

SupplementsRProgrsDataGeneticCrosses

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# Program -1: R- codes for analysis of full diallel data using Hayman (1954)
approach
# Full Diallel-- Hayman approach

# Read data
FullD<- read.table("DFLR4Hayman.txt", header = TRUE)
attach(FullD)
Rep<- FullD$Rep
P1<- FullD$P1
P2<- FullD$P2
Yield<- FullD$DFLR

NP<- c(10)
NRep<- c(3)
#.....Create matrices
NRep1<- (NRep +1)

Z<- array(0,c(NRep1, NP, NP))
count<- c(0)

for(k in 1:NRep) {for(i in 1:NP){for(j in 1:NP){
  count<- (count+1 )
  Z[Rep[count],P1[count],P2[count]]<- c(Yield[count]) } } }

#..... Totals over the blocks
for(k in 1:NRep){Z[NRep1 , ,]=Z[NRep1 , ,]+Z[k , ,] }

#..... Degrees of freedom and Anova skeleton
assqB<- (0) ; bssqB<- (0) ; cssqB<- (0); dssqB<- (0); tssqB<- (0)
b1ssqB<- (0) ; b2ssqB<- (0); b3ssqB<- (0)
Blockss<- (0); GrandTot<- (0)

aDF<- (NP-1) ; bDF<- (NP*(NP-1)/2) ; cDF<- (NP-1) ; dDF<- (NP-1)*(NP-2)/2;
tDF<- NP*NP-1
b1DF<- 1 ; b2DF<- (NP-1) ; b3DF<- ( NP*(NP-3)/2)
BlockDF<- (NRep-1)

axBDF<- (NP-1)*(NRep-1) ; bxBDF<- (NP*(NP-1)/2)*(NRep-1) ; cxBDF<-
(NP-1)*(NRep-1) ; dxBDF<- (NP-1)*(NP-2)*(NRep-1)/2; txBDF<- (NP*NP-1)*(NRep-1)
b1xBDF<- (NRep-1) ; b2xBDF<- (NP-1)*(NRep-1) ; b3xBDF<- (
NP*(NP-3)/2)*(NRep-1)

DoF<- c(aDF, bDF, b1DF, b2DF, b3DF, cDF, dDF,tDF)
XBDoF<- c(axBDF, bxBDF, b1xBDF, b2xBDF, b3xBDF, cxBDF, dxBDF, txBDF)

Source<- c("a", "b", "b1", "b2", "b3", "c", "d", "total")
XBSource<- c("a x Block", "b x Block", "b1 x Block", "b2 x Block", "b3 x
Block", "c x Block", "d x Block", "total x Block")

SumSq<- matrix(0, 8, NRep, dimnames = list(c("a", "b", "b1", "b2", "b3", "c",
"d", "total"),c("Block1", "Block2", "Block3")))
#.....Sum of squares

for(k in 1:NRep1){
# Compute block-wise

# Generate totals
Y<- array(0,c(NP, NP))
Y<- Z[k , ,]
YT<- t(Y)

#Compute the row sums , column sums and various sums of squares

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SupplementsRProgrsDataGeneticCrosses

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Yrsum<- rowSums(Y)
Ycsum<- colSums(Y)

Ysum<- sum(Y)
assq<- sum((Yrsum+Ycsum)^2)/2/NP - 2*Ysum^2/NP^2
bssq<- sum((Y+YT)^2)/4 -assq-Ysum^2/NP^2

cssq<- sum((Yrsum-Ycsum)^2)/2/NP
dssq<- sum((Y-YT)^2)/4 - cssq
tssq<- sum(Y^2)-Ysum^2/NP^2

self<- diag(Y)
selfsum<- sum(self)

b1ssq<- (Ysum-NP*selfsum)^2/NP/NP/(NP-1)
b2ssq<- (sum((Yrsum+Ycsum-NP*self)^2) - (2*Ysum-NP*selfsum)^2/NP)/NP/(NP-2)
b3ssq<- sum((Y+YT)^2)/4 - sum(self^2) - sum((Yrsum+Ycsum-2*self)^2)/2/(NP-2) +
(Ysum-selfsum)^2/(NP-1)/(NP-2)

