# p8130_hw3_xj2249

*xj2249*

*2019/10/24*

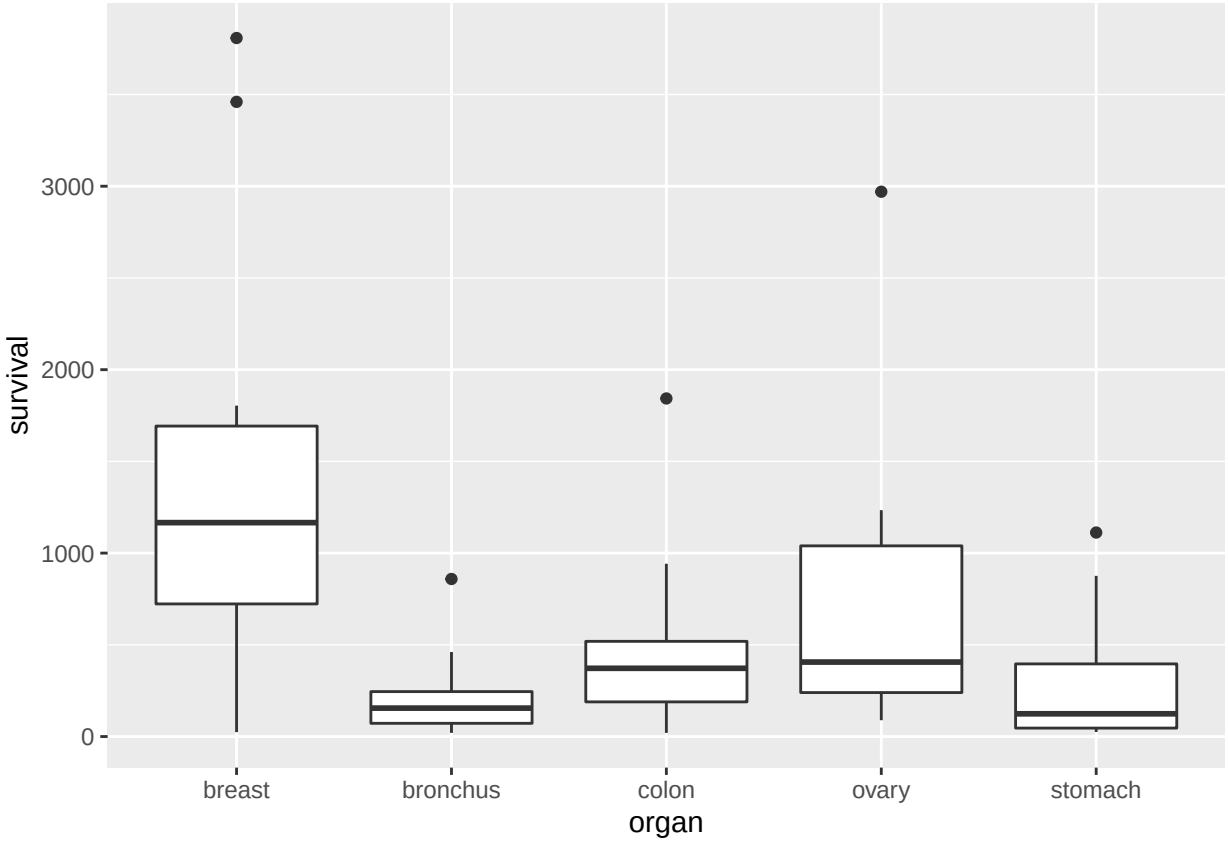
## Problem2

### a)

```
sur_df <- read_csv("./SurvCancer.csv") %>%
        janitor::clean_names() %>%
        mutate(organ = str_to_lower(organ),
               organ = factor(organ))
```

```
## Parsed with column specification:
## cols(
##   SURVIVAL = col_double(),
##   ORGAN = col_character()
## )
```

```
# boxplot
sur_df %>%
        ggplot(aes( x =  organ, y = survival)) +
        geom_boxplot()
```




```
# descriptive statistics
sur_df %>%
        group_by(organ) %>%
        summarise( n = n(),
                   mean = mean(survival),
                   median = median(survival),
                   sd = sd(survival),
                   IQR = IQR(survival),
                   min = min(survival),
                   max = max(survival)
                  ) %>%
        knitr::kable()
```

| organ | n | mean | median | sd | IQR | min | max |
|---|---|---|---|---|---|---|---|
| breast | 11 | 1395.9091 | 1166 | 1238.9667 | 969.50 | 24 | 3808 |
| bronchus | 17 | 211.5882 | 155 | 209.8586 | 173.00 | 20 | 859 |
| colon | 17 | 457.4118 | 372 | 427.1686 | 330.00 | 20 | 1843 |
| ovary | 6 | 884.3333 | 406 | 1098.5788 | 799.75 | 89 | 2970 |
| stomach | 13 | 286.0000 | 124 | 346.3096 | 350.00 | 25 | 1112 |

