Two-way ANOVA without replication

This version of the ANOVA is used when there is only one **observation** in each block. Each **treatment** is represented once only in each block and the treatments are allocated to positions in a random manner. This design is known as a randomized block design or a randomized complete block design (Fig. WEA1.).

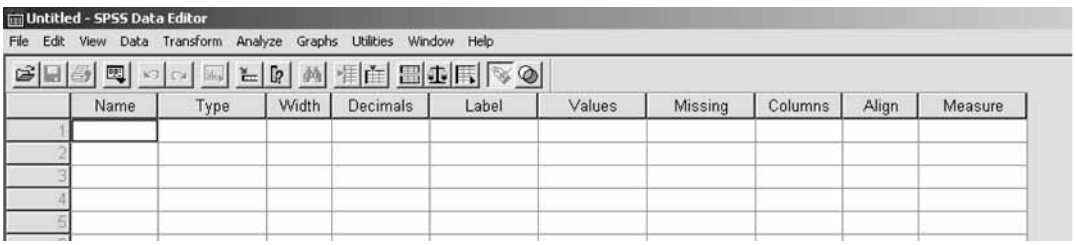
Fig. WEA1. A randomized block design.

	TREATMENTS				
Block 1	T1	T5	T2	T3	T4
Block 2	T3	T2	T5	T4	T1
Block 3	T4	T1	T3	T5	T2
Block 4	T1	T4	T2	T3	T5
Block 5	T2	T5	T4	T1	T3
Block 6	T3	T1	T2	T4	T5
Block 7	T5	T3	T4	T1	T2

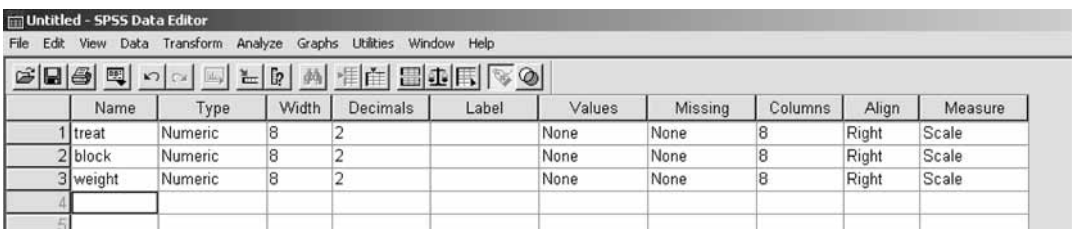
An example of this type of design could occur where tomato plants have been fed with different feed formulations and grown in a polytunnel. The treatments within each block stretch across the width of the polytunnel. The blocks spread down the length of the polytunnel, and hence experience different environmental conditions. By using a randomized block design and a two-way ANOVA without replication, the variability can be partitioned into variability due to treatment and variability due to environment. Hence the effect of the treatments can be investigated without the environmental effect masking the outcome of the test.

In this trial, fruit would be harvested at a certain date and the mass recorded (in grams). The data are given in the spreadsheet shown in step 2.

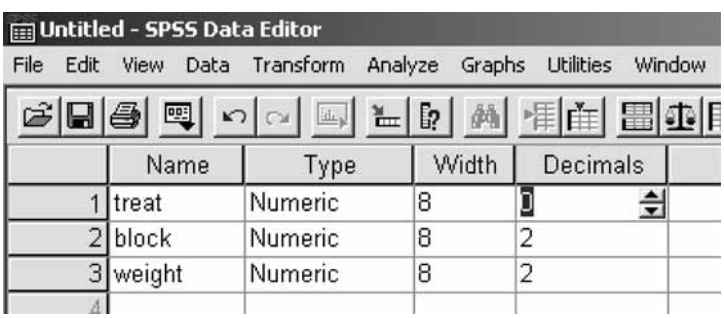
Step 1: Set up the variables
When SPSS starts up, select '**variable** view' using the tabs at bottom-left. You should get something like this:



