

Working Draft

Not to be Cited

Computing Biometrics at ICARDA

Volume I

**Compiled by M. Singh
Computer and Biometrics Services Unit
ICARDA**



**International Center for Agricultural Research in the Dry Areas
P. O. Box 5466, Aleppo, Syria**

January 1994

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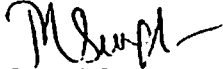
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0. Introduction

Biometric consultations often lead to the exploration of secrets of data using a number of computing biometric tools. During the course of scientist-biometrician interactive sessions, a number of computing biometric modules for specialized applications were sorted out. This volume contains ten such modules. It also has a number of modules for generating the most commonly used experimental designs. For each module, we provide brief sections on introduction, areas of application, keywords, input/output, location of program, location of sample data and results, client(s), etc. Outputs running over large number of pages are not included in this document. However, they are available on a diskette.

Anyone interested in these programs is most welcome to ask for a copy of the programs and may also share them with other researchers, particularly working with National Agricultural Research Systems in West Asia and North Africa.

These programs are written in Genstat, but volunteers are most welcome to code them in other computing languages as well.


Murari Singh
Sr. Biometrician

26 January 1994
Tel Hadya, Aleppo

**Computer and Biometrics Services Unit
ICARDA**

Serial Number -001

GENSTAT Modules in Computing Biometrics

Title: Analysis of multi-locational trials conducted in randomized complete blocks

1. Introduction:

This program analyses data from multi-locational variety trials conducted in randomized complete blocks. It displays individual location data analysis, combined analysis of variance to evaluate GxE interaction, Partitions GxE in heterogeneity of linear regressions, computes stability indices, clustering of environments and of genotypes and estimates of variance components for genotypes, GxE interaction and plots.

2. Areas of application and keywords:

Plant breeding and genetics, Physiology, Crop improvement.

Multi-locational varietal trials, combined analysis of variance, GxE interactions, stability indices, heterogeneity of regressions, clustering, variance components.

3. Input/Output:

Input:

Plot-wise values of replications, genotypes, locations levels, yield variable(s).

Output:

Individual location ANOVA, means, se, %cv, combined analysis of variance, partitioning of GxE interaction in heterogeneity of linear regressions, stability indices, clustering of environments and of genotypes, estimates of variance components for genotypes, GxE interaction and plots.

4. Location of the program:

Program:

A:\CompBiom\93\MLVT1.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\MLVT1.Txt

Results:

A:\CompBiom\93\MLVT1.opt

6. Client(s)

All plant breeders at ICARDA

7. Date

January 1994

8. Comments

M. Singh

Program:

```
*****  
      GENSTAT program for analyzing multi-locational variety trials  
      conducted in randomized complete blocks.  
*****
```

```
OPEN 'MLVT1.Txt';CH=2;FI=IN  
Scalar Nlines  
Read[ch=2]Nlines  
Skip[ch=2] Nlines  
Scal NRep, NGeno,NLoc  
Read [ch=2] NRep,NGeno,NLoc
```

```
Scal NObs, NGxNL  
Calc NObs=NGeno*NLoc*NRep  
Calc NGxNL=NGeno*NLoc
```

```
Unit [NObs]
```

```
Fact [Leve=NGeno] Geno  
Fact [Leve=NLoc] Loc  
Fact [Leve=NRep] Rep  
Read [Ch=2] Rep,Geno,Loc,Yield
```

```
* ===== Below is only for statistical programmers use ===== *
```

```
* 1. Individual locations analysis *
```

```
Bloc Rep/Loc  
Trea Geno
```

```
Vari[Nval=NGeno] Mean[1...NLoc], GenoMean
```

```
For I=1...NLoc ; MN=Mean[1...NLoc]  
Rest Yield; Cond=Loc.EQ.I  
Anov [Prin=A;SE=M;Fpro=Y] Yield  
Akeep Geno; Means=TDum  
Equa TDum;MN  
Dele[Rede=Y] TDum  
Rest Yield  
Endf
```

```
Vari[Nval=NLoc] LocMean
```

" 2. Combined ANOVA over locations "

Bloc Loc/Rep/Geno
Trea Geno*Loc
Anov [Print=A;SE=M;FPRO=Y] Yield
Akeep Geno;Means=TDum
Equa TDum; GenoMean
Dele[Rede=Y] TDum

Akeep Loc; Means=TDum
Equa TDum; LocMean
Dele[Rede=Y] TDum

Fact[Leve=NGeno; Valu=1...NGeno] GenoNum
Prin GenoNum,Mean[1...NLoc],GenoMean; field=7
Prin[orie=a] LocMean ;fiel=7

" 3. Partition GxE Int in heterogeneity of linear regressions"

Trea Geno*Pol(Loc;1;LocMean)
Anov [Print=A;SE=M;FPRO=Y] Yield

" 4. Compute stability indices "

Vari[nvalu=NGeno] GenoCV
Calc GenoCV=100.*Sqrt(Vvar(IP(Mean[1...NLoc])))/GenoMean

Matr [Rows=NGeno; Colu=NLoc] GE : & [Rows=NLoc; Colu=NGeno] EG
Equa IP(Mean[1...NLoc]); EG
Calc GE=Tran(EG)

Vari[Nval=NLoc] GMean[1...NGeno]
Equa GE; IP(GMean[1...NGeno])

Dele GE, EG

Vari[Nval=NGxNL] GEData
Equa IP(Mean[1...NLoc]); GEData

Vari[Nval=NGeno] Slope,DeviMs, Wricke,Pla_Pet,Plaisted, Shukla

For I=1...NGeno ; Y=GMean[1...NGeno]
Model Y ; Fitt=F
Fit[prin=*] LocMean
RKeep ; Est=Est ; Devi=SS ; DF=df
Calc Slope\${I} =Est \${2} : & DeviMs \${I} =SS/df

"

Graph Y,F; LocMean; symb='o','.'; Meth=p,c

▪
Endf

Fact[Leve=NGeno; Nval=NGxNL] Geno1
Fact[Leve=NLoc; Nval=NGxNL] Loc1
Vari[Nval=NGxNL] GEInt

Gene Loc1, Geno1
Bloc
Trea Loc1+Geno1
Anov GEData; Res=GEInt

Dele GEData

Calc GEInt=GEInt*GEInt
Tabu [Class=Geno1] GEInt; Tota=TDum

Equa TDum; Wricke
Dele[Rede=Y] TDum

Scal SsGE
Calc SsGE=Sum(Wricke)

Calc Pla_Pet=(NGeno*Wricke+SsGE)/(2*(NGeno-1)*(NLoc-1))
Calc Plaisted=(-NGeno*Wricke/(NGeno-1)+SsGE)/((NGeno-2)*(NLoc-1))
Calc Shukla = (NGeno*Wricke - SsGE/(NGeno-1))/(NGeno-2)/(NLoc-1)

▪ Correlation between indices ▪
Corr[Print=c] GenoMean, Slope, DeviMs,GenoCV,Wricke,Pla_Pet,Plaisted,Shukla
Print GenoNum, GenoMean, Slope, DeviMs,GenoCV,Wricke,Pla_Pet,Plaisted,Shukla

Graph Slope; GenoMean; Symb=GenoNum
Graph GenoCV; GenoMean; Symb=GenoNum
Graph DeviMs; GenoMean; Symb=GenoNum
Graph Wricke; GenoMean; Symb=GenoNum

Vari[nval=NGeno]RGenoMn,RSlope,RDeviMs,RGenoCV,RWricke,RPla_Pet,RPlaist,RShukla

For D= GenoMean, Slope, DeviMs,GenoCV,Wricke,Pla_Pet,Plaisted,Shukla ; \
DD= RGenoMn, RSlope, RDeviMs,RGenoCV,RWricke,RPla_Pet,RPlaist,RShukla
Sort[dire=d; Groups=f] D
Calc DD=Int(f)
endf

▪ Correlations between ranks ▪
Corr[Prin=c]RGenoMn, RSlope, RDeviMs,RGenoCV,RWricke,RPla_Pet,RPlaist,RShukla

▪ 5. Clustering of Environments ▪

Symm[Rows=NLoc] Simi

```
Scal Type;5  
Fsim[Simi=Simi] GMean[1...NGeno]; Test=Type  
Hclu[ Prin=a,d] Simi  
Dele[Rede=Y] Simi
```

*** 6. Clustering of Genotypes ***

```
Symm[Rows=NGeno] Simi  
Scal Type;5  
Fsim[Simi=Simi] Mean[1...NLoc]; Test=Type  
Hclu[ Prin=a,d] Simi  
Dele[Rede=Y] Simi
```

*** 7. Estimation of variance components***

```
Vcom[Fix=Loc] Loc+Loc.Rep+Geno+Loc.Geno  
REML Yield
```

```
Clos  
Stop
```

GENSTAT Modules in Computing Biometrics

Title: Path coefficients analysis

1. Introduction:

This program performs the path analyses to evaluate direct and indirect contributions of correlated variables on a dependent variable.