if(k <= NRep){
assqB<- (assqB + assq) ; bssqB<- (bssqB + bssq) ; cssqB<- (cssqB+cssq);
dssqB<- (dssqB + dssq); tssqB<- (tssqB+tssq)
b1ssqB<- (b1ssqB+b1ssq) ; b2ssqB<- (b2ssqB+b2ssq); b3ssqB<- (b3ssqB + b3ssq)
SumSqB<-c(assqB, bssqB, b1ssqB, b2ssqB, b3ssqB, cssqB, dssqB, tssqB)

SumSq[, k]<-c(assq, bssq,b1ssq, b2ssq, b3ssq, cssq, dssq, tssq)
}

if(k == NRep1){
SumSqT<- (c(assq, bssq,b1ssq, b2ssq, b3ssq, cssq, dssq, tssq)/NRep)
xBSumSq<- (SumSqB - SumSqT)
MeanSqT<- SumSqT/DoF
xBMeanSqT<- XBSumSq/xBDoF
FProb<- pf( (MeanSqT/xBMeanSqT), DoF, xBDoF, lower.tail=FALSE )

print(data.frame(Source, DoF,SumSq,SumSqB,SumSqT,MeanSqT,xBSource,
xBDoF,xBSumSq,xBMeanSqT,FProb))
} }
#..... OVER

# Program- 2: R- codes for analysis of Complete Diallel Crosses data using
Griffing Method 4 approach
# Griffing CDC Type 4 Method + Models I & II

# Read data
Griff4<- read.table("DFLR4Griffing4.txt", header = TRUE)
attach(Griff4)

Rep<- Griff4$Rep
P1<- Griff4$P1
P2<- Griff4$P2
Yield<- Griff4$DFLR

#-----
NP<- c(10)
NCrs<- (NP*(NP-1)/2)
NRep<- c(3)
NPM1<- (NP-1)
NRep1<- (NRep+1)
#Create matrices
NObs<- NRep*NP*(NP-1)/2

# degrees of freedom
RepDF<- (NRep -1)
CrsDF<- (NP*(NP-1)/2 -1 )
gcaDF<- (NP-1)

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SupplementsRProgrsDataGeneticCrosses
scaDF<- (CrsDF -gcaDF)
TotDF<- (NObs-1)
ResDF<- (TotDF - RepDF - CrsDF)
DF<- c(RepDF, CrsDF,ResDF, TotDF)

Z<- array(0,c(NRep1, NP, NP))
count<- c(0)
rv<- c(1)
for(k in 1:NRep) {for(i in 1:NPM1){for(j in (i+1):NP){
  count<- (count+1 )
  Z[Rep[count],P1[count],P2[count]]<- c(Yield[count]) } } }

# Sums of squares at cross level
#Totals over the blocks
RepSS<- (0)
TotSS<- (0)
GTot<- (0)
for(k in 1:NRep){
Z[NRep1 , ,]=Z[NRep1 , ,]+Z[k , ,]

repTot<- (sum(Z[k , ,]))
RepSS<- RepSS + (repTot)^2
GTot<- GTot+repTot
TotSS<- (TotSS +sum(Z[k , ,]^2) )
}

CF<- (GTot^2/NObs)
RepSS<- (RepSS/NCrs - CF)
TotSS<- (TotSS -CF)

#..... Cross(Genotype) means, Cross SS and error mean square
CrsSS<- ( sum(Z[NRep1 , , ]^2)/NRep - CF )
ResSS<- (TotSS - RepSS - CrsSS)

SumSq<- c(RepSS, CrsSS,ResSS, TotSS)

#Mean squares and variance ratios and F-prob
MeanSq<- (SumSq/DF)
Vr<- array("", c(4))
FProb<- array("",c(4))

