

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.).

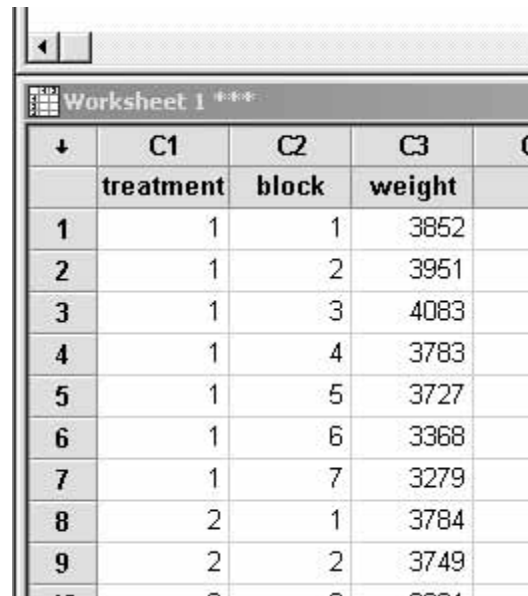
Fig. WEA1. A randomized block design

| | 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, and 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.

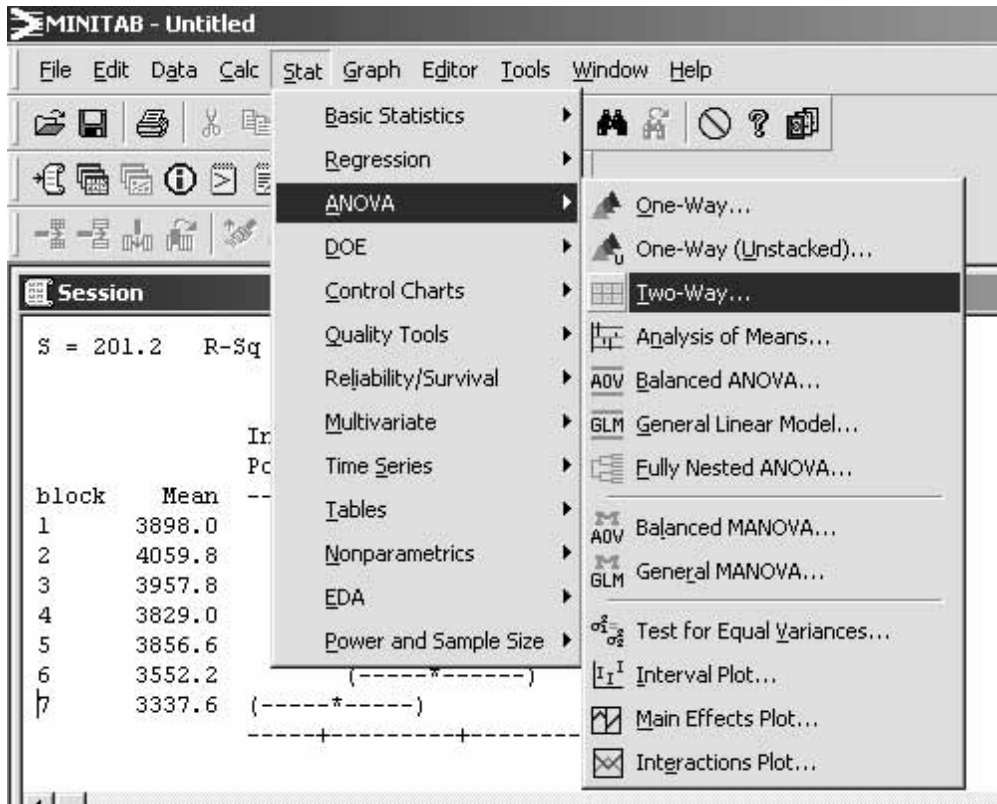
In this trial, fruit would be harvested at a certain date and the mass recorded (in grams). The data are given in the spreadsheet shown in step 2.

Step 1. Enter the data into the worksheet window of Minitab, using sensible headings for the columns.