2. Areas of application and keywords:

Plant breeding and genetics, Physiology, Crop improvement.
Path analysis, direct and indirect effects.

3. Input/Output:

Input:

Values of explanatory variable(s) and variable to be explained over a number of genotypes or experimental units.

Output:

Correlation matrix, vector of path coefficients, matrix of direct and indirect effects in correlation, contribution of direct and indirect effects in variation.

4. Location of the program:

Program:

A:\CompBiom\92\Path.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\Path.Txt

Results:

A:\CompBiom\93\Path.Out

6. Client(s)

All plant breeders at ICARDA

7. Date

January 1993

8. Comments

M. Singh

Program:

Path Coefficient Analysis

Scalar NObs, NVar, 42, 6
Scalar NXVar
Calc NXVar=NVar-1
UNITS [NObs]
OPEN 'PATH.TXT'; CH=2; FILETYPE=INPUT

* There are 6 variables V[1...6] where V[6] is dependent on other V[1...5]
variables which are correlated themselves *

READ [CH=2; Form=1(-4,6)] V[1...NVar]

SYMM[ROWS=NVar]RXPY
SYMM[ROWS=NXVar] RXX
VARI [NVALUES=NXVar] RXY,PATH
DIAG[ROWS=NXVar] DPATH
MATR[ROWS=NXVar;COLU=NXVar]MRXY

SSPM[TERMS=V[1...NVar]] SSPM;RXPY
FSSPM[PRINT=C] SSPM
CALC RXPY=CORR(RXPY)
EQUA RXPY;IP(RXX,RXY)
CALC PATH=PROD(INV(RXX);RXY)
EQUA PATH;DPATH
CALC MRXY=PROD(RXX;DPATH)

PRINT ' Correlations ', RXPY
PRINT ' Correlations and Path coefficients ', RXY,PATH
PRINT ' Decomposition of correlation into direct and indirect effects', MRXY

CALC MRXY=PROD(DPATH;RXX)
CALC MRXY=PROD(MRXY;DPATH)
CALC MRXY=2*MRXY-DPATH*DPATH
SCAL RESS
CALC RESS = 1-SUM(RXY*PATH)

PRINT ' Contribution of direct and indirect effects in variability',MRXY
PRINT ' Contribution of Residuals in variability', RESS

CLOS
STOP

Output:

Genstat 5 Release 2.2 (Vax/VMS5) 24-JAN-1994 14:10:25.76
 Copyright 1990, Lawes Agricultural Trust (Rothamsted Experimental Station)

```

1 *****
-2
-3           Path Coefficient Analysis
-4
-5 *****
6
7 Scalar NObs, NVar; 42, 6
8 Scalar NXVar
9 Calc NXVar=NVar-1
10 UNITS [NObs]
11 OPEN 'PATH.TXT'; CH=2; FILETYPE=INPUT
12
13 " There are 6 variables V[1...6] where V[6] is dependent on other V[1...5]
-14 variables which are correlated themselves "
15
16 READ [CH=2; Form=!(4,6)] V[1...NVar]
  
```

Identifier	Minimum	Mean	Maximum	Values	Missing
V[1]	82.3	131.1	172.5	42	0
V[2]	103.0	123.0	166.0	42	0
V[3]	6.15	11.92	19.72	42	0
V[4]	11.00	17.76	25.00	42	0
V[5]	14.90	23.44	38.10	42	0
V[6]	0.0	627.6	12312.0	42	0 Skew

```

17
18
19
20 SYMM[ ROWS=NVar]RXPY
21 SYMM[ ROWS=NXVar] RXX
22 VARI [ NVALUES=NXVar] RXY,PATH
23 DIAG[ROWS=NXVar] DPATH
24 MATR[ ROWS=NXVar;COLU=NXVar]MRXY
25
26 SSPM[TERMS=V[1...NVar] ] SSPM;RXPY
27 FSSPM[PRINT=C] SSPM
  
```

*** Degrees of freedom ***

Correlations: 40

*** Correlation matrix ***

V[1]	1	1.000		
V[2]	2	0.536	1.000	
V[3]	3	-0.008	-0.119	1.000

```
V[4]      4 0.545 0.777 0.083 1.000
V[5]      5 0.424 0.751 -0.082 0.753 1.000
V[6]      6 0.213 0.167 0.004 0.280 0.356 1.000
```

```
      1 2 3 4 5 6
```

```
28 CALC RXPY=CORR(RXPY)
29 EQUA RXPY;IP(RXX,RXY)
30 CALC PATH=PROD(INV(RXX);RXY)
31 EQUA PATH;DPATH
32 CALC MRXY=PROD(RXX;DPATH)
33
34 PRINT ' Correlations ', RXPY
```

Correlations

RXPY

1	1.0000					
2	0.5357	1.0000				
3	-0.0084	-0.1189	1.0000			
4	0.5445	0.7765	0.0833	1.0000		
5	0.4239	0.7512	-0.0823	0.7527	1.0000	
6	0.2127	0.1672	0.0036	0.2803	0.3562	1.0000
	1	2	3	4	5	6

```
35 PRINT ' Correlations and Path coefficients ', RXY,PATH
```

Correlations and Path coefficients

RXY	0.2127	0.1672	0.0036	0.2803	0.3562
PATH	0.1340	-0.3673	-0.0123	0.1415	0.4679

```
36 PRINT ' Decomposition of correlation into direct and indirect effects', MRXY
```

Decomposition of correlation into direct and indirect effects

MRXY

	1	2	3	4	5
1	0.1340	-0.1968	0.0001	0.0770	0.1983
2	0.0718	-0.3673	0.0015	0.1099	0.3515
3	-0.0011	0.0437	-0.0123	0.0118	-0.0385
4	0.0730	-0.2852	-0.0010	0.1415	0.3522
5	0.0568	-0.2759	0.0010	0.1065	0.4679

```
37
```

```
38 CALC MRXY=PROD(DPATH;RXX)
```

```

39 CALC MRXY=PROD(MRXY;DPATH)
40 CALC MRXY=2*MRXY-DPATH*DPATH
41 SCAL RESS
42 CALC RESS = 1-SUM(RXY*PATH)
43
44 PRINT ' Contribution of direct and indirect effects in variability',MRXY

```

Contribution of direct and indirect effects in variability

	MRXY				
	1	2	3	4	5
1	0.01795	-0.05272	0.00003	0.02064	0.05314
2	-0.05272	0.13492	-0.00107	-0.08071	-0.25820
3	0.00003	-0.00107	0.00015	-0.00029	0.00094
4	0.02064	-0.08071	-0.00029	0.02002	0.09965
5	0.05314	-0.25820	0.00094	0.09965	0.21890

```

45 PRINT ' Contribution of Residuals in variability', RESS

```

RESS

Contribution of Residuals in variability 0.8267

```

46
47 CLOS
48 STOP

```

***** End of job. Maximum of 15108 data units used at line 32 (34606 left)

GENSTAT Modules in Computing Biometrics

Title **Testing parallelism of linear regressions**

1. Introduction:

This program performs the linear regression analyses to compare the parallelism of regression lines over levels of a factor.

2. Areas of application and keywords:

Agronomy, Micro-biology, Physiology, Crop improvement.
Comparison of slopes and intercepts.

3. Input/Output:

Input:

Values of levels of the factor (over which the regression lines would be compared), values of independent (or X) variable and of dependent (or Y) variable for each unit.

Output:

Accumulated analysis of variance, estimates of intercepts and slopes, tests for equality of slopes and equality of intercepts.

4. Location of the program:

Program:

A:\CompBiom\92\Parallel.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

(Simulated inside the program)

Results:

A:\CompBiom\93\Parallel.Out

6. Client(s)

Dr. P. White, PFLP

7. Date

January 1993

8. Comments

M. Singh

Program:

Comparing slopes and intercepts of Y on X over levels of a factor

Scalar NObs, NLevel; 40, 4

UNITS [NObs]

FACT[LEVE=NLevel; VALU=10(1...NLevel)] GENO

CALC X=URAN(564328)

CALC Y=URAND(97654391)+3.4*URAN(431)*URAN(321)

* in above X and Y are generated but in actual practice you will read values in them"

SCAL SS0,SS1,SS2,MS0,DF0,DF1,DF2,DFSLOPE,DFINT,FSLOPE,PRSLOPE,FINT,PR_INT

MODEL Y

TERMS[FULL=Y] GENO/X

FIT [CONS=0; PRINT=m,s,e,a] GENO/X

RKEEP DF=DF0; DEVI=SS0

CALC MS0=SS0/DF0

"

Test of slope equivalence. FIT a common slope.