CrsVr<- (CrsSS/CrsDF)/(ResSS/ResDF)
CrsFPr<- pf(CrsVr, CrsDF, ResDF, lower.tail=FALSE )
Vr[2]<- CrsVr
FProb[2]<- CrsFPr
Source<- c("Rep", "Cross", "Residual", "Total")
print(data.frame(Source, DF,SumSq,MeanSq,Vr, FProb))

#..... Compute Combining ability analysis of variance

# Here on selected items will be converted to the level of mean over
replications
ResSS<- ResSS/NRep
ResMS<- ResSS/ResDF
CrsSS<- (CrsSS/NRep)
CrsMS<- (CrsSS/CrsDF)

# For gcas and scas

# Generate a matrix of Y totals
Y<- array(0,c(NP, NP))
Y<- Z[NRep1 , ,]/NRep

gtot<- (GTot/NRep)

TotPar<- (rowSums(Y) + colSums(Y))

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SupplementsRProgrsDataGeneticCrosses
gcaSS<- (sum(( TotPar )^2)/(NP-2) - 4*gtot^2/NP/(NP-2) )
gcaMS<- (gcaSS/gcaDF)
scaSS<- (CrsSS - gcaSS)
scaMS<- (scaSS/scaDF)

Source<- c("gca", "sca", "Error")

DoF<- c(gcaDF, scaDF, ResDF)
SS<- c(gcaSS, scaSS, ResSS)
MS<- SS/DoF
Vr<- array("", c(3))
FProb<- array("",c(3))
Vr<- MS/ResMS

FProb<- pf(Vr, DoF, ResDF, lower.tail=FALSE )
Vr[3]<- c("")
FProb[3]<- c("")
print(data.frame(Source, DoF,SS,MS,Vr, FProb))

#..... Estimates of effects

Effects<- array(0, c(NP, NP))

for(i in 1:NP) Effects[i,i]<- ( (NP*TotPar[i] - 2*gtot)/NP/(NP-2) ) #gca s
for(i in 1:NPM1){ for(j in (i+1):NP){Effects[i,j]=Y[i,j] - gtot* 2/NP/(NP-1)
-Effects[i,i]-Effects[j,j]} } #sca s

print(Effects)

# Standard errors
SEs<- array(0, c(6))

" .....Calculate SEs"
Sig2ePrime<- (ResMS)
Desc<- c("SE of est. mu", "SE of gca: gi", "SE of sca:sij, i<>j", "SED gi-gj",
"SED sij-sik, i<>j, k; j<>k", "SED sij-skl, i<>j, k, l; j<>k, l,; k<>l")
SEs[1]<- sqrt(Sig2ePrime* 2/NP/(NP-1)) # " SE of mu "
SEs[2]<- sqrt(Sig2ePrime* (NP-1)/NP/(NP-2) ) # " SE of gca: gi"
SEs[3]<- sqrt(Sig2ePrime* (NP-3)/(NP-1) ) # SE of sca: sij , i<>j "

SEs[4]<- sqrt(Sig2ePrime* 2/(NP-2) ) # "SED gi-gj"
SEs[5]<- sqrt(Sig2ePrime* 2*(NP-3)/(NP-2)) # "SED sij-sik, i<>j, k; j<>k"
SEs[6]<- sqrt(Sig2ePrime* 2*(NP-4)/(NP-2)) # "SED sij-skl, i<>j, k, l;
j<>k, l,; k<>l"

print(data.frame(Desc , SEs))

#Model II: lines assumed having random effects: Varcomponents: S2GCA, S2SCA,
S2Reci"

# '....Model II: lines assumed having random effects: Varcomponents: S2GCA,
S2SCA...'

VarComp<- array(0,c(3))
SEVarComp<- array(0, c(3))

# estimates "
VarComp[1]<- ( MS[1] - MS[2])/(NP-2) #"sigma2g= varcomp for gi"
VarComp[2]<- ( MS[2] - MS[3]) #sigma2s=varcomp for sij"

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SupplementsRProgrsDataGeneticCrosses
VarComp[3]<- MS[3] # "Sigma2e' = error var divided by
Rep"

