Working Draft

Not to be Cited

Computing Biometrics at ICARDA

Volume II

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

January 1995

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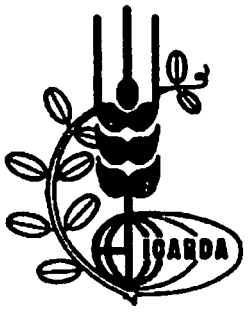

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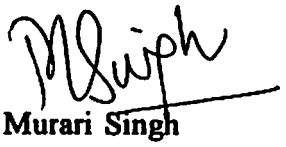
Contents:

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 the eight of such modules. 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.

Seven of these programs are written in Genstat and one in FORTRAN, but volunteers are most welcome to code them in other computing languages as well.



Murari Singh
Sr. Biometrician

2 January 1995

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 incomplete blocks

1. Introduction:

This program analyses data from multi-locational variety trials conducted in incomplete blocks. It displays individual location data analysis, combined analysis over locations to evaluate GxE interaction, computes stability indices, clustering of environments and of genotypes and estimates of variance components for genotypes, heritability estimates.

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, clustering, variance components, heritability.

3. Input/Output:

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

Output:
Individual location ANOVA, means, se, %cv, combined analysis over locations, stability indices, clustering of environments and of genotypes, estimates of variance components for genotypes, heritability.

4. Location of the program:

Program:
A:\CompBiom\94\MLVT2.gen
(Software: GENSTAT 5 Rel 3.1)

5. Location of illustrative data and results:

Data:
A:\CompBiom\94\MLVT2.Txt
Results:
A:\CompBiom\94\MLVT2.opt

6. Client(s)

All plant breeders at ICARDA

7. Date

November 1994

8. Comments

M. Singh

Program:

```
" ************************************************************************
        GENSTAT program for analyzing multi-locational variety trials
        conducted in incomplete blocks.

        Software environment: Genstat 5 Rel 3.1

************************************************************************ "

OPEN 'MLVT2.Txt';CH=2;FI=IN
Scalar Nlines
Read[ch=2]Nlines
Skip[ch=2] Nlines

Scal NRep, NBlk,NGeno,NLoc
Read [ch=2] NLoc,NRep,NBlk,NGeno

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
Fact [Leve=NBlk] Blk
Read [Ch=2] Loc, Rep,Blk, Geno,Yield



" ======  Below is only for statistical programmers use =======  "


" 1.  Individual locations analysis "

Vcomp[Fixed=Rep+Geno]Rep/Blk+Geno

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

For I=1...NLoc     ; MN=Mean[1...NLoc]
Rest Yield; Cond=Loc.EQ.I
Reml[prin=m,c,means,s,w] Yield
Vkeep Geno; Means=TDum
Equa TDum;MN
Dele[Rede=Y] TDum
Rest Yield
Endf
```

```
Vari[Nval=NLoc] LocMean

" 2. Combined analysis over locations "

Vcomp[Fixed=Rep+Geno*Loc]Loc+Loc.Rep/Blk+Geno/Loc
Reml[prin=m,c,means,s,w] Yield
Vkeep Geno; Means=TDum
Equa TDum; GenoMean
Dele[Rede=Y]  TDum

Vkeep 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. Compute stability indices "

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


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

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

    Dele GE, EG

Vari[ Nval=NGxNL] GEData
Equa  !P(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
Vari[values=1...NGeno]Order0,Order1
For D= GenoMean, Slope, DeviMs,GenoCV,Wricke,Pla_Pet,Plaisted,Shukla ; \
   DD= RGenoMn, RSlope, RDeviMs,RGenoCV,RWricke,RPla_Pet,RPlaist,RShukla
Sort[dire=D; Index=D] Order0
Sort Order0,Order1
Calc DD=Order1
endf

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

" 4. Clustering of Environments "

Symm[Rows=NLoc] Simi
```

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

" 5. Clustering of Genotypes "
Symm[Rows=NGeno] Simi
Fsim[Simi=Simi] Mean[1...NLoc]; Test=Euclidean
Hclu[ Prin=a,d] Simi
Dele[Rede=Y] Simi

" 6. Estimation of variance components"

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


" 7. Estimation of heritabilities"

" 7.1 From individual environments"

SCAL SGg2,SGe2,h2
Scal Vgg,Vge,Vee,Bias, Seh2
symm[3] Vcov
symm[2] Vcov_r

For i=1...NLoc

Rest Yield; Loc.eq.i

"  Using incomplete block design: block effects random "

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

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

PRINT SGg2,SGe2,h2,Bias,Seh2

" Under complete blocks "

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

VKEEP[SIGMA2=SGe2;vcov=Vcov_r] Geno; COMP=SGg2
EQUA Vcov_r ; Ip(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

PRINT SGg2,SGe2,h2,Bias,Seh2

rest Yield
Endf

" 8.2 Overall environments"

SCALAR SGg2,SGe2,SGi2,SGb2,Vgg,Vee,Vii,Vgi,Vge,Vie, h2, Bias,Se
  SYMM[4] Vcov
    Symm[3] Vcov_r

" Under incomplete blocks: Block effects random "

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

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)
           CALC Se=Vgg+h2*h2*Se-2*h2*(Vgg+Vgi+Vge)
               CALC Se=h2*SQRT(Se)/SGg2

Print h2, Bias, Se

" Under complete blocks "

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

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)
      CALC Se=Vgg+h2*h2*Se-2*h2*(Vgg+Vgi+Vge)
       CALC Se=h2*SQRT(Se)/SGg2

Print h2, Bias, Se


Clos
Stop
```

Output: Not included

Computer and Biometrics Services Unit
ICARDA

Serial Number -002

FORTRAN Modules in Computing Biometrics

Title: **Estimation and testing significance of genotypic and phenotypic correlations between traits using data from randomized complete block design.**

1. Introduction:

This program performs bivariate analysis of variance to compute genotypic, phenotypic and environmental correlations between traits observed using a randomized complete block design. For details, see Singh , M. 1992. Genotypic and Phenotypic correlations in Plant Traits. ICARDA-033:May 1992. International Center for Agricultural research in the Dry Areas, P.O. Box 5466, Aleppo, Syria. pp 279.

2. Areas of application and keywords:

Plant breeding and genetics,Crop improvement.

3. Input/Output:

Input:
Plot-wise values of replications (i.e. complete blocks), genotype, variable(s).

Output:
Bivariate analysis of variance, estimates of genotypic variance, phenotypic variance, environmental variance, and covariances between pairs of traits, for a given number of sets of traits

4. Location of the program:

Program:
A:\CompBiom\94\Genocorr.exe
A:\CompBiom\94\Genocorr.for
(Software: FORTRAN Program)

5. Location of illustrative data and results:

Data:
A:\CompBiom\94\Genocorr.txt
Results:
A:\CompBiom\94\Genocorr.out

6. Client(s)

Plant breeders

7. Date

June 1994 (First edition January 1991)

8. Comments

M. Singh

Program:

```
      REAL HH(31)
      REAL ZZ(31,4,28), X(4,28),Y(4,28)
      INTEGER IN(4), IOUT(4)
      DATA IN /3,10,17,25/
      DATA IOUT /9,16,24,31/
C=============================================================
C  FOR  A STUDENT FROM A NARS
      TYPE*, ' NV,NB , NRN'
      READ(1,*) NV,NB,NRN
      NTOT=NV*NB
      DO 50 I=1,NTOT
      READ (5,*) I1,I2,(HH(K),K=3,31)
      DO 55 J=1,NB
      DO 55 K=1,NV
 55   ZZ(K,I1,I2)=HH(K)
  50 CONTINUE
      DO 65 ISET=1,4
      WRITE (6,911) ISET
 911  FORMAT(/,'********** SET OF VARIABLES**** = ', I5,/)
      IOUT0=IOUT(ISET)
      IOUT1=IOUT(ISET)-1
      IN0=IN(ISET)
      DO 60 K=IN0,IOUT1
      K1=K+1
      DO 60 KK=K1,IOUT0
      WRITE (6,912) K,KK
 912  FORMAT(/,'********** NUMBERS OF VARIABLES IN PAIR = ',I4,I4,/)
      DO 70 J=1,NB
      DO 70 I=1,NV
      Y(J,I)=ZZ(K,J,I)
 70   X(J,I) =ZZ(KK,J,I)
      CALL CORR(NV,NB,X,Y,NRN)
 60   CONTINUE
 65   CONTINUE
C 10   CONTINUE
      STOP
      END
      SUBROUTINE CORR( NV,NB,X,Y,NRN)
      REAL  X(4,30),Y(4,30), TX(30),TY(30),BX(4),BY(4)
      V=NV
      B=NB
      DO 50 J=1,NB
      BX(J)=0.
 50   BY(J)=0.
      DO 60 I=1,NV
      TX(I)=0.
  60  TY(I)=0.
      GX=0.
      GY=0.
      GXX=0.
```

```
      GYY=0.
      GXY=0.
      DO 100 J=1,NB
      DO 100 I=1,NV
      YIJ=Y(J,I)
      XIJ=X(J,I)
      BX(J)=BX(J)+XIJ
      BY(J)=BY(J)+YIJ
      TX(I)=TX(I)+XIJ
      TY(I)=TY(I)+YIJ
      GX=GX+XIJ
      GY=GY+YIJ
      GXX=GXX+XIJ*XIJ
      GYY=GYY+YIJ*YIJ
      GXY=GXY+XIJ*YIJ
100   CONTINUE
      CFX=GX*GX/V/B
      CFY=GY*GY/V/B
      CFXY=GX*GY/V/B
      GXX=GXX-CFX
      GYY=GYY-CFY
      GXY=GXY-CFXY
      BSX=0.
      BSY=0.
      BSXY=0.
      TSX=0.
      TSY=0.
      TSXY=0.
      DO 110 J=1,NB
      BSX=BSX+BX(J)*BX(J)
      BSXY=BSXY+BX(J)*BY(J)
110   BSY=BSY+BY(J)*BY(J)
      DO 120 I=1,NV
      HX=TX(I)/B
      HY=TY(I)/B
      TSX=TSX+TX(I)*TX(I)
      TSXY=TSXY+TX(I)*TY(I)
120   TSY=TSY+TY(I)*TY(I)
      BSX=BSX/V-CFX
      BSY=BSY/V-CFY
      TSX=TSX/B-CFX
      TSY=TSY/B-CFY
      BSXY=BSXY/V-CFXY
      TSXY=TSXY/B-CFXY
      DFB=B-1
      DFT=V-1
      DFTO=V*B-1
      DFE=(B-1)*(V-1)
      ERRX=GXX-BSX-TSX
      ERRY=GYY-BSY-TSY
      ERRXY=GXY-BSXY-TSXY
```

