Factorial design (CRD-ab) tutorial

For this experiment we will have a 2 factor factorial design with each factor having 2 levels..

Problem description
Nitrogen dioxide (NO2) is an automobile emission pollutant, but less is known about its effects than those of other pollutants, such as particulate matter. Several animal models have been studied to gain an understanding of the effects of NO2. Sherwin and Layfield (1976) studied protein leakage in the lungs of mice exposed to 0.5 part per million (ppm) NO2 for 10, 12, and 14 days. Half of a total group of 36 animals were exposed to the NO2; the other half served as controls. Control and experimental animals were matched on the basis of weight, but this aspect will be ignored in the analysis since the matching did not appear to influence the results. The response is the percent of serum fluorescence. High serum fluorescence values indicate a greater protein leakage and some kind of insult to the lung tissue. The data is available at U:_MT Student File Area\hjkim\STAT375\SPSS tutorial\SerumFluorescnence.sav.

	Serum fluorescence		
	10 Days	12 Days	14 days
Control	143	179	76
	169	160	40
	95	87	119
	111	115	72
	132	171	163
	150	146	78
Exposed	152	141	119
	83	132	104
	91	201	125
	86	242	147
	150	209	200
	108	114	178

In SPSS, the data should be entered the following manner.

Analysis of Factorial Design

Now we can begin our analysis of the data. We click on Analyze-General Linear Model-Univariate in the pull down menus to start the process. This will take you to the Univariate window. We will need to define which of the variables is the dependent variable and which are the factor variables. After moving each of them to the proper field, we can choose several options from the menus.
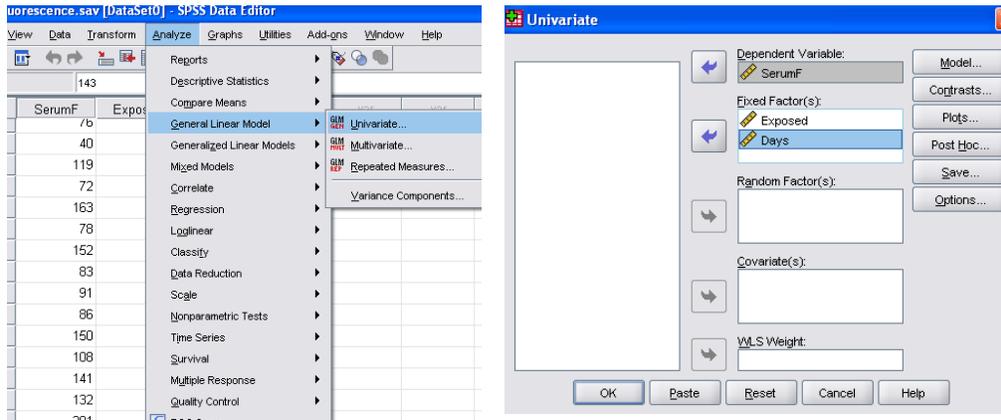
Profile Plot and Main effect plot
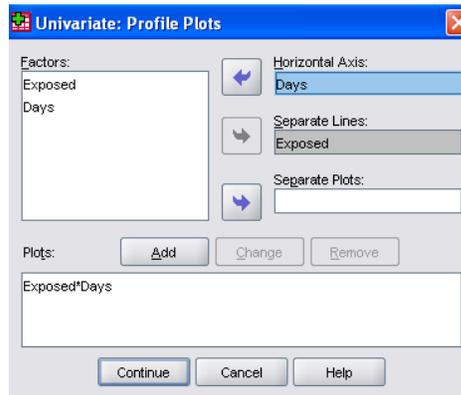
Clicking on the **Plot** button will bring up the profile plot window. We can create both of the interaction plot (Exposed*Days and Days*Exposed) by placing each of the factors in on the respective axis and hitting the **Add** button. After defining the plots we hit **Continue** return to the **Univariate** window.

Note that by placing a factor to Horizontal Axis only, we can generate main effect plot. If there is no interaction effect, generating main effect plots will be useful.
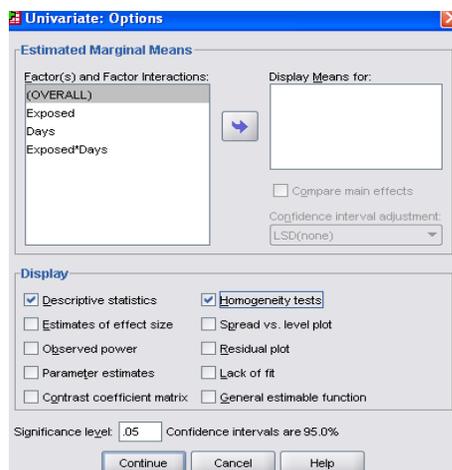
Once in the **Univariate** window click on the **options** button to bring up the **Options** window. There are several available options but the ones that we will commonly use will be the descriptive statistics and Homogeneity tests. After clicking the appropriate box hit the **Continue** button and then the OK button on the **Univariate** window.