SEVarComp[1]<- sqrt( 2*(MS[1])^2/(NP-1)/(NP-2) + 4*(NP-3)*(MS[2])^2/NP/(NP-2)
) # " SE of Sigma2g"
SEVarComp[2]<- sqrt( 4*(MS[2])^2/NP/(NP-3) + 2*MS[3]^2/DoF[3]/(NP-2) ) # "SE
of Sigma2s"
SEVarComp[3]<- sqrt( (2*MS[3])^2/ResDF )

#Prin ' If a variance component is negative, replace it by zero and adjust
associated estimates accordingly'
print(data.frame(Source, DoF, VarComp, SEVarComp))

# Estimation of genetic parameters: In breeding coeficient = 1 assumed"
print(c(" Estimates of components of variance for additive and dominance
effects"))

Genetic<- c("Additive variance(Sigma2A)", "Dominance variance(Sigma2D)")
EstGenetic<- array(0, c(2))
SEEstGenetic<- array(0, c(2))

EstGenetic<- c(2*VarComp[1], VarComp[2])
SEEstGenetic<- c(2*SEVarComp[1], SEVarComp[2])

print(data.frame(Genetic, EstGenetic, SEEstGenetic))
#.....OVER

# Program- 3: R- codes for analysis of Partial Diallel Crosses in Incomplete
Blocks data using
# Singh and Hinkelmann (1998) approach
# Full Diallel-- Incomplete Block Design approach

# Read data
PDCIB<- read.table("DFLR4PDCIB1.txt", header = TRUE)
attach(PDCIB)

Blk<- PDCIB$Rep
P1<- PDCIB$P1
P2<- PDCIB$P2
Geno<- PDCIB$Geno
Yield<- PDCIB$DFLR

#-----
NP<- (10)
NBlk<- (3)
NCMax<- NP*(NP-1)/2
P1P2<- (P2+(P1-1)*NP)

#.....Generate factor of the crosses
Cross<- sort(unique.default(P1P2), na.last = TRUE)
NC<- length(Cross)
Par1<- 1+as.integer(Cross/NP-0.001)
Par2<- Cross-(Par1-1)*NP
print(cbind(Cross, Par1, Par2))

#Cross vs Parent Matrix: Z
Z<- matrix(0, NC,NP)

for(i in 1:NC){
  for(j in 1:NP){
    Z[i,j]=(Par1[i]==j | Par2[i]==j)+2*(Par1[i]==j & Par2[i]==j) } }

#Cross vs Block matrix: Sai: S (NC x NBlk)
S<- table(P1P2, Blk)

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SupplementsRProgrsDataGeneticCrosses

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# Row and colmnn sums and diagonals
qvec<- rowSums(S); kvec<- colSums(S)
qd<- diag(qvec) ; kd<- diag(kvec)

print(kvec)
#Find Cross totals and Block totals

CrstTot<- as.vector( tapply(Yield, P1P2, sum))
BlkTot<- as.vector(tapply(Yield, Blk, sum))
#Compute C and Q matrices

C<- (qd - S %**% solve(kd) %**% t(S))
Q<- (CrstTot - S %**% solve(kd) %**% BlkTot)
ZCZ<- t(Z) %**% C %**% Z

Cinv<- solve(C + (1/sum(qvec))* qvec %**% t(qvec))

ZCZinv<- matrix(0, NP, NP)
ZCZinv<- solve( t(Z) %**% (C + (1/sum(qvec))* qvec %**% t(qvec)) %**% Z )

#..... Compute SS

CF<- (sum(BlkTot)**2/sum(kd))
BlkSS<- c(t(BlkTot) %**% solve(kd) %**% BlkTot - CF)

CrossSS<- c( t(Q) %**% Cinv %**% Q )
gcaSS<- c( t(Q) %**% Z %**% ZCZinv %**% t(Z) %**% Q )
scaSS<- ( CrossSS - gcaSS)

TotSS<- (sum(Yield**2) - CF)
ResSS<- (TotSS - BlkSS-CrossSS)

