STAT 571B, Homework
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Code at https://github.com/kyclark/stat571/tree/master/hw02

1. Montgomery 3.3

One-way ANOVA

```
Source       DF      SS      MS       F        P
Factor        3    36.15   <MST>    <F>      <P>
Error      <DFE>   <SSE>   <MSE>
Total        19   196.04
```

```
DFE = N - a               = 20 - 4           = 16
SSE = SS(Total) / SST = 196.04 - 36.15 = 159.89
MST = SST / DFT           = 36.15 / 3        = 12.05
MSE = SSE / DFE           = 159.89 / 16      = 9.993
F   = MST / MSE           = 12.05 / 9.993    = 1.206
P   = F (Signal, Noise) = F (DFT, DFE) = F (1.206, 3, 16) = 0.3395
```

2. Montgomery 3.22 (skip part d)

a) Do the three circuits have the same response time?

```
> dat = read.delim("~/work/stat571/hw02/3.22.dat")
> dat$circuit = factor(dat$circuit) # to turn integers into factors
> amod = aov(response ~ circuit, data=dat)
> amod.sum = unlist(summary(amod))
> amod.sum['Pr(>F)1']
     Pr(>F)1
0.0004023258
```

P < α = 0.01 ∴ reject H0 (no difference), response times are different

b) Tukey Honest Significant Difference

This uses the standard TukeyHSD test in R:

```
> TukeyHSD(amod, conf.level=0.99)
  Tukey multiple comparisons of means
    99% family-wise confidence level

Fit: aov(formula = response ~ circuit, data = dat)

$circuit
     diff        lwr       upr      p adj
2-1  11.4    2.123163 20.676837 0.0023656
3-1  -2.4 -11.676837   6.876837 0.6367043
3-2 -13.8 -23.076837  -4.523163 0.0005042
```

I found a second library called "multcomp" that gives the same results with a little better emphasis on the differences:

```
> library("multcomp")
> tmod <- glht(amod, linfct = mcp(circuit="Tukey"))
> summary(tmod)
```

        Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: aov(formula = response ~ circuit, data = dat)

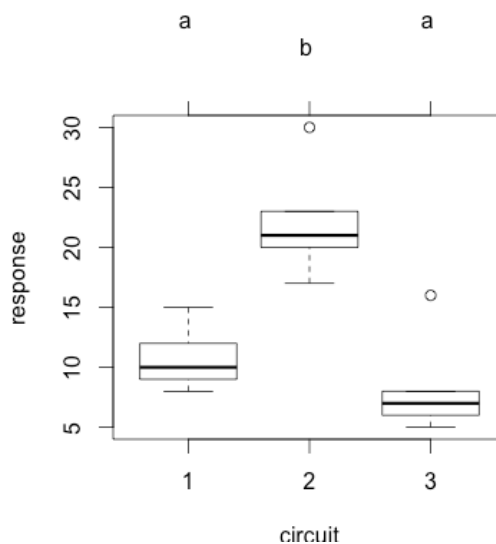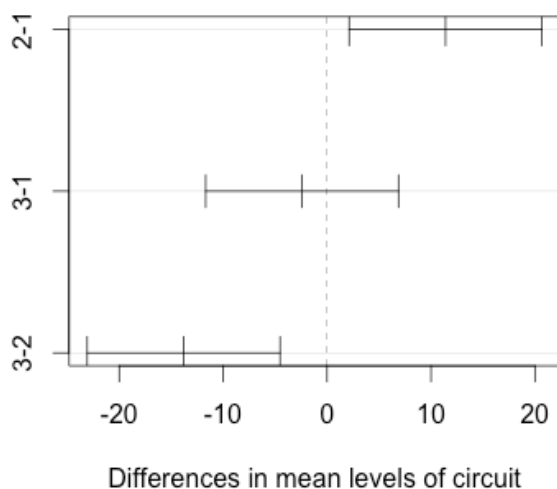Linear Hypotheses:
           Estimate Std. Error t value Pr(>|t|)
2 - 1 == 0   11.4   2.6   4.385   0.0024 **
3 - 1 == 0   -2.4   2.6 -0.923   0.6367
3 - 2 == 0   -13.8   2.6 -5.308   <0.001 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

The combination 3-1 is the most significantly similar (overlap "0" in plot below, left). The others are different. The graph on the left shows that the differences between 3 and 1 include 0, so no significant difference. The graph on the right shows the grouping of 1 and 3 into "a" and the others (2-1, 2-3) into "ab."