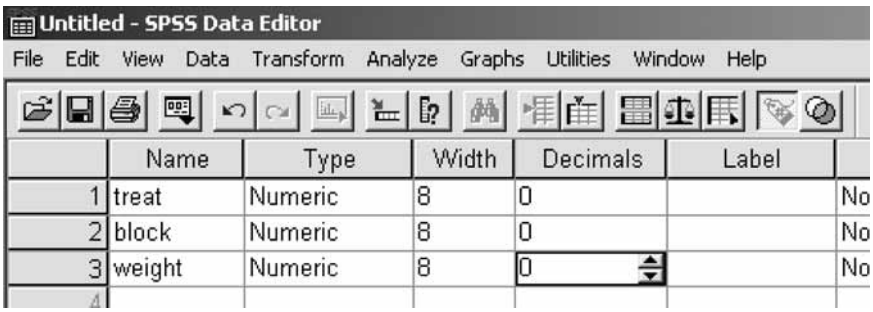
The three variables we have are treat(ment), block and weight (of crop) (SPSS variable names can be a maximum of eight characters long). Type their names into the first three name cells. Default properties are set for each variable.



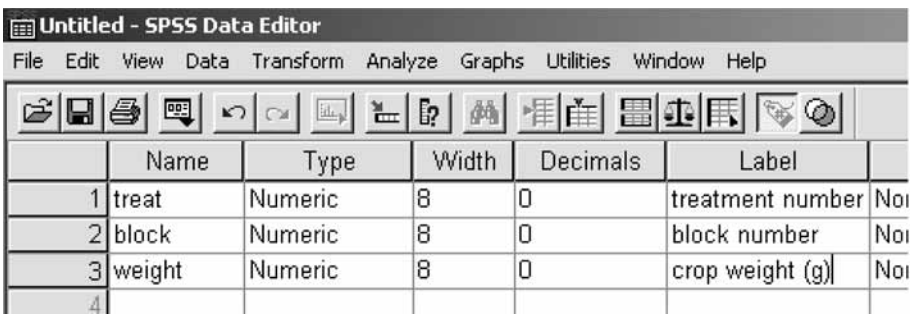
These are all numeric variable, and all integers, so the 'Decimals' property needs changing to 'zero'. To change it, click in the 'decimals' cell in row 1, and use the 'up-and-down' arrows that appear to adjust the number of decimal places to 0.



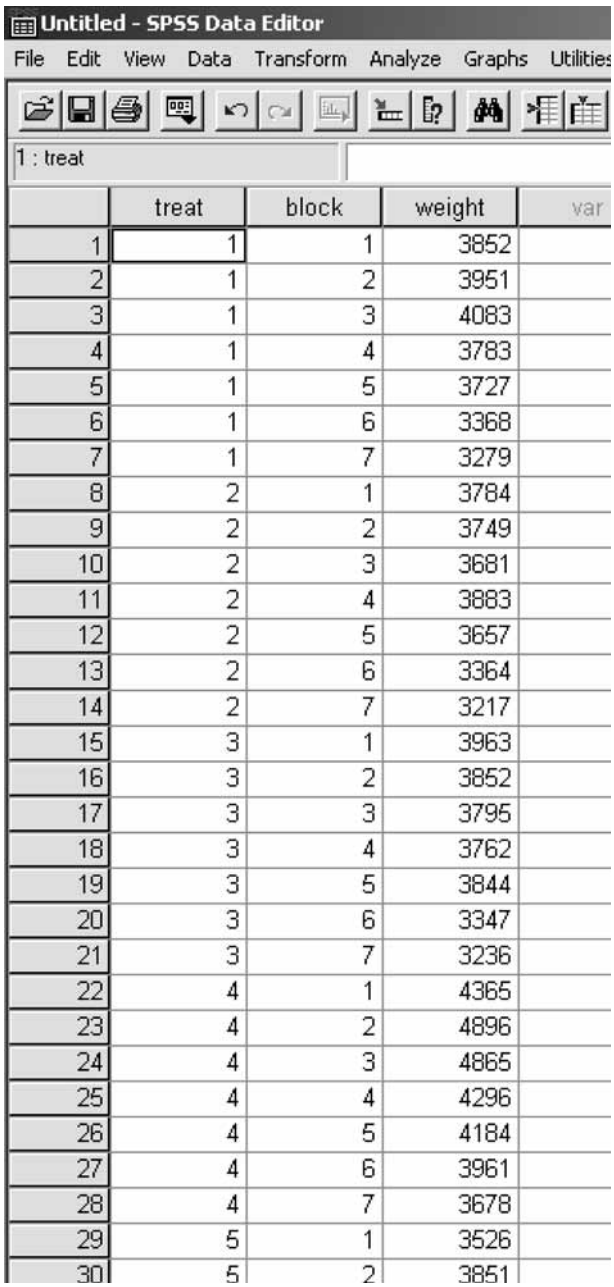
Repeat for the other two variables.



