
## Log(scale)  0.616      0.265  2.32  0.02
##
## Scale= 1.85
##
## Weibull distribution
## Loglik(model)= -51.6   Loglik(intercept only)= -51.6
## Number of Newton-Raphson Iterations: 7
## n= 76
```

2b

For the Weibull regression for Group 2 only, the Scale parameter is estimated as 1.85 and the standard error is estimated as 1.303434. I think we might need to use delta method here. That is, if $\sqrt{(n)}(X_n - \theta) \rightarrow N(0, \sigma^2)$, then $\sqrt{(n)}(g(X_n) - g(\theta)) \rightarrow N(0, \sigma^2(g'(\theta))^2)$.

(Notice that the Log(scale)= 0.616 and Scale= 1.85, which is $= \exp(0.616)$.)

```
##           Value Std. Error
## 0.6158380  0.2650022
```

```
##           Value Std. Error
## 1.851207  1.303434
```

2c

$H_0: \beta_{shape} = 1$. I assume we are still working with Group 2 only.

LR test: There is evidence to use a more complex Weibull distribution to fit the data over the Exponential model ($p = 0.007592901$). For an Exponential model for the survival time, the Scale parameter is set to 1 (Shape = 1 / Scale = 1 too), but here we reject the Exponential model so we reject the $H_0: \beta_{shape} = 1$.

```
## [1] 7.127063
```

```
## [1] 0.007592901
```

Wald test: There is evidence to use a more complex Weibull distribution. Here again we reject the $H_0: \beta_{shape} = 1$ (Wald test statistics = 5.403432, $p = 0.0200972$).

```
## [1] 5.403432
```

```
## [1] 0.0200972
```

2d

Since we reject the $H_0: \beta_{shape} = 1$, we have evidence that a more complex Weibull distribution to fit the data over the Exponential model. A Weibull regression model is preferred.

(Recall the Exponential distribution is a special case of Weibull distribution.)

2e

Weibull regression model results:

```
##
## Call:
## survreg(formula = Surv(Time, Delta) ~ factor(Z), data = Kidney,
##         dist = "weibull")
##           Value Std. Error      z      p
## (Intercept) 3.597      0.339 10.61 <2e-16
## factor(Z)2  0.623      0.469  1.33  0.18
## Log(scale)  0.129      0.167  0.77  0.44
##
## Scale= 1.14
##
## Weibull distribution
## Loglik(model)= -122   Loglik(intercept only)= -122.9
##  Chisq= 1.93 on 1 degrees of freedom, p= 0.16
## Number of Newton-Raphson Iterations: 7
## n= 119
```

2f

On average, the other group (Group 2: patients utilized a percutaneous placement of their catheter) does better although it is not statistically significant ($p=0.18$). The other group is estimated to be $\exp(0.623) = 1.864042$ times the reference group (Group 1: patients utilized a surgically placed catheter).

```
## factor(Z)2
##    1.864042
```

2g

$H_0: \beta_{catheter} = 0$.

```
##
## Call:
## survreg(formula = Surv(Time, Delta) ~ factor(Z), data = Kidney,
##         dist = "weibull")
##           Value Std. Error      z      p
## (Intercept) 3.597      0.339 10.61 <2e-16
## factor(Z)2  0.623      0.469  1.33  0.18
## Log(scale)  0.129      0.167  0.77  0.44
##
## Scale= 1.14
##
## Weibull distribution
## Loglik(model)= -122   Loglik(intercept only)= -122.9
##   Chisq= 1.93 on 1 degrees of freedom, p= 0.16
## Number of Newton-Raphson Iterations: 7
## n= 119

##
## Call:
## survreg(formula = Surv(Time, Delta) ~ 1, data = Kidney, dist = "weibull")
##           Value Std. Error      z      p
## (Intercept) 3.887      0.316 12.30 <2e-16
## Log(scale)  0.117      0.165  0.71  0.48
##
## Scale= 1.12
##
## Weibull distribution
## Loglik(model)= -122.9   Loglik(intercept only)= -122.9
## Number of Newton-Raphson Iterations: 6
## n= 119
```

Likelihood ratio test: We fail to reject $H_0: \beta_{catheter} = 0$ (LR test statistics = 1.928084, $p = 0.1649682$).

