

Assignment #7 — Due Friday, October 29, 2010, by 4:00 P.M.

Turn in homework to your TA's mailbox using this sheet as the cover page.

Fill in your name and also circle the *lecture section in which you are registered* and circle the *discussion section you expect to attend* to pick up this assignment.

Name:

Lecture 1 (Larget). **311:** Tu 1:00 - 2:15pm **312:** Th 8:00 - 9:15am **313:** We 1:00 - 2:15pm

Lecture 2 (Hanlon). **321:** Tu 1:00 - 2:15pm **322:** We 2:30 - 3:45pm **323:** We 1:00 - 2:15pm

Please answer the following questions.

1. p. 277, Problem 11 in the textbook.
2. p. 277, Problem 12 in the textbook.
3. p. 278, Problem 14 in the textbook.
4. Follow the example in the R handout to take $B = 10000$ bootstrap samples from the data for problem 14 on page 278. Report and interpret a 95% confidence interval for the mean. Repeat this for a second bootstrap sample of size 10000. Do the endpoints of the confidence interval change (up to the level of rounding)? In addition, use the `t.test()` function to find a 95% confidence interval based on normal distributions in the population. Compare the interval found using the bootstrap with that found using the t distribution.
5. The following data was from the previous assignment.

	CMT	ECMO	Total
Die	4	1	5
Live	6	28	34
Total	10	29	39

Follow the examples in the R handout and use R to find p-values for the null hypothesis that these variables are independent versus the one-sided alternative that the CMT (conventional medical treatment) group is more likely to die than the ECMO (Extracorporeal membrane oxygenation) group using:

- (a) Fisher's exact test with `fisher.test()`.
- (b) The χ^2 test with `chisq.test()`.
- (c) The G-test using the function described in the handout.

Your solutions do not need to interpret the results. Do include the R commands you use to create the matrix and carry out each test. You only need to show the calculated p-values, not all output.

6. The file `lizards.txt` contains data described in Example 12.3 on page 287 of the textbook. Follow the examples in the R handout to (1) draw a graph to compare the two samples; and (2) conduct a *permutation test* for the null hypothesis that the average population horn lengths for living and killed lizards are equal versus the alternative that the average is smaller for killed lizards. Here, a permutation test is identical to a *randomization test*. The distinction in nomenclature is that typically a randomization test is for when the groups are *experimental* (such as random assignment of treatment groups) and a permutation test is for when groups are *observational*. Find a p-value and interpret the results in the context of the problem.