AUGMENT 1: A MICROCOMPUTER BASED PROGRAM TO ANALYZE AUGMENTED RANDOMIZED COMPLETE BLOCK DESIGN

R. C. Agrawal and R. L. Sapra

National Bureau of Plant Genetic Resources,
Pusa Campus, New Delhi 110 012

A user friendly computer program named AUGMENT1 has been developed in GWBASIC supported on MS-DOS at the Documentation unit of NBPGR to analyse the data of Augmented Randomized Complete Block Designs. The programme takes care of both equal as well as unequal number of new entries/lines in different blocks for a set of quantitative descriptors. The output of the detailed analysis for individual descriptors includes two kinds of ANOVA tables, adjusted values for the new entries and 4 kinds of standard errors for testing different contrasts. The results of the analysis are stored in a text file and can be conveniently taken on a hard copy. The copy of the programme can be had from the Director, NBPGR, New Delhi.

Key words :   Augment 1, PC based program, augmented design, analysis

Augmented Designs suggested by Federer (1956) are being extensively used by the germplasm evaluators for the preliminary evaluation of their germplasm trials in respect of quantitative idescriptos particularly when the number of accessions are unmanageable and the quantity of the genetic material is not sufficient to go for even two replications. Statistical analysis of such designs is slightly cumbersome as compared to that of Randomized Block Designs. The most commonly used Augmented Design is the Augmented Randomized Complete Block Design (RCBD) in which only check varieties are repeated a number of times and new accessions (to be tested) appear only once (Federer, 1956; Federer and Raghavrao, 1975). Because of its simplicity and usefulness, this design is also practiced in fields of entomology, pathology, chemistry, physiology, agronomy and perhaps others for combining screening experiments on new material and preliminary testing experiments on promising material. Because of its wide use in these fields and mainly in the genetic resources environment, a programme named AUGMENT 1 has been developed to analyse the data of such designs.

Basic concepts about Augmented RCBD

We illustrate the concept with some hypothetical example for ease in understanding the programme

Suppose, we have 4 check varieties say C_i, i = 1 to 4; 10 new accessions (which are to be tested) say A_i, i = 1 to 10 of Sorghum and three blocks (b=3)

In the layout of this experiment, there have to be 7 plots (4 for checks and 3 for new varieties) in any two blocks and 8 plots (4 for checks and 4 for new varieties) in the remaining third block. We are assuming that the 1st and 3rd block are having 7 plots each and 2nd block is having 8 plots. For random allocation of these accessions in the experiment, we have to proceed as —

(i) Allot 4 check varieties to each block randomly. In this process, say following is the arrangement —

Blocks	Entries							
	1	2	3	4	5	6	7	8
1	C_1		C_3		C_4	C_2		
2	C_3	C_1		C_4	C_2			
3	C_1		C_2	C_4	C_3			

The 8th plot is only for 2nd block.

(ii) 10 new varieties are allotted randomly·in the remaining plots of the 3 blocks. This way 22 plots are randomly occupied by 4 checks and 10 new accessions. The final arrangement looks like-

Blocks	Entries							
	1	2	3	4	5	6	7	8
1	C_1	A_9	C_3	A_2	C_4	C_2	A_1	
2	C_3	C_1	A_3	C_4	C_2	A_8	A_{10}	A_5
3	C_1	A_4	C_2	C_4	C_3	A_7	A_6	

For the analysis purpose, let us assume-

v = Number of check varieties

V = Number of new varieties

b = Number of blocks

n_i = Number of new varieties in ith block

$$N = \sum_{i=1}^{b} (v + n_i) = \text{Total number of plots}$$

ANOVA

Sources of Variation	d.f.	Sum of Squares
Blocks (Ignoring treatments)	b − 1	B
Treatments (eliminating blocks)	v + v − 1	SScn
Check varieties	v − 1	SSc
New varieties and (checks vs. new varieties)	V	SSn
Error	(v − 1) (b − 1)	SSe
Blocks (eliminating treatments)	b − 1	SSb
Treatments (ignoring blocks)	v + V − 1	T
Check varieties	v − 1	SSc
New varieties	v − 1	SSn(1)
Checks vs new varieties	1	SSn(2)
Error	(v − 1) (b − 1)	SSe

Standard Errors

Four kinds of standard errors for comparing mean differences are as follow-

(i) Between two check variety means

$$SE(1) = \frac{\sqrt{2MS\ (E)}}{b}$$

(ii) Between two new varieties in the same block

$$SE(2) = \sqrt{2\ MS\ (E)}$$

(iii) Between two new varieties not in the same block

$$SE\ (3) = \sqrt{2\left(1 + \frac{1}{v}\right)MS\ (E)}$$

(iv) Between a check variety and a new variety

$$SE\ (4) = \sqrt{\left(1 + \frac{1}{b} + \frac{1}{v} + \frac{1}{bv}\right)MS\ (E)}$$

Adjusted values

For comparison of new varieties, it is essential to adjust them for the block effects. For finding the adjusted value of a new accession, we have the following formula-

> Adjusted value of a new accession = Unadjusted value of that accession - (Mean of the check varieties in the block where this new accession occurs - overall mean of the check varieties)

About the program AUGMENT 1

The AUGMENT 1 has been developed for equal as well as unequal number of new accessions in each block. The program requires 6 files namely, AUGMENT 1.EXE, BRUN40.EXE, BRUN40.LIB, HELP.AUG, AUGT2.EXE and HELP.EXE. For installation of the programme, create a directory C: \AUGMEN and all the above mentioned files must be copied in this directory. To run the program, one has to simply type augment1 in the C:\AUGMEN directory followed by Enter key.