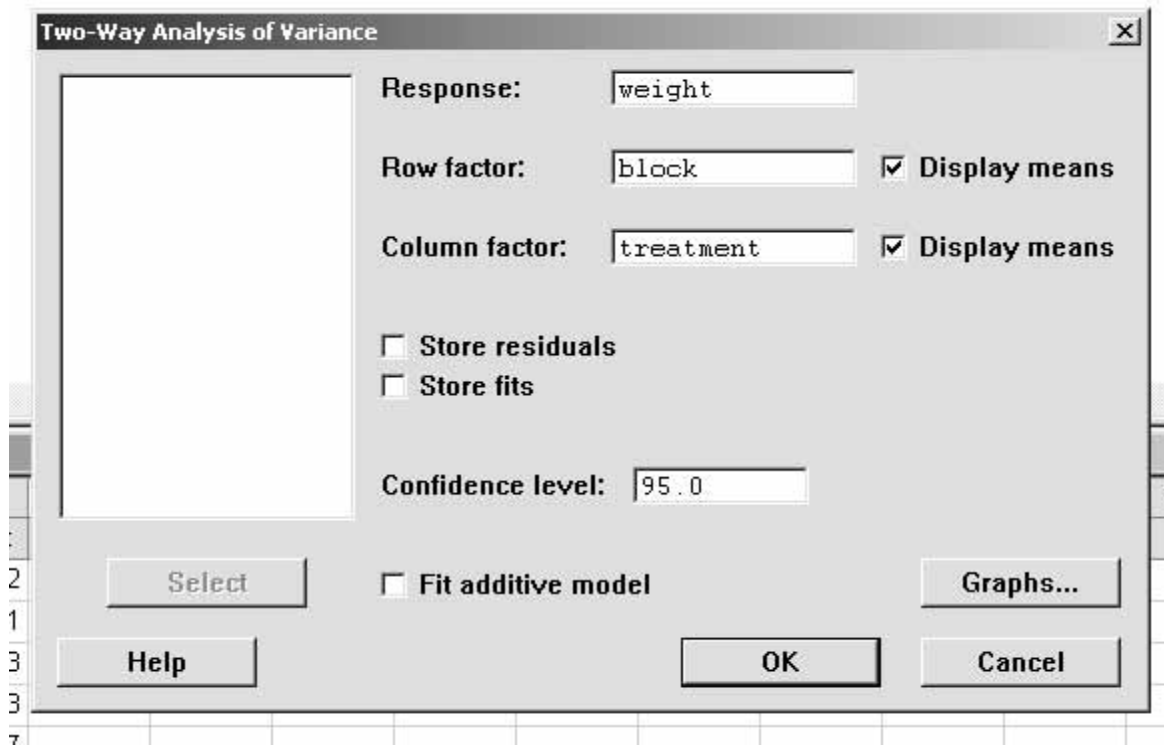


| | C1 | C2 | C3 | C4 |
|---|-----------|-------|--------|----|
| | treatment | block | weight | |
| 1 | 1 | 1 | 3852 | |
| 2 | 1 | 2 | 3951 | |
| 3 | 1 | 3 | 4083 | |
| 4 | 1 | 4 | 3783 | |
| 5 | 1 | 5 | 3727 | |
| 6 | 1 | 6 | 3368 | |
| 7 | 1 | 7 | 3279 | |
| 8 | 2 | 1 | 3784 | |
| 9 | 2 | 2 | 3749 | |

Step 2. Analyse the data. Go to 'Stat', 'ANOVA', 'Two-Way'.



Transfer 'weight' from the left-hand window to the 'Response' window by clicking on it to highlight it, the clicking on 'Select' to make the transfer. In the same way, transfer 'block' to the 'Row factor' window, and 'treatment' to the 'Column factor' window.



Click on 'OK', and the results will appear in the 'Session' window.

Two-way ANOVA: weight versus block, treatment

| Source | DF | SS | MS | F | P |
|-----------|----|---------|--------|-------|-------|
| Block | 6 | 1897834 | 316306 | 7.81 | 0.000 |
| Treatment | 4 | 2604883 | 651221 | 16.09 | 0.000 |
| Error | 24 | 971649 | 40485 | | |
| Total | 34 | 5474367 | | | |