It might be good to add labels to help us remember exactly what the variables represent. Type something sensible in each of the 'label' cells.

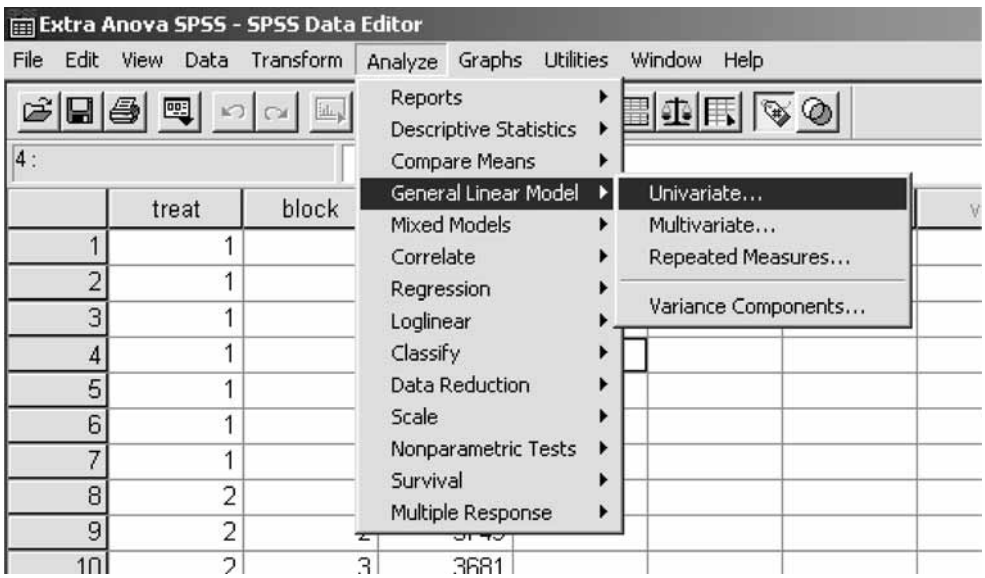


Transfer to data view by using the tabs at bottom-left.
Enter the data.

