

APL Scripts used in Rifkin, et al., Genetic architecture of divergence: the selfing syndrome in *Ipomoea lacunosa*

I. Estimating within- and between-module pairwise trait phenotypic correlations and standard errors

A. Program PHENCORRMODMEANS

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PHENCORRMODMEANS
A THIS PROGRAM CALCULATES MEANS AND STANDARD ERRORS OF PHENOTYPIC
A CORRELATIONS FOR WITHIN- AND BETWEEN-MODULE TRAIT PAIRS

A THIS PROGRAM CALLS PROGRAM 'STATS2'

INPUT←ΔOVERLAPCORR      A INPUT VARIABLE
TYPE←1
ROWS←1↑ΡINPUT
CLUSTERMODS←'N'          A NOTE: 'Y' IF WANT FOR CLUSTER MODULES, 'N' IF
FOR ANATOMICAL MODULES
AVECORRMAT←5 5Ρ0          A INITIALIZE CORRELATION MATRIX
AVESEMAT←5 5Ρ0            A INITIALIZE STANDARD ERROR MATRIX

I←0
RETI:I←I+1                A MODULE 1 LOOP

J←I-1
RETJ:J←J+1                A MODULE 2 LOOP

STMT1← 'IND←((INPUT[;1]∈ΔTRAITIND',(⊤I),')∧(INPUT[;2]∈ΔTRAITIND',(⊤
J),'))/↑ROWS'
      A ΔTRAITIND1, . . . ΔTRAITIND5 LIST TRAIT NUMBERS ASSOCIATED WITH
      INDIVIDUAL MODULES

STMT2← 'IND←((INPUT[;1]∈ΔTRAITIND',(⊤I),'A)∧(INPUT[;2]∈ΔTRAITIND',(⊤
J),'A))/↑ROWS'
STMT2A← 'IND2←((INPUT[;1]∈ΔTRAITIND',(⊤J),'A)∧(INPUT[;2]∈ΔTRAITIND',
(⊤I),'A))/↑ROWS'
$STMT1  A MAKES INDEX OF TRAIT INDICES FOR PAIR OF TRAITS I,J
→(~CLUSTERMODS='N')/DOWN1  A DON'T EXECUTE IF ANALYZING CLUSTER MOD
ULES
$STMT2
$STMT2A          A NOTE: EXECUTE BOTH STATEMENTS 2 AND 2A BECAUSE IND1
AND IND2 MAY CONTAIN DIFFERENT ELEMENTS
IND←IND,IND2
DOWN1:CORRS←,↑INPUT[IND;3]  A PAIRWISE TRAIT CORRELATIONS FOR MODUL
ES I,J

STATS2 CORRS  A CALCULATE STATISTICS ON CORRELATIONS
AVECORRMAT[I;J]←AVECORRMAT[J;I]←MEAN    A PLACE AVE CORRELATION FOR M
ODULE 1 IN AVECORRMAT
AVESEMAT[I;J]←AVESEMAT[J;I]←STDERR  A PLACE SE IN AVESEMAT
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→(J<5)/RETJ
→(I<5)/RETI

□TCLF
'AVERAGE (SE) CORRELATIONS WITHIN AND BETWEEN MODULES FOR PHENOTYPIC
CORRELATION OF TYPE ',TYPE
□TCLF
'MODULE           1           2           3           4
      5'
□TCLF
' 1',(6 3AVECORRMAT[1;1])'',(6 4AVESEMAT[1;1]),',(6 3AVE
CORRMAT[1;2]),',(6 4AVESEMAT[1;2]),',(6 3AVECORRMAT[1;3]),
',(6 4AVESEMAT[1;3]),',(6 3AVECORRMAT[1;4]),',(6 4AVESEM
AT[1;4]),',(6 3AVECORRMAT[1;5]),',(6 4AVESEMAT[1;5]),'
□TCLF
' 2',(6 3AVECORRMAT[2;1])'',(6 4AVESEMAT[2;1]),',(6 3AVE
CORRMAT[2;2]),',(6 4AVESEMAT[2;2]),',(6 3AVECORRMAT[2;3]),
',(6 4AVESEMAT[2;3]),',(6 3AVECORRMAT[2;4]),',(6 4AVESEM
AT[2;4]),',(6 3AVECORRMAT[2;5]),',(6 4AVESEMAT[2;5]),'
□TCLF
' 3',(6 3AVECORRMAT[3;1])'',(6 4AVESEMAT[3;1]),',(6 3AVE
CORRMAT[3;2]),',(6 4AVESEMAT[3;2]),',(6 3AVECORRMAT[3;3]),
',(6 4AVESEMAT[3;3]),',(6 3AVECORRMAT[3;4]),',(6 4AVESEM
AT[3;4]),',(6 3AVECORRMAT[3;5]),',(6 4AVESEMAT[3;5]),'
□TCLF
' 4',(6 3AVECORRMAT[4;1])'',(6 4AVESEMAT[4;1]),',(6 3AVE
CORRMAT[4;2]),',(6 4AVESEMAT[4;2]),',(6 3AVECORRMAT[4;3]),
',(6 4AVESEMAT[4;3]),',(6 3AVECORRMAT[4;4]),',(6 4AVESEM
AT[4;4]),',(6 3AVECORRMAT[4;5]),',(6 4AVESEMAT[4;5]),'
□TCLF
' 5',(6 3AVECORRMAT[5;1])'',(6 4AVESEMAT[5;1]),',(6 3AVE
CORRMAT[5;2]),',(6 4AVESEMAT[5;2]),',(6 3AVECORRMAT[5;3]),
',(6 4AVESEMAT[5;3]),',(6 3AVECORRMAT[5;4]),',(6 4AVESEM
AT[5;4]),',(6 3AVECORRMAT[5;5]),',(6 4AVESEMAT[5;5]),'
□TCLF
□TCLF
□TCLF
'PROGRAM PHENCORRMODMEANS FINISHED. '

```

B. Program STATS2

STATS2 X
 A THIS PROGRAM CALCULATES MEAN, VARIANCE, STDDEV ETC.
 A FOR A VECTGOR OF NUMBERS

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MEAN←+/X÷ρX
DIFF←X-MEAN
VAR←(+/DIFF★2) ÷(-1+ρX)
STDDEV←VAR★.5
STDERR←STDDEV÷((ρX)★.5)
CV←STDDEV÷MEAN

```

C. Program SHUFFLECORRS

SHUFFLECORRS

A THIS PROGRAM SHUFFLES PHENOTYPIC CORRELATIONS ASSIGNED TO DIFFERENT MODULES AND DETERMINES PROBABILITY
A THAT DIFFERENCE BETWEEN WITHIN- AND BETWEEN-MODULE AVERAGES IS GREATER THAN THAT OBSERVED.

CLUSTERMODS←'N' A NOTE: 'Y' IF WANT FOR CLUSTER MODULES, 'N' IF FOR ANATOMICAL MODULES

OBSCORRS←|ΔOVERLAPCORR[;3] A ΔOVERLAPCORR HAS PHENOTYPIC CO
RELATIONS IN COLUMN 3
OBSTYPE←ΔOVERLAPCORR[;6] A 1 IF WITHIN-MODULE CORRELATION
, 0 IF BETWEEN-MODULE CORRELATION

\$(CLUSTERMODS='N')/|OBSCORRS←|ΔOVERLAPCORRA[;3]' A EXECUTE IF USING
ANATOMICAL MODULES
\$(CLUSTERMODS='N')/|OBSTYPE←ΔOVERLAPCORRA[;6]'

IND1←(OBSTYPE=1)/|ρOBSTYPE A INDEX FOR WITHIN-MODULE CORRELATION
S
IND0←(OBSTYPE=0)/|ρOBSTYPE A INDEX FOR BETWEEN-MODULE CORRELATION
NS

NUM1←ρIND1
NUM0←ρIND0

OBSAVE1←(+/OBSCORRS[IND1])÷ρIND1 A OBSERVED AVERAGE OF WITHIN-MODULE CORRELATIONS
OBSAVE0←(+/OBSCORRS[IND0])÷ρIND0 A OBSERVED AVERAGE OF BETWEEN-MODULE CORRELATIONS

OBSDIFF←OBSAVE1-OBSAVE0 A OBSERVED DIFFERENCE

□TCLF
'OBSERVED MEAN WITHIN-MODULE CORRELATION: ',OBSAVE1 A LIST
OBSERVED VALUES
'OBSERVED MEAN BETWEEN-MODULE CORRELATION: ',OBSAVE0
□TCLF
'OBSERVED DIFFERENCE: ',OBSDIFF

SHUFFDIFFS←0ρ0 A INITIATE VARIABLE THAT WILL HAVE SHUFFLED DIFFERENCES

I←0
RETI:I←I+1
RAND←231?231 A INDEX FOR SHUFFLED VALUES

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NEWTYPE←OBSTYPE[RAND]      A SHUFFLE OBSTYPE (E.G. SHUFFLE WHETHER WITHIN- OR BETWEEN- MODULE CORRELATION)

IND1←(NEWTYPE=1)/ $\rho$ OBSTYPE      A INDEX FOR WITHIN-MODULE CORRELATION
S
IND0←(NEWTYPE=0)/ $\rho$ OBSTYPE      A INDEX FOR BETWEEN-MODULE CORRELATIONS

AVE1←(+/OBSCORRS[IND1])÷ $\rho$ IND1      A CALCULATE AVERAGE FOR WITHIN-MODULE SHUFFLED CORRELATIONS
AVE0←(+/OBSCORRS[IND0])÷ $\rho$ IND0      A CALCULATE AVERAGE FOR BETWEEN-MODULE SHUFFLED CORRELATIONS

SHUFFDIFF←AVE1-AVE0          A CALCULATE WITHIN- MINUS BETWEEN-MODULE DIFFERENCE

SHUFFDIFFS←SHUFFDIFFS,SHUFFDIFF      A ADD DIFFERENCE TO SHUFFDIFFS
→(I<1000)/RETI

PROP←(+/SHUFFDIFFS≥OBSDIFF)÷1000    A CALCULATE PROPORTION OF SHUFFLED DIFFERENCES GREATER THAN OR EQUAL TO OBSERVED DIFFERENCE
□TCLF
'PROPORTION OF SHUFFLED DIFFERENCES GREATER THAN OBSERVED: ',PROP
□TCLF
'PROGRAM SHUFFLCORRS FINISHED. VECTOR OF SHUFFLED DIFFERENCES IN VARIABLE ''SHUFFDIFFS''.'

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D. Input variable ΔOVERLAPCORR

COLUMNS OF ΔOVERLAPCORR

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COL1 TRAIT NUMBER FOR TRAIT 1 OF PAIR (CORRESPONDS TO
      TRAIT IN ΔTRAITNAMES)
COL2 TRAIT NUMBER FOR TRAIT 2 OF PAIR
COL3 PAIRWISE PHENOTYPIC CORRELATIONS
COL4 PAIRWISE QTL OVERLAP (ALL QTLS)
COL5 PAIRWISE QTL OVERLAP (GWS QTSL)
COL6 1 IF WITHIN-MODULE PAIR, 0 IF BETWEEN-MODULE PAIR

```

E. Trait Index Variables

ΔTRAITIND1	1 2 3 4 5 6 7
ΔTRAITIND2	8 9 10
ΔTRAITIND3	11 12 13
ΔTRAITIND4	14 15 16 17
ΔTRAITIND5	18 19 20 21 22

F. Trait names and number codes

	C	A
Cor_Length	1.1	1.1
Cor_tissue_Length	1.2	1.2

Cor_Width	1.3	1.3
L_over_W	1.4	1.4
LV_over_L	1.5	1.5
Style_Length	1.6	1.6
LnNectaruLPlusOne	1.7	5.1
more_than_one_flower_on_cyme	2.1	2.1
flowers_per_cyme_greater_than_one	2.1	2.1
Cyme_length	2.2	2.2
Day_germ	2.3	3.1
Internode_1_day_21	3.1	3.2
Internode_2_day_21	3.2	3.3
Internode_3_day_21	3.3	3.4
avg.number	4.1	4.1
Pollen_per_flower	4.2	4.2
avg.size	4.3	4.3
more_than_one_flower_per_day	4.4	3.5
neg_recip_L1_adj	5.1	3.6
neg_recip_L2_adj	5.2	3.7
neg_recip_L3_adj	5.3	3.8
Number_leaves_day_21	5.4	3.9
Height_mm_day_21	5.5	3.11

Column A: trait number codes for cluster traits

Column B: trait number codes for anatomical traits

II. Calculate pairwise trait overlap and averages within and between modules and test for differences

A. Program CALCQTLOVERLAP

CALCQTLOVERLAP

A THIS PROGRAM CALCULATES QTL OVERLAPS FOR ALL PAIRWISE TRAIT COMBINATIONS, AVERAGES FOR MODULE PAIRS, AND PERFORMS BOOTSTRAP ON THEM.
A CALLS PROGRAMS CONSTRUCTOVERLAP, CALCOVERLAPAVES, REPORTOVERLAP AND SHUFFLEOVERLAP

GWSONLY←'Y' A Y IF USE GWS QTLS ONLY, N IF ALL QTLS

DELETE←7 A 7 MEANS DELETE NOTHING

TRAITQTL←ΔMASTERDATA[;2 4 5] A SEE BELOW FOR LISTING OF ΔMASTERDATA COLUMNS.

TRAITCODES←ΔMASTERDATA[;1] A LIST OF TRAIT CODE NUMBERS

IND←(~TRAITCODES∈(6.1,6.2))/1ρTRAITCODES A LIST TRAITS TO EXCLUDE (FOR N_FLOWERS AND EVER_FLOWERED)

TRAITQTL←TRAITQTL[IND ;] A EXCLUDE THOSE TRAITS

TRAITCODES←TRAITCODES[IND] A EXCLUDE THOSE TRAITS FROM TRAITCODES

SIGNIFICANCE←ΔMASTERDATAq[IND ; 3] A CHANGE AS APPROPRIATE

ROWS←1↑ρTRAITQTL

A ACTIVATE NEXT THREE LINES IF WANT GWS ONLY

→(~GWSONLY='Y')/SKIP

GWINDEX←(SIGNIFICANCE=1)/!ROWS A INDEX OF QTL'S THAT ARE SIGNIFICANT GENOME WIDE

TRAITQTL←TRAITQTL[GWINDEX ;] A EXECUTE THESE TWO STATEMENTS IF WANT TO DO ANALYSIS USING JUST GENOMEWIDE QTLS

TRAITCODES←TRAITCODES[GWINDEX]

SKIP:

ANOTE: CAN CHANGE METHOD OF CALCULATING QTL OVERLAP BY CHANGING CONSTRUCTOVERLAP

CONSTRUCTOVERLAP A CALL CONSTRUCTOVERLAP

CALCOVERLAPAVES A CALL CALCOVERLAPAVES

OBSAVEOVERLAP←AVEMAT A SAVE OBSERVED VALUES OF AVERAGE PAIRWISE QTL OVERLAPS WITHIN AND BETWEEN MODULES

OBSSEOVERLAP←SEMAT A SAVE STANDARD ERRORS OF AVERAGE PAIRWISE QTL OVERLAP

ΔOBSMEANWITHIN←MEANWITHIN A OVERALL OVERLAP WITHIN MODULES(ALL MODULES COMBINED)

ΔOBSMEANBETWEEN←MEANBETWEEN A OVERALL OVERLAP BETWEEN MODULES (ALL MODULES COMBINED)

ΔOLDDIFF←MEANWITHIN-MEANBETWEEN A DIFFERENCE BETWEEN ABOVE TWO VALUES

