

**Manual for MREMLM (version 12/15/2001): A  
program for the estimation of covariance components,  
genetic parameters, and genetic predictions of additive  
and nonadditive intra and interbreed genetic effects in  
multibreed populations**

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 Animal Breeding Mimeo Series (2002), Dept. Animal Sciences, Univ. Florida  
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## **Manual for MREMLEM (version 12/15/2001): A program for the estimation of covariance components, genetic parameters, and genetic predictions of additive and nonadditive intra and interbreed genetic effects in multibreed populations**

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## **PREFACE**

The current MREMLEM version (12/15/2001):

- 1) is modular, largely written in FORTRAN 95, and makes extensive use of dynamic memory allocation,
- 2) modifications done during 2001 were tested with small beef and dairy multibreed data sets from Colombia, Thailand, and the USA,
- 3) can analyze beef and dairy cattle data using calf-dam (i.e., animal), sire-maternal grandsire, and sire models,
- 4) accounts for intra and interbreed direct, maternal, additive, nonadditive (intralocus) genetic, and intra and interbreed environmental effects,
- 5) uses regression to account for additive and nonadditive intra and interbreed genetic group effects,
- 6) can handle any number of base breeds, restricted solely by the memory requirements (which could be substantial),
- 7) needs to account only for the breed group combinations present in the existing animals in a multibreed data set, not on all possible combinations of parental breed group combinations,
- 8) computes additive and nonadditive genetic, environmental, and phenotypic covariances for pairs of breeds and for all breed group combinations present in a multibreed data set,
- 9) generates multibreed additive, multibreed nonadditive, and total (additive + nonadditive) genetic predictions, or multibreed additive, intra and interbreed nonadditive, and total genetic predictions,
- 10) has a flexible interface to define fixed environmental and regression genetic group effects,
- 11) accepts any number of main effects, and up to six levels of nested and cross-classified fixed effects,
- 12) allows fixed effects to be all subclass effects (1s and 0s) or a combination of subclass and regression effects (1s, 0s, other numbers),
- 13) generates outputs of estimates of covariance components and

- genetic parameters and of genetic predictions suitable for printing mimeographs, and
- 14) generates a file of genetic predictions suitable for further analysis using other computer packages (e.g., Quattro Pro, Excel).

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**NOTE: Because the MREMLEM system is under continuous modifications and enhancements it will contain bugs that are likely to show up during the analysis of new data sets or unusual models.**  
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## PROGRAM CHARACTERISTICS AND COMPUTING ALGORITHMS

- 1) The MREMLEM program computes additive and nonadditive direct and maternal genetic and environmental variances and covariances in inbred and noninbred multibreed populations composed of ANY NUMBER OF BASE BREEDS.
- 2) The estimation procedure used is Restricted Maximum Likelihood (REML, Patterson and Thompson (1971), Biometrika 58:545; Corbeil and Searle (1976), Technometrics 18:31).
- 3) Computations are carried out using a Generalized Expectation-Maximization (GEM) algorithm (Dempster et al. (1975), J. Royal Stat. Soc., Ser. B, 38:1). A description of the covariance component methodology which this computer program is based upon is given in Elzo (1994), J. Anim. Sci. 72:3055-3065, Elzo (1996), J. Anim. Sci. 74:317-328, and Elzo and Wakeman (1998), J. Anim. Sci. 76:1290-1332.
- 4) Covariances are estimated using a two-step procedure. Firstly, the Cholesky elements of the genetic (additive and nonadditive) and environmental covariances are estimated using a Generalized Expectation-Maximization (GEM) algorithm. Secondly, covariance matrices and matrices of genetic parameters (heritability and interactibility ratios, correlations) are computed.
- 5) Convergence criterion  $vcconv = \sqrt{ssdif/ssim1}$ , where  
 $ssdif = \text{sum of squares of differences between absolute values of covariance estimates in GEM iterations } i \text{ and } i - 1,$   
 $ssim1 = \text{sum of squares of covariance estimates in GEM iteration } i - 1.$
- 6) No standard errors of estimation of covariance components are computed.
- 7) In addition to estimating covariances, the MREMLEM program computes:
  - a. ratios of variances (heritabilities, interactibilities),
  - b. correlations (additive and nonadditive genetic, environmental, and phenotypic), and
  - c. additive, nonadditive, and total genetic predictions for all animals in the model.

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## PROGRAM FILES (Written by M. A. Elzo, 2001; unless otherwise noted)

**common99-R01.f90** = module with the definition of global variables, parameters, dynamic and static arrays, computation of memory requirements.

**commonproglm.f90** = module containing the default program limits.

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commonsubr.f90 = module containing subroutines used by all other modules.

convergence.f90 = module that computes the GEM convergence criteria.

defprepmmme.f90 = module that reads pedigree and data files, and sets ups the
structure of the mixed model equations according to the model used.

fspak99-R01.f90 = module containing the fspak subroutines (Perez-Enciso,
Misztal, and Elzo, 1994).

kindsMREMLEM.f90 = module that defines the kinds of variables used in MREMLEM.

mmedirsol.f90 = module that compute direct solutions for the mme using the
sparse matrix algorithm from fspak.

mremlcovest2b.f90 = module that computes 2-breed multibreed covariances and
genetic parameters for nbgcom parental breed group combinations.

mremlcovestmb.f90 = module that computes m-breed multibreed covariances and
genetic parameters for all parental breed group combinations, for m > 2,
present in a multibreed data set.

mreml_Estep.f90 = module that performs the computations of the E-step of the
GEM algorithm (prediction of additive and nonadditive genetic values in the
mixed model, i.e., solve the mme).

mreml_Mstep.f90 = module that performs the computations of the M-step of the
GEM algorithm (estimation of base additive, nonadditive, and environmental
covariances).

mremlprog99-R01.f90 = main program; used to read parameters and to control
the specific subroutines that estimate multibreed covariance components and
that predict genetic values.

sublibrary.f90 = module that contain generic subroutines used by all other
modules.
*****
```

## MODIFYING THE SIZE OF THE PROGRAM

The size of the program will be automatically modified for most variables through dynamic allocation of resources. A few default parameters are still being defined in input file iproglim (defined below), but this file will likely be eliminated in future versions of MREMLEM.

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## MODELS FOR THE MIXED MODEL EQUATIONS

**CALF-DAM** (animal model = AM)

**SIRE-MATERNAL GRANDSIRE** (smgs model = SMGSM)

## SIRE (sire model = SM)

### FIXED EFFECTS

- 1) Any number of main effects, e.g., contemporary group.
- 2) Up to six cross-classified effects, e.g., age of dam x sex of calf interaction (subclass and regression effects allowed)
- 3) Up to six nested effects, e.g., Age of dam within breed group of dam and sex of calf (subclass and regression effects allowed)
- 4) Additive genetic regression groups (direct, maternal separately)
  - a. Additive breed group of calf and dam (AM)
  - b. Additive breed group of sire and mgs (SMGSM)
  - c. Additive breed group of sire (SM)
- 5) Nonadditive genetic regression groups (direct, maternal separately)
  - a. Intralocus Interbreed Breed Group of Sire x Breed Group of Dam Interaction (AM, SMGS, SM)
  - b. Intralocus Interbreed Breed Group of Mgs x Breed Group of Mgd Interaction (AM, SMGS, SM)
- 6) Regression genetic group due to breed of maternal granddams (SMGSM) Breed of dam (SM) (direct, maternal jointly)

### RANDOM EFFECTS

- 1) Calf additive direct genetic effects (AM)  
Sire additive direct genetic effects (SMGSM, SM)  
(Subclass form)
- 2) Dam additive maternal genetic effects (AM)  
Mgs additive maternal genetic effects (SMGSM)  
(Subclass form)
- 3) Sire intralocus intrabreed and interbreed nonadditive direct genetic effects (sire x breed-group-of-dam interactions; AM, SMGSM, SM)  
(Regression form)
- 4) Maternal grandsire intralocus intra and interbreed nonadditive maternal genetic effects (mgs x breed-group-of-mgd interactions; AM, SMGSM)  
(Regression form)
- 5) Residual effects  
(Subclass form)

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### BATCH FILE = xmremlem.bat

