Math 3080 § 1.	**Spectrophotometer Example:**	Name: Example
Treibergs	**One-Factor Random Effects ANOVA**	Jan. 22, 2014

Today's example was motivated from problem 13.14.9 of Walpole, Myers, Myers and Ye, *Probability and Statistics for Engineers and Scientists, 7th ed.*, Prentice Hall 2002. It is an example of a one-factor random effects model.

For a single factor, the ANOVA is run the same way with the same f-statistic and rejection region. However, in the Random Effects model, the factors (laboratories) are assumed to be a random sample from all laboratories, and the null hypothesis is

$$\mathcal{H}_0 : \sigma_A^2 = 0$$

In this case we are unable to reject the null hypothesis, and conclude that there is no significant evidence that the laboratory variance is nonzero.

In case the treatment variance component is significant, we can estimate it from the mean squares of the ANOVA table. The estimators follow from the expected mean squares in the balanced random effects model. Since

$$E(MSE) = \sigma^2$$
$$E(MSTr) = \sigma^2 + J\sigma_A^2$$

it follows that estimators are

$$\widehat{\sigma^2} = MSE,$$
$$\widehat{\sigma_A^2} = \frac{MSTr - MSE}{J}.$$

The diagnostic plots show that it is plausible that assumptions hold. The plot of residuals vs. fitted values shows that the variances for the three treatments are somewhat different, although not significantly as the analysis shows. The QQ-normal plot of the standardized residuals follows the 45° line nicely indicating that there is no evidence that normality assumption is violated.

Data Set Used in this Analysis :

```
# Math 3082        Spectrophotometer  Data    1-19-2014
#
# Data from  Walpole, Myers & Myers,
# Probability and Statistics for Engineers and Scientists, 6th ed, Prentice
# Hall, Upper Saddle River NJ, 1998. Testing for HIV antibodies, a
# spectrophotometer measured the optical density, absorbance of light at a
# particular wavelength, of blood samples. The blood sample is positive if  it
# exceeds a certain cutoff value that is determined by the control samples for
# that run. Researchers are interested in in comparing the laboratory
# variability for the positive control values. The data represent positive
# control values for ten different runs at four randomly selected laboratories.
#
Laboratory Density
1 8.880000000e-001
1 9.830000000e-001
1 1.047000000e+000
1 1.087000000e+000
1 1.125000000e+000
```

```
1 9.970000000e-001
1 1.025000000e+000
1 9.690000000e-001
1 8.980000000e-001
1 1.018000000e+000
2 1.065000000e+000
2 1.226000000e+000
2 1.332000000e+000
2 9.580000000e-001
2 8.160000000e-001
2 1.015000000e+000
2 1.071000000e+000
2 9.050000000e-001
2 1.140000000e+000
2 1.051000000e+000
3 1.325000000e+000
3 1.069000000e+000
3 1.219000000e+000
3 9.580000000e-001
3 8.190000000e-001
3 1.140000000e+000
3 1.222000000e+000
3 9.950000000e-001
3 9.280000000e-001
3 1.322000000e+000
4 1.232000000e+000
4 1.127000000e+000
4 1.051000000e+000
4 8.970000000e-001
4 1.222000000e+000
4 1.125000000e+000
4 9.900000000e-001
4 8.750000000e-001
4 9.300000000e-001
4 7.750000000e-001
```