```

OTCLF
'GWSONLY = ', GWSONLY
REPORTOVERLAP      A CALL REPORTOVERLAP TO REPORT RESULTS

SHUFFLEOVERLAP      A CALL SHUFFLEOVERLAP TO TEST WHETHER AVERAGE OVERLAPS
WITHIN AND BETWEEN MODULES DIFFER

OTCLF
'PROGRAM CALCQTLOVERLAP FINISHED. DELETE = ', DELETE
'   OUTPUT IN VARIABLES ''OBSAVEOVERLAP'', ''OBSSEOVERLAP''
'   ''MEANWITHIN'', ''SEWITHIN'', ''MEANBETWEEN'', ''SEBETWEEN''
'   ''ΔOBSMEANWITHIN'', ''ΔOBSMEANBETWEEN'', ''ΔOLDDIFF''.

```

B. Program CONSTRUCTOVERLAP

CONSTRUCTOVERLAP
A THIS PROGRAM CONSTRUCTS QTL OVERLAP MATRIX FOR ALL QTLS
A CALLED BY CALCQTLOVERLAP

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QTLNUMS←1@TRAITCODES      A TRAITCODES IS VECTOR OF TRAIT CODES ASSOCIATED WITH INDIVIDUAL QTLS
TRAITCODES2←TRAITCODES
TRAITQTL2←TRAITQTL      A COL1 CHROMOSOME, COL2 QTL CI LOWER BOUND,
COL3 QTL CI UPPER BOUND

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TRSH←TRAITCODES2
TRSH2←1@TRAITCODES2
UNIQUE←(TRSH≠TRSH2)/TRAITCODES2      A UNIQUE TRAIT CODES
NUNIQUE←ρUNIQUE
DIM←ρUNIQUE      A NUMBER OF TRAITS

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SIZE←ρTRAITCODES2      A TOTAL NUMBER OF QTLS
NUMMAT1←NUMMAT2←MAT←(DIM,DIM)ρ0      A INITIALIZE OVERLAP MATRICES

```

A MAT IS DIM X DIM MATRIX. EACH ELEMENT WILL EVENTUALLY BE THE NUMBER OF QTLS THAT OVERLAP FOR A PAIR OF TRAITS
A NUMMAT1 IS A DIM X DIM MATRIX. EACH ELEMENT WILL BE THE TOTAL NUMBER OF QTLS FOR TRAIT 1 FOR CALCULATING JACCARD INDEX
A ONLY THE ABOVE DIAGONAL ENTRIES ARE RELEVANT, AND THERE WILL BE 0'S WHEN THERE ARE NO OVERLAPPING QTLS FOR A TRAIT PAIR
A NUMMAT2 IS ANALOGOUS MATRIX FOR TRAIT 2

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OVERLAPMATAALL←(DIM,DIM)ρ0      A INITIALIZE MATRIX FOR JACCARD INDICES

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LINES1←0 6ρ0
I←0
RETI:I←I+1      A QTL1 LOOP
J←I
RETJ:J←J+1      A QTL2 LOOP
→(J>SIZE)/DOWN

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LINEI<-TRAITQTL2[I;]    A GET QTL DATA FOR QTL1 (CHROMOSOME, CI LOW, C
I HIGH)
LINEJ<-TRAITQTL2[J;]    A GET QTL DATA FOR QTL2

TEST1<-TRAITCODES[I]=TRAITCODES[J]
→(TEST1=1)/RETJ           A SKIP IF TRAITCODES IDENTICAL

TEST1<-LINEI[1]=LINEJ[1]   A QTL1 AND QTL2 ON SAME CHROMOSOME?
→(TEST1=0)/RETJ           A IF NOT, SKIP AND LEAVE ZERO IN MATRIX

TEST<-((LINEI[3]=LINEJ[2])∨(LINEJ[3]=LINEI[2]))      A
→(TEST=1)/RETJ           A SKIP IF CONFIDEN
CE INTERVALS ABUT
CRIT1<-(LINEI[2]≥LINEJ[2]) ∧ (LINEI[2]≤LINEJ[3])      A THESE FOUR LIN
ES DETERMINE WHETHER QTL PAIR OVERLAP
CRIT2<-(LINEI[3]≥LINEJ[2]) ∧ (LINEI[3]≤LINEJ[3])      A THEY DETERMI
NE WHETHER DIFFERENT CRITERIA ARE MET
CRIT3<-(LINEJ[2]≥LINEI[2]) ∧ (LINEJ[2]≤LINEI[3])
CRIT4<-(LINEJ[3]≥LINEI[2]) ∧ (LINEJ[3]≤LINEI[3])      A ONE OF THE FOUR
CRITERIA MUST BE TRUE

TEST2<-CRIT1∨CRIT2∨CRIT3∨CRIT4
→(TEST2=0)/RETJ           A SKIP OF NO OVERLAP

A IF GET TO HERE, QTL 1 AND 2 ON DIFFERENT CHROMOSOMES AND OVERLAP
CODE1<-TRAITCODES2[I]      A TRAIT NUMBER FOR QTL1
CODE2<-TRAITCODES2[J]      A TRAIT NUMBER FOR QTL2
INDEX1<-(UNIQUE=CODE1)/!ρUNIQUE
INDEX2<-(UNIQUE=CODE2)/!ρUNIQUE

NUM1<-+/(TRAITCODES2=CODE1)
NUM2<-+/(TRAITCODES2=CODE2)      A TEST2 =1 IF THERE IS OVERLAP
→(TEST2=1)/*MAT[ INDEX1;INDEX2 ]←MAT[ INDEX2;INDEX1 ]←MAT[ INDEX2;INDEX1 ]
+1'  A IF THERE IS OVERLAP, ADD 1 IN MAT FOR ENTRIES I,J AND J,I
→(TEST2=1)/*NUMMAT1[ INDEX1;INDEX2 ]←NUMMAT1[ INDEX2;INDEX1 ]←NUM1'      A
IF THERE IS OVERLAP, ENTER NUMBER OF QTLS FOR TRAIT I
→(TEST2=1)/*NUMMAT2[ INDEX1;INDEX2 ]←NUMMAT2[ INDEX2;INDEX1 ]←NUM2'      A
IF THERE IS OVERLAP, ENTER NUMBER OF QTLS FOR TRAIT J

→RETJ

DOWN:→(I<(SIZE-1))/RETI

A REMAINING LINES CALCULATE JACCARD INDEX OF OVERLAP FOR EACH TRAIT
COMBINATION

SIZE2<-1↑ρMAT
K<-0
RETK:K<-K+1      A LOOP FOR TRAIT 1

L<-K
RETL:L<-L+1      A LOOP FOR TRAIT 2

→(MAT[K;L]=0)/DOWN2      A IF NO OVERLAPPING QTLS FOR A TRAIT PAIR, SKIP

```

```

AVE←(MAT[K;L])÷(NUMMAT1[K;L]+NUMMAT2[K;L]-MAT[K;L])      A CALCULATE
JACCARD INDEX FOR TRAIT PAIR
ΔOVERLAPMATALL[K;L]←ΔOVERLAPMATALL[L;K]←AVE      A ENTER JACCARD INDEX
INTO ΔOVERLAPMATALL

DOWN2:→(L<SIZE2)/RETL
→(K<(SIZE2-1))/RETK

```

C. Program CALCOVERLAPAVES

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CALCOVERLAPAVES;I;J
A THIS FUNCTION CALCULATES AVERAGE QTL OVERLAPS FOR MODULE PAIRS
A CALLED BY PROGRAM CALCQTLOVERLAP
A CALLS PROGRAM EXTRACTUPPERTRIANGLE
A IT USES ΔOVERLAPMATALL PRODUCED BY PROGRAM CONSTRUCTOVERLAP, A 22
X 22 MATRIX OF TRAIT OVERLAPS

SQUARESW←SQUARESB←0ρ0      A SQUARESW IS A VECTOR THAT WILL HOLD ALL
WITHIN-MODULE TRAIT-PAIR OVERLAPS
A SQUARESB IS A VECTOR THAT WILL HOLD ALL
BETWEEN-MODULE TRAIT-PAIR OVERLAPS
NW←NB←0ρ0                  A NW IS VECTOR OF NUMBER OF TRAIT PAIRS IN
EACH MODULE
A NB IS VECTOR OF NUMBER OF TRAIT PAIRS IN
EACH BETWEEN-MODULE COMBINATION
LTRAITCODES2←1TRAITCODES2      A CONVERTS TRAITCOES (E.G. 2.1)
INTO INTEGERS (2)
CODES1←(1 2 3 4 5)εLTRAITCODES2/1 2 3 4 5      A LIST OF MODULES
SIZECODES1←ρCODES1            A NUMBER OF MODULES
NUNIQUE←ρUNIQUE              A NUMBER OF UNIQUE TRAITC
ODES
AVEMAT←(SIZECODES1,SIZECODES1)ρ0      A INITIALIZE MATRIX THAT
WILL HOLD AVERAGE OVERLAPS FOR MODULE PAIRS
SEMAT←(SIZECODES1,SIZECODES1)ρ0      A INITIALIZE CORRESPONDIN
G STANDARD ERROR MATRIX
LUNIQUE ←LUNIQUE                A CONVERTS UNIQUE TRAIT
CODES INTO INTEGERS

MAXI←MAXJ←+/(1 2 3 4 5)εLTRAITCODES2      A SETS MAXIMUM NUMBER OF
MODULES FOR LOOPS

I←0
RETI:I←I+1      A FIRST MODULE LOOP

IND←(LUNIQUE=CODES1[I])/1ρLUNIQUE      A VECTOR OF TRAIT NUMBERS FOR
TRAITS IN MODULE I

*(1=ρIND)/* →JMP '
E

SQUARE←ΔOVERLAPMATALL[IND;IND]      A PICK OUT MATRIX OVERLAPS COR
RESPONDING TO MODULE I

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SIZE←1↑ρSQUARE

EXTRACTUPPERTRIANGLE SQUARE
ARE AND PUT IN VECTOR TRIVEC
AVE←+/TRIVEC÷(ρTRIVEC)
F TRAITS IN MODULE I
DIFFS←TRIVEC-AVE
    ERROR OF AVERAGE
VAR←(+/DIFFS★2)÷(-1+ρTRIVEC)
VARMEAN←VAR÷(ρTRIVEC)
STDERR←VARMEAN★.5
AVEMAT[I;I]←AVE
SEMAT[I;I]←STDERR

SQUARESW←SQUARESW,TRIVEC
OR MODULE TO SQUARESW
NW←NW,ρTRIVEC
MODULE TO NW

JMP:J←I
RETJ:J←J+1

→(J>MAXJ)/DOWN

INDI←(LUNIQUE=CODES1[I])/ιρLUNIQUE      A INDEX OF TRAIT CODES FOR MOD
ULE I
INDJ←(LUNIQUE=CODES1[J])/ιρLUNIQUE      A INDEX OF TRAIT CODES FOR MOD
ULE J

SQUARE←,ΔOVERLAPMALL[INDJ;INDI]          A PICK OUT PAIRWISE OVERLAPS F
OR BETWEEN-MODULE PAIRS FOR MODULES I AND J
DIM1←ρSQUARE
AVE←+/SQUARE÷DIM1
S
DIFF←SQUARE-AVE
ANDAR ERROR
VAR←+(DIFF★2)÷(DIM1-1)
VARMEAN← VAR÷DIM1
STDERR←VARMEAN★.5

SIZE1←ρINDI
SIZE2←ρINDJ

AVEMAT[I;J]←AVEMAT[J;I]←AVE
SEMAT[I;J]←SEMAT[J;I]←STDERR

SQUARESB←SQUARESB,SQUARE
RESB
NB←NB,(SIZE1×SIZE2)
B

→(J<MAXJ)/RETJ

→(I<(MAXI))/RETI

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```

DOWN:AVEBETWEEN<-(+/SQUARESB)÷(+/NB)      A CALCULATE OVERALL AVERAGE OV
ERLAP FOR BETWEEN-MODULE PAIRS
AVEWITHIN<-(+/SQUARESW)÷(+/NW)      A CALCULATE OVERALL AVERAGE OV
ERLAP FOR WITHIN-MODULE PAIRS

STATS2 SQUARESW
MEAN AND STANDARD ERROR BETWEEN AND WITHIN MODULES
MEANWITHIN<-MEAN
A NOTE THAT MEAN STATEMENTS ARE REDUNDANT WITH THE TWO LINES STARTING AT DOWN:
SEWITHIN<-STDERR
STATS2 SQUARESB
MEANBETWEEN<-MEAN
SEBETWEEN<-STDERR

AVEMODULEMAT<-(5,5)P0

UNIQUEA<-UNIQUE

OTCLF
'PROGRAM CALCOVERLAPAVES FINISHED. DATA IN VARIABLES ''AVEMAT'' AND
''AVEMODULEMAT''.'

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D. Program REPORTOVERLAP

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REPORTOVERLAP ;I ;J
A THIS PROGRAM FORMATS OUTPUT OF PROGRAM QTLOVERLAP
A THIS PROGRAM IS CALLED BY CALCQTLOVERLAP

AVEMATFORMAT<-OTCLF,'MODULE ',(11 0$CODES1[1]),(16 0$(1$CODES1)) A TH
IS VARIABLE WILL CONTAIN THE PRINTED OUTPUT
MAXI<-MAXJ<-PCODES1      A NUMBER OF MODULES
I<-0
RETI:I<I+1    A ROW LOOP
LINE<-OTCNL,' ',($CODES1[I]),'           ' A INITIATE ROW OF AVEMATFORMAT
J<-0
RETJ:J<J+1    A COLUMN LOOP
LINE<-LINE,((8 3)$AVEMAT[I;J]),' (',(5 3$SEMAT[I;J]),')' A ADD COLU
MN VALS TO ROW
→(J<MAXJ)/RETJ

AVEMATFORMAT<-AVEMATFORMAT,OTCNL,LINE      A ADD LINE TO AVEMATFORMAT
OBSAVEMATFORMAT<-AVEMATFORMAT      A NOT NEEDED
→(I<MAXI)/RETI

AVEMATFORMAT      A PRINT MODULE AVERAGE OVERLAPS AND SE'S
OTCLF
OTCLF
'MEAN OVERLAP (SE) WITHIN MODULES ',(8 4$MEANWITHIN),' (',(6 4$SEWI
THIN),')
'MEAN OVERLAP (SE) BETWEEN MODULES ',(8 4$MEANBETWEEN),' (',(6 4$SEB
ETWEEN),')

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□TCLF
'DIFFERENCE BETWEEN WITHIN- AND BETWEEN- MODULE OVERLAP ',8 4† ΔOLDD
IFF

E. Program SHUFFLEOVERLAP

SHUFFLEOVERLAP

Δ THIS PROGRAM PERMUTES THE QTL'S TO CALCULATE SIGNIFICANCE OF DIFFERENCE IN OVERLAP FOR WITHIN-
Δ AND BETWEEN-MODULE AVERAGE OVERLAP
Δ CALLED BY PROGRAM CALCQTLOVERLAP

OLDDIFF←ΔOLDDIFF Δ SAVE ΔOLDDIFF THIS IS THE OBSERVED
DIFFERENCE BETWEEN WITHIN- AND BETWEEN- MODULE AVERAGE OVERLAPS
ORIGTRAITCODES←TRAITCODES2 Δ SAVE TRAITCODES2, VECTOR OF TRAIT CODES (E.G. 1.1, 1.2, . . . 2.1, ETC) FOR QTLS
DIMCODES←#TRAITCODES2 Δ NUMBER OF QTLS

SHUFFLEDIFFS←0#0 Δ INITIALIZE VECTOR THAT WILL SAVE WITHIN MINUS BETWEEN OVERLAP AVERAGE DIFFERENCES

KK←0
RETKK:KK←KK+1

TEST←(L(KK÷100))=(KK÷100) Δ TEST FOR KK EVENLY DIVIDED BY 100.
Δ (TEST)'''KK = '' ,KK'
100

INDEX←DIMCODES?DIMCODES Δ CREATE INDEX TO RANDOMLY PERMUTE TRAIT CODES
TRAITCODES2←ORIGTRAITCODES[INDEX] Δ CREATE RANDOMLY PERMUTED TRAIT CODES

SHCONSTRUCTOVERLAP Δ ANALAGOUS TO PROGRAM CONSTRUCTOVERLAP
; CONSTRUCTS OVERLAP MATRIX

CALCOVERLAPAVES Δ CALCULATE AVERAGE OVERLAPS FOR MODULE COMBINATIONS

SHDIFF←MEANWITHIN-MEANBETWEEN Δ CALCULATE DIFFERENCE BETWEEN WITHIN- AND BETWEEN- MODULE MEANS
SHUFFLEDIFFS←SHUFFLEDIFFS,SHDIFF Δ ADD DIFFERENCE TO SHUFFLEDIFFS

→(KK<1000)/RETKK

PROP←(+/(SHUFFLEDIFFS≥OLDDIFF))÷1000 Δ CALCULATE PROPORTION OF REPLICATES IN WHICH DIFF IS GREATER THAN OBSERVED DIFF

□TCLF
'PROPORTION OF SHUFFLE DIFFERENCES ≥ ORIGINAL DIFFERENCE = ',PROP,'
(1,000 SHUFFLES)'

□TCLF
'PROGRAM SHOVERLAP FINISHED.'

F. Program SHCONSTRUCTOVERLAP

SHCONSTRUCTOVERLAP

A THIS PROGRAM CONSTRUCTS QTL OVERLAP MATRIX FOR ALL QTLS FOR BOOTSTRAPPING
A ENTRY I,J = 0 IF NO OVERLAP, =1 IF OVERLAP
A CALLED BY SHUFFLEOVERLAP
A SEE PROGRAM CONSTRUCTOVERLAP FOR MORE DETAILED EXPLANATION OF CODE

NUNIQUE \leftarrow ρUNIQUE
DIM \leftarrow ρUNIQUE