```
=====
@ECHO OFF
rem ##### (Specific batch file for MAB data set)#####
REM xmremmab.bat *** (Specific batch file for MAB data set)***
rem #####
REM dir = c:\home\pkg\mremlem2001\RunRelease_mab\
copy PARAM mremlem99.paramsmz
copy PARAM param.011002.MREMLEM

rem #####
rem struct_pedigree_file_mab_ufl_mremlem2001 = struct_pedigree_file_mab_ufl
```

```

rem struct_data_file_mab_ufl_mremlem2001 = struct_data_file_mab_ufl
rem                                         + new fields (e.g., age of dam)
rem #####
copy struct_pedigree_file_mab_ufl_mremlem2001 struct_pedigree_file
copy struct_data_file_mab_ufl_mremlem2001     struct_data_file

rem #####
rem Run MREMLEM
rem #####
c:\home\pkg\mremlem2001\Debug\mremlem2001.exe %1 %2 %3 %4

copy MBEOOUT mbeout.011002.bdmwdm.smgs_GENPRED_a
copy MBEOOUT mremmabo.011002.bdmwdm.a3n33e3_a.smgs_GENPRED_a
copy WRTSOL bulsol.011002.bdmwdm.a3n33e3_a.smgs_GENPRED_a

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```

## INPUT FILES: Read in *free* format.

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INPUT FILE 1 = parameter file (PARAM)
INPUT FILE 2 = default program limits (IPROGLIM)
INPUT FILE 3 = structure of pedigree file (STRUCT_PEDIGREE_FILE)
INPUT FILE 4 = structure of data file (STRUCT_DATA_FILE)
INPUT FILE 5 = pedigree file (PEDIG)
INPUT FILE 6 = data file (LCSET)
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## OUTPUT FILES

```

OUTPUT FILE 1 = general output file (MBEOOUT)
OUTPUT FILE 2 = covariances and genetic parameter estimates (RESULTS)
OUTPUT FILE 3 = genetic predictions file (WRTSOL)
```

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```

## REMARKS

- 1) Convergence criterion in file MBEOOUT = vcconv(iter).
- 2) The five lines for each animal in file WRTSOL correspond to:
  - a) line 1: predicted genetic values
  - b) line 2: standard error of prediction (sep)
  - c) line 3: ratio (prediction/genetic standard deviation)
  - d) line 4: (sep/ genetic standard deviation)
  - e) line 5: BIF accuracy = 1 - (sep/ genetic standard deviation)

```

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## DESCRIPTION OF INPUT FILES

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**INPUT FILE 1 = parameter file (PARAM)**


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```

'begin headings'
***** ANGUS-BRAHMAN MULTIBREED GENETIC EVALUATION *****
***** --> 3-TRAIT GENETIC COVARIANCES - 2-TRAIT GENETIC PREDICTIONS <--- *****
***** BIRTH WEIHGT - WEANING WEIGHT *****
***** IF MREMLEM HANGS UP -> INCREASE frnze slightly in IPROGLIM *****
***** ... and if this does not solve the problem, check the program !!!! *****
***** Program MREMLEM (12/23/2001) *****
***** Author: Mauricio A. Elzo *****
***** University of Florida *****
***** Dept. Animal Sciences *****
***** Room 202D, Bldg 459 *****
***** P O Box 110910 *****
***** Tel: (352) 392-7564 *****
***** Fax: (352) 392-7564 *****
***** Email: elzo@animal.ufl.edu *****
***** READ [1] *****
***** Date: 12/23/2001
***** (dir) = c:\home\pkg\mremlem2001\runrelease_mab\
***** Batch Program: c:\home\pkg\mremlem2001\runrelease\xmremlem.bat
***** Executable: c:\home\pkg\mremlem2001\debug\mremlem2001.exe
'
***** Output File (MBEOUT): (dir)mbeout.122301.bdmwdm.smgs_gencov_a'
'
***** Pedigree file (PEDIG): (dir)mabped_all.111601.ipar-isex-sire'
***** Data file (LCSET): (dir)mabcset_all.111601'
'
***** Run: gen prior c(i,j) = g '
***** env prior c(i,j) = p BW and WW
***** Parameter File Prior: Covariance Estimates from single-trait runs'
'
***** Compare: (dir)MBEOUT.062001.Correct_W98_and_Correct_W2000'
'
***** end headings'
'begin headings'
***** READ [1b] DATA SET NAME'
'end headings'
'Angus-Brahman Multibreed Data Set'
'begin headings'
***** READ [1c] DATA SET CODE'
'end headings'
'angus-brahman'
'begin headings'
***** jmodel = 1 = (p1)var(1) + (p2)var(2) + (p3)var(3)'
'      = 2 = (1)var(1) + (p2)[var(2) - var(1)] + (p3)var(3)'
'janmod = 1 = calf-dam model'

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```

' = 2 = sire-mgs model'
' inbred = 1 = assume no inbreeding in the population (bubi)'
' = 2 = account for inbreeding approximately (abubi)'
' = 3 = account for inbreeding completely (inrbui)'
' irsub = 1 = (add sub, nad sub)'
' = 2 = (add sub, nad reg)'
' = 3 = (add reg, nad reg)'
'      --- do not use <====> insufficient storage space'
' jadm = 1 = joint .5 direct and maternal mgs effects'
' = 2 = separate .5 direct and maternal mgs effects'
' lrmmesol = 0 = do NOT print mme solutions'
' = 1 = compute and print mme solutions (ADD SUB, NAD SUB)'
'      print animal diagonal blocks of lsh inverse'
'      after MREMLEM converges'
' = 2 = compute and print mme solutions (ADD SUB, NAD REG)'
'      print animal diagonal blocks of lsh inverse'
'      after MREMLEM converges'
' = 3 = compute and print mme solutions (ADD SUB, NAD SUB, TOT SUB)'
'      print animal diagonal blocks of lsh inverse'
'      after MREMLEM converges'
'*****'
'READ [2] JMODEL JANMOD INBRED IRSUB JADM LRMMESOL'
'end headings'
      1          2          2          2          2          3
'begin headings'
'*****'
' jnzrec = 1 = consider calves with any number of nonzero traits'
' = 0 = consider only calves with measurements on ALL traits'
' knwnmgs = 0 = do NOT delete calves w/o mgs or with fictitious mgs'
' = 1 = delete calves w/o mgs'
' nfixeff = n = number of fixed effects'
'indbug(0) = 0 = DO NOT BUILD ANY TYPE OF GENETIC GROUPS FOR BULLS'
' = 1 = Accumulated Subclass Grouping Strategy - All Animals'
' = 2 = Accumulated Subclass Grouping Strategy - Base Animals'
' = 3 = SEPARATE REGRESSION grouping strategy (====> nbugr = 0)'
'indbug(1) = 0 = DO NOT BUILD SUBCLASS BULL GROUPS'
' = 1 = ACCUMULATED SUBCLASS BULL GROUPS according to ancestors'
'      identified ONLY'
' = 2 = ACCUMULATED SUBCLASS BULL GROUPS according to breed group'
'      combination and ancestors identified'
' = 3 = SEPARATE REGRESSION grouping strategy (====> nbugr = 0)'
' = 4 = ACCUMULATED SUBCLASS BULL GROUPS according to breed group'
'      combination ONLY'
' = 5 = ACCUMULATED REGRESSION grouping strategy'
'*****'
' (locont) do jfm=1,nenvef'
' (effmod) #CGE NOT increased by +2'
' Contemporary Group - Age of Dam'
' Nonren BW - Nonren WW'
' WORKS - frnze=.03 (up from .02) Sanmartinero-Brahman'
' Renum BW - Renum WW'
' WORKS - frnze=.03 (up from .02) Sanmartinero-Brahman'
' Renum BW - Nonren WW'
' WORKS - frnze=.03 (up from .02) Sanmartinero-Brahman'
' Nonren BW - Renum WW'
' WORKS - frnze=.03 (up from .02) Sanmartinero-Brahman'
' WORKS - frnze=.06 (up from .03) Angus-Brahman'
'READ [2a] JNZREC KNWNMGS NFIXEFF INDBUG(0) INDBUG(1)'
'end headings'
      1          0          2          3
'begin headings'

