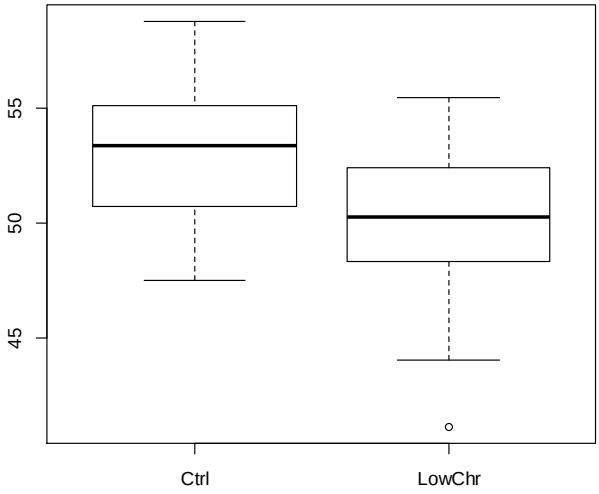
STAT511 HW#6 KEY
36 points total, 2 points per problem unless otherwise noted

#1 Rat Liver (Two Sample problem)

A. Boxplot



B. (**4 pts**)
H0: $\sigma_1^2 = \sigma_2^2$
F= 0.7898
p-value= 0.7373
Fail to Reject H0; cannot conclude that the variances are different.

C. P-value = 0.6789
Fail to Reject H0; cannot conclude that the variances are different.

D. The conclusions from both tests are the same. We do not have evidence that the variances are different. Use pooled variance t-test.

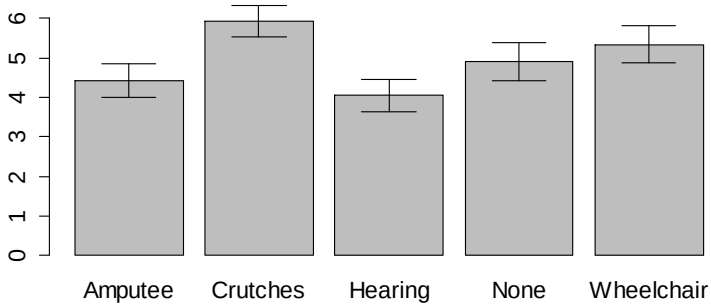
E. (**4 pts**)
H0: $\mu_1 = \mu_2$
t= 2.1709
p-value = 0.041
Reject H0; conclude there is a difference between the means.

F. ANOVA table

```
            Df Sum Sq Mean Sq F value Pr(>F)
Trt          1  66.25   66.25   4.713  0.041 *
Residuals   22 309.26   14.06
```

#3 Handicap (ANOVA)

A. Bar Plot (**4 pts**)



B. **(4 pts)**

H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5$

F= 2.862

p-value = 0.0301

Reject H0; conclude not all the means are the same

C. Pairwise Comparisons

contrast	estimate	SE	df	t.ratio	p.value
Amputee - Crutches	-1.4928571	0.6171922	65	-2.419	0.0184
Amputee - Hearing	0.3785714	0.6171922	65	0.613	0.5418
Amputee - None	-0.4714286	0.6171922	65	-0.764	0.4477
Amputee - Wheelchair	-0.9142857	0.6171922	65	-1.481	0.1433
Crutches - Hearing	1.8714286	0.6171922	65	3.032	0.0035
Crutches - None	1.0214286	0.6171922	65	1.655	0.1028
Crutches - Wheelchair	0.5785714	0.6171922	65	0.937	0.3520
Hearing - None	-0.8500000	0.6171922	65	-1.377	0.1732
Hearing - Wheelchair	-1.2928571	0.6171922	65	-2.095	0.0401
None - Wheelchair	-0.4428571	0.6171922	65	-0.718	0.4756

D. LSD(0.05) = 1.233

E. Means Display (**4 pts**)

Hearing	Amputee	None	Wheelchair	Crutches
4.05	4.42	4.90	5.34	5.92

Handicap	lsmean	SE	df	lower.CL	upper.CL	.group
Hearing	4.050000	0.4364208	65	3.178407	4.921593	1
Amputee	4.428571	0.4364208	65	3.556979	5.300164	12
None	4.900000	0.4364208	65	4.028407	5.771593	123
Wheelchair	5.342857	0.4364208	65	4.471265	6.214450	23
Crutches	5.921429	0.4364208	65	5.049836	6.793021	3

F. Based on the plot of residuals vs fitted values which shows equal scatter, the assumption of equal variances seems reasonable.

#R Code

```
#Q1
RatLiver <-
read.csv("c:/hess/STAT511_FA11/HW_2015/HW6/RatLiver.csv")
str(RatLiver)
boxplot(Enzyme ~ Trt, data = RatLiver)
var.test(Enzyme ~ Trt, data = RatLiver)
library(car)
leveneTest(Enzyme ~ Trt, data = RatLiver, center = "median")
t.test(Enzyme ~ Trt, data = RatLiver, var.equal = TRUE)
Fit <- aov(Enzyme ~ Trt, data = RatLiver)
summary(Fit)

#Q2
library(Sleuth3)
data(case0601)
str(case0601)
#A
library(plyr)
SumStats <- ddply(case0601, c("Handicap"), summarise,
               n    = length(Score),
               mean = mean(Score),
               sd   = sd(Score),
               se   = sd / sqrt(n) )
library(gplots)
with(barplot2(mean, plot.ci = TRUE, ci.l = mean-se, ci.u =
mean+se, names = Handicap), data = SumStats)
#B
OneWayFit <- aov(Score ~ Handicap, data=case0601)
summary(OneWayFit)
#C
library(multcompView)
library(lsmeans)
lsout <- lsmeans(OneWayFit, pairwise ~ Handicap, adjust = "none"
)
#D
qt(0.975,65)*sqrt(2.666)*sqrt(2/14)
#E
cld(lsout, adjust = "none")
#F
plot(OneWayFit)
```