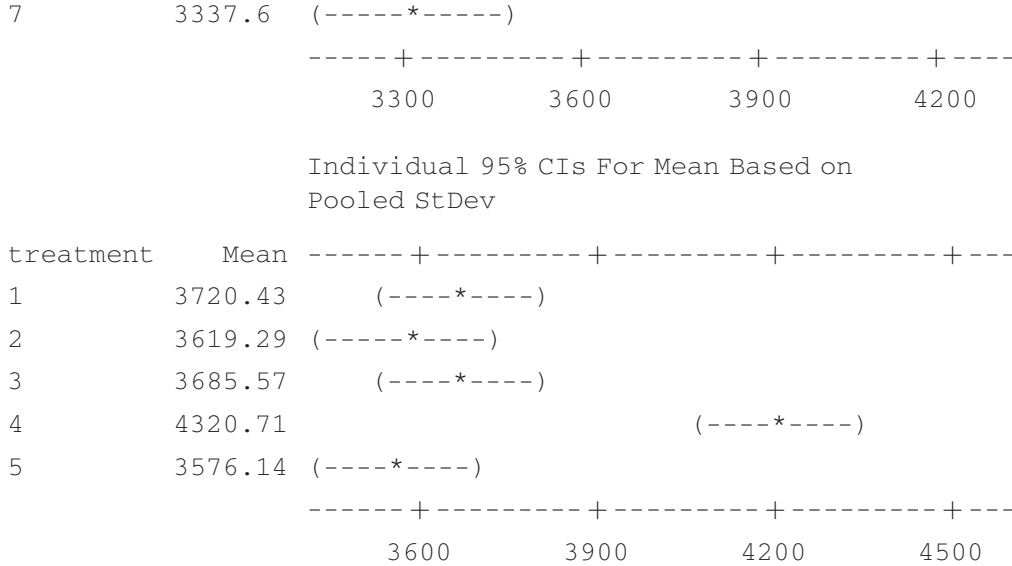
S = 201.2

R-Sq = 82.25%

R-Sq(adj) = 74.86%

Individual 95% CIs For Mean Based on
Pooled StDev

| block | Mean | CI |
|-------|--------|---------------|
| 1 | 3898.0 | (-----*-----) |
| 2 | 4059.8 | (-----*-----) |
| 3 | 3957.8 | (-----*-----) |
| 4 | 3829.0 | (-----*-----) |
| 5 | 3856.6 | (-----*-----) |
| 6 | 3552.2 | (-----*-----) |



Step 3. Decide what the results mean.

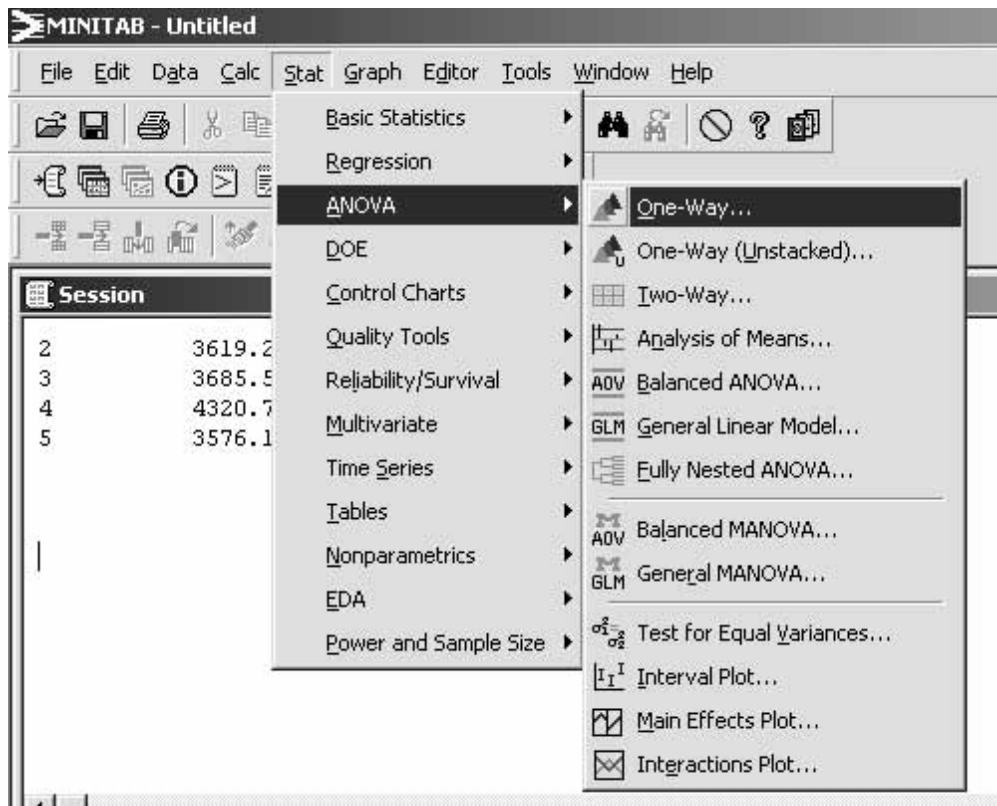
The F value for the blocks is 7.81, and the corresponding p value is less than 0.001. This indicates a significant ($F = 7.81$, $p = 0.001$) relationship between weight of tomatoes produced and the block in which the plant was located.

The F value for the treatments is 16.09, and the corresponding p value is less than 0.001. This indicates a significant ($F = 7.81$, $p = 0.001$) relationship between weight of tomatoes produced and the treatment they received.

