AUG1Way- analyses similar trials conducted in augmented designs with one-way blocking system for evaluating a single factor such as genotype. The genotypes are automatically grouped as tests or checks.

This document contents:

1. Title and brief description of the procedure
2. Steps, user is required to follow for using this module

1. Title and brief description of the procedure:

Title: AUG1Way- analyses similar trials conducted in augmented designs with one-way blocking system for evaluating a single factor such as genotype. The genotypes are automatically grouped as tests or checks.

Brief description:

This program analyses similar trials conducted in augmented designs with one-way blocking system for evaluating a single treatment factor such as genotype (W.T. Federer.1961. Augmented designs with one-way elimination of heterogeneity, Biometrics, 17:447-473). The program automatically groups the genotypes as tests (with less than average replications) or as checks (with more than or equal to average replications). The analysis produces a) Regression analyses of variance with a sequential partition of genotype variation into variation due to checks vs. tests, between checks alone, and between tests alone; b) REML (residual/restricted maximum likelihood) estimates for the genotypes best linear unbiased estimates (BLUEs) assuming block effects and genotype effects as fixed, c) REML (residual/restricted maximum likelihood) estimates for the genotypes best linear unbiased predictor (BLUPs) estimates assuming block effects and genotype effects as random. It also produces in a separate file standard error of differences of BLUEs and BLUPs and a list of t-values for significance levels of 0.1%, 1%, 5%, 10% and 20% to aid compute LSDs (least significant differences) for genotypes comparisons.

2. Steps, User is required to follow for using this module:

Step1.

Prepare your data using a familiar data management system, say, MS Excel. For example, the Excel columns are your data on trial number, replications, treatments, yield, plant height etc.

Step 2.

Save the file in Step 1 as a Text file.

Step 3.

Copy the header (top lines of the Sample input-file and paste on the top of your text file).

Step 4.

Read carefully and modify, as indicated in the specific places, these top lines to suit your experimental details (e.g. on the number of trials, replications, treatment levels, variable to be analyzed etc).

Step 5.

Save this file for analysis.

Step 6.

Open the intranet and click the link … GO related to this module.

Step 7.

It will open an email for you. Now you should attach that file and send.

Note:

After processing, the BioComputing system will return you an e-mail containing your data file, and output file(s). The output file may contain errors if your input file is not prepared correctly, or, the data is non-analyzable using the above procedure.