```
## [1] 1.928084
```

```
## [1] 0.1649682
```

Wald test: Again, we fail to reject $H_0: \beta_{catheter} = 0$ (Wald test statistics = 1.764698, $p = 0.1840396$).

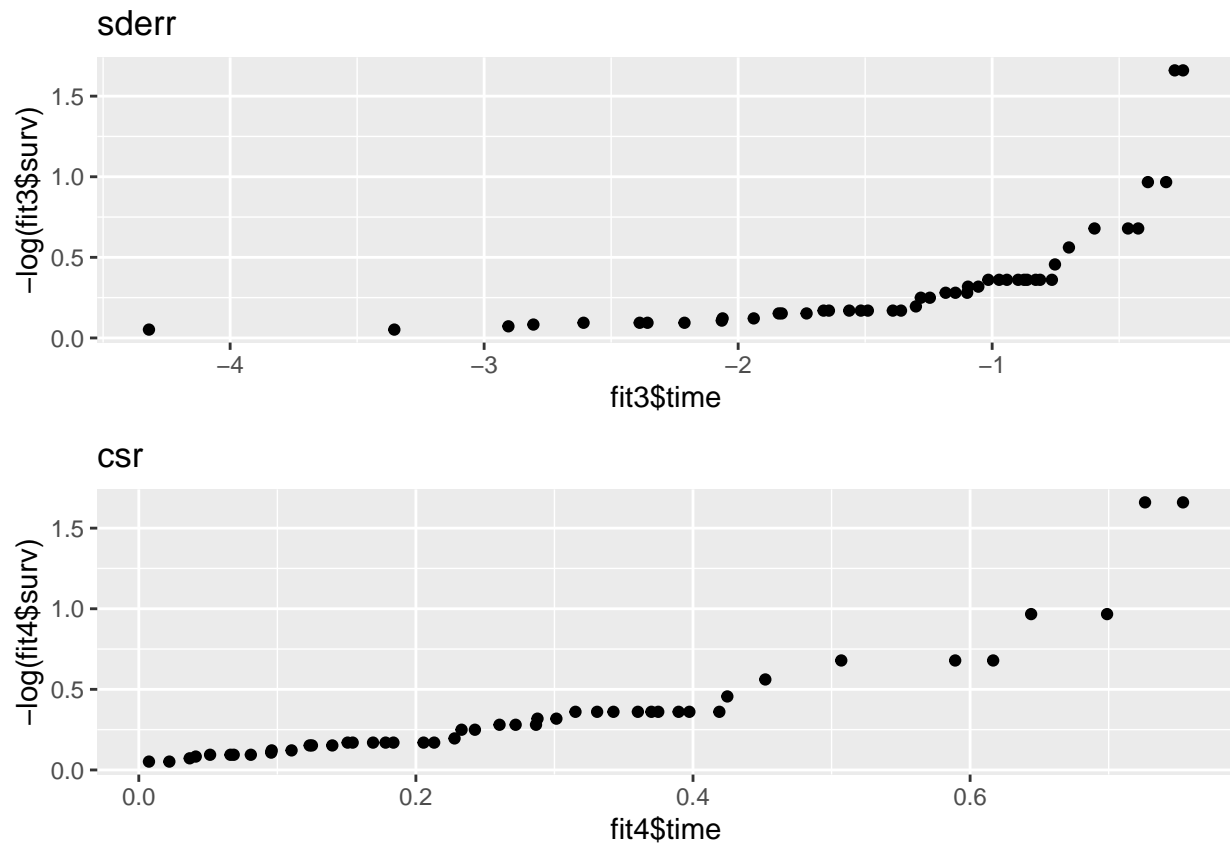
```
## [1] 1.764698
```

```
## [1] 0.1840396
```

2h

Weibull regression model may not be a good fit.

Page 3 of Lecture 23 slide says if a Weibull model holds, after obtaining the KM estimator \hat{S} based on U_i (standardized residuals), we should plot $-\log S(U_i)$ vs U_i and check if a straight line goes through the origin. No. For the KM estimator \hat{S} based on r_i (Cox-snell residuals), we should plot $-\log S(r_i)$ vs r_i and check to see if there is a straight line with slope = 1. Not quite either.



Note. Assume that page 3 of Lecture 23 slide is indeed correct, then this is different from plot of $\log(-\log(\text{survival function}))$ vs. $\log(\text{time})$ for Weibull model from Lab4-R-1.pdf.

3

3a

Weibull regression model results with `age`, `bmi`, `hr`, `sho`, `chf` as covariates:

```
##
## Call:
## survreg(formula = Surv(time, fstat) ~ age + bmi + hr + factor(sho) +
##       factor(chf), data = Data_1, dist = "weibull")
##               Value Std. Error      z      p
## (Intercept)  14.7381      1.4818  9.95 < 2e-16
## age          -0.0923      0.0127 -7.29 3.0e-13
## bmi           0.0909      0.0297  3.06 0.00225
## hr           -0.0185      0.0052 -3.55 0.00038
## factor(sho)1 -2.0301      0.4810 -4.22 2.4e-05
## factor(chf)1 -1.3673      0.2741 -4.99 6.1e-07
## Log(scale)    0.6176      0.0584 10.57 < 2e-16
##
## Scale= 1.85
##
## Weibull distribution
## Loglik(model)= -1648.7   Loglik(intercept only)= -1752.5
##  Chisq= 207.49 on 5 degrees of freedom, p= 7.1e-43
## Number of Newton-Raphson Iterations: 6
## n= 500
```

All of these covariates have significant effects on survival time. p-values are included in **3b**.

3b

It is estimated that the mean (or median) survival time will decrease by 8.168477% ($= (1 - \exp(-0.0923)) * 100$) (or $\exp(-0.0923) = \mathbf{0.9118316}$ times) with one unit increase of `age`. `age` has significant effect on the survival time ($p = 3.0e-13$).

It is estimated that the mean (or median) survival time will increase by 9.09% (or $\exp(0.0909) = \mathbf{1.095159}$ times) with one unit increase of `bmi`. `bmi` has significant effect on the survival time ($p = 0.00225$).

It is estimated that the mean (or median) survival time will decrease by 1.832993% ($= (1 - \exp(-0.0185)) * 100$) (or $\exp(-0.0185) = \mathbf{0.9816701}$ times) with one unit increase of `hr`. `hr` has significant effect on the survival time ($p = 0.00038$).

CORRECTED. The other group is times the reference group. This makes more sense since now that the reference groups (`sho = 0`: No cardiogenic shock & `chf = 0`: No congestive heart complications) should have better survival.

The other group (`sho = 1`: Yes cardiogenic shock) is estimated to be $\exp(-2.0301) = \mathbf{0.1313224}$ times the reference group (`sho = 0`: No cardiogenic shock). `sho` has significant effect on the survival time ($p = 2.4e-05$).

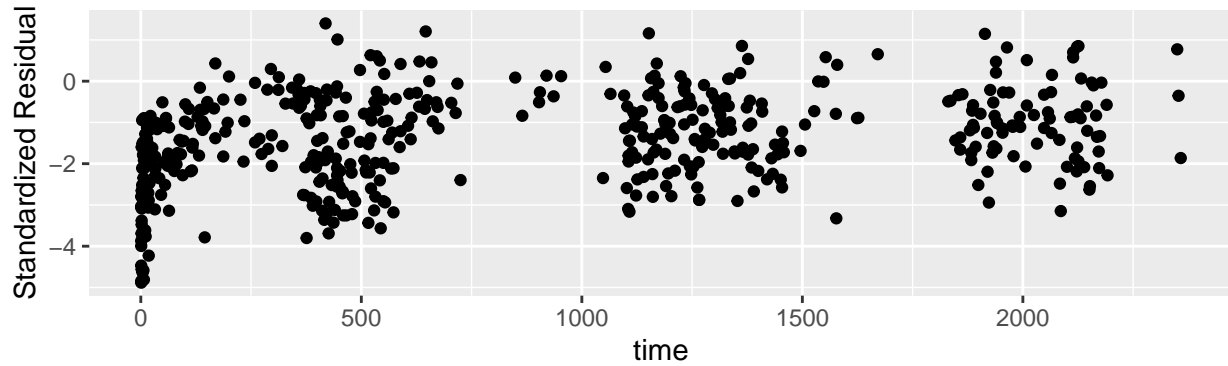
The other group (`chf = 1`: Yes congestive heart complications) is estimated to be $\exp(-1.3673) = \mathbf{0.254794}$ times the reference group (`chf = 0`: No congestive heart complications). `chf` has significant effect on the survival time ($p = 6.1e-07$).