SumSq<- c(BlkSS, CrossSS, gcaSS, scaSS, ResSS, TotSS)
#.....DFS
BlkDF<- (NBlk-1)
CrossDF<- (NC-1)
gcaDF<- (NP-1)
scaDF<- (CrossDF - gcaDF)
TotDF<- (length(Yield)-1)
ResDF<- (TotDF - (BlkDF + CrossDF))
Sigma2<- (ResSS/ResDF)
DoF<- c(BlkDF, CrossDF, gcaDF, scaDF, ResDF, TotDF)
MeanSq<- (SumSq/DoF)
FProb<- pf( (MeanSq/Sigma2), DoF, ResDF, lower.tail=FALSE)
FProb[1]<- c("") ; FProb[5]<- c("") ; FProb[6]<- c("")

Source<- c( "Blocks", "Crosses", "gca", "sca", "Residual", "Total")
data.frame(Source, DoF, SumSq, MeanSq, FProb)

#gca estimates and SEs

Sigma2
VCovGca<- ( Sigma2* ZCZinv )
VCovGca

gcaEst<- ( ZCZinv %**% t(Z) %**% Q )

gcaSeEst<- sqrt(diag(VCovGca))
Parents<- c(1:NP)
data.frame(Parents, gcaEst, gcaSeEst)
#.....OVER

#Datasets for days to 50% flowering

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SupplementsRProgrsDataGeneticCrosses

# Data for full diallel - Hayman (1954) analysis	Rep	P1	P2	DFLR
1	1	1	1	120.13
1	1	1	2	128.56
1	1	1	3	102.33
1	1	1	4	106.80
1	1	1	5	106.33
1	1	1	6	111.10
1	1	1	7	116.20
1	1	1	8	129.00
1	1	1	9	129.00
1	1	1	10	110.89
1	2	1	1	117.63
1	2	2	2	127.80
1	2	2	3	96.67
1	2	2	4	105.75
1	2	2	5	105.67
1	2	2	6	116.20
1	2	2	7	115.40
1	2	2	8	132.89
1	2	2	9	131.50
1	2	2	10	116.20
1	3	1	1	102.78
1	3	2	2	105.80
1	3	3	3	104.75
1	3	3	4	105.60
1	3	3	5	108.14
1	3	3	6	112.40
1	3	3	7	126.00
1	3	3	8	126.11
1	3	3	9	119.43
1	3	3	10	109.70
1	4	1	1	103.50
1	4	2	2	107.00
1	4	3	3	95.71
1	4	4	4	107.14
1	4	5	5	108.60
1	4	6	6	114.22
1	4	7	7	111.20
1	4	8	8	118.00
1	4	9	9	129.00
1	4	10	10	111.33
1	5	1	1	105.78
1	5	2	2	107.00
1	5	3	3	95.38
1	5	4	4	100.60
1	5	5	5	109.11
1	5	6	6	112.89
1	5	7	7	113.50
1	5	8	8	129.00
1	5	9	9	125.38
1	5	10	10	110.29
1	6	1	1	109.33
1	6	2	2	109.57
1	6	3	3	99.67
1	6	4	4	104.50
1	6	5	5	103.60
1	6	6	6	113.00
1	6	7	7	112.78
1	6	8	8	121.60
1	6	9	9	127.00
1	6	10	10	109.00
1	7	1	1	107.40
1	7	2	2	112.71
1	7	3	3	94.20