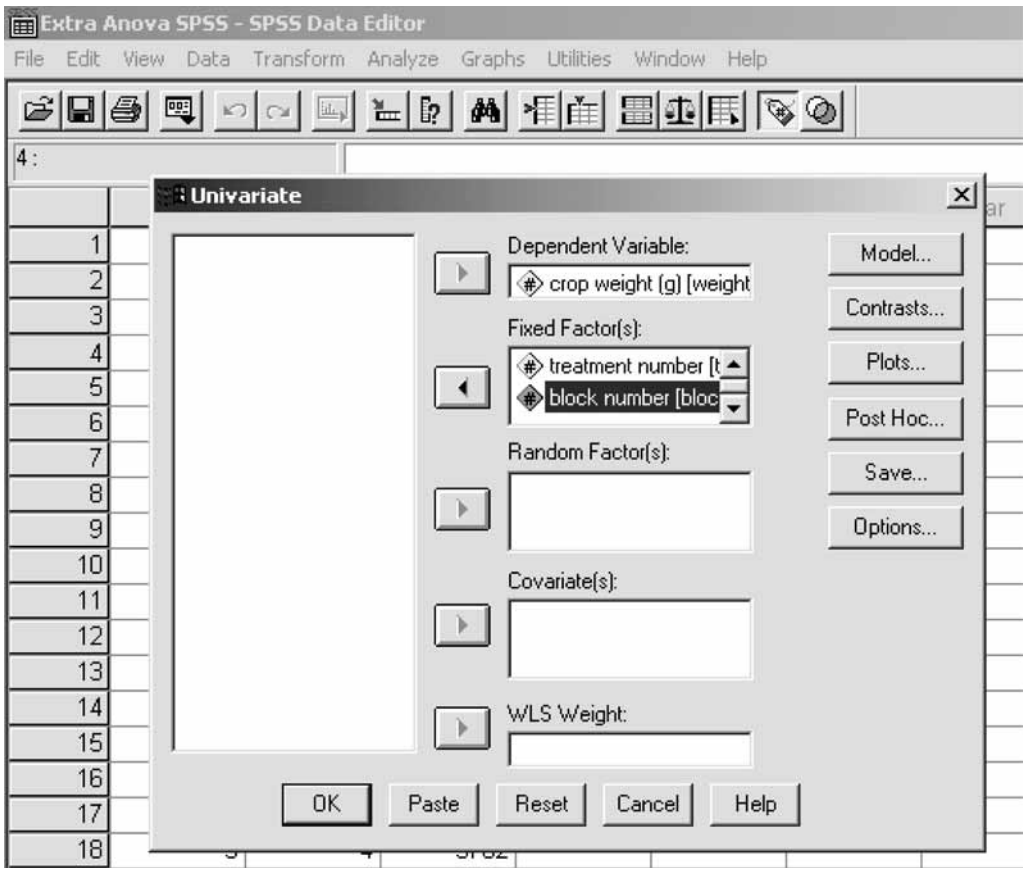


	treat	block	weight	var
1	1	1	3852	
2	1	2	3951	
3	1	3	4083	
4	1	4	3783	
5	1	5	3727	
6	1	6	3368	
7	1	7	3279	
8	2	1	3784	
9	2	2	3749	
10	2	3	3681	
11	2	4	3883	
12	2	5	3657	
13	2	6	3364	
14	2	7	3217	
15	3	1	3963	
16	3	2	3852	
17	3	3	3795	
18	3	4	3762	
19	3	5	3844	
20	3	6	3347	
21	3	7	3236	
22	4	1	4365	
23	4	2	4896	
24	4	3	4865	
25	4	4	4296	
26	4	5	4184	
27	4	6	3961	
28	4	7	3678	
29	5	1	3526	
30	5	2	3851	

