Homework 5
MATH 4830, Spring 2006
due Thurs. Feb. 23

1. Example from class. A botanist is interested in comparing the growh response of dwarf pea stems to two different levels of the hormone idoleacetic acid (IAA). Using 16-day-old pea plants, she obtains 5-millimeter sections and floats these sections on solutions with different hormone concentrations to observe the effect of the hormone on the growth of the peas stem. Let X and Y be the independent growths that can be atributed to the hormone during the first 26 hours after sectioning for $(0.5)(10)^{-4}$ and 10^{-4} levels of concentration of IAA.

The data is growth in millimeters and can be read into R by:

```
> pea <- read.table("http://www-math.cudenver.edu/~bbailey/4830/pea.dat'', header=T)
```

(a) Make a new R object `newpea` that is a list with components: `newpea$X` and `newpea$Y` and contains the growth from the two groups. You can do this by the list command,

```
> newpea <- list(X=pea$growth[pea$group==1], Y=pea$growth[pea$group==2])
```

It should look like:

```
> newpea
$X
 [1] 0.8 1.8 1.0 0.1 0.9 1.7 1.0 1.4 0.9 1.2 0.5

$Y
 [1] 1.0 0.8 1.6 2.6 1.3 1.1 2.4 1.8 2.5 1.4 1.9 2.0 1.2
```

(b) Make boxplots of X and Y. Add an informative title to the plot using the `title` command.

(c) We want to test $\mathrm{H}_0 : \mu_X = \mu_Y$ against $\mathrm{H}_A : \mu_X < \mu_Y$, assuming the populations are normally distributed with equal variances.

Use the R function `t.test`. (Don't forget to give the appropriate alternative and set var.equal=TRUE. What is the p-value of the test. At the $\alpha = 0.05$ level state your conclusion.

Calculate the t-statistic by hand. How does it compare with the t-value given by R?

2. Use the R dataset `sleep`. Don't forget to use the data command to have access to this data. For example,

```
> data(sleep)
```

(a) Use the help file and give a description of the dataset sleep.

(b) Make a new R object `newsleep` that is a list with components: `newsleep$g1` and `newsleep$g2` and contains the extra hours of sleep for the two groups. You can do this by the list command,

```
> newsleep <- list(g1=sleep$extra[sleep$group==1], g2=sleep$extra[sleep$group==2])
```

It should look like:

```
> newsleep
$g1
 [1]  0.7 -1.6 -0.2 -1.2 -0.1  3.4  3.7  0.8  0.0  2.0

$g2
 [1]  1.9  0.8  1.1  0.1 -0.1  4.4  5.5  1.6  4.6  3.4
```

(c) Make boxplots of group 1 and group 2. Add an informative title to the plot.

(d) Use the R function `t.test` to test the hypothesis of equality of the two population means against the two-sided alternative. You can make the assumption of equal population variances. What is the p-value of the test? Read p. 49, Section 2.5.3 of your text. What is your conclusion based on your p-value?

(e) Try out the R function `var.test` to test the hypothesis of equality of population variances used in (d).