ACS Publisher

Journal of Extension System

Year 2020, Volume-36, Issue-2 (December)

ISSN 0970-2989 ***(Print)***
ISSN 2582-273X ***(Online)***

Development of Web Based Analysis Tool for Augmented Randomized Complete Block Design (ARCBD)

Vinay Kumar[1], Sarita Rani[2], Ram Niwas[3], O.P. Sheoran[4], *and* Komal Malik[5]

[1,2,3]Assistant Professor, [4]Professor, Department of Mathematics and Statistics CCS HAU, Hisar-125004, [5]Assistant Professor, Govt. College Nalwa, Hisar-125004

ARTICLE INFO

Keywords: Block design, Augmented Design, Fixed effect model, Random effect model.

ABSTRACT

In biological and field experiments, the Augmented Randomized Complete Block Design (ARCBD) is widely used for screening and selection of a large number of germplasm lines/ varieties/entries/test treatments with non replicated test treatments and replicated control treatments to estimate the experimental error. A web based online module for analysis of ARCBD was developed using scripting language Active Server Pages (ASP) based on server client architecture. The data have been taken from Federer (1956) and output compared accordingly. The outputs produced by the module are in agreement with the output generated from SAS package. An attempt was made to provide a user friendly interface for entering/ pasting the data, characters names, number of observations and number of characters for analysis of augmented randomized complete block design. The module produces different output tables such as check x block table, block effects, control means and control effects, adjusted mean for test genotypes and genotypic effects. It also computes sum of squares in the analysis of variance tables after ignoring/eliminating treatment and eliminating/ignoring blocks for block and treatment effects, respectively. Critical difference table for comparing different mean differences at 5% and 1% level of significance is also given. A complete procedure is also provided in the help file to make a user friendly interface for analysis of the design.

Introduction

Experimental Designs plays an important role on establishing an interface between theoretical results and statistical applications in several fields like agriculture, industry and biological experiments. Block designs are useful in experiments requiring eliminations of heterogeneity in one or two direction. Randomized block design (RBD) or any such design becomes inadequate or inefficient under the following two conditions (i) when seeds of test genotypes are small in quantity so that replications are not possible (ii) when large numbers of germplasm collections are to be evaluated limited facility of uniform land becomes a bottleneck. Such a huge collection (in 100's or 1000's) apparently can't be accommodated in randomized block design as soil heterogeneity becomes unmanageable. In absence of error term (error variance) in the Analysis of Variance (ANOVA), without replications, test of significance cannot be applied. However, both these problems can be surmounted by employing Augmented design. These experimental situations may also occur in the fields of entomology, pathology and chemistry, physiology, microbiology

*Corresponding author.
E-mail address: vinay.stat@gmail.com (Vinay Kumar)
Received 20-10-2020; Accepted 19-11-2020

and agronomy and perhaps others for screening experiments on new material and preliminary testing of experiments on promising material. In some other cases (e.g. physics), a single observation on new material may be desirable because of relatively low variability in the experimental material. These types of situations came to be known to Federer around 1955 in screening new strains of sugarcane and soil fumigants used in pineapples.

Analysis and designing for Augmented (Hoonuiaku) designs is available in Federer (1956, 1961), Federer and Raghavarao (1975), Federer, Nair, and Raghavarao (1997), Iram et al. (2017), Morsy et al. (2016), Sharma and Kumari (2015), You et al. (2013).

Methodology and Results

An augmented design is any standard experimental design where control treatments augmented with additional treatments in the complete block, incomplete block, in the row, in the column etc. The blocks in an augmented design may be of unequal size. There are two categories of experimental situations, the material for the tests is scarce and the experimenter cannot afford to replicate the treatments. However, enough material is available for the replications of controls. In second category of experiments, more than one replications of test treatment is possible. In case of test treatments with single replications i.e. for the first type of experiments Federer (1956) proposed three models such as (i) Augmented completely randomized design (Augmented design I), (ii) Augmented randomized complete block design (Augmented design II), Augmented Latin Square Design (Augmented Design III). Additionally, randomized incomplete block designs (RIBD) where a portion of treatments may be included in a small blocks resulting in incomplete blocks layout. Lattice Designs are special cases of incomplete block designs. Alpha and lattice designs are replicated designs. But, augmented designs are suitable for un-replicated treatments.

