Statistical Analysis Step-by-Step Using Statistical Calculator for Pooled Analysis

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Methodology

We follow the steps described below to get the data analyzed and finding its outputs:

Step 1: Type www.psbvb.in in any browser that will open the following web page:

Step 2: Then click on Statistical Analysis which will open the page given below:

Step 3: There are number of items on the statistical calculator. You can click on any one of them according to your need, for example, click on pooled analysis.

Step 4: Click on Statistical Calculator of pooled analysis, then that page will download the calculator within a second. You can keep it in your computer or laptop forever. Next, you click on the downloaded file which is an excel file and a data

spreadsheet will open up. Here you can analyse upto 23 number of treatments,upto 6 number of replications and upto 6 number of Location / Year / Season. Now you can put your data directly in the given spreadsheet or copy from other sheet and paste it here.

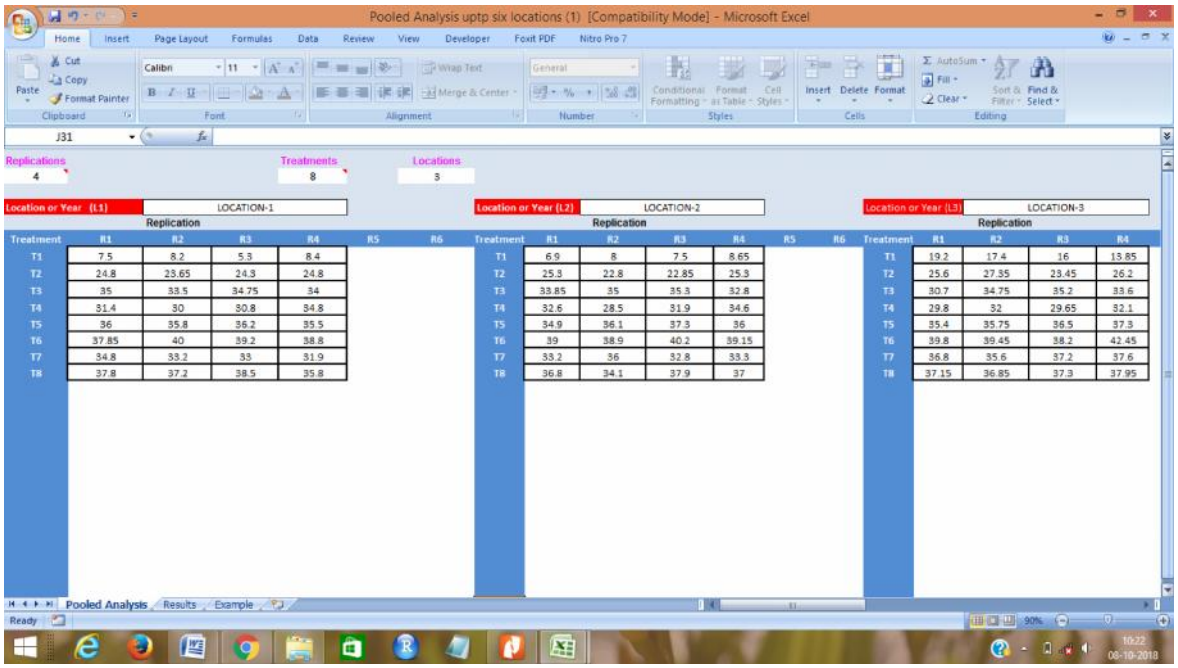
Example 3.5: An Experiment was conducted in RBD in three locations with eight varieties and four replications. The data regarding yield of wheat (Kg./plot) are given below in table. Analyze the data and draw your conclusions.

