#### <u>8.2.1(b)</u>

> var1=c(32.1,30.6,33.7,29.7)
> var2=c(34.5,32.6,34.6,31.0)
> t.test(var1,var2,paired=TRUE)

Paired t-test

data: var1 and var2
t = -4.8833, df = 3, p-value = 0.01642
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-2.7253027 -0.5746973

Let muD be the population mean difference in the two varieties of wheat (lbs). Since p=0.016<0.05=alpha we reject H0: muD=0 at the 5% level. On average, variety 2 provides between 0.6 and 2.7 lbs more wheat per plot of land with 95% confidence.

### <u>8.2.4</u>

> mcpp= c( 1.1, 1.3, 1.0, 1.7, 1.4, 0.1, 0.5, 1.6,-0.5) > placebo=c( 0.0,-0.3, 0.6, 0.3,-0.7,-0.2, 0.6, 0.9,-2.0) > t.test(mcpp,placebo,paired=TRUE)

#### Paired t-test

data: mcpp and placebo
t = 4.1703, df = 8, p-value = 0.003121
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
0.4470396 1.5529604

Let muD be the population mean difference in weight loss (kgs) from MCPP vs. placebo. Since p=0.003<0.01=alpha, we reject H0: muD=0 at the 1% significance level. On average, C=MCPP provides between 0.4 and 1.6 kgs more weight loss than placebo with 95% confidence.

#### <u>8.2.6</u>

> treated=c(69.50,67.00,70.75,68.50,66.75,68.50,69.50,69.00,66.75,69.00, + 69.50,69.00,70.50,68.00,69.00) > control=c(70.00,69.00,69.50,69.25,67.75,66.50,68.75,70.00,66.75,68.50, + 69.00,69.75,70.25,66.25,68.25) > t.test(treated,control,paired=TRUE)

Paired t-test

data: treated and control t = 0.4043, df = 14, p-value = 0.6921alternative hypothesis: true difference in means is not equal to 0 95 percent confidence interval: -0.5021850 0.7355184

> t.test(treated,control)

Welch Two Sample t-test

data: treated and control t = 0.2535, df = 27.875, p-value = 0.8018 alternative hypothesis: true difference in means is not equal to 0 95 percent confidence interval: -0.8262934 1.0596267

(a) The 95% confidence interval is (-0.50,0.74) degrees C. This is done the correct way, pairing treated and untreated from the same carcass.

(b) The wrong 95% confidence interval is much (1.5 times) bigger, (-0.83,1.06).

# <u>8.4.5</u>

Let etaD be the median difference in numbers of seizures from valproate vs. placebo within individuals. We want to test H0: etaD=0 versus HA: etaD<0, that valproate lowers the mean number of seizures. We can use R's sum function to count the number of positive differences.

```
> placebo= c(37,52,63, 2,25,29,15,52,19,12, 7, 9,65,52, 6,17,54,27,36, 5)
> valproate=c( 5,22,41, 4,32,20,10,25,17,14, 8, 8,30,22,11, 1,31,15,13, 5)
> sum(valproate-placebo>0)
[1] 5
> binom.test(5,20,alternative="less")
```

Exact binomial test

data: 5 and 20 number of successes = 5, number of trials = 20, p-value = 0.02069

Since p=0.02<0.05=alpha, we reject H0: etaD=0 at the 5% level and conclude HA: etaD<0, that valproate significantly reduces the mean number of seizures within individuals.

## <u>8.4.6</u>

Let etaD be the median difference in numbers of displays of dominance for Northern vs. Carolina. We want to test H0: etaD=0 vs. HA: etaD not equal 0.

> northern=c( 0, 0, 0, 2, 0, 2, 1, 0)
> carolina=c( 9, 6,22,16,17,33,24,40)
> sum(northern-carolina>0)
[1] 0
> binom.test(0,8)

Exact binomial test

data: 0 and 8 number of successes = 0, number of trials = 8, p-value = 0.007812

Since p=0.008<0.05=alpha, we reject H0: etaD=0 at the 5% level. There is a significant difference in dominance displays between pairs of birds.