c) graphical comparison

I used the following information on the means of the three groups to create the attached graph.

```
> mean(dat[dat$circuit == 1, "response"])
[1] 10.8
> mean(dat[dat$circuit == 2, "response"])
[1] 22.2
> mean(dat[dat$circuit == 3, "response"])
[1] 8.4
> summary(amod)
          Df Sum Sq Mean Sq F value   Pr(>F)
circuit    2  543.6   271.8   16.08 0.000402 ***
Residuals 12  202.8    16.9
```

The mean square of the residuals is 16.9 which I multiplied by 3 standard deviations to find the span of the scaled t-distribution:

sqrt(MSE/n) = sqrt(16.9/15) = 1.06 * 3SD = 3.09

e) Choose either circuit 1 or 3 as they have the lower response times which would be desirable for a shutoff valve.

f) The plot of residuals shows a random distribution of residuals, so basic analysis of variance assumptions are satisfied.

Residuals response ~ circuit
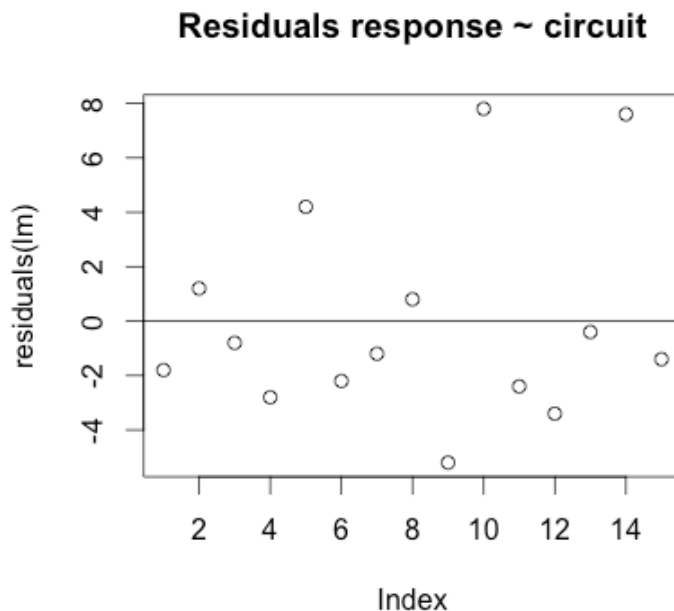
Further, plot of residuals vs fitted and QQ plots show basic variance is acceptable (though we can see outliers in rows 10 and 14):
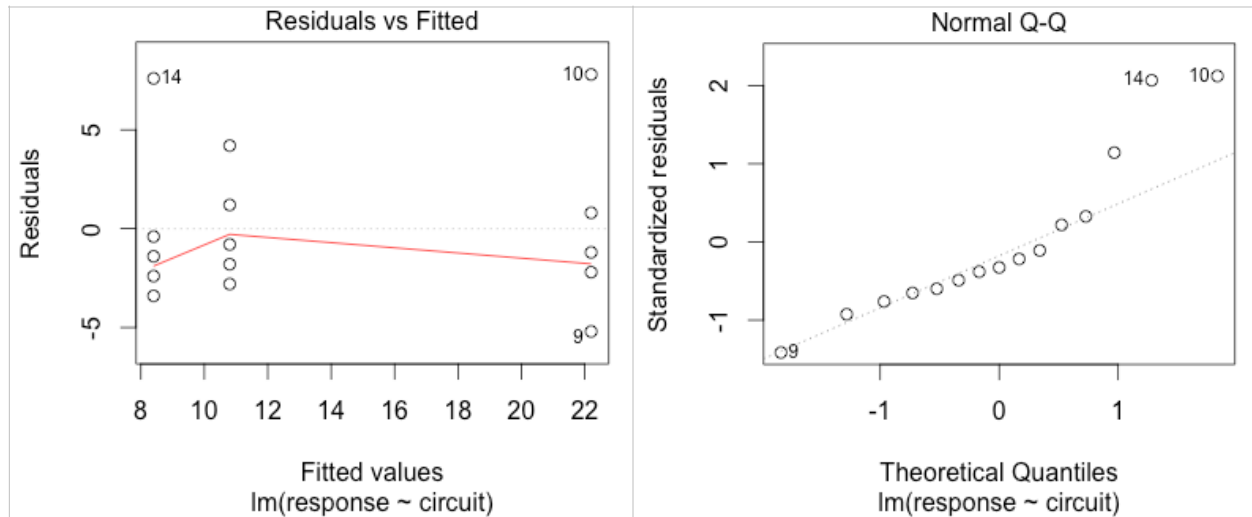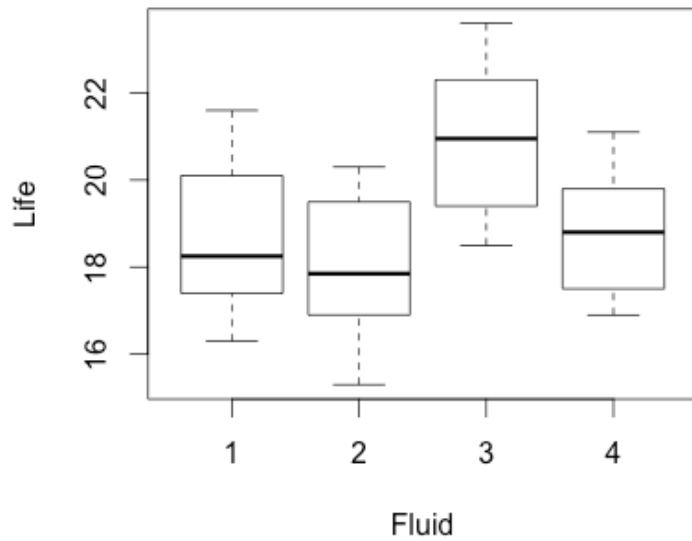