"

TERMS GENO*X

FIT X+GENO

RKEEP DF=DF1; DEVI=SS1

CALC DFSLOPE=DF1-DF0

CALC FSLOPE=(SS1-SS0)/DFSLOPE/MS0

CALC PRSLOPE=1-FPRO(FSLOPE;DFSLOPE;DF0)

PRINT DFSLOPE, DF0, FSLOPE,PRSLOPE

"

TEST FOR INTERCEPT DIFFERENCES

"

FIT X+X.GENO

RKEEP DF=DF2; DEVI=SS2

CALC DFINT=DF2-DF0

CALC FINT=(SS2-SS0)/DFINT/MS0

CALC PR_INT=1-FPRO(FINT;DFINT;DF0)

PRINT DFINT, DF0, FINT,PR_INT

CLOSE

STOP

Output:

Genstat 5 Release 2.2 (Vax/VMS5) 24-JAN-1994 14:19:45.88
Copyright 1990, Lawes Agricultural Trust (Rothamsted Experimental Station)

```
1 *****  
-2 Comparing slopes and intercepts of Y on X over levels of a factor  
-3 *****  
4  
5 Scalar NObs; 40  
6 UNITS [NObs]  
7 FACT[LEVE=4; VALU=10(1...4)] GENO  
8 CALC X=URAN(564328)  
9 CALC Y=URAND(97654391)+3.4*URAN(431)*URAN(321)  
10 * in above X and Y are generated but in actual practice you will read values  
-11 in them"  
12  
13 SCAL SS0,SS1,SS2,MS0,DF0,DF1,DF2,DFSLOPE,DFINT,FSLOPE,PRSLOPE,FINT,PR_INT  
14  
15 MODEL Y  
16 TERMS[FULL=Y] GENO/X  
17 FIT [CONS=O; PRINT=m,s,e,a] GENO/X
```

17.....

***** Regression Analysis *****

Response variate: Y
Fitted terms: GENO + X.GENO

*** Summary of analysis ***

	d.f.	s.s.	m.s.	v.r.
Regression	8	8.375	1.04689	11.36
Residual	32	2.949	0.09215	
Total	40	11.324	0.28310	
Change	-7	-0.509	0.07273	0.79

Residual variance exceeds variance of Y variate

* MESSAGE: The following units have high leverage:
16 0.54

*** Estimates of regression coefficients ***

	estimate	s.e.	t
GENO 1	0.339	0.186	1.83
GENO 2	0.372	0.211	1.77
GENO 3	-0.079	0.447	-0.18
GENO 4	0.593	0.229	2.60
X.GENO 1	0.250	0.290	0.86
X.GENO 2	-0.093	0.408	-0.23
X.GENO 3	0.840	0.606	1.39
X.GENO 4	-0.276	0.379	-0.73

*** Accumulated analysis of variance ***

Change	d.f.	s.s.	m.s.	v.r.
- Constant	-1	-7.86604	7.86604	85.37
+ GENO	4	8.07571	2.01893	21.91
+ X.GENO	4	0.29944	0.07486	0.81
Residual	32	2.94865	0.09215	
Total	39	3.45777	0.08866	

18 RKEEP DF=DF0; DEVI=SS0
19 CALC MS0=SS0/DF0

20 "
 -21 Test of slope equivalence. FIT a common slope.
 -22 "
 23
 24 TERMS GENO*X
 25 FIT X+GENO

25.....

***** Regression Analysis *****

Response variate: Y
 Fitted terms: Constant + X + GENO

*** Summary of analysis ***

	d.f.	s.s.	m.s.	v.r.	
Regression	4	0.236	0.05891	0.64	
Residual	35	3.222	0.09206		
Total	39	3.458	0.08866		
Change	-4	-0.236	0.05891	0.64	

Residual variance exceeds variance of Y variate

*** Estimates of regression coefficients ***

	estimate	s.e.	t
Constant	0.421	0.142	2.97
X	0.101	0.190	0.53
GENO 2	-0.138	0.137	-1.01
GENO 3	0.033	0.140	0.24
GENO 4	-0.034	0.136	-0.25

26 RKEEP DF=DF1; DEVI=SS1
 27 CALC DFSLOPE=DF1-DF0
 28 CALC FSLOPE=(SS1-SS0)/DFSLOPE/MS0
 29 CALC PRSLOPE=1-FPRO(FSLOPE;DFSLOPE;DF0)
 30 PRINT DFSLOPE, DF0, FSLOPE,PRSLOPE

DFSLOPE	DF0	FSLOPE	PRSLOPE
3.000	32.00	0.9893	0.4102

31
 32 "
 -33 TEST FOR INTERCEPT DIFFERENCES
 -34 "
 35 FIT X+X.GENO

35.....

***** Regression Analysis *****

Response variate: Y

Fitted terms: Constant + X + X.GENO

*** Summary of analysis ***

	d.f.	s.s.	m.s.	v.r.
Regression	4	0.327	0.08182	0.91
Residual	35	3.130	0.08944	
Total	39	3.458	0.08866	
Change	-4	-0.327	0.08182	0.91

Residual variance exceeds variance of Y variate

* MESSAGE: The following units have high leverage:
16 0.40

*** Estimates of regression coefficients ***

	estimate	s.e.	t
Constant	0.385	0.113	3.40
X	0.188	0.211	0.89
X.GENO 2	-0.304	0.239	-1.27
X.GENO 3	0.037	0.195	0.19
X.GENO 4	-0.151	0.216	-0.70

36 RKEEP DF=DF2; DEVI=SS2
37 CALC DFINT=DF2-DF0
38 CALC FINT=(SS2-SS0)/DFINT/MS0
39 CALC PR_INT=1-FPRO(FINT;DFINT;DF0)
40 PRINT DFINT, DF0, FINT,PR_INT

DFINT	DF0	FINT	PR_INT
3.000	32.00	0.6578	0.5841

41
42 CLOSE
43 STOP

***** End of job. Maximum of 14622 data units used at line 24 (35092 left)

**Computer and Biometrics Services Unit
ICARDA**

Serial Number - 004

GENSTAT Modules in Computing Biometrics

Title: Fitting genetic ratios

1. Introduction:

This program fits genetic ratios to the categories (representing values of qualitative traits) created by the effects of major genes. It fits the specified genetic ratios to the phenotypic frequencies observed in

- i. two categories,
- ii. three categories and
- iii. four categories.

2. Areas of application and keywords:

Plant breeding and genetics
Genetic ratios, Chi-square

3. Input/Output:

Input:

Frequencies in the categories

Output:

Expected frequencies, chi-squares, probabilities

4. Location of the program:

Program:

A:\CompBiom\93\ratio.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\ASCROS6.TXT

Results:

A:\CompBiom\93\ASCROS6.OPT

6. Client(s)

Mr. M. Labdi, LP

7. Date

December 1993

8. Comments

M. Singh

Program:

Unit{313}

Open 'Ascros6.txt' ; ch=2; fi=in

Fact[leve=7; labe=l(P1,P2,F1,F2,BC1,BC2,CHK)] Gen
Read[ch=2; form=l(-1,1,-2,3)]Gen,SC15,SC21,SC21%; frep=La

" Cases of two classes "

SCAL Ncases; 9

Vari[valu=1...Ncases]Case

Vari[nval=Ncases] R,S,RPS, NR,NS,N, Chi1,Chi2,Pr1,Pr2

Read R,S

1 3 13 3 9 7 15 1 55 9 63 1 37 27 25 39 11 5 :

Calc RPS=R+S

For Y=SC21,SC15,SC21% ; dd=4,4,40

Rest Y; cond=Gen.eq.4

Calc NR=Sum(Y.le.dd) : & N=Nobs(Y) : & NS=N-NR

Calc Chi1=((NR-N*R/RPS)**2)/(N*R/RPS)+((NS-N*S/RPS)**2)/(N*S/RPS)

Calc Chi2=(RPS/N/S)*(NR-N*S/RPS)**2+(RPS/N/R)*(NS-N*R/RPS)**2

Calc Pr1=1-Chisq(Chi1;1): Calc Pr2=1-Chisq(Chi2;1)

Print Case,R,S,NR,NS,N,Chi1,Pr1,Chi2,Pr2 ; fiel=3(4),7(9); deci=6(0),4(4)

Endf

dele R,S,RPS, NR,NS, Chi1,Chi2,Pr1,Pr2

" Case of three classes "

SCAL Ncases; 5

Vari[valu=1...Ncases]Case

Vari[nval=Ncases] R1,R2,R3, R,N1,N2,N3,N,Prob, Chi

Read R1,R2,R3

12 3 1 7 8 1 9 16 39 9 6 1 9 3 4

:

Calc R=R1+R2+R3

For Y=SC21,SC15,SC21% ; d1=4,4,40 ; d2=6,6,60

Rest Y; Cond=Gen.eq.4

Calc N1=Sum(Y.le.d1): & N3=Sum(Y.gt.d2): & N=Nobs(Y): & N2=N-N1-N3

Calc Chi=(R/N/R1)*(N1-N*R1/R)**2+(R/N/R2)*(N2-N*R2/R)**2+(R/N/R3)*(N3-N*R3/R)**2

Calc Prob=1-chisq(Chi;2)

Prin Case,R1,R2,R3,N1,N2,N3,N,Chi, Prob; fiel=8(6),2(9); deci=8(0),2(4)

Endf

" Case of four classes "

SCAL Ncases; 3

Vari[valu=1...Ncases]Case

Vari[nval=Ncases] R1,R2,R3,R4, R,N1,N2,N3,N4,N,Prob, Chi

Read R1,R2,R3,R4

9 3 3 1 27 9 9 9 27 27 9 1

:

Calc R=R1+R2+R3+R4

For Y=SC21,SC15,SC21% ; d1=3,3, 20; d2=4,4,40; d3=6,6,60

Rest Y; Cond=Gen.eq.4

Calc N1=Sum(Y.le.d1): & N2=Sum(Y.gt.d1.and.Y.le.d2)

Calc N4=Sum(Y.gt.d3): & N=Nobs(Y): & N3=N-N1-N2-N4

Calc Chi=(R/N/R1)*(N1-N*R1/R)**2+(R/N/R2)*(N2-N*R2/R)**2+ \
(R/N/R3)*(N3-N*R3/R)**2+(R/N/R4)*(N4-N*R4/R)**2

Calc Prob=1-chisq(Chi;3)

Prin Case,R1,R2,R3,R4,N1,N2,N3,N4,N,Chi, Prob; fiel=10(5),2(9); deci=10(0),2(4)

Endf

clos

stop

**Computer and Biometrics Unit
ICARDA**

Serial Number -005

GENSTAT Modules in Computing Biometrics

Title: Estimation of genetic components of generation means

1. Introduction:

This program fits models to estimate components m , d , h , i , j and l of generation means using data from the parents, F1, F2 and backcross families. It facilitates joint scaling tests and selection of genetic models.

2. Areas of application and keywords:

Plant breeding and genetics
Components of generation means, joint scaling tests, genetic modelling

3. Input/Output:

Input:

Plant-wise data from the six families (P1,P2,F1,F2,BC1, BC2) of a cross evaluated in blocks.

Output:

Models; analysis of deviation; estimates of parameters.

4. Location of the program:

Program:

A:\CompBiom\93\mdh.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\ASCROS6.TXT

Results:

A:\CompBiom\93\mdh6.OPT

6. Client(s)

Mr. M. Labdi, LP

7. Date

December 1993

8. Comments

M. Singh

Program:

Unit[313]

Open 'AScros6.txt'; ch=2; fi=in

```
Fact[leve=7; labe=lt(P1,P2,F1,F2,BC1,BC2,CHK)] Gen
Fact[Leve=2] Rep : & [leve=5]Plant :&[leve=20] Pot
Vari[Nval=6]Mean,DF,SS, Wet, SE
Vari[valu=6(1)] M : &[valu=1,-1,0,0,5,-.5] D :&[valu=0,0,1,.5,.5,.5]H
Vari[valu=2(1,0,.25)] I:&[valu=4(0),.25,-.25]J:&[valu=0,0,1,3(.25)]L
Print M,D,H,I,J,L
Text[values=P1,P2,F1,F2,BC1,BC2] Family
Read[ch=2]Rep,Gen,Pot,Plant,SC15,SC21,SC21%; frep=Le,La,le,le
```

```
For Y=SC21,SC21%,SC15
```

```
For i=1...6
```

```
Print 'Generation Number is =', i
```

```
Rest Y ; cond=Gen.eq.i
```

```
Hist Y
```

```
Bloc Rep/Pot/Plant
```

```
Anov[prin=a] Y
```

```
Akeep Terms=Rep.Pot.Plant; ss=ss;df=df
```

```
Calc Mean[i]=Mean(Y); & DF[i]=df :& SSS[i]=ss
```

```
Calc Wet[i]=Nobs(Y)/(ss/df)
```

```
Rest Y
```

```
Endf
```

```
Calc SE=1/Sqrt(Wet)
```

```
Print Family,Mean,SE,Wet, DF,SS
```

```
Model[Weight=Wet; Disp=1] Mean
```

```
Terms [Full=y] M,D,H,I,J,L
```

```
Fit[ cons=o; fprob=y;tprob=y]M
```

```
Add D : & H : & I : & J : & L
```

```
Fit[Cons=O;Fpro=Y;Tprob=Y] M,D,H,J
```

```
Add L
```

```
Fit[Cons=O;Fpro=Y;Tprob=Y] M,D,H,L
```

```
Fit[Cons=O;Fpro=Y;Tprob=Y] M,D,H,I,L
```

```
Fit[ cons=o; fprob=y;tprob=y]M
```

```
Add H
```

```
Endf
```

```
Clos
```

```
Stop
```

**Computer and Biometrics Services Unit
ICARDA**

Serial Number-006

GENSTAT Modules in Computing Biometrics

Title: Estimation of heritability from a single environment trial

1. Introduction:

This program computes estimate of heritability (in broad sense) from a single variety trial conducted in blocks. It provides an estimate of its asymptotic standard error.

2. Areas of application and keywords:

Plant breeding and genetics

Heritability in broad sense, standard error, incomplete blocks

3. Input/Output:

Input:

Plot-wise values of replications, blocks, genotypes and traits

Output:

Estimates of variance components (for plots, blocks within replication, genotypes), heritability and standard error.

4. Location of the program:

Program:

A:\CompBiom\93\Herit1.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\Herit1.txt

Results:

A:\CompBiom\93\Herit1.opt

6. Client(s)

Dr. S. Ceccarelli, CP

7. Date

January 1994

8. Comments

M. Singh

Program:

UNIT[50]

***** Heritability from a single trial ***** *

* ***** 1. Declare various structures *****

```
FACT[LEV=2] Rep :& [Lev=5]Blk : &[Lev=25]Geno
SCAL SGg2,SGe2,h2
Scal Vgg,Vge,Vee,Bias, Seh2
symm[3] Vcov
symm[2] Vcov_r
```

* ***** 2. Read data values *****

```
OPEN 'Herit1.TXT';CH=2;FI=IN
READ[CH=2;END=*; Form=!(5,-34)] Rep,Blk,Geno,CY[1...2]
```

```
FOR Y=CY[1...2]
```

* Using incomplete block design: block effects random *

* ***** 3.1 Compute variance components *****

```
VCOMP[fixed=Rep] RANDOM=Rep/Blk+Geno
REML[print=*] Y
```

* ***** 3.2 Compute heritability and its SE *****

```
VKEEP[SIGMA2=SGe2;vcov=Vcov] Geno; COMP=SGg2
CALC Vgg,Vge,Vee=Vcov$(2,3,3; 2,2,3)
CALC h2=SGg2/(SGg2+SGe2)
CALC One_h22=(1-h2)**2
CALC Bias=One_h22*((1-h2)*Vgg-h2*Vge)/(h2*SGe2*SGe2)
CALC Seh2=(1-h2)*SQRT(One_h22*Vgg-2*h2*(1-h2)*Vge+Vee*h2**2)/SGe2
```

* ***** 3.3 Print heritability and SE *****

```
PRINT h2,Bias,Seh2
```

* Under complete blocks *

* ***** 3.1 Compute variance components *****

```
VCOMP[fixed=Rep] RANDOM=Rep+Geno
REML[print=*] Y
```

* ***** 3.2 Compute heritability and its SE *****

```
VKEEP[SIGMA2=SGe2;vcov=Vcov_r] Geno; COMP=SGg2
EQUA Vcov_r ; !p(Vgg,Vge,Vee)
```

```
CALC h2=SGg2/(SGg2+SGe2)
CALC One_h22=(1-h2)**2
CALC Bias=One_h22*((1-h2)*Vgg-h2*Vge)/(h2*SGe2*SGe2)
CALC Seh2=(1-h2)*SQRT(One_h22*Vgg-2*h2*(1-h2)*Vge+Vec*h2**2)/SGe2
```

```
" ***** 3.3 Print heritability and SE *****
```

```
PRINT h2,Bias,Seh2
```

```
endif
```

```
clos: stop
```

Output:

Genstat 5 Release 2.2 (Vax/VMS5) 18-JAN-1994 08:06:20.43
Copyright 1990, Lawes Agricultural Trust (Rothamsted Experimental Station)

```
1
2 UNIT[50]
3
4 ***** Heritability from a single trial *****
5
6 * ***** 1. Declare various structures *****
7
8 FACT[LEV=2] Rep :& [Lev=5]Blk : &[Lev=25]Geno
9 SCAL SGg2,SGe2,h2
10 Scal Vgg,Vge,Vee,Bias, Seh2
11 symm[3] Vcov
12 symm[2] Vcov_r
13
14 * ***** 2. Read data values *****
15 OPEN 'Herit1.TXT';CH=2;FI=IN
16 READ[CH=2;END=*; Form=1(5,-34)] Rep,Blk,Geno,CY[1...2]

Identifier Minimum Mean Maximum Values Missing
CY[1] 2707 4809 6733 50 0
CY[2] 2940 4187 5213 50 0
17
18 FOR Y=CY[1...2]
19
20
21 * Using incomplete block design: block effects random *
22
23
24 * ***** 3.1 Compute variance components *****
25 VCOMP[fixed=Rep] RANDOM=Rep/Blk+Geno
26 REML[print=*] Y
27
28
29 * ***** 3.2 Compute heritability and its SE *****
30 VKEEP[SIGMA2=SGe2;vcov=Vcov] Geno; COMP=SGg2
31 CALC Vgg,Vge,Vee=Vcov$[2,3,3; 2,2,3]
32 CALC h2=SGg2/(SGg2+SGe2)
33 CALC One_h22=(1-h2)**2
34 CALC Bias=One_h22*((1-h2)*Vgg-h2*Vge)/(h2*SGe2*SGe2)
35 CALC Seh2=(1-h2)*SQRT(One_h22*Vgg-2*h2*(1-h2)*Vge+Vee*h2**2)/SGe2
36
37
38 * ***** 3.3 Print heritability and SE *****
39 PRINT h2,Bias,Seh2
40
41 * Under complete blocks *
42
```

```

43 * ***** 3.1 Compute variance components *****
44 VCOMP[fixed=Rep] RANDOM=Rep+Gcno
45 REML[print=*] Y
46
47
48 * ***** 3.2 Compute heritability and its SE *****
49 VKEEP[SIGMA2=SGe2;vcov=Vcov_r] Gcno; COMP=SGg2
50 EQUA Vcov_r ; lp(Vgg,Vge,Vee)
51 CALC h2=SGg2/(SGg2+SGe2)
52 CALC One_h22=(1-h2)**2
53 CALC Bias=One_h22*((1-h2)*Vgg-h2*Vge)/(h2*SGe2*SGe2)
54 CALC Seh2=(1-h2)*SQRT(One_h22*Vgg-2*h2*(1-h2)*Vge+Vee*h2**2)/SGe2
55
56
57 * ***** 3.3 Print heritability and SE *****
58 PRINT h2,Bias,Seh2
59
60 endf

```

h2	Bias	Seh2
0.4724	0.07582	0.1707

h2	Bias	Seh2
0.4340	0.07792	0.1657

- * MESSAGE: Estimate for variance component 1 at iteration 1 is negative
A small positive value will be used next iteration.
- * MESSAGE: Estimate for variance component 1 at iteration 2 is negative
A small positive value will be used next iteration.
- * MESSAGE: Estimate for variance component 1 at iteration 3 is negative
A small positive value will be used next iteration.
- * MESSAGE: Estimate for variance component 1 at iteration 4 is negative
A small positive value will be used next iteration.
- * MESSAGE: Estimate for variance component 1 at iteration 5 is negative
A small positive value will be used next iteration.

***** Warning (Code VC 21). Statement 3 in For Loop
Command: REML[print=*] Y

Negative component has been reset to a positive value on final iteration

The results from this analysis should be compared with results obtained by removing the 1 negative component(s) from the RANDOM model, as estimates of components and standard errors from the current model may be misleading.

h2	Bias	Seh2
0.3241	0.1151	0.1846

h2	Bias	Seh2
0.3347	0.1105	0.1813

61 clos: stop

***** End of job. Maximum of 22674 data units used at line 60 (27040 left)

GENSTAT Modules in Computing Biometrics

Title: Estimates of heritability from multi-locational trials

1. Introduction:

This program computes estimate of heritability (in broad sense) from multi-locational variety trials conducted in blocks. It provides an estimate of its asymptotic standard error.

2. Areas of application and keywords:

Plant breeding and genetics

Heritability in broad sense, standard error, incomplete blocks, multi-locational trials, GxE interaction

3. Input/Output:

Input:

Plot-wise values of locations, replications, blocks, genotypes and traits

Output:

Estimates of variance components (for plots and blocks within replications, GxE interaction, genotype), heritability and standard error.

4. Location of the program:

Program:

A:\CompBiom\93\Herit2.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\Herit2.txt

Results:

A:\CompBiom\93\Herit2.opt

6. Client(s)

Dr. S. Ceccarelli, CP

7. Date

January 1994

8. Comments

M. Singh

Program:

```
" ***** Heritability from multi-environments ***** "
```

UNIT[200]

```
" ***** 1. Declare various structures ***** "
```

FACT[lev=4] Loc: &[LEV=2] Rep :& [Lev=5]Blk : &[Lev=25]Geno
SCALAR SGg2,SGe2,SGi2,Vgg,Vee,Vii,Vgi,Vge,Vie, h2, Se, Bias
SYMM[4] Vcov
Symm[3] Vcov_r

```
" ***** 2. Read data values ***** "
```

OPEN 'herit2.TXT';CH=2;FI=IN
READ[CH=2;END=*] Loc,Rep, Blk,Geno,V[1...9]

FOR Y=V[1...2]

```
" Under incomplete blocks: Block effects random "
```

```
" ***** 3.1 Compute variance components ***** "
```

VCOMP[abso=Loc; Fixed=Loc/Rep] RANDOM=Loc+Loc.Rep+Loc.Rep.Blk+Geno+Geno.Loc
REML[print=s] Y

```
" ***** 3.2 Compute heritability and its SE ***** "
```

VKEEP[SIGMA2=SGe2;vcov=Vcov] Geno+Geno.Loc; COMP=SGg2,SGi2
CALC Vgg,Vgi,Vii,Vge,Vie,Vee=Vcov\$[2,3,3,4,4,4;2,2,3,2,3,4]
CALC h2=SGg2/(SGg2+SGi2+SGe2)
CALC Bias =h2*(Vgg-h2*(Vgg+Vgi+Vge))/SGg2/SGg2
CALC Se=Vgg+Vii+Vee+2*(Vgi+Vge+Vie) : & Se=Vgg+h2*h2*Se-2*h2*(Vgg+Vgi+Vge)
CALC Se=h2*SQRT(Se)/SGg2

```
" ***** 3.3 Print heritability and SE ***** "
```

Print h2, Bias, Se
" Under complete blocks "

```
" ***** 3.1 Compute variance components ***** "
```

VCOMP[abso=Loc; Fixed=Loc/Rep] RANDOM=Loc+Loc.Rep+Geno+Geno.Loc
REML[print=s] Y

```
" ***** 3.2 Compute heritability and its SE ***** "
```

VKEEP[SIGMA2=SGe2;vcov=Vcov_r] Geno+Geno.Loc; COMP=SGg2,SGi2
EQUA Vcov_r ; !p(Vgg,Vgi,Vii,Vge,Vie,Vee)
CALC h2=SGg2/(SGg2+SGi2+SGe2)
CALC Bias =h2*(Vgg-h2*(Vgg+Vgi+Vge))/SGg2/SGg2
CALC Se=Vgg+Vii+Vee+2*(Vgi+Vge+Vie) : & Sc=Vgg+h2*h2*Sc-2*h2*(Vgg+Vgi+Vge)
CALC Se=h2*SQRT(Se)/SGg2

```
" ***** 3.3 Print heritability and SE ***** "
```

Print h2, Bias, Se
ENDF
clos: stop

GENSTAT Modules in Computing Biometrics

Title: Critical period of weed competition

1. Introduction:

This program computes the estimate of critical period of weed interference and its asymptotic standard error when the relationship of the yield with duration of weed-free time is linear and the relationship of the yield with duration of weed-infested time is (i). linear and (ii). logistic. Lentil data have been used to illustrate the procedure over four environments.

2. Areas of application and keywords:

Weed Science, Agronomy

Critical period, weed-interference, estimates, standard error, lentil.

3. Input/Output:

Input:

Values of environment, duration treatments, yield variables

Output:

Estimates of critical period of weed-interference, standard errors and the summary, estimates of parameters of linear and logistic models fitted.

4. Location of the program:

Program:

A:\CompBiom\93\Critical.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

A:\CompBiom\93\Critical.Txt

Results:

A:\CompBiom\93\Critical.opt

6. Client(s)

Dr. B.E. Abu-Irmaileh, LP

7. Date

January 1994

8. Comments

M. Singh

Program:

Analysis of data on lentils for

1. fitting equations on period of weed interference,
2. estimation of Critical Period, asymptotic standard error and confidence intervals.