```
      SGEX=ERRX/DFE
      SGEY=ERRY/DFE
      SGEXY=ERRXY/DFE
      SGGX=(TSX/DFT-SGEX)/B
      SGGY=(TSY/DFT-SGEY)/B
      SGGXY=(TSXY/DFT-SGEXY)/B
      SGPX=SGGX+SGEX
      SGPY=SGGY+SGEY
      SGPXY= SGGXY+SGEXY
      ROG=-99.
      IF((SGGX.GT.0.).AND.(SGGY.GT.0.)) ROG=SGGXY/SQRT(SGGX*SGGY)
      ROE=SGEXY/SQRT(SGEX*SGEY)
      ROPA=TSXY/SQRT(TSX*TSY)
      ROP=-99.
      IF((SGPX.GT.0.).AND.(SGPY.GT.0.)) ROP=SGPXY/SQRT(SGPX*SGPY)
C       WRITE(7,800) NV,NB,SGGX,SGGY,SGEX,SGEY,ROG,ROE,ROP,ROPA
C 800  FORMAT(10X, 2(I4,X),3X,4(F12.5,X),4(F10.6,X))
      WRITE(6,900)
C       WRITE(6,*) DFB,BSX,BSY,BSXY
C       WRITE(6,*) DFT,TSX,TSY,TSXY
C       WRITE(6,*) DFE,SGEX,SGEY,ERRXY
      BSX=BSX/DFB
      BSY=BSY/DFB
      TSX=TSX/DFT
      TSY=TSY/DFT
 900  FORMAT( X,' ******* BIVARIATE ANALYSIS OF VARIANCE ***')
      BSXY=BSXY/DFB
      TSXY=TSXY/DFT
      WRITE(6,*) DFB,BSX,BSY,BSXY
      WRITE(6,*) DFT,TSX,TSY,TSXY
      WRITE(6,*) DFE,SGEX,SGEY,SGEXY
      WRITE(6,*) SGPX,SGPY,SGPXY
      WRITE(6,*) NV,NB,SGGX,SGGY,SGEX,SGEY,ROG,ROE,ROP,ROPA
      HX2=SGGX/(SGGX+SGEX)
      HY2=SGGY/(SGGY+SGEY)
      WRITE( 6,*) HX2,HY2
      CALL SIMG(NV,NB,HX2,HY2,ROE,ROG,NRN)
      CALL SIMP(NV,NB,HX2,HY2,ROE,ROP,NRN)
      RETURN
      END
      SUBROUTINE SIMG(NV,NB,HX2,HY2,ROE,ROG,NRN)
      REAL ST(2),VR(2),RM(2,4)
      REAL PLEV(10),RLEV(2,10),HV1(5000),HV2(5000)
      DATA PLEV/ .005,.01,.025,.05,.1,.90,.95,.975,.99,.995/
C
C     **********************************************
C       This presents simulated significance levels  and
c       simulated moments of r(g),  approximate variances,and
c       probability of invalid estimates of rho(g)  when population
c                    rho(g)=0.
c       Bivariate normal distribution assumed.
```

```
c     ***********************************************
C
      NPT=10
      NST=2
      ZMN=0.
      ZSD=1.
      CALL G05CBF(0)
      B=NB
      V=NV
      Q=V-1.
      F=Q*(B-1.)
      NQ=Q
      NF=F
C
c              note  :   above vhx , vhy are in square form
c                vhx,vhy =var(g)/( var(g)+var(e) )
C                                APPROXIMATION
      XL2=1./HX2-1.
      YL2=1./HY2-1.
      XL=SQRT(XL2)
      YL=SQRT(YL2)
      HX=SQRT(HX2)
      HY=SQRT(HY2)
      SG1=SQRT(B+XL2)
      SG2=SQRT(B+YL2)
      SE1=XL
      SE2=YL
C                  approximations : untransformed, arcsin
C           Genotype correlation  r(g) : VR(1) , VR(2)
      ROE2=ROE*ROE
      VR(1)=1./Q+(XL2+YL2)/B/Q+(1.+ROE2)*XL2*YL2/B/F
      VR(2)=VR(1)
      ROPA=ROE*XL*YL/(SG1*SG2)
C     ---------- SIMULATION PART----------
C
C
      DO 155 I=1,NST
      DO 156 J=1,4
  156 RM(I,J)=0.
  155 CONTINUE
      NVC=0
      DO 555 II=1,NRN
C     GENERATE WISHART VARIABLES GXX,GYY,GXY WITH NQ,SG1,SG2,ROPA
      N=NQ
      RHO=ROPA
      SGX=SG1
      SGY=SG2
c
      XX=0.
      YY=0.
      XY=0.
```

```
      DO 100 I=1,N
      H1=G05DDF(ZMN,ZSD)
      H2=G05DDF(ZMN,ZSD)
      H2=(RHO*H1+H2*SQRT(1.-RHO*RHO))*SGY
      H1=H1*SGX
      XX=XX+H1*H1
      YY=YY+H2*H2
      XY=XY+H1*H2
  100 CONTINUE
      GXX=XX
      GYY=YY
      GXY=XY
C     GENARATE WISHART VARIABLES EXX,EYY,EXY WITH NF,SE1,SE2,ROE
      RHO=ROE
      N=NF
      SGX=SE1
      SGY=SE2
c
      XX=0.
      YY=0.
      XY=0.
      DO 200 I=1,N
      H1=G05DDF(ZMN,ZSD)
      H2=G05DDF(ZMN,ZSD)
      H2=(RHO*H1+H2*SQRT(1.-RHO*RHO))*SGY
      H1=H1*SGX
      XX=XX+H1*H1
      YY=YY+H2*H2
      XY=XY+H1*H2
  200 CONTINUE
      EXX=XX
      EXY=XY
      EYY=YY
C
      D1=(GXX/Q-EXX/F)/B
      D2=(GYY/Q-EYY/F)/B
      IF((D1.LE.0.).OR.(D2.LE.0.)) GOTO 555
      H=(GXY/Q-EXY/F)/B/SQRT(D1*D2)
C
      IF(ABS(H).GT.1.) GOTO 555
      ST(1)=H
      ST(2)=ASIN(H)
      NVC=NVC+1
      HV1(NVC)=ST(1)
      HV2(NVC)=ST(2)
C
      DO 240 I=1,NST
      HH=1.
      STI=ST(I)
      DO 250 J=1,4
      HH=HH*STI
```

```
      RM(I,J)=RM(I,J)+HH
  250 CONTINUE
  240 CONTINUE
  555 CONTINUE
      PERC=1.-FLOAT(NVC)/FLOAT(NRN)
C
      NNRN=NVC
      FNRN=NNRN
      IF(NVC.LE.1) GOTO 1
C
      DO 260 I=1,NST
      DO 270 J=1,4
  270 RM(I,J)=RM(I,J)/FNRN
      RM(I,3)=RM(I,3)/RM(I,2)/SQRT(RM(I,2))
      RM(I,4)=RM(I,4)/RM(I,2)/RM(I,2)-3.
  260 CONTINUE
C       write mean=bias as 10* mean ; SD= 10* standard deviation
      DO 280 I=1,NST
      RM(I,1)=10.*RM(I,1)
  280 RM(I,2)=10.*SQRT(RM(I,2))
      VR(1)=10.*SQRT(VR(1))
  290 VR(2)=10.*SQRT(VR(2))
C
C     ARRANGE HV1, HV2 IN ASCENDING ORDER OF MAGNITUDE
      CALL ORDER(NVC,HV1)
      CALL ORDER(NVC,HV2)
C
      DO 320 K=1,NPT
      INT1=FNRN*PLEV(K)
      RLEV(1,K)=HV1(INT1)
      RLEV(2,K)=HV2(INT1)
  320 CONTINUE
      WRITE(6,906) HX2,HY2,ROE,NV,NB,PERC,RM(1,1),RM(1,2),VR(1),
     +RM(1,3),RM(1,4),(RLEV(1,J),J=1,NPT)
      WRITE(6,907) RM(2,1),RM(2,2),VR(2),RM(2,3),RM(2,4),
     +(RLEV(2,J),J=1,NPT)
  906 FORMAT(2X,2(F3.1,X),F3.1,X,I3,X,I2,X,F4.2,
     +3X,F5.2,X,F5.3,X,F5.2,X,F5.2,X,F5.2,3X,10(F5.3,X))
  907 FORMAT(28X,F5.2,X,F5.2,X,F5.2,X,F5.2,X,F5.2,3X,10(F5.2,X))
    1 RETURN
      END
      SUBROUTINE SIMP(NV,NB,HX2,HY2,ROE,ROP,NRN)
      REAL ST(2),VR(2),RM(2,4)
      REAL PLEV(10),RLEV(2,10),HV1(5000),HV2(5000)
      DATA PLEV/ .005,.01,.025,.05,.1,.90,.95,.975,.99,.995/
C     ****************************************************************
C       This presents simulated moments ,critical values , approximate
C       variances of rho(pb), and probability of invalid estimates
c       of rho(pb) when   population rho(pb) =0.
c        Bivariate normal distribution assumed   .
C     ****************************************************************
```

```
C
      NPT=10
      NST=2
      ZMN=0.
      ZSD=1.
      CALL G05CBF(0)
      B=NB
      V=NV
      Q=V-1.
      F=Q*(B-1.)
      NQ=Q
      NF=F
c              note  :   above vhx , vhy are in square form
c                vhx,vhy =var(g)/( var(g)+var(e) )
C                              APPROXIMATION
      XL2=1./HX2-1.
      YL2=1./HY2-1.
      XL=SQRT(XL2)
      YL=SQRT(YL2)
      HX=SQRT(HX2)
      HY=SQRT(HY2)
      SG1=SQRT(B+XL2)
      SG2=SQRT(B+YL2)
      SE1=XL
      SE2=YL
C                  approximations : untransformed, arcsin
C     Phenotype correlation  r(gb) : VR(1),VR(2)
      ROG=-ROE*XL*YL
      VR(1)=(1.+(B-1.)*(1.+ROG*ROG)*HX2*HY2)/B/Q
      VR(2)=VR(1)
      ROPA=(1.-B)*ROE*XL*YL/SG1/SG2
C     ---------- SIMULATION PART----------
C
C
      DO 155 I=1,NST
      DO 156 J=1,4
  156 RM(I,J)=0.
  155 CONTINUE
      NVC=0
      DO 555 II=1,NRN
C     GENERATE WISHART MATRIX GXX,GYY,GXY WITH NQ, SG1,SG2,ROPA
      N=NQ
      RHO=ROPA
      SGX=SG1
      SGY=SG2
      XX=0.
      YY=0.
      XY=0.
      DO 100 I=1,N
      H1=G05DDF(ZMN,ZSD)
      H2=G05DDF(ZMN,ZSD)
```

```
      H2=(RHO*H1+H2*SQRT(1.-RHO*RHO))*SGY
      H1=H1*SGX
      XX=XX+H1*H1
      YY=YY+H2*H2
      XY=XY+H1*H2
  100 CONTINUE
      GXX=XX
      GYY=YY
      GXY=XY
C     GENERATE WISHART MATRIX EXX,EXY,EYY WITH NF, SE1,SE2,ROE
      N=NF
      RHO=ROE
      SGX=SE1
      SGY=SE2
      XX=0.
      YY=0.
      XY=0.
      DO 200 I=1,N
      H1=G05DDF(ZMN,ZSD)
      H2=G05DDF(ZMN,ZSD)
      H2=(RHO*H1+H2*SQRT(1.-RHO*RHO))*SGY
      H1=H1*SGX
      XX=XX+H1*H1
      YY=YY+H2*H2
      XY=XY+H1*H2
  200 CONTINUE
      EXX=XX
      EXY=XY
      EYY=YY
C
      D1=(GXX/Q-EXX/F)/B
      D2=(GYY/Q-EYY/F)/B
      IF((D1.LE.0.).OR.(D2.LE.0.)) GOTO 555
      H=(GXY+EXY)/SQRT((GXX+EXX)*(GYY+EYY))
      IF(ABS(H).GT.1.) GOTO 555
      ST(1)=H
      ST(2)=ASIN(H)
      NVC=NVC+1
      HV1(NVC)=ST(1)
      HV2(NVC)=ST(2)
C
      DO 240 I=1,NST
      HH=1.
      STI=ST(I)
      DO 250 J=1,4
      HH=HH*STI
      RM(I,J)=RM(I,J)+HH
  250 CONTINUE
  240 CONTINUE
  555 CONTINUE
      PERC=1.-FLOAT(NVC)/FLOAT(NRN)
```