```

```

'*****!
' lenreccdat = length of the data record'
' lenrecped = length of the pedigree record'
' prtrencoldat = sequentially renumbered column to be printed'
' (check if renumbering is correct)'
'*****!
'READ [3] LENRECDAT  LENRECPED  PRTRENCOLDAT'
'end headings'
      101          27          00
'begin headings'
'*****!
'READ [3a] PARAMETERS FROM edped'
'numidped = # id per animal and its ancestors in the pedigree file (PEDIG)'
'numiddat = # id per animal and its ancestors in the data file (LCSET)'
'numidped numiddat'
'*****!
'end headings'
      3          2
'begin headings'
'*****!
'numanped = # animals in each pedigree record'
'numbreedgeval = # breeds in the data set'
'numwrintfields = # non-grouped integer fields'
'maxnumcg = # contemporary groups'
'numtraits = # defined traits in the data set (= ntdat)'
'numwrcharfields = # character fields'
'*****!
'READ [3b] PARAMETERS FROM edped'
'numanped numbreedgeval numwrintfields maxnumcg numtraits numwrcharfields'
'end headings'
      5          2          59          2          19          1
'begin headings'
'*****!
' mxiter = maximum number of mremlem iterations, and indicator to compute'
'         genetic parameters and genetic predictions only'
'         = -1 => compute genetic parameters (herit, interact, corr) **ONLY**'
'         = 0 => compute genetic parameters **AND** genetic predictions'
'         = 1 or larger => compute MREMLEM covariances, gen par, and gen pred'
' iterpr = frequency of printing of GEM iteration results'
' fconv = overall convergence criterion (cconv < fconv)'
' ioptn = type of algorithm used to invert the lhs of the mme (not used)'
'         = 2 = luginv   (full-stored inversion) (not used)'
'         = 3 = g2swepl (full-stored inversion) (not used)'
'         = 4 = fi5152  (full-stored inversion) (not used)'
'         = 6 = solf52  (sparse-stored inversion) (not used)'
'         = 5 = solf60  (sparse-stored inversion) (not used)'
'         = 7 = solf61  (sparse-stored inversion) '
' jckg = indicator
'         = 1 = check that aga = a, where a = lhs (not used) '
'         = 0 = else
'*****!
'READ [4] MXITER  ITERPR    FCONV     ZDJN     IOPTN   JCKG'
'end headings'
      0       010     .1E-3     .1E-10      7       1
'begin headings'
'*****!
'READ [5] MXJTER  JTERPR    FCONVJ    RMULTMAX  JGRCOV  JBGBUL'
'end headings'
      12       021     .1E-1     1.0D0      0       0
'begin headings'
'*****!

```

```

'READ [6] JRESTR  JRATIO      SMALNU1      JRESCORE'
'end headings'
    2222      3      .0100      1
'begin headings'
'*****'
'READ [7] MXDSOL  IROSOL  IRND  MAXRND  IPRND'
'end headings'
    40000     -1      0      20      20
'begin headings'
'*****'
' kdfyr = year of birth of the oldest calves in the data set'
' lstyryr = year of birth of the youngest calves in the data set'
'*****'
'READ [8] KDFYR  LSTYR'
'end headings'
    1987    2010
'begin headings'
'*****'
' nbr = number of breeds'
' nbg = number of breed groups'
' idenbf = denominator for breed fractions'
' divbg = divisor used to compute breed groups'
'     = (idenbf/nbg)+.0000001'
' nt = number of traits analized'
' nblk = number of genetic blocks'
'     = 1 = additive genetic effects only'
'     = 2 = add and nonadd interbreed intralocus genetic effects'
'*****'
'READ [9] NBR  NBG  NT  NGLBK'
'end headings'
    2      5      2      2
'begin headings'
'*****'
'READ [9a] NAMES AND ACRONYMS OF BREEDS CONSIDERED IN THE ANALYSIS'
'end headings'
    'ANGUS'          'A'
    'BRAHMAN'        'B'
'begin headings'
'*****'
'READ [9b] PEDIGREE CODES, PEDIGREE NAMES, LOCATION OF SEQUENTIAL NUMBERS,
' AND LOCATIONS OF BREED 1 FRACTIONS IN THE DATA FILE'
'CODE = 0 (ZERO) IF AN ANCESTOR IS *** NOT *** PRESENT IN THE DATA FILE'
'*** THE PEDIGREE CODES (1 TO 7) APPLY TO THE PEDIGREE AND THE DATA FILES ***'
'*****'
' CODE NAME                      LOC_SEQ_#   LOC_FR_BR_1'
'end headings'
    1 'ANIMAL(CODE=1)'           2                  3
    2 'SIRE(CODE=2)'            6                  7
    3 'DAM(CODE=3)'             10                 11
    0 'PATERNAL GRANDSIRE(CODE=4)' 0                  0
    0 'PATERNAL GRANDDAM(CODE=5)' 0                  0
    6 'MATERNAL GRANDSIRE(CODE=6)' 14                 15
    7 'MATERNAL GRANDDAM(CODE=7)' 18                 19
'begin headings'
'*****'
'READ [10] LOCATION OF THE YEAR OF BIRTH OF THE CALF AND THE DAM, AND THEIR'
' CORRESPONDING PERPETUAL BIRTH DATES'
'loccafyr locdamyr locprcraf locprpdam locdamage'
'end headings'
    21      34      23      35      -1
'begin headings'

