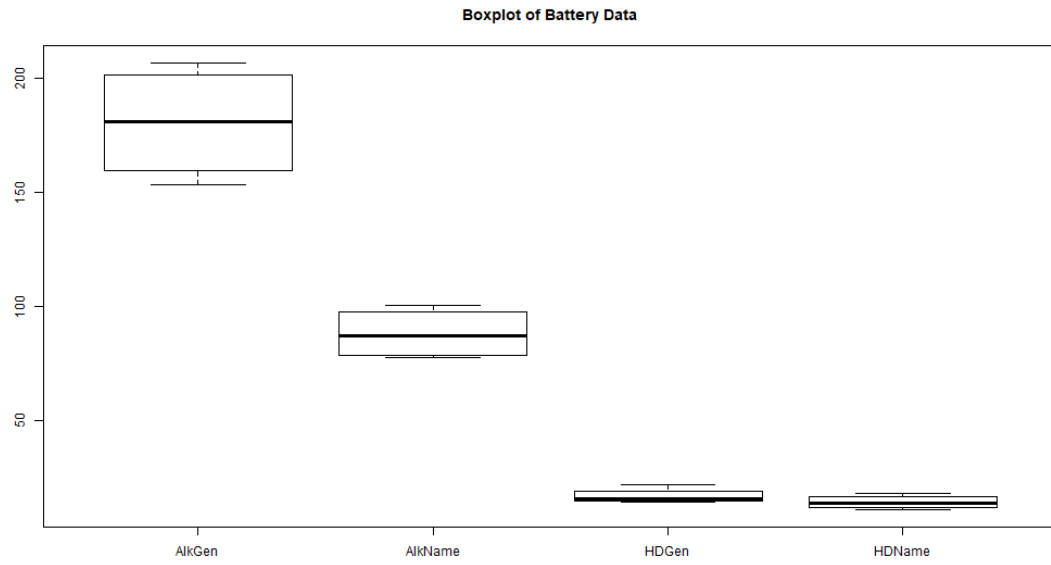

STAT 461: Homework 6

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October 17, 2018

PROBLEM 1



PROBLEM 2

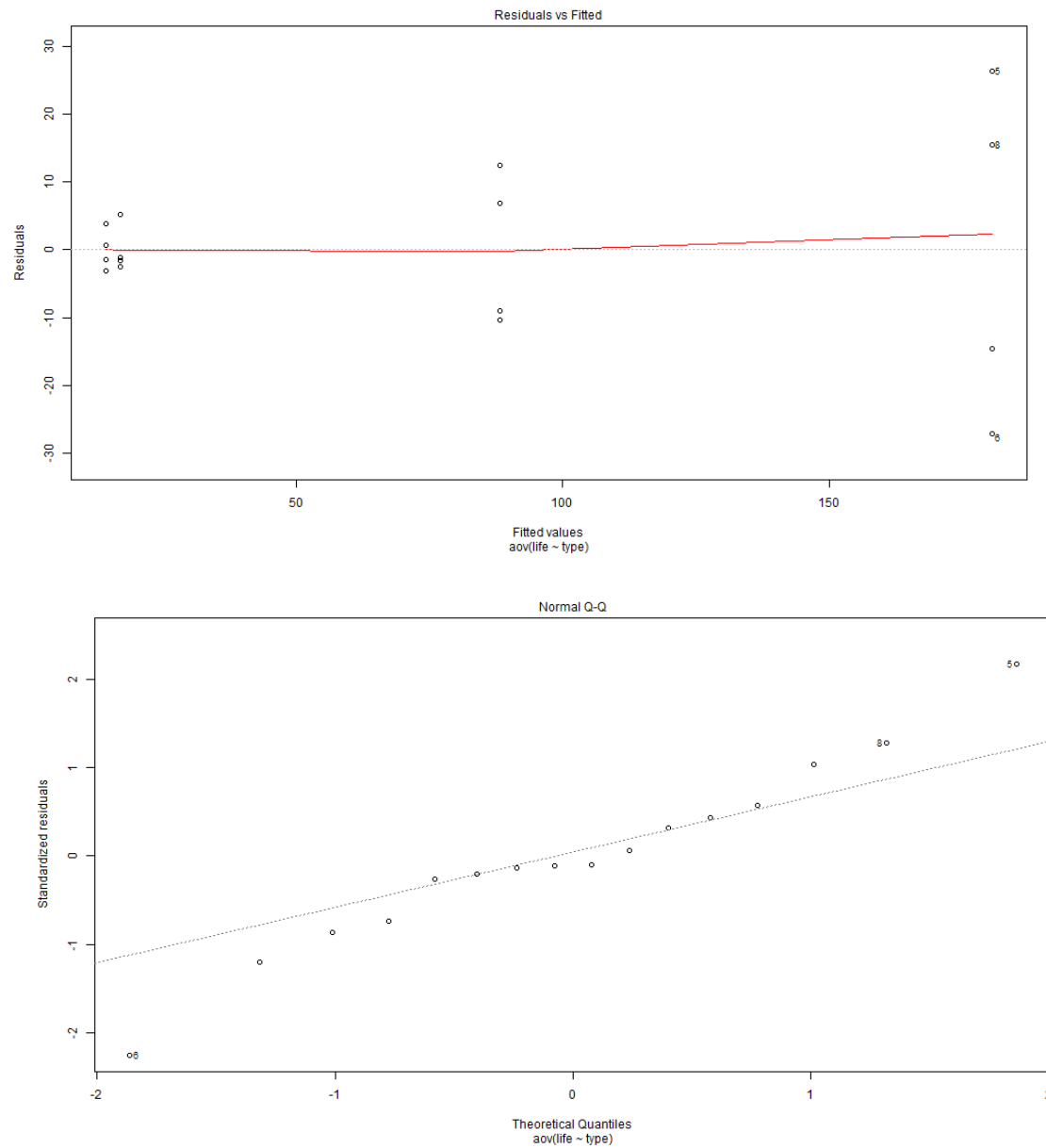
a)

$$Y_{it} = \mu + \tau_i + \epsilon_{it}, \quad \epsilon_{it} \sim N(0, \sigma^2)$$

$i = \text{AlkName}, \text{AlkGen}, \text{HDName}, \text{HDGen}$

$t = 1, \dots, r_i; \quad r_{\text{AlkName}} = r_{\text{AlkGen}} = r_{\text{HDName}} = r_{\text{HDGen}} = 4$

b)



c)

No. The Residuals vs Fitted plots clearly show an increasing trend in the residuals.