3. Montgomery 3.23

a) Do the fluids differ?

```
> dat = read.delim("~/work/stat571/hw02/3.23.long.dat")
> dat$fluid = factor(dat$fluid) # to turn integers into factors
> amod = aov(life ~ fluid, data=dat)
> amod.sum = unlist(summary(amod))
> amod.sum['Pr(>F)1']
   Pr(>F)1
0.05246316
```
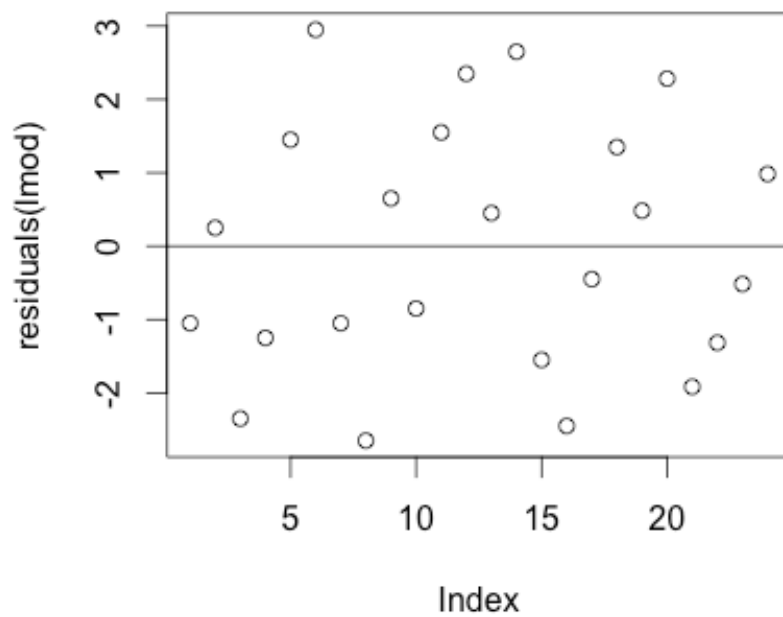
$P > \alpha = 0.05 \therefore$ fail to reject null hypothesis, fluids are not significantly different