Unit[72]

Fact[Leve=4] Env: Fact[Leve=18]TRT

Open 'Critical.txt'; CH=2;FI=IN

Scalar Skipline

Read[ch=2] Skipline

Skip[ch=2]Skipline

Read[CH=2; Form=!(4,-5)] Env,TRT,GY,SY

Calc GY=10.*GY : & SY=10.*SY " To convert to kg/ha unit "

Fact[Leve=2] WF_W : Calc WF_W=Newl(TRT;! (9(1,2)))

Fact[Leve=10] WF: Calc WF=Newl(TRT;! (1...9,9(10)))

Fact[Leve=10] W: Calc W=Newl(TRT;! (9(10),1,2,3...9))

Dele TRT

Vari WeekWF,WeekW

Calc WeekWF=(INT(WF)-1)*2: Calc WeekW=(INT(W)-1)*2

Scal A1,A2,B1,B2,B,M,C,A

Scal Var_A1,Cov_A1B1,Var_B1,Var_A2,Cov_A2B2,Var_B2, Df1,Df2

Scal Var_B, Cov_BM,Var_M, Cov_BC,Cov_MC,Var_C, Cov_BA,Cov_MA,Cov_CA,Var_A

Vari[Nval=2] EstLin

Vari[Nval=4] EstLog

Symm[Rows=2] VcovLin

Symm[Rows=4] VcovLog

Matr[Rows=1;Colu=4] Deri

Scal G,Fun,Time,CP,SE, V11,V12,V22, Tval, H1,LAasymp,UAsymp,LExact,UExact,FLog

For Y=GY,SY

For J=1...4

Rest Y,WeekWF; Cond=WF_W.eq.1.and.Env.eq.J

Model Y

Fit[Prin=m,s,e,c] WeekWF

Rkeep EST=EstLin;Vcov=VcovLin; DF=Df1

Equa EstLin;!P(A1,B1) : & VcovLin; !P(Var_A1,Cov_A1B1,Var_B1)

Rest Y, WeekWF

Rest Y,WeekW; Cond=WF_W.eq.2.and.Env.eq.J

Model Y

```

Fit[Prin=m,s,e,c] WeekW
Rkeep EST=EstLin;Vcov=VcovLin; DF=Df2
Equa EstLin;!P(A2,B2) : & VcovLin; !P(Var_A2,Cov_A2B2,Var_B2)

* Critical period estimates, se, exact and asymptotic 95% confidence limits
under linear-linear model *

Calc CP=(A2-A1)/(B1-B2) : Calc V11=Var_A1+Var_A2:& V12=- (Cov_A1B1+Cov_A2B2)
Calc V22=Var_B1+Var_B2: Calc Tval=Fed(0.95;1;Df1+Df2) :& Tval=SQRT(Tval)

Calc G=Tval*Tval*V22/(B1-B2)**2
Calc H1=SQRT(V11+CP*CP*V22-2*CP*V12-G*(V11-V12*V12/V22))
Calc LExact= ( CP- G*V12/V22- Tval*H1/(B1-B2) )/(1-G)
Calc UExact= ( CP- G*V12/V22+ Tval*H1/(B1-B2) )/(1-G)
Calc SE=SQRT(V11+CP*CP*V22-2*CP*V12)/ABS(B1-B2)
Calc LAsymp=CP-NED(.975)*SE : CALC UAsymp=CP+NED(.975)*SE

Print CP,SE,LAsymp, UAsymp,LExact,UExact

* Critical period estimates and standard errors : Approximate
Linear-Logistic relationship *
Model Y
Fitc[Curve=Logistic;Prin=m,s,e,c] WeekW
Rkeep EST=EstLog; Vcov=VcovLog
Equa EstLog;!P(B,M,C,A) : & VcovLog ; \
!P(Var_B, Cov_BM,Var_M, Cov_BC,Cov_MC,Var_C, Cov_BA,Cov_MA,Cov_CA,Var_A)

* Solve for CP*

Expr Diff; valu=!E(Fun=(A1+B1*Time-A-C/(1+Exp(-B*(Time-M))))**2)
Model[Function=Fun]
Rcycle Time;Init=CP
Fitn[Calc=Diff]

Print Time,Fun

Calc FLog=A+C/(1+Exp(-B*(Time-M)))
Calc Deri$[1;4] =1 :& Deri$[1;3]=(FLog-A)/C
Calc Deri$[1;2]=-B*(C+A-FLog)*(FLog-A)/C
Calc Deri $[1;1] =(Time-M)*(C+A-FLog)*(FLog-A)/C
Calc SE=Qproduct(Deri;VcovLog)+Var_A1+Time*Time*Var_B1+2*Time*Cov_A1B1
Calc SE=SQRT(SE)/ABS(B1-B*(C+A-FLog)*(FLog-A)/C)
Calc LAsymp=CP-NED(.975)*SE : Calc UAsymp=CP+NED(.975)*SE

PRINT Time,SE,LAsymp,UAsymp

Rest Y, WeekW
Endf
Endf
clos
stop

```

**Computer and Biometrics Services Unit
ICARDA**

Serial Number-009

GENSTAT Modules in Computing Biometrics

Title: Modelling of seed germination with time and temperature

1. Introduction:

This program models seed germination with temperature and times. For each genotype and temperature combination in the experiment, it fits a logistic model to the cumulative percentage germination as a function of time, computes time (D50%) to 50% germination, computes rate ($R50\% = 1/D50$) of germination as inverse of this time. Optimum temperature is estimated by modelling D50% by quadratic divided by quadratic function in temperature. The linear function in times are fitted to R50% for cases below the optimum temperature. The base temperature is estimated with standard error.

2. Areas of application and keywords:

Plant Physiology, abiotic stress

Temperature stress, base temperature, germination, wheat

3. Input/Output:

Input:

For a number of genotype and temperature, number of seeds germinated, total number of seeds used for different times in hours.

Output:

Estimates of base temperature, optimum temperature, R50%, D50%

4. Location of the program:

Program:

A:\CompBiom\93\Germ_Mod.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

ICARDA VAX [murari.CP.maha]BWTH1.dat

ICARDA VAX [murari.CP.maha]BWTH2.dat

ICARDA VAX [murari.CP.maha]Coeff3.Opt

Results:

ICARDA VAX [murari.CP.maha]Maha1.opt

6. Client(s)

Dr. V. Mahalakshmi, CP

7. Date

December 1993

8. Comments

M. Singh

Program:

```
Unit[30]
Vari[nvalu=35] Fullrow
Open 'bwth2.dat'; ch=2;fi=in ;width=180
open 'coeff1.opt';ch=3;fi=out
Scal Ncases; 196
Scal Col,Row,Temp,Geno, B,M,C,A, Tot, Rbarsq
Scal[valu=*] Bmis,Mmis,Cmis,Amis
Read [ch=2; end=*] Time
for i=1...Ncases
Read[ch=2;end=*] Fullrow
Calc Row,Col,Temp,Geno=Fullrow$[1...4]: & Y=Fullrow$[!(6...35)]
Calc Tot=Sum(Y)
If Tot.le.12
  Calc D50,Rbarsq=0,0 : & B,M,C,A=Bmis,Mmis,Cmis,Amis

Print[ch=3;ipri=*] i, Row,Col,Geno,Temp,Rbarsq,B,M,C,A,D50;fiel=4(4),2(6),5(9) \
; deci=4(0),2,2,5(3)
Else
Calc Y=Cum(Y) : Calc Y=(Y/Tot)*100.
Model Y ; Fitt=F
Fitc[ curve=log] Time
Graph[ncol=35;nrow=16] Y, F;Time; Meth=p,c
Rkeep Est=Est ;df=df;devi=ss
Calc Rbarsq=100.*(1-ss/df/var(Y))
Equa Est; Ip(B,M,C,A)
Calc D50=M-Log((C+A-50)/(50-A))/B
Print[ch=3;ipri=*] i, Row,Col,Geno,Temp,Rbarsq,B,M,C,A,D50;fiel=4(4),2(6),5(9) \
; deci=4(0),2,2,5(3)
Endif
endif

clos
stop
```

```
Unit[25]
Vari[nvalu=30] Fullrow
Open 'bwth1.dat'; ch=2;fi=in ;width=180
open 'coeff2.opt';ch=3;fi=out
Scal Ncases; 196
Scal Col,Row,Temp,Geno, B,M,C,A, Tot, Rbarsq
Scal[valu=*] Bmis,Mmis,Cmis,Amis
Read [ch=2; end=*] Time
for i=1...Ncases
Read[ch=2;end=*] Fullrow
Calc Row,Col,Temp,Geno=Fullrow$[1...4]: & Y=Fullrow$[!(6...30)]
Calc Tot=Sum(Y)
If Tot.le.12
```

```

Calc D50,Rbarsq=0,0 : & B,M,C,A=Bmis,Mmis,Cmis,Amis

Print[ch=3;ipri=*] i, Row,Col,Geno,Temp,Rbarsq,B,M,C,A,D50;fiel=4(4),2(6),5(9) \
; deci=4(0),2,2,5(3)
Else
Calc Y=Cum(Y) : Calc Y=(Y/Tot)*100.
Model Y ; Fitt=F
Fitc[ curve=log] Time
Graph[ncol=35;nrow=16] Y, F;Time; Meth=p,c
Rkeep Est=Est ;df=df;devi=ss
Calc Rbarsq=100.*(1-ss/df/var(Y))
Equa Est; lp(B,M,C,A)
Calc D50=M-Log((C+A-50)/(50-A))/B
Print[ch=3;ipri=*] i, Row,Col,Geno,Temp,Rbarsq,B,M,C,A,D50;fiel=4(4),2(6),5(9) \
; deci=4(0),2,2,5(3)
Endif
endif

clos
stop