```

```

*****!
'READ [11] LOCATION OF THE NT EVALUATED TRAITS IN THE DATA RECORD'
'      (LTRDAT(I),I=1,NT)'
'end headings'
     83      84
'begin headings'
*****!
'READ [11a] MULTIPLIER FOR THE NT EVALUATED TRAITS'
'      (TRMULT(I),I=1,NT)'
'end headings'
     .1E+1 .1E+1
'begin headings'
*****!
'READ [11b] STATISTICAL MODEL'
'*** LOCATION = POSITIVE NUMBER IF EFFECT PRESENT IN STRUCT_DATA_FILE'
'      = NEGATIVE NUMBER IF NEW EFFECT GENERATED BY MREMLEM'
'*** MAXIMUM NUMBER OF NESTED EFFECTS = 6 (maxnested=6) -> INCREASE IF NEEDED ***'
'PRINT EFFECT TRAIT #NESTED LOCATIONS AND NAMES OF NESTED EFFECTS'
'      (jfm)      EFFECTS'
*****!
'end headings'
   1      1      1      1      80 'Cont Group'
   1      1      2      1      81 'Cont Group'
   1      2      1      3      -1 'Age Dam'
                  24 'Sex Calf'
                  11 'Fr Br1 Dam'
   1      2      2      3      -1 'Age Dam'
                  29 'New Sex Calf'
                  11 'Fr Br1 Dam'

'begin headings'
*****!
'READ [14] INDICATOR FOR DIRECT (1) AND DIR & MAT (2) EFFECTS FOR EACH TRAIT'
'      (IDMTR(I),I=1,NT)'
'end headings'
     2      2
'begin headings'
*****!
'READ [15] NUMBER OF LOCI PER BLOCK'
'      (ISTLOC(I),I=1,NGBLK)'
'end headings'
     1      1      2
'begin headings'
*****!
'READ [16] NONADDITIVE SET TO BE ANALYZED (DEFINED IN SUBR NADWG)'
'      NADSET'
'end headings'
     33
'begin headings'
*****!
'READ [17] NUMBER OF POPULATIONS PER GEN COV BLOCK (ADD, NAD1, NAD2)'
'      (NGEF(I),I=1,NGBLK)'
'end headings'
     3      3
'begin headings'
*****!
'READ [18] NUMBER OF POPULATIONS FOR ENV COV BLOCK'
'      NENMAT'
'end headings'
     3
'begin headings'
*****!

```

```

'READ [19] ***** ADDITIVE GENETIC COVARIANCE PRIORS *****
' add[11] add[22] add[12]'
'end headings'
   6.268      6.173      5.252      (bwd,bwd)
   .0          .0          .0          wwd)
  -0.342     -0.160      0.056      bwm)
   .0          .0          .0          wwm)
  61.179     68.471    134.857      (wwd,wwd)
   .0          .0          .0          bwm)
 -13.813     -0.556     18.448      wwm)
   6.700      7.058      1.575      (bwm,bwm)
   .0          .0          .0          wwm)
  49.396     167.695     18.270      (wwm,wwm)

'begin headings'
*****!
'READ [19a] ***** NONADDITIVE GENETIC COVARIANCE PRIORS *****
' nad[11] nad[22] nad[12]'
'end headings'
   6.502      6.343      6.038      (bwd,bwd)
   .0          .0          .0          wwd)
   0.147      0.286      0.036      bwm)
   .0          .0          .0          wwm)
  85.969     84.725     67.552      (wwd,wwd)
   .0          .0          .0          bwm)
  29.235      2.296     26.935      wwm)
   6.860      6.226      6.195      (bwm,bwm)
   .0          .0          .0          wwm)
  67.297     56.467     86.071      (wwm,wwm)

'begin headings'
*****!
'READ [20] ***** ADDITIVE GENETIC COVARIANCE ESTIMATES *****
' add[11] add[22] add[12]'
'end headings'
   5.572      5.646      4.311      (BWD,BWD)
   1.027      1.637      7.256      WWD)
  -0.494     -0.257      0.038      BWM)
  -0.078      1.775     -1.356      WWM)
  58.490     67.547    132.544      (WWD,WWD)
   0.310      0.853      1.919      BWM)
 -13.329     -0.575     17.727      WWM)
   5.964      6.237      2.006      (BWM,BWM)
   0.320      2.948     -0.340      WWM)
  47.446     156.718     31.851      (WWM,WWM)

'begin headings'
*****!
'READ [20a] ***** NONADDITIVE GENETIC COVARIANCE ESTIMATES *****
' nad[11] nad[22] nad[12]'
'end headings'
   5.953      5.758      5.349      (BWD,BWD)
   0.854      1.156      1.364      WWD)
   0.194      0.346      0.140      BWM)
   0.403      0.154      0.614      WWM)
  82.099     83.671     65.092      (WWD,WWD)
   0.662      0.126      0.806      BWM)
  28.435      2.462     26.724      WWM)
   6.323      5.619      5.618      (BWM,BWM)
   0.775      0.549      1.337      WWM)
  65.414     53.642     84.029      (WWM,WWM)

'begin headings'
*****!
'READ [21] ***** ENVIRONMENTAL COVARIANCE PRIORS *****

```

```

' env[11]  env[22]  env[12]'
'end headings'
    43.816    49.309    35.059          (bw,bw)
    .0        .0        .0            (ww)
   427.047   372.904   288.933          (ww,ww)

'begin headings'
***** READ [21a] ***** ENVIRONMENTAL COVARIANCE ESTIMATES *****
' env[11]  env[22]  env[12]'
'end headings'
    12.149    13.597    16.752      (BW,BW)
    31.305    37.254    20.486        (WW)
   379.076   298.182   261.814      (WW,WW)

'begin headings'
***** READ [22] ***** PRINT SELECTED 2-BREED COVARIANCE ESTIMATES *****
' Read npcovset and matrix lprcovest(0:3,3,np covset)'
' npcovset = number of 2-breed sets of [add,nad,env] cov matrices to be printed'
' lprcovest(0,i,k) = number of [add, nad, env] cov matrices for 2-breed'
'           printing of parameter estimates for set k'
' lprcovest2b(0,1,k)=naddmat2b for set k'
' lprcovest2b(0,2,k)=nnadmat2b for set k'
' lprcovest2b(0,3,k)=nenvmat2b for set k'
' lprcovest(j,1,k) = location of add cov matrices for set k in an nbr mult popn'
' lprcovest(j,2,k) = location of nad cov matrices for set k in an nbr mult popn'
' lprcovest(j,3,k) = location of env cov matrices for set k in an nbr mult popn'
' *** SEE READ [19a], [20a], and [21a] for number and location of these matrices'
***** end headings'

    1                  np covset
    3      3      3      lprcovest2b(j=0,i={1,3},iprcovset=1)
    1      2      3      lprcovest2b(j={1,lprcovest2b(0,1,k)},i=1,iprcovset=1)
    1      2      3      lprcovest2b(j={1,lprcovest2b(0,2,k)},i=2,iprcovset=1)
    1      2      3      lprcovest2b(j={1,lprcovest2b(0,3,k)},i=3,iprcovset=1)

=====
=====
```

