# 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

- o enter your name for the IV in the "Within-subject Factor Name" box (pettype)
- o enter the number of conditions of the IV in the "Number of levels" window (2)
- o click the "Add" button
- o 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 mamlnum /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

(OVERALL)	: Display Means for:
Pettype	•
	Compare main effects
	Confidence interval adjustment LSD(none)
Display	
Descriptive statistics	Transformation matrix
Estimates of effect size	Homogeneity tests
Observed power	Spread vs. level plot
	Residual plot
Parameter estimates	The look of fit
Parameter estimates           SCP matrices	

**Descriptive Statistics** 

	Mean	Std. Deviation	N
number of reptiles at store	9.25	4.267	12
number of fish at store	23.92	9.605	12
number of mammals	21.50	12.866	12

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"

#### **Tests of Within-Subjects Effects**

Measure:MEASURE\_1

Source		Type III Sum of Squares	df	Mean Square	F	Sig.
Pettype	Sphericity Assumed	1484.056	2	742.028	22.222	.000
	Greenhouse-Geisser	1484.056	1.672	887.492	22.222	.000
	Huynh-Feldt	1484.056	1.937	766.233	22.222	.000
	Lower-bound	1484.056	1.000	1484.056	22.222	.001
Error(Pettype)	Sphericity Assumed	734.611	22	33.391		
	Greenhouse-Geisser	734.611	18.394	39.937		
	Huynh-Feldt	734.611	21.305	34.481		
	Lower-bound	734.611	11.000	66.783		

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 Comparions 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 mamlnum /WSFACTOR=Pettype 3 /METHOD=SSTYPE(3) /EMMEANS=TABLES(Pettype) compare(Pettype) /PRINT=DESCRIPTIVE /WSDESIGN=Pettype

← asks for pairwise comparisons among WG conditions

## **Estimated Marginal Means**

## Pettype

Estimates

Measure: MEASURE_1								
			95% Confidence Interval					
Pettype	Mean	Std. Error	Lower Bound	Upper Bound				
1	9.250	1.232	6.539	11.961				
2	23.917	2.773	17.814	30.020				
3	21.500	3.714	13.325	29.675				

Pairwise Comparisons

Measure: MEASURE\_1

		Mean Difference (I-			95% Confiden Differ	ce Interval for ence <sup>b</sup>
(I) Pettype	(J) Pettype	J)	Std. Error	Sig. <sup>b</sup>	Lower Bound	Upper Bound
1	2	-14.667	1.990	.000	-19.046	-10.287
	3	-12.250	2.826	.001	-18.470	-6.030
2	1	14.667	1.990	.000	10.287	19.046
	3	2.417	2.179	.291	-2.380	7.213
3	1	12.250	2.826	.001	6.030	18.470
	2	-2.417	2.179	.291	-7.213	2.380

Based on estimated marginal means

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

b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

SPSS does not show the compute t-values for the pairwise comparisons. They can obtained as t = Mean Difference / Std.Error. For Reptiles vs Fish, this would be t = -14.667 / 1.990 = 7.370

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.

## 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



Fish = 23.92

Mammals = 21.50

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 spread sheet.

Applying these LSD/HSD values to the pairwise comparisons... Reptiles = 9.25

, .pp.jgeee .					
Pair	<b>→</b>	Reptiles v Fish	Reptiles v Mammals	Fish v Mammals	
Mean Difference	<b>→</b>	14.667 <	12.250 <	> 2.417	
LSD Result	<b>→</b>	<	<	=	
HSD Result	<b>→</b>	<	<	=	
RH:		The researcher hypothesiz animals, fewer reptiles, an	zed that stores would tend to dia d an intermediate number of ma	splay more fish than other types a ammals.	of
	→	<	<	<	

	→	<	<	<	
RH: support?	<b>→</b>	Supported	Supported	Not supported	➔ Partial Support

## 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 then into the "Paired Variables" window

## **SPSS Syntax**



		Paired variables.			Options
<ul> <li>strnum</li> <li>type or reptile department [reptdept]</li> <li>rating of reptile quality - 1-10 scale [reptgood]</li> <li>number of reptiles at store [reptnum]</li> <li>type of fish available [fishdept]</li> <li>rating of fish quality - 1-10 scale [fishgood]</li> <li>number of fish at store [fishnum]</li> <li>type of store [chair]</li> <li>number of mammals [mamInum]</li> </ul>	~	Pair 1 2 3 4	Variable1     Variable2       Image: Provide the state of the	······································	

**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.

Paired Samples Statistics						
		Mean	N	Std. Deviation		
Pair 1	number of reptiles at store	9.25	12	4.267		
	number of fish at store	23.92	12	9.605		
Pair 2	number of reptiles at store	9.25	12	4.267		
	number of mammals	21.50	12	12.866		
Pair 3	number of fish at store	23.92	12	9.605		
	number of mammals	21.50	12	12.866		

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.

## Paired Samples Test

		Paired Differences				
		Mean	Std. Deviation	1 1	df	Sig. (2-tailed)
Pair 1	number of leptiles at store - number of fish at store	-14.667	6.893	-7.371	11	.000
Pair 2	number of leptiles at store - number of mammals	-12.250	9.790	-4.335	11	.001
Pair 3	number of fish at store - number of mammals	2.417	7.549	1.109	11	.291

## **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.