```

Unit[392]

" Note that Coeff3.opt has contents of Coeff1.opt and Coeff2.Opt, putting coeff2.opt below the Coeff1.opt "

```
Open 'coeff3.opt'; ch=2;fi=in
```

```
Fact[leve=15] Geno
Read[ch=2;End=*;Form=l(-3,2,-5,1)] Geno,Temp,D50
```

```
Vari[nval=14] OpTemp, BaseT,SeBaseT,Slope,SeSlope,Rsq
```

```
Scal TOpt1,TOpt2, A,B,C,D,E
For i=1...13,15;j=1...14
Rest Temp,D50 ; cond=Geno.eq.l.and.D50.ne.0
```

```
Model D50 ;fitt=F
Fitc[curve=qdq] Temp
Rkeep Est=Est ;Devi=ss;df=df
Calc Rsq$[j]=100*(1-ss/df/var(D50))
```

```
Equa Est;lp(D,E,B,C,A)
```

```
Calc TOpt1=SQRT((2*B*E)**2-4*C*E*(B*D-C))
Calc TOpt2=(-2*B*E-TOpt1)/2./C/E
Calc TOpt1=(-2*B*E+TOpt1)/2./C/E
```

```
Print i, TOpt1,TOpt2
```

```

If TOpt2.ge.35
  Calc TOpt2=26
Endif

Print i, TOpt1,TOpt2
Calc OpTemp$[j]=TOpt2
Graph D50,F;Temp;Symb='o','.'; meth=p,c
Rest D50,Temp

Rest R50,D50, Temp , F; Cond=Temp.le.TOpt2.and.Geno.eq.i.and.D50.ne.0
Calc R50=1/D50

Model R50; Fitt=F
Fit Temp
Rkeep Est=Est1 ; Vcov=Vcov
Scal Btemp
Calc Btemp=-Est1$[1]/Est1$[2]
Print i,Btemp
Calc BaseT$[j] =Btemp
Calc Slope$[j] =Est1$[2]
Calc SeSlope$[j]=Sqrt(Vcov$[2;2])
Calc SeBaseT$[j]=ABS(Btemp)*SQRT(Vcov$[1;1]/(Est1$[1])**2+ \
      Vcov$[2;2]/(Est1$[2])**2-2.*Vcov$[2;1]/Est1$[1]/Est1$[2])
Graph R50,F;Temp;Symb='o','.'; meth=p,c

Rest R50,D50,Temp,F

Endf
Fact[leve=14; valu=1...14] Genotype
Calc Slope=1000*Slope :& SeSlope=1000*ScSlope

Print Genotype, Rsq, OpTemp,BaseT,SeBaseT,Slope,SeSlope;fiel=9
Scal Chsq,PrChi,wmean

Calc wmean=sum(BaseT/SeBaseT/SeBaseT)/Sum(1/SeBaseT/SeBaseT)
Calc Chsq=Sum(((BaseT-wmean)/SeBaseT)**2)
Calc PrChi=1-Chsq(Chsq;13)
Prin Chsq,PrChi

Calc wmean=sum(Slope/SeSlope/SeSlope)/Sum(1/SeSlope/SeSlope)
Calc Chsq=Sum(((Slope-wmean)/SeSlope)**2)
Calc PrChi=1-Chsq(Chsq;13)
Prin Chsq,PrChi

Rest BaseT,SeBaseT; cond=BaseT.ge.0
Calc wmean=sum(BaseT/SeBaseT/SeBaseT)/Sum(1/SeBaseT/SeBaseT)
Calc Chsq=Sum(((BaseT-wmean)/SeBaseT)**2)
Calc PrChi=1-Chsq(Chsq;11)
Prin Chsq,PrChi
clos
stop

```

GENSTAT Modules in Computing Biometrics

Title: Classification of isolates using disease development data

1. Introduction:

This program has been written to analyze reaction of a number of isolates in terms of disease scores on three chickpea genotypes (susceptible, moderately resistant and resistant). The scores were observed on a number of days on the same plants. There are two programs in the same file.

Program 1: For each date and isolate, it gives the analysis of contrasts used for classification of the isolate. The probability values of contrast guides the classification of the isolate.

Program 2: It does the following:

i. For each isolate and each genotype, it computes an average score (over plants) for each date, fits exponential curves corresponding to each genotype and compares the parallelism of the exponential curves, for each isolate. The differences, in the constant, slope and shape parameters of the disease progress curves of the three genotypes can be used to classify the isolate.

ii. It also computes the observed area under the disease progress curve for each plant and each genotype. These areas are then subjected to the analysis of contrasts as in (1).

2. Areas of application and keywords:

Plant Pathology, biotic stress

Chickpea, classification of isolates, areas under disease progress curve, scores, exponential curves

3. Input/Output:

Input:

Disease scores, for each experimental date, plant, genotype and isolate.

Output:

Analysis of variance of contrasts, probability values, estimates of disease progress curves, accumulated analysis of variance under exponential curves, area under disease progress curves.

4. Location of the program:

Program:

A:\CompBiom\94\Dis_curv.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

ICARDA VAX [murari.LP.FWeigand]ASCo2.Txt

Results:

ICARDA VAX [murari.LP.FWeigand]*.Opt

6. Client(s)

Drs. F. Weigand and S. Udupa, LP

7. Date

January 1994

8. Comments

M. Singh

Program:

- ° Program 1: To compare contrasts for classification of isolates °
- ° Program 1: To compare contrasts for classification of isolates °
- ° Program 1: To compare contrasts for classification of isolates °
- ° Program 1: To compare contrasts for classification of isolates °

Unit{6624}

Open 'Asco2.txt' ; ch=2

Skip[ch=2]5

Fact[leve=23] Iso : &[leve=3]Geno : &[leve=12]Date : &[leve=8]Plant

Gene Iso,Geno,Date,Plant

Read[ch=2;Form=1(-3,8)] Score

Matr[Rows=1t(W_M_R,W_MR_S);Colu=3; Valu=0,-1,1, 2,-1,-1]WCon

Matr[Rows=1t(S_S_M,S_SM_R);Colu=3; Valu=-1,1,0, -1,-1,2]SCon

Matr[Rows=1t(SS_S_R,SS_SR_M);Colu=3; Valu=-1,0,1, -1,2,-1]SSCon

Bloc

For j=12,11,10,8,7,6,5,4,3,2,1

For i=1...23

Rest Score ; cond=Iso.eq.i.and.Date.eq.j

Print ' Sampling date ', j, ' Isolate number ', j

Trea Reg(Geno;2;WCon)

Anov[prin=a,m;se=m;fpro=y] Score

Trea Reg(Geno;2;SCon)

Anov[prin=a,m;se=m;fpro=y] Score

Trea Reg(Geno;2;SSCon)

Anov[prin=a,m;se=m;fpro=y] Score

rest Score

Endf : Endf

clos

stop

- ° Program 2: To compare disease development curves to classify the isolates °
- ° Program 2: To compare disease development curves to classify the isolates °
- ° Program 2: To compare disease development curves to classify the isolates °
- ° Program 2: To compare disease development curves to classify the isolates °

Unit{36}

Open 'Asco2.txt' ; ch=2

Skip[ch=2]5

Fact[leve=12] Date : &[leve=3]Geno

Gene Geno,Date

Device 5

Pen 1,2,3;line=1; meth=m

```

Vari[nval=24]A,R,B,ArPred,ArObs,RBar
Fact[leve=3;nval=24]Lines
Fact[leve=8; nval=24]Plants
Gene Lines,Plants