## INPUT FILE 2 = default program limits (IPROGLIM)

```
=====
```

```

'begin headings'
***** Program MREMLEM (12/23/2001) *****
***** Author: Mauricio A. Elzo      *****
***** University of Florida      *****
***** Dept. Animal Sciences      *****
***** Room 202D, Bldg 459      *****
***** P O Box 110910      *****
***** Tel: (352) 392-7564      *****
***** Fax: (352) 392-7564      *****
***** Email: elzo@animal.ufl.edu *****
***** MREMLEM PROGRAM LIMITS *****
***** IPROGLIM -> INPUT FILE FOR MODULE commonproglim (06/18/2001) *****
' maxiter = maximum number of multibreed GEM iterations'
' mxbuls = maximum number of animals that can be evaluated by MREMLEM'
```

```

'      (mxbuls is limited by the # equations that can be stored in'
'      core using the linker subr's !!!)'
'***** Used by read_pedigreefile to resequence evaluated animals !!!! *****
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'integer,parameter :: maxiter=200'
'integer,parameter :: mxbuls=400      ! smz test settings: 2 traits {d,m}'
'integer,parameter :: mxbuls=184      ! smz test settings: 2 traits {d,m}'
'integer,parameter :: mxbuls=4200     ! PREC620 settings: 2 traits {d,m}'
'integer,parameter :: mxbuls=2200     ! PREC620 settings: 3 traits {d,m}'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'READ [1] maxiter      mxbuls'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'end headings'
          200           233           15800 (mavail < largest 4-byte integer)

'begin headings'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'frnze = fraction of nonzero elements in the lhs of the mme'
'real,parameter :: frnze=.0012 ! for the rc data set'
'real,parameter :: frnze=.0012 ! for the smz data set'
'real,parameter :: frnze=.0200 ! Latest setting: smz data set (05/30/2001)'
-----
'tmulmav = multiplier to correct excess memory requirements for fspak '
'real,parameter :: tmulmav=.20 ! for the rc and smz data sets'
'real,parameter :: tmulmav=.15 ! NEW value (05/30/2001) -> smz data set'
'tmulmav=.40 ! new value (06/27/2001) for revised_allocations'
-----
'tmulmlptr2 = multiplier to correct excess memory requirements by hash'
'            (due to mlptr1 >> actual number of mme)'
'NOTE: tmulmlptr2 MUST be modified for EACH data set !!!! (06/12/2001)'
'      tmulmlptr2 is NOT used by revised_allocations'
'real,parameter :: tmulmlptr2=.40 ! NEW value (06/13/2001) -> smz data set and
real(rk)'
'real,parameter :: tmulmlptr2=.35 ! NEW value (06/12/2001) -> smz data set and
real(8)'
'real,parameter :: tmulmlptr2=.99 ! TEST value (06/12/2001) -> smz data set'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'READ [2] frnze      tmulmav    tmulmlptr2'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'end headings'
          0.06          0.40          0.40

'begin headings'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'mxdimt = dimension of full-stored matrices (aaa,ag,aga,ggg,dif)'
'      (used to solve mme directly using the sweep operator)'
'      mxdimt is too small to be useful for more than a single herd'
'      ==> max(meqtot)=mxdimt if mme are solved by dense procedures'
'      ==> must install a sparse option to solve large systems of mme'
'mxbusb = max number of bull contributions to G inverse (giam, mremlem_Estep)'
'mbuinf = max number of pieces of information needed per bull for G inverse'
'maxupd = max number of vectors with covariance information (e.g., remcov(.,maxupd)'
'integer,parameter :: mxdimt=0020,mxbusb=10,mbuinf=15,maxupd=21'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'READ [3] mxdimt      mxbusb      mbuinf      maxupd'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!
'end headings'
          20           10           15           21

'begin headings'
***** !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!

```

```

'mxnbr = max number of breeds allowed in the program'
'mxsex = max number of sexes allowed in the program'
'mxdas = max number of age of dam categories'
'mxfxef = max number of subclass fixed effects'
'integer,parameter :: mxnbr=2,mxsex=3,mxdas=3,mxfxef=10'
'*****'
'READ [4] mxnbr      mxsex      mxdas      mxfxef'
'*****'
'end headings'
3           3           3           10

'begin headings'
'*****'
'READ [5] -> KEEP AS PARAMETERS !!! DO *NOT* READ THEM !!!!'
'*****'
'for subr irescov, irescovinv'
'mxim = indicator (im = 1, sire known only, and im = 2, sire and mgs known)'
'          (im = 1, animal known only, and im = 2, animal and dam known)'
'          (two categories only)'
'mkanc = number of combinations of sire and mgs, or animal and dam identified'
'          (four combinations in all)'
'maxxnt = maximum number of traits allowed by trait-combination function'
'          The new algorithm allows for combinations of up to 32 traits, but'
'          given the huge sizes of the resulting arrays using mxnt, the'
'          value of mxnt will be kept at 2 (or 4) for now (8/11/94).'
'          informational parameter, i.e., not used by mremlem !!!'
'integer,parameter :: mxim=2,mkanc=4,maxxnt=32'
'*****'
'end headings'

'begin headings'
'*****'
'mxnt = max number of traits'
'mxdm = max number of direct and maternal effects per trait'
'mxnbg = max number of breed groups'
'mxanef = max number of animal effects'
'          = 2 ==> sire and mgs; animal and dam'
'          = 3 ==> sire, mgs, perm env; animal, dam, perm env'
'mxgref = max number of sets of genetic group effects'
'          = 2 ==> sire group and mgs group sets; animal group and dam group sets'
'          = 3 ==> sire grp, mgs grp, penv grp sets; animal grp, dam grp, penv grp sets'
'For BEEF CATTLE'
'integer,parameter :: mxnt=2,mxdm=2,mxnbg=5,mbgcommmax=20,mxanef=2,mxgref=2 ! Beef'
'For DAIRY CATTLE <== TEST these parameters for memory requirements !!!'
'integer,parameter :: mxnt=2,mxdm=1,mxnbg=5,mbgcommmax=20,mxanef=1,mxgref=1 ! Dairy'
'*****'
'READ [6] mxnt      mxdm      mxnbg      mbgcommmax      mxanef      mxgref'
'*****'
'end headings'
3           2           5           15           2           2

'begin headings'
'*****'
'mntdat = max number of traits per input record'
'mxelin = max number of elements per input record'
'integer,parameter :: mntdat=20,mxelin=100'
'*****'
'READ [7] mntdat      mxelin'
'*****'
'end headings'
20          100

```

```
'begin headings'
*****!
'mgblk = max number of additive and nonadditive genetic blocks'
'      per bull (sire-mgs model), calf (calf-dam model)'
'mxadbl = max number of additive genetic blocks'
'mxnabl = max number of nonadditive genetic blocks'
'maxncg = max number of contemporary group equations for direct solns'
'integer,parameter :: mgblk=2,mxadbl=1,mxnabl=1,maxncg=0110'
*****!
'READ [8] mgblk      mxadbl      mxnabl      maxncg'
*****!
'end headings'
2          1          1          110
=====
```