```
      FNRN=NVC
      IF(NVC.LE.1)  GOTO 1
C
      DO 260 I=1,NST
      DO 270 J=1,4
  270 RM(I,J)=RM(I,J)/FNRN
      RM(I,3)=RM(I,3)/RM(I,2)/SQRT(RM(I,2))
      RM(I,4)=RM(I,4)/RM(I,2)/RM(I,2)-3.
  260 CONTINUE
c       write mean=bias as 10* mean ; SD= 10* standard deviation
      DO 280 I=1,NST
      RM(I,1)=10.*RM(I,1)
  280 RM(I,2)=10.*SQRT(RM(I,2))
      VR(1)=10.*SQRT(VR(1))
      VR(2)=10.*SQRT(VR(2))
C
      CALL ORDER(NVC,HV1)
      CALL ORDER(NVC,HV2)
      DO 320 K=1,NPT
      INT1=FNRN*PLEV(K)
      RLEV(1,K)=HV1(INT1)
      RLEV(2,K)=HV2(INT1)
  320 CONTINUE
      WRITE(6,908) HX2,HY2,ROE,NV,NB,PERC,RM(1,1),RM(1,2),VR(1),
     +RM(1,3),RM(1,4),(RLEV(1,J),J=1,NPT)
      WRITE(6,909) RM(2,1),RM(2,2),VR(2),RM(2,3),RM(2,4),
     +(RLEV(2,J),J=1,NPT)
  908 FORMAT(2X,2(F3.1,X),F3.1,X,I3,X,I2,X,F4.2,
     +3X,F4.2,X,F5.3,X,F5.3,X,F5.2,X,F5.2,3X,10(F5.3,X))
  909 FORMAT(28X,F4.2,X,F5.3,X,F5.3,X,F5.2,X,F5.2,3X,10(F5.2,X))
    1 RETURN
      END
      SUBROUTINE ORDER(N,X)
      REAL X(5000)
C     ARRANGE X IN ASCENDING ORDER OF MAGNITUDE
      DO 5 I=2,N
      IF (X(I)-X(I-1))1,5,5
    1 TEMP=X(I)
      IM=I-1
      DO 3 J=1,IM
      L=I-J
      IF (TEMP-X(L))2,4,4
    2 X(L+1)=X(L)
    3 CONTINUE
      X(1)=TEMP
      GOTO 5
    4 X(L+1)=TEMP
    5 CONTINUE
      RETURN
      END
```

Output Not included

Computer and Biometrics Services Unit
ICARDA

Serial Number -003

GENSTAT Modules in Computing Biometrics

Title: **Analysis of data from Diallel experiments-I**

1. Introduction:

This program analyses data from a diallel experiment using
i) Hayman's method: to estimate components of variation, Vr-Wr graphs,
ii) Griffing's method III and both models for estimating combining ability effects and genetic variance components.

2. Areas of application and keywords:

Plant breeding and genetics,Crop improvement.

3. Input/Output:

Input:
Plot-wise values of replications, blocks, first parent, second parent, variable(s).

Output:

Griffing's approach:	Gca, sca's estimates and se's, estimates of gca and sca variances
Hayman's approach:	Estimates of components of variation and se's, Parent -offsprings array variances/covariances (Vr -Wr), tests on validity of model, estimate of products of the two allels frequencies, number of dominant genes, heritability in broad sense and narrow sense etc. These for F1's data and also for F2's data;

Heterosis and inbreeding coefficients.

4. Location of the program:

Program:
A:\CompBiom\94\Diallel1.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:
A:\CompBiom\94\diallel1.Txt
Results:
A:\CompBiom\94\diallel1.opt

6. Client(s)

Mr. M. Labdi and Dr. K. B. Singh

7. Date

February 1994

8. Comments

M. Singh

Program:

```
"*****************************************************************************

Estimation of components of variation using
                    - Hayman's approach  and
                    - Griffing's approach.

******************************************************************************
******************************************************************************
"



Scal NRep,NBlk,Np, Coeff ; 2,8,8,1

Scal NG, NGAll
Calc NG=Int(Np*(Np+1)/2)
Calc NGAll=Np*Np

Calc Unit=NGAll*NRep
Unit[Unit]



" *********************  Read Data from Labdi's file ********* "

Fact[leve=NRep]Rep:&[leve=NBlk]Blk

Fact[leve=NGAll;labe=!t( P1,F12,F13,F14,F15,F16,F17,F18, \
                  P2,F23,F24,F25,F26,F27,F28, P3,F34,F35,F36,F37,F38, \
   P4,F45,F46,F47,F48, P5,F56,F57,F58, P6,F67,F68, P7,F78, P8, \
    S12,S13,S14,S15,S16,S17,S18,\
   S23,S24,S25,S26,S27,S28, S34,S35,S36,S37,S38, \
   S45,S46,S47,S48, S56,S57,S58, S67,S68, S78)] Geno


Open 'Diallel1.txt' ; ch=2; fi=in
Scal Nlines
Read[Ch=2]Nlines
Skip[ch=2]Nlines
Read[ch=2] Rep,Blk,Geno,NPlants, SC1,SC1%, SC2,SC2%, SC3,SC3% ;frep=le,le,la
Scal Sigma2
Scal SigRep,SigBlk,DfRep,DfBlk,DfError
Scalar E
Scal DfPlotEr
Vari[nval=NGAll] GMean0
```

```
Vari[nval=NG]GMean

For Yield = SC1 ",SC1%, SC2,SC2%, SC3,SC3% "

Vcomp[fixed=Rep+Geno]Rep/Blk+Geno
Reml Yield
Vkeep[sigma2=Sigma2] Geno; Means=MT
Equa MT; GMean0
Calc E=Sigma2/NRep
Calc DfRep=NRep-1: & DfBlk=NRep*(NBlk-1)
Calc DfPlotEr=NRep*NGAll-DfRep-DfBlk-(NGAll-1)


Vari[Nvalu=NG]ParF1,ParF2,GMean
Scal ij,ij1
Calc ij=1
For i=1...Np
For j=i...Np
Calc ParF1$[ij]=GMean0$[ij]
If i.eq.j
   Calc ParF2$[ij]=ParF1$[ij]
   else
   Calc ij1=Np*(Np+1)/2+ij-i
   Calc ParF2$[ij]=GMean0$[ij1]
endif
Calc ij=ij+1
Endf:Endf


" ********** Generate Parent levels ***************"

Fact[leve=Np;Nval=NG]P1,P2
Scal ij
Calc ij=0
For i=1...Np : For j=i...Np
Calc ij=ij+1
Calc P1$[ij]=Int(i)   : & P2$[ij]=Int(j)
Endf : Endf


Print P1,P2,ParF1,ParF2



"*********** Griffing's method ************ "

Vari [nval=NG]G[1...Np],SCAEff[1,2]

For i=1...Np;GG=G[1...Np]
Calc GG=(P1.eq.i)+(P2.eq.i)
Endf
```

```
Scal Mn
For Dum=ParF1,ParF2; SCA=SCAEff[1,2]
Calc Mn=Mean(Dum)

" Griffing model I "

Calc Dum=Dum-Mn
Model Dum ; fitt=SCA
Fit [prin=m,s;fpro=y] G[1...Np]
Rkeep DF=df;devi=ss
Fit [cons=o;prin=m,e] G[1...Np]
Calc SCA=Dum-SCA

"  Griffing model II "

Scal SeS2G,SeS2S,SeS2A,SeS2D,Sigma2G,Sigma2S,Sigma2A,Sigma2D,GCAMS
Calc Sigma2S=ss/df-Sigma2/NRep
Calc GCAMS=((Nobs(Dum)-1)*Var(Dum)-ss)/(Np-1): & Sigma2G=(GCAMS-ss/df)/(Np+2)
Calc SeS2G=sqrt(  (2*GCAMS**2+4*(ss/df)**2/Np/(Np+2) )/(Np-1)/(Np+2)  )
Calc SeS2S=sqrt(   4*(ss/df)**2/Np/(Np-1)+2*(Sigma2/NRep)**2/DfPlotEr )
Calc Sigma2A=2*Sigma2G
Calc SeS2A=2*SeS2G
Calc Sigma2D=Sigma2S
Calc SeS2D=SeS2S
Print E,Sigma2G,SeS2G,Sigma2S,SeS2S,Sigma2A,SeS2A,Sigma2D,SeS2D
Calc Dum=Dum+Mn
Endf
Rest ParF1,SCAEff[1],ParF2,SCAEff[2] ; cond=P1.ne.P2
print P1,P2,ParF1,SCAEff[1],ParF2,SCAEff[2] ;fiel=10
Rest P1,P2,ParF1,SCAEff[1],ParF2,SCAEff[2]
Scal SeGca, SeSca
Calc SeGca=sqrt((Np-1)*Sigma2/NRep/Np/(Np+2))
Calc SeSca=sqrt((Np*Np+Np+2)*Sigma2/NRep/(Np+1)/(Np+2)) "lines i <> j unequal"
Prin SeGca, SeSca



"  Parents + F1 s "
Calc GMean=ParF1

"
********** Notations used **********

1. Statistics available
P1, P2, GMean :      vectors (NG) of first parent, second parent and
                     resultig offspring (adjusted) mean
                     (over blocks/replicates) respectively
VoLo                   Variance of parent means (parent variability)
Vr                    Vector (Np) of variance of each of Np arrays
V1L1                   Mean(Vr): mean of array variances (bar Vr )
Wr                    Vector (Np) of covariances betwen parents and
```

```
                their offsprings for each array
WoLo1             Mean(Wr): mean of Np covariances in Wr
VoL1              Variance of means of arrays
ML1               mean of parents
MLo               mean of their nxn progenies

2. Variance components to be estimated

E                  sigma2/reps
                  expected environmental component of variation

D                  = VoLo-E
                  component of variation due to additive effects

H1                 =VoLo -4WoLo1+4V1L1 -(3Np-2)E/(n

          MDD: degree of dominance
          GenesPN: uv average: Positive negative gene freq product
          GenesDR : proportion of dominant and recessive genes
          CorrP  : correlation between parental order of dominance
                   and parental measurements

           NGGD: number of groups of genes exhibiting dominance
           h2ns : heritability in narrow sense
           h2bs : heritability in broad sense

"


" **********Variance of parents VoLo ********** "

Scalar VoLo
Rest GMean; Cond=P1.eq.P2
Calc VoLo=Var(GMean)
Rest GMean

"********** Compute  Vr , Wr, VrWr **********"

Vari[Nval=Np]Vr,Wr,WrVr,Fr,ArM,Vhelp,PMean,WrLim,WrPred,WrB1
Fact[leve=Np;valu=1...Np; nval=Np]Parents

For i=1...Np
Rest GMean; Cond=P1.eq.i.or.P2.eq.i
Calc Vr$[i]=Var(GMean)
Calc ArM$[i]=Mean(GMean)
Rest GMean
Rest GMean; Cond=P1.eq.i.and.P2.eq.i; saveset=set
Calc PMean$[i]=GMean$[set]
Rest GMean
Endf
```

```
" ******** Compute V1L1, VoL1,WoLo1 ******** "

Scal V1L1,VoL1,WoLo1
Calc V1L1=Mean(Vr)
Calc VoL1=Var(ArM)

For i=1...Np
Rest GMean; Cond=P1.eq.i.or.P2.eq.i; saveset=set
Calc Vhelp=GMean$[set]
Calc Wr$[i]=Covariance(PMean;Vhelp)
Endf
Calc WoLo1=Mean(Wr)

Scal ML1,MLo

Rest GMean; Cond=P1.eq.P2
Calc ML1=Mean(GMean)
Rest GMean; Cond=P1.ne.P2
Calc MLo=Mean(GMean)
Calc MLo=((Np-1)*MLo+ML1)/Np
Rest GMean

