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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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
GENSTAT Modules in Computing Biometrics

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

1. Introduction:
This program analyses data from multi-localional 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-localitional 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
Scalar NRep, NGeno, NLoc
Read [ch=2] NRep, NGeno, NLoc

Scalar 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 l=1...NLoc ; MN=Mean[1...NLoc]
Rest Yield; Cond=Loc, EQ.1
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[ore=a] LocMean ;fie=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(P(Mean[1...NLoc])))))/GenoMean

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

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

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

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

Delete GEData

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

Equa TDum; Wricke
    Dele[Rede=y] TDum

Scale 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

Var[nval=NGeno] RGenoMn, RSlope, RDeviMs, RGenoCV, RWricke, RPla_Pet, RPlaisted, RShukla

For D= GenoMean, Slope, DeviMs, GenoCV, Wricke, Pla_Pet, Plaisted, Shukla ; D
    DD= RGenoMn, RSlope, RDeviMs, RGenoCV, RWricke, RPla_Pet, RPlaisted, RShukla
Sort[dire=desc; Groups=3] D
Calc DD=Int(f) D
endf

" Correlations between ranks "
Corr[Print=c] RGenoMn, RSlope, RDeviMs, RGenoCV, RWricke, RPla_Pet, RPlaisted, RShukla

" 5. Clustering of Environments "

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

* 7. Estimation of variance components *
REML Yield

Clos
Stop
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=!(4,6)] V[1...NVar]

SYMM[ ROWS=NVar] RXPY
SYMM[ ROWS=NXVar] RX
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 RXY; IF(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 RES
CALC RES = 1-SUM(RXY*PATH)

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

CLOS
STOP
Path Coefficient Analysis

Scalar NOb, NVar; 42, 6  
Scalar NXVar  
Calc NXVar=NVar-1  
UNITS [NOb]  
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]  

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 1231.0 42 0 Skew  

SYMM[ ROWS=NVar] RXPY  
SYMM[ ROWS=NXVar] RX  
VARI [ NVALUES=NXVar] RX,PATH  
DIAG[ROWS=NXVar] DPATH  
MATR[ ROWS=NXVar;COLU=NXVar] MRXY  
SSPM[TERMS=V[1...NVar] ] SSPM;RXPY  
FSSPM[PRINT=C] SSPM  

*** Degrees of freedom ***
Correlations: 40

*** Correlation matrix ***

V[1] 1.000  
V[2] 0.536 1.000  
V[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 RXY=CORR(RXY)
29 EQUA RXY;IP(RXX,RXY)
30 CALC PATH=PROD(INV(RXX);RXY)
31 EQUA PATH;DPATH
32 CALC MRXY=PROD(RXX;DPATH)
33
34 PRINT ' Correlations ', RXY

Correlations
RXY
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)

12
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

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.01795</td>
<td>-0.05272</td>
<td>0.00003</td>
<td>0.02064</td>
<td>0.05314</td>
</tr>
<tr>
<td>2</td>
<td>-0.05272</td>
<td>0.13492</td>
<td>-0.00107</td>
<td>-0.08071</td>
<td>-0.25820</td>
</tr>
<tr>
<td>3</td>
<td>0.00003</td>
<td>-0.00107</td>
<td>0.00015</td>
<td>-0.00029</td>
<td>0.00094</td>
</tr>
<tr>
<td>4</td>
<td>0.02064</td>
<td>-0.08071</td>
<td>-0.00029</td>
<td>0.02002</td>
<td>0.09965</td>
</tr>
<tr>
<td>5</td>
<td>0.05314</td>
<td>-0.25820</td>
<td>0.00094</td>
<td>0.09965</td>
<td>0.21890</td>
</tr>
</tbody>
</table>

PRINT ' Contribution of Residuals in variability', RESS

RESS

Contribution of Residuals in variability  0.8267

CLOS
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=] GENO/X
FIT [CONS=O; PRINT=m,s,c,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
Comparing slopes and intercepts of Y on X over levels of a factor

Scalar NObs; 40
UNITS [NObs]
FACT|LEVE=4; VALU=10(1...4)] GENO
CALC X=URAN(364328)
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"