### **INPUT FILE 3 = structure of pedigree file (*STRUCT\_PEDIGREE\_FILE*)**

=====

```
'begin headings'
*****!
'STRUCTURE OF THE MULTIBREED ANGUS-BRAHMAN PEDIGREE FILE'
'LOCATION  NAME OF EFFECT      TYPE      MAXNUMSUB      DENOMINATOR'
*****!
'end headings'
1  'Parent Indicator      ' 'subclass'   '-1'    1
2  'Sex Indicator        ' 'subclass'   '-1'    1
3  'Charact Ident Animal' 'subclass'   '-1'    1
4  'Ingeger Ident Animal' 'subclass'   '-1'    1
5  'Seq Number Animal    ' 'subclass'   '-1'    1
6  'Fractn Br 1 Animal  ' 'regression' '1'     32
7  'Fractn Br 1 Animal  ' 'regression' '1'     32
8  'Charact Ident Sire   ' 'subclass'   '-1'    1
9  'Ingeger Ident Sire  ' 'subclass'   '-1'    1
10 'Seq Number Sire      ' 'subclass'   '-1'    1
11 'Fractn Br 1 Sire    ' 'regression' '1'     32
12 'Fractn Br 1 Sire    ' 'regression' '1'     32
13 'Charact Ident Dam   ' 'subclass'   '-1'    1
14 'Ingeger Ident Dam   ' 'subclass'   '-1'    1
15 'Seq Number Dam       ' 'subclass'   '-1'    1
16 'Fractn Br 1 Dam     ' 'regression' '1'     32
17 'Fractn Br 1 Dam     ' 'regression' '1'     32
18 'Charact Ident Mgs   ' 'subclass'   '-1'    1
19 'Ingeger Ident Mgs   ' 'subclass'   '-1'    1
20 'Seq Number Mgs       ' 'subclass'   '-1'    1
21 'Fractn Br 1 Mgs     ' 'regression' '1'     32
22 'Fractn Br 1 Mgs     ' 'regression' '1'     32
23 'Charact Ident Mgd   ' 'subclass'   '-1'    1
24 'Ingeger Ident Mgd   ' 'subclass'   '-1'    1
25 'Seq Number Mgd       ' 'subclass'   '-1'    1
26 'Fractn Br 1 Mgd     ' 'regression' '1'     32
27 'Fractn Br 1 Mgd     ' 'regression' '1'     32
=====
```

### **INPUT FILE 4 = structure of data file (*STRUCT\_DATA\_FILE*)**

=====

```
'begin headings'
```

```
*****
' STRUCTURE OF THE EDITED MULTIBREED ANGUS-BRAHMAN DATA FILE'
'LOCATION NAME OF EFFECT      TYPE      MAXNUMSUB  DENOMINATOR  RENUMBER'
*****
'end headings'
1   'Int Number Animal    ' 'subclass'   -1       1       0
2   'Seq Number Animal    ' 'subclass'   -1       1       0
3   'Fractn Br 1 Animal  ' 'regression' 1        32      0
4   'Fractn Br 2 Animal  ' 'regression' 1        32      0
5   'Int Number Sire     ' 'subclass'   -1       1       0
6   'Seq Number Sire     ' 'subclass'   -1       1       0
7   'Fractn Br 1 Sire   ' 'regression' 1        32      0
8   'Fractn Br 2 Sire   ' 'regression' 1        32      0
9   'Int Number Dam     ' 'subclass'   -1       1       0
10  'Seq Number Dam     ' 'subclass'   -1       1       0
11  'Fractn Br 1 Dam   ' 'regression' 1        32      0
12  'Fractn Br 2 Dam   ' 'regression' 1        32      0
13  'Int Number Mgs    ' 'subclass'   -1       1       0
14  'Seq Number Mgs    ' 'subclass'   -1       1       0
15  'Fractn Br 1 Mgs   ' 'regression' 1        32      0
16  'Fractn Br 2 Mgs   ' 'regression' 1        32      0
17  'Int Number Mgd    ' 'subclass'   -1       1       0
18  'Seq Number Mgd    ' 'subclass'   -1       1       0
19  'Fractn Br 1 Mgd   ' 'regression' 1        32      0
20  'Fractn Br 2 Mgd   ' 'regression' 1        32      0
21  'YEARSET calf      ' 'subclass'   40      1       1 hash renum
22  'TRP PreWean calf  ' 'subclass'   60      1       1 hash renum
23  'Birth Date calf   ' 'regression' 1        1       0
24  'Sex calf          ' 'subclass'   2        1       1 hash renum
25  'SUR PreWean calf  ' 'subclass'   16      1       1 hash renum
26  'DZDAT calf        ' 'regression' 1        1       0
27  'RFD calf          ' 'subclass'   16      1       1 hash renum
28  'CASDAT calf        ' 'regression' 1        1       0
29  'New Sex calf      ' 'subclass'   3        1       1 hash renum
30  'Weaning Date calf ' 'regression' 1        1       0
31  'TRP PostWean calf ' 'subclass'   60      1       1 hash renum
32  'TRP PostYearl calf ' 'subclass'   60      1       1 hash renum
33  'Slaughter Date calf ' 'regression' 1        1       0
34  'YEARSET dam        ' 'subclass'   40      1       1 hash renum
35  'Birth Date dam    ' 'regression' 40      1       0
36  'AGE0 calf          ' 'regression' 1        1       0
37  'BWT calf           ' 'regression' 1        1       0
38  'AIGLEN calf        ' 'regression' 1        1       0
39  'CEase               ' 'subclass'   4        1       1 hash renum
40  'AGE1 calf          ' 'regression' 1        1       0
41  'WT1 calf           ' 'regression' 1        1       0
42  'AGE2 calf          ' 'regression' 1        1       0
43  'WT2 calf           ' 'regression' 1        1       0
44  'AGE3 calf          ' 'regression' 1        1       0
45  'WT3 calf           ' 'regression' 1        1       0
46  'AGE4 calf          ' 'regression' 1        1       0
47  'WT4 calf           ' 'regression' 1        1       0
48  'AGE5 calf          ' 'regression' 1        1       0
49  'WT5 calf           ' 'regression' 1        1       0
50  'AGE6 calf          ' 'regression' 1        1       0
51  'WT6 calf           ' 'regression' 1        1       0
52  'AGE7 calf          ' 'regression' 1        1       0
53  'WT7 calf           ' 'regression' 1        1       0
54  'AGEE calf           ' 'regression' 1        1       0
55  'WWT calf            ' 'regression' 1        1       0
56  'AGE8 calf          ' 'regression' 1        1       0
```

