**SPSS: k Within-Groups ANOVA & Post Hoc Tests**

**Application:** To compare the means of two or more quantitative variables obtained from dependent samples (repeated measures or matched groups). The two or more scores might be the same variable measured at different times or under different conditions, comparable variables measured at the same time, or some combination.

**Research Hypothesis:** The data come from the Pet shop database. The researcher hypothesized that stores would tend to display more fish than other types of animals, fewer reptiles, and an intermediate number of mammals.

**H0: for this analysis:** Pet stores display the same mean number of reptiles, fish and mammals.

**Analyze ➔ General Linear Model ➔ Repeated Measures**

- **Repeated Measures Definition Window**
  - enter your name for the IV in the “Within-subject Factor Name” box (pettype)
  - enter the number of conditions of the IV in the “Number of levels” window (2)
  - click the “Add” button
  - click the “Define” button

- **Repeated Measures window** — highlight the variables that are the DV score for each condition and click the arrow

- **Options** — check the “Descriptives” box

**SPSS Syntax**

```
GLM reptnum fishnum mammnum /WSFACTOR=Pettype 3
/METHOD=SSTYPE(3)
/PRINT=DESCRIPTIVE
/WSDESIGN=Pettype.
```

- DV for each IV condition
- name of WG IV & # conditions
- get descriptive stats
- tells that Pettype is a WG IV
Remember, even if the printout shows it, never report \( p = .000 \), because that would suggest there is no possibility of a Type 1 error. Instead, report \( p < .001 \)

The p-value of means that there is less than a .1% chance that this result is a Type I error

Use the “Sphericity Assumed” df, Mean Square Error & p
LSD Pairwise Comparisons Using SPSS

SPSS will perform the analysis, but not via the GUI! If you click on the “Post Hoc” button it brings up the screen, but you can’t select anything. But, we can get the LSD (uncorrected) results by using syntax.

GLM reptnum fishnum mammnum
/WSFACTOR=Pettype 3
/METHOD=SSTYPE(3)
/EMMEANS=TABLES(Pettype) compare(Pettype)  
/PRINT=DESCRIPTIVE
/WSDESIGN=Pettype

Estimated Marginal Means

Pettype

<table>
<thead>
<tr>
<th>Measure</th>
<th>MEASURE_1</th>
<th>95% Confidence Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pettype</td>
<td>Mean</td>
<td>Std. Error</td>
</tr>
<tr>
<td>1</td>
<td>9.250</td>
<td>1.232</td>
</tr>
<tr>
<td>2</td>
<td>23.917</td>
<td>2.773</td>
</tr>
<tr>
<td>3</td>
<td>21.500</td>
<td>3.714</td>
</tr>
</tbody>
</table>

Pairwise Comparisons

<table>
<thead>
<tr>
<th>(I) Pettype</th>
<th>(J) Pettype</th>
<th>Mean Difference[^a]</th>
<th>Std. Error</th>
<th>Sig[^b]</th>
<th>95% Confidence Interval for Difference[^c]</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>-14.617[^a]</td>
<td>1.990</td>
<td>.000</td>
<td>-19.046 -10.287</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>-12.210[^a]</td>
<td>2.826</td>
<td>.001</td>
<td>-18.470 -6.030</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>14.617[^a]</td>
<td>1.990</td>
<td>.000</td>
<td>10.287 19.046</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>2.417</td>
<td>2.179</td>
<td>.291</td>
<td>-2.380 7.213</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>12.210[^a]</td>
<td>2.926</td>
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<td>.291</td>
<td>-7.213 2.380</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* The mean difference is significant at the .050 level.

^a Adjustments for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

Notice that each pairwise comparison is presented twice!
Reptile vs Fish = Fish vs Reptile
Be sure you get the direction of each significant mean difference right!!

Reptiles < Fish
Reptiles < Mammals
Fish = Mammals

These LSD p-values can also be used for Bonferroni tests. Had we been interested in only the comparison of Reptile vs Fish and Reptile vs Mammals, we would want to test each using \( p = .05 / 2 = .025 \).