MODEL Y
TERMS[FULL=Y] GENO/X
FIT [CONS=O; PRINT=m,s,e,a] GENO/X
***** Regression Analysis *****

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

*** Summary of analysis ***

<table>
<thead>
<tr>
<th></th>
<th>d.f.</th>
<th>s.s.</th>
<th>m.s.</th>
<th>v.r.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Regression</td>
<td>8</td>
<td>8.375</td>
<td>1.04689</td>
<td>11.36</td>
</tr>
<tr>
<td>Residual</td>
<td>32</td>
<td>2.949</td>
<td>0.09215</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>40</td>
<td>11.324</td>
<td>0.28310</td>
<td></td>
</tr>
</tbody>
</table>

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 ***

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

*** Accumulated analysis of variance ***

<table>
<thead>
<tr>
<th></th>
<th>d.f.</th>
<th>s.s.</th>
<th>m.s.</th>
<th>v.r.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Change</td>
<td>-1</td>
<td>-7.86604</td>
<td>7.86604</td>
<td>85.37</td>
</tr>
<tr>
<td>+ GENO</td>
<td>4</td>
<td>8.07571</td>
<td>2.01893</td>
<td>21.91</td>
</tr>
<tr>
<td>+ X.GENO</td>
<td>4</td>
<td>0.29944</td>
<td>0.07486</td>
<td>0.81</td>
</tr>
<tr>
<td>Residual</td>
<td>32</td>
<td>2.94865</td>
<td>0.09215</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>39</td>
<td>3.45777</td>
<td>0.08866</td>
<td></td>
</tr>
</tbody>
</table>

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 ***

<table>
<thead>
<tr>
<th></th>
<th>estimate</th>
<th>s.e.</th>
<th>t</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>0.421</td>
<td>0.142</td>
<td>2.97</td>
</tr>
<tr>
<td>X</td>
<td>0.101</td>
<td>0.190</td>
<td>0.53</td>
</tr>
<tr>
<td>GENO 2</td>
<td>-0.138</td>
<td>0.137</td>
<td>-1.01</td>
</tr>
<tr>
<td>GENO 3</td>
<td>0.033</td>
<td>0.140</td>
<td>0.24</td>
</tr>
<tr>
<td>GENO 4</td>
<td>-0.034</td>
<td>0.136</td>
<td>-0.25</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>DFSLOPE</th>
<th>DF0</th>
<th>FSLOPE</th>
<th>PRSLOPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.000</td>
<td>32.00</td>
<td>0.9893</td>
<td>0.4102</td>
</tr>
</tbody>
</table>

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

18
***** Regression Analysis *****

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

*** Summary of analysis ***

<table>
<thead>
<tr>
<th></th>
<th>d.f.</th>
<th>s.s.</th>
<th>m.s.</th>
<th>v.r.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Regression</td>
<td>4</td>
<td>0.327</td>
<td>0.08182</td>
<td>0.91</td>
</tr>
<tr>
<td>Residual</td>
<td>35</td>
<td>3.130</td>
<td>0.08944</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>39</td>
<td>3.458</td>
<td>0.08866</td>
<td></td>
</tr>
<tr>
<td>Change</td>
<td>-4</td>
<td>-0.327</td>
<td>0.08182</td>
<td>0.91</td>
</tr>
</tbody>
</table>

Residual variance exceeds variance of Y variate

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

*** Estimates of regression coefficients ***

<table>
<thead>
<tr>
<th></th>
<th>estimate</th>
<th>s.e.</th>
<th>t</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>0.385</td>
<td>0.113</td>
<td>3.40</td>
</tr>
<tr>
<td>X</td>
<td>0.188</td>
<td>0.211</td>
<td>0.89</td>
</tr>
<tr>
<td>X.GENO 2</td>
<td>-0.304</td>
<td>0.239</td>
<td>-1.27</td>
</tr>
<tr>
<td>X.GENO 3</td>
<td>0.037</td>
<td>0.195</td>
<td>0.19</td>
</tr>
<tr>
<td>X.GENO 4</td>
<td>-0.151</td>
<td>0.216</td>
<td>-0.70</td>
</tr>
</tbody>
</table>