57	'WT8 calf	' regression'	1	1	0
58	'AGE9 calf	' regression'	1	1	0
59	'WT9 calf	' regression'	1	1	0
60	'AGE10 calf	' regression'	1	1	0
61	'WT10 calf	' regression'	1	1	0
62	'AGE11 calf	' regression'	1	1	0
63	'WT11 calf	' regression'	1	1	0
64	'AGE12 calf	' regression'	1	1	0
65	'WT12 calf	' regression'	1	1	0
66	'AGE13 calf	' regression'	1	1	0
67	'WT13 calf	' regression'	1	1	0
68	'AGE14 calf	' regression'	1	1	0
69	'WT14 calf	' regression'	1	1	0
70	'AGE15 calf	' regression'	1	1	0
71	'WT15 calf	' regression'	1	1	0
72	'AGE16 calf	' regression'	1	1	0
73	'WT16 calf	' regression'	1	1	0
74	'AGE17 calf	' regression'	1	1	0
75	'WT17 calf	' regression'	1	1	0
76	'FINAL AGE calf	' regression'	1	1	0
77	'FINALWT calf	' regression'	1	1	0
78	'SL AGE calf	' regression'	1	1	0
79	'SL WT calf	' regression'	1	1	0
80	'BWT cont grp	' subclass '	30	1	1 hash renum
81	'WWT cont grp	' subclass '	309	1	1 hash renum
82	'GESTATION LENGTH	' regression'	1	1	0
83	'BIRTH WEIGHT	' regression'	1	1	0
84	'WEANING WEIGHT 205D	' regression'	1	1	0
85	'PWG 205D TO 365D	' regression'	1	1	0
86	'PWG 205D TO 550D	' regression'	1	1	0
87	'PWG 365D TO 550D	' regression'	1	1	0
88	'WEIGHT 365D	' regression'	1	1	0
89	'WEIGHT 550D	' regression'	1	1	0
90	'SLAUGHTER AGE	' regression'	1	1	0
91	'WT GAIN BIRTH-100D	' regression'	1	1	0
92	'WT GAIN 100D-200D	' regression'	1	1	0
93	'WT GAIN 200D-300D	' regression'	1	1	0
94	'WT GAIN 300D-400D	' regression'	1	1	0
95	'WT GAIN 400D-500D	' regression'	1	1	0
96	'WEIGHT 100D	' regression'	1	1	0
97	'WEIGHT 200D	' regression'	1	1	0
98	'WEIGHT 300D	' regression'	1	1	0
99	'WEIGHT 400D	' regression'	1	1	0
100	'WEIGHT 500D	' regression'	1	1	0
101	'Charact Ident Animal'	' subclass '	-1	1	0

```

'begin headings'
*****!
' Create new variable: Age of Dam'
*****!
' renumreccdat(locdamage)= 0 = no transformation'
' renumreccdat(locdamage)= 1 = days to months'
' renumreccdat(locdamage)= 2 = days to year subclasses'
' renumreccdat(locdamage)= 3 = days to years'
' renumreccdat(locdamage)= 4 = months to years'
' renumreccdat(locdamage)= 9 = days to years (original agedamsub code)'
*****!
'NEW VARIABLES READ FROM FILE STRUCT_DATA_FILE (NOT IN THE DATA FILE)'
'LOCATION NAME OF EFFECT          TYPE          MAXNUMSUB DENOMINATOR RENUMBER'
*****!
'end headings'

```

-1      'Age Dam Yr                          ' 'subclass'                          3                          1                          9    agedamsub

## INPUT FILE 5 = pedigree file (PEDIG)

**Example of pedigree records from the Angus-Brahman Multibreed Herd of the University of Florida (boldfaced every other record for clarity)**

```

1 1 "CCR PATHFINDER 152W      "       62      143 20 12 "
"        0 20 12 "           0      0 20 12 "           0      0 20 12 "
0 0 20 12
1 1 "WHS DICHEO ESTO 0257    "       61      144 0 32 "
"        0 0 32 "           0      0 0 32 "           0      0 0 32 "
0 0 0 32
1 1 "CHARGER OF BRINKS     "       60      145 8 24 "
"        0 0 32 "           0      0 32 0 "           0      0 16 16 "
0 0 0 32
1 1 "BN1800 INDU-ANGUS     "       58      146 16 16 "
"        0 0 32 "           0      0 32 0 "           0      0 32 0 "
0 0 32 0
1 1 "BRINKS EQUALIZER      "       57      147 24 8 "
"        0 0 32 0 "           0      0 0 32 "           0      0 16 16 "
0 0 32 0
1 1 "B A R POWER PLAY 59    "       56      148 32 0 "
"        0 32 0 "           0      0 32 0 "           0      0 32 0 "
0 0 32 0
1 1 "711                   "       55      149 20 12 "
"        0 20 12 "           0      0 20 12 "           0      0 20 12 "
0 0 20 12
1 1 "PARTIN                 "       54      150 0 32 "
"        0 0 32 "           0      0 0 32 "           0      0 0 32 "
0 0 0 32
1 1 "HARDEE 4                "       53      151 8 24 "
"        0 0 32 "           0      0 32 0 "           0      0 16 16 "
0 0 0 32
1 1 "93U (2X4 2)            "       50      152 20 12 "
"        0 20 12 "           0      0 20 12 "           0      0 20 12 "
0 0 20 12
1 1 "MWF ROCKY 74/8          "       49      153 20 12 "
"        0 20 12 "           0      0 20 12 "           0      0 20 12 "
0 0 20 12
1 1 "BALDWIN TAG 185          "       48      154 32 0 "
"        0 32 0 "           0      0 32 0 "           0      0 32 0 "
0 0 32 0
1 1 "G D A R RAINMAKER 340    "       47      155 32 0 "
"        0 32 0 "           0      0 32 0 "           0      0 32 0 "
0 0 32 0
1 1 "WR SUVAL14               "       46      156 0 32 "
"        299021 66 0 32 "         0      0 0 32 "           0      0 0 32 "
0 0 0 32

```

1	1	"TTT MR. S. SUVA69			45	157	0	32 "		0	0	0	32 "
"		299021	66	0 32 "									
0		0 0 32		"	0	0	0	32 "					"
1	1	"SUGARLAND'S ESTO	53 11/5	"	44	158	0	32 "		0	0	0	32 "
"		0	0 32 "										"
0		0 0 32		"	0	0	0	32 "					"
1	1	"JDH CREIGHTON MANSO	321/5	"	43	159	0	32 "		0	0	0	32 "
"		0	0 32 "										"
0		0 0 32		"	0	0	0	32 "					"
1	1	"IW'S REXCRATA278		"	42	160	0	32 "		0	0	0	32 "
"		0	0 32 "										"
0		0 0 32		"	0	0	0	32 "					"
1	1	"D N R SHORTCUT		"	41	161	8	24 "		0	0	16	16 "
"		0	0 32 "										"
0		0 0 32		"	0	0	32	0 "					"
1	1	"MR CLAYDESTA801P2-803T11		"	40	162	8	24 "		0	0	16	16 "
"		0	0 32 "										"
0		0 0 32		"	0	0	32	0 "					"
1	1	"WB MR WRANGLER 819X4		"	39	163	16	16 "		0	0	0	32 "
"		0	0 32 0 "										"
0		0 0 32		"	0	0	0	32 "					"
1	1	"WB MR. HOSS 801X2		"	38	164	24	8 "		0	0	16	16 "
"		0	0 32 0 "										"
0		0 32 0		"	0	0	0	32 "					"