```

SIZE $\leftarrow$ ρTRAITCODES2      A TOTAL NUMBER OF QTLS
NUMMAT1 $\leftarrow$ NUMMAT2 $\leftarrow$ MAT $\leftarrow$ (DIM,DIM) $\rho$ 0      A INITIALIZE OVERLAP MATRIX
ΔOVERLAPMATALL $\leftarrow$ (DIM,DIM) $\rho$ 0
I $\leftarrow$ 0
RETI:I $\leftarrow$ I+1      A QTL1 LOOP

J $\leftarrow$ I
RETJ:J $\leftarrow$ J+1      A QTL2 LOOP
 $\rightarrow$ (J>SIZE)/DOWN
LINEI $\leftarrow$ TRAITQTL2[I;]  A GET QTL DATA FOR QTL1  (CHROMOSOME, CI LOW, C
I HIGH)
LINEJ $\leftarrow$ TRAITQTL2[J;]  A GET QTL DATA FOR QTL2
TEST1 $\leftarrow$ LINEI[1]=LINEJ[1]  A QTL1 AND QTL2 ON SAME CHROMOSOME?
 $\rightarrow$ (TEST1=0)/RETJ      A IF NOT, SKIP AND LEAVE ZERO IN MATRIX

TEST $\leftarrow$ ((LINEI[3]=LINEJ[2]) $\vee$ (LINEJ[3]=LINEI[2]))
 $\rightarrow$ (TEST=1)/RETJ
CRIT1 $\leftarrow$ (LINEI[2] $\geq$ LINEJ[2])  $\wedge$  (LINEI[2] $\leq$ LINEJ[3])      A THESE TWO LINE
S TEST WHETHER THERE IS OVERLAP
CRIT2 $\leftarrow$ (LINEI[3] $\geq$ LINEJ[2])  $\wedge$  (LINEI[3] $\leq$ LINEJ[3])
CRIT3 $\leftarrow$ (LINEJ[2] $\geq$ LINEI[2])  $\wedge$  (LINEJ[2] $\leq$ LINEI[3])
CRIT4 $\leftarrow$ (LINEJ[3] $\geq$ LINEI[2])  $\wedge$  (LINEJ[3] $\leq$ LINEI[3])

TEST2 $\leftarrow$ CRIT1 $\vee$ CRIT2 $\vee$ CRIT3 $\vee$ CRIT4
CODE1 $\leftarrow$ TRAITCODES2[I]
CODE2 $\leftarrow$ TRAITCODES2[J]
INDEX1 $\leftarrow$ (UNIQUE=CODE1)/ $\nu$ ρUNIQUE
INDEX2 $\leftarrow$ (UNIQUE=CODE2)/ $\nu$ ρUNIQUE

NUM1 $\leftarrow$ +(TRAITCODES2=CODE1)
NUM2 $\leftarrow$ +(TRAITCODES2=CODE2)
 $\rightarrow$ (TEST2=1)/*MAT[ INDEX1; INDEX2 ] $\leftarrow$ MAT[ INDEX2; INDEX1 ] $\leftarrow$ MAT[ INDEX2; INDEX1 ]
+1'          A IF THERE IS OVERLAP, ENTER 1 IN MAT FOR ENT
RIES I,J AND J,I
 $\rightarrow$ (TEST2=1)/*NUMMAT1[ INDEX1; INDEX2 ] $\leftarrow$ NUMMAT1[ INDEX2; INDEX1 ] $\leftarrow$ NUM1 '
 $\rightarrow$ (TEST2=1)/*NUMMAT2[ INDEX1; INDEX2 ] $\leftarrow$ NUMMAT2[ INDEX2; INDEX1 ] $\leftarrow$ NUM2 '

A  $\rightarrow$ ((CODE1=4.3) $\vee$ (CODE2=4.3)) $\wedge$ (TEST2=1))/'''CODE1 = ''',CODE1  $\diamond$  ''COD
E2 = ''',CODE2  $\diamond$  LINEI  $\diamond$  LINEJ  $\diamond$  TRSH $\square$ '
```

```

->RETJ

DOWN:→(I<(SIZE-1))/RETI

SIZE2←1↑ρMAT

K←0
RETK:K←K+1

L←K
RETL:L←L+1

→(MAT[K;L]=0)/DOWN2
AVE←0.5×((MAT[K;L]÷NUMMAT1[K;L]) + (MAT[K;L]÷NUMMAT2[K;L]))

△OVERLAPMATALL[K;L]←△OVERLAPMATALL[L;K]←AVE

DOWN2:→(L<SIZE2)/RETL
→(K<(SIZE2-1))/RETK

```

G. Program EXTRACTUPPERTRIANGLE

EXTRACTUPPERTRIANGLE X;I;J
 A THIS PROGRAM EXTRACTS UPPER TRIANGLE OF A SQUARE MATRIX X AND COVERS TO VECTOR 'TRIVEC'.

```

DIM←1↑ρX
TRIVEC←0ρ0
I←0
RETI:I←I+1
J←I
RETJ:J←J+1
TRIVEC←TRIVEC,X[I;J]
→(J<DIM)/RETJ
→(I<(DIM-1))/RETI

```

H. Variables

AMASTERDATA (ALL QTLS) AND AMASTERDATA1 (ONLY GWS QTLS)

COL1	TRAIT CODE
COL2	CHROMOSOME
COL3	GWS (1) OR CWS (0)
COL4	CI LOWER BOUND (CM)
COL5	CI UPPER BOUND (CM)
COL6	CI MIDPOINT (CM)
COL7	IGNORE
COL8	ADDITIVE EFFECT OF CORD ALLELE
COL9	DOMINANCE DEVIATION (RELATIVE TO ZERO, THE AVERAGE)

OF THE TWO HOMOZYGOTES)
COL10 NUMBER OF LINES WITH LL GENOTYPE
COL11 NUMBER OF LINES WITH CL GENOTYPE
COL12 NUMBER OF LINES WITH CC GENOTYPE
COL13 UNIQUE ID FOR QTL

III. Randomization test. Assigns QTLs to random positions in genome and calculates probability obtain pattern of overlaps similar to observed

A. Program MAKEMODULES

MAKEMODULES

```
A THIS PROGRAM MAKES VARIABLES ΔMODULE1, ΔMODULE2, ETC.  
A MATRIX COLUMNS ARE  
A COL1 MODULE TRAIT NUMBER (=DECIMAL PART OF TRAITCODE)  
A COL2 CHROMOXOME  
A COL3 GWS (1) OR CWS (0)  
A COL4 CI LOWER BOUND (CM)  
A COL5 CI UPPER BOUND (CM)  
A COL6 CI LOWER BOUND (BP)  
A COL7 CI UPPER BOUND (BP)  
  
II<-0  
RETII:II<II+1  
IND<((ΔMASTERDATA[,1])=II)/11↑ρΔMASTERDATA  
Q<-ΔMASTERDATA[,1:5]  
Q[,1]<-(Q[,1]-II)×10  
CONVTRAITQTLS Q  
STMT<'ΔMODULE',(¶II),'  
↓STMT  
→(II<5)/RETII  
  
□TCLF  
'PROGRAM MAKEMODULES FINISHED. OUTPOUT IN VARIABLES ''ΔMODULEX'', X  
ε(1,2,3,4,5)'
```

B. Program CALCMODOVERLAP

CALCMODOVERLAP X

```
A THIS PROGRAM CALCULATES QTL OVERLAPS WITHIN A MODULE FOR JOANNA'S  
DATA AND PERFORMS BOOTSTRAP ON THEM.  
A X IS VARIABLE ΔMODULEI, WHERE iε1, . . . , 5
```

```
TRAITQTL<-ΔMASTERDATA[,2 3 4]          A READ IN DATA FROM ΔMASTERDATA  
TRAITCODES<-ΔMASTERDATA[,1]              A READ IN TRAIT CODES FROM ΔMASTER  
DATA  
IND<(~TRAITCODESε(2.4,2.5))/1ρTRAITCODES    A ELIMINATE QTL AND TRAIT  
CODES FOR TRAITCODES 2.4, AND 2.5 (REDUNDANT CODES)  
TRAITQTL<-TRAITQTL[,1:5]  
TRAITCODES<-TRAITCODES[,1:5]  
  
GWSONLY<'Y'                                A Y IF ANALYZE GWS QTL ONLY  
  
→(~GWSONLY='Y')/SKIP                      A SKIP IF WANT TO ANALYZE ALL QTL  
A RUN NEXT THREE LINES IF WANT TO ANALYZE ONLY GWS QTLS; THEY ELIMIN  
ATE CWS QTLS  
Q<-X[,3]  
IND<(Q=1)/1ρQ  
X<-X[,1:5]
```

```

SKIP:OBSTRAITQTL<X          A PLACE X INTO VARIABLE WITH QTL INFORMATION FOR MODULE

CONSTRUCTMODOOVERLAP OBSTRAITQTL    A CALL CONSTRUCTMODOOVERLAP

OBSAVEOVERLAP<+/+/ΔOVERLAPMATALL÷(DIM×(DIM-1))   A CALCULATE AVERAGE OVERLAP FOR MODULE
OBSOVERLAPMATALL<ΔOVERLAPMATALL           A SAVE OBSERVED OVERLAP MATRIX AS THIS VARIABLE

□TCLF
'OBSERVED AVERAGE OVERLAP = ',OBSAVEOVERLAP          A PRINT OBSERVED OVERLAP FOR MODULE

□TCLF
'STARTING RANDOMIZATION TEST'

MODAVEOVERLAP<0P0      A INITIALIZE VARIABLE TO CONTAIN AVERAGE OVERLAPS FOR RANDOMIZATION REPLICATES

LL<0
RETLL:LL<LL+1          A RANDOMIZATION LOOP

RANDOMIZEPOSITIONS      A CALL PROGRAM RANDOMIZEPOSITIONS; PRODUCES VARIABLE NEWTRAITQTL

CONSTRUCTMODOOVERLAP NEWTRAITQTL      A CALL CONSTRUCTMODOOVERLAP
AVEOVERLAP<+/+/ΔOVERLAPMATALL÷(DIM×(DIM-1))   A CALCULATE AVERAGE OVERLAP FOR REPPLICATE
MODAVEOVERLAP<MODAVEOVERLAP ,AVEOVERLAP        A APPEND AVERAGE OVERLAP TO LIST

→(LL<1000)/RETLL

□TCLF
'MODULE',(%MOD),' RESULTS'
□TCLF
'OBSERVED AVERAGE OVERLAP = ',OBSAVEOVERLAP
□TCLF
PROP<(+/MODAVEOVERLAP≥OBSAVEOVERLAP)÷1000      A CALCULATE PROPORTION OF REPLICATES WITH OVERLAP ≥ OBSERVED
'PROPORTION OF RANDOMIZED TRIALS WITH AVERAGE OVERLAP GREATER THAN OBSERVED = ',PROP
□TCLF

□TCLF
'PROGRAM CALCMODOOVERLAP FINISHED. DELETE = ',DELETE
' OUTPUT IN VARIABLES ''MODAVEOVERLAPP'', ''OBSSEOVERLAP''.'

```

C. Program CONSTRUCTMODOOVERLAP

CONSTRUCTMODOOVERLAP Y

```

A THIS PROGRAM CONSTRUCTS QTL OVERLAP MATRIX FOR ALL QTLS
A ENTRY I,J = 0 IF NO OVERLAP, =1 IF OVERLAP
A CALLED BY PROGRAM CALCQTLOVERLAP
A Y IS VARIABLE WITH TRAITQTL INFORMATION WITH SAME COLUMNS AS ΔMODU
LE1

TRAITQTL←Y
TRAITCODES←Y[,1]

A NEXT FOUR LINES IDENTIFY UNIQUE TRAITCODES
TRSH←TRAITCODES
TRSH2←~1ΦTRAITCODES
UNIQUE←(TRSH≠TRSH2)ΦTRAITCODES
NUNIQUE←ρUNIQUE
DIM←ρUNIQUE           A NUMBER OF UNIQUE TRAIT CODES

SIZE←ρTRAITCODES      A TOTAL NUMBER OF QTLS
NUMMAT1←NUMMAT2←MAT←(DIM,DIM)ρ0      A INITIALIZE OVERLAP MATRIX
ΔOVERLAPMATAALL←(DIM,DIM)ρ0          A INITIALIZE FINAL OVERLAP MATRIX
; DIM IS NUMBER OF TRAITS IN MODULE      A WILL CONTAIN JACCARD OVERLAP IND
ICES FOR PAIRS OF TRAITS IN MODULE
A LINES2←0 8ρ0                  A INITIALIZE VARIABLE TO HOLD NEW DATA

I←0
RETI:I←I+1           A QTL1 LOOP

J←I
RETJ:J←J+1           A QTL2 LOOP
→(J>SIZE)/DOWN
LINEI←TRAITQTL[I,]   A GET QTL DATA FOR QTL1 (CHROMOSOME, CI LOW, CI
HIGH)
LINEJ←TRAITQTL[J,]   A GET QTL DATA FOR QTL2

TEST←ρLINEI
*(TEST≠7)Φ'ΦTCLF Φ LINEI '        A CHECK TO ENSURE LINE HAS 7 ELEMENTS

TEST1←LINEI[1]=LINEJ[1]      A 1 IF BOTH QTLS FOR SAME TRAIT
→(TEST1=1)/RETJ            A SKIP IF BOTH QTLS FOR SAME TRAIT

TEST1←LINEI[2]=LINEJ[2]      A QTL1 AND QTL2 ON SAME CHROMOSOME?
→(TEST1=0)/RETJ            A IF SO, SKIP AND LEAVE ZERO IN MATRIX

TEST←((LINEI[4]=LINEJ[3])∨(LINEJ[4]=LINEI[3]))
→(TEST=1)/RETJ              A SKIP OF CI'S A
BUT
CRIT1←(LINEI[3]≥LINEJ[3]) ∧ (LINEI[3]≤LINEJ[4])      A THESE FOUR LIN
ES TEST WHETHER THERE IS OVERLAP USING MARKER POSITIONS (CM)
CRIT2←(LINEI[4]≥LINEJ[3]) ∧ (LINEI[4]≤LINEJ[4])
CRIT3←(LINEJ[3]≥LINEI[3]) ∧ (LINEJ[3]≤LINEI[4])
CRIT4←(LINEJ[4]≥LINEI[3]) ∧ (LINEJ[4]≤LINEI[4])

```

```

A TEST←((LINEI[7]=LINEJ[6])∨(LINEJ[7]=LINEI[6]))
A →(TEST=1)/RETJ
A CRIT1←(LINEI[6]≥LINEJ[6]) ∧ (LINEI[6]≤LINEJ[7])      A THESE FOUR L
INES TEST WHETHER THERE IS OVERLAP USING BP POSITIONS; ALTERNATIVE
A CRIT2←(LINEI[7]≥LINEJ[6]) ∧ (LINEI[7]≤LINEJ[6])      A TO LINES A
BOVE
A CRIT3←(LINEJ[6]≥LINEI[6]) ∧ (LINEJ[6]≤LINEI[7])
A CRIT4←(LINEJ[7]≥LINEI[6]) ∧ (LINEJ[7]≤LINEI[7])

TEST2←CRIT1∨CRIT2∨CRIT3∨CRIT4                      A CONDITION FOR OVERLAP

→(TEST2=0)/RETJ                                      A IF NO OVERLAP, SKIP

A LINES2←LINES2,[1](LINEI[1 2 4 5],LINEJ[1 2 4 5])

CODE1←TRAITCODES[I]                                    A TRAIT CODE FOR TRAIT I
CODE2←TRAITCODES[J]                                    A TRAIT CODE FOR TRAIT J
INDEX1←(UNIQUE=CODE1)/↑UNIQUE                         A INDEX FOR UNIQUE ELEMENT EQUAL TO
CODE 1
INDEX2←(UNIQUE=CODE2)/↑UNIQUE                         A INDEX FOR UNIQUE ELEMENT EQUAL TO
CODE 2