PROBLEM 2

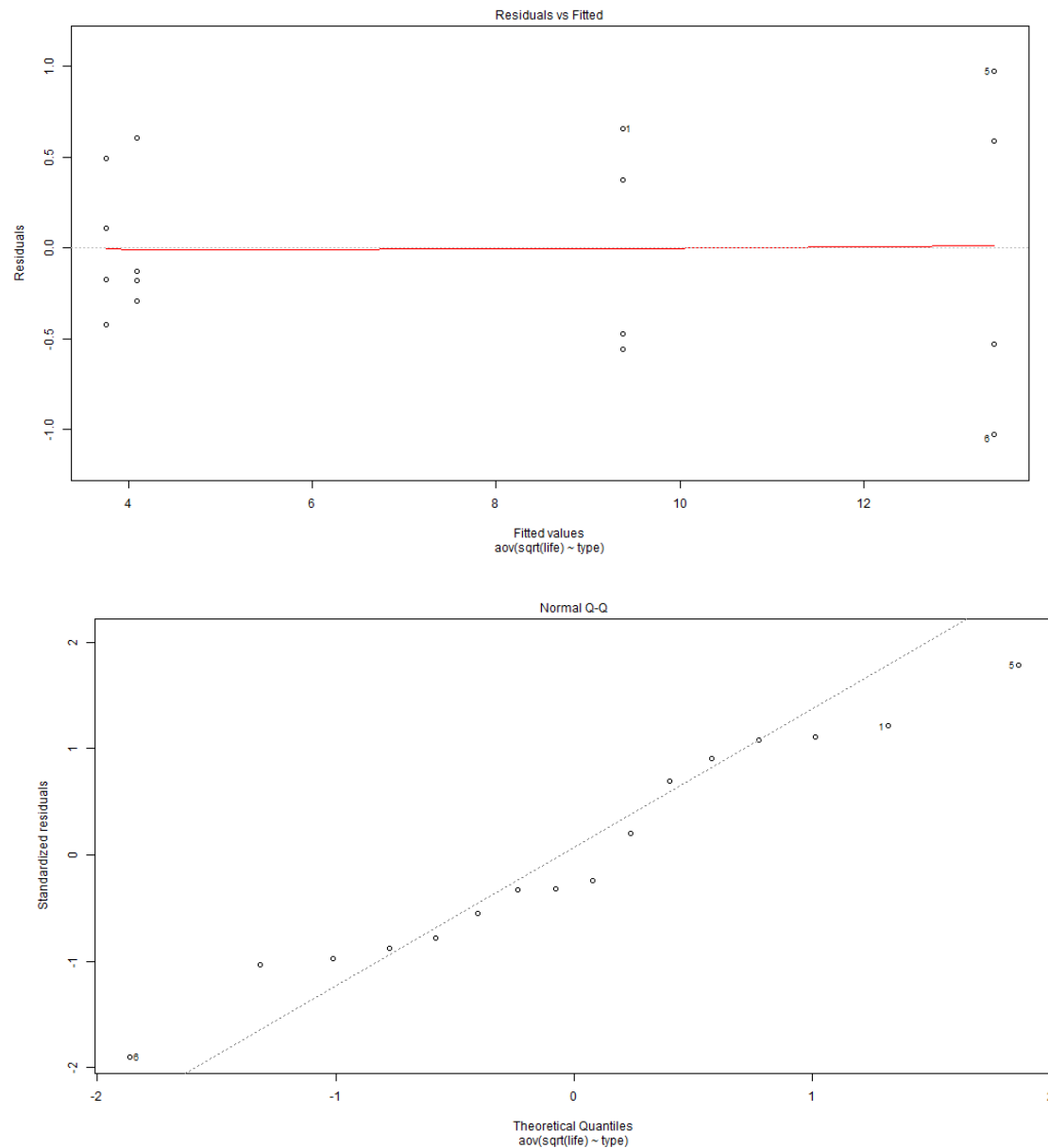
a)

$$\sqrt{Y_{it}} = \mu + \tau_i + \epsilon_{it}, \quad \epsilon_{it} \sim N(0, \sigma^2)$$

$i = \text{AlkName}, \text{AlkGen}, \text{HDName}, \text{HDGen}$

$t = 1, \dots, r_i; \quad r_{\text{AlkName}} = r_{\text{AlkGen}} = r_{\text{HDName}} = r_{\text{HDGen}} = 4$

b)



c)

The Residuals vs Fitted plot is better than the original model, but there is still somewhat of a trend.

