Stat 296 Fall 2007
Solutions to Assignment #2

Exercise 2, page 73: Since there are 3 data points for treatment #1 and 3 data points for treatment #2, the total number of possible permuted samples is $\frac{6!}{3!3!} = 20$. We can list them all as follows:

Permuted Sample	Treatment 1	Treatment 2	Difference of means
1	10 12 15	17 19 50	-16.33333
2	10 12 17	15 19 50	-15
3	10 12 19	15 17 50	-13.66667
4	10 12 50	15 17 19	7
5	10 15 17	12 19 50	-13
6	10 15 19	12 17 50	-11.66667
7*	10 15 50	12 17 19	9
8	10 17 19	12 15 50	-10.33333
9	10 17 50	12 15 19	10.33333
10	10 19 50	12 15 17	11.66667
11	12 15 17	10 19 50	-11.66667
12	12 15 19	10 17 50	-10.33333
13	12 15 50	10 17 19	10.33333
14	12 17 19	10 15 50	-9
15	12 17 50	10 15 19	11.66667
16	12 19 50	10 15 17	13
17	15 17 19	10 12 50	-7
18	15 17 50	10 12 19	13.66667
19	15 19 50	10 12 17	15
20	17 19 50	10 12 15	16.33333

*observed sample

Suppose that μ_1 denotes the true mean for Treatment #1 and that μ_2 denotes the true mean for Treatment #2. If we are interested in testing $H_0 : \mu_1 = \mu_2$ vs. $H_A : \mu_1 > \mu_2$, then since the observed difference of means was 9, and since there are 9 permuted differences greater than or equal to 9, we conclude that the one-sided p-value is $\frac{9}{20} = 0.45$. Hence, there is not nearly enough evidence to reject H_0.

Exercise 3, page 73: As in Exercise 2, there are 20 possible permuted samples.

Permuted Sample	Treatment 1	Treatment 2	Difference of medians
1	10 12 15	17 19 50	-7
2	10 12 17	15 19 50	-7
3	10 12 19	15 17 50	-5
4	10 12 50	15 17 19	-5
5	10 15 17	12 19 50	-4
6	10 15 19	12 17 50	-2
7*	10 15 50	12 17 19	-2
8	10 17 19	12 15 50	2
9	10 17 50	12 15 19	2
10	10 19 50	12 15 17	4
11	12 15 17	10 19 50	-4
12	12 15 19	10 17 50	-2
13	12 15 50	10 17 19	-2
14	12 17 19	10 15 50	2
15	12 17 50	10 15 19	2
16	12 19 50	10 15 17	4
17	15 17 19	10 12 50	5
18	15 17 50	10 12 19	5
19	15 19 50	10 12 17	7
20	17 19 50	10 12 15	7

*observed

If we are interested in testing $H_0 : \theta^1_{0.5} = \theta^2_{0.5}$ vs. $H_A : \theta^1_{0.5} > \theta^2_{0.5}$, then since the observed difference of medians was -2, and since there are 14 permuted differences greater than or equal to -2, we conclude that the one-sided p-value is $\frac{14}{20} = 0.70$. Hence, there is not nearly enough evidence to reject H_0.

Exercise 4, page 73: Suppose that μ_1 denotes carapace lengths (in mm) of crayfish from Section 1 of a stream in Kansas, and suppose that μ_2 denotes carapace lengths (in mm) of crayfish from Section 2 of a stream in Kansas. Consider testing the hypotheses $H_0 : \mu_1 = \mu_2$ vs. $H_A : \mu_1 \neq \mu_2$.

(a) Using SAS to perform the permutation test, we find a p-value of 0.0238. Hence, at the $\alpha = 0.05$ level, we would reject H_0, and conclude that there is significant evidence to conclude that carapace lengths differ between sections.

(b) Using SAS to perform the Wilcoxon rank-sum test, we find a p-value of 0.0303. Hence, at the $\alpha = 0.05$ level, we would reject H_0, and conclude that there is significant evidence to conclude that carapace lengths differ between sections.

If, instead, you decided to use $H_A : \mu_1 > \mu_2$, then the appropriate p-value for (a) is 0.0152 and for (b) is 0.0152.

```
data carapace;
input Section Length;
datalines;
1 5
1 11
1 16
1 8
1 12
2 17
2 14
2 15
2 21
2 19
2 13
;
run;

proc npar1way data=carapace anova scores=data;
class section;
exact scores=data;
var length;
run;
```

```
                    The NPAR1WAY Procedure
                  Data Scores Two-Sample Test

                Statistic (S)                52.0000

                Normal Approximation
                Z                            -2.1567
                One-Sided Pr <  Z             0.0155
                Two-Sided Pr > |Z|            0.0310

                Exact Test
                One-Sided Pr <=  S            0.0152
                Two-Sided Pr >= |S - Mean|    0.0238
```

```
proc npar1way data=carapace wilcoxon correct=no;
class section;
exact wilcoxon;
var length;
run;
```

```
                                   The NPAR1WAY Procedure
                                  Wilcoxon Two-Sample Test

                              Statistic (S)               18.0000

                              Normal Approximation
                              Z                           -2.1909
                              One-Sided Pr <  Z            0.0142
                              Two-Sided Pr > |Z|           0.0285

                              t Approximation
                              One-Sided Pr <  Z            0.0266
                              Two-Sided Pr > |Z|           0.0533

                              Exact Test
                              One-Sided Pr <=  S           0.0152
                              Two-Sided Pr >= |S - Mean|   0.0303
```