NUM1←+/TRAITCODES=CODE1                                A NUMBER OF QTLS WITH UNIQUE CODE =
CODE1
NUM2←+/TRAITCODES=CODE2                                A NUMBER OF QTLS WITH UNIQUE CODE =
CODE2

↓(TEST2=1)/*MAT[ INDEX1 ; INDEX2 ]←MAT[ INDEX2 ; INDEX1 ]←MAT[ INDEX2 ; INDEX1 ]
+1'          A IF THERE IS OVERLAP, INCREMENT ENTRY I,J IN MAT BY 1
↓(TEST2=1)/*NUMMAT1[ INDEX1 ; INDEX2 ]←NUMMAT1[ INDEX2 ; INDEX1 ]←NUM1'
          A IF OVERLAP, ENTER THE NUMBER OF QTLS FOR TRAIT I IN N
UMMAT1
↓(TEST2=1)/*NUMMAT2[ INDEX1 ; INDEX2 ]←NUMMAT2[ INDEX2 ; INDEX1 ]←NUM2'
          A IF OVERLAP, ENTER THE NUMBER OF QTLS FOR TRAIT I IN N
UMMAT2

→RETJ

DOWN:→(I<(SIZE-1))/RETI

A NEXT PART OF PROGRAM TAKES DATA FROM MAT, NUMMAT1 AND NUMMAT2 AND
CALCULATES JACCARD INDEX FOR EACH PAIR OF TRAITS      IN MODULE

SIZE2←1↑PMAT      A NUMBER OF TRAITS IN MODULE

K←0
RETK:K←K+1        A TRAIT K LOOP

L←K
RETL:L←L+1        A TRAIT L LOOP

→(MAT[K;L]=0)/DOWN2        A IF NO OVERLAP FOR TRAITS K AND L, SKIP

```

```

AVE<- (MAT[K;L])÷(NUMMAT1[K;L]+NUMMAT2[K;L]-MAT[K;L])      A THIS IS TH
E JACCARD INDEX

ΔOVERLAPMATALL[K;L]<-ΔOVERLAPMATALL[L;K]<-AVE    A PUT JACCARD INDEX INT
O ΔOVERLAPMATALL

DOWN2:→(L<SIZE2)/RETL
→(K<(SIZE2-1))/RETK

→0

□TCLF
'PROGRAM CONSTRUCTOVERLAP FINISHED. TRAITCODE ',(DELETE),'. MATRIX
IN VARIABLE ''MAT''.'

```

D. Program RANDOMIZEPOSITIONS

RANDOMIZEPOSITIONS

A THIS PROGRAM RANDOMIZES THE POSITIONS OF THE QTLS IN A GIVEN MODUL
E
A CALLED BY CALCMODOVERLAP

```

NEWTRAITQTL<-0 7P0      A INITIALIZE VARIABLE FOR RANDOMIZED QTLS

SIZE<-1↑OBSTRAITQTL      A NUMBER OF ROWS IN MATRIX OF QTL INFORMATION
MAXII<-SIZE              A MAXIMUM VALUE OF II FOR II LOOP
II<-0
RETIID:II<-II+1          A
LINE<-OBSTRAITQTL[II;]    A CHOOSE QTL II
NEWLINE<-LINE[1]           A CHOOSE LINE CORRESPONDING TO RANDOMIZED Q
TL II

A NEXT LINES CHOOSE CHROMOSOME RANDOMLY
MAXDEN<-ACHROMDENSITIES[15]      A ACHROMDENSITIES IS VECTOR OF CU
MULATIVE CHROMOSOME SIZES ; MAXDEN IS
                                A TOTAL SUM OF CHROMOSOME SI
ES
RAND<-?MAXDEN              A RANDOM NUMBER FOR CHOOSING CHR
OMOSOME
LINKGRP<-1+(+/RAND≥ACHROMDENSITIES ) A CHOOSE CHROMOSOME
A (RAND=MAXDEN)/*LINKGRP<-15'      A IN CASE RAND=MAXDEN, MAKE LINK
GRP 15

NEWLINE<-NEWLINE,LINKGRP      A ADD LINKAGE GROUP NUMBER TO NEWLINE

QTLSIZE<-LINE[7]-LINE[6]      A SIZE OF QTL 1.5 LOD INTERVAL IN BP
QTLHALFSIZE<-QTLSIZE÷2      A HALF SIZE OF QTL LOD INTERVAL

```

```

IND<- (ΔCUMDENSITY[ ;1 ]=LINKGRP )/11↑ρΔCUMDENSITY      A INDEX FOR ENTRIES
CORRESPONDING TO CHROMOSOME LINKGRP
PART<-ΔCUMDENSITY[ IND; ]                         A SELECT PART OF ΔCUMDENSITY CORRES-
ONDING TO CHROMOSOME LINKGRP
MAX<-Γ/PART[ ;3 ]                                     A MAXIMUM VALUE OF CUMULATIVE GENE D-
ENSITY FOR CHROMOSOME
RAND2<-?MAX                                         A RANDOM NUMBER UP TO MAX
WINDOW<-1+(+/PART[ ;3 ]≤RAND2)                      A WINDOW CORRESPONDING TO CUMULATIVE
GENE NUMBER ≤ RAND2
BASEPOS<- (WINDOW-1)×50000                          A BP POSITION OF START OF WINDOW
RAND3<-?50000                                         A RANDOM POSITION IN WINDOW
POSITION<-BASEPOS+RAND3                            A POSITION OF MIDDLE OF QTL

LOWER<-POSITION-QTLHALFSIZE                         A LOWER POSITION OF QTL (I.E. 1.5 L-
OD CI OF QTL)
UPPER<-POSITION+QTLHALFSIZE                        A UPPER POSITION OF QTL

‡(LOWER<0)/*POSITION<POSITION-LOWER'           A IF LOWER POSITION < 0, THE
N DEFINE NEW LOWER POSITION AS POSITION-LOWER
‡(UPPER>ΔLGSIZESBP[LINKGRP])//*DIFF<UPPER-ΔLGSIZESBP[LINKGRP] ◊ POSIT-
ION<POSITION-DIFF'   A IF UPPER POSITION > MAX POSITION
                           A THEN REDUCE POSITION BY OV-
ERAGE
LOWER<-POSITION-QTLHALFSIZE                         A POSITION OF LOWER BOUND OF
CI                                                 A POSITION OF UPPER BOUND OF
UPPER<-POSITION+QTLHALFSIZE                         CI

NEWLINE<-NEWLINE,LINE[3 4 5],LOWER,UPPER            A MAKE LINE FOR QTL APPENDI-
NG LOWER AND UPPER BOUNDS FOR NEW QTL POSITION
NEWTRAITQTL<-NEWTRAITQTL,[1]NEWLINE               A APPEND NEWLINE TO NEWTRAI-
TQTL; COLS 3,4 AND 5 OF LINE ARE GWS (1 OR 0),
                                                 A ORIGINAL CI LOWER
BOUND IN CM, AND ORIGINAL CI UPPER BOUND IN CM

→(II<MAXII)/RETII

```

F. Program CALCMODOVERLAP2

```

CALCMODOVERLAP2
A THIS PROGRAM CALCULATES QTL OVERLAPS WITHIN A MODULE FOR JOANNA'S
DATA AND PERFORMS BOOTSTRAP ON THEM.
A THIS PROGRAM IS ESSENTIALLY SAME AS CALCMODOVERLAP, EXCEPT IT PER-
FORMS THE ANALYSIS FOR ALL MODULES
A SIMULTANEOUSLY AND FOR OVERALL WITHIN- VS. BETWEEN- MODULE AV-
ERAGES
A BECAUSE OF THIS SIMILARITY, ANNOTATION IS NOT AS COMPLETE

GWSONLY<'N'
MAXMM<5    A 4 FOR ANATOMICAL MODULES, 5 FOR CLUSTER MODULES

CUMOVERLAP<0ρ0
MM<0

```

```

RETMM:MM<MM+1

STMT←'TRAITQTL←AMODULE',(FMM)      A USE A OR B FOR LESS-CONSERVATIVE
E AND CONSERVATIVE SNP SETS, RESPECTIVELY
$STMT

TRAITCODES←TRAITQTL[;1]

→(~GWSONLY='Y')/SKIP
A RUN NEXT FOUR LINES IF WANT TO ANALYZE ONLY GWS QTLS
Q←TRAITQTL[;3]
IND←(Q=1)/1PQ
TRAITQTL←TRAITQTL[IND;]
TRAITCODES←TRAITQTL[;1]

SKIP:OBSTRAITQTL←TRAITQTL

TEST←1↑PTRAITQTL
→(TEST<2)/DOWN

CONSTRUCTMODOVERLAP OBSTRAITQTL

TRIANGLE ΔOVERLAPMATAALL
CUMOVERLAP←CUMOVERLAP,VEC

DOWN:→(MM<MAXMM)/RETMM

OBSOVERLAP←(+/CUMOVERLAP)÷Pcumoverlap

□TCLF
'OBSERVED AVERAGE OVERLAP WITHIN MODULES = ',OBSOVERLAP

□TCLF
'STARTING RANDOMIZATION TEST'

MODAVEOVERLAP←0P0

LL←0
RETLL:LL←LL+1

CUMOVERLAP←0
NN←0
RETNN:NN←NN+1

STMT←'TRAITQTL←AMODULE',(FNN)      A USE A OR B FOR LESS-CONSERVATIVE
AND CONSERVATIVE SNP SETS, RESPECTIVELY
$STMT

TRAITCODES←TRAITQTL[;1]

A RUN NEXT FOUR LINES IF WANT TO ANALYZE ONLY GWS QTLS
Q←TRAITQTL[;3]
IND←(Q=1)/1PQ
TRAITQTL←TRAITQTL[IND;]
TRAITCODES←TRAITQTL[;1]

```

```

TEST←1↑ρTRAITQTL
→(TEST<2)/DOWN2

RANDOMIZEPOSITIONS

CONSTRUCTMODOVERLAP NEWTRAITQTL
TRIANGLE ΔOVERLAPMATAALL
CUMOVERLAP←CUMOVERLAP,VEC
DOWN2:→(NN<5)/RETNN

AVEOVERLAP←(+/CUMOVERLAP)÷ρCUMOVERLAP

MODAVEOVERLAP←MODAVEOVERLAP,AVEOVERLAP

→(LL<1000)/RETLL

□TCLF
'OBSERVED AVERAGE OVERLAP = ',OBSOVERLAP
□TCLF
PROP←(+/MODAVEOVERLAP≥OBSOVERLAP)÷1000
'PROPORTION OF RANDOMIZED TRIALS WITH AVERAGE OVERLAP GREATER THAN O
BSERVED = ',PROP
□TCLF

□TCLF
'PROGRAM CALCMODOVERLAP2 FINISHED. DELETE = ',DELETE
' OUTPUT IN VARIABLES ''MODAVEOVERLAPP'', ''OBSSEOVERLAP'''.

```

G. Variables used

ΔGENEDENSITY, HAS THREE COLUMNS:

COL1	LINKAGE GROUP
COL2	NUMBER OF 50KB WINDOW
COL3	NUMBER OF GENES IN WINDOW

ΔOVERLAPMATAALL

an N x N matrix, where N is number of traits in module
entry i,j is the Jaccard Index of overlap for traits i and j

IV. Calculation of correlation between phenotypic correlations and QTL overlaps

A. This correlation is calculated in SAS using the following input from variable ΔOVERLAPCORR:

ΔOVERLAPCORR is a MATRIX WITH FOLLOWING COLUMNS:

COL1 Trait 1 (Trait code)
COL2 Trait 2 (Trait code)
COL3 Phenotypic correlation
COL4 Jaccard Index overlap (all QTLs)
COL5 Jaccard Index overlap (only GWS QTLs)
COL6 1 if within-module trait pair, 0 if between-module

B. Calculated correlation between module average correlation and module average QTL overlaps manually, then made variables ΔAVEOVERLAPCORR (for cluster modules) and ΔAVEOVERLAPCORR2 (for anatomical modules) with following columns:

COL1 Module I
COL2 Module J
COL3 Average Jaccard overlap (all QTLs)
COL4 Average Jaccard overlap (only GWS QTLs)
COL5 Average phenotypic correlation

NOTE: a value of 99 indicates data unavailable because of too few QTLs or traits

C. Program PERMUTEAVEOVCORR

PERMUTEAVEOVCORR

A THIS PROGRAM PERMUTES PHENOTYPIC CORRELATIONS TO TEST SIGNIFICANCE OF CORRELATION BETWEEN MODULE AVERAGE OVERLAP
A AND AVERAGE PHENOTYPIC CORRELATION
A THIS PROGRAM CALLS PROGRAM CALCCORR

CLUSTERMOD←'N' A Y IF ANALYSIS FOR CLUSTER MODULES, N IF FOR ANATOMICAL MODULES

X←ΔAVEOVERLAPCORR[;3 5] A READ IN OVERLAP (ALL QTLS) AND PHENOTYPIC CORRELATION
Y←ΔAVEOVERLAPCORR[;4 5] A READ IN OVERLAP (GWS QTLS) AND PHENOTYPIC CORRELATION
*(CLUSTERMOD='N')/'X←ΔAVEOVERLAPCORR2[;3 5]' A IF ANALYZING ANATOMICAL MODELS, PERFORM ANALOGOUS READINS
*(CLUSTERMOD='N')/'Y←ΔAVEOVERLAPCORR2[;4 5]'

IND1←(X[,1]≠99)/1↑ρX A INDEX OF ENTRIES WITHOUT MISSING VALUES
X←X[IND1;] A KEEP ENTRIES WITHOUT MISSING VALUES
IND2←(Y[,1]≠99)/1↑ρY A INDEX OF ENTRIES WITHOUT MISSING VALUES
Y←Y[IND2;] A KEEP ENTRIES WITHOUT MISSING VALUES

```

XX←X          A PRESERVE X FOR LATER USE
YY←Y          A PRESERVE Y

CALCCORR X      A CALCULATE CORRELATION BETWEEN OVERLAP (AL
L QTLS) AND PHENOTPYIC CORRELATION
OBSCORR1←CORR   A SAVE CORRELATION AS OBSCORR1
CALCCORR Y      A CALCULATE CORRELATION BETWEEN OVERLAP (GW
S QTLS) AND PHENOTPYIC CORRELATION
OBSCORR2←CORR   A SAVE AS OBSCORR2

A PRINTOUT CALCULATED INFORMATION

$(CLUSTERMOD='Y')/'OTCLF ◊ ''ANALYSIS FOR CLUSTER MODULES.''''
$(CLUSTERMOD='N')/'OTCLF ◊ ''ANALYSIS FOR ANATOMICAL MODULES.'''''