PROBLEM 4

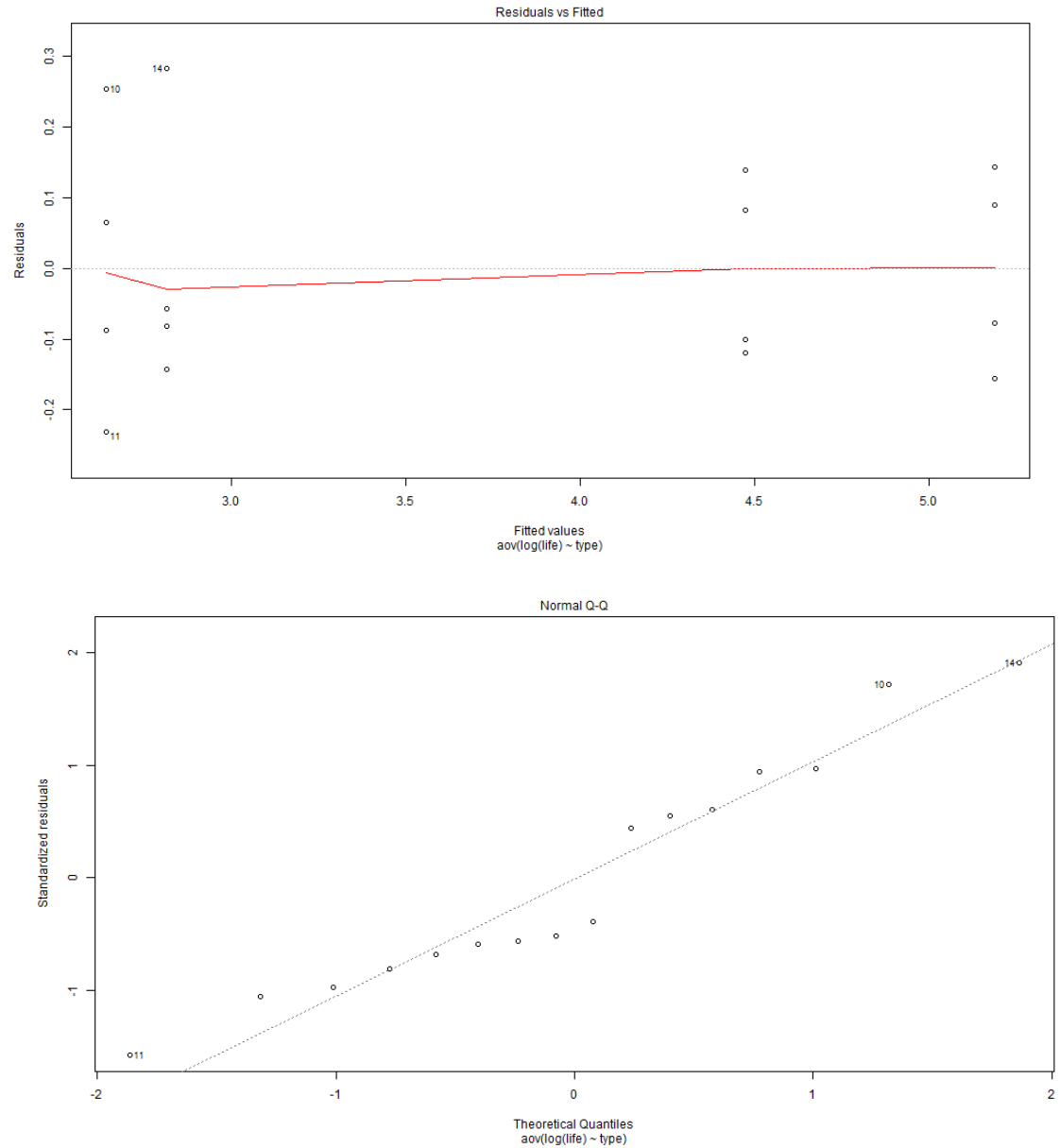
a)

$$\log(Y_{it}) = \mu + \tau_i + \epsilon_{it}, \quad \epsilon_{it} \sim N(0, \sigma^2)$$

$i = \text{AlkName}, \text{AlkGen}, \text{HDName}, \text{HDGen}$

$t = 1, \dots, r_i; \quad r_{\text{AlkName}} = r_{\text{AlkGen}} = r_{\text{HDName}} = r_{\text{HDGen}} = 4$

b)



c)

No. The Residuals vs Fitted plots clearly show an decreasing trend in the residuals.