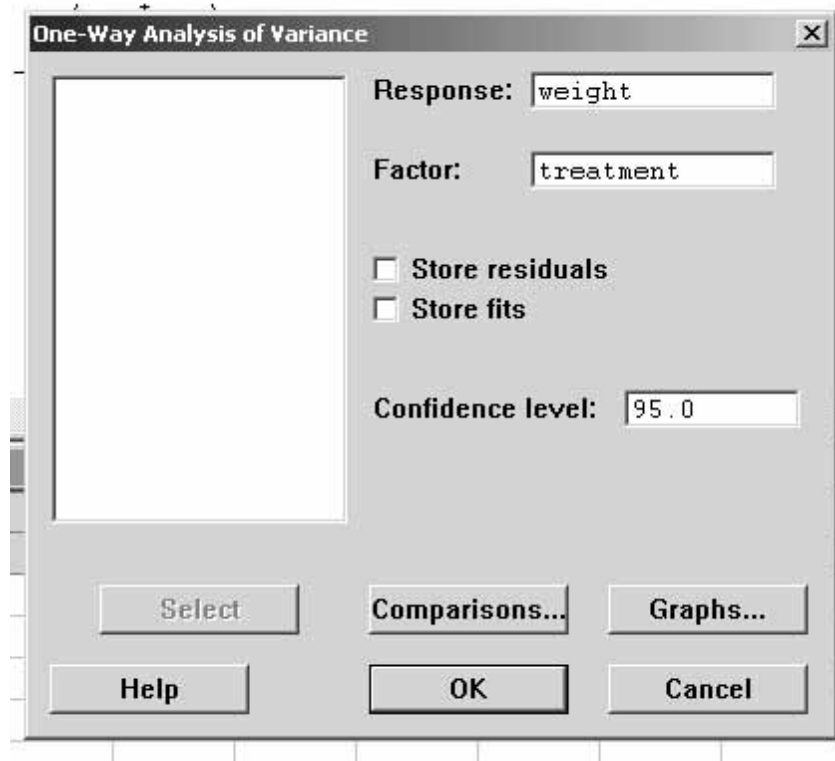
Step 4. Find out which differences are significant.

For this, we need a Tukey's test, and this will have to be done for blocks and for treatments separately.

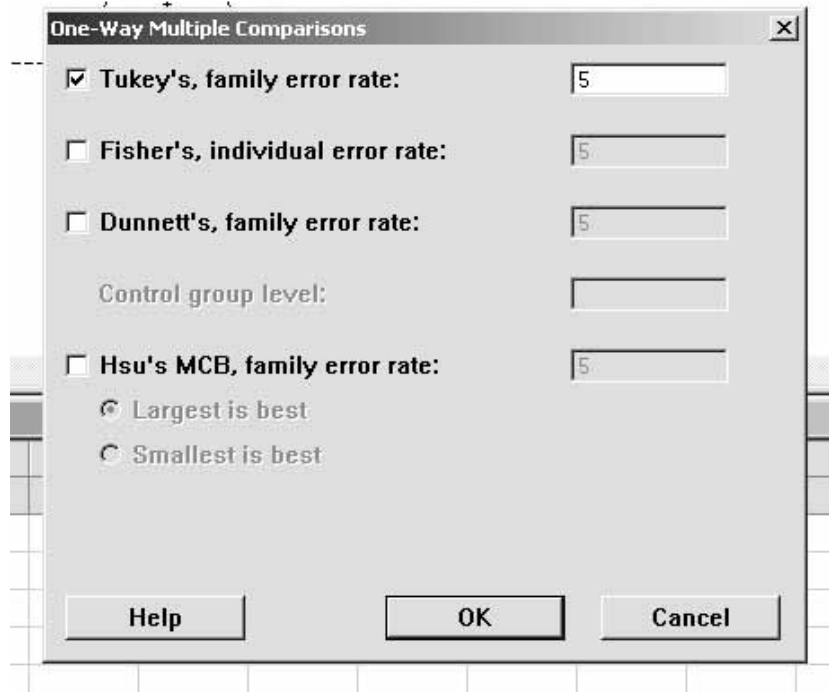
For blocks (which is what we are really interested in), go to 'Stat', 'ANOVA', 'One-Way'.



Transfer 'weight' and 'treatment' into the 'Response' and 'Factor' windows respectively.



Click on 'Comparisons', and select 'Tukey's'. The default 'family error rate' (5%) corresponds to $p = 0.05$, so this is OK.



Click on 'OK', and then on 'OK' again. The results will appear in the 'Session' window.