OTCLF
'CORRELATION FOR ALL QTLS ', OBSCORR1
'CORRELATION FOR GWS QTLS ', OBSCORR2

A START PERMUTAIOTNS

OTCLF
'STARTING PERMUTATIONS '

RANDCORRS1←0ρ0    A INITIALIZE VARIABLE FOR CORRELATION BETWEEN OV
ERLAP (ALL QTLS) AND PHENOTPYIC CORRELATION (CORRELATION 1)
RANDCORRS2←0ρ2    A INITIALIZE VARIABLE FOR CORRELATION BETWEEN OV
ERLAP (GWS QTLS) AND PHENOTPYIC CORRELATION (CORRELATION 2)
ROWS1←1↑ρXX       A SIZE OF VARIABLE WITH DATA FOR CORRELATION 1
ROWS2←1↑ρYY       A SIZE OF VARIABLE WITH DATA FOR CORRELATION 2

I←0
RETI:I←I+1        A PERMUTATION LOOP

X←XX              A DATA FOR CORRELATION 1
Y←YY              A DATA FOR CORRELATION 2

RAND1←ROWS1?ROWS1  A MAKE INDEX FOR PERMUTING COLUMN 1 OF X
X[;1]←X[RAND1;1]  A PERMUTE COLUMN 1 OF X
RAND2←ROWS2?ROWS2  A MAKE INDEX FOR PERMUTING COLUMN 1 OF Y
Y[;1]←Y[RAND2;1]  A PERMUTE COLUMN 1 OF Y

CALCCORR X          A CALCULATE CORRELATION 1
CORR1←CORR          A SAVE AS CORR1
CALCCORR Y          A CALCULATE CORRELATION 2
CORR2←CORR          A SAVE AS CORR2
RANDCORRS1←RANDCORRS1,CORR1  A APPEND TO RANDCORRS1
RANDCORRS2←RANDCORRS2,CORR2  A APPEND TO RANDCORRS2

→(I<1000)/RETI

OTCLF
SUM1←+/ (RANDCORRS1≥OBSCORR1)  A SUM OF CORRELATIONS ≥ OBSERVED COR
RELATION 1

```

```

SUM2<+/((RANDCORRS2≥OBSCORR2))      A SUM OF CORRELATIONS ≥ OBSERVED COR
RELATION 2
PROP1←SUM1÷1000                      A CONVERT SUMS TO PROPORTIONS
PROP2←SUM2÷1000
'PROP GREATER THAN OBSERVED (ALL QTLS) ',PROP1
'PROP GREATER THAN OBSERVED (GWS QTLS) ',PROP2

□TCLF
'PROGRAM PERMUTEAVEOVCCORR FINISHED '

```

D. Program CALCCORR

```

CALCCORR X
A THIS PROGRAM CALCULATES CORRELATION BETWEN TWO COLUMNS IN X
ROWS←1↑ΡX
MEANS←+/[1]X÷ROWS
X1←,X[;1]
X2←,X[;2]
DIFF1←X1-MEANS[1]
DIFF2←X2-MEANS[2]
COV←+/(DIFF1×DIFF2)÷ROWS
VAR1←+/(DIFF1★2)÷ROWS
VAR2←+/(DIFF2★2)÷ROWS
CORR←COV÷((VAR1×VAR2)★.5)
A □TCLF
A 'THE CORRELATION IS ',CORR

```

V. Predicting genetic correlations from QTL properties

A. Program PREDICTCORR

PREDICTCORR

▷ THIS PROGRAM PREDICTS PAIRWISE TRAIT GENETIC CORRELATIONS FROM QTL OVERLAP AND EFFECT SIZES
▷ INPUT IS VARIABLE ΔMIDPOINTS (SEE BELOW)
▷ CALLS PROGRAMS CALCCOV3, CALCCORR AND TRIANGLE

ALLQTLS←'N' ▷ 'Y' MEANS ALL QTLS USED, 'N' MEANS ONLY GWS QTLS USED

ΔMIDPOINTSA←ΔMIDPOINTS ▷ USE ΔMIDPOINTS FOR LESS-CONSERVATIVE QT LS, ΔMIDPOINTS1 FOR GWS QTLS

ΔTOTRHEA←ΔTOTRHE1 ▷ USE ΔTOTRHE FOR LESS-CONSERVATIVE QT LS, ΔTOTRHE1 FOR GWS QTLS

QTLDATA←ΔMASTERDATA ▷ USE ΔMASTERDATA FOR LESS-CONSERVATIVE QTL SET, ΔMASTERDATA1 FOR CONSERVATIVE DATASET

TRAITCODES←ΔMASTERDATA[;1] ▷ AND USE ΔMASTERDATA FOR LESS-CONSERVATIVE QTL SET, ΔMASTERDATA1 FOR CONSERVATIVE DATASET

IND←(~TRAITCODES∈(2.4,2.5,6.1,6.2))/1ρTRAITCODES ▷ LIST TRAITS TO EXCLUDE NOTE: 2.4 AND 2.5 ARE ALTERNATES FOR 2.1 AND 2.2

▷ ↳(ALLQTLS='N')/'IND←(~TRAITCODES∈(3.1,3.2,3.3,2.4,2.5))/1ρTRAITCODES' ▷ USE THIS FOR JUST FLOWER AND NECTAR TRAIT ANALYSIS

TRAITCODES←TRAITCODES[IND] ▷ EXCLUDE TRAITCODES FOR EXCLUDED TRAITS FROM ABOVE

QTLDATA←QTLDATA[IND;] ▷ EXCLUDE TRAITS FROM QTL DATA

QTLDATAB←QTLDATA ▷ PRESERVE QTLDATA

UNIQCODES←1.1,1.2,1.3,1.4,1.5,1.6,1.7,2.1,2.2,2.3,3.1,3.2,3.3,4.1,4.2,4.3,4.4,5.1,5.2,5.3,5.4,5.5 ▷ UNIQUE TRAIT CODES

▷ ↳(ALLQTLS='N')/'UNIQCODES←1.1,1.2,1.3,1.4,1.5,1.6,1.7,2.1,3.2,3.3,4.3,5.1,5.2,5.3,5.4' ▷ USE THIS FOR JUST FLOWER AND NECTAR TRAIT ANALYSIS

▷ ↳(ALLQTLS='N')/'ΔTOTRHEA←ΔTOTRHEA[1 2 3 4 5 6 7 11 12 13;]' ▷ USE THIS FOR JUST FLOWER AND NECTAR TRAIT ANALYSIS

MAXJ←ρUNIQCODES ▷ MAXIMUM VALUE FOR J LOOP

MAXI←MAXJ-1 ▷ MAXIMUM VALUE FOR I LOOP

AA MIDPOINTS←0 4ρ0 ▷ THIS VARIABLE HOLDS MIDPOINTS OF OVERLAP INTERVALS FOR QTLS THAT OVERLAP

 ▷ FIRST TWO COLUMNS ARE QTL UNIQUE ID, THIRD IS LG AND FOURTH IS MIDPOINT

 ▷ DOESN'T NEED TO BE RUN IF ALREADY HAVE ΔMIDPOINT S

GENCORRS←((ρUNIQCODES),(ρUNIQCODES))ρ0 ▷ INITIALIZE MATRIX FOR PAIRWISE TRAIT PREDICTED GENETIC CORELATIONS

OVERLAPMAT←((ρUNIQCODES),(ρUNIQCODES))ρ0

```

I<-0
RETI:I<I+1    A FIRST TRAIT LOOP

J<I
RETJ:J<J+1    A SECOND TRAIT LOOP

TRAITCODEI<UNIQCODES[I]
TRAITCODEJ<UNIQCODES[J]

IND1<(TRAITCODES=UNIQCODES[I])/1@TRAITCODES      A INDEX OF QTLS FOR TRA
IT WITH TRAITCODES = UNIQCOEDES[I]
PART1<QTLDATA[IND1;]                            A EXTRACT QTLDATA FOR T
HAT TRAIT
IND2<(TRAITCODES=UNIQCODES[J])/1@TRAITCODES      A INDEX OF QTLS FOR TRA
IT WITH TRAITCODES = UNIQCOEDES[J]
PART2<QTLDATA[IND2;]                            A EXTRACT QTLDATA FOR T
HAT TRTAIT

OVERLAPS<0 4@0      A NUMBERS ARE QTNUMBERS FROM PARTS 1 AND 2 FOR OVE
RLAPPING QTL

MAXII<1↑@PART1      A MAXIMUM VALUE FOR II IN II LOOP
MAXJJ<1↑@PART2      A MAXIMUM VALUE FOR JJ IN JJ LOOP

II<0
RETI:II<II+1      A PART1 LOOP

JJ<0
RETJJ:JJ<JJ+1      A PART2 LOOP

LINEII<PART1[II;]  A GET QTL DATA FOR QTL1 (CHROMOSOME, CI LOW, CI H
IGH)
LINEJJ<PART2[JJ;]  A GET QTL DATA FOR QTL2

TEST1<LINEII[2]=LINEJJ[2]      A QTL1 AND QTL2 ON SAME CHROMOSOME?
→(TEST1=0)/DOWN              A IF NOT, SKIP AND LEAVE ZERO IN MATRIX

TEST<((LINEII[5]=LINEJJ[4])∨(LINEJJ[5]=LINEII[4]))      A DO NOT COUNT AS
→(TEST=1)/DOWN
OVERLAP IF CI'S ABUT
CRIT1<(LINEII[4]≥LINEJJ[4]) ∧ (LINEII[4]≤LINEJJ[5])      A THESE FOUR
LINES TEST WHETHER THERE IS OVERLAP
CRIT2<(LINEII[5]≥LINEJJ[4]) ∧ (LINEII[5]≤LINEJJ[5])
CRIT3<(LINEJJ[4]≥LINEII[4]) ∧ (LINEJJ[4]≤LINEII[5])
CRIT4<(LINEJJ[5]≥LINEII[4]) ∧ (LINEJJ[5]≤LINEII[5])

TEST2<CRIT1∨CRIT2∨CRIT3∨CRIT4      A CRITERION FOR OVERLAP
→(TEST2=0)/DOWN                  A IF NO OVERLAP, GO DOWN

```

```

OVERLAPS←OVERLAPS,[1](II,JJ,LINEII[13],LINEJJ[13])      A COLUMNS: II
, JJ, QTL ID NUMBER FOR QTL II, QTL ID NUMBER FOR QTL JJ

A THIS NEXT SET OF 6 LINES CALCULATES MIDPOINTS OF OVERLAP INTERVALS
AND STORES IN VARIABLE MIDPOINTS
A THEY NEEDN'T BE RUN IF 4MIDPOINTS HAS BEEN CREATED

A TEMP←LINEII[3 4],LINEJJ[3 4]                      A TEMP2←@TEMP
A TEMP3←TEMP[TEMP2]
A INTERVAL←TEMP3[2 3]
A MIDPOINT←(+/INTERVAL)÷2
A MIDPOINTS←MIDPOINTS,[1](LINEII[12],LINEJJ[12],LINEII[2],MIDPOINT)

DOWN:→(JJ<MAXJJ)/RETJJ

→(II<MAXII)/RETII

MAXK←1↑POVERLAPS          A NUMBER OF ROWS IN VARIABLE OVERLAPS, MAXIM
K VALUE FOR K LOOP

A CREATE VARIABLES TO CONTAIN ADDITIVE AND DOMINANCE EFFECTS OF OVER
LAPPING QTL PAIRS
ADDEFF←0 4P0  A VARIABLE HAS COLUMNS: COLS 1 AND 2: ADDITIVE EFFECT
OF C ALLELE FOR QTLS I AND J COLS 3 AND 4: QTL ID'S FOR QTLS I AND J
NOTE: 'Additive effect' in this context is the average trait value o
f the means for an individual homozygous for a particular allele
DOMEFF←0 4P0  A VARIABLE HAS ANALAGOUS COLUMNS
NOTE: 'dominance effect' in this context is the average trait value
of heterozygous individuals

SIZE←1↑POVERLAPS
→(SIZE=0)/DOWN4          A IF NO OVERLAPPING QTLS, SKIP TO DOWN4

A START PROCESSING OVERLAPPING QTLS

K←0
RETK:K←K+1  A THIS LOOP ADDS ADDITIVE AND DOMINANCE EFFECTS FOR OVERL
APPING QTLS

AVALS←(PART1[OVERLAPS[K;1];8],PART2[OVERLAPS[K;2];8],OVERLAPS[K;3 4])
)  A ADDITIVE EFFECTS OF C ALLELE FOR THE TWO OVERLAPPING QTLS PLUS
QTL ID'S
DVALS←(PART1[OVERLAPS[K;1];9],PART2[OVERLAPS[K;2];9],OVERLAPS[K;3 4])
)  A DOMINANCE DEVIATION FOR THE TWO OVERLAPPING QTLS PLUS QTL ID'S

ADDEFF←ADDEFF,[1]AVALS          A APPEND ADDITIVE EFFECT VALUES
DOMEFF←DOMEFF,[1]DVALS          A APPEND DOMINANCE EFFECT VALUES

→(K<MAXK)/RETK

A START PROCESSING TRAIT PAIR THAT HAS NO OVERLAPPING QTLS
A NEXT SET OF LINES ADDS ADDITIVE AND DOMINANCE EFFECT FOR QTLS IN
PART1 THAT DO NOT OVERLAP WITH ANY IN PART2

```

```

DOWN4:MAXL←1↑ρPART1      A MAXIMUM VALUE OF L FOR L LOOP
L←0
RETL:L←L+1                A LOOP FOR QTLS IN PART1

TEST←L≤OVERLAPS[,1]
→(TEST=1)/DOWN2          A SKIP IF QTL OVERLAPS A QTL IN PART2

ADDEFF←ADDEFF,[1](PART1[L;8],0,PART1[L;13],0)      A ADD ADDITIVE
EFFECT TO ADDEFF FOR QTL OF TRAIT 1, 0'S FOR TRAIT 2
DOMEFF←DOMEFF,[1](PART1[L;9],0,PART1[L;13],0)      A ADD DOMINANCE
EFFECT TO DOMEFF FOR QTL OF TRAIT 2, 0'S FOR TRAIT 1

DOWN2:→(L<MAXL)/RETL

A NEXT SET OF LINES ADDS ADDITIVE AND DOMINANCE EFFECT FOR QTLS IN
PART2 THAT DO NOT OVERLAP WITH ANY IN PART1

MAXLL←1↑ρPART2          A MAXIMUM VALUE OF LL FOR LL LOOP
LL←0
RETL:L←LL+1              A LOOP FOR QTLS IN PART2

TEST←LL≤OVERLAPS[,2]
→(TEST=1)/DOWN3          A SKIP IF QTL OVERLAPS A QTL IN PART1

ADDEFF←ADDEFF,[1](0,PART2[LL;8],0,PART2[LL;13])    A ADD ADDITIVE
EFFECT TO ADDEFF FOR QTL OF TRAIT 2, 0'S FOR TRAIT 1
DOMEFF←DOMEFF,[1](0,PART2[LL;9],0,PART2[LL;13])    A ADD DOMINANCE
EFFECT TO DOMEFF FOR QTL OF TRAIT 2, 0'S FOR TRAIT 1

DOWN3:→(LL<MAXLL)/RETL

CALCCOV3      A CALL PROGRAM CALCCOV3, WHICH CALCULATES GENETIC CORREL
ATIONS FROM ADDEFF AND DOMEFF VARIABLES

GENCORRS[I;J]←R      A ADD PREDICTED GENETIC CORRELATION TO GENCORRS FO
R TRAIT PAIR I,J

→(J<MAXJ)/RETJ

→(I<MAXI)/RETI

TRIANGLE GENCORRS      A MAKES UPPER TRIANGLE OF GENCORRS INTO VECTO
R 'VEC'
NPOINTS←0.5×(PUNIQCODES)×(-1+PUNIQCODES)  A NUMBER OF ELEMENTS IN 'V
EC'; COULD ALSO USE JUST NPOINTS←PVEC
DATA←((NPOINTS,1)ρΔPHENCORRVEC),(NPOINTS,1)ρVEC  A COL1: PHENOTYPIC
CORRELATIONS, COL2: GENCORRS
‡(ALLQTLS='N')/DATA←((NPOINTS,1)ρΔPHENCORRVEC[ΔGWSIND2]),(NPOINTS,1
)ρVEC'  A ALTERNATE STATEMENT IF USING ONLY GWS QTLS
BIAS←DATA[,2]-DATA[,1]          A BIAS = PREDICTED G
ENETIC CORRELATION - PHENOTYPIC CORRELATION
DATA←DATA,(NPOINTS,1)ρBIAS        A ADD BIAS AS COLUMN
OF DATA

```

```

CALCCORR DATA[;1 2]
OBSCORR1←CORR          A CORRELATION BETWEEN PHENOTYPIC CORRELATION
AND PREDICTED GENETIC CORELATION
CALCCORR DATA[;1 3]
OBSCORR2←CORR          A CORRELATION BETWEEN PHENOTYPIC CORRELATION
AND BIAS

IND←(DATA[;2]≠0)/11↑ρDATA  A INDEX FOR VALUES OF DATA IN WHICH PRE
DICTED GENETIC CORRELATION IS NOT 0
DATA2←DATA[ IND;1]         A DATA FOR ONLY TRAIT PAIRS FOR WHICH PP
REDICTED GENETIC CORRELATION IS NOT 0
CALCCORR DATA2[;1 2]
OBSCORR1A←CORR           A CORRELATION BETWEEN PHENOTYPIC CORRELATION
AND PREDICTED GENETIC CORELATION
CALCCORR DATA2[;1 3]
OBSCORR2A←CORR           A CORRELATION BETWEEN PHENOTYPIC CORRELATION
AND BIAS

```

