Assignment 3 -- Solutions

September 23, 2010 (due Sept 30)

1. Was Tyrannosaurus Rex Warm-Blooded?

It is known that the oxygen isotopic composition of vertebrate bone phosphate is related to the body temperature at which the bone forms. Differences in means at different bone sites would indicate nonconstant temperatures throughout the body. Minor temperature differences would be expected in warm-blooded animals. The dataset "bone_oxygen.txt" on the course website (http://compbio.med.harvard.edu/BMI713/) shows several measurements of the oxygen isotopic composition of bone phosphate in each of 6 bone specimens from a single Tyrannosaurus rex skeleton. (Data modified from R. E. Barrick, and W. J. Showers, "Thermophysiology of *Tyrannosaurus rex*: Evidence from Oxygen Isotopes", *Sciences* 265 (1994): 222-224.)

Read the data file "bone_oxygen.txt" from the course website, and save it as a data frame in R: t.rex <- read.table("http://compbio.med.harvard.edu/BMI713/bone_oxygen.txt", header=T, sep="\t")

a. Is there any evidence that the oxygen isotopic composition of proximal caudal bone is different from that of mid-caudal bone? Please state the null hypothesis H_0 and the alternative hypothesis H_1 , choose a proper test for the comparison, and calculate the test statistic, p-value, and the 95% confidence interval for the true mean difference. Can the observed difference be attributed to chance?

Denote the mean of the oxygen isotopic composition of the proximal caudal bone as μ , and the mean of the oxygen isotopic composition of the mid-caudal bone as μ .

The null hypothesis H_0 is $\mu = \mu z$, and the alternative hypothesis H_1 is $\mu z \neq \mu z$.

We can use unpaired t-test to test whether the means of the oxygen isotopic composition of proximal and mid-caudal bones are different.

If we assume that the variances are equal:

The difference of sample means is

$$\bar{X}_1 - \bar{X}_2 = 11.132 - 11.554 = -0.422$$

and the pooled sample standard deviation is

$$s = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}} = \sqrt{\frac{0.137 + 0.194}{6 + 5 - 2}} = 0.192.$$

The t-statistic is

$$t - statistic = \frac{\overline{X}_1 - \overline{X}_2}{s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} = \frac{-0.422}{0.192 \times \sqrt{\frac{1}{6} + \frac{1}{5}}} = -3.63,$$

and the degree of freedom is 6 + 5 - 2 = 9.

The p-value is 0.0055 (given by 2*pt(-3.63, 9) in R).

The 95% confidence interval for true mean difference is

$$(\overline{X}_1 - \overline{X}_2) \pm t_{9,0.97} (s \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}) = -0.422 \pm 2.262 \times 0.192 \times \sqrt{\frac{1}{6} + \frac{1}{5}} = -0.422 \pm 0.263.$$

Or we can perform t-test in R:

```
> t.test(prox, mid, paired = FALSE, var.equal = TRUE)
       Two Sample t-test
data: prox and mid
t = -3.6357, df = 9, p-value = 0.005437
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-0.6851087 -0.1595580
sample estimates:
mean of x mean of y
11.13167 11.55400
```

If we assume that variances are not equal, and perform t-test in R:

```
> t.test(prox, mid, paired = FALSE, var.equal = FALSE)
      Welch Two Sample t-test
data: prox and mid
t = -3.5348, df = 7.35, p-value = 0.008807
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-0.7021563 -0.1425104
sample estimates:
mean of x mean of y
11.13167 11.55400
```

Since the p-value is less than 0.01, we can reject the null hypothesis that the means of oxygen composition of the two bones are equal.

b. Suppose the samples are from normal populations, use *F*-test to test if the oxygen isotopic compositions of proximal and mid-caudal bones have equal variances. What is the degree of freedom?

```
The F-statistic is F = \frac{{s_1}^2}{{s_2}^2} = \frac{0.0274}{0.0485} = 0.565, which is greater than F_{0.025}(6-1, 5-1) = 0.00055,
```

so there is no evidence for different population variances.

Or we can calculate the p-value as 2*pf(0.565,5,4) in R, which gives 0.54.

The degree of freedom is (5, 4).

We can also perform F-test in R:

```
> var.test(prox, mid)
       F test to compare two variances
data: prox and mid
F = 0.5649, num df = 5, denom df = 4, p-value = 0.5434
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.0603283 4.1737317
sample estimates:
ratio of variances
         0.5649426
```

c. Is there evidence that the means are different for all the 6 different bones? Calculate the sum of squares and mean squares for within and between groups, construct an ANOVA table, perform the F-test and find the p-value. What inference can you make? (R hints: aov function can be used to fit an ANOVA model, and summary function can be used to summarize the results of model fitting functions.)

ANOVA Table:

Source of Variation	Sum of Squares	df	Mean Square	F-statistic	p-value
Between	3.3705	5	0.67410	8.82	8.7e-5
Within	1.7586	23	0.07646		
Total	5.1291	28			

There is strong evidence that the means are different for all the 6 different bones.

We can use the aov function in R for ANOVA:

2. True or false. If the answer is false, please explain the reason briefly.

- **a.** The significance level α of a test is equal to the probability that the null hypothesis is true. *False,* α *is the probability of a Type I error under the null hypothesis.*
- **b.** If the significance level α of a test is decreased, the power would be expected to increase. *False, power would generally decrease as the significance level is decreased.*
- **c.** The power of a test is equal to the probability that the null hypothesis is rejected. False, the power of a test is equal to the probability that the null hypothesis is rejected when it is false.
- **d.** A type I error occurs when the test statistic falls in the rejection region of the test. False, a type I error occurs when the test statistic falls in the rejection region given that the null hypothesis is true.
- **e.** The power of a test is determined by the null distribution of the test statistic. *Partially true, the power of a test is also determined by the alternative distribution(s).*