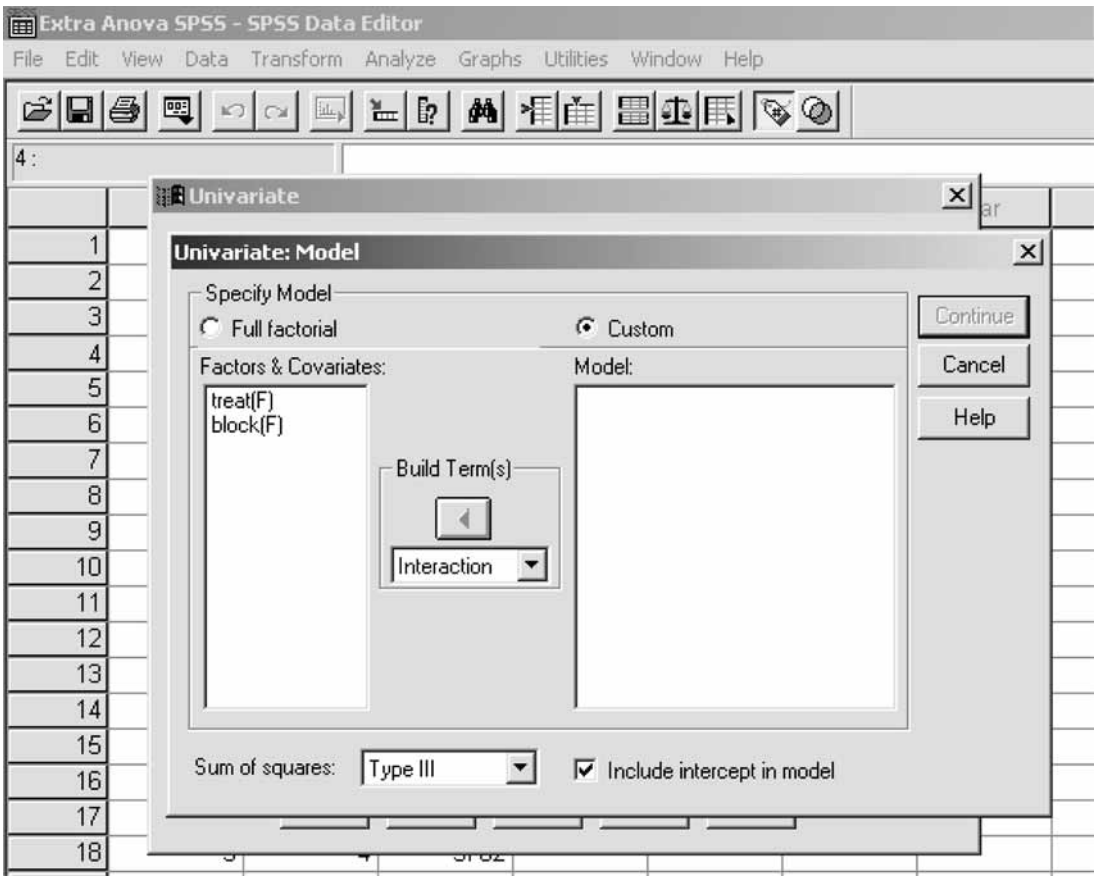
Step 2: Perform the test.
Go to 'Analyze', 'General Linear Model', 'Univariate'.



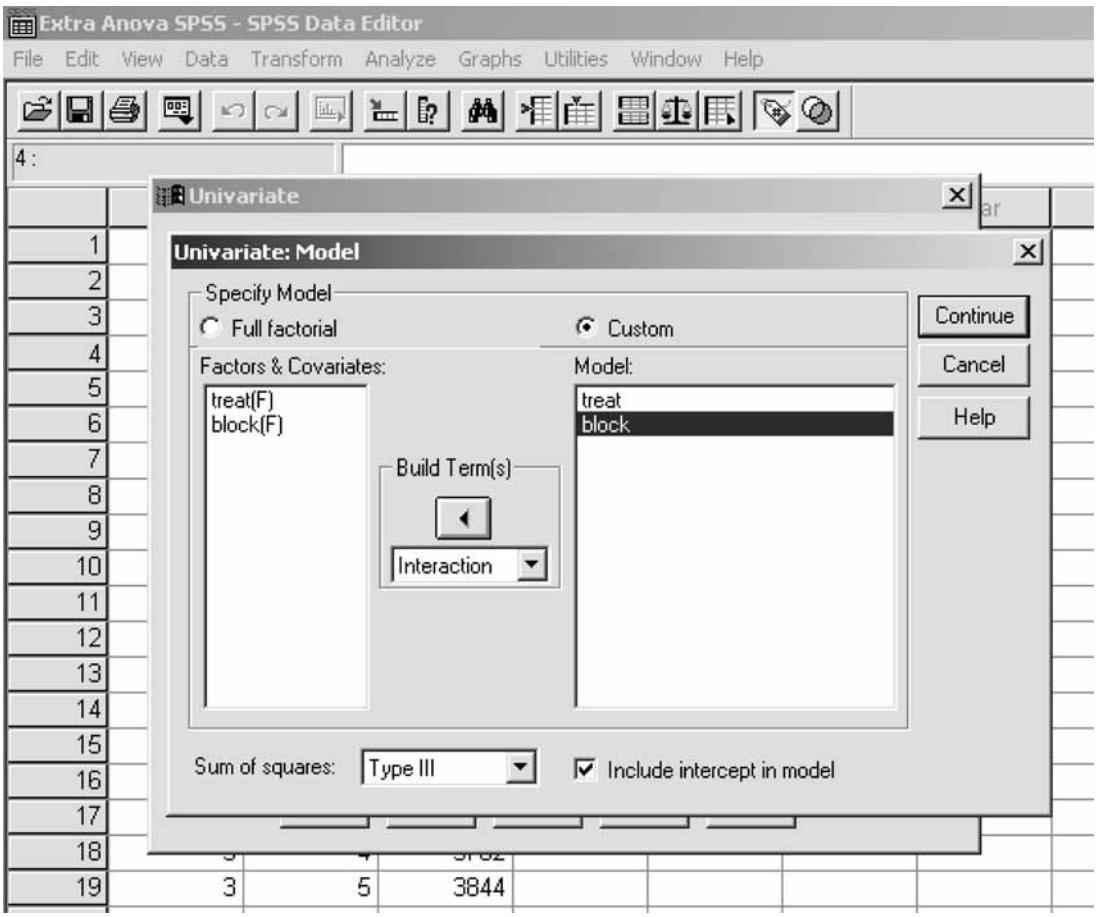
The dependent variable is the crop weight. Click on weight to highlight it, then click on the appropriate arrow to transfer it across into the '**dependent variable**' window. In the same way, transfer both 'treat' and 'block' into the 'fixed factor(s)' window.