```

```

Matr[ Rows=lt(W_M_R,W_MR_S);Colu=3; Valu=0,-1,1, 2,-1,-1]WCon
Matr[ Rows=lt(S_S_M,S_SM_R);Colu=3; Valu=-1,1,0, -1,-1,2]SCon
Matr[ Rows=lt(SS_S_R,SS_SR_M);Colu=3; Valu=-1,0,1, -1,2,-1]SSCon
Vari[valu=(1,6(2),3,0,3,2,1)3]ArCoeff

```

```

For i=1...23
Print ' Isolate number is ', i

```

```

Read[ch=2;End=*; Form=l(-2,9)] Time,h[1...8]
Calc h[9]=Vmean(lp(h[1...8]))

```

```

" Fitting on mean values over plants"
Model h[9]
Terms Time*Geno
Fitc[curve=exp;prin=*; Fpro=y]Time
Add[prin=*; Fpro=y]Geno
Add[prin=*; Fpro=y]Time.Geno
Add[nonl=s;prin=m,s,a,e; Fpro=y]
Rkeep Est=Est[9]

```

```

" Fitting over each geno and plant"

```

```

" Observed area under the curve "

```

```

Scal ij
Calc ij=0
Scal Nob

```

```

For j=1...3
For y=h[1...8]
Calc ij=ij+1

```

```

Rest y,ArCoeff; Geno.eq.j

```

```

Calc Nob=Nobs(y)
If Nob.gt.4
Calc ArObs[ij]=Sum(y* ArCoeff)/2
Else
Calc ArObs[ij]=l(*)
Endif
Rest y,ArCoeff
Endf
Endf

```

```
Bloc
Trea Reg(Lines;2;WCon)
Anov[prin=a,m,%;se=m;fpro=y] ArObs
Trea Reg(Lines;2;SCon)
Anov[prin=a;fpro=y] ArObs
Trea Reg(Lines;2;SSCon)
Anov[prin=a;fpro=y] ArObs

endf

clos
stop
```

GENSTAT Modules in Computing Biometrics

Title: Random sampling and randomization in experimental designs

1. Introduction:

This series of programs generate random samples and randomized plans for five experimental designs. These are given as assignments with explanation on running the GENSTAT and storing the output.

2. Areas of application and keywords:

Field experimentation and survey
Random sampling, randomization

3. Input/Output:

Input:

Population size, sample size, number of replications, levels of treatment factors.

Output:

Randomly selected units, randomized field plans.

4. Location of the program:

Program:

A:\CompBiom\93\Random.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

(parameters in side the program)

Results:

(not stored)

6. Client(s)

Trainees of Elementaries in Biometrics (25 Jan 1994)

7. Date

Jan 1994

8. Comments

M. Singh

Assignment 1: Randomize N (=30, say) numbers and draw a random sample of size M (=20, say) out of N.

Usage: Randomization and random sampling.

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign1.Gen.

```
Scalar N,M ; 30,20
Factor[Levels=N; Nvalues=N] Whole
Factor[Levels=N; Nvalues=M] Sample
Generate Whole
Randomize Whole
Equate Whole; Sample
Print Sample
Stop
```

Step 2: To see the results on the screen, use

Genstat Assign1.gen

Step 3: To store results in a file , say Assign1.Res, use

Genstat Assign1.gen , Assign1.res

Assignment 2: Generate a randomized plan for an experiments to evaluate 5 genotypes of barley and conducted in an RCB design with 4 replications.

Usage: Planning your experiments in RCBD

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign2.Gen.

```
Scalar NRep, NGeno; 4, 5
Scalar NPlots
Calc NPlots=NRep*NGeno

Unit[NPlots]
Factor[Levels=NRep] Rep
Factor[Levels=NGeno] Geno
Generate Rep,Geno

Randomize[Bloc=Rep/Geno] Geno

Fact[leve=NPlots]Plot
Generate Plot
Print Plot, Rep,Geno
Stop
```

**Step 2: To see the results on the screen, use
Genstat Assign2.gen**

**Step 3: To store results in a file , say Assign2.Res, use
Genstat Assign2.gen , Assign2.res**

Assignment 3: Generate a randomized plan for an experiments to evaluate effects of 3 levels of nitrogen on 5 genotypes of barley and conducted as full factorial in an RCB design with 4 replications.

Usage: Planning your experiments in RCBD

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign3.Gen.

```
Scalar NRep, NNitr,NGeno; 4, 3, 5

Scalar NPlots
Calc NPlots=NRep*NNitr*NGeno

Unit[NPlots]
Factor[Levels=NRep] Rep
Factor[Levels=NNitr] Nitrogen
Factor[Levels=NGeno] Geno
Generate Rep,Nitrogen,Geno

Scalar NNiGe
Calculate NNiGe=NNitr*NGeno
Fact[Levels=NNiGe] Plots
Generate Plots

Randomize[Bloc=Rep/Plots] Nitrogen,Geno
Print Rep, Plots,Nitrogen,Geno
Stop
```

Step 2: To see the results on the screen, use

Genstat Assign3.gen

Step 3: To store results in a file , say Assign3.Res, use

Genstat Assign3.gen , Assign3.res

Assignment 4: Generate a randomized plan for an experiments to evaluate effects of 3 levels of nitrogen on 5 genotypes of barley and conducted as split-plot in an RCB design with nitrogen as main plots , genotypes as sub-plot treatments and with 4 replications.

Usage: Planning your experiments in split-plots in RCBD

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign4.Gen.

```
Scalar NRep, NNitr,NGeno; 4, 3, 5
```

```
Scalar NPlots
```

```
Calc NPlots=NRep*NNitr*NGeno
```

```
Unit[NPlots]
```

```
Factor[Levels=NRep] Rep
```

```
Factor[Levels=NNitr] Nitrogen
```

```
Factor[Levels=NGeno] Geno
```

```
Generate Rep,Nitrogen,Geno
```

```
Fact[Levels=NPlots] Plots
```

```
Generate Plots
```

```
Randomize[Bloc=Rep/Nitrogen/Geno] Nitrogen,Geno
```

```
Print Plots,Rep,Nitrogen,Geno
```

```
Stop
```

Step 2: To see the results on the screen, use

```
Genstat Assign4.gen
```

Step 3: To store results in a file , say Assign4.Res, use

```
Genstat Assign4.gen , Assign4.res
```

Assignment 5: Generate a randomized plan for an experiments to evaluate effects of 3 levels of nitrogen on 4 spacings and conducted as strip-plot in an RCB design with 4 replications.

Usage: Planning your experiments in strip-plots in RCBD

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign5.Gen.

```
Scalar NRep, NNitr,NSpace; 4, 3, 4
```

```
Scalar NPlots
```

```
Calc NPlots=NRep*NNitr*NSpace
```

```
Unit[NPlots]
```

```
Factor[Levels=NRep] Rep
```

```
Factor[Levels=NNitr] Nitrogen
```

```
Factor[Levels=NSpace] Spacing
```

```
Generate Rep,Nitrogen,Spacing
```

```
Fact[Levels=NPlots] Plots
```

```
Generate Plots
```

```
Randomize[Bloc=Rep/(Nitrogen*Spacing)] Nitrogen,Spacing
```

```
Print Plots,Rep,Nitrogen,Spacing
```

```
Stop
```

Step 2: To see the results on the screen, use

```
Genstat Assign5.gen
```

Step 3: To store results in a file , say Assign5.Res, use

```
Genstat Assign5.gen , Assign5.res
```

Assignment 6: Generate a randomized plan for an experiments to evaluate effects of 3 levels of nitrogen , 4 spacings and 2 genotypes conducted as split-strip-plot in an RCB design with 4 replications (genotypes in sub-plots).

Usage: Planning your experiments in split-strip-plots in RCBD

Attempt:

Step 1: Prepare an ASCII file using VMS or DOS editor, with the following contents. Let the name of this file be Assign6.Gen.

```
Scalar NRep, NNitr,NSpace,NGeno; 4, 3, 4,2
```

```
Scalar NPlots
```

```
Calc NPlots=NRep*NNitr*NSpace*NGeno
```

```
Unit[NPlots]
```

```
Factor[Levels=NRep] Rep
```

```
Factor[Levels=NNitr] Nitrogen
```

```
Factor[Levels=NSpace] Spacing
```

```
Factor[Levels=NGeno] Geno
```

```
Generate Rep,Nitrogen,Spacing,Geno
```

```
Fact[Levels=NPlots] Plots
```

```
Generate Plots
```

```
Randomize[Bloc=Rep/(Nitrogen*Spacing)/Geno]Nitrogen,Spacing,Geno
```

```
Print Plots,Rep,Nitrogen,Spacing,Geno
```

```
Stop
```

Step 2: To see the results on the screen, use

```
Genstat Assign6.gen
```

Step 3: To store results in a file , say Assign6.Res, use

```
Genstat Assign6.gen , Assign6.res
```

***** End of Computing Biometrics Volume I *****