Secondly, in case of test treatments with many replications, the second type of experiments is in fact a follow up of the first type of experiments. In these types of experiments generally the screenings of experiments for the purpose to identify the promising test treatments is performed. Once these are identified, then a further experimentation is carried out with the tests treatments identified as promising. In these experiments, it is possible to replicate the tests also besides replicating the controls. In this category a standard design (RCB design, BIB design, Latin Square, nested, etc) in test treatments is supplemented with the additional control treatments. Generally all the controls appear together. So, considering the importance of augmented design, web based module for analysis of augmented randomized complete block design is developed for the users and the procedure is described below.

In proposed experiment, online module for analysis of augmented design for randomized complete block design was developed using scripting language ASP (Active Server Pages) based on server client architecture. The module used the techniques described by Federer (1956). The following were the key steps in the modules:

1. Preparation of data submitted for analysis
2. Compute blocks totals for entries, block effect, mean effect and check effects
3. Compute adjusted mean of test varieties and their genotypic effects
4. Computation of sum of squares, mean square, degrees of freedom, F values and p-values of F tests needed for analysis of variance table
5. Compute critical differences to compare various means
6. Display the results in tabular form.

Data arrangement for analysis included the blocks, controls/checks and the entries/varieties coded as 1, 2 & 3 ; C1, C2, C3, C4, …, and V1, V2, V3, … , respectively. These codes in MS Excel as per following criteria:

Table 1 (Field Layout of Augmented Design II)

Blocks	Experimental Units						
	1	**2**	**3**	**4**	**5**	**6**	**7**
1	*V8* (74)	*C3* (78)	*C4* (78)	*V3* (70)	*C1* (83)	*C2* (77)	*V7* *(75)*
2	*C4* (91)	*C2* (81)	*C1* (79)	*C3* (81)	*V1* (79)	*V5* (78)	
3	*V4* (96)	*C3* (87)	*C1* (92)	*V2* (89)	*C4* (81)	*C2* (79)	*V6* (82)

Table 2 Check × Block

	B1	**B2**	**B3**	**Total**
C1	83.000	79.000	92.000	254.000
C2	77.000	81.000	79.000	237.000
C3	78.000	81.000	87.000	246.000
C4	78.000	91.000	81.000	250.000
Total	316.000	332.000	339.000	

Table 3 Block Effects

	R(1)	**R(2)**	**R(3)**
Block Effects	-3.250	0.750	2.500

Table 4 Control Means and Control Effects

	C(1)	**C(2)**	**C(3)**	**C(4)**
Control Mean	84.667	79.000	82.000	83.333
Control Effect	3.604	-2.063	0.938	2.271

a) first column denotes the codes of block number
b) Second column denotes the codes of controls/checks (C1, C2, …) and entries/varieties (V1, V2, ...)
c) Third column contains the observed value of control or variety each character in separate column. For example, if we want to analyze the data on yield, numbers of tillers, numbers of spike lets and root length, then the third column contains the observed data for yield, fourth, fifth and sixth columns contain data for numbers of tillers, numbers of spike lets and root length, respectively.

For testing the validity of results obtained from module, the data have been taken from (Federer, 1956) and output has been compared. The outputs produced by the module are in agreement with the output generated from SAS package.

Table 5 Adjusted Test Genotypes Means/Adjusted Test Treatments

Test Genotype	Observed Mean	Adjusted Mean	Genotype Effect
V1	79.000	78.250	-2.813
V2	89.000	86.500	5.438
V3	70.000	73.250	-7.813
V4	96.000	93.500	12.438
V5	78.000	77.250	-3.813
V6	82.000	79.500	-1.563
V7	75.000	78.250	-2.813
V8	74.000	77.250	-3.813

For illustration purpose, the field layout of Augmented Randomized Complete Block design. The observed data is shown in table 1.