PROBLEM 5

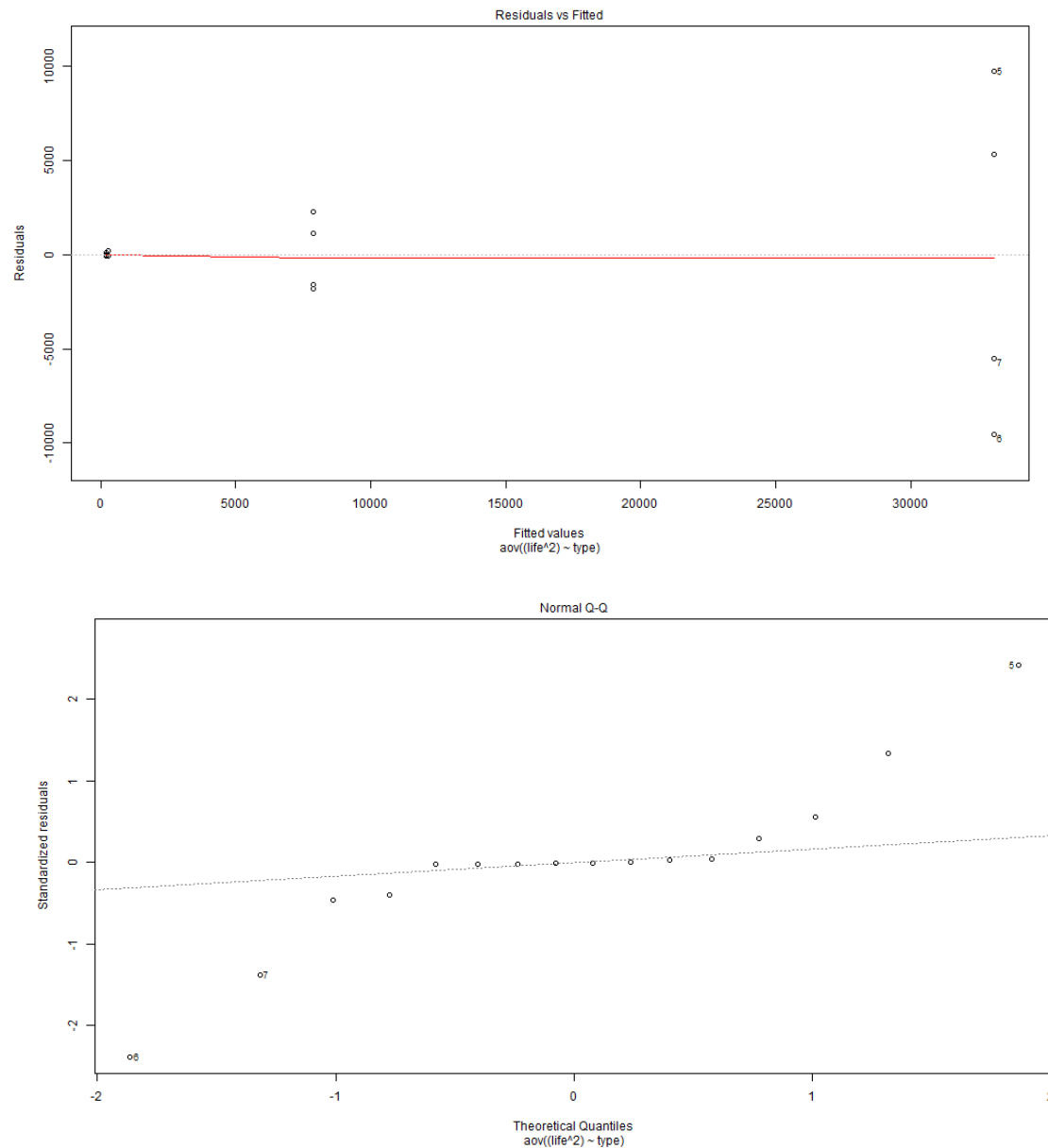
a)

$$Y_{it}^2 = \mu + \tau_i + \epsilon_{it}, \quad \epsilon_{it} \sim N(0, \sigma^2)$$

$i = \text{AlkName}, \text{AlkGen}, \text{HDName}, \text{HDGen}$

$t = 1, \dots, r_i; \quad r_{\text{AlkName}} = r_{\text{AlkGen}} = r_{\text{HDName}} = r_{\text{HDGen}} = 4$

b)



c)

No. The Residuals vs Fitted plots clearly show a significantly increasing trend in the residuals.