## b)

Hypothesis:

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 \quad vs \quad H_1 : \text{not all means are equal}$$

Significance level:$\alpha = 0.01$

Assumptions:(1)Independence (2)equal variance (3)normality

Decision rule: Reject $H_0$: if $F_{stats} > F_{4,59,1-\alpha/2} = F_{4,59,0.995} = 4.148$ Fail to reject $H_0$: if $F_{stats} < F_{4,59,0.995}$

Interpretation: Since $F_{stats} = 6.433 > F_{4,59,1-\alpha/2} = F_{4,59,0.995} = 4.148$, we reject $H_0$ and conclude that there is a significant difference in average survival time among different cancer groups.

```
sur_aov <- aov(survival ~ organ, data = sur_df)

pander(sur_aov)
```

Table 2: Analysis of Variance Model

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|---|---|---|---|---|---|
| **organ** | 4 | 11535761 | 2883940 | 6.433 | 0.0002295 |
| **Residuals** | 59 | 26448144 | 448274 | NA | NA |

## c) how to adjust 0.05 to 0.01

1) Bonferroni

```
pairwise.t.test(sur_df$survival, sur_df$organ, p.adj = 'bonferroni')
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  sur_df$survival and sur_df$organ
##
##          breast  bronchus colon   ovary
## bronchus 0.00025 -        -       -
## colon    0.00608 1.00000  -       -
## ovary    1.00000 0.38575  1.00000 -
## stomach  0.00153 1.00000  1.00000 0.75283
##
## P value adjustment method: bonferroni
```

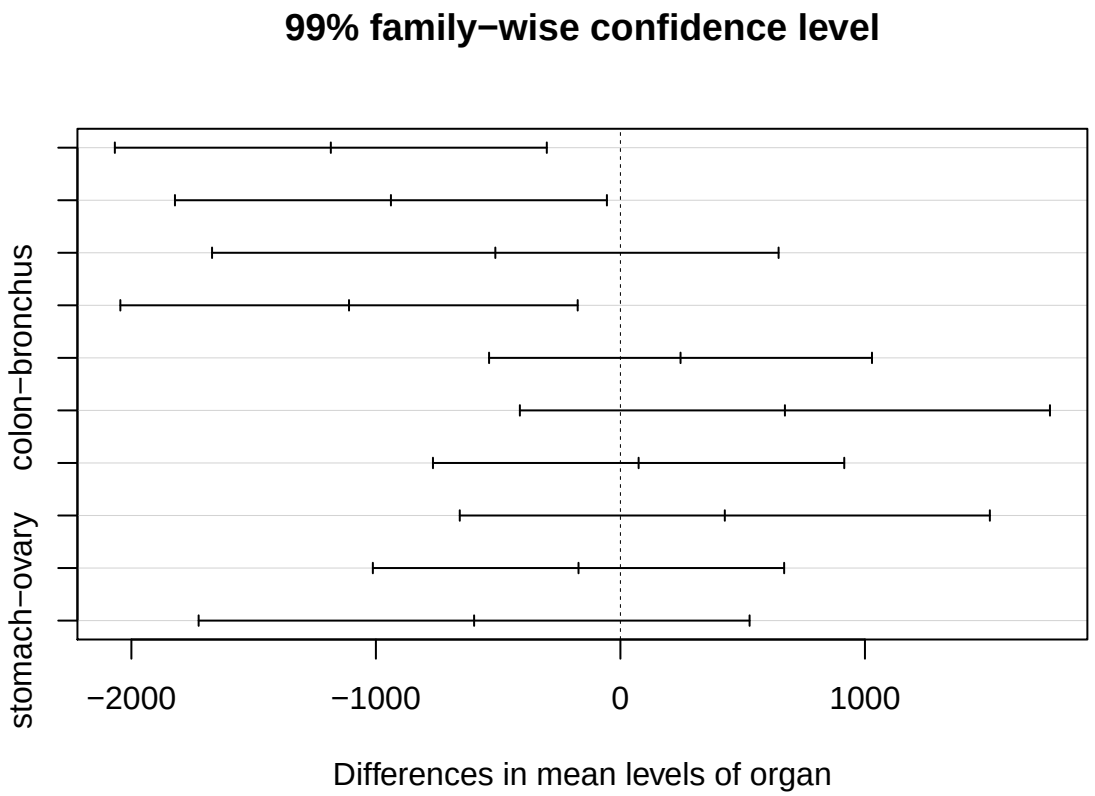
2) Tukey

```
TukeyHSD(sur_aov,conf.level = 0.99) ## 0.99???
```

```
##   Tukey multiple comparisons of means
##     99% family-wise confidence level
##
## Fit: aov(formula = survival ~ organ, data = sur_df)
##
## $organ
##                         diff        lwr        upr     p adj
## bronchus-breast  -1184.32086 -2067.6073 -301.03446 0.0002385
## colon-breast      -938.49733 -1821.7837  -55.21093 0.0053072
```

```
## ovary-breast      -511.57576 -1670.0752  646.92367 0.5630900
## stomach-breast   -1109.90909 -2045.0583 -174.75983 0.0013962
## colon-bronchus     245.82353  -537.1262 1028.77324 0.8208402
## ovary-bronchus     672.74510  -411.1997 1756.68989 0.2271084
## stomach-bronchus    74.41176  -766.6111  915.43467 0.9981461
## ovary-colon        426.92157  -657.0232 1510.86636 0.6659115
## stomach-colon     -171.41176 -1012.4347  669.61114 0.9568289
## stomach-ovary     -598.33333 -1724.9413  528.27467 0.3772923
```

```
TukeyHSD(sur_aov,conf.level = 0.99) %>% plot()
```