Two data files are required for running this programme -

(1) Data file for check varieties

(2) Data file for unreplicated treatments (new accessions).

The input files (1) & (2) must be ASCII files and the fields must be delimited by commas. For file (1) the fields must be in the following order:

replication no., check variety no., ch.1, ch.2, ...

where as for file (2), the order of the fields must be:

replication no., ch.1, ch.2, ...

where ch.1, ch.2, etc. are the characters to be analysed.

Hardware requirements

1. IBM Compatible PC XT/AT with a minimum of 256 KB RAM.

2. Hard Disk with a minimum free space of 124 KB to load the program.

3. MS-DOS Ver 3.0 (or higher).

Limitations

The programme has the following limitations

(1) No. of replications should not exceed 100.

(2) No. of check varieties should not exceed 10.

(3) No. of characters/descriptors should not exceed 20.

However these limits can be increased (depending upon the computer's memory) by changing the dimensions in the source program.

Sample exercise

The following example has been taken from Federer (1956). Four hypothetical varieties (check varieties A, B, C, D) and eight hypothetical seedlings (new

accessions (e, f, g, h, i, j, k, l) are used. The layout of the experiment is shown below —

Blocks					Entries			
1.	Variety or seedling	l	C	D	g	A	B	k
	Yield	74	78	78	70	83	77	75
2.	Variety or seedling	D	B	A	C	e	i	
	Yield	91	81	79	81	79	78	
3.	Variety or seedling	h	C	A	f	D	B	j
	Yield	96	87	92	89	81	79	82

Blocks 1 and 3 contain 7 entries each, and block 2 contains 6 entries. Following are the two sample input data files (CHKFILE and ACCFILE for yield of check varieties and new accessions respectively) created in the format mentioned earlier for analyzing the data of this example.

Input Files

CHKFILE	ACCFILE
1,1,83	1,74
1,2,77	1,70
1,3,78	1,75
1,4,78	2,79
2,1,79	2,78
2,2,81	3,96
2,3,81	3,89
2,4,91	3,82
3,1,92	
3,2,79	
3,3,87	
3,4,81	

An output file containing the results of analysis can be had in ASCII mode. The output for the present example is given below -

Output file for sample exercise

AUGMENTED RANDOMIZED COMPLETE BLOCK DESIGN
ANALYSIS FOR THE DATA FILE (CHECK VARIETIES)—CHKFILE
AND FOR DATAFILE (UNREPLICATED TRAEATMENTS)—ACCFILE
NO. OF REPLICATIONS/BLOCK = 3
NO. OF TREATMENTS OR CHECK VARIETIES = 4
NO. OF CHARACTERS/DESCRIPTORS = 1

ANOVA (Character 1)

Source	D.F.	S.S.	M.S.	F˙
Blocks (Ignoring treatments)@	2	360.06	180.03	6.67
Treatments (eliminating blocks)	11	285.10	25.92	0.96
Check varieties	3	52.92	17.64	0.65
U.R. varieties and check vs. U.R.# varieties	8	232.19	29.02	1.08
Error	6	161.83	26.97	
Total	19	807.00		
Blocks (eliminating treatments)	2	69.50	34.75	·1.29
Treatments (ignoring blocks)	11	575.67	52.33	1.94
Check varieties	3	52.92	17.64	0.65
U.R. varieties	7	505.88	72.27	2.68
U.R. varieties vs. checks	1	16.88	16.88	0.63
ERROR	6	161.83	26.97	

@ The S. S. of Blocks (eliminating treatments) is calculated after taking into consideration the mean effects, check variety effect and block effect. The S.S. of blocks (ignoring treatments) is the usual S.S. of blocks by considering the new accessions as single replicates.
# U.R. - Unreplicated new accessions
*

ADJUSTED VALUES

Treat No.	Block No.	Ch. No.	Obs. value	Adj. value
1	1	1	74.00	77.25
2	1	1	70:00	73.25
3	1	1	75.00	78.25
4	2	1	79.00	77.25
5	2	1	78.00	77.25
6	3	1	96.00	93.50
7	3	1	89.00	86.50
8	3	1	82.00	79.50

STANDARD ERRORS OF DIFFERENCES

FOR CHARACTER NO. (1) :

S.E. BETWEEN ANY 2 REPL. TREAT. : 4.24

S.E. BETWEEN ANY 2 TREAT. IN THE SAME REPL. : 8.21

S.E. BETWEEN ANY 2 UNREPL. TREAT. IN THE SAME REPL. : 8.21

S.E. BETWEEN REPL. TREAT. 9AVERAGED OVER ALL REPL.) AND UNREPL. TREAT. : 6.70

REFERENCES

Federer, W.T. 1956. Augmented (or Hoonuiaku) Designs. *Hawaiian Planter's Record* **55** (2) : 191-208.

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