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

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>DFINT</td>
<td>DF0</td>
<td>FINT</td>
<td>PR_INT</td>
</tr>
<tr>
<td>3.000</td>
<td>32.00</td>
<td>0.6578</td>
<td>0.5841</td>
</tr>
</tbody>
</table>

41
42 CLOSE
43 STOP

******* End of job. Maximum of 14622 data units used at line 24 (35092 left)
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=lt(P1,P2,F1,F2,BC1,BC2,CHK)] Gcn
Read[ch=2; form=lt(-1,1,-2,3)]Gcn,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,SC21,SC21%; dd=4,4,40
Rest Y; cond=Gcn.eq.4
Calc NR=Sum(Y.le.dd); & N=Nobs(Y) & NS=N-NR
Calc Chi1=((NR-N*R/RPS)**2)/(NR/N/RPS)+(NS-N*S/RPS)**2)/(NS/N/RPS)
Calc Chi2=(RPS/N/S)**2+(RPS/N/R)**2+(NS-N*S/RPS)**2
Calc Pr1=1-Chisq(Chi1;1); Calc Pr2=1-Chisq(Chi2;1)
Print Case,R,S, NR, NS, N, Chi1, Chi2, Pr1, Pr2; fiel=3(4),7(9); deci=6(0),4(4)
Endf
delc 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
1 2 3 1 7 8 1 9 16 39 6 1 9 3 4
Calc R=R1+R2+R3

For Y=SC21,SC21,SC21%; d1=4,4,40; d2=6,6,60
Rest Y; Cond=Gcn.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)**2+(R/N/R2)**2+(R/N/R3)**2+(N1-N*R1/R)**2
Calc Prob=1-chisq(Chi;2)
Print 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, R1,N1,N2,N3,N4,N,Prob, Chi
Read R1, R2, R3, R4
9 3 3 1 2 7 9 9 9 2 7 2 7 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)**2+(N2-N*R2/R)**2 +
(R/N/R3)**2+(N3-N*R3/R)**2+(R/N/R4)**2+(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
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[lev=7; labe=lt(P1,P2,F1,F2,BC1,BC2,CHK)] Gen
Vari[Val=6]Mean,DF,SS, Wet, SE
Vari[Val=6(1)] M : & [Val=1,1,0,5,5] D : & [Val=0,0,1,5,5,5] H
Vari[Val=2(1,0,25)] I : & [Val=4(0),25,25] J : & [Val=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
Blec Rep/Pot/Plant
Anov[prin=a] Y
Akeep Terms=Rep,Pot,Plant; ss=ss; df=df
Calc Mean[i]=Mean(Y); & DF[i]=df ; & SS[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=0; pprob=y; pprob=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=0; pprob=y; pprob=y] M
Add H
Endf

Close
Stop

24
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 ***** *

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=1(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[SGG2=SGG2;vcov=Vcov] Geno; COMP=SGG2
CALC Vgg,Vge,Vee=Vcov$[2,3,3; 2,2,3]
CALC h2=SGG2/(SGG2+SGG2)
CALC One_h22=(1-h2)**2
CALC Bias=One_h22*((1-h2)*Vgg*h2*Vge)/(h2*SGG2*SGG2)
CALC Seh2=(1-h2)*SQRT(One_h22*Vgg*2*h2*(1-h2)*Vge+Vee*h2**2)/SGG2

***** 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[SGG2=SGG2;vcov=Vcov_r] Geno; COMP=SGG2
EQUA Vcov_r = lp(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+Vee*h2**2)/SGe2

**** 3.3 Print heritability and SE ****
PRINT h2,Bias,Seh2

endf
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
9  SCAL SGg2,SGe2,h2
10  Scal Vgg,Vge,Vee,Bias, Sch2
11  symm[3] Vcov
12  symm[2] Vcov_r
13
14  * ***** 2. Read data values ******
15  OPEN "Heritl.TXT";CH=2;Fl=IN
16  READ[CH=2;END=*, Form=(5,34)] Rep,Blk,Geno,CY[1...2]