Calc WrVr=Wr+Vr
Calc WrLim=Sqrt(Vr*VoLo)
Model Wr; Fitt=WrPred
Fit Vr
Rkeep Est=Est; Vcov=Vcov;DF=DF
Scal Int, Slope
Equat Est; Ip(Int,Slope)

Calc Fr=2*(VoLo-WoLo1+V1L1-Wr-Vr)-2*(Np-2)*E/Np


Scal Tsq, Prob

" 1.  Test b=1 "
Calc Tsq =(Slope-1)**2/Vcov$[2;2]
Calc Prob=1-Fpro(Tsq;1;DF)
Print Tsq,DF,Prob

" 2.  Test the Validity of Hypothesis"

Calc Tsq=(Np-2)*(Var(Vr)-Var(Wr))**2/(Var(Vr)*Var(Wr)- \
        (Covariance(Wr;Vr))**2)/4
Calc Prob=1-Fpro(Tsq;4;DF)
Prin Tsq,DF,Prob


" ********** Components of variation **********"
```

```
Scal D,F,H1,H2,h2,s2,Np2,Np3
Calc Np2=Np*Np : & Np3=Np*Np2
Calc D=VoLo-E :& F=2*VoLo-4*WoLo1-2*(Np-2)*E/Np
Calc H1=VoLo-4*WoLo1+4*V1L1-(1+4*(Np-1)/Np/Coeff)*E
Calc H2=4*V1L1-4*VoL1-4*(Np-1)*(1+(Np-1)/Coeff)*E/Np2
Calc h2=4*(ML1-MLo)**2-4*(Np-1)*E/Np2

"*************** Standard errors ****************"

Calc s2=0.5*Var((Wr-Vr))
Calc SeD=Sqrt(s2*(1+1/Np)) :& SeF=Sqrt(s2*(4+20/Np-16/Np2+16/Np3))
Calc SeH1=Sqrt(s2*(1+41/Np-12/Np2+4/Np3)) : & SeH2=sqrt(s2*(36/Np))
Calc Seh2=Sqrt(s2*(16+16/Np2-32/Np3+16/Np/Np3)/Np)
Calc SeE=sqrt(s2/Np)
Print s2, D,SeD,F,SeF,H1,SeH1,H2,SeH2,h2,Seh2,E,SeE

Calc WrB1=D/4-H1/4+Vr
Print Parents,Vr,Wr,WrVr,Fr,ArM,PMean,WrLim,WrPred,WrB1
Print VoLo,V1L1,VoL1,WoLo1,ML1,MLo
Graph WrB1,WrLim,WrPred,Wr;Vr; symb=Parents; meth=c,c,c,p
Graph WrVr;PMean; symb=Parents; meth=p

" Other parameters on genes "
Scal MDD,GenesPN,GenesDR,CorrP, NGGD,h2ns,h2bs

Calc MDD=sqrt(H1/D) : & GenesPN=H2/4/H1
Calc GenesDR=(sqrt(4*D*H1)+F)/(sqrt(4*D*H1)-F)
Calc NGGD=h2/H2
Calc CorrP= Correlation(WrVr;PMean)

" Recalculate F as mean of Fr"
Calc F=Mean(Fr)

Calc h2ns=(0.5*D+0.5*H1-.5*H2-.5*F)/(.5*D+.5*H1-.25*H2-.5*F+E)
Calc h2bs=(0.5*D+0.5*H1-.25*H2-.5*F)/(.5*D+.5*H1-.25*H2-.5*F+E)

Prin MDD,GenesDR,GenesPN,CorrP, NGGD,h2ns,h2bs, F


" Most dominant and recessive parents"

Scal XPlus, XMinus, AFreq,aFreq, YDom,YRec
Scal YD,YR
Calc XPlus=(1+sqrt(1-4*(WoLo1-V1L1)/VoLo))/2
Calc XMinus=(1-sqrt(1-4*(WoLo1-V1L1)/VoLo))/2

print XPlus,XMinus

  If XPlus.gt.1
       Calc XPlus=XPlus-1
    Else
```

```
  Endif

  If XMinus.gt.1
       Calc XMinus=XMinus-1
    Else
  Endif

  If XPlus.lt.0
       Calc XPlus=0.
    Else
  Endif

  If XMinus.lt.0
       Calc XMinus=0.
    Else
  Endif

print XPlus,XMinus

Scal XPlus0,XMinus0
Calc XPlus0=XPlus: Calc XMinus0=1-XPlus0
Calc YDom=ML1+Slope*(VoLo*XMinus0*(XMinus0+1)-WoLo1-V1L1)
Calc YRec=ML1+Slope*(VoLo*XPlus0*(XPlus0+1)-WoLo1-V1L1)
Print XPlus0, XMinus0,YDom,YRec

Calc XMinus0=XMinus :Calc XPlus0=1-XMinus0
Calc YDom=ML1+Slope*(VoLo*XMinus0*(XMinus0+1)-WoLo1-V1L1)
Calc YRec=ML1+Slope*(VoLo*XPlus0*(XPlus0+1)-WoLo1-V1L1)
Print XPlus0, XMinus0,YDom,YRec


"   Parents + F2 's ********************** "


Calc GMean=ParF2


" **********Variance of parents VoLo *************** "

Scalar VoLo
Rest GMean; Cond=P1.eq.P2
Calc VoLo=Var(GMean)
Rest GMean

"********** Compute  Vr , Wr, VrWr  ****************"

Vari[Nval=Np]Vr,Wr,WrVr,Fr,ArM,Vhelp,PMean,WrLim,WrPred
Fact[leve=Np;valu=1...Np; nval=Np]Parents
```

```
For i=1...Np
Rest GMean; Cond=P1.eq.i.or.P2.eq.i
Calc Vr$[i]=Var(GMean)
Calc ArM$[i]=Mean(GMean)
Rest GMean
Rest GMean; Cond=P1.eq.i.and.P2.eq.i; saveset=set
Calc PMean$[i]=GMean$[set]
Rest GMean
Endf

" ******** Compute V1L1, VoL1,WoLo1 ******** "

Scal V1L2,VoL2,WoLo2
Calc V1L2=Mean(Vr)
Calc VoL2=Var(ArM)

For i=1...Np
Rest GMean; Cond=P1.eq.i.or.P2.eq.i; saveset=set
Calc Vhelp=GMean$[set]
Calc Wr$[i]=Covariance(PMean;Vhelp)
Endf
Calc WoLo2=Mean(Wr)

Scal ML1,MLo

Rest GMean; Cond=P1.eq.P2
Calc ML1=Mean(GMean)
Rest GMean; Cond=P1.ne.P2
Calc MLo=Mean(GMean)
Calc MLo=((Np-1)*MLo+ML1)/Np
Rest GMean

Calc WrVr=Wr+Vr
Calc WrLim=Sqrt(Vr*VoLo)
Model Wr; Fitt=WrPred
Fit Vr
Rkeep Est=Est; Vcov=Vcov;DF=DF
Scal Int, Slope
Equat Est; Ip(Int,Slope)

Print VoLo,V1L2,VoL2,WoLo2,ML1,MLo
Scal Tsq, Prob

" 1.  Test b=1 "
Calc Tsq =(Slope-1)**2/Vcov$[2;2]
Calc Prob=1-Fpro(Tsq;1;DF)
Print Tsq,DF,Prob

" 2.  Test the Validity of Hypothesis"

Calc Tsq=(Np-2)*(Var(Vr)-Var(Wr))**2/(Var(Vr)*Var(Wr)- \
```

```
          (Covariance(Wr;Vr))**2)/4
Calc Prob=1-Fpro(Tsq;4;DF)
Prin Tsq,DF,Prob


" ********** Components of variation **********"

Scal D,F,H1,H2,h2,s2,Np2,Np3
Calc Np2=Np*Np : & Np3=Np*Np2
Calc D=VoLo-E :& F=4*VoLo-8*WoLo1-4*(Np-2)*E/Np
Calc H1=4*VoLo-16*WoLo2+16*V1L2-4*(5*Np-4)*E/Np
Calc H2=16*V1L2-16*VoL2-16*(Np-1)*E/Np
Calc h2=16*(ML1-MLo)**2-16*(Np-1)*E/Np


"********** Standard errors **********"

Calc s2=0.5*Var((Wr-Vr))
Calc SeD=Sqrt(s2*(1+1/Np)) :& SeF=Sqrt(s2*(16+80/Np-64/Np2+6/Np3))
Calc SeH1=Sqrt(s2*(16+656/Np-192/Np2+64/Np3)) : & SeH2=sqrt(s2*(576/Np))
Calc Seh2=Sqrt(s2*(256+256/Np2-512/Np3+256/Np/Np3)/Np)
Calc SeE=Sqrt(s2/Np)
Print s2,D,SeD,F,SeF,H1,SeH1,H2,SeH2,h2,Seh2,E,SeE

Calc WrB1=D/4-H1/4+Vr
Print Parents,Vr,Wr,WrVr,ArM,PMean,WrLim,WrPred,WrB1
Print VoLo,V1L1,VoL1,WoLo1,ML1,MLo
Graph WrB1,WrLim,WrPred,Wr;Vr; symb=Parents; meth=c,c,c,p
Graph WrVr;PMean; symb=Parents; meth=p

" Other parameters on genes "
Scal MDD,GenesPN,GenesDR,CorrP, NGGD,h2ns,h2bs

Calc MDD=sqrt(H1/4/D) : & GenesPN=H2/4/H1
Calc GenesDR=(sqrt(4*D*H1)/4+F/2)/(sqrt(4*D*H1)/4-F/2)
Calc NGGD=h2/H2
Calc CorrP= Correlation(WrVr;PMean)
Calc h2ns=D/4/(D/4+H1/16-F/8+E)

Prin MDD,GenesDR,GenesPN,CorrP, NGGD,h2ns


" Most dominant and recessive parents"

Scal XPlus, XMinus, AFreq,aFreq, YDom,YRec
Scal YD,YR
Calc XPlus= (1+sqrt(1-4*GenesPN))/2
Calc XMinus=(1-sqrt(1-4*GenesPN))/2

print XPlus,XMinus
```

```
  If XPlus.gt.1
       Calc XPlus=XPlus-1
    Else
  Endif

  If XMinus.gt.1
       Calc XMinus=XMinus-1
    Else
  Endif

  If XPlus.lt.0
       Calc XPlus=0.
    Else
  Endif

  If XMinus.lt.0
       Calc XMinus=0.
    Else
  Endif

print XPlus,XMinus

Scal XPlus0,XMinus0
Calc XPlus0=XPlus: Calc XMinus0=1-XPlus0
Calc YDom=ML1+Slope*(VoLo*XMinus0*(XMinus0+1)-WoLo2-V1L2)
Calc YRec=ML1+Slope*(VoLo*XPlus0*(XPlus0+1)-WoLo2-V1L2)

Print XPlus0, XMinus0,YDom,YRec

Calc XMinus0=XMinus :Calc XPlus0=1-XMinus0
Calc YDom=ML1+Slope*(VoLo*XMinus0*(XMinus0+1)-WoLo2-V1L2)
Calc YRec=ML1+Slope*(VoLo*XPlus0*(XPlus0+1)-WoLo2-V1L2)
Print XPlus0, XMinus0,YDom,YRec



********** Heterosis and inbreeding depression ************ "


Scal  i1, Np1,HMPar,HMPar%,HBPar,HBPar%,IDep,IDep%, PrHMPar,PrHBPar,PrIDep
Calc Np1=Np-1
For i=1...Np1
Calc i1=i+1
For j=i1...Np
Rest ParF1,ParF2; P1.eq.i.and.P2.eq.j
Calc MidPar=(PMean$[i]+PMean$[j])/2
Calc  HMPar=Mean(ParF1)-MidPar
Calc Fval=HMPar**2/(3.5*Sigma2/NRep)
Calc PrHMPar=1-FPro(Fval;1;df)

Calc  HMPar%=(HMPar/MidPar)*100.
```

```
Calc SupPar=PMean$[i]*(PMean$[j].lt.PMean$[i])+ \
                    PMean$[j]*(PMean$[j].ge.PMean$[i])
Calc HBPar=Mean(ParF1)-SupPar
Calc Fval=HBPar**2/(2.*Sigma2/NRep)
Calc PrHBPar=1-FPro(Fval;1;df)
Calc HBPar%=(HBPar/SupPar)*100.