Output

Besides the usual descriptive statistics you will see output for Levene's test of equal variance. Without going into the details of the test it checks the null hypothesis of equal variances using F test.

$$H_o : \sigma_1^2 = \sigma_2^2 = \sigma_3^2 = \sigma_4^2 \qquad H_A : \text{At least one variance is different}$$

By looking at the p-value (Sig) we can see if the null is rejected. As P-value is greater than .05, we would not reject the null hypothesis, but instead conclude that there is no evidence that the variances are unequal.

Levene's Test of Equality of Error Variances[a]

Dependent Variable:SerumF

F	df1	df2	Sig.
.904	5	30	.491

Tests the null hypothesis that the error variance of the dependent variable is equal across groups.

a. Design: Intercept + Exposed + Days + Exposed * Days

The standard ANOVA from SPSS contains several lines that we will not use for our analysis. I suggest deleting those lines from the output. This can easily be done by double clicking on the ANOVA in the output window, which bring up the editor mode. Use your mouse to highlight the desired lines and hit delete. After cleaning up the output you should be left with the ANOVA as we typically use it. We begin by checking to see if there are significant interactions amongst the factors. We see that the interaction (Exposed*Days) is not significant, (p-value= .086), so we should check to see if the main effects of Exposed or Days are significant. The profile plots are not exactly parallel, but they are not too far away from parallel.

Tests of Between-Subjects Effects

Dependent Variable:SerumF

Source	Type III Sum of Squares	Df	Mean Square	F	Sig.
Exposed	4356.000	1	4356.000	2.840	.102
Days	11867.389	2	5933.694	3.868	.032
Exposed * Days	8184.500	2	4092.250	2.668	.086
Error	46019.000	30	1533.967		
Corrected Total	70426.889	35			

a. R Squared = .347 (Adjusted R Squared = .238)
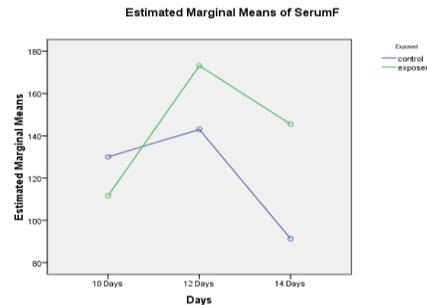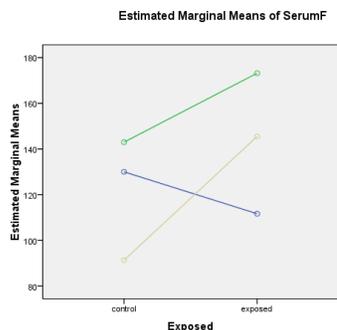
We see that the main effect Exposed is not significant (p-value = .102) but Days is significant (p-value = .032). The main effect plot is generated by going back to plot option.

Estimated Marginal Means of SerumF
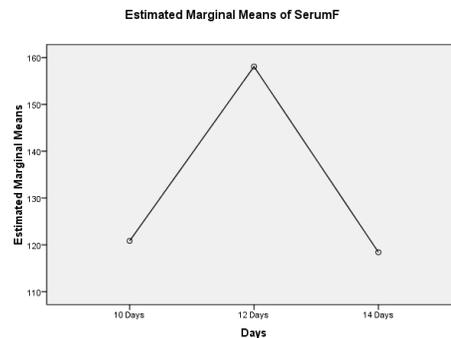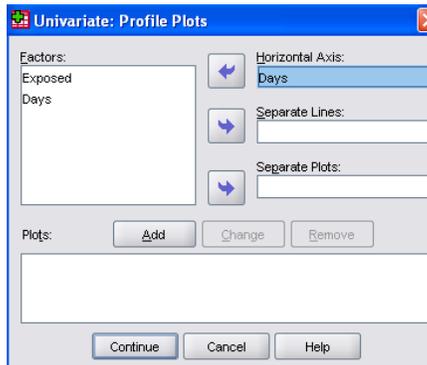
Post Hoc Test

LSD, HSD, and Scheffe's s will be used as a post hoc test. The post hoc test is need to be done only for Days since it is only significant factor. By clicking **post hoc** in **Univariate** window, you will see post hoc window. Place Days to the **Post Hoc Tests for** and clck LSD, Tukey, and Scheffe. This will generate output including the following homogeneous subsets.
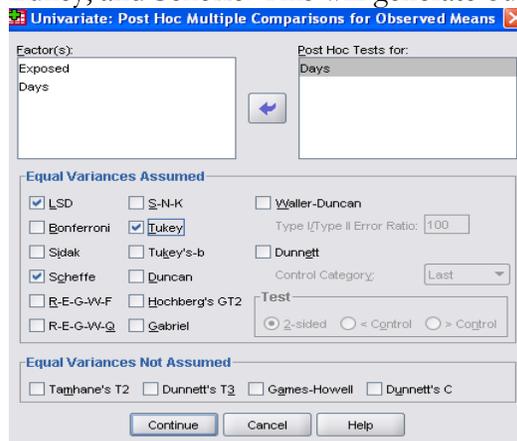
Homogeneous subsets