<table>
<thead>
<tr>
<th>Identifier</th>
<th>Minimum</th>
<th>Mean</th>
<th>Maximum</th>
<th>Values</th>
<th>Missing</th>
</tr>
</thead>
<tbody>
<tr>
<td>CY[1]</td>
<td>2707</td>
<td>4809</td>
<td>6733</td>
<td>50</td>
<td>0</td>
</tr>
<tr>
<td>CY[2]</td>
<td>2940</td>
<td>4187</td>
<td>5213</td>
<td>50</td>
<td>0</td>
</tr>
</tbody>
</table>

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 Sch2=(1-h2)*SQR(T(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,Sch2
40
41  * Under complete blocks *
42
43
44

28
```
* 3.1 Compute variance components
VCOMP[fixed=Rep] RANDOM=Rep+Geno
REML[print=+] Y

* 3.2 Compute heritability and its SE
VKEEP[SIGMA2=SGe2;cov=Vcov_r|Geno; COMP=SGe2
EQUA Vcov_r ; lP(Vgg,Vge,Vce)
CALC h2=SGe2/(SGe2+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+Vce*h2**2)/SGe2

* 3.3 Print heritability and SE
PRINT h2,Bias,Seh2
endf

<table>
<thead>
<tr>
<th>h2</th>
<th>Bias</th>
<th>Seh2</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.4724</td>
<td>0.07582</td>
<td>0.1707</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>h2</th>
<th>Bias</th>
<th>Seh2</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.4340</td>
<td>0.07792</td>
<td>0.1657</td>
</tr>
</tbody>
</table>

* 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.

<table>
<thead>
<tr>
<th>h2</th>
<th>Bias</th>
<th>Seh2</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.3241</td>
<td>0.1151</td>
<td>0.1846</td>
</tr>
<tr>
<td>h2</td>
<td>Bias</td>
<td>Seh2</td>
</tr>
<tr>
<td>0.3347</td>
<td>0.1105</td>
<td>0.1813</td>
</tr>
</tbody>
</table>

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(20)

* ***** 1. Declare various structures *****
FACT{lev=4} Loc: &{lev=2} Rep: &{lev=5} Blk: &{lev=25} Geno
SCALAR Sg2, Sge2, Sgi2, Vgg, Vce, Vii, Vgi, Vge, Vle, h2, S, Se, Bias
SYM{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 *****
REML[print=s] Y

* ***** 3.2 Compute heritability and its SE *****
VKEEP[SIGMA2=Sge2; vcov=Vcov] Geno+Geno.Loc; COMP=Sg2, Sgi2
CALC Vgg, Vgi, Vii, Vge, Vle, Vce, Vcov=[2,3,4,4,4,2,3,2,3,4]
CALC h2=Sg2/(Sg2+Sgi2+Sge2)
CALC Bias=-h2*(Vgg-h2*(Vgg+Vgi+Vge))/Sg2/Sg2
CALC Se=Vgg+Vii+Vce+2*(Vgi+Vge+Vle) & Se=Vgg+h2*h2*Se-2*h2*(Vgg+Vgi+Vge)
CALC Se=h2*SRT(Se)/Sg2

* ***** 3.3 Print heritability and SE *****
Print h2, Bias, Se

* Under complete blocks *

* ***** 3.1 Compute variance components *****
REML[print=s] Y

* ***** 3.2 Compute heritability and its SE *****
VKEEP[SIGMA2=Sge2; vcov=Vcov_r] Geno+Geno.Loc; COMP=Sg2, Sgi2
EQUA Vcov_r; lp(Vgg, Vgi, Vii, Vge, Vle, Vce)
CALC h2=Sg2/(Sg2+Sgi2+Sge2)
CALC Bias=-h2*(Vgg-h2*(Vgg+Vgi+Vge))/Sg2/Sg2
CALC Se=Vgg+Vii+Vce+2*(Vgi+Vge+Vle) & Se=Vgg+h2*h2*Se-2*h2*(Vgg+Vgi+Vge)
CALC Se=h2*SRT(Se)/Sg2

* ***** 3.3 Print heritability and SE *****
Print h2, Bias, Se
ENDF
close: stop

31
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]


Open 'Critical.txt'; CH=2;Fl=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

Scalar A1,A2,B1,B2,B,M,C,A
Scalar Var_A1,Cov_A1B1,Var_B1,Var_A2,Cov_A2B2,Var_B2, Df1, Df2
Scalar 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
Scalar G, Fun, Time, CF, SE, V11, V12, V22, Tval, H1, LAsymp, 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; IP(A1,B1) : & VcovLin; IP(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; IP(A2,B2) & VcovLin; IP(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 LAsym=CP-Ned(.975)*SE : CALC UAsym=CP+Ned(.975)*SE

Print CP,SE,LAsym, UAsym,LExact,UExact

* Critical period estimates and standard errors : Approximate
  - Linear-Logistic relationship *
  Print|Curve=Logistic;Prin=m,s,e,c] WeekW
  Rkeep EST=EstLog; Vcov=VcovLog
  Equa EstLog; IP(B,M,C,A) &: VcovLog ;
  IP(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=IF(Fun=(A1+B1*Time-A-C/(1+Exp(-B*(Time-M)))))**2
