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**GENSTAT PROGRAMS FOR SUMMARY TABLES FROM
RBD AND LATTICE DESIGNS**

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GENSTAT PROGRAMS FOR SUMMARY TABLES FROM RBD AND LATTICE DESIGNS

INTRODUCTION

Data sets from multilocational trials have to be processed as soon after the growing season as possible to allow genotypic assessment over environments. Forming two-way tables with margins for each variable allows this assessment. Since randomized block and lattice designs are often used at ICRISAT Centre and West African centers, programs for these designs have been developed for producing summary tables.

In all programs genotype names and corresponding numbers, yield ranks, percentage of check or percentage of grand mean, standard error, mean and coefficient of variation are presented. The programs also provide means and percentage trial mean with their rankings across all the environments.

All the following programs are available in the sub-directory [BG.MACRO] and it is suggested that scientists wishing to use these programs copy them.

**RANDOMIZED BLOCK DESIGN USING CHECK MEAN FOR
CALCULATING PERCENTAGE OF MEAN**

(RBDCHECK.SUM)

This program is developed for preparing a summary table from a randomized block design. The global identifiers the user has to specify in the program are given below:

| | | |
|--------|---------|---|
| NR | SCALAR | No. of replications |
| NT | SCALAR | No. of treatments |
| NV | SCALAR | No. of variables |
| NTEST | SCALAR | No. of test entries |
| NCHECK | SCALAR | No. of check entries |
| NCMEAN | SCALAR | Check entry number used for calculating percentage of mean |
| CENTRY | VARIATE | check entry numbers |
| TEST | VARIATE | test entry numbers |
| NN1 | NAMES | test entry names |
| NN2 | NAMES | check entry names |

RESTRICTIONS: The data for the yield should be the first variable with other characters following.

Example:

```
'REFE'   RBDCHECK
'UNIT'   $ 75
'SCAL'   NR=3: NT=25: NV=3
'SCAL'   NCHECK=4: NTEST=21
'VARI'   CENTRY=20,21,22,25
'TEST'   TEST=1...19,23,24
'NAME'   NN1=A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,W,X
'NAME'   NN2=T,U,V,Y
'INPU'   2
:
r
'CLOSE'
'STOP'
```

**RANDOMIZED BLOCK DESIGN USING GRAND MEAN FOR
CALCULATING PERCENTAGE OF MEAN**

(RBDMEAN.SUM)

This program is developed for preparing a summary table from a randomized block design. The global identifiers the user has to specify in the program are given below:

| | | |
|--------|---------|----------------------|
| NR | SCALAR | No. of replications |
| NT | SCALAR | No. of treatments |
| NV | SCALAR | No. of variables |
| NTEST | SCALAR | No. of test entries |
| NCHECK | SCALAR | No. of check entries |
| CENTRY | VARIATE | check entry numbers |
| TEST | VARIATE | test entry numbers |
| NN1 | NAMES | test entry names |
| NN2 | NAMES | check entry names |

RESTRICTIONS: The data for the yield should be the first variable with other characters following.

Example:

```
'REFE'      RBDCHECK
'UNIT'      $ 75
'SCAL'      NR=3; NT=25; NV=3
'SCAL'      NCHECK=4; NTEST=21
'VARI'      CENTRY=20,21,22,25
'TEST'      TEST=1...19,23,24
'NAME'      NN1=A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,W,X
'NAME'      NN2=T,U,V,Y
'INPU'      2

'CLOSE'
'STOP'
```

**SUMMARY OF ACROSS ENVIRONMENTS MEAN FROM
RANDOMIZED BLOCK DESIGNS**

(ACROSS.RBD)

This program is designed to make a two-way table of genotypes and environments. The user should define in the program the following identifiers:

| | | |
|--------|---------|----------------------|
| NR | SCALAR | No. of replications |
| NT | SCALAR | No. of treatments |
| NV | SCALAR | No. of variables |
| NCHECK | SCALAR | No. of check entries |
| NTEST | SCALAR | No. of test entries |
| NL | SCALAR | No. of locations |
| CENTRY | VARIATE | check entry numbers |
| TEST | VARIATE | test entry numbers |
| NN1 | NAMES | test entry names |
| NN2 | NAMES | check entry names |

RESTRICTIONS: The yield data should be the first variable in all the files. The data should always go in the replication order (first replication data for all the entries first, 2nd replication next and so on).