Arrange the data as given below in excel of any text editor

1	C1	83
1	C2	77
1	C3	78
1	C4	78
1	V3	70
1	V7	75
1	V8	74
2	C1	79
2	C2	81
2	C3	81
2	C4	91
2	V1	79
2	V5	78
3	C1	92
3	C2	79
3	C3	87
3	C4	81
3	V4	96
3	V2	89
3	V6	82

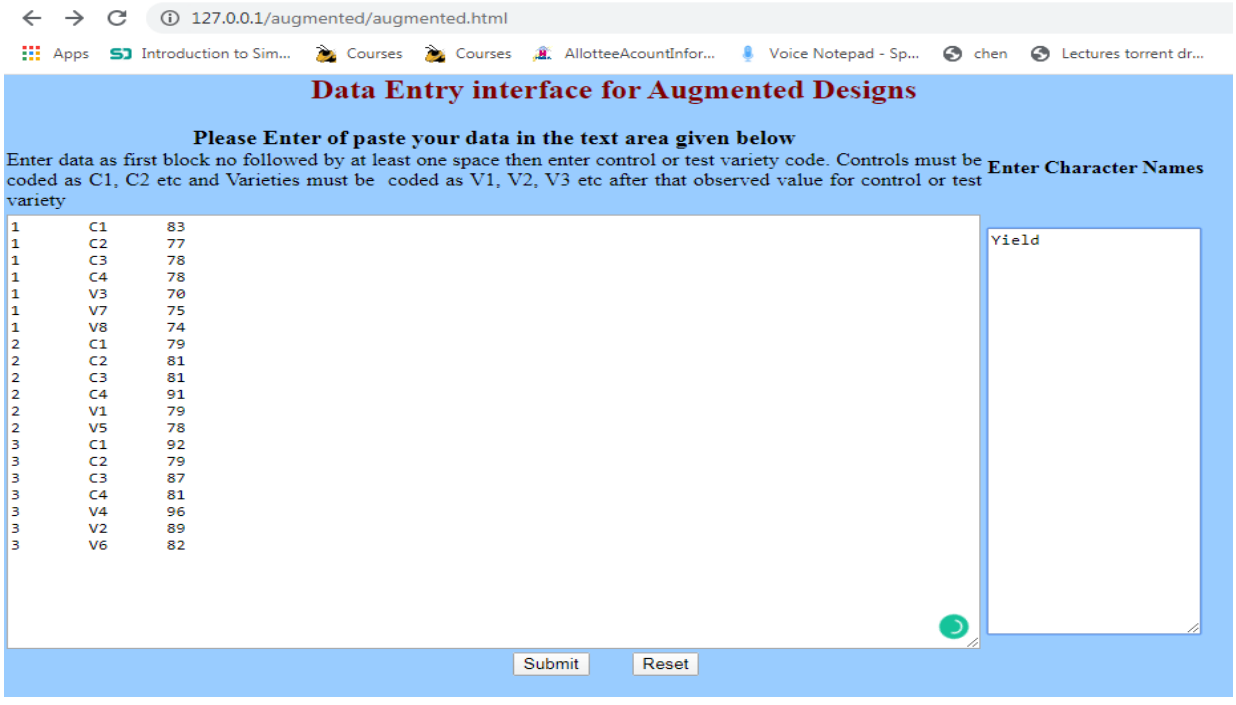

Figure 1 Screenshot of Data Entry Interface

Table 6 For Analysis of Variance

Source of Variation	DF	Sum of Squares	Mean Squares	F-Calculated	Significance
Block (ignoring treatments)	2	360.071	180.036	6.675	0.02981
Treatments (eliminating blocks)	11	285.095	25.918	0.961	0.54992
Checks	3	52.917	17.639	0.654	0.60917
Varieties+ Checks vs. Varieties	8	232.179	29.022	1.076	0.47793
Error	6	161.833	26.972		
Total	19	807.000			