```

□TCLF
'CORRELATION OF PHENOTYPIC CORRELATIONS AND PREDICTED CORRELATIONS:
',OBSCORR1
'    WITH ZEROS REMOVED:
',OBSCORR1A
'CORRELATION OF BIAS AND PHENOTYPIC CORRELATIONS: ',OBSCORR2
'    WITH ZEROS REMOVED: ',OBSCORR2A

```

□TCLF

'PROGRAM PREDICTCORR FINISHED. OUTPUT IN VARIABLE ''GENCORRS''.'

B. Program CALCCOV3

CALCCOV3

A THIS PROGRAM CALCULATES PREDICTED GENETIC COVARIANCE, VARIANCES AND GENETIC CORRELATION FOR A PAIR OF TRAITS TAKING GENOTYPE FREQS INTO ACCOUNT

A CALLED BY PROGRAM 'PREDICTCORR'

A X VARIABLE ADDEFF, Y IS VARIABLE DOMEFF FROM PREDICTCORR

```

KKMAX←1↑ρADDEFF          A NUMBER OF ROWS IN VARIABLE ADDEFF

PAIRS←ΔMIDPOINTSA[;1 2]    A VARIABLE WITH ALL PAIRS OF QTLS THAT
OVERLAP; NUMBERS ARE QTL IDs FOR QTL1 AND QTL2; ΔMIDPOINTS FOR ALL
QTL, ΔMIDPOINTS1 FOR GWS QTL

VARCOV←0 3ρ0                A INITIALIZE VARIABLE; COL 1: GENETIC
COVARIANCE, COLS 2 AND 3: GENETIC VARIANCES OF TRAITS I AND J

SAVELINE1←0 12ρ0             A INITIALIZE VARIABLE WITH FOLLOWING C
OLUMNS:
                                A COL 1 ADDITIVE EFFECT OF QTL I
                                A COL 2 DOMINANCE EFFECT OF QTL I
                                A COL 3 ADDITIVE EFFECT OF QTL J

```

```

A COL 4 DOMINANCE EFFECT OF QTL J
A COL 5 QTL ID FOR QTL I
A COL 6 QTL ID FOR QTL J
A COL 7 PROPORTION OF INDIVIDUALS HOMO
ZYGOUS FOR CORDAT ALLELE
A COL 8 PROPORTION OF INDIVIDUALS HETE
ROZYGOUS
A COL 9 PROPORTION OF INDIVIDUALS HOMO
ZYGOUS FOR LACUNOSA ALLELE
A COL 10 MEAN VALUE FOR QTL I
A COL 11 MEAN VALUE FOR QTL J
A COL 12 GENETIC COVARIANCE BETWEEN QT
LS I AND J

A THIS SEGMENT CALCULATES PREDICTED GENETIC COVARIANCE
KK←0
RETKK:KK←KK+1          A LOOP FOR PROCESSING ADDEFF AND DOMEFF
LINEA←ADDEFF[KK;]        A READIN LINE KK OF ADDEFF
AEFFECTS←LINEA[1 2]      A ADDITIVE EFFECTS OF THE TWO QTLS
LINED←DOMEFF[KK;]        A READ IN LINE KK OF DOMEFF
DEFFECTS←LINED[1 2]      A DOMINANCE DEVIATION OF THE TW QTLS
PAIR←2 1PLINEA[3 4]      A QTL PAIR UNIQUE IDS

COV←0      A INITIALIZE PREDICTED GENETIC COVARIANCE TO 0
FLAG←1      A 1 INDICATES OVERLAPPING QTL; 0 INDICATES NOT OVERLAPPING
QTLS
TEST←(AEFFECTS[1]≠0)∧(AEFFECTS[2]≠0)      A TEST FOR WHETHER OVERLAP
PING QTLS

↑(TEST=0)∨'FLAG=0' →DOWN'           A SET FLAG = 0 AND LEAVE COV = 0 IF
ONE OR BOTH ADDITIVE EFFECTS = 0

A CALCULATE COVARIANCE FOR QTL PAIR

IND←(,PAIRS^.=PAIR)/↑↑PAIRS      A ROW INDEX OF QTL PAIR IN ΔMIDPOINT
S
TEST←0=PAIR
↑(TEST=1)∨'PAIR←2 1PLINEA[4 3]' →IND←(,PAIRS^.=PAIR)/↑↑PAIRS      A TEST IF PAIR IN VARIABLE 'PAIRS'
A IF NOT IN 'PAIRS', REVERSE ORDER OF PAIR
IND←(,PAIRS^.=PAIR)/↑↑PAIRS      A ROW INDEX OF QTL PAIR IN ΔMIDPOINT
S
TEST←0=PAIR
↑(TEST=1)∨'→DOWN'                A SKIP OF PAIR NOT IN 'PAIRS'

NUMS←,ΔMIDPOINTSA[IND;6 7 8]
A VECTOR OF NUMBER OF INDIVIDUALS WITH CC, CL AND WITH LL GEN
OTYPE

→(0=+/NUMS)/DOWN4      A IF NO INDIVIDUALS, GO TO DOWN4

PROPCC←NUMS[1]÷(+/NUMS)      A PROPORTION OF INDIVIDUALS WITH CC GENOTYPE
PE
PROPCL←NUMS[2]÷(+/NUMS)
PROPLL←NUMS[3]÷(+/NUMS)

```

```

MEAN1<- (PROPCC×AEFFECTS[1]) + ((PROPCL)×DEFFECTS[1]) - (PROPLL×AEFFECTS[1])
] ) A MEAN EFFECT FOR QTL1
MEAN2<- (PROPCC×AEFFECTS[2]) - ((PROPCL)×DEFFECTS[2]) - (PROPLL×AEFFECTS[2]
] ) A MEAN EFFECT FOR QTL2

PROD1<-PROPCC×(AEFFECTS[1]-MEAN1)×(AEFFECTS[2]-MEAN2)
A CALCULATE COVARIANCE
PROD2<-PROPCL×(DEFFECTS[1]-MEAN1)×(DEFFECTS[2]-MEAN2)
PROD3<-PROPLL×((-1×AEFFECTS[1])-MEAN1)×((-1×AEFFECTS[2])-MEAN2)
COV<-PROD1+PROD2+PROD3
NEWLINE<- (AEFFECTS, DEFFECTS, (,PAIR), PROPCC, PROPCL, PROPLL, MEAN1, MEAN
2, COV) A NEWLINE WITH CALCULATED DATA; SAME COLUMNS AS SAVELINE1 (S
EE ABOVE)
SAVELINE1<-SAVELINE1, [1]NEWLINE A ADD NEWLINE TO SAVELINE1

DOWN:
A THIS SECTION CALCULATES GENETIC VARIANCES OF INDIVIDUAL TRAITS

A CALCULATE VARIANCES
VARI<-VARJ<-0 A INITIALIZE VARIABLES FOR VARIANCES OF TRAITS I AND
J
PAIR2<,PAIR A VECTOR OF TRAIT ID'S

→(AEFFECTS[1]=0)/DOWN2 A SKIP FOR QTL1 IF EFFECT IS 0

A CALCULATE VARIANCE FOR QTL1
IND<- (MASTERDATA[,13]=PAIR2[1])/11↑ρMASTERDATA A INDEX FOR QTL WI
TH SAME ID AS QTL I
LINEI<,MASTERDATA[IND,] A SELECT CORRESPONDING LINE FROM MAST
ERDATA
AEFFECT<-LINEI[8] A ADDITIVE EFFECT OF THIS QTL
DOMEFFECT<-LINE[9] A DOMINANCE EFFECT OF THIS QTL
NUMS<-LINEI[12 11 10] A NUMBERS OF CC, CL AND LL INDIVIDUALS
AT QTL

PROPCC<-NUMS[1]÷+/NUMS A PROPORTION OF INDIVIDUALS HOMOZYGOUS
FOR CORD ALLELE
PROPCL<-NUMS[2]÷+/NUMS A PROPORTION OF INDIVIDUALS HETEROZYGO
US
PROPLL<-NUMS[2]÷+/NUMS A PROPORTION OF INDIVIDUALS HOMOZYGOUS
FOR LACUNOSA
DOWN1A:MEAN1<- (PROPCC×AEFFECT)+((PROPCL)×DOMEFFECT)-(PROPLL×AEFFECT)
A MEAN EFFECT FOR QTL1

A CALCULATE GENETIC VARIANCE OF QTL I
SQUARE1<-PROPCC×((AEFFECT-MEAN1)★2)
SQUARE2<-PROPCL×((DOMEFFECT-MEAN1)★2)
SQUARE3<-PROPLL×((((-1×AEFFECT)-MEAN1)★2)
VARI<-SQUARE1+SQUARE2+SQUARE3

DOWN2:
A CALCULATE VARIANCE FOR QTL J
VARJ<-0
→(AEFFECTS[2]=0)/DOWN3 A SKIP FOR QTL2 IF EFFECT IS 0

```

```

A CALCULATE VARIANCE FOR QTL2
IND<- (MASTERDATA[,13]=PAIR2[2])/11↑ρMASTERDATA      A FOLLOWING LINES
ANALOGOUS TO ABOVE
LINEJ<- ,MASTERDATA[IND;]
AEFFECT<-LINEJ[8]
DOMEFFECT<-LINEJ[9]
NUMS<-LINEJ[12 11 10]

PROPCC<-NUMS[1]÷+/NUMS
PROPCL<-NUMS[2]÷+/NUMS
PROPLL<-NUMS[2]÷+/NUMS

DOWN2A:MEAN2<- (PROPCC×AEFFECT)+((PROPCL)×DOMEFFECT)-(PROPLL×AEFFECT)
A MEAN EFFECT FOR QTL1

A CALCULATE GENETIC VARIANCE FOR TRAIT J
SQUARE1<-PROPCC×((AEFFECT-MEAN2)★2)
SQUARE2<-PROPCL×((DOMEFFECT-MEAN2)★2)
SQUARE3<-PROPLL×((( -1×AEFFECT)-MEAN2)★2)
VARJ<-SQUARE1+SQUARE2+SQUARE3

DOWN3:

VARCOV<-VARCOV,[1](COV,VARI,VARJ)      A ADD COVARIANCE, AND VARIANCES O
F TRAITS I AND J TO VARCOV

DOWN4:→(KK<KKMAX)/RETKK

SUM<-+/[1]VARCOV      A SUM COVARIANCES AND VARIANCES TO GET TOTAL GENE
TIC COVARIANCE AND VARIANCES FROM ALL QTLS
R<-SUM[1]÷((SUM[2]×SUM[3])★.5)      A CALCULATE PREDICTED GENETIC CORREL
ATION FROM TOTAL COVARIANCE AND VARIANCES

```

C. Program TRIANGLE

```

TRIANGLE X
A THIS PRPGRAM MAKES A VECTOR 'VEC' OUT OF THE UPPER TRIANGLE (NOT I
NCLUDING DIAGONAL) OF A MATRIX

VEC<-0ρ0
MAXI<-1+1↑ρX
I<-0
RETI:I<I+1

MAXJ<1↑ρX
J<I
RETJ:J<J+1
VEC<-VEC,X[I;J]

→(J<MAXJ)/RETJ
→(I<MAXI)/RETI

```

→0

OTCLF

'PROGRAM TRIANGLE FINISHED. DATA IN VARIABLE ''VEC''. '

D. Program SHUFFLEPRED

SHUFFLEPRED

▷ THIS PROGRAM SHUFFLES QTLS TO CALCULATE PROBABILITY OF CORRELATION BETWEEN PHENOTYPIC CORRELATIONS AND PREDICTED GENETIC CORRELATIONS

▷ CAN RUN THIS FOR COMBINATIONS OF GWS OR ALL QTLS AND ALL TRAITS OR JUST FLOWER AND NECTAR TRAITS

▷ CHANGE TITLE APPROPRIATELY BELOW

▷ IN PREDICTCORR, INDICATE ALLQTLS = 'Y' OR 'N' (NO MEANS JUST FLOWER AND NECTAR TRAITS)

▷ IN PREDICTCORR USE EITHER △MIDPOINTS OR △MIDPOINTS1, △MASTERDATA OR △MASTERDATA1, AND △TOTRHE OR △TOTRHE1, FOR LESS OR MORE CONSERVED QTLS

▷ IN PREDICTCORR2 USE EITHER △MIDPOINTS OR △MIDPOINTS1

TITLE←'GWS QTLS' ▷ A TITLE TO PRINT
SCORRS1←SCORRS2←SCORRS1A←SCORRS2A←0P0 ▷ VARIABLES TO HOLD OUTPUT FROM SHUFFLING QTLS

PREDICTCORR ▷ RUN PREDICTCORR TO OBTAIN 'OBSERVED' PREDICTED GENETIC CORRELATIONS

IJ←0

RETIJ:IJ←IJ+1 ▷ LOOP FOR SHUFFLED REPLICATES

TEST←(IJ÷100)=L(IJ÷100)

✳(TEST=1)/*'REPS COMPLETED ',IJ' ▷ A LIST PROGRESS THROUGH LOOP

PREDICTCORR2 ▷ CALL PROGRAM PREDICTCORR2 (SIMILAR TO PREDICTCORR), WHICH PRODUCES VALUES OF CORRELATIONS
 ▷ FROM SHUFFLED DATA

SCORRS1←SCORRS1, SHUFcorr1 ▷ ADD CORRELATION BETWEEN PREDICTED GENETIC CORRELATIONS (ALL QTLS) AND PHENOTYPIC CORRELATIONS (ALL QTLS)

SCORRS2←SCORRS2, SHUFcorr2 ▷ ADD CORRELATION BETWEEN PREDICTED GENETIC CORRELATIONS (GWS QTLS) AND PHENOTYPIC CORRELATIONS

SCORRS1A←SCORRS1A, SHUFcorr1A ▷ ANALOGOUS TO SCORRS1 EXCEPT DOE SN'T INCLUDE DATA FOR PAIRS FOR WHICH PRED GEN CORRELATION IS 0

SCORRS2A←SCORRS2A, SHUFcorr2A ▷ ANALOGOUS TO SCORRS2 EXCEPT DOE SN'T INCLUDE DATA FOR PAIRS FOR WHICH PRED GEN CORRELATION IS 0

→(IJ<1000)/RETIJ

SUM1←+/SCORRS1≥OBSCORR1 ▷ SUM OF SHUFFLED VALUES ≥ OBSERV ED VALUES

SUM2←+/SCORRS2≥OBSCORR2

SUM1A←+/SCORRS1A≥OBSCORR1A

SUM2A←+/SCORRS2A≥OBSCORR2A

```

DTCLF
TITLE
DTCLF
'CORRELATION BETWEEN PHENOTYPIC CORRELATIONS AND PREDICTED GENETIC C
ORRELATION'
'    OBSERVED CORRELATION: ',OBSCORR1
'    PROPORTION OF SHUFFLED CORRELATIONS ≥ OBSERVED: ',SUM1÷1000
DTCLF
'    CORRELATION WITH ZEROS REMOVED'
'    OBSERVED CORRELATION: ',OBSCORR1A
'    PROPORTION OF SHUFFLED CORRELATIONS ≥ OBSERVED: ',SUM1A÷1000
DTCLF
'CORRELATION BETWEEN PHENOTYPIC CORRELATIONS AND BIAS'
'    OBSERVED CORRELATION: ',OBSCORR2
'    PROPORTION OF SHUFFLED CORRELATIONS ≥ OBSERVED: ',SUM2÷1000
DTCLF
'    CORRELATION WITH ZEROS REMOVED: '
'    OBSERVED CORRELATION: ',OBSCORR2A
'    PROPORTION OF SHUFFLED CORRELATIONS ≥ OBSERVED: ',SUM2A÷1000

```

E. Program PREDICTCORR2

PREDICTCORR2
 A THIS PROGRAM PREDICTS PAIRWISE TRAIT GENETIC CORRELATIONS FROM QTL
 OVERLAP AND EFFECT SIZES FOR RANDOM ASSIGNMENT OF TRAITS TO QTLS
 A IT IS ESSENTIALLY SAME AS PROGRAM PREDICTCORR, BUT IS SLIGHTLY MO
 DIFIED BECAUSE IT IS CALLED BY SHUFFLEPRED
 A SEE PREDICTCORR FOR MORE DETAILED ANNOTATION

```

QTLDATA<-QTLDATAB

MIDNUMS<-ΔMIDPOINTS[;1 2]