R Session:

```
R version 2.14.0 (2011-10-31)
Copyright (C) 2011 The R Foundation for Statistical Computing
ISBN 3-900051-07-0
Platform: i386-apple-darwin9.8.0/i386 (32-bit)

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  Natural language support but running in an English locale

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```
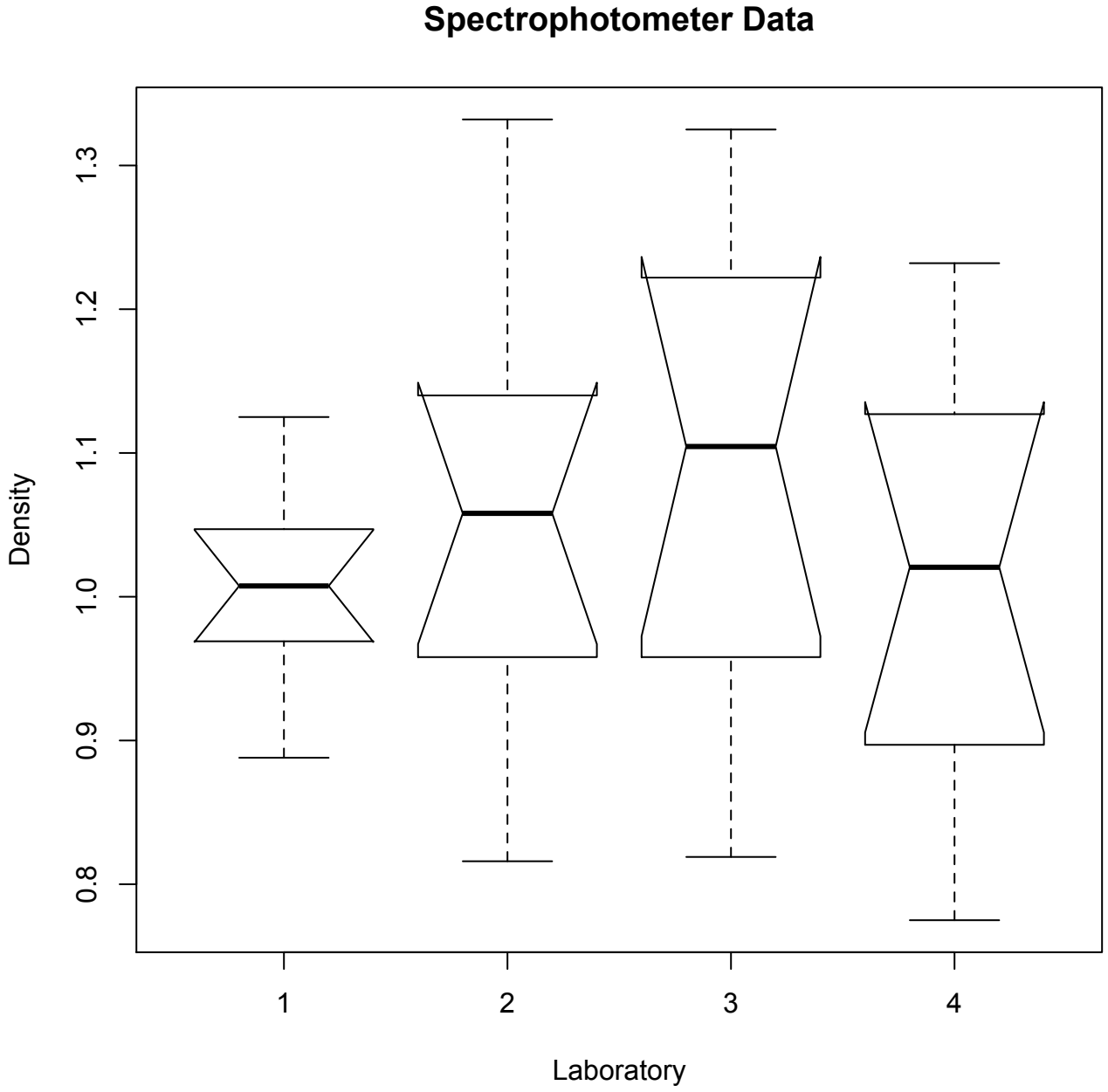
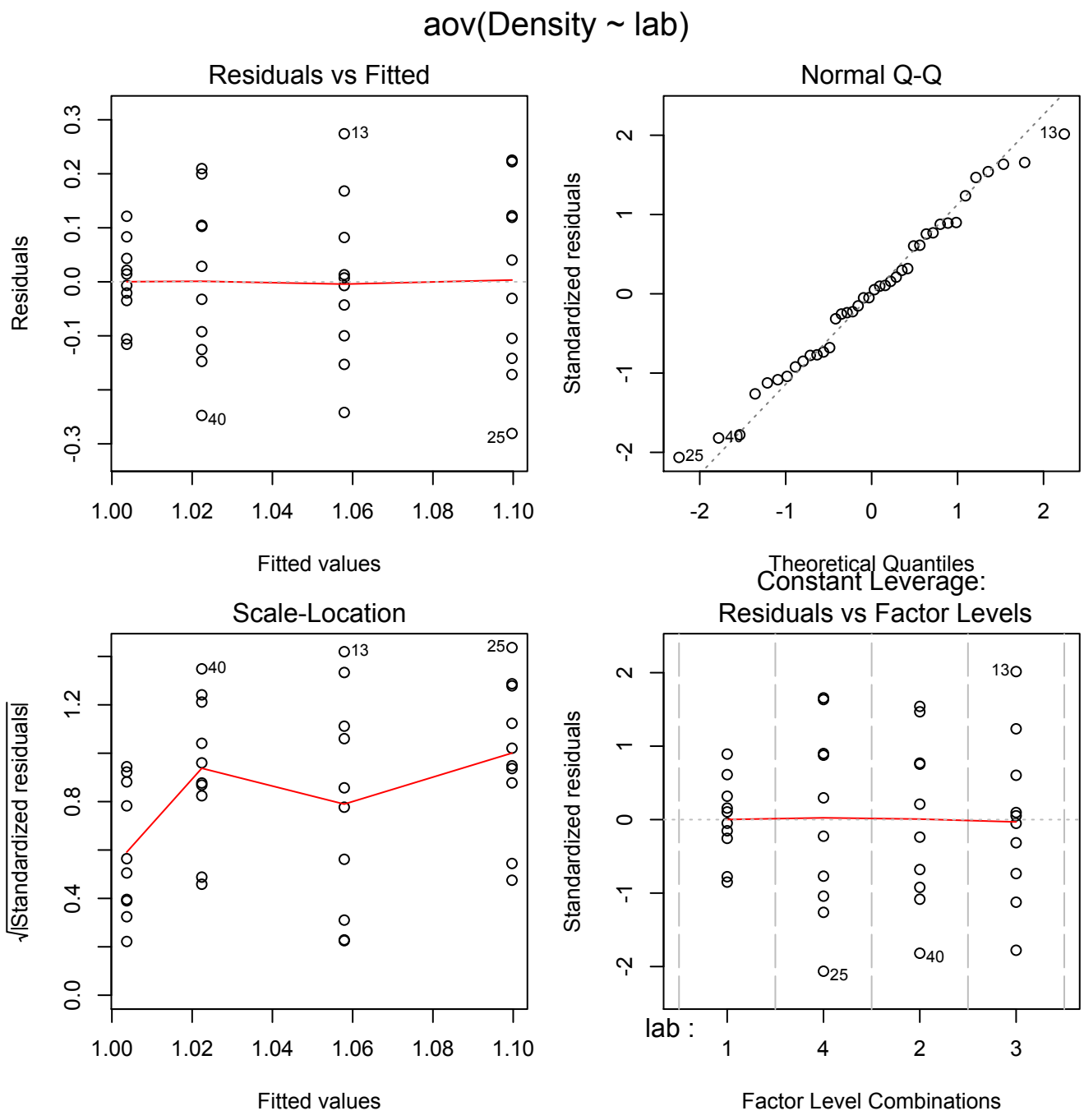