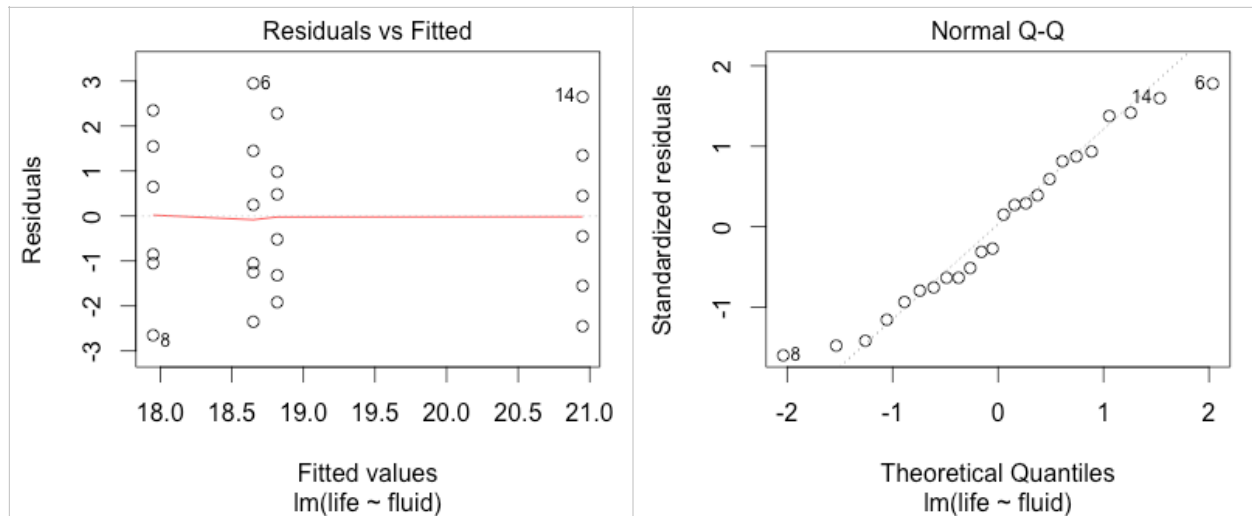**b)** *I would select fluid 3 as it has the longest life:*

c) *Plot of residuals is random, so basic analysis of variance satisfied.*

Residuals life ~ fluid

Other graphs of residuals vs fitted and QQ show good variance, too:

Residuals vs Fitted — lm(life ~ fluid)

Normal Q-Q — lm(life ~ fluid)

4. Montgomery 3.28

a) Do all five materials have the same effect on mean failure time?

```
> dat = read.delim("~/work/stat571/hw02/3.28.dat")
> dat$material = factor(dat$material)
> amod = aov(failure ~ material, data=dat)
> amod.sum = unlist(summary(amod))
> amod.sum['Pr(>F)1']
     Pr(>F)1
0.003785956
```

Very small p-value to support null hypothesis ∴ there is a difference.

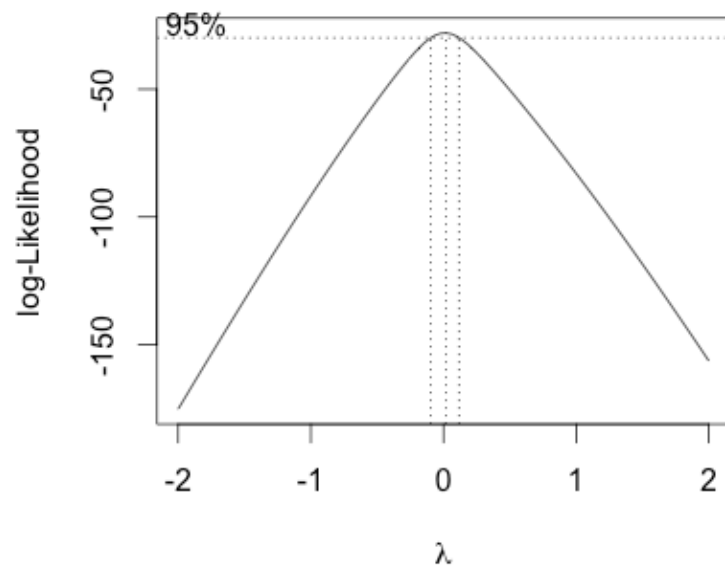**b)** *Plot of residuals vs predicted shows poor variance (opening funnel to right).*

Residuals vs Fitted

Residuals vs Fitted
lm(failure ~ material)
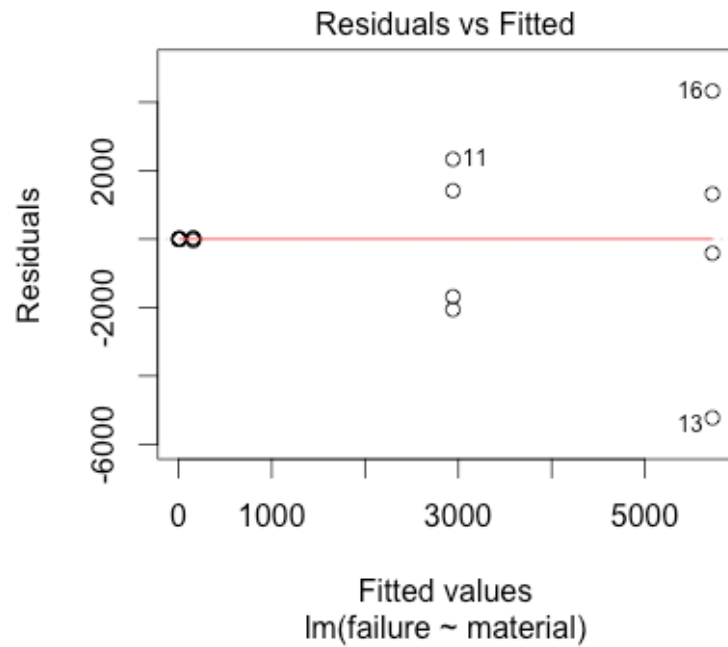
c) Transform "failure" by log