TRAITCODES<-QTLDATA[;1]           A AND USE ΔMASTERDATA1 FOR CONSERVAT
IVE DATASET

IND<-(~TRAITCODES€(2.4,2.5))/`ρTRAITCODES   A LIST TRAITS TO EXCLUDE
NOTE: 2.4 AND 2.5 ARE ALTERNATES FOR 2.1 and 2.2

A `*(ALLQTLS='N')/' IND<-(~TRAITCODES€(3.1,3.2,3.3,2.4,2.5))/`ρTRAITCOD
ES'   A USE THIS FOR JUST FLOWER AND NECTAR TRAIT ANALYSIS

TRAITCODES<-TRAITCODES[IND]
QTLDATA<-QTLDATA[IND;1]
CODES<-,QTLDATA[;1]
NUM<-ρCODES
ORDER<-NUM?NUM

QTLDATA[;1]<-CODES[ORDER]
TRAITCODES<- CODES[ORDER]

MAXJ<-ρUNIQCODES
MAXI<-MAXJ-1

```

```

MIDPOINTS←0 4ρ0   A THIS VARIABLE HOLDS MIDPOINTS OF OVERLAP INTERVALS FOR QTLS THAT OVERLAP
                    A FIRST TWO COLUMNS ARE QTL UNIQUE ID, THIRD IS LG AND FOURTH IS MIDPOINT
GENCORRS←((ρUNIQCODES),(ρUNIQCODES))ρ0
AVETRHES←((ρUNIQCODES),(ρUNIQCODES))ρ0
OVERLAPMAT←((ρUNIQCODES),(ρUNIQCODES))ρ0

I←0
RETI:I←I+1      A FIRST TRAIT LOOP

J←I
RETJ:J←J+1      A SECOND TRAIT LOOP

TRAITCODEI←UNIQCODES[I]
TRAITCODEJ←UNIQCODES[J]

IND1←(TRAITCODES=UNIQCODES[I])/1ρTRAITCODES
PART1←QTLDATA[IND1;]
IND2←(TRAITCODES=UNIQCODES[J])/1ρTRAITCODES
PART2←QTLDATA[IND2;]

OVERLAPS←0 4ρ0   A NUMBERS ARE QTLNUMBERS FROM PARTS 1 AND 2 FOR OVERLAPPING QTL

MAXII←1↑ρPART1
MAXJJ←1↑ρPART2

II←0
RETII:II←II+1    A PART1 LOOP

JJ←0
RETJJ:JJ←JJ+1    A PART2 LOOP

LINEII←PART1[II;] A GET QTL DATA FOR QTL1 (CHROMOSOME, CI LOW, CI HIGH)
LINEJJ←PART2[JJ;] A GET QTL DATA FOR QTL2

TEST1←LINEII[2]=LINEJJ[2]      A QTL1 AND QTL2 ON SAME CHROMOSOME?
→(TEST1=0)/DOWN              A IF NOT, SKIP AND LEAVE ZERO IN MATRIX

TEST←((LINEII[5]=LINEJJ[4])∨(LINEJJ[5]=LINEII[4]))          A DO NOT COUNT AS
→(TEST=1)/DOWN
OVERLAP IF CI'S ABUT
CRIT1←(LINEII[4]≥LINEJJ[4]) ∧ (LINEII[4]≤LINEJJ[5])        A THESE TWO LINES TEST WHETHER THERE IS OVERLAP
CRIT2←(LINEII[5]≥LINEJJ[4]) ∧ (LINEII[5]≤LINEJJ[5])
CRIT3←(LINEJJ[4]≥LINEII[4]) ∧ (LINEJJ[4]≤LINEII[5])
CRIT4←(LINEJJ[5]≥LINEII[4]) ∧ (LINEJJ[5]≤LINEII[5])

TEST2←CRIT1∨CRIT2∨CRIT3∨CRIT4
→(TEST2=0)/DOWN

OPAIR←2 1ρ(LINEII[13],LINEJJ[13])

```

```

TESTPAIR<+/, (MIDNUMS^.=OPAIR)
  &(TESTPAIR=0)/*TEMP<OPAIR[2; 1],OPAIR[1;1] ◊ OPAIR<-2 1@TEMP'
TESTPAIR2<+/, (MIDNUMS^.=OPAIR)

  &(TESTPAIR2=0)/*TESTPAIR2 NOT IN DATASET'' ◊ →0'

OVERLAPS<OVERLAPS,[1](II,JJ,LINEII[13],LINEJJ[13])

A TEMP<LINEII[3 4],LINEJJ[3 4]           A THIS NEXT SET OF 6 LINES CA
LCULATES MIDPOINTS OF OVERLAP INTERVALS AND STORES IN VARIABLE MIDPO
INTS
A TEMP2←@TEMP
A TEMP3←TEMP [ TEMP2 ]
A INTERVAL←TEMP3[2 3]
A MIDPOINT←(+/INTERVAL)÷2
A MIDPOINTS←MIDPOINTS,[1](LINEII[12],LINEJJ[12],LINEII[2],MIDPOINT)

DOWN:→(JJ<MAXJJ)/RETJJ

→(II<MAXII)/RETII

MAXK←1↑ρOVERLAPS

ADDEFF←0 4ρ0
DOMEFF←0 4ρ0

SIZE←1↑ρOVERLAPS
→(SIZE=0)/DOWN4

K←0
RETK:K←K+1 A THIS LOOP ADDS RHE FOR OVERLAPPING QTLS

AVALS←(PART1[OVERLAPS[K;1];8],PART2[OVERLAPS[K;2];8],OVERLAPS[K;3 4])
)   A ADDITIVE EFFECT OF C ALLELE FOR THE TWO OVERLAPPING QTLS
DVALS←(PART1[OVERLAPS[K;1];9],PART2[OVERLAPS[K;2];9],OVERLAPS[K;3 4])
)   A DOMINANCE DEVIATION FOR THE TWO OVERLAPPING QTLS

ADDEFF←ADDEFF,[1]AVALS
DOMEFF←DOMEFF,[1]DVALS

→(K<MAXK)/RETK

DOWN4:MAXL←1↑ρPART1
L←0
RETL:L←L+1

TEST←L≤OVERLAPS[,1]
→(TEST=1)/DOWN2

ADDEFF←ADDEFF,[1](PART1[L;8],0,PART1[L;13],0)
DOMEFF←DOMEFF,[1](PART1[L;9],0,PART1[L;13],0)

DOWN2:→(L<MAXL)/RETL

MAXLL←1↑ρPART2

```

```

LL←0
RETLL:LL←LL+1

TEST←LL≤OVERLAPS[ ;2 ]
→(TEST=1)/DOWN3

ADDEFF←ADDEFF,[1](0,PART2[LL;8],0,PART2[LL;13])
DOMEFF←DOMEFF,[1](0,PART2[LL;9],0,PART2[LL;13])

DOWN3 :→(LL<MAXLL)/RETLL

CALCCOV3

GENCORRS[I;J]←R

→(J<MAXJ)/RETJ
→(I<MAXI)/RETI

TRIANGLE GENCORRS
NPOINTS←0.5×(ρUNIQCODES)×(-1+ρUNIQCODES)
DATA←((NPOINTS,1)ρΔPHENCORRVEC), (NPOINTS,1)ρVEC
↳(ALLQTLS='N')/'DATA←((NPOINTS,1)ρΔPHENCORRVEC[ΔGWSIND2]), (NPOINTS,1)
)ρVEC'
BIAS←DATA[ ;2 ]-DATA[ ;1 ]
DATA←DATA,(NPOINTS,1)ρBIAS

CALCCORR DATA[ ;1 2 ]
SHUFCORR1←CORR
CALCCORR DATA[ ;1 3 ]
SHUFCORR2←CORR

IND←(DATA[ ;2 ]≠0)/1↑ρDATA
DATA2←DATA[ IND; ]
CALCCORR DATA2[ ;1 2 ]
SHUFCORR1A←CORR
IND←(DATA[ ;3 ]≠0)/1↑ρDATA
DATA2←DATA[ IND; ]
CALCCORR DATA2[ ;1 3 ]
SHUFCORR2A←CORR

```

A 'PROGRAM PREDICTCORR FINISHED. OUTPUT IN VARIABLES ''GENCORRS'' AND ''AVETRRES''. '

F. Program PREDGENCORRMODMEANS

PREDGENCORRMODMEANS

A THIS PROGRAM CALCULATES MEANS AND STANDARD ERRORS FOR WITHIN- AND BETWEEN-MODULE PAIRS FOR PREDICTED GENETIC CORRELATIONS

INPUT←ΔPHENVSPREDGEN A USE THIS OR ΔPHENVSPREDGEN1 FOR LESS CONSERVATIVE OR CONSERVATIVE QTL SETS.
A THIS VARIABLE HAS FOLLOWING COLUMNS:
A COL1 PHENOTYPIC CORRELATIONS
A COL2 PREDICTED GENETIC CORRELATIONS

INED (PVE)	A COL3 AVERAGE TOTAL PERCENT VARIANCE EXPLA
	A COL4 AVERAGE TOTAL RELATIVE HOMOZYGOUS EF
FECT (RHE)	

A INPUT←ΔOVERLAPCORR1[;1 2], INPUT

A FIRST SET OF COMMANDS CREATES VARIABLE CATCODES. EACH ROW CORRESPONDS TO ONE OF THE TRAIT PAIRS, AND INDICATES WHICH MODULE THAT TRAIT PAIR BELONGS TO

CATCODES←0 2P0

ALLQTLS←'N'	A 'Y' IF ALL QTLS, 'N' OF ONLY GWS QTLS
WITHINCORRS←0P0	A INITIALIZE VARIABLE FOR ALL WITHIN-MODULE CORRELATIONS
BETWCORRS←0P0	A INITIALIZE VARIABLE FOR ALL BETWEEN-MODULE CORRELATIONS
UCODES←1.1 1.2 1.3 1.4 1.5 1.6 1.7 2.1 2.2 2.3 3.1 3.2 3.3 4.1 4.2 4 .3 4.4 5.1 5.2 5.3 5.4 5.5	A UNIQUE TRAIT CODES
+(ALLQTLS='N')/UCODES←1.1,1.2,1.3,1.4,1.5,1.6,1.7,2.1,3.2,3.3,4.3,5 .1,5.2,5.3,5.4'	A USE THIS WHEN ANALYZING ONLY GWS DATA

MAXL←PUCODES	A MAXIMUM L VALUE FOR L LOOP
MAXK←MAXL-1	A MAXIMUM K VALUE FOR K LOOP

K←0	
RETK:K←K+1	A TRAIT K LOOP
L←K	
RETL:L←L+1	A TRAIT L LOOP

CODE1←UCODES[K]	A TRAIT CODE FOR TRAIT K
CODE2←UCODES[L]	A TRAIT CODE FOR TRAIT L

CATCODES←CATCODES,[1]((LCODE1),(LCODE2))	A APPEND INTEGER PORTION OF TRAIT CODES
→(L<MAXL)/RETL	
→(K<MAXK)/RETK	

A NEXT SET OF LINES CALCULATES WITHIN- AND BETWEEN-MODULE AVERAGE PREDICTED GENETIC CORRELATIONS AND SE

TYPE←1
ROWS←1↑PINPUT A NUMBER OF TRAIT PAIRS

AVECORRMAT←5 5P0	A INITIALIZE VARIABLES FOR OUTPUT; THIS IS MATRIX OF AVERAGE MODULE CORRELATIONS
AVESEMAT←5 5P0	A MATRIX OF SE OF AVERAGE MODULE CORRELATIONS
NUMMMAT←5 5P0	A VARIABLE THAT WILL CONTAIN NUMBER OF CORRELATIONS FOR MODULES I AND J

MAXI←MAXJ←5 A SET MAXIMA FOR I AND J FOR I AND J LOOPS

I←0
RETI:I←I+1 A TRAIT I LOOP

```

J←I-1
RETJ:J←J+1           A TRAIT K LOOP

CATIND←(,CATCODES^.= 2 1ρ(I,J))/11↑ρCATCODES      A INDEX OF CATCODES
CORRESPONDING TO I,J

CORRS←INPUT[CATIND;2]      A EXTRACT CORRELATIONS CORRESPONDING TO
THOSE CATCODES   NOTE: TAKING ABSOLUTE VALUES OF CORRELATIONS
NUMMAT[I;J]←ρCORRS      A NUMBER OF CORRELATIONS FOR MODULE PAIR
I,J

*(I=J)/*WITHINCORRS←WITHINCORRS,CORRS'          A IF WITHIN-MODULE CORRELAT
IONS, ADD CORRELATIONS TO WITHINCORRS
*(I≠J)/*BETWCORRS←BETWCORRS,CORRS'            A IF BETWEEN-MODULE CORRELA
TIONS, ADD CORRELATIONS TO BETWCORRS

TEST←2≤ρCORRS           A 0 IF ≤ 2 CORRELATIONS, 1
IF > 2 CORRELATIONS

*(TEST=1)/*STATS2 CORRS ◊ AVECORMAT[I;J]←MEAN ◊ AVESEMAT[I;J]←STDERR
◊ →DOWN'             A IF > 2 CORRELATIONS, CALCULATE MEAN AND SE
                     A AND ENTER INTO MATRICES
TEST2←1=ρCORRS          A 1 IF ONLY ONE CORRELATION, 0 IF NO CO
RRELATIONS
*(TEST2=1)/*AVECORMAT[I;J]←CORRS ◊ AVESEMAT[I;J]←99'    A IF ONLY
1 CORRELATION, ENTER CORR INTO AVECORMAT, AND 99 (MISSING DATA) INT
O SE MATRIX
*(TEST2=0)/*AVECORMAT[I;J]←99 ◊ AVESEMAT[I;J]←99'        A IF NO CO
RRELATIONS, ENTER 99 INTO BOTH MATRICES

DOWN:→(J<5)/RETJ

→(I<5)/RETI

STATS2 WITHINCORRS      A CALCULATE STATISTICS ON ALL WITHIN-MODULE COR
RELATIONS
WITHINMEAN←MEAN          A MEAN
WITHINSE←STDERR          A STANDARD ERROR

STATS2 BETWCORRS         A CALCULATE STATISTICS FOR ALL BETWEEN-MODULE C
ORRELATIONS
BETWMEAN←MEAN
BETWSE←STDERR

A FOLLOWING LINES SET UP OUTPUT FOR PRINTING
LINE1←LINE2←LINE3←LINE4←LINE5←'
K1←0
RETK1:K1←K1+1
LINE1←LINE1,'',(6 4↑AVESEMAT[1;K1]),'
LINE2←LINE2,'',(6 4↑AVESEMAT[2;K1]),'
LINE3←LINE3,'',(6 4↑AVESEMAT[3;K1]),'
LINE4←LINE4,'',(6 4↑AVESEMAT[4;K1]),'
LINE5←LINE5,'',(6 4↑AVESEMAT[5;K1]),'
→(K1<5)/RETK1

```

```

OTCLF
' AVERAGE (SE) CORRELATIONS WITHIN AND BETWEEN MODULES FOR GENETIC CO
RRELATION OF TYPE ',TYPE
OTCLF
'MODULE      1          2          3          4          5 '
OTCLF
'   1  ',10 4AVECORRMAT[1;]
LINE1
OTCLF
'   2  ',10 4AVECORRMAT[2;]
LINE2
OTCLF
'   3  ',10 4AVECORRMAT[3;]
LINE3
OTCLF
'   4  ',10 4AVECORRMAT[4;]
LINE4
OTCLF
'   5  ',10 4AVECORRMAT[5;]
LINE5

OTCLF
' AVERAGE WITHIN-MODULE CORRELATION (SE): ',WITHINMEAN,WITHINSE
' AVERAGE BETWEEN-MODULE CORRELATION (SE): ',BETWMEAN,BETWSE

→0

'PROGRAM PREDGENCORMODMEANS FINISHED. '

```

G. Program PERMUTEAVECORRS

PERMUTEAVECORRS

A THIS PROGRAM PERMUTES PHENOTYPIC CORRELATIONS TO TEST SIGNIFICANCE
OF CORRELATION BETWEEN MODULE AVERAGE PHEN CORRELATIONS

A AND AVERAGE PREDICTED GENETIC CORRELATION

CLUSTERMOD←'Y' A Y IF ANALYSIS FOR CLUSTER MODULES, N IF FOR ANATOMICAL MODULES

```

X←ΔAVEPHENVSPREGEN[,2 1]           A AVERAGE PREDICTED GENETIC CORRELAT
IONS (ALL QTLS) AND AVERAGE PHENOTYPIC CORRELATIONS
Y←ΔAVEPHENVSPREGEN[,3 1]           A AVERAGE PREDICTED GENETIC CORRELAT
IONS (GWS QTLS) AND AVERAGE PHENOTYPIC CORRELATIONS
A *(CLUSTERMOD='N')/X←ΔAVEOVERLAPCORR2[,3 5]'    A ANALAGOUS TO ABO
VE
A *(CLUSTERMOD='N')/Y←ΔAVEOVERLAPCORR2[,4 5]'

IND1←(X[,1]≠99)/1↑ρX
X←X[IND1,]                         A DELETE ENTRIES WITH MISSING DATA
IND2←(Y[,1]≠99)/1↑ρY
Y←Y[IND2,]                         A DELETE ENTRIES WITH MISSING DATA
XX←X                                A SAVE X FOR LATER
YY←Y                                A SAVE Y FOR LATER

```

```

CALCCORR X          A CALL CALCCORR TO CALCULATE CORRELATION F
OR ALL QTLS
OBSCORR1←CORR      A SAVE CORRELATION
CALCCORR Y          A CALL CALCCORR TO CALCULATE CORRELATION F
OR GWS QTLS
OBSCORR2←CORR      A SAVE CORRELATION

A PRINT TITLE
↳(CLUSTERMOD='Y')//DTCLF ◊ "'ANALYSIS FOR CLUSTER MODULES.''''
↳(CLUSTERMOD='N')//DTCLF ◊ "'ANALYSIS FOR ANATOMICAL MODULES.'''''