3) Dunnett Test

```
glht(sur_aov, linfct = mcp(organ = "Dunnett")) %>% summary()
```

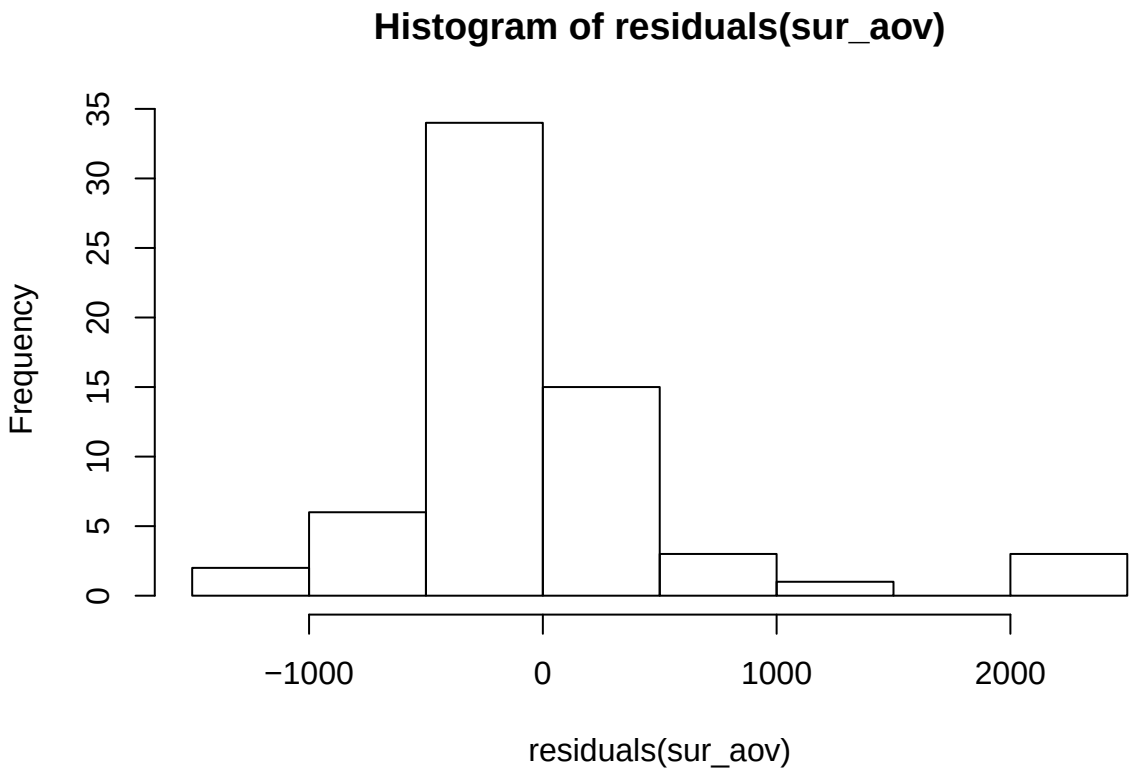
```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Dunnett Contrasts
##
##
## Fit: aov(formula = survival ~ organ, data = sur_df)
##
## Linear Hypotheses:
##                          Estimate Std. Error t value Pr(>|t|)
## bronchus - breast == 0  -1184.3      259.1  -4.571  < 0.001 ***
## colon - breast == 0      -938.5      259.1  -3.622  0.00225 **
```

```
## ovary - breast == 0      -511.6      339.8  -1.506  0.36676
## stomach - breast == 0   -1109.9      274.3  -4.046  < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

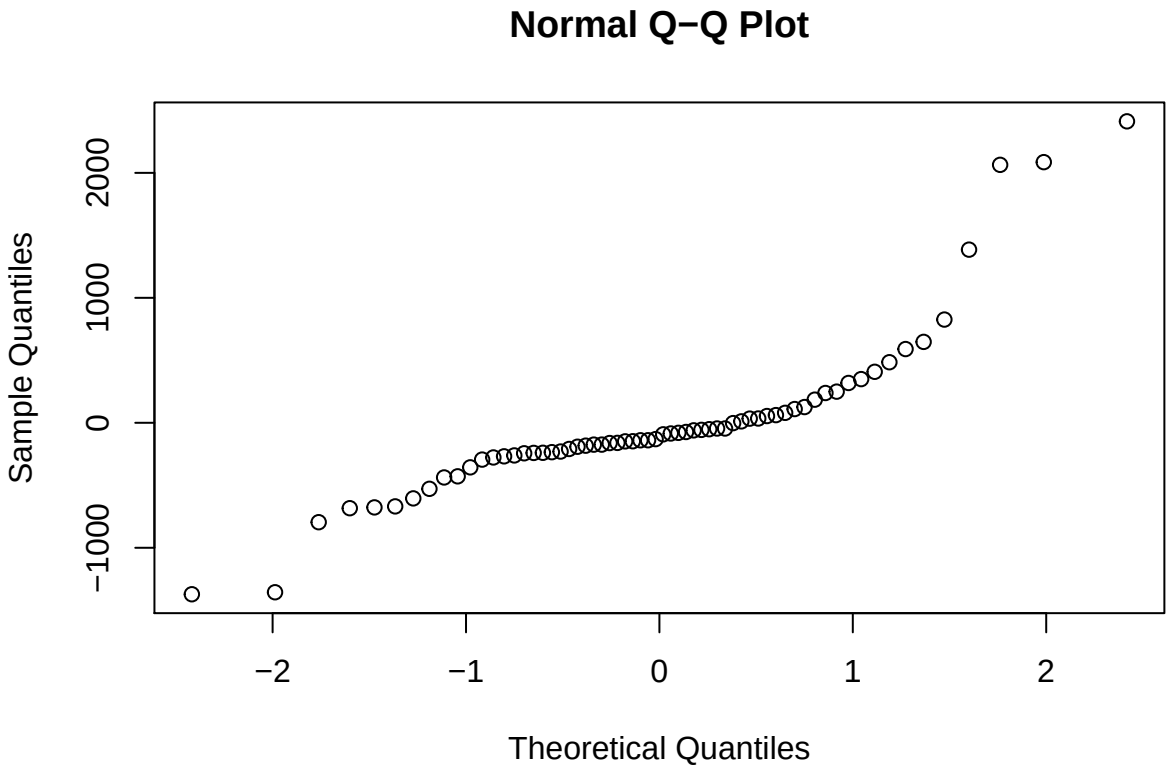
## d)

i) check the normality assumption

```
# first, try a hist/density plot.
hist(residuals(sur_aov))
```




```
# check the normality (of residuals) assumption
qqnorm(residuals(sur_aov))
```




As the QQ-plot shows, the normality assumption is questionable. Therefore, we can Kruskal Wallis test to fix the problem.
ii) KW test

```
kruskal.test(survival ~ organ, data = sur_df) %>% pander()
```

Table 3: Kruskal-Wallis rank sum test: `survival` by `organ` The p-value is 0.005, at a significance level 0.01, we reject $H_0$ and conclude that there is a significant difference in average survival time among different cancer groups. The p-value of kw-test is 0.004798, much larger than that of the anova test(0.0002295), which shows that kw-test is harder to reject $H_0$ and it's more conservative and less powerful.

| Test statistic | df | P value |
|---|---|---|
| 14.95 | 4 | 0.004798 * * |

# Problem3