SupplementsRProgrsDataGeneticCrosses

1	7	4	103.67
1	7	5	105.00
1	7	6	107.80
1	7	7	121.43
1	7	8	129.50
1	7	9	122.75
1	7	10	124.50
1	8	1	118.50
1	8	2	120.67
1	8	3	118.50
1	8	4	118
1	8	5	112.71
1	8	6	117.13
1	8	7	115.56
1	8	8	141.30
1	8	9	127.67
1	8	10	112.25
1	9	1	120.57
1	9	2	122.40
1	9	3	108.40
1	9	4	112.43
1	9	5	106.13
1	9	6	111.14
1	9	7	117.00
1	9	8	118.00
1	9	9	128.57
1	9	10	129.60
1	10	1	106.11
1	10	2	110.25
1	10	3	97.38
1	10	4	101.00
1	10	5	100.56
1	10	6	105.75
1	10	7	106.88
1	10	8	121.83
1	10	9	119.20
1	10	10	112.37
2	1	1	121.00
2	1	2	124.80
2	1	3	102.17
2	1	4	110.60
2	1	5	109.17
2	1	6	111.80
2	1	7	119.00
2	1	8	131.22
2	1	9	131.67
2	1	10	115.80
2	2	1	121.00
2	2	2	130.00
2	2	3	100.80
2	2	4	110.80
2	2	5	107.29
2	2	6	117.00
2	2	7	121.90
2	2	8	126.89
2	2	9	126.33
2	2	10	114.40
2	3	1	107.56
2	3	2	106.22
2	3	3	101.25
2	3	4	99.67
2	3	5	106.71
2	3	6	111.50
2	3	7	111.20
2	3	8	120.89
2	3	9	118.80

SupplementsRProgrsDataGeneticCrosses

2	3	10	115.44
2	4	1	102.60
2	4	2	105.89
2	4	3	94.50
2	4	4	108.50
2	4	5	113.80
2	4	6	113.67
2	4	7	111.60
2	4	8	117.25
2	4	9	131.83
2	4	10	108.71
2	5	1	108.20
2	5	2	105.67
2	5	3	93.25
2	5	4	101.83
2	5	5	111.44
2	5	6	111.75
2	5	7	118.00
2	5	8	125.25
2	5	9	115.33
2	5	10	111.00
2	6	1	108.13
2	6	2	109.33
2	6	3	102.00
2	6	4	105.00
2	6	5	105.56
2	6	6	115.67
2	6	7	112.10
2	6	8	125.33
2	6	9	121.00
2	6	10	110.60
2	7	1	113.60
2	7	2	113.00
2	7	3	96.86
2	7	4	100.33
2	7	5	104.88
2	7	6	107.00
2	7	7	117.00
2	7	8	128.80
2	7	9	121.30
2	7	10	116.57
2	8	1	128.00
2	8	2	129.50
2	8	3	108.00
2	8	4	115
2	8	5	110.40
2	8	6	118.43
2	8	7	121.00
2	8	8	130.00
2	8	9	134.25
2	8	10	113.86
2	9	1	122.20
2	9	2	122.75
2	9	3	105.86
2	9	4	116.00
2	9	5	117.33
2	9	6	106.13
2	9	7	114.25
2	9	8	118.00
2	9	9	132.25
2	9	10	113.00
2	10	1	107.86
2	10	2	111.29
2	10	3	102.63
2	10	4	106.00
2	10	5	102.71

SupplementsRProgrsDataGeneticCrosses

2	10	6	105.25
2	10	7	106.00
2	10	8	121.67
2	10	9	121.00
2	10	10	110.43
3	1	1	120.75
3	1	2	124.00
3	1	3	106.20
3	1	4	107.60
3	1	5	107.60
3	1	6	111.00
3	1	7	114.90
3	1	8	129.25
3	1	9	127.13
3	1	10	110.22
3	2	1	104.56
3	2	2	127.25
3	2	3	105.60
3	2	4	109.50
3	2	5	112.83
3	2	6	112.67
3	2	7	119.80
3	2	8	124.30
3	2	9	132.70
3	2	10	111.22
3	3	1	104.50
3	3	2	111.67
3	3	3	100.00
3	3	4	106.25
3	3	5	103.00
3	3	6	110.00
3	3	7	112.50
3	3	8	122.00
3	3	9	119.22
3	3	10	111.20
3	4	1	107.00
3	4	2	102.50
3	4	3	97.00
3	4	4	105.50
3	4	5	105.83
3	4	6	110.00
3	4	7	109.22
3	4	8	114.00
3	4	9	127.80
3	4	10	110.67
3	5	1	107.33
3	5	2	114.13
3	5	3	104.50
3	5	4	102.00
3	5	5	106.63
3	5	6	111.20
3	5	7	119.00
3	5	8	118.60
3	5	9	127.40
3	5	10	107.33
3	6	1	112.60
3	6	2	116.86
3	6	3	101.40
3	6	4	100.43
3	6	5	102.22
3	6	6	113.33
3	6	7	114.40
3	6	8	120.00
3	6	9	125.70
3	6	10	111.00
3	7	1	118.60

