# 36-402/608   Homework #5   due 10:30AM 2/18

1. Moon phases and behavior (20 points, 5 each)

   There have been many studies of moon phases and behavior. The data for this problem represent the daily accident rate for the US national highway system over 30 lunar months of 29 days each. (Ignore the complication that a lunar month is 29.5 days). Because accidents are counts and because the monthly boxplots showed skewed distributions, the outcome is recoded as the square root of the daily accident rate (sqrtAcc). Here is the raw data:
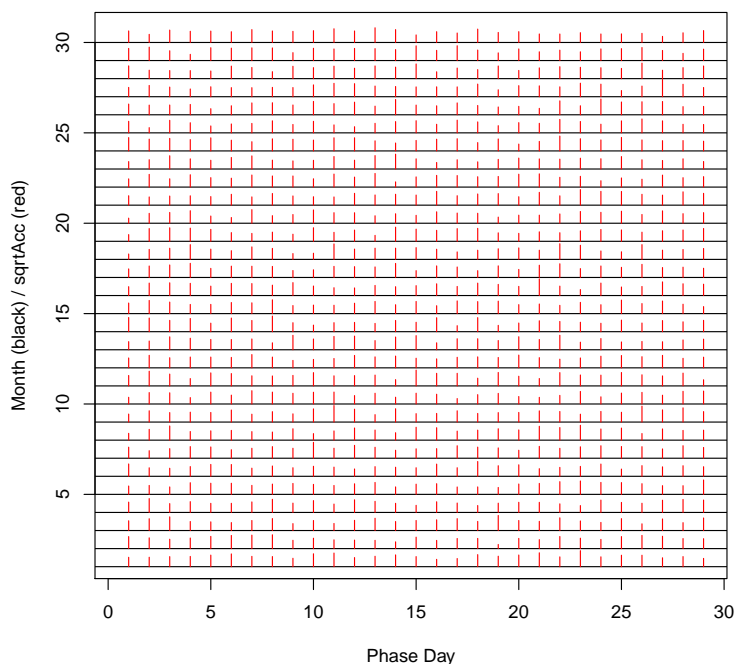
   (a) Here is an ANOVA comparing the first three weeks of the lunar month (full moon through new moon to first quarter) to the last week (first quarter to full moon):

```
last8Days = factor(day>=22)
summary(aov(sqrtAcc~last8Days))
#              Df Sum Sq Mean Sq F value  Pr(>F)
# last8Days     1    611  611.40   5.982 0.01465 *
# Residuals   868  88717  102.21
fit.contrast(aov(sqrtAcc~last8Days), "last8Days", rbind(LminusF=c(-1,1)))
#                   Estimate Std. Error  t value    Pr(>|t|)
# last8DaysLminusF 1.875634  0.7668781 2.445805 0.01465055
```

   What is the standard interpretation of these results?

(b) Now I will tell you that 25 ANOVAs were run, each with a different split of the month, starting with lunar days (1 through 2) vs. (3 through 29), then (1 through 3) vs. (4 through 29), and continuing up to (1 through 26) vs. (27 through 29). Only the ANOVA with the smallest p-value was reported. Why is this procedure inappropriate?

(c) Knowing that 25 tests were done, state what multiple comparisons correction approach is most appropriate, how you would apply it, and what your new conclusion is.

(Note: These data were simulated completed randomly.)

2. Brick strength (20 points, 5 each)

Bricks were prepared in 10 batches of 10 bricks each with each batch treating two brick with each of five additives, A through E.

```
br=aov(strength~additive+batch, brick)
summary(br)
#             Df  Sum Sq Mean Sq F value    Pr(>F)
# additive    4  605.12 151.280 12.0812 7.752e-08 ***
# batch       9   86.24   9.583  0.7653    0.6485
# Residuals  86 1076.89  12.522


planned = rbind(CDEvsAB=c(-1/2,-1/2,1/3,1/3,1/3),
                AvsB=c(1,-1,0,0,0),
                EvsCD=c(0,0,-1/2,-1/2,1),
                CvsD=c(0,0,1,-1,0))
library(gmodels)
round(fit.contrast(br, "additive", planned, conf.int=0.95), 3)
#                  Estimate Std. Error t value Pr(>|t|) lower CI upper CI
# additiveCDEvsAB    4.667      0.722   6.461    0.000    3.231    6.103
# additiveAvsB      -0.564      1.119  -0.504    0.616   -2.789    1.661
# additiveEvsCD      2.438      0.969   2.515    0.014    0.511    4.364
# additiveCvsD       0.010      1.119   0.009    0.993   -2.214    2.235


TukeyHSD(br, "additive", ordered=TRUE)
#       diff        lwr       upr     p adj
# B-A 0.5640 -2.5541336 3.682134 0.9867666
# D-A 4.1310  1.0128664 7.249134 0.0034999
# C-A 4.1415  1.0233664 7.259634 0.0033938
# E-A 6.5740  3.4558664 9.692134 0.0000008
# D-B 3.5670  0.4488664 6.685134 0.0166799
# C-B 3.5775  0.4593664 6.695634 0.0162306
```

```
# E-B 6.0100   2.8918664 9.128134 0.0000065
# C-D 0.0105  -3.1076336 3.128634 1.0000000
# E-D 2.4430  -0.6751336 5.561134 0.1959570
# E-C 2.4325  -0.6856336 5.550634 0.1995642
```

(a) What are your conclusions about the planned contrasts?

(b) What additional contrasts can be reported as statistically significant?

(c) What p-values should you report for the comparisons of groups B vs. A, D vs. C, and D vs A?

(d) If it now looks interesting to compare AB vs CD, what correction method should you use?

3. Gene array (10 points, 5 each) A gene array experiment is performed using an analysis that consists of 500,000 t-tests.

(a) If you were to use a Bonferroni correction, what p-value would you need to be less than to call a comparison statistically significant?

(b) What specific problem would this approach lead to?

4. Math test (50 points)

What is the square root of 9?