```
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[R.app GUI 1.42 (5933) i386-apple-darwin9.8.0]

[Workspace restored from /home/1004/ma/treibergs/.RData]
[History restored from /home/1004/ma/treibergs/.Rhistory]

> tt=read.table("M3082DataSpectrophotometer.txt", header=T)
> tt
   Laboratory Density
1           1   0.888
2           1   0.983
3           1   1.047
4           1   1.087
5           1   1.125
6           1   0.997
7           1   1.025
8           1   0.969
9           1   0.898
10          1   1.018
11          2   1.065
12          2   1.226
13          2   1.332
14          2   0.958
15          2   0.816
16          2   1.015
17          2   1.071
18          2   0.905
19          2   1.140
20          2   1.051
21          3   1.325
22          3   1.069
23          3   1.219
24          3   0.958
25          3   0.819
26          3   1.140
27          3   1.222
28          3   0.995
29          3   0.928
30          3   1.322
31          4   1.232
32          4   1.127
33          4   1.051
34          4   0.897
35          4   1.222
36          4   1.125
37          4   0.990
38          4   0.875
```

```
39          4   0.930
40          4   0.775
> attach(tt)
> lab = ordered(Laboratory)


> ###################### BOXPLOT AND SUMMARIZE DATA ############################
> #

> boxplot(Density~lab, notch=T,xlab="Laboratory",ylab="Density",
  main="Spectrophotometer Data")

Warning message:
In bxp(list(stats = c(0.888, 0.969, 1.0075, 1.047, 1.125, 0.816,  :
  some notches went outside hinges ('box'): maybe set notch=FALSE

> tapply(Density,lab,summary)
$`1`
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.8880  0.9725  1.0080  1.0040  1.0420  1.1250

$`2`
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.8160  0.9722  1.0580  1.0580  1.1230  1.3320

$`3`
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.8190  0.9672  1.1040  1.1000  1.2210  1.3250

$`4`
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.7750  0.9052  1.0200  1.0220  1.1260  1.2320

> #
> ######################## RUN ANOVA ##################################################
>
> t1=aov(Density~lab)
> summary(t1)
            Df Sum Sq Mean Sq F value Pr(>F)
lab          3 0.0537 0.01791   0.871  0.465
Residuals   36 0.7401 0.02056

>
> ###################### MODEL-CHECKING DIAGNOSTIC PLOTS ########################
>
> opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
   mar = c(4.1, 4.1, 2.1, 1.1))
> plot(t1)
> par(opar)
> >
```


Spectrophotometer Data
Density
0.8
0.9
1.0
1.1
1.2
1.3
1
2
3
4
Laboratory


aov(Density ~ lab)
Residuals vs Fitted
Residuals
Fitted values
Normal Q-Q
Standardized residuals
Theoretical Quantiles
Scale-Location
√|Standardized residuals|
Fitted values
Constant Leverage:
Residuals vs Factor Levels
Standardized residuals
lab :
Factor Level Combinations