Calc  IDep=Mean(ParF1)-Mean(ParF2)
Calc Fval=IDep**2/(2.0*Sigma2/NRep)
Calc PrIDep=1-FPro(Fval;1;df)
Calc IDep%=(IDep/Mean(ParF1))*100.

Print i,j,HMPar,HMPar%,PrHMPar,HBPar,HBPar%,PrHBPar,IDep,IDep%,PrIDep; \
   fiel=10;deci=3
Endf
Endf

Rest ParF1,ParF2

Endf

Clos
stop
```

Output: **Not included here**

Computer and Biometrics Services Unit
ICARDA

Serial Number -004

GENSTAT Modules in Computing Biometrics

Title: Comparing parallelism of non-linear curves-I

1. Introduction:

This program shows steps for comparing a number of (ten standard) non-linear curves over the levels of a grouping factor, when the model errors are homoscedastic. It provides the sum of squares due to common parameters, changes due to constant terms, changes due to slopes and change due to separate non-linear parameters. It has illustrations using data from experiments conducted by Pasture, Forage and Live-stock program.

2. Areas of application and keywords:

Comparing non-linear curves.

3. Input/Output:

Input:

Levels of grouping factor, values of x-variables, values of y-variable (variable to be modelled)

Output:

Model, summary of regression analysis, accumulated analysis, estimates and standard errors

4. Location of the program:

Program:

Diskette :\CompBiom\94\CurveHom.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

Diskette :\CompBiom\94\CurveHom.Txt

Results:

Diskette :\CompBiom\94\CurveHom.opt

6. Client(s)

Dr. S. Christiansen,PFLP

7. Date

Mar 1994

8. Comments

M. Singh

Program

```
" ANALYSIS OF PART II. Germination test. repeated over 6 months: monthly
  and bi-weekly measurements on percentage of hard seeds above ground
   and percentage of hard seeds below ground.
        AHARD  : % hard seeds above ground
        BHARD  : % hard seeds below ground

 These are means over reps and management.

Source: Dr. S. Christiansen
"
UNIT[84]
Open ' Scott_curve.txt'; ch=2; fi=in
FACT[LEVE=7; LABE=IT(V2614,V2647,V2650,V2660,LC,MR,MN)] ACC
READ[ch=2] ACC,TIME, AHARD,BHARD; FREP=LEV

VARI[ VALU=(0,1,1.5,2,2.5,3.,3.5,4.,4.5,5.,5.5,6.)7] MONTH

MODEL AHARD ; fitt=f
TERMS MONTH*ACC
FITC[ CURVE=QDQ;prin=m,s;fpro=y] MONTH
ADD[prin=m,s;fpro=y] ACC
ADD[prin=m,s;fpro=y] MONTH.ACC
ADD[PRIN=M,E,S,A; fpro=y;tpro=y;NONL=SEPARATE]

Vari[nvalu=12]Fit[1...7],Mon[1...7]
Equa lp(f,MONTH); lp(Fit[1...7],Mon[1...7])
Graph Fit[1...7];Mon[1...7] ; meth=c
Graph Fit[1...7];Mon[1...7] ; meth=c; symb='1','2','3','4','5','6','7'


" Model BHARD using logistic.

 Since BHARD is not meaningful for MR,MN , so use the data for only
 five accessions.

"
Vari[nvalu=60] bhard,Month
Fact[leve=5;labe=lt(V2614,V2647,V2650,V2660,LC);Nvalu=60] Acc

Equat BHARD; bhard
Equat MONTH; Month
Equat ACC; Acc

MODEL bhard; fitt=fit
TERMS Acc*Month
FITC[ CURVE=logistic;prin=m,s;fpro=y] Month
ADD[prin=m,s;fpro=y] Acc
ADD[prin=m,s;fpro=y] Month.Acc
ADD[PRIN=M,E,S,A; fpro=y;tpro=y;NONL=SEPARATE]
```

```
Equa lp(fit,Month); lp(Fit[1...5],Mon[1...5])
Graph Fit[1...5];Mon[1...5] ; meth=c
Graph Fit[1...5];Mon[1...5] ; meth=c; symb='1','2','3','4','5'


clos
stop
```

Output : Not included here

Computer and Biometrics Services Unit
ICARDA

Serial Number -005

GENSTAT Modules in Computing Biometrics

Title: Comparing parallelism of non-linear curves-II

1. Introduction:

This program shows steps for comparing a number of (ten standard) non-linear curves over the levels of a grouping factor, when the model errors are heteroscedastic over the levels of grouping factor. It provides the sum of squares due to common parameters, changes due to constant terms, changes due to slopes and change due to separate non-linear parameters. It has illustrations using data from experiments conducted by Pasture, Forage and Live-stock program.

2. Areas of application and keywords:

Comparing non-linear curves.

3. Input/Output:

Input:
Levels of grouping factor, values of x-variables, values of y-variable (variable to be modelles)

Output:
Estimation and test for heterogeneous errors over levels of the grouping factor, model, summary of regression analysis, accumulated analysis, estimates and standard errors

4. Location of the program:

Program:
Diskett :\CompBiom\94\CurveHet.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:
Diskette :\CompBiom\94\CurveHet.Txt
Results:
Diskette :\CompBiom\94\CurveHet.opt

6. Client(s)

Dr. S. Christiansen,PFLP

7. Date

Mar 1994

8. Comments

M. Singh

Program:

```
" ANALYSIS OF PART II. Germination test. repeated over 6 months: monthly
  and bi-weekly measurements on percentage of hard seeds above ground
   and percentage of hard seeds below ground.
        AHARD  : % hard seeds above ground
        BHARD  : % hard seeds below ground
 These are means over reps and management.

Source: Dr. S. Christiansen

      Error variances may be heterogeneous

"
UNIT[84]
Open ' Scott_curve.txt'; ch=2; fi=in
FACT[LEVE=7; LABE=IT(V2614,V2647,V2650,V2660,LC,MR,MN)] ACC
READ[ch=2] ACC,TIME, AHARD,BHARD; FREP=LEV

VARI[ VALU=(0,1,1.5,2,2.5,3.,3.5,4.,4.5,5.,5.5,6.)7] MONTH

" Estimate error variances and test their homogeneity"
Scal NL ; 7
Scal h1,h2,h3,h4;0,0,0,0
Scal chisq, prob

For i=1...NL
Rest AHARD, Wet; ACC.eq.i
MODEL AHARD ; fitt=f
FITC[ CURVE=QDQ;prin=m,s,e;fpro=y] MONTH

Rkeep devi=ss; df=df
Calc h1=h1+df*log(ss/df)
Calc h2=h2+ss
Calc h3=h3+df
Calc Wet=df/ss
Calc h4=h4+1/df
Rest AHARD, Wet

Endf

Calc chisq=(h3*log(h2/h3)-h1)/(1+(h4-1/h3)/3/(NL-1))
Calc prob=1-chisq(chisq;NL-1)
Print chisq,prob

MODEL [weight=Wet]AHARD ; fitt=f
TERMS MONTH*ACC
FITC[ CURVE=QDQ;prin=m,s;fpro=y] MONTH
ADD[prin=m,s;fpro=y] ACC
ADD[prin=m,s;fpro=y] MONTH.ACC
ADD[PRIN=M,s,a,e; fpro=y;tpro=y;NONL=SEPARATE]
```

```
Vari[nvalu=12]Fit[1...7],Mon[1...7]
Equa lp(f,MONTH); lp(Fit[1...7],Mon[1...7])
Graph Fit[1...7];Mon[1...7] ; meth=c
Graph Fit[1...7];Mon[1...7] ; meth=c; symb='1','2','3','4','5','6','7'

clos
stop
```

Output: Not included

Computer and Biometrics Services Unit
ICARDA

Serial Number -006

GENSTAT Modules in Computing Biometrics

Title: **Analysis of long-term rotational trials: 1. Estimation of main effects and interactions.**

1. Introduction:

This program performs analysis of data from two-course rotation systems in terms of evaluating the main effects and interactions of the treatment factors and cropp rotations.

2. Areas of application and keywords:

Long-term rotation trials, repeated measures, two-course rotations, barley rotations

3. Input/Output:

Input:
Factor values of treatment, crop rotation, year, variable(s)

Output:
Analysis of variance table, tables ofmeans and their standard errors.

4. Location of the program:

Program:
Diskett :\CompBiom\94\LTRT1*.gen (12 files)
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:
Diskette :\CompBiom\94\LTRT1*.txt (3 files)
Results:
Diskette :\CompBiom\94\LTRT1*.OUT (12 files)

6. Client(s)

Dr. M. Jones, FRMP

7. Date

1992/1993/1994

8. Comments

M. Singh

Programs:

File LTRT11.GEN

```
 UNIT[ 288]
 OPEN 'B_LVF1.TXT'; CH=2;FI=IN
 FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
 Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
 FACT[LEVE=22] TREAT
 FACT[ LEVE=3] REP
 FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
 READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

" This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on 3 rotations (B/V,B/F,B/B0; Three fertility
 treatments (N20:P60 0: 0,0:0 0:0,N20:P30 N20:P30 N20:30,0:0 N20:30);
  two sites (TelHadya, Breda),
6 years (Y83_84,Y84_85...Y88_89). We generate 2 Series (Odd, Even), 3 cycles
(First, Second, Third).

"
FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;l((1,2,3,4)4,5,5,6,6,6,6))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;l(1,1,2,2,3,3))
FACT[LEVE=3; Labe=lt('-F','+F',F_Others)] FERT1
CALC FERT1=NEWL(TREAT;l(3,3,2,3, 3,3,3,3, 3,3,3,3, 3,3,1,3, 1,2,  3,2,1,2))
dele TREAT
PRINT LOC,REP, ROTA, YEAR, FERT1,GY,ST; fiel=5(13),2(6); deci=2

for i=1,2 : for j=3,5,6
REST GY,ST; cond=LOC.eq.i.AND.ROTA.EQ.j
Tabu[class= REP, FERT1, YEAR,SERIES] GY,ST; TOTA=TBGY,TBSY
print[ miss='  '] TBGY,TBSY; field=6; deci=2
endf: endf

clos: stop
```

File LTRT12.GEN

```
" ********

This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on
      3 rotations (B/V,B/F,B/B0;
```

```
      3 fertility treatments
        (N20:P60 0: 0,0:0 0:0,N20:P30 N20:P30 N20:30,0:0 N20:30);
      2 sites (TelHadya, Breda),
      6 years (Y83_84,Y84_85...Y88_89).
        We generate 2 Series (Odd, Even), 3 cycles (First, Second, Third).