SupplementsRProgrsDataGeneticCrosses

3	7	2	126.33
3	7	3	108.75
3	7	4	118
3	7	5	109.50
3	7	6	123.33
3	7	7	115.50
3	7	8	132.20
3	7	9	122.33
3	7	10	114.71
3	8	1	121.67
3	8	2	138.33
3	8	3	105.00
3	8	4	109.17
3	8	5	109.57
3	8	6	111.88
3	8	7	121.67
3	8	8	141.00
3	8	9	127.50
3	8	10	115.83
3	9	1	107.25
3	9	2	115.89
3	9	3	98.75
3	9	4	109.00
3	9	5	102.00
3	9	6	106.71
3	9	7	109.57
3	9	8	123.00
3	9	9	126.70
3	9	10	113.50
3	10	1	112.57
3	10	2	95.10
3	10	3	102.67
3	10	4	102.63
3	10	5	109.89
3	10	6	122.88
3	10	7	119.43
3	10	8	113.50
3	10	9	113.38
3	10	10	110.78

data for Griffing 4 method

Rep	P1	P2	DFLR
1	1	2	128.56
1	1	3	102.33
1	1	4	106.80
1	1	5	106.33
1	1	6	111.10
1	1	7	116.20
1	1	8	129.00
1	1	9	129.00
1	1	10	110.89
1	2	3	96.67
1	2	4	105.75
1	2	5	105.67
1	2	6	116.20
1	2	7	115.40
1	2	8	132.89
1	2	9	131.50
1	2	10	116.20
1	3	4	105.60
1	3	5	108.14
1	3	6	112.40
1	3	7	126.00
1	3	8	126.11
1	3	9	119.43
1	3	10	109.70

SupplementsRProgrsDataGeneticCrosses

1	4	5	108.60
1	4	6	114.22
1	4	7	111.20
1	4	8	118.00
1	4	9	129.00
1	4	10	111.33
1	5	6	112.89
1	5	7	113.50
1	5	8	129.00
1	5	9	125.38
1	5	10	110.29
1	6	7	112.78
1	6	8	121.60
1	6	9	127.00
1	6	10	109.00
1	7	8	129.50
1	7	9	122.75
1	7	10	124.50
1	8	9	127.67
1	8	10	112.25
1	9	10	129.60
2	1	2	124.80
2	1	3	102.17
2	1	4	110.60
2	1	5	109.17
2	1	6	111.80
2	1	7	119.00
2	1	8	131.22
2	1	9	131.67
2	1	10	115.80
2	2	3	100.80
2	2	4	110.80
2	2	5	107.29
2	2	6	117.00
2	2	7	121.90
2	2	8	126.89
2	2	9	126.33
2	2	10	114.40
2	3	4	99.67
2	3	5	106.71
2	3	6	111.50
2	3	7	111.20
2	3	8	120.89
2	3	9	118.80
2	3	10	115.44
2	4	5	113.80
2	4	6	113.67
2	4	7	111.60
2	4	8	117.25
2	4	9	131.83
2	4	10	108.71
2	5	6	111.75
2	5	7	118.00
2	5	8	125.25
2	5	9	115.33
2	5	10	111.00
2	6	7	112.10
2	6	8	125.33
2	6	9	121.00
2	6	10	110.60
2	7	8	128.80
2	7	9	121.30
2	7	10	116.57
2	8	9	134.25
2	8	10	113.86
2	9	10	113.00