SPSS does not show the compute t-values for the pairwise comparisons. They can obtained as \( t = \text{Mean Difference} / \text{Std.Error} \). For Reptiles vs Fish, this would be \( t = -14.667 / 1.990 = 7.370 \).
LSD & HSD using the Post Hoc “Computators”

SPSS does not provide post hoc analyses for all ANOVA models (e.g., WG designs). Also, there may be occasions when you want to compare means from a study that didn’t post analyses, or did them differently than you would have preferred. One additional advantage of using these is that you can provide your readers with the LSD or HSD values that were the basis of your post hoc tests.

http://psych.unl.edu/psycrs/statpage/escomp.exe  http://psych.unl.edu/psycrs/statpage/computator_131a.xls

The two Computators will produce slightly different results, and those results might be slightly different from the SPSS results, because they all use slightly different t-table values and Student’s t-table values. The specific table (with the applied sample size rounding) can be seen for the xls version if you extend the right side of the spreadsheet.

Applying these LSD/HSD values to the pairwise comparisons…  Reptiles = 9.25  Fish = 23.92  Mammals = 21.50

<table>
<thead>
<tr>
<th>Pair</th>
<th>Reptiles v Fish</th>
<th>Reptiles v Mammals</th>
<th>Fish v Mammals</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean Difference</td>
<td>14.667 &lt;</td>
<td>12.250 &lt;</td>
<td>&gt; 2.417</td>
</tr>
<tr>
<td>LSD Result</td>
<td>&lt;</td>
<td>&lt;</td>
<td>=</td>
</tr>
<tr>
<td>HSD Result</td>
<td>&lt;</td>
<td>&lt;</td>
<td>=</td>
</tr>
</tbody>
</table>

**RH:** The researcher hypothesized that stores would tend to display more fish than other types of animals, fewer reptiles, and an intermediate number of mammals.

<table>
<thead>
<tr>
<th>RH: support?</th>
<th>&lt;</th>
<th>&lt;</th>
<th>&lt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Supported</td>
<td>Supported</td>
<td>Not supported</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Partial Support</td>
</tr>
</tbody>
</table>

4
Post Hoc Follow-ups using t-tests

SPSS does not compute post hoc tests for within-groups comparisons. However it is simple enough to obtain pairwise comparisons of the means using paired t-tests. The results closely correspond with an LSD analysis -- both produce uncorrected p-values.

**Analyze ➔ Compare Means ➔ Paired-Samples T test**
- Highlight the conditions/variables of each pair
- Use the arrow to move them into the “Paired Variables” window

**SPSS Syntax**

\[
\text{T-TEST PAIRS= reptnum fishnum maminum} \text{ WITH}\n\text{ /MISSING=ANALYSIS} (PAIRED)
\]

The 3 condition pairs

**RH:** The researcher hypothesized that stores would tend to display more fish than other types of animals, fewer reptiles, and an intermediate number of mammals.

These results tell us that

As hypothesized - more fish than reptiles in these stores.

As hypothesized – more mammals then reptiles in these stores.

Contrary to the hypothesis – equivalent numbers of fish and mammals.

These p-values can also be used for Bonferroni tests. Had we been interested in only the comparison of Chain v Private & Private v Coop, we would want to test each using \( p = .05 / 2 = .025 \).
Reporting the Results

Results based on the LSD tests

Table 1 summarizes the data for the numbers of animals displayed at the stores. There was a significant difference among the distributions of the three types of animals (F(2,22) = 22.22, p < .001, Mse = 33.391). Pairwise comparisons using LSD revealed that, consistent with the research hypothesis, more fish than reptiles were displayed on average and also more mammals than reptiles were displayed on average (p < .01 for each). However, contrary to the research hypothesis, there was not a significant difference between the average number of fish and mammals displayed (p = .291). These results provide partial support for the research hypothesis.

Results based on the pairwise t-tests

Table 1 summarizes the data for the numbers of animals displayed at the stores. There was a significant difference among the distributions of the three types of animals (F(2,22) = 22.22, p < .001, Mse = 33.391). Pairwise comparisons using LSD revealed that, consistent with the research hypothesis, more fish than reptiles were displayed on average, t(11) = 7.371, p < .001, and also more mammals than reptiles were displayed on average, t(11) = 4.335, p = .001. However, contrary to the research hypothesis, there was not a significant difference between the average number of fish and mammals displayed. These results provide partial support for the research hypothesis.