```
## (Intercept)          age          bmi          hr factor(sho)1 factor(chf)1
## 2.515905e+06 9.118060e-01 1.095176e+00 9.816856e-01 1.313270e-01 2.548066e-01
## Log(scale)
## 1.854546e+00
```

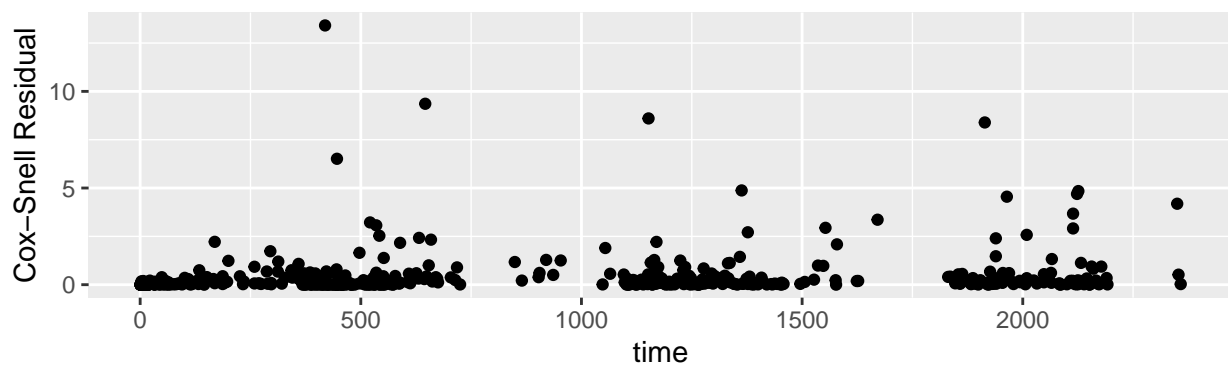
3c

Standardized residuals (sderr) take negative values and are symmetric except at the left end. Cox-snell residuals (csr) are always positive. If the Weibull regression is a correct fit, then the residuals should follow ?? distribution. I think we should proceed with the 3rd and 4th plot on the next page.

Standardized residuals from Weibull regression

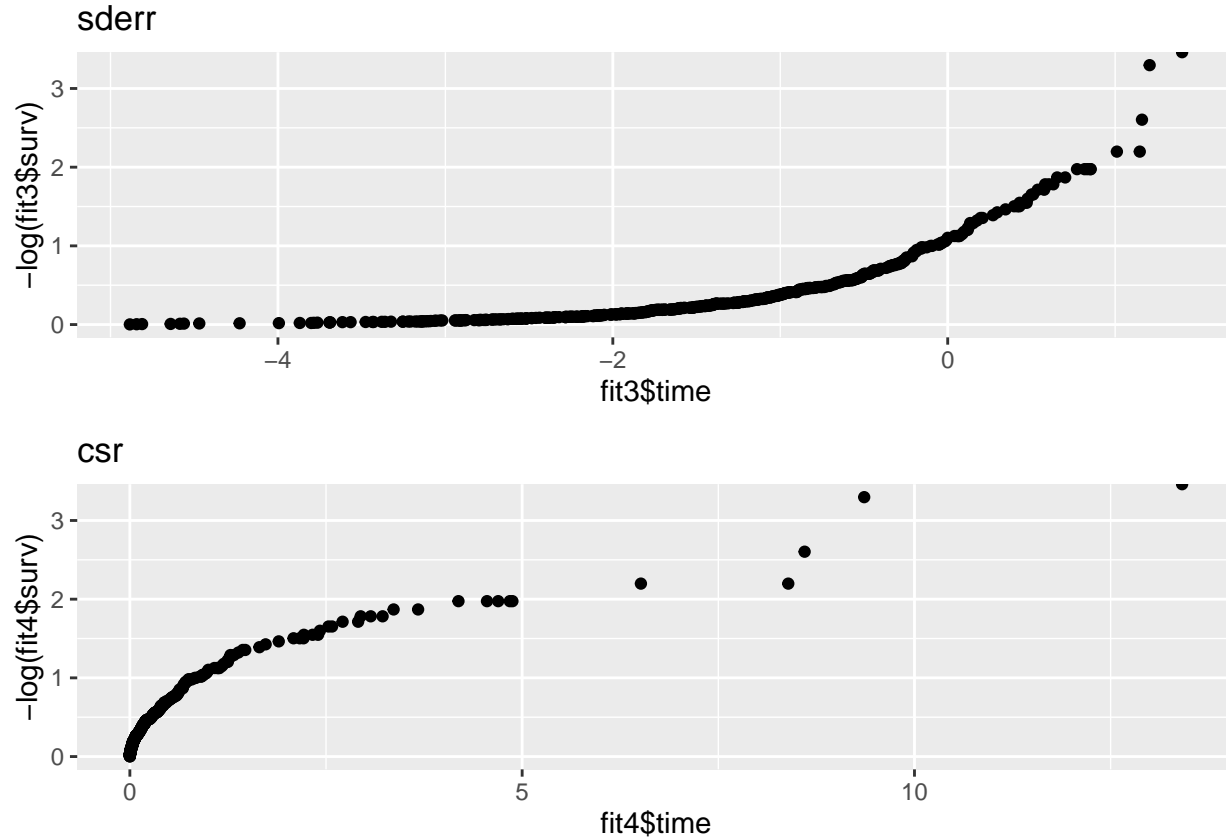


Cox-Snell residuals from Weibull regression

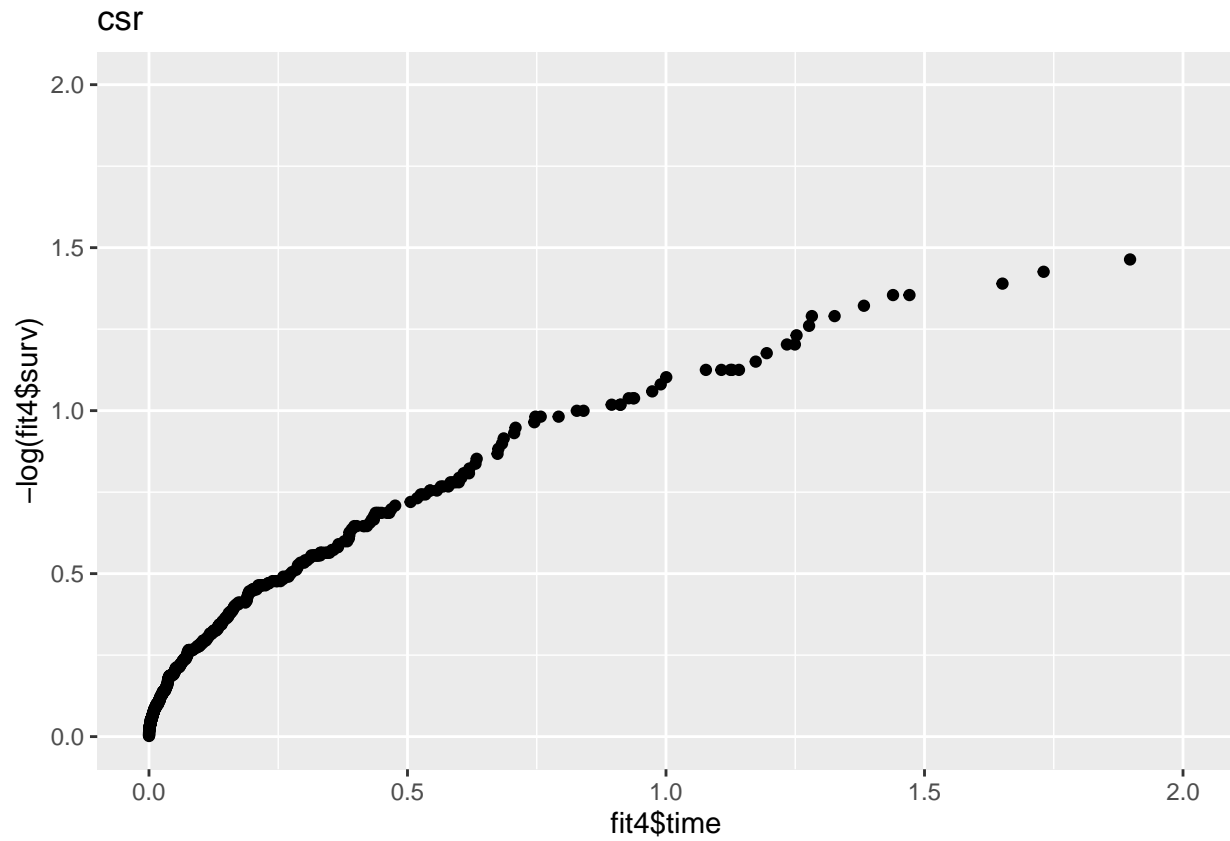


Here I follow Page 3 of Lecture 23 slide again. Weibull regression may not a good fit since the 1st plot of $-\log(\text{survival})$ vs time does not appear straight and does not go through the origin and the 2nd plot does not appear linear with slope = 1.

Note. In the sderr plot, survival function is estimated using the standardized residuals. In the csr plot, survival function is estimated using the Cox-Snell residuals.



We should a straight line with slope = 1 so Weibull regression is a good fit.



3d

Fitting the the Weibull regression if the Weibull regression is not appropriate for the data would result in inaccurate estimates for the parameter of interest, incorrect coefficient for the scale parameter and unreliable results.