**** Analysis of data for individual locations,years, rotations******
"

  UNIT[ 288]
  OPEN 'B_LVF1.TXT'; CH=2;FI=IN
  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
  FACT[LEVE=22] TREAT
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
  READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;!((1,2,3,4)4,5,5,6,6,6,6))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;!(1,1,2,2,3,3))
FACT[LEVE=3; Labe=lt('-F','+F',F_Others)] FERT1
CALC FERT1=NEWL(TREAT;!(3,3,2,3, 3,3,3,3, 3,3,3,3, 3,3,1,3, 1,2,  3,3,1,2))
dele TREAT

" FOR B/V,B/F and b/b"


for i=1: for j=1: for k=3
rest GY,ST;cond=LOC.eq.i.and.YEAR.eq.j.and.ROTA.eq.k

BLOC REP/FERT1
TREA FERT1
ANOV[SE=M;FPRO=Y; FACT=4] GY ; FITT=F1; RESI=R1
GRAPH R1;F1
endf: endf: endf

clos:stop


File      LTRT13.GEN

" ********

This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on
      3 rotations (B/V,B/F,B/B);
      3 fertility treatments
```

```
      (N20:P60 0: 0,0:0 0:0,N20:P30 N20:P30 N20:30,0:0 N20:30);
    2 sites (TelHadya, Breda),
    6 years (Y83_84,Y84_85...Y88_89).
      We generate 2 Series (Odd, Even), 3 cycles (First, Second, Third).

**** Analysis of data for individual locations, rotations******
"

 UNIT[ 288]
 OPEN 'B_LVF1.TXT'; CH=2;FI=IN
 FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
 Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
 FACT[LEVE=22] TREAT
 FACT[ LEVE=3] REP
 FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
 READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;l((1,2,3,4)4,5,5,6,6,6,6))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;l(1,1,2,2,3,3))
FACT[LEVE=3; Labe=lt('-F','+F',F_Others)] FERT1
CALC FERT1=NEWL(TREAT;l(3,3,2,3, 3,3,3,3, 3,3,3,3, 3,3,1,3, 1,2,  3,3,1,2))
dele TREAT

" FOR B/V,B/F and b/b"

for i=1: for k=3
rest GY,ST;cond=LOC.eq.i.and.ROTA.eq.k

BLOC REP/FERT1
TREA FERT1
BLOC SERIES.REP.FERT1/CYCLE
TREA FERT1*SERIES*CYCLE +SERIES.REP/CYCLE-REP.FERT1.SERIES/CYCLE
ANOV[SE=M;FPRO=Y; FACT=4] GY; FITT=F1; RESI=R1
GRAPH R1;F1
endf: endf

clos:stop

File      LTRT14.GEN


" ********

This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on
      3 rotations (B/V,B/F,B/B0;
      3 fertility treatments
```

```
      (N20:P60 0: 0,0:0 0:0,N20:P30 N20:P30 N20:30,0:0 N20:30);
    2 sites (TelHadya, Breda),
    6 years (Y83_84,Y84_85...Y88_89).
      We generate 2 Series (Odd, Even), 3 cycles (First, Second, Third).

**** Analysis of data combined over locations or/and rotations******
"

  UNIT[ 288]
  OPEN 'B_LVF1.TXT'; CH=2;FI=IN
  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
  FACT[LEVE=22] TREAT
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
  READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;l((1,2,3,4)4,5,5,6,6,6,6))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;l(1,1,2,2,3,3))
FACT[LEVE=3; Labe=lt('-F','+',F_Others)] FERT1
CALC FERT1=NEWL(TREAT;l(3,3,2,3, 3,3,3,3, 3,3,3,3, 3,3,1,3, 1,2,  3,3,1,2))
dele TREAT

" FOR B/V,B/F and b/b"

" for Tel Hadya (i.e. LOC=1)  only but combined over rotations B_V,B_F,B_B"

FACT[LEVE=4; labe=lt(B_V,B_F,B_B, Others)] ROTA1
CALC ROTA1=NEWL(ROTA;l(4,4,1,4,2,3))
     DELE ROTA

REST GY,F1,R1; COND=LOC.EQ.1.AND.ROTA1.LT.4.AND.FERT1.LT.3

BLOC SERIES.REP.FERT1.ROTA1/CYCLE
TREA FERT1*ROTA1*SERIES*CYCLE +SERIES.REP/CYCLE-REP.(FERT1*ROTA1).SERIES/CYCLE
ANOV[SE=M;FPRO=Y; FACT=4] GY; FITT=F1; RESI=R1
GRAPH R1;F1

" for only B_V rotation(i.e. ROTA1=1)but over both locations TelHadya and Breda"

REST GY,F1,R1; COND=ROTA1.eq.1.AND.FERT1.LT.3
BLOC LOC.SERIES.REP.FERT1/CYCLE
TREA LOC*FERT1*SERIES*CYCLE+REP.SERIES.LOC/CYCLE \
      -REP.FERT1.SERIES.LOC/CYCLE
ANOV[SE=M;FPRO=Y;FACT=5] GY;FITT=F1;RESI=R1
GRAPH R1;F1


" Combined over all rotations and locations "
```

```
REST GY,F1,R1; COND=ROTA1.LT.4.AND.FERT1.LT.3
BLOC LOC.SERIES.REP.FERT1.ROTA1/CYCLE
TREA LOC*FERT1*ROTA1*SERIES*CYCLE+REP.SERIES.LOC/CYCLE \
      -REP.(FERT1*ROTA1).SERIES.LOC/CYCLE
ANOV[SE=M;FPRO=Y;FACT=5] GY;FITT=F1;RESI=R1
GRAPH R1;F1
clos
stop
```

File LTRT21.GEN

```
"
    This program illustrates analysis of data on Long-term rotational trials
conducted by Dr. M. Jones, FRMP and has been preprepared for training on
Long-term rotational trials, 7-18 Mar 93 conducted by Dr. M. Jones,FRMP,ICARDA.
The data in file HAYTDM6.txt are on hay and total barley dry matter produced
from
            2 rotations: Barley/Vetch and Barley/(Vetch+Barley)
            4 fertility treatments (20:60 0:0 20:30 0:30 20:0 0:60 0:0 0:0
            6 years(1983/84 ... 1988/89)
            3 reps
            2 sites
"
UNITS[288]
OPEN ' HAYTDM6.TXT' ; CH=2;FI=IN

 FACT[ LEVE=2; Labels=!t(TelHadya, Breda)] LOC
 FACT[LEVE=22] TREAT
 FACT[ LEVE=3] REP
 FACT[LEVE=6; Labe=!t(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
READ [CH=2] LOC,YEAR,REP,TREAT,HAY,TDM ; frep=lev

FACT[LEVE=6; labe=!t(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;!((1,2,3,4)4,5,5,6,6,6,6))
Fact[ leve=2; Labels=!t(Odd, Even)] SERIES
CALC SERIES=NEWL(YEAR;!(1,2,1,2,1,2))
FACT[LEVE=3; Labe=!t(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;!(1,1,2,2,3,3))

FACT[LEVE=5;Labe=!t('20:60 0:0','20:30 0:30','20:0 0:60','0:0 0:0',F_others)] \
            FERT1
CALC FERT1 = NEWL(TREAT;!(5,5,1,1, 5,5,2,2, 5,5,3,3, 5,5,4,4, 6(5)))

dele TREAT
PRINT LOC,REP, ROTA, YEAR, FERT1,HAY,TDM; fiel=5(13),2(6); deci=2

for i=1,2 :  for j=3,4

print i,j
rest HAY,TDM; cond=LOC.eq.i.AND.ROTA.EQ.j
```

```
Tabu[class= FERT1,YEAR,SERIES,REP] HAY,TDM; TOTA=TBHAY,TBTDM
print[ miss=' '] TBHAY,TBTDM; field=6; deci=2

endf : endf
clos: stop
```

File LTRT22.GEN

```
" ***********
```

This program illustrates analysis of data on Long-term rotational trials conducted by Dr. M. Jones, FRMP and has been preprepared for training on Long-term rotational trials, 7-18 Mar 93 conducted by Dr. M. Jones,FRMP,ICARDA. The data in file HAYTDM6.txt are on hay and total barley dry matter produced from

2 rotations: Barley/Vetch and Barley/(Vetch+Barley)
4 fertility treatments (20:60 0:0 20:30 0:30 20:0 0:60 0:0 0:0
6 years(1983/84 ... 1988/89)
3 reps
2 sites

```
**** Analysis of data for individual locations,years, rotations******
"
UNITS[288]
OPEN ' HAYTDM6.TXT' ; CH=2;FI=IN

  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
READ [CH=2] LOC,YEAR,REP,TREAT,HAY,TDM ; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;I((1,2,3,4)4,5,5,6,6,6,6))
Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
CALC SERIES=NEWL(YEAR;I(1,2,1,2,1,2))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;I(1,1,2,2,3,3))

FACT[LEVE=5;Labe=lt('20:60 0:0','20:30 0:30','20:0 0:60','0:0 0:0',F_others)] \
            FERT1
CALC FERT1 = NEWL(TREAT;I(5,5,1,1, 5,5,2,2, 5,5,3,3, 5,5,4,4, 6(5)))

dele TREAT

rest TDM;cond=LOC.eq.1.and.YEAR.eq.1.and.ROTA.eq.3

BLOC REP/FERT1
TREA FERT1
ANOV[PRINT=a,m,mi,%cv; SE=M;FPRO=Y] TDM ; FITT=F1; RESI=R1
GRAPH R1;F1
```

```
clos:stop
```

File LTRT23.GEN

```
" ***********
```

This program illustrates analysis of data on Long-term rotational trials conducted by Dr. M. Jones, FRMP and has been preprepared for training on Long-term rotational trials, 7-18 Mar 93 conducted by Dr. M. Jones,FRMP,ICARDA. The data in file HAYTDM6.txt are on hay and total barley dry matter produced from

2 rotations: Barley/Vetch and Barley/(Vetch+Barley)
4 fertility treatments (20:60 0:0 20:30 0:30 20:0 0:60 0:0 0:0
6 years(1983/84 ... 1988/89)
3 reps
2 sites

```
**** Analysis of data for individual location and rotation combinations *****
"
UNITS[288]
OPEN ' HAYTDM6.TXT' ; CH=2;FI=iN

  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
READ [CH=2] LOC,YEAR,REP,TREAT,HAY,TDM ; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;I((1,2,3,4)4,5,5,6,6,6,6))
Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
CALC SERIES=NEWL(YEAR;I(1,2,1,2,1,2))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;I(1,1,2,2,3,3))

FACT[LEVE=5;Labe=lt('20:60 0:0','20:30 0:30','20:0 0:60','0:0 0:0',F_others)] \
          FERT1
CALC FERT1 = NEWL(TREAT;I(5,5,1,1, 5,5,2,2, 5,5,3,3, 5,5,4,4, 6(5)))

dele TREAT

rest TDM;cond=LOC.eq.1.and.ROTA.eq.3.and.FERT1.lt.5

BLOC SERIES.REP.FERT1/CYCLE
TREA FERT1*SERIES*CYCLE +SERIES.REP/CYCLE-REP.FERT1.SERIES/CYCLE
ANOV[ SE=M;FPRO=Y] TDM ; FITT=F1; RESI=R1

GRAPH R1;F1

clos:stop
```

File LTRT24.GEN

```
" ***********
    This program illustrates analysis of data on Long-term rotational trials
conducted by Dr. M. Jones, FRMP and has been preprepared for training on
Long-term rotational trials, 7-18 Mar 93 conducted by Dr. M. Jones,FRMP,ICARDA.
The data in file HAYTDM6.txt are on hay and total barley dry matter produced
from
            2 rotations: Barley/Vetch and Barley/(Vetch+Barley)
            4 fertility treatments (20:60 0:0 20:30 0:30 20:0 0:60 0:0 0:0
            6 years(1983/84 ... 1988/89)
            3 reps
            2 sites

**** Analysis of data combined over location or/and rotations *****
"
UNITS[288]
OPEN ' HAYTDM6.TXT' ; CH=2;FI=IN

  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
READ [CH=2] LOC,YEAR,REP,TREAT,HAY,TDM ; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;l((1,2,3,4)4,5,5,6,6,6,6))
Fact[ leve=2; Labels=lt(Odd, Even)] SERIES
CALC SERIES=NEWL(YEAR;l(1,2,1,2,1,2))
FACT[LEVE=3; Labe=lt(First, Second, Third)] CYCLE
CALC CYCLE=NEWL(YEAR;l(1,1,2,2,3,3))