DTCLF
'CORRELATION FOR ALL QTLS ', OBSCORR1
'CORRELATION FOR GWS QTLS ', OBSCORR2

A BEGIN PERMUTATION ANALYSIS
DTCLF
'STARTING PERMUTATIONS '

RANDCORRS1←0Ρ0      A VARIABLE TO HOLD PERMUTATION CORRELATIONS FOR AL
L QTLS
RANDCORRS2←0Ρ2      A VARIABLE TO HOLD PERMUTATION CORRELATIONS FOR GW
S QTLS
ROWS1←1↑ΡXX         A NUMBER OF ROWS IN XX
ROWS2←1↑ΡYY         A NUMBER OF ROWS IN YY

I←0
RETI:I←I+1          A PERMUTATION LOOP

X←XX                A RETRIEVE SAVED DATA
Y←YY

RAND1←ROWS1?ROWS1   A INDEX OF RANDOMIZED ROWS IN X
X[;1]←X[RAND1;1]    A PERMUTE PHENOTYPIC CORRELATIONS
RAND2←ROWS2?ROWS2   A INDEX OF RANDOMIZED ROWS IN Y
Y[;1]←Y[RAND2;1]    A PERMUTE PHENOTYPIC CORRELATION

CALCCORR X          A CALC CORRELATION FOR ALL QTLS
CORR1←CORR          A VALUE OF CORRELATION
CALCCORR Y          A CALC CORRELATION FOR GWS QTLS
CORR2←CORR          A VALUE OF CORRELATION
RANDCORRS1←RANDCORRS1,CORR1  A APPEND CORRELATION TO RANDCORRS1 AND
    RANDCORRS2
RANDCORRS2←RANDCORRS2,CORR2

→(I<1000)/RETI

DTCLF
SUM1←+/ (RANDCORRS1≥OBSCORR1)    A NUMBER OF PERMUTATION CORRELATIONS
    ≥ OBSERVED (ALL QTLS)
SUM2←+/ (RANDCORRS2≥OBSCORR2)    A NUMBER OF PERMUTATION CORRELATIONS
    ≥ OBSERVED (GWS QTLS)
PROP1←SUM1÷1000                 A PROPORTION OF PERMUTATION CORRELAT
IONS ≥ OBSERVED (ALL QTLS)

```

```

PROP2←SUM2÷1000          A PROPORTION OF PERMUTATION CORRELAT
IONS ≥ OBSERVED (GWS QTLS)
'PROP GREATER THAN OBSERVED (ALL QTLS) ',PROP1
'PROP GREATER THAN OBSERVED (GWS QTLS) ',PROP2

DTCLF
'PROGRAM PERMUTEAVEOVCCORR FINISHED '

```

H. Program PERMUTEBIAS

PERMUTEBIAS

A THIS PROGRAM COMPUTES SIGNIFICANCE OF CORRELATIONS BETWEEN BIAS AND PHENOTYPIC CORRELATIONS
A BIAS IS PREDICTED GENETIC CORRELATION MINUS OBSERVED PHENOTYPIC CORRELATION

```

XX←X←ΔPHENVSPREDGEN      A ALL QTLS; SEE BELOW FOR DESCRIPTION OF THI
S VARIABLE
YY←Y←ΔPHENVSPREDGEN1     A ONLY GWS QTLS
ROWSX←1↑ρX                A NUMBER OF ROWS IN X
ROWSY←1↑ρY                A NUMBER OF ROWS IN Y

BIASX←(ROWSX,1)ρ(X[,2]-X[,1])   A CALCULATE BIAS
BIASY←(ROWSY,1)ρ(Y[,2]-Y[,1])   A CALCULATE ABSOLUTE VALUE OF BIAS
ABIASX←|BIASX
ABIASY←|BIASY

COLS1X←X[,1],BIASX        A MAKE MATRIX FOR ANALYZING PHEN CORR VS BIAS
COLS1Y←Y[,1],BIASY

CALCCORR COLS1X           A CALCULATE CORRELATION
OBSCORR1X←CORR             A STORE CORRELATION
CALCCORR COLS1Y
OBSCORR1Y←CORR

IND1←(X[,2]≠0)/1ROWSX    A GET RID OF LINES WITH PREDICTED GEN CORR
= 0
COLS2X←COLS1X[IND1,]
IND2←(Y[,2]≠0)/1ROWSY
COLS2Y←COLS1Y[IND2,]

CALCCORR COLS2X           A CALCULATE AND STORE CORRELATIONS FOR DATA
WITHOUT GEN CORR = 0
OBSCORR2X←CORR
CALCCORR COLS2Y
OBSCORR2Y←CORR

DTCLF
'CORRELATION OF BIAS VS. PHEN CORR, ALL QTLS, ALL POINTS ', OBSCORR1
X
'CORRELATION OF BIAS VS. PHEN CORR, GWS QTLS, ALL POINTS ', OBSCORR1
Y

```

```
'CORRELATION OF BIAS VS. PHEN CORR, ALL QTLS, NON-0 POINTS ', OBSCOR
R2X
'CORRELATION OF BIAS VS. PHEN CORR, GWS QTLS, NON-0 POINTS ', OBSCOR
R2Y
```

A BEGIN PERMUTATIONS

```
CORRS1X←CORRS1Y←CORRS2X←CORRS2Y←0ρ0      A INITIALIZE VARIABLES TO HOLD
CORRELATIONS FROM PERMUTATIONS
```

I←0

```
RETI:I←I+1          A PERMUTATION LOOP
```

```
X←XX          A RETRIEVE DATA
```

```
Y←YY
```

```
ROWSX←1↑ρX
```

```
ROWSY←1↑ρY
```

```
BIASX←(ROWSX,1)ρ(X[,2]-X[,1])      A CALCULATE BIAS AND ABSOLUTE VA
LUE OF BIAS
```

```
BIASY←(ROWSY,1)ρ(Y[,2]-Y[,1])
```

```
ABIASX←|BIASX
```

```
ABIASY←|BIAZY
```

```
COLS1X←X[,1],BIASX      A MAKE MATRICES FOR CALCULATING CORRELATIONS
COLS1Y←Y[,1],BIAZY
```

```
ROWSX←1↑ρCOLS1X      A NUMBER OF DATA PAIRS FOR CORRELATIONS
ROWSY←1↑ρCOLS1Y
```

```
RAND1←ROWSX?ROWSX      A INDEX OF PERMUTED ROWS IN COLS1X
```

```
COLS1X[,2]←COLS1X[RAND1;2]      A PERMUTE PHENOTPYIC CORELATION
```

```
RAND2←ROWSY?ROWSY
```

```
COLS1Y[,2]←COLS1Y[RAND2;2]
```

```
CALCCORR COLS1X      A CALCULATE AND STORE CORRELATIONS
```

```
CORR1X←CORR
```

```
CALCCORR COLS1Y
```

```
CORR1Y←CORR
```

```
CORRS1X←CORRS1X,CORR1X      A APPEND CORRELATIONS
CORRS1Y←CORRS1Y,CORR1Y
```

```
IND1←(X[,2]≠0)/1ROWSX      A GET RID OF LINES WITH PREDICTED GEN CORR
= 0
```

```
COLS2X←COLS1X[IND1; ]
```

```
IND2←(Y[,2]≠0)/1ROWSY
```

```
COLS2Y←COLS1Y[IND2; ]
```

A PERMUTE, CALCULATE AND APPEND CORRELATIONS AS ABOVE

```
ROWSX←1↑ρCOLS2X
```

```
ROWSY←1↑ρCOLS2Y
```

```
RAND1←ROWSX?ROWSX
```

```
COLS2X[,2]←COLS2X[RAND1;2]
```

```
RAND2←ROWSY?ROWSY
```

```

COLS2Y[,2]←COLS2Y[RAND2,2]

CALCCORR COLS2X
CORR2X←CORR
CALCCORR COLS2Y
CORR2Y←CORR

CORRS2X←CORRS2X,CORR2X
CORRS2Y←CORRS2Y,CORR2Y

→(I<1000)/RETI

□TCLF
♀ CALCULATE NUMBER OF PERMUTATION CORRELATIONS ≥ OBSERVED CORRELATIO
N
SUM1← +/CORRS1X≤OBSCORR1X
SUM2← +/CORRS1Y≤OBSCORR1Y
SUM3← +/CORRS2X≤OBSCORR2X
SUM4← +/CORRS2Y≤OBSCORR2Y

'PROPORTIONS GREATER THAN OBSERVED'
' ALL QTLS, ALL TRAIT PAIRS ', SUM1÷1000
' GWS QTLS, ALL TRAIT PAIRS ', SUM2÷1000
' ALL QTLS, NON-0 PAIRS ', SUM3÷1000
' GWS QTLS, NON-0 PAIRS ', SUM4÷1000

□TCLF
'PROGRAM PERMUTEPIAS FINISHED.'

```

I. Variables used by above programs

ΔMIDPOINTS

```

COL1: QTL1 ID
COL2: QTL2 ID
COL3: LINKAGE GROUP
COL4: MIDPOINT OF OVERLAP INTERVAL (CM)
COL5: NEAREST MARKER POSITION (CM)
COL6: NUMBER OF INDIVIDUALS WITH CC GENOTYPE AT MARKER POSITION
COL7: NUMBER OF INDIVIDUALS WITH CL GENOTYPE AT MARKER POSITION
COL8: NUMBER OF INDIVIDUALS WITH LL GENOTYPE AT MARKER POSITION

```

ΔPHENVSPREDGEN (ALL QTL) AND
 ΔPHENVSPREDGEN1 (GWS QTL) HAVE FOLLOWING COLUMNS:

```

COL 1 PHENOTYPIC CORRELATIONS
COL 2 PREDICTED GENETIC CORRELATIONS
COL 3 AVERAGE TOTAL PVE
COL 4 AVERAGE TOTAL RHE

```

NOTE: THIRD AND 4TH COLUMNS PRODUCED BY FOLLOWING PROGRAM:

MAKEAVETOTPVE

A THIS PROGRAM CALCULATES AVERAGE TOTAL PVE AND AVERAGE TOTAL RHE FOR ALL TRAIT COMBINATIONS
A RESULTING VECTOR PUT INTO THIRD AND FOURTH COLUMNS OF ΔPHENVSPREDGEN AND ΔPHENVSPREDGEN1
A READS IN VECTOR ATOTPVE

ALLQTLS←'N' A 'Y' MEANS ALL QTLS USED, 'N' MEANS ONLY GWS QTLS USED

UNIQCODES←1.1,1.2,1.3,1.4,1.5,1.6,1.7,2.1,2.2,2.3,3.1,3.2,3.3,4.1,4.2,4.3,4.4,5.1,5.2,5.3,5.4,5.5 A UNIQUE TRAIT CODES

‡(ALLQTLS='N')/'UNIQCODES←1.1,1.2,1.3,1.4,1.5,1.6,1.7,2.1,3.2,3.3,4.3,5.1,5.2,5.3,5.4' A USE THIS FOR JUST FLOWER AND NECTAR TRAIT ANALYSIS

IND←(ATOTPVE[;1]∈UNIQCODES)/↑↑pATOTPVE A INDEX OF ROWS OF ATOTPVE WITH TRAIT CODES ∈ UNIQCODES
TOPVVE←ATOTPVE[IND;] A EXTRACT THOSE ROWS

NUMCODES←MAXJ←pUNIQCODES A NUMBER OF UNIQCODES, MAXIMUM VALUE OF J IN LOOP J
MAXI←MAXJ-1 A MAXIMUM VALUE OF I IN LOOP I
AVEPVEVEC←0p0 A INITIALIZE VECTOR TO HOLD AVERAGE TOT AL PVE FOR PAIR OF TRAITS
AVETRHEVEC←0p0 A INITIALIZE VECTOR TO HOLD AVERAGE TOT AL RHE FOR PAIR OF TRAITS

I←0
RETI:I←I+1 A LOOP FOR TRAIT I
J←I
RETJ:J←J+1 A LOOP FOR TRAIT J

CODE1←UNIQCODES[I] A UNIQUE CODE FOR TRAIT I
CODE2←UNIQCODES[J] A UNIQUE CODE FOR TRAIT J

IND1←(TOPVVE[;1]=CODE1)/↑NUMCODES A INDEX OF ROWS OF TOPVVE WITH UNIQUE CODE = CODE1
TOPVVE1←TOPVVE[IND1;2] A EXTRACT TOTAL PVE FOR TRAIT I
TOTRHE1←TOPVVE[IND1;3] A EXTRACT TOTAL RHE FOR TRAIT I
IND2←(TOPVVE[;1]=CODE2)/↑NUMCODES A INDEX OF ROWS OF TOPVVE WITH UNIQUE CODE = CODE2
TOPVVE2←TOPVVE[IND2;2] A EXTRACT TOTAL PVE FOR TRAIT J
TOTRHE2←TOPVVE[IND2;3] A EXTRACT TOTAL RHE FOR TRAIT J
AVEPVE←(TOPVVE1+TOPVVE2)÷2 A CALCULATE AVERAGE TOTAL PVE
AVETRE←(TOTRHE1+TOTRHE2)÷2 A CALCULATE AVERAGE TOTAL RHE
AVEPVEVEC←AVEPVEVEC, AVEPVE A APPEND AVERAGES TO APPROPRIATE VECTORS
AVETRHEVEC←AVETRHEVEC, AVETRE

→(J<MAXJ)/RETJ
→(I<MAXI)/RETI

DTCLF

'PROGRAM MAKEAVETOTPVE FINISHED. OUTPUT IN VECTORS ''AVEPVEVEC'' AND
D ''AVETRHEVEC''. '

△AVEPHENVSPREDGEN

COL 1 AVERAGE PHENOTYPIC CORRELATIONS
COL 2 AVERAGE PREDICTED GENETIC CORRELATIONS (ALL QTLS)
COL 3 AVERAGE PREDICTED GENETIC CORRELATIONS (GWS QTLS)

NOTE: THESE ARE WITHIN- AND BETWEEN-MODULE AVERAGE
CORRELATIONS

△AVEOVERLAPCORR (all QTLS) and △AVEOVERLAPCORR2 (GWS QTLs)

COL 1 MODULE NUMBER FOR MODULE I
COL 2 MODULE NUMBER FOR MODULE J
COL 3 AVERAGE PREDICTED GENETIC CORRELATIONS (ALL QTLS)
COL 4 AVERAGE PREDICTED GENETIC CORRELATIONS (GWS QTLS)
COL 5 AVERAGE PHENOTYPIC CORRELATIONS

NOTE: THESE ARE WITHIN- AND BETWEEN-MODULE AVERAGE
CORRELATIONS

△TOTPVE THIS VARIABLE HAS 3 COLUMNS:

COL1 TRAIT NUMBER
COL2 TOTAL PERCENT VARIANCE EXPLAINED (PVE)
COL3 TOTAL RELATIVE HOMOZYGOUS EFFECT (RHE)
(0 MEANS NO RHE DATA AVAILABLE)