Example:

```
'REFE'   RBDCHECK
'UNIT'   $ 75
'SCAL'   NR=3: NT=25: NV=3
'SCAL'   NCHECK=4: NTEST=21 :NL=2
'VARI'   CENTRY=20,21,22,25
'TEST'   TEST=1...19,23,24
'NAME'   NN1=A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,W,X
'NAME'   NN2=T,U,V,Y
'INPU'   2
:
'CLOSE'
'STOP'
```

NOTE: The user has to change the 'PRINT' statements at the end of the program depending on the number of environments. The following statements are for 2 environments.

```
'PRIN/P' .....V(1),R2(1),V(2),R2(2)
:           .....VV(1),R3(1),VV(2),R3(2)
```

Supposing the user has 4 environments, then the 'PRINT' statement will be

```
'PRIN/P' .....V(1),R2(1),V(2),R2(2),V(3),R2(3),V(4),R2(4)
:           .....VV(1),R3(1),VV(2),R3(2),VV(3),R3(3),VV(4),R3(4)
```

TRIPLE/SQUARE LATTICE DESIGNS

(LATTICE.SUM)

This program has been developed to make a summary table of characteristics from triple or square lattice designs with any number of replications. The user has to define in the program the following identifiers:

| | | |
|--------|---------|--|
| NT | SCALAR | No. of treatments |
| NV | SCALAR | No. of variables |
| SREP | FACTOR | Repeat of the design |
| UREP | FACTOR | No. of replications |
| BWR | FACTOR | No. of blocks within replications |
| PLOT | FACTOR | Plots within blocks |
| NCHECK | SCALAR | No. of check entries |
| NTEST | SCALAR | No. of test entries |
| CENTRY | VARIATE | check entry numbers |
| TEST | VARIATE | test entry numbers |
| PRCNT | INTEGER | indicate 1 - if percentage is based on check entry or else 2 if it is on grand mean |
| NCMEAN | SCALAR | check number to be used for calculating percentage of mean; 0 - if the grand mean is taken for percentage. |
| NN1 | NAMES | test entry names |
| NN2 | NAMES | check entry names |

RESTRICTIONS: The data for the yield should be the first variable with other characters following.

```
'REFE' SQLAT
'UNIT' $ 100
'SCAL' NT=25; NR=4; NV=2; NCMEAN=20
'SCAL' NCHCK=4 : NTEST=21
'INTE' PRCNT=1
'VARI' CENTRY=20,21,22,25
'VARI' TEST=1..19,23,24
'NAME' NN1=A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,W,X
'NAME' NN2=T,U,V,Y
'FACT' SREP $ 1=100(1) : UREP $ 4
'FACT' BWR $ 5 : PLOT $ 5=(1..5)20
'FACT' TREAT $ 25
```

```
'CLOSE'
'STOP'
```

**SUMMARY OF ACROSS ENVIRONMENTS MEAN FROM
TRIPLE/SQUARE LATTICE DESIGNS**

(LATTICE.ACR)

This program is designed to make a two-way table of genotypes and environments. The user should define the following identifiers in the program:

| | | |
|--------|---------|-----------------------------------|
| NR | SCALAR | No. of replications |
| NT | SCALAR | No. of treatments |
| NV | SCALAR | No. of variables |
| SREP | FACTOR | Repeat of the design |
| UREP | FACTOR | No. of replications |
| BWR | FACTOR | No. of blocks within replications |
| PLOT | FACTOR | Plots within blocks |
| NCHECK | SCALAR | No. of check entries |
| NTEST | SCALAR | No. of test entries |
| CENTRY | VARIATE | check entry numbers |
| TEST | VARIATE | test entry numbers |
| NN1 | NAMES | test entry names |
| NN2 | NAMES | check entry names |

RESTRICTIONS: The yield data should be the first variable in all the files.

Example:

```
'REFE' SOLAT
'UNIT' $ 100
'SCAL' NT=25: NR=4: NV=2: NL=2
'SCAL' NCHCK=4 : NTEST=21
'VARI' CENTRY=20,21,22,25
'VARI' TEST=1...19,23,24
'NAME' NN1=A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,W,X
'NAME' NN2=T,U,V,Y
'FACT' SREP $ 1=100(1) : UREP $ 4
'FACT' BWR $ 5 : PLOT $ 5=(1...5)20
'FACT' TREAT $ 25
:
'CLOSE'
'STOP'
```

NOTE: The user has to change the 'PRINT' statements at the end of the program depending on the number of environments. The following statements are for 2 environments.

```
'PRIN/P' ..... ,V(1),R2(1),V(2),R2(2)
: ..... ,VV(1),R3(1),VV(2),R3(2)
```

Supposing the user has 4 environments, then the 'PRINT' statement will be

```
'PRIN/P' ..... ,V(1),R2(1),V(2),R2(2),V(3),R2(3),V(4),R2(4)
: ..... ,VV(1),R3(1),VV(2),R3(2),VV(3),R3(3),VV(4),R3(4)
```