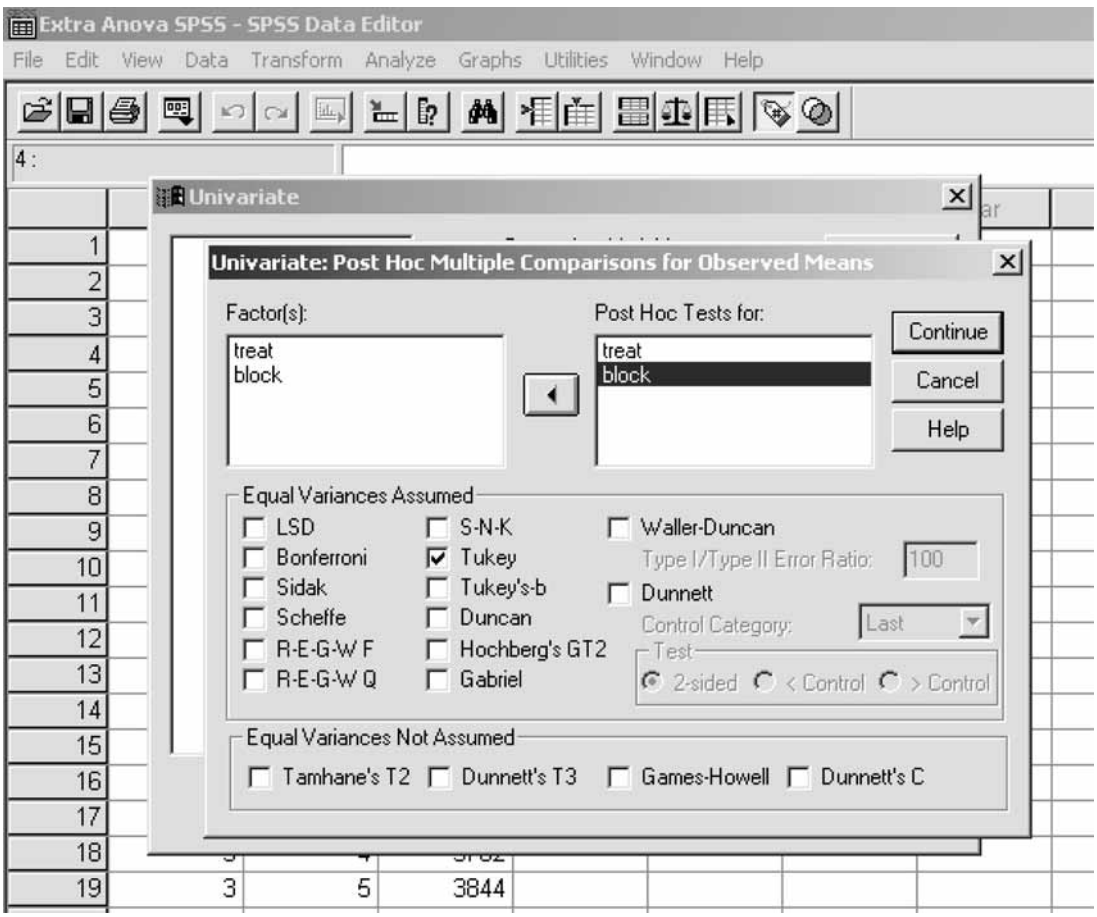
We need to set up the model appropriately. Click on 'Model', and select 'Custom'.