SerumF

	Days	N	Subset 1	Subset 2
Tukey HSD[a]	14 Days	12	118.42	
	10 Days	12	120.83	120.83
	12 Days	12		158.08
	Sig.		.987	.067
Scheffe[a]	14 Days	12	118.42	
	10 Days	12	120.83	
	12 Days	12	158.08	
	Sig.		.061	

Means for groups in homogeneous subsets are displayed.
Based on observed means.
The error term is Mean Square(Error) = 1533.967.

a. Uses Harmonic Mean Sample Size = 12.000.

Note: If there is an interaction effect, doing post hoc test is a little bit more complicated. First, you need make a new column in data window for interaction that will recognize all the different combinations. To make a new column, say interaction, go do **Transform** and **Compute** as below. It will bring **Compute Variable** window.
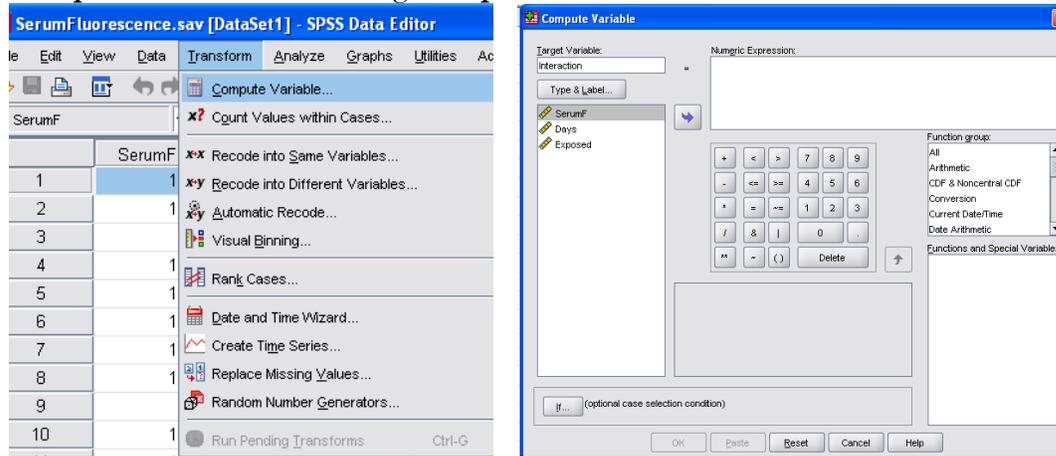
Put variable name in **Target variable**. Click **If** button at the bottom of the **Compute Variable** window. This will bring **Compute variable: If case window**
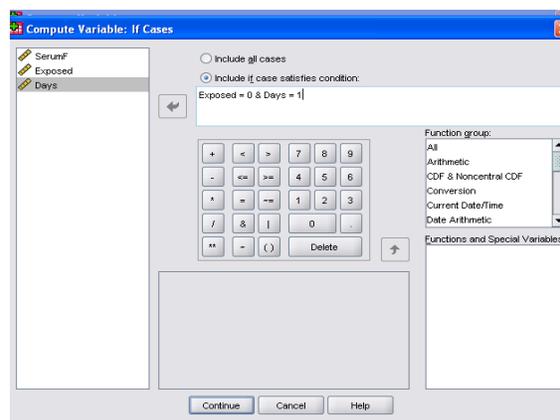
Click **Include if case satisfies condition** and write the condition as the picture in the left side. Click **Continue**.
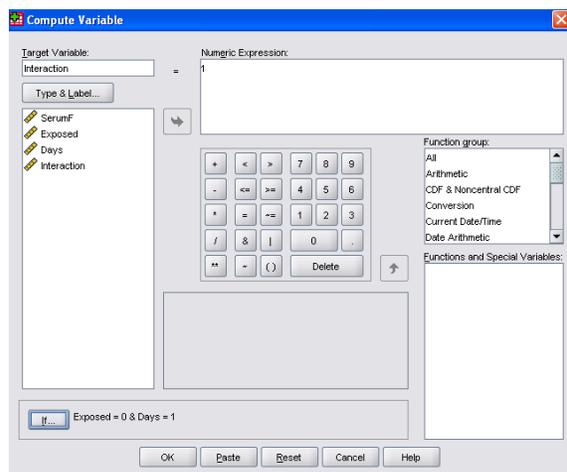
Type desired group number in **Numeric Expression.**
Repeat this for all possible treatment combination. Here, 2*3 =6 groups should be defined.

Then run post hoc test (Analyze-General Linear Model- Univariate) for interaction.

Again, the current dataset do not have a significant interaction, thus this step is not necessary.