Professor Notes About the "Hypothesis Testing" Homework

- On question 2 in the first section, make sure to multiply the result from `distrib()` by two because the alternative hypothesis is the two-tailed "not equals" situation. Also make sure (before multiplying by two) to find the area into the nearest tail (i.e., to the left if the observed statistic is less than the hypothesized mean or to the right if the observed statistic is greater than the hypothesized mean).
- On all questions, make sure to use the standard error rather than the standard deviation.
- The hypotheses should be written "mathematically" rather than as sentences (see the key below).
- I did not include the graphs from `distrib()` simply to save space. It is good practice to carefully examine those figures.
- In the "beetle" question,
  - Note that the data.frame had to be filtered to contain only the "Halticus.oleracea" species.
  - Make sure to define μ when stating the hypotheses.
  - The last question should be a sentence that answers the researcher's research hypothesis about whether the mean thorax size was greater than 190 mm or not.

P-Value Calculations and Decisions

1. The p-value is "the probabiity of observing a sample mean of 73 or less if the population mean is 80." The null hypothesis is rejected because the p-value (=0.0276)$< \alpha$.
2. The p-value is "the probabiity of observing a sample mean of 1370 or 'different' if the population mean is 1500." The null hypothesis is not rejected because the p-value (=0.3041)$> \alpha$.

Beetle Size

1. $H_A : \mu > 190$ vs. $H_0 : \mu = 190$, where μ is the mean thorax length (μm) for all *Halticus oleracea* beetles in this population.
2. $\bar{x}$=194.167 μm.
3. p-value=0.103.
4. Do not reject H_0 because the p-value $> \alpha$.
5. The average thorax length for all *Halticus oleracea* beetles in this population does not appear to be greater than 190 μm.

R Appendix.

```
library(NCStats)

# P-values
distrib(73,mean=80,sd=20/sqrt(30))
2*distrib(1370,mean=1500,sd=800/sqrt(40))

## Beetle question
setwd("c:/stats")
d <- read.csv("Beetles.csv")
d <- filterD(d,species=="Halticus.oleracea")
Summarize(~thorax,data=d,digits=3)
distrib(194.167,mean=190,sd=14/sqrt(18),lower.tail=FALSE)
```