PROBLEM 6

The square root model clearly has the nicest looking Residuals vs Fitted plots.

PROBLEM 7

As shown below, there are significant differences for every pair other than HD Generic vs HD Name-brand.

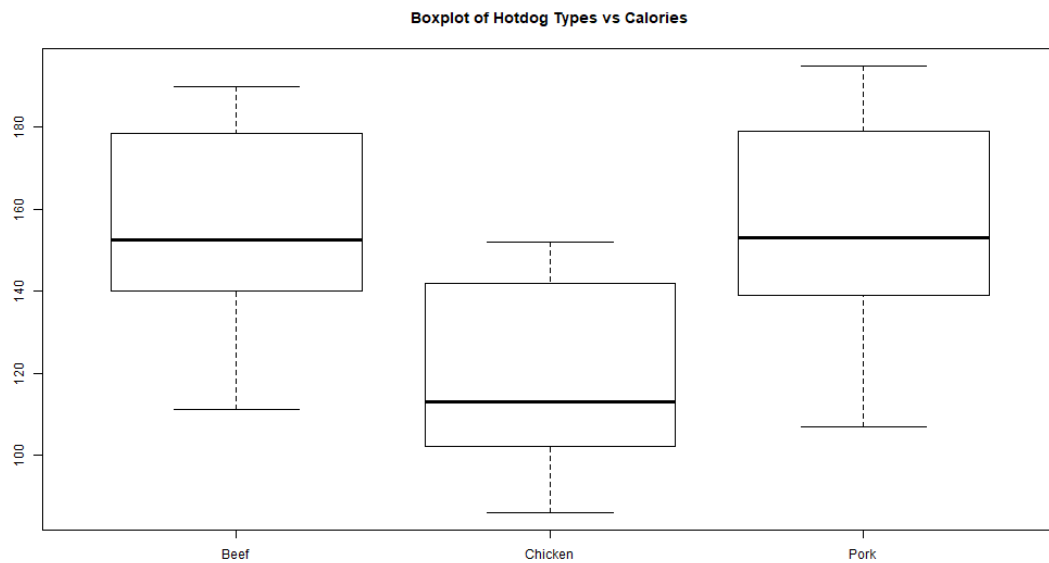
- Alk Gen > Alk Name
- Alk Gen > HD Gen
- Alk Gen > HD Name
- Alk Name > HD Gen
- Alk Name > HD Name
- HD Gen = HD Name

```
1 > contrast(sqrtLifeLSM, method='pairwise')
2 contrast      estimate      SE df t.ratio p.value
3 AlkGen - AlkName 4.0374808 0.4427383 12   9.119 <.0001
4 AlkGen - HDGen   9.3166850 0.4427383 12  21.043 <.0001
5 AlkGen - HDName  9.6541649 0.4427383 12  21.806 <.0001
6 AlkName - HDGen  5.2792042 0.4427383 12  11.924 <.0001
7 AlkName - HDName 5.6166841 0.4427383 12  12.686 <.0001
8 HDGen - HDName   0.3374799 0.4427383 12   0.762 0.8697
```

Listing 1: Pairwise Comparisons for Sqrt Model

PROBLEM 8

Below is a boxplot for the calories vs types of hotdog:



Following this is the pairwise comparison of the types of hotdog vs calories. This comparison shows us that the following differences in types exist:

- Beef has higher calories than chicken
- Beef and pork have no significant calorie difference
- Pork has higher calories than chicken

```
1 > contrast(hotdogLSM, method='pairwise')
2 contrast      estimate      SE df t.ratio p.value
3 Beef - Chicken  38.085294  7.738831  51   4.921  <.0001
4 Beef - Pork    -1.855882  7.738831  51  -0.240  0.9688
5 Chicken - Pork -39.941176  8.046454  51  -4.964  <.0001
```