Select ‘treat’, and click on the arrow to transfer it across into the ‘Model’ window. Repeat for ‘block’.



Click on 'Continue' to return to the 'Univariate' dialogue box.
We need to include a Tukey test to help unravel the significance of the results. Click on 'Post Hoc'; select treat and block in turn, and clock on the arrow to transfer them across into the 'Post hoc tests for' window. Make sure that 'Tukey' is selected.



Click on 'Continue', and then on 'OK'. The output will appear in a separate window.

Univariate Analysis of Variance

Between-Subjects Factors

		N
treatment number	1	7
	2	7
	3	7
	4	7
	5	7
block number	1	5
	2	5
	3	5
	4	5
	5	5
	6	5
	7	5

Tests of Between-Subjects Effects

Dependent Variable: crop weight (g)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	4502717.200(a)	10	450271.720	11.122	.000
Intercept	501266486.429	1	501266486.429	12381.417	.000
TREAT	2604883.429	4	651220.857	16.085	.000
BLOCK	1897833.771	6	316305.629	7.813	.000
Error	971649.371	24	40485.390		
Total	506740853.000	35			
Corrected Total	5474366.571	34			

a R Squared = .823 (Adjusted R Squared = .749)

Post Hoc Tests

Treatment number

Multiple Comparisons

Dependent Variable: crop weight (g)
Tukey HSD

(I) treatment number	(J) treatment number	Mean Difference (I – J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
1	2	101.14	107.551	.878	−215.71	417.99
	3	34.86	107.551	.997	−281.99	351.71
	4	−600.29(*)	107.551	.000	−917.13	−283.44
	5	144.29	107.551	.669	−172.56	461.13
2	1	−101.14	107.551	.878	−417.99	215.71
	3	−66.29	107.551	.971	−383.13	250.56
	4	−701.43(*)	107.551	.000	−1018.28	−384.58
	5	43.14	107.551	.994	−273.71	359.99
3	1	−34.86	107.551	.997	−351.71	281.99
	2	66.29	107.551	.971	−250.56	383.13
	4	−635.14(*)	107.551	.000	−951.99	−318.29
	5	109.43	107.551	.845	−207.42	426.28
4	1	600.29(*)	107.551	.000	283.44	917.13
	2	701.43(*)	107.551	.000	384.58	1018.28
	3	635.14(*)	107.551	.000	318.29	951.99
	5	744.57(*)	107.551	.000	427.72	1061.42
5	1	−144.29	107.551	.669	−461.13	172.56
	2	−43.14	107.551	.994	−359.99	273.71
	3	−109.43	107.551	.845	−426.28	207.42
	4	−744.57(*)	107.551	.000	−1061.42	−427.72

Based on observed means.
* The mean difference is significant at the .05 level.

Homogeneous Subsets

crop weight (g)

Tukey HSD

treatment number	N	Subset 1	Subset 2
5	7	3576.14	
2	7	3619.29	
3	7	3685.57	
1	7	3720.43	
4	7		4320.71
Sig.		.669	1.000

Means for groups in homogeneous subsets are displayed. Based on Type III Sum of Squares
The error term is Mean Square(Error) = 40485.390.
a Uses Harmonic Mean Sample Size = 7.000.
b Alpha = .05.