One-way ANOVA: weight versus treatment

| Source | DF | SS | MS | F | P |
|-----------|----|---------|--------|------|-------|
| treatment | 4 | 2604883 | 651221 | 6.81 | 0.001 |
| Error | 30 | 2869483 | 95649 | | |
| Total | 34 | 5474367 | | | |

S = 309.3 R-Sq = 47.58% R-Sq(adj) = 40.59%

Individual 95% CIs For Mean Based on Pooled StDev

| Level | N | Mean | StDev | CI |
|-------|---|--------|-------|---------------|
| 1 | 7 | 3720.4 | 295.8 | (-----*-----) |
| 2 | 7 | 3619.3 | 240.0 | (-----*-----) |
| 3 | 7 | 3685.6 | 278.2 | (-----*-----) |
| 4 | 7 | 4320.7 | 445.5 | (-----*-----) |
| 5 | 7 | 3576.1 | 239.3 | (-----*-----) |

-----+-----+-----+-----+-----
 3500 3850 4200 4550

Pooled StDev = 309.3

If the process is repeated to give the significance of the blocks, the following output is obtained:

One-way ANOVA: weight versus block

| Source | DF | SS | MS | F | P |
|--------|----|---------|--------|------|-------|
| block | 6 | 1897834 | 316306 | 2.48 | 0.048 |
| Error | 28 | 3576533 | 127733 | | |
| Total | 34 | 5474367 | | | |

S = 357.4 R-Sq = 34.67% R-Sq(adj) = 20.67%

Individual 95% CIs For Mean Based on Pooled StDev

| Level | N | Mean | StDev |
|-------|---|--------|-------|
| 1 | 5 | 3898.0 | 306.5 |
| 2 | 5 | 4059.8 | 472.9 |
| 3 | 5 | 3957.8 | 568.6 |
| 4 | 5 | 3829.0 | 313.9 |
| 5 | 5 | 3856.6 | 202.6 |
| 6 | 5 | 3552.2 | 277.1 |
| 7 | 5 | 3337.6 | 192.2 |

Pooled StDev = 357.4

Tukey 95% Simultaneous Confidence Intervals
All Pairwise Comparisons among Levels of block

Individual confidence level = 99.64%

block = 1 subtracted from:

| block | Lower | Center | Upper |
|-------|---------|--------|-------|
| 2 | -555.9 | 161.8 | 879.5 |
| 3 | -657.9 | 59.8 | 777.5 |
| 4 | -786.7 | -69.0 | 648.7 |
| 5 | -759.1 | -41.4 | 676.3 |
| 6 | -1063.5 | -345.8 | 371.9 |
| 7 | -1278.1 | -560.4 | 157.3 |

block = 2 subtracted from:

| block | Lower | Center | Upper |
|-------|---------|--------|-------|
| 3 | -819.7 | -102.0 | 615.7 |
| 4 | -948.5 | -230.8 | 486.9 |
| 5 | -920.9 | -203.2 | 514.5 |
| 6 | -1225.3 | -507.6 | 210.1 |
| 7 | -1439.9 | -722.2 | -4.5 |

block = 3 subtracted from:

| block | Lower | Center | Upper | |
|-------|---------|--------|-------|---------------|
| 4 | -846.5 | -128.8 | 588.9 | (-----*-----) |
| 5 | -818.9 | -101.2 | 616.5 | (-----*-----) |
| 6 | -1123.3 | -405.6 | 312.1 | (-----*-----) |
| 7 | -1337.9 | -620.2 | 97.5 | (-----*-----) |

-----+-----+-----+-----+-----+
-800 0 800 1600

block = 4 subtracted from:

| block | Lower | Center | Upper | |
|-------|---------|--------|-------|---------------|
| 5 | -690.1 | 27.6 | 745.3 | (-----*-----) |
| 6 | -994.5 | -276.8 | 440.9 | (-----*-----) |
| 7 | -1209.1 | -491.4 | 226.3 | (-----*-----) |

-----+-----+-----+-----+-----+
-800 0 800 1600

block = 5 subtracted from:

| block | Lower | Center | Upper | |
|-------|---------|--------|-------|---------------|
| 6 | -1022.1 | -304.4 | 413.3 | (-----*-----) |
| 7 | -1236.7 | -519.0 | 198.7 | (-----*-----) |

-----+-----+-----+-----+-----+
-800 0 800 1600

block = 6 subtracted from:

| block | Lower | Center | Upper | |
|-------|--------|--------|-------|---------------|
| 7 | -932.3 | -214.6 | 503.1 | (-----*-----) |

-----+-----+-----+-----+-----+
-800 0 800 1600

The overall F value is 2.48, and the corresponding p value is 0.048 – just significant at $p = 0.05$.

The only significant difference here (confidence interval not including zero) is the comparison of block 2 with block 7.