Table 7 Analysis of Variance (Block Adjusted)

Source of Variation	DF	Sum of Squares	Mean Squares	F-Calculated	Significance
Blocks (eliminating treatments)	2	69.500	34.750	1.288	0.34237
Treatment (ignoring blocks)	11	575.667	52.333	1.940	0.21468
Checks	3	52.917	17.639	0.654	0.60917
Varieties	7	505.875	72.268	2.679	0.12526
Check vs Varieties	1	16.875	16.875	0.626	0.45907
Error	6	161.833	26.972		
Total	19	807.000			

Table 8 For Critical Difference

Comparison type	C.D. at 5 %	C.D. at 1 %
Between two Control Mean	10.376	15.721
Between two varieties in same block	17.972	27.230
Between two varieties not in same block	20.093	30.444
Between variety and control	16.406	24.857

Copy the data and paste it in text area provided in the data entry interface. Also enter the character name in the text area for character name as shown in the screenshot

After entering the data and character names press "Submit" button. Once the data is submitted for analysis, results will be displayed on separate new web page……Finally, it shows the output tables such as Table 2,3,4,5, 6,7 and 8.

Conclusion

The present study enlightens the web based analysis module for augmented randomized complete block design when number of seeds is a limitation or a single observation on new material may be desirable because of relatively low variability in the experimental material. Online module for analysis of augmented randomized complete block design is developed using scripting language ASP (Active Server Pages) based on server client architecture. The data have been taken from Federer (1956) and output has been compared. The outputs produced by the module are in agreement with the output generated from SAS package. The module produces different output tables such as check x block table, block effects, control means and control effects, adjusted mean for test genotypes and genotypic effects, sum of squares in the analysis of variance tables after ignoring/eliminating treatment and eliminating/ignoring blocks for block and treatment, respectively, critical difference (C.D.) table for comparing different mean differences at 5% and 1% level of significance with a user friendly, free and easily accessible online at http://14.139.232.166/Augmented/augmentedmain.html

References

Federer, W.T. (1956). Augmented designs. Hawaiian planter record, 55,191-208.

Federer, W. T. (1961). Augmented designs with one way eliminations of heterogeneity. Biometrics, 17, 447-473.

Federer, W. T and Raghavarao D. (1975). On Augmented Designs. Biometrics, 31, 35-39.

Federer, W.T., Nair, R.C. and Raghavarao, D. (1997). Some augmented row-column designs. Biometrics, 31, 361-374.

Iram Saba, Parvaze A. Sofi*, N.A. Zeerak, R.R. Mir and Musharib Gull (2017): Using Augmented Design for Evaluation of Common Bean (Phaseolus vulgaris L.) Germplasm, International Journal of

Current Microbiology and Applied Sciences, Vol. 6(7), 246-254. doi: https://doi.org/10.20546/ijcmas.2017.607.029

Morsy A. R. and Hayam S. A. Fateh (2016): EVALUATION AND SELECTION OF SOYBEAN GENOTYPES FOR YIELD PERFORMANCE USING AUGMENTED DESIGN, https://www.researchgate.net/publication/311856630

Sharma, V., and S. Kumari (2015). Augmented design: Data analysis. Sher-e-Kashmir Univ. of Agric. Sci. and Tech. of Jammu (SKUAST-Jammu), India. 2015-02-04 06:46:35.http://www.biotecharticles.com/AgricultureArticle/Augmented-Design-Data-Analysis-3317.html

You F M, Duguid S D, Thambugala D, Cloutier S (2013). Statistical analysis and field evaluation of the type 2 modified augmented design (MAD) in phenotyping of flax (Linum usitatissimum) germplasms in multiple environments. Aust. J. Crop Sci. 7(11):1789-1800.