SupplementsRProgrsDataGeneticCrosses

3	1	2	124.00
3	1	3	106.20
3	1	4	107.60
3	1	5	107.60
3	1	6	111.00
3	1	7	114.90
3	1	8	129.25
3	1	9	127.13
3	1	10	110.22
3	2	3	105.60
3	2	4	109.50
3	2	5	112.83
3	2	6	112.67
3	2	7	119.80
3	2	8	124.30
3	2	9	132.70
3	2	10	111.22
3	3	4	106.25
3	3	5	103.00
3	3	6	110.00
3	3	7	112.50
3	3	8	122.00
3	3	9	119.22
3	3	10	111.20
3	4	5	105.83
3	4	6	110.00
3	4	7	109.22
3	4	8	114.00
3	4	9	127.80
3	4	10	110.67
3	5	6	111.20
3	5	7	119.00
3	5	8	118.60
3	5	9	127.40
3	5	10	107.33
3	6	7	114.40
3	6	8	120.00
3	6	9	125.70
3	6	10	111.00
3	7	8	132.20
3	7	9	122.33
3	7	10	114.71
3	8	9	127.50
3	8	10	115.83
3	9	10	113.50

data for PDC in incomplete blocks (Singh and Hinkelmann 1998)

Rep	P1	P2	DFLR
1	1	2	128.56
1	1	3	102.33
1	1	4	106.80
1	1	5	106.33
1	1	6	111.10
1	1	7	116.20
1	1	9	129.00
1	2	3	96.67
1	2	4	105.75
1	2	5	105.67
1	2	6	116.20
1	2	7	115.40
1	2	8	132.89

SupplementsRProgrsDataGeneticCrosses

1	2	10	116.20
1	3	4	105.60
1	3	5	108.14
1	3	6	112.40
1	3	7	126.00
1	3	8	126.11
1	3	9	119.43
1	3	10	109.70
1	4	6	114.22
1	4	7	111.20
1	4	8	118.00
1	4	9	129.00
1	4	10	111.33
1	5	6	112.89
1	5	7	113.50
1	5	8	129.00
1	5	9	125.38
1	5	10	110.29
1	6	7	112.78
1	6	8	121.60
1	6	9	127.00
1	6	10	109.00
1	7	8	129.50
1	7	9	122.75
1	7	10	124.50
1	8	9	127.67
1	8	10	112.25
2	1	2	124.80
2	1	3	102.17
2	1	4	110.60
2	1	5	109.17
2	1	6	111.80
2	1	7	119.00
2	1	9	131.67
2	2	3	100.80
2	2	4	110.80
2	2	5	107.29
2	2	6	117.00
2	2	7	121.90
2	2	8	126.89
2	2	10	114.40
2	3	4	99.67
2	3	5	106.71
2	3	6	111.50
2	3	7	111.20
2	3	8	120.89
2	3	9	118.80
2	3	10	115.44
2	4	6	113.67
2	4	7	111.60
2	4	8	117.25
2	4	9	131.83
2	4	10	108.71
2	5	6	111.75
2	5	7	118.00
2	5	8	125.25
2	5	9	115.33
2	5	10	111.00
2	6	7	112.10
2	6	8	125.33

SupplementsRProgrsDataGeneticCrosses

2	6	9	121.00
2	6	10	110.60
2	7	8	128.80
2	7	9	121.30
2	7	10	116.57
2	8	9	134.25
2	8	10	113.86
2	9	10	113.00
3	1	2	124.00
3	1	3	106.20
3	1	4	107.60
3	1	5	107.60
3	1	6	111.00
3	1	7	114.90
3	1	8	129.25
3	1	9	127.13
3	1	10	110.22
3	2	3	105.60
3	2	4	109.50
3	2	5	112.83
3	2	6	112.67
3	2	7	119.80
3	2	8	124.30
3	2	10	111.22
3	3	4	106.25
3	3	5	103.00
3	3	6	110.00
3	3	7	112.50
3	3	8	122.00
3	3	9	119.22
3	4	6	110.00
3	4	7	109.22
3	4	8	114.00
3	4	9	127.80
3	4	10	110.67
3	5	6	111.20
3	5	7	119.00
3	5	8	118.60
3	5	9	127.40
3	5	10	107.33
3	6	7	114.40
3	6	8	120.00
3	7	10	114.71
3	8	9	127.50
3	8	10	115.83
3	9	10	113.50