First perform a Box-Cox test to determine lambda:

```
> library('MASS')
> bc = boxcox(failure ~ material, data=dat, lambda = seq(-2, 2, .1))
> with(bc, x[which.max(y)])
[1] 0.02020202
```
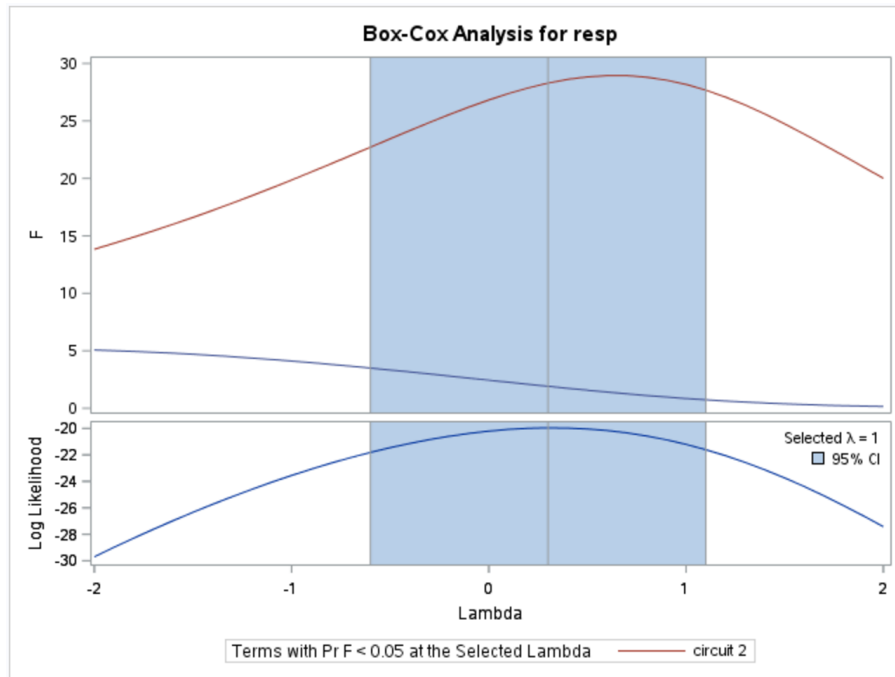

SAS agrees:

```
data circuits;
input circuit resp @@;
```

```
datalines;
1 9 1 12 1 10 1 8 1 15
2 20 2 21 2 23 2 17 2 30
3 6 3 5 3 8 3 16 3 7
;
run;

proc transreg data=circuits;
model boxcox(resp/convenient lambda=-2.0 to 2.0 by 0.1)=class(circuit);
run;
```
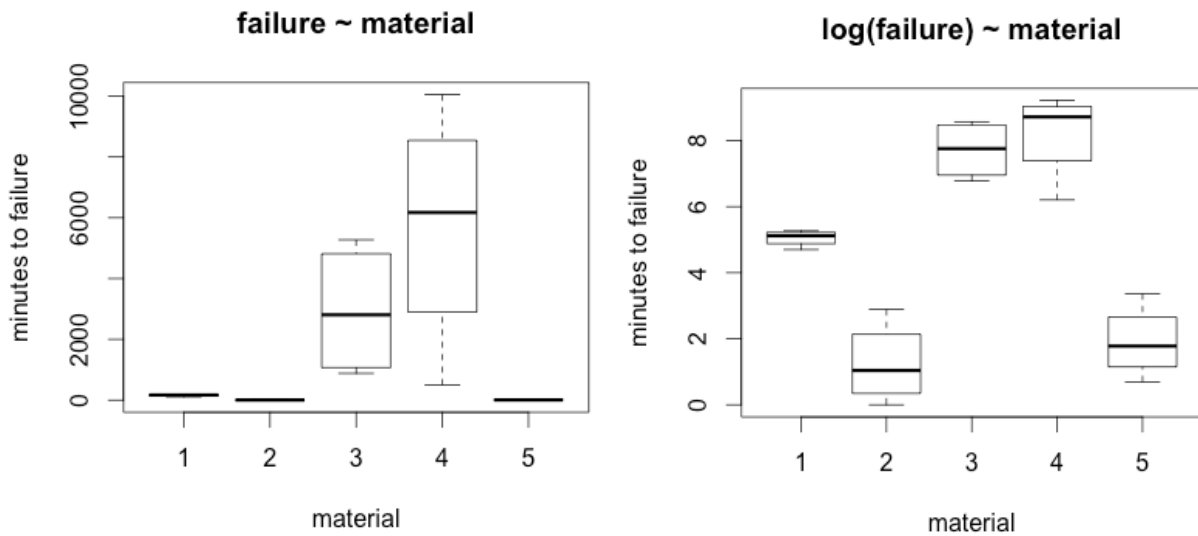