Model[Function=Fun]
Recycle 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 LAsym=CP-Ned(.975)*SE : Calc UAsym=CP+Ned(.975)*SE

PRINT Time,SE,LAsym, UAsym

Rest Y, WeekW
   Endf
   Endf
clos
stop

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Computer and Biometrics Services Unit
ICARDA

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]
Var[nvalu=35] Fullrow
Open 'bwhth2.dat'; ch=2;fl=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;ficle=4(4),2(6),5(9) 
      ; deci=4(0),2,2,5(3)
   Else
   Calc Y=Sum(Y) : Calc Y=(Y/Tot)*100.
   Model Y; Fltt=F
   Ftcv[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;ficle=4(4),2(6),5(9) 
      ; deci=4(0),2,2,5(3)
endif

endf

clos
stop

Unit[25]
Var[nvalu=30] Fullrow
Open 'bwhth1.dat'; ch=2;fl=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

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

Print[ch=3; i pari=*] i, Row, Col, Geno, Temp, Rbarsq, B, M, C, A, D50; flei=4(4),2(6),5(9) \\
    ; decl=4(0),2,2,5(3)
Else
Calc Y=Sum(Y) : Calc Y=(Y/Tot)*100.
Model Y ; Fit=F
Fit[ curve=log] Time
Graph[ncol=35; nrow=16] Y, F; Time; Meth=p, c
Rkeep 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; i pari=*] i, Row, Col, Geno, Temp, Rbarsq, B, M, C, A, D50; flei=4(4),2(6),5(9) \\
    ; decl=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[level=15] Geno
Read[ch=2; End=*; Form=(1,-3,2,-5,1)] Geno, Temp, D50

Var[avail=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.land. D50. ne.0

Model D50 ; fit=F
Fit[curve=qdq] Temp
Rkeep 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.l.0.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$[j]=Btemp
Calc SeSlope$[j]=Sqrt(Vcov$[2;2])
Calc SeBaseT$[j]=ABS(Btemp)*SQRRT(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*SeSlope

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

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

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

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

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

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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=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

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
Var[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=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
Var[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=1(-2,9)] Time,h[1...8]
Calc h[9]=Vmean(h[1...8])

* Fitting on mean values over plants*
Model h[9]
Terms Time*Geno
Fit[curve=exp;prin=*, Fpro=y]Time
Add[prin=*, Fpro=y]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]=1(^*)
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

ddf

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

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Assignment 1: Randomize \( N (=30, \text{say}) \) numbers and draw a random sample of size \( M (=20, \text{say}) \) 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


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 RCB

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, NNit, NGeno; 4, 3, 5
Scalar NPLOTS
Calc NPLOTS=NRep*NNit*NGeno

Unit[NPLOTS]
Factor[Levels=NRep] Rep
Factor[Levels=NNit] Nitrogen
Factor[Levels=NGeno] Geno
Generate Rep,Nitrogen,Geno

Scalar NNiGe
Calculate NNiGe=NNit*NGeno
Factor[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 RCB

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
    
    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

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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 RCB

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[Blc = 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 **************************