Exercise 5, page 73: Suppose that μ_1 denotes nest heights (in metres) of species A of woodland nesting birds, and that μ_2 denotes nest heights (in metres) of species B of woodland nesting birds. Consider testing the hypotheses $H_0 : \mu_1 = \mu_2$ vs. $H_A : \mu_1 \neq \mu_2$. Using SAS to perform a Wilcoxon rank-sum test gives a p-value of 0.0556. At the $\alpha = 0.05$ level we would not reject H_0, but at the $\alpha = 0.06$ level we would reject H_0. It is up to you to decide if this is significant or not. If, instead, the alternative is $H_A : \mu_1 > \mu_2$, then the corresponding p-value is 0.0278.

```
data nesting;
input Species$ Height;
datalines;
A 5.1
A 9.4
A 7.2
A 8.1
A 8.8
B 2.5
B 4.2
B 6.9
B 5.5
B 5.3
;
run;

proc npar1way data=nesting wilcoxon correct=no;
class Species;
exact wilcoxon;
var Height;
run;
```

```
                The NPAR1WAY Procedure
              Wilcoxon Two-Sample Test

        Statistic (S)               37.0000

        Normal Approximation
        Z                            1.9845
        One-Sided Pr >  Z            0.0236
        Two-Sided Pr > |Z|           0.0472

        t Approximation
        One-Sided Pr >  Z            0.0392
        Two-Sided Pr > |Z|           0.0785

        Exact Test
        One-Sided Pr >=  S           0.0278
        Two-Sided Pr >= |S - Mean|   0.0556
```

Exercise 7, page 74: Suppose that μ_1 denotes the number of siblings that students in an introductory statistics class whose hometown is rural have, and let μ_2 denote the number of siblings that students in an introductory statistics class whose hometown is urban have. Consider testing the hypotheses $H_0 : \mu_1 = \mu_2$ vs. $H_A : \mu_1 \neq \mu_2$.

(a) Using SAS to perform the Wilcoxon rank-sum test, we find a p-value of 0.0010. Hence, at the $\alpha = 0.01$ level, we would reject H_0, and conclude that there is overwhelming evidence to conclude that the number of siblings differs between urban students and rural students. If, instead, you decided to use $H_A : \mu_1 > \mu_2$, then the appropriate p-value is 0.0004144.

(b) In order to conduct the two sample t-test, we begin by calculating $\overline{X_1} = 2.0417$, $S_1 = 1.3345$ and $\overline{X_2} = 1.2353$, $S_2 = 1.8210$, and noting that sample size 1 is $m = 24$ and sample size 2 is $n = 17$. This gives a test statistic of

$$T = \frac{\overline{X_1} - \overline{X_2}}{\sqrt{1/n + 1/m}\sqrt{\frac{(m-1)S_1^2+(n-1)S_2^2}{m+n-2}}} = \frac{2.0417 - 1.2353}{\sqrt{1/17 + 1/24}\sqrt{\frac{23(1.3345)^2+16(1.8210)^2}{39}}} = 1.639.$$

Using t-table with $df = 39$ (use the normal table instead), we find a test statistic of 1.639 corresponds to a two-sided p-value of $2 \times 0.0505 = 0.101$. This is not very significant evidence against H_0. The result is so different than (a) primarily because of the outlier 8 in the urban group. This skews the data tremendously and suggests that the assumption of approximate normality that the t-test requires is violated. Hence, in this example, the t-test result is invalid.

```
data siblings;
input Hometown$ Number;
datalines;
R 3
R 2
R 1
R 1
R 2
R 1
R 3
R 2
R 2
R 2
R 2
R 5
R 1
R 4
```

```
R 1
R 1
R 1
R 1
R 6
R 2
R 2
R 2
R 1
R 1
U 1
U 0
U 1
U 1
U 0
U 0
U 1
U 1
U 1
U 8
U 1
U 1
U 1
U 0
U 1
U 1
U 2
;
run;

proc npar1way data=siblings wilcoxon correct=no;
class Hometown;
exact wilcoxon;
var Number;
run;
```

```
                         The NPAR1WAY Procedure
                        Wilcoxon Two-Sample Test

                  Statistic (S)                 246.5000

                  Normal Approximation
                  Z                              -3.1707
                  One-Sided Pr <  Z               0.0008
                  Two-Sided Pr > |Z|              0.0015

                  t Approximation
                  One-Sided Pr <  Z               0.0015
                  Two-Sided Pr > |Z|              0.0029

                  Exact Test
                  One-Sided Pr <=  S           4.144E-04
                  Two-Sided Pr >= |S - Mean|      0.0010
```

Exercise 8, page 74: If we perform the permutation test on the data in Exercise 7, then the p-value that SAS outputs for the two-sided test is 0.1131. This is quite close to the t-test approximation in 7(b). Statistical theory suggests that for large samples under appropriate conditions, the permutation test and the t-test will give essentially the same p-value. This example suggests such a fact.

```
proc npar1way data=siblings anova scores=data;
 class Hometown;
 exact scores=data;
 var Number;
 run;
```

```
                      The NPAR1WAY Procedure
                   Data Scores Two-Sample Test

               Statistic (S)                21.0000

               Normal Approximation
               Z                            -1.6049
               One-Sided Pr <  Z             0.0543
               Two-Sided Pr > |Z|            0.1085

               Exact Test
               One-Sided Pr <=  S            0.0637
               Two-Sided Pr >= |S - Mean|    0.1131
```