FACT[LEVE=5;Labe=lt('20:60 0:0','20:30 0:30','20:0 0:60','0:0 0:0',F_others)] \
            FERT1
CALC FERT1 = NEWL(TREAT;l(5,5,1,1, 5,5,2,2, 5,5,3,3, 5,5,4,4, 6(5)))

dele TREAT

" **** For Telhadya(LOC=1) but combined over B/V and B/BV ***** "

rest TDM;cond=LOC.eq.1.and.(ROTA.eq.3.or.ROTA.eq.4).and.FERT1.lt.5
BLOC SERIES.REP.FERT1.ROTA/CYCLE
TREA FERT1*ROTA*SERIES*CYCLE +SERIES.REP/CYCLE-REP.(FERT1*ROTA).SERIES/CYCLE
ANOV[SE=M;FPRO=Y; FACT=4] TDM ; FITT=F1;  RESI=R1
GRAPH R1;F1

" **** For B/V but combined over both locations ***** "

rest TDM;cond=ROTA.eq.3.and.FERT1.lt.5
BLOC LOC.SERIES.REP.FERT1/CYCLE
```

```
TREA LOC*FERT1*SERIES*CYCLE+REP.SERIES.LOC/CYCLE-REP.FERT1.SERIES.LOC/CYCLE
ANOV[SE=M;FPRO=Y; FACT=4] TDM ; FITT=F1; RESI=R1
GRAPH R1;F1

" **** Combined over locations and B/V and B/BV ***** "

rest TDM;cond=(ROTA.eq.3.or.ROTA.eq.4).and.FERT1.lt.5
BLOC LOC.SERIES.REP.FERT1.ROTA/CYCLE
TREA LOC*FERT1*ROTA*SERIES*CYCLE+REP.SERIES.LOC/CYCLE \
        -REP.(FERT1*ROTA).SERIES.LOC/CYCLE
ANOV[SE=M;FPRO=Y; FACT=5] TDM ; FITT=F1; RESI=R1
GRAPH R1;F1

clos: stop

File      LTRT31.GEN

"
    This prog is prepared for training on Long-term rotational trials,
     7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on continuous barley (B/B); four fertility
 treatments (N20:P60 N20:60, N0:P0 N20:P60 N20:P60 N0:P0, N0:P0,N0:P0);
  two sites (TelHadya, Breda),
     6 years (Y83_84,Y84_85...Y88_89).
"

  UNIT[ 288]
  OPEN 'B_LVF1.TXT'; CH=2;FI=IN
  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[leve=2] SERIES
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
  READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;l((1,2,3,4)4,5,5,6,6,6,6))


FACT[LEVE=5;Labe=lt('20:60 20:60','20:60 0:0','0:0 0:0','0:0 20:60',F_Others)]\
                FERT
CALC FERT=NEWL(TREAT;l(18(5),1,2,3,4))

dele TREAT, SERIES

" FOR B/B "

FOR I=1...2 :FOR J=1...3 : FOR K=1...4
REST GY,ST; COND=ROTA.EQ.6.AND.LOC.EQ.I.AND.REP.EQ.J.AND.FERT.EQ.K
PRINT LOC,REP, FERT,YEAR,GY,ST; fiel=4(13),2(6); deci=2
```

```
ENDF: ENDF: ENDF

REST GY,ST; COND=ROTA.EQ.6
Tabu[class= LOC,FERT, YEAR,REP] GY,ST; TOTA=TBGY,TBSY
print[ miss='  '] TBGY,TBSY; field=6; deci=2

FACT[LEVE=5] FERTX
CALC FERTX=FERT
FOR I=1...2 :FOR J=1...3 : FOR K=1...4
REST GY,ST; COND=ROTA.EQ.6.AND.LOC.EQ.I.AND.REP.EQ.J.AND.FERTX.EQ.K
PRINT[RL=INT;CL=INT] LOC,REP, FERTX,YEAR,GY,ST; fiel=4(13),2(6); deci=2
ENDF: ENDF: ENDF

clos: stop

File      LTRT32.GEN

" **********
 This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File B_LVF1.TXT has data on continuous barley (B/B); four fertility
 treatments (N20:P60 N20:60, N0:P0 N20:P60 N20:P60 N0:P0, N0:P0,N0:P0);
  two sites (TelHadya, Breda),
6 years (Y83_84,Y84_85...Y88_89).

****** Individual locations and polynomial contrasts over years

"

  UNIT[ 288]
  OPEN 'B_LVF1.TXT'; CH=2;FI=IN
  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[leve=2] SERIES
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
  READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;!((1,2,3,4)4,5,5,6,6,6,6))


FACT[LEVE=5;Labe=lt('20:60 20:60','20:60 0:0','0:0 0:0','0:0 20:60',F_Others)]\
                FERT
CALC FERT=NEWL(TREAT;!(18(5),1,2,3,4))

dele TREAT, SERIES

" FOR B/B "
REST GY; COND=ROTA.EQ.6
```

```
REST GY  ; COND=LOC.EQ.1.AND.ROTA.eq.6.and.FERT.LT.5

BLOC REP/(YEAR*FERT)

TREA YEAR*FERT
ANOV[SE=M;FPRO=Y] GY ; FITT=F1 ;RESI=R1
GRAPH R1;F1

BLOC
TREA POL(YEAR;4)*REP*FERT
ANOV[PRINT=A] GY

clos : stop
```

File LTRT33.GEN

```
" **********
 This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.
 File B_LVF1.TXT has data on continuous barley (B/B); four fertility
 treatments (N20:P60 N20:60, N0:P0 N20:P60 N20:P60 N0:P0, N0:P0,N0:P0);
  two sites (TelHadya, Breda),
6 years (Y83_84,Y84_85...Y88_89).

****** Combined over locations and polynomial contrasts over years

"

  UNIT[ 288]
  OPEN 'B_LVF1.TXT'; CH=2;FI=IN
  FACT[ LEVE=2; Labels=lt(TelHadya, Breda)] LOC
  FACT[LEVE=22] TREAT
  FACT[leve=2] SERIES
  FACT[ LEVE=3] REP
  FACT[LEVE=6; Labe=lt(Y83_84,Y84_85,Y85_86,Y86_87,Y87_88,Y88_89)] YEAR
  READ [ch=2] TREAT, LOC,REP,YEAR,SERIES,GY,ST; frep=lev

FACT[LEVE=6; labe=lt(B_P, B_PB, B_V, B_VB, B_F, B_B)] ROTA
CALC ROTA=NEWL(TREAT;I((1,2,3,4)4,5,5,6,6,6,6))


FACT[LEVE=5;Labe=lt('20:60 20:60','20:60 0:0','0:0 0:0','0:0 20:60',F_Others)]\
                FERT
CALC FERT=NEWL(TREAT;I(18(5),1,2,3,4))

dele TREAT, SERIES

" FOR B/B "
REST GY; COND=ROTA.EQ.6

REST GY  ; COND=ROTA.eq.6.and.FERT.LT.5
```

```
BLOC LOC/REP/(YEAR*FERT)
TREA YEAR*LOC*FERT
ANOV[SE=M;FPRO=Y] GY ; FITT=F1;RESI=R1
GRAPH R1;F1

BLOC
TREA POL(YEAR;5)*LOC*REP*FERT
ANOV[PRINT=A;FACT=4] GY

clos  : stop

File      LTRT34.GEN
"  **********
 This prog is prepared for training on Long-term rotational trials,
  7-18 Mar 93 conducted by FRMP, ICARDA.

 File CONT_BAR.TXT has data on continuous barley (B/B); four fertility
 treatments (N20:P60 N20:60, N0:P0 N20:P60 N20:P60 N0:P0, N0:P0,N0:P0);
  two sites (TelHadya, Breda),
6 years (Y83_84,Y84_85...Y88_89).

****** Polynomial contrast computed for analysis

"
  UNIT[ 6]
  OPEN 'CONT_BAR.TXT'; CH=2;FI=IN
VARI[VALU= -5,-3,-1,1,3,5] Linear
VARI[VALU= 5, -1,-4,-4,-1,5] Quadra
VARI[VALU= -5, 7, 4, -4, -7, 5]Cubic
VARI[VALU= 1, -3, 2, 2, -3, 1] Quartic
VARI[VALU= -1, 5, -10, 10, -5, 1] Quintic
VARI[NVAL=24] GLin,GQua,GCub,GQuar,GQui,SLin,SQua,SCub,SQuar,SQui

FOR I=1...24
READ[CH=2; END=*; FORM=I(-4,2)] GY,ST

CALC GLin $[I] = SUM(GY*Linear) : CALC GQua $[I] =SUM(GY*Quadra)
CALC GCub $[I] = SUM(GY*Cubic)  : CALC GQuar $[I]= SUM(GY*Quartic)
CALC GQui $[I] = SUM(GY*Quintic)

CALC SLin $[I] =SUM(ST*Linear) : CALC SQua $[I] =SUM(ST*Quadra)
CALC SCub $[I] =SUM(ST*Cubic)  : CALC SQuar $[I]=SUM(ST*Quartic)
CALC SQui $[I] =SUM(ST*Quintic)

endf

  FACT[ LEVE=2; Labels=!t(TelHadya, Breda); values=12(1,2)] LOC
  FACT[ LEVE=3; values=4(1...3)2] REP
FACT[leve=4; Labe=!t('20:60 20:60','20:60 0:0','0:0 0:0','0:0 20:60') ; \
                valu=(1...4)6] FERT
```

```
BLOC LOC/REP/FERT
TREA LOC*FERT
FOR Y=GLin,GQua,GCub,GQuar,GQui
ANOV[SE=M;FPRO=Y] Y
endf

clos  : stop

poly   n=6
  lin = -5,-3,-1,1,3,5
quadr = 5, -1,-4,-4,-1,5
cubic = -5 7 4 -4 -7 5
quart =  1 -3 2 2 -3 1
quint = -1 5 -10 10 -5 1
```

Outputs : Not included

Computer and Biometrics Services Unit
ICARDA

Serial Number -007

GENSTAT Modules in Computing Biometrics

Title: Modelling germination in wheat- A robust method

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. The relationship between D50% and temperature was roughly appearing like a quadratic divided by linear (qdl) function in temperature for each of the genotypes. Estimation of this function is essential to obtain optimum temperature and hence the base temprature. However, the fit was not very satisfactory when all the data points were used. Scatter and fitted plots were examined to notice the presence of few suspected outliers (suspected by high standardized residuals). Then, we decided to fit the model again without such points {i.e. the points where standardized residuals were outside (-2,2) interval}, and the suspected outliers were identified again.This process was iterated and was found to converge within five iterations (convergence in terms of residual mean square, values of the estimates of qdl parameters, and the suspected outliers whose numbers varied from 1 to 5 on an average of 50 sample points). The experience was similar with each of the 18 genotypes. With a loss of few points or degree of freedom,the gain was enormous (minimun increase in %R-square(adj) exceeded 20%). 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\94\Germ_Rob.gen
(Software: GENSTAT 5)

5. Location of illustrative data and results:

Data:

ICARDA VAX [murari.CP.maha.assad]Ger1.dat, Ger2.dat, Temp1.mea, Temp2.mea

Results:

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

6. Client(s)

Dr. V. Mahalakshmi,CP

7. Date

June 1994

8. Comments

M. Singh

Program:

```
" Program 2: Lag phase "