		LOCATION-1		
variety	R1	R2	R3	R4
1	7.5	8.2	5.3	8.4
2	24.8	23.65	24.3	24.8
3	35	33.5	34.75	34
4	31.4	30	30.8	34.8
5	36	35.8	36.2	35.5
6	37.85	40	39.2	38.8
7	34.8	33.2	33	31.9
8	37.8	37.2	38.5	35.8

		LOCATION-2		
variety	R1	R2	R3	R4
1	6.9	8	7.5	8.65
2	25.3	22.8	22.85	25.3
3	33.85	35	35.3	32.8
4	32.6	28.5	31.9	34.6
5	34.9	36.1	37.3	36
6	39	38.9	40.2	39.15
7	33.2	36	32.8	33.3
8	36.8	34.1	37.9	37

		LOCATION-3		
variety	R1	R2	R3	R4
1	19.2	17.4	16	13.85
2	25.6	27.35	23.45	26.2
3	30.7	34.75	35.2	33.6
4	29.8	32	29.65	32.1
5	35.4	35.75	36.5	37.3
6	39.8	39.45	38.2	42.45
7	36.8	35.6	37.2	37.6
8	37.15	36.85	37.3	37.95

Step 5: Put Number of Replications =4, Number of Tretments=8, Number of Location =3 and Name of Location= Location 1,Location 2, Location 3 in the following page.



Step 6: Now you click on print command and that will start analysis and produces the results in a printable format. If a printer is attached to computer, then you can take a print out of the results. Otherwise, you can see your result in a print preview mode. see the page below:

Output

ANOVA for LOCATION-1

Source	DF	SS	MS	F- value	p-value	
TREATMENTS	7	2975.24	425.03	282.53**	0.00	
REPLICATIONS	3	1.06	0.35	0.24	0.87	
ERROR	21	31.59	1.50			
TOTAL	31	3007.90				

Grand total =	972.75	Root MSE =	1.23
S E (d) =	0.87	Grand Mean =	30.40
Critical Difference =	1.80	C V =	4.03%
R Square =	0.99	S E(m)=	0.61

ANOVA for LOCATION-2

Source	DF	SS	MS	F- value	p-value	
TREATMENTS	7	2918.18	416.88	193.18**	0.00	
REPLICATIONS	3	4.20	1.40	0.65	0.59	
ERROR	21	45.32	2.16			
TOTAL	31	2967.70				

Grand total =	974.50	Root MSE =	1.47
S E (d) =	1.04	Grand Mean =	30.45
Critical Difference =	2.16	C V =	4.82%
R Square =	0.98	S E(m)=	0.73

ANOVA for LOCATION-3

Source	DF	SS	MS	F- value	p-value	
TREATMENTS	7	1653.85	236.26	97.86**	0.00	
REPLICATIONS	3	4.97	1.66	0.69	0.57	
ERROR	21	50.70	2.41			
TOTAL	31	1709.519297				

Grand total =	1028.15	Root MSE =	1.55
S E (d) =	1.10	Grand Mean =	32.13
Critical Difference =	2.28	C V =	4.84%
R Square =	0.97	S E(m)=	0.78

Location's	df	MSE
L1	21	1.50
L2	21	2.16
L3	21	2.41

According to Hartley's test the Variances are equal; It means MSEs are homogeneous

If MSEs are heterogeneous, then we use Aitken's Transformation to the data for pooled analysis