Listing 2: Pairwise Comparisons for Hotdogs

CODE APPENDIX

```
1 #####
2 #### Setup
3 #####
4 ## Install and load libraries
5 # ipak function taken from: https://gist.github.com/stevenworthington/3178163
6 ipak <- function(pkg) {
7   new.pkg <- pkg[!(pkg %in% installed.packages()[, "Package"])]
8   if (length(new.pkg))
9     install.packages(new.pkg, dependencies = TRUE)
10   sapply(pkg, require, character.only = TRUE)
11 }
12 packages <- c("ggplot2", "reshape2", "gridExtra", "TSA", "astsa", "orcutt",
13              "nlme", "fGarch", "vars", "lsmeans")
14 ipak(packages)
15
16 #####
17 #### Data Input
18 #####
19 type<-c("AlkName", "AlkName", "AlkName", "AlkName", "AlkGen", "AlkGen",
20         "AlkGen", "AlkGen", "HDName", "HDName", "HDName", "HDName",
21         "HDGen", "HDGen", "HDGen", "HDGen")
22
23 life<-c(100.668, 77.734, 79.210, 95.063, 206.880, 153.347, 165.980, 196.000,
24         14.951, 18.063, 11.111, 12.840, 15.340, 22.090, 15.734, 14.440)
25
26 batt<-data.frame(type=type, life=life)
27
28 #####
29 #### Problem 1
30 #####
31 png("./figures/battery-boxplot.png", width = 1024, height = 576)
32   boxplot(life ~ type, main="Boxplot of Battery Data")
33 dev.off()
34
35 #####
36 #### Problem 2
37 #####
38 ## Part B
39 lifeAnova = aov(life~type, data=batt)
40 summary(lifeAnova)
41
42 png("./figures/original-ResidualVsFitted.png", width = 1024, height = 576)
43   plot(lifeAnova, 1)
44 dev.off()
45
46 png("./figures/original-QQ.png", width = 1024, height = 576)
47   plot(lifeAnova, 2)
48 dev.off()
49
50 #####
51 #### Problem 3
52 #####
53 ## Part B
54 sqrtLifeAnova = aov(sqrt(life)~type, data=batt)
55 summary(sqrtLifeAnova)
56
57 png("./figures/root-ResidualVsFitted.png", width = 1024, height = 576)
58   plot(sqrtLifeAnova, 1)
59 dev.off()
60
61 png("./figures/root-QQ.png", width = 1024, height = 576)
62   plot(sqrtLifeAnova, 2)
63 dev.off()
64
```

```

65 #####
66 #### Problem 4
67 #####
68 ## Part B
69 logLifeAnova = aov(log(life)~type, data=batt)
70 summary(logLifeAnova)
71
72 png("./figures/log-ResidualVsFitted.png", width = 1024, height = 576)
73   plot(logLifeAnova,1)
74 dev.off()
75
76 png("./figures/log-QQ.png", width = 1024, height = 576)
77   plot(logLifeAnova,2)
78 dev.off()
79
80 #####
81 #### Problem 5
82 #####
83 ## Part B
84 squareLifeAnova = aov((life^2)~type, data=batt)
85 summary(squareLifeAnova)
86
87 png("./figures/square-ResidualVsFitted.png", width = 1024, height = 576)
88   plot(squareLifeAnova,1)
89 dev.off()
90
91 png("./figures/square-QQ.png", width = 1024, height = 576)
92   plot(squareLifeAnova,2)
93 dev.off()
94
95 #####
96 #### Problem 7
97 #####
98 sqrtLifeLSM = lsmeans(sqrtLifeAnova, ~ type)
99 contrast(sqrtLifeLSM, method='pairwise')
100
101 #####
102 #### Problem 8
103 #####
104 hotdog=read.table("hotdogs.txt",header=TRUE)
105
106 png("./figures/hotdog-boxplot.png", width = 1024, height = 576)
107   boxplot(hotdog$Calories~hotdog$Type, main="Boxplot of Hotdog Types vs Calories")
108 dev.off()
109
110 hotdogModel = aov(Calories ~ Type, data=hotdog)
111 summary(hotdogModel)
112 hotdogLSM = lsmeans(hotdogModel, ~Type)
113 contrast(hotdogLSM, method='pairwise')

```