Unit[864]
Open 'coeff12.opt'; ch=2
Fact[leve=18]Geno
Read[ch=2] Cases,Geno,Temp,Rsq,BEst,MEst,CEst,AEst,D50
Vari Indicate
Calc Indicate=0

Vari[nval=18]Msq,Rsq, Df, OpTemp, BaseT,SeBaseT,Slope,SeSlope

For i=1...18
rest Lag,MEst,BEst,CEst,AEst,Temp ; cond=Geno.eq.i.and.D50.gt.0
Calc Lag=MEst-(1/BEst)*Log(-1-CEst/AEst)

rest Temp,f,Lag,res ; cond=Geno.eq.i.and.D50.gt.0

Model Lag;fitt=f
Fitc[prin=*] Temp
Rkeep Resi=res

Calc res=abs(res)

For[ntimes=5]
Rest Temp,Lag,f,res
rest Temp,f,res,Indicate, Lag ; cond=Geno.eq.i.and.D50.gt.0.and.res.le.2
Model Lag;fitt=f
Fitc[prin=*]  Temp
Rkeep Resi=res
calc res=abs(res)
Endf
Calc Indicate=Indicate+1

Model Lag;Fitted=Fval
Fitc Temp
graph Lag,Fval;Temp
rest Lag,MEst,BEst,CEst,AEst,Temp

endf
Rest Indicate

Rest Lag, Temp, Geno ; Indicate.gt.0

Model Lag
Terms Temp+Geno+Geno.Temp
Fitc[prin=m,s; Fprob=y] Temp
Add [prin=m,s; Fprob=y]Geno
Add [prin=m,s;Fprob=y] Geno.Temp
```

```
Add[print=m,s,a,e; noni=s; Fprob=y;Tprob=y ]

clos: stop

clos
stop



 " Program 1: Base temperature"
Unit[864]
Open 'coeff12.opt'; ch=2
Fact[leve=18]Geno
Read[ch=2] Cases,Geno,Temp,Rsq,B1,M1,C1,A1,D50

Scal A,B,C,D, TOPT,df,ss
Vari[nval=18]Msq,Rsq, Df, OpTemp, BaseT,SeBaseT,Slope,SeSlope

Device 5

Pen 1, 2 ; meth=p,m

For i=1...18

rest Temp,f,res, D50,R50 ; cond=Geno.eq.i.and.D50.gt.0
Calc R50=1/D50
Model D50;fitt=f
Fitc[curve=qdl ; prin=*] Temp
Rkeep Resi=res

"Dgraph D50,f; Temp ; pen=1,2"
Calc res=abs(res)

For[ntimes=5]
Rest Temp,D50,f,res
rest Temp,D50,f,res ; cond=Geno.eq.i.and.D50.gt.0.and.res.le.2
Model D50;fitt=f
Fitc[curve=qdl;prin=*;fprob=y] Temp
Rkeep Resi=res
calc res=abs(res)
Endf

"Dgraph D50,f; Temp ; pen=1,2"

Rkeep df=df; devi=ss ; Est=Est
Calc Msq$[i]=ss/df : & Rsq$[i]=(1-ss/df/var(D50))*100. :& Df$[i]=df
CALC D,B,C,A=Est$[1...4]
Calc TOPT=(sqrt(B*D/C)-1)/D
Calc OpTemp$[i]=TOPT

Rest R50,Temp,D50,f,res
```

```
Rest R50,Temp; Geno.eq.i.and.D50.gt.0.and.res.le.2.and.Temp.le.TOPT
Model R50
Fit[prin=*] Temp
Rkeep Est=Est1 ; Vcov=Vcov
Scal Btemp
Calc Btemp=-Est1$[1]/Est1$[2]

Calc BaseT$[i] =Btemp
Calc Slope$[i] =Est1$[2]
Calc SeSlope$[i]=Sqrt(Vcov$[2;2])
Calc SeBaseT$[i]=ABS(Btemp)*SQRT(Vcov$[1;1]/(Est1$[1])**2+ \
        Vcov$[2;2]/(Est1$[2])**2-2.*Vcov$[2;1]/Est1$[1]/Est1$[2])

Rest R50,D50,Temp

Endf

Fact[leve=18; valu=1...18] Genotype
Calc Slope=1000*Slope :& SeSlope=1000*SeSlope

Print Genotype, Rsq, OpTemp,BaseT,SeBaseT,Slope,SeSlope ;fiel=9
Scal Chsq,PrChi,wmean,Sewmean
Calc wmean=sum(BaseT/SeBaseT/SeBaseT)/Sum(1/SeBaseT/SeBaseT)
Calc Chsq=Sum(((BaseT-wmean)/SeBaseT)**2)
Calc PrChi=1-Chisq(Chsq;17)
Calc Sewmean=sqrt(1/Sum(1/SeBaseT/SeBaseT))
Prin Chsq,PrChi,wmean,Sewmean

Calc wmean=sum(Slope/SeSlope/SeSlope)/Sum(1/SeSlope/SeSlope)
Calc Chsq=Sum(((Slope-wmean)/SeSlope)**2)
Calc PrChi=1-Chisq(Chsq;17)
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-Chisq(Chsq;14)
Calc Sewmean=sqrt(1/Sum(1/SeBaseT/SeBaseT))
Prin Chsq,PrChi,wmean,Sewmean



clos
stop



Unit[48]
Open 'Ger2.dat'; ch=2 ; width=320
Open 'Temp2.mea';ch=3
```

```
Scal Rep,Rep1,Temp,Temp1,Cham, Cham1,TMeas, Geno
Scal Temp,Geno, B,M,C,A, Tot, Rbarsq
Scal[valu=*] Bmis,Mmis,Cmis,Amis

Read[ch=2; end=*] Time
Vari[nval=52]Fullrow

Open 'coeff2.opt';ch=4;fi=out

For[ntimes=72]
Read[ch=3;end=*] Rep1,Temp1,Cham1,TMeas
For[ntimes=6]
Read[ch=2;end=*] Fullrow


Calc Temp, Cham,Rep,Geno=Fullrow$[1...4]
Calc Y=Fullrow$[!(5...52)]
Calc Tot=Sum(Y)

If Tot.le.12
   Calc D50,Rbarsq=0,0 : & B,M,C,A=Bmis,Mmis,Cmis,Amis

Print[ch=4;ipri=*] Geno,TMeas,Rbarsq,B,M,C,A,D50;fiel=4,2(6),5(9);deci=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=4; ipri=*] Geno,TMeas,Rbarsq,B,M,C,A,D50;fiel=4,2(6),5(9);deci=2,2,5(3)

Endif

Endf
Endf

clos
stop


Note: Coeff12.opt is file  (Coeff1.opt +Coeff2.opt) combined over
      experients 1 and 2
```

Computer and Biometrics Services Unit
ICARDA

Serial Number -008

GENSTAT Modules in Computing Biometrics

Title: Modelling absorbance due to rhizobia under salinity

1. Introduction:

This program models absorbance percentage in various rhizobia strain with time under two salinity levels. For each rhizobium and salinity level combination in the experiment, it fits a logistic model to the cumulative percentage germination as a function of time, computes lag phase, maximum growth, slope (at pint of inflection). These parameters are then subjected to regression on rhizobia and salinity leading to their predictions.

2. Areas of application and keywords:

Plant Physiology, abiotic stress, biotic stress, chickpea

3. Input/Output:

Input:

For a number of rhizobia, salinity, absorption %, over different times in hours.

Output:

Estimates of lag phase, slope, maximum growth rate. Predictions.

4. Location of the program:

Program:

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

5. Location of illustrative data and results:

Data:

ICARDA VAX [murari.LP.MCS.Adlan]Absorb.txt

Results:

ICARDA VAX [murari.LP.MCS.ADLAN]Absorb.out

6. Client(s)

Mr. Adlan, (M.Sc. stiudent at AUB, Lebanon)

7. Date

September 1994

8. Comments

M. Singh

```
Program
"
Data on response of rhizobia to salinity in terms of absorbance over
a period of seven days. 18 rhizobia, 2 salinity levels.
Lab expt. conducted at T.Hadya during August 1993 by Mr. Adlan, ARC, Sudan.
This work is for his M.Sc. degree. Supervisor: Dr. M. C. Saxena.

Time is in hours. Asorbence in Absorbence unit
"

Unit[72]
Vari[nval=14]Absorb,Time:   & [nvalu=17] Fullrow
Open 'Adlanr.yyy'; ch=2;fi=in
Skip[ch=2]1
Scal Ncases; 72
Scal SRhiz,SSalin,SSampl, SB,SM,SC,SA,SRbar, AbsLast
Scal[valu=*] Bmis,Mmis,Cmis,Amis, Miss
Scal  Two; 2
Vari[valu=0,4,22,28,46,52,70,76,94,100,118,124,142,148] Time
Fact[leve=18]Rhiz: &[leve=2]Salin,Sampl
Vari B,M,C,A,Rbarsq
Fact[leve=2;valu=72(1); labe=!t(Responsive,Constant) ] ID
For i=1...Ncases

Read[ch=2;end=*] Fullrow
Calc (SRhiz,SSalin,SSampl)=Fullrow$[1...3] : & Absorb=Fullrow$[!(4...17)]
      If NOBS(Absorb).eq.0
         Calc SB,SM,SC,SA,SRbar=Miss
         Calc (B,M,C,A)$[i]=SB,SM,SC,SA
         Calc Rbarsq$[i]=SRbar
         Calc ID$[i]=Int(Two)
         Print SRhiz,SSalin,SSampl
         Calc (Rhiz,Salin,Sampl)$[i]=Int(SRhiz,SSalin,SSampl)
      else

Rest Absorb; Time.ne.0.
Model   Absorb ; Fitt=F
Fitc[ curve=log; print=*] Time
Rest Absorb


Rkeep Est=Est ;df=df;devi=ss
Calc SRbar=100.*(1-ss/df/var(Absorb))
Calc Rbarsq$[i]=SRbar
Calc (Rhiz,Salin,Sampl)$[i]=Int(SRhiz,SSalin,SSampl)
Equa Est; !p(SB,SM,SC,SA)
Calc (B,M,C,A)$[i]=SB,SM,SC,SA
"Graph[ncol=35;nrow=16] Absorb, F;Time; Meth=p,c"
endif

endf
```

```
" Time90:  Time to Gamma=90% of (A+C): maximum growth"

Calc Slop=B*C/4 : & Lag=M-(1/B)*Log(-1-C/A): & MaxGr=A+C
Scal Gamma   ;0.90
Calc Time90=M-(1/B)*Log(-1+C/( (A+C)*Gamma-A) )
Calc Lag16=M-(1/B)*Log(-1+C/(0.016-A) )
Calc Lag16=Lag16*(Lag16.ge.0)

Open 'adlan1.opt'; ch=2;fi=ou
Outp 2

Vari [valu=72(1)] Sel
Calc Sel=Sel+(Rhiz.eq.5.and.Salin.eq.2)+(Rhiz.eq.18.and.Salin.eq.2)
Calc Lag1=Lag*(Lag.ge.0)

For y=Slop,Lag,Lag1,Lag16,MaxGr,Time90 "B,M,C,A"
Model y
Rest y; Sel.eq.1
Fit[prin=m,s,a; fprob=y] Rhiz+Salin+Rhiz*Salin
Rest y
Print ' ******** Warning: do not extract estimates for rhiz,sal=(5,2), (18,2)'
Pred[prin=p,s; alias=ignore;comb=p]Rhiz
Pred[prin=p,s;alias=ignore;comb=p]Salin
Pred[prin=p,s;alias=ignore;comb=p]Salin,Rhiz
endf

Print Rhiz,Salin,Sampl,ID,Rbarsq, M,Slop,Lag,MaxGr,Time90; Fiel=8


clos :stop
```

Output : Not included