Block number

Multiple Comparisons

Dependent Variable: crop weight (g)
Tukey HSD

(I) block number	(J) block number	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
1	2	−161.80	127.256	.858	−570.44	246.84
	3	−59.80	127.256	.999	−468.44	348.84
	4	69.00	127.256	.998	−339.64	477.64
	5	41.40	127.256	1.000	−367.24	450.04
	6	345.80	127.256	.137	−62.84	754.44
	7	560.40(*)	127.256	.003	151.76	969.04
2	1	161.80	127.256	.858	−246.84	570.44
	3	102.00	127.256	.983	−306.64	510.64
	4	230.80	127.256	.552	−177.84	639.44
	5	203.20	127.256	.686	−205.44	611.84
	6	507.60(*)	127.256	.008	98.96	916.24
	7	722.20(*)	127.256	.000	313.56	1130.84

(I) block number	(J) block number	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
3	1	59.80	127.256	.999	−348.84	468.44
	2	−102.00	127.256	.983	−510.64	306.64
	4	128.80	127.256	.946	−279.84	537.44
	5	101.20	127.256	.983	−307.44	509.84
	6	405.60	127.256	.053	−3.04	814.24
	7	620.20(*)	127.256	.001	211.56	1028.84
4	1	−69.00	127.256	.998	−477.64	339.64
	2	−230.80	127.256	.552	−639.44	177.84
	3	−128.80	127.256	.946	−537.44	279.84
	5	−27.60	127.256	1.000	−436.24	381.04
	6	276.80	127.256	.344	−131.84	685.44
	7	491.40(*)	127.256	.011	82.76	900.04
5	1	−41.40	127.256	1.000	−450.04	367.24
	2	−203.20	127.256	.686	−611.84	205.44
	3	−101.20	127.256	.983	−509.84	307.44
	4	27.60	127.256	1.000	−381.04	436.24
	6	304.40	127.256	.245	−104.24	713.04
	7	519.00(*)	127.256	.007	110.36	927.64
6	1	−345.80	127.256	.137	−754.44	62.84
	2	−507.60(*)	127.256	.008	−916.24	−98.96
	3	−405.60	127.256	.053	−814.24	3.04
	4	−276.80	127.256	.344	−685.44	131.84
	5	−304.40	127.256	.245	−713.04	104.24
	7	214.60	127.256	.631	−194.04	623.24
7	1	−560.40(*)	127.256	.003	−969.04	−151.76
	2	−722.20(*)	127.256	.000	−1130.84	−313.56
	3	−620.20(*)	127.256	.001	−1028.84	−211.56
	4	−491.40(*)	127.256	.011	−900.04	−82.76
	5	−519.00(*)	127.256	.007	−927.64	−110.36
	6	−214.60	127.256	.631	−623.24	194.04

Based on observed means.
* The mean difference is significant at the .05 level.

Homogeneous Subsets

crop weight (g)

Tukey HSD

		Subset		
block number	N	1	2	3
7	5	3337.60		
6	5	3552.20	3552.20	
4	5		3829.00	3829.00
5	5		3856.60	3856.60
1	5		3898.00	3898.00
3	5		3957.80	3957.80
2	5			4059.80
Sig.		.631	.053	.552

Means for groups in homogeneous subsets are displayed. Based on Type III Sum of Squares
The error term is Mean Square Error) = 40485.390.
a Uses Harmonic Mean Sample Size = 5.000.
b Alpha = .05.

Step 3: Decide what the results mean.

(a) In the second table, the *F* values for treatment and block are 16.085 and 7.813 respectively. Both of these are significant at better than $p = 0.001$.

(b) The Tukey test results for treatment (the 'Homogenous subsets' table) indicate that treatment 4 is significantly different from the others, and that the others are not significantly different from each other.

(c) The Tukey test results for block (the 'multiple comparisons table) indicate that:

(i) Block 7 is significantly different from all other blocks except block 6;

(ii) Block 2 is significantly different from both block 7 and block 6.