Combined block design of experiment and ANOVA table with transformation

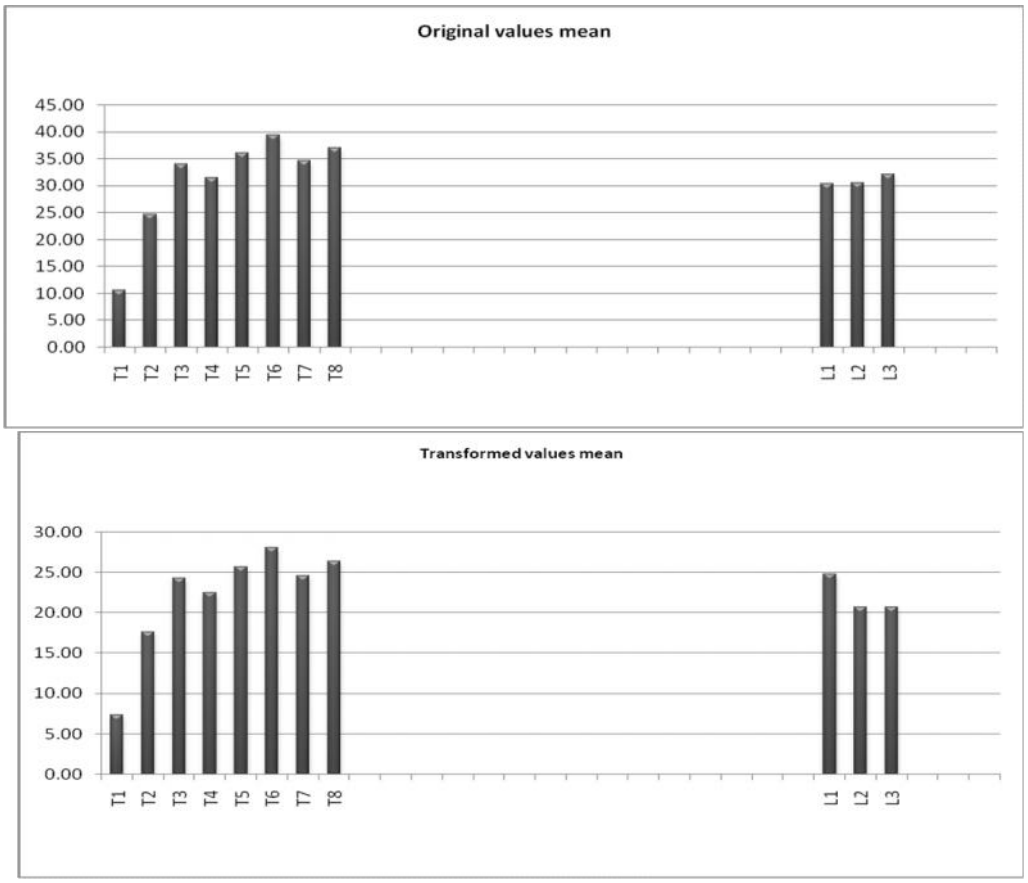
SOURCE	DF	SS	MS	Fcal	p-value	
TREATMENTS	7	3808.95	544.14	544.14 **	0.00	
LOCATIONS	2	355.11	177.55	177.55 **	0.00	
REP in loc	9	4.71	0.52	0.52		
treat*loc	14	206.06	14.72	14.72 **	0.00	
ERROR	63	63.00	1.00			
TOTAL	95	4437.83				
	SE	CD			GM=	22.06
Location	0.25	0.50			CV=	4.53
Treatment	0.41	0.82			Root MSE	1
TRT*Loc	0.71	1.41			R Square =	0.99

combined block design experiment ANOVA table without transformation

SOURCE	DF	SS	MS	Fcal	p-value	
TREATMENTS	7	7347.12	1049.59	518.17 **	0.00	
LOCATIONS	2	61.98	30.99	15.30 **	0.00	
REP in loc	9	10.23	1.14	0.56		
treat*loc	14	200.16	14.30	7.06 **	0.00	
ERROR	63	127.61	2.03			
TOTAL	95	7747.10				
	SE	CD			GM=	30.99
Location	0.36	0.71			CV=	4.59
Treatment	0.58	1.16			Root MSE=	1.42
TRT*Loc	1.01	2.01			R Square =	0.98

** Significant at the 0.01 level

Treatment	Mean (Original)	Mean (Transformation)
T1	10.58	7.32
T2	24.70	17.59
T3	34.04	24.29
T4	31.51	22.49
T5	36.06	25.71
T6	39.42	28.08
T7	34.62	24.60
T8	37.03	26.42
L1	30.40	24.78
L2	30.45	20.73
L3	32.13	20.68



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3. Biometrical Methods in Quantitative Genetic Analysis, R.K. Singh and B. D. Chaudhary, Kalyani Publishers.