Box-Cox Analysis for resp

*As the lambda is closest to 0, log transformation is chosen.*

```
> dat$log.failure = log(dat$failure)
> boxplot(failure ~ material, data=dat, main = 'failure ~ material', ylab =
'minutes to failure', xlab = 'material')
> boxplot(log.failure ~ material, data=dat, main = 'log(failure) ~ material',
ylab = 'minutes to failure', xlab = 'material')
```

failure ~ material
log(failure) ~ material

The above boxplots show the normalizing effect of transforming the minutes-to-failure data by natural logarithm. ANOVA analysis and scatterplots further support this change by an increase p-value and better distribution of residuals, respectively.

```
> amod2 = aov(log.failure ~ material, data=dat)
> amod2.sum = unlist(summary(amod2))
> amod2.sum['Pr(>F)1']
    Pr(>F)1
1.176093e-07
```


Residuals log(failure) ~ material
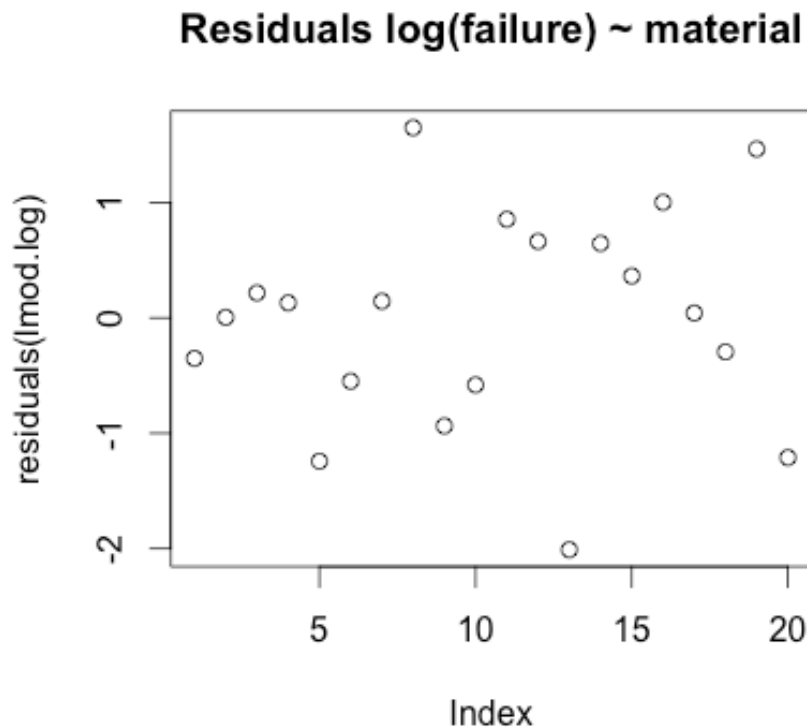
5. Montgomery 3.51

```
> dat = read.delim("~/work/stat571/hw02/3.23.long.dat")
> dat$fluid = factor(dat$fluid)
> kruskal.test(life ~ fluid, data=dat)

        Kruskal-Wallis rank sum test

data:  life by fluid
Kruskal-Wallis chi-squared = 6.2177, df = 3, p-value = 0.1015
```

Previous p-value was 0.52 which was greater than α = 0.05, so this p-value reconfirms failure to reject null hypothesis.