## **INPUT FILE 6 = data file (*LCSET*)**

**Example of growth data records from the Angus-Brahman Multibreed Herd of the University of Florida (boldfaced every other record for clarity)**

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## DESCRIPTION OF OUTPUT FILES

### OUTPUT FILE 1 = general output file (*MBEOUT*)

Contains:

- 1) A transcript of the input parameters, structure of pedigree and data files, and memory requirements,
- 2) Follow up indicators of the status of the MREMLM at various points during the GEM iterations: subroutine calls, specific parameter values, changes in covariance estimates, scoring and GEM convergence values.
- 3) Estimates of intrabreed and interbreed additive genetic, nonadditive genetic, and environmental covariances, and convergence values at every GEM iteration.
- 4) Estimates of multibreed additive and nonadditive genetic, environmental, and phenotypic covariances at convergence.
- 5) Estimates of multibreed additive (heritabilities) and nonadditive (interactibilities) genetic ratios, additive and nonadditive genetic correlations, environmental correlations, and phenotypic correlations at GEM convergence.
- 6) Multibreed additive, nonadditive, and total genetic predictions for all animals in the model, or multibreed additive, intralocus intrabreed and interbreed nonadditive, and total genetic predictions for all animals, after GEM convergence.

### File MBEOUT: Estimates of Covariances and Genetic Parameters.

```
=====
(mremlem_covest2b) [Add,Nad,Env] Covariance Estimates, set 1 MREMLM iter 0
=====

(addwg2b) additive genetic weights of the 5 BASE breed group combinations
bgi bgs bgd      breed 11      breed 22      breed 12
 1   1   1      0.00000000      1.00000000      0.00000000
 2   1   3      0.25000000      0.75000000      0.25000000
 3   1   5      0.50000000      0.50000000      0.00000000
 4   5   3      0.75000000      0.25000000      0.25000000
 5   5   5      1.00000000      0.00000000      0.00000000

(addwg2b) additive genetic weights for the combination of 5 BASE breed group combinations
bgi bgs bgd      breed 11      breed 22      breed 12
 1   1   1      0.00000000      1.00000000      0.00000000
 2   1   2      0.12500000      0.87500000      0.18750000
 3   1   3      0.25000000      0.75000000      0.25000000
 4   1   4      0.37500000      0.62500000      0.18750000
 5   1   5      0.50000000      0.50000000      0.00000000
 6   2   2      0.25000000      0.75000000      0.37500000
 7   2   3      0.37500000      0.62500000      0.43750000
 8   2   4      0.50000000      0.50000000      0.37500000
 9   2   5      0.62500000      0.37500000      0.18750000
10   3   3      0.50000000      0.50000000      0.50000000
11   3   4      0.62500000      0.37500000      0.43750000
12   3   5      0.75000000      0.25000000      0.25000000
13   4   4      0.75000000      0.25000000      0.37500000
14   4   5      0.87500000      0.12500000      0.18750000
15   5   5      1.00000000      0.00000000      0.00000000

(nadcovwg2b) nonadditive genetic weights used to construct multibreed
covariances for nbg2bcom mating combinations
i   j      nad 11      nad 12      nad 13
1   1   0.00000000   1.00000000   0.00000000
1   2   0.00000000   0.75000000   0.25000000
1   3   0.00000000   0.50000000   0.50000000
1   4   0.00000000   0.25000000   0.75000000
1   5   0.00000000   0.00000000   1.00000000
2   2   0.06250000   0.56250000   0.37500000
```

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2   3   0.12500000  0.37500000  0.50000000
2   4   0.18750000  0.18750000  0.62500000
2   5   0.25000000  0.00000000  0.75000000
3   3   0.25000000  0.25000000  0.50000000
3   4   0.37500000  0.12500000  0.50000000
3   5   0.50000000  0.00000000  0.50000000
4   4   0.56250000  0.06250000  0.37500000
4   5   0.75000000  0.00000000  0.25000000
5   5   1.00000000  0.00000000  0.00000000

(nadcovwg2bbasemat) nonadditive genetic weights used to construct
MATERNAL nonadditive covariances for nbg2b base breed group combinations
    i     j     nad 11      nad 12      nad 13
1   1   0.00000000  1.00000000  0.00000000
1   2   0.00000000  0.50000000  0.50000000
1   3   0.00000000  0.00000000  1.00000000
1   4   0.50000000  0.00000000  0.50000000
1   5   1.00000000  0.00000000  0.00000000
2   2   0.00000000  0.50000000  0.50000000
2   3   0.00000000  0.00000000  1.00000000
2   4   0.50000000  0.00000000  0.50000000
2   5   1.00000000  0.00000000  0.00000000
3   3   0.00000000  0.00000000  1.00000000
3   4   0.50000000  0.00000000  0.50000000
3   5   1.00000000  0.00000000  0.00000000
4   4   0.50000000  0.00000000  0.50000000
4   5   1.00000000  0.00000000  0.00000000
5   5   1.00000000  0.00000000  0.00000000

(gparemit2b) DIRECT NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
  1   1   1   0.0000  1.0000  0.0000  1.0000  0.0000  1.0000  0.0000
  2   1   2   0.0000  1.0000  0.2500  0.7500  0.0000  0.7500  0.2500
  3   1   3   0.0000  1.0000  0.5000  0.5000  0.0000  0.5000  0.5000
  4   1   4   0.0000  1.0000  0.7500  0.2500  0.0000  0.2500  0.7500
  5   1   5   0.0000  1.0000  1.0000  0.0000  0.0000  0.0000  1.0000
  6   2   2   0.2500  0.7500  0.2500  0.7500  0.0625  0.5625  0.3750
  7   2   3   0.2500  0.7500  0.5000  0.5000  0.1250  0.3750  0.5000
  8   2   4   0.2500  0.7500  0.7500  0.2500  0.1875  0.1875  0.6250
  9   2   5   0.2500  0.7500  1.0000  0.0000  0.2500  0.0000  0.7500
 10  3   3   0.5000  0.5000  0.5000  0.5000  0.2500  0.2500  0.5000
 11  3   4   0.5000  0.5000  0.7500  0.2500  0.3750  0.1250  0.5000
 12  3   5   0.5000  0.5000  1.0000  0.0000  0.5000  0.0000  0.5000
 13  4   4   0.7500  0.2500  0.7500  0.2500  0.5625  0.0625  0.3750
 14  4   5   0.7500  0.2500  1.0000  0.0000  0.7500  0.0000  0.2500
 15  5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000

(gparemit2b) MATERNAL NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd bgmgs bgmgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
  1   1   1   1   1   0.0000  1.0000  0.0000  1.0000  0.0000  1.0000  0.0000
  2   1   2   1   3   0.0000  1.0000  0.5000  0.5000  0.0000  0.5000  0.5000
  3   1   3   1   5   0.0000  1.0000  1.0000  0.0000  0.0000  0.0000  1.0000
  4   1   4   3   5   0.5000  0.5000  1.0000  0.0000  0.5000  0.0000  0.5000
  5   1   5   5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000
  6   2   2   1   3   0.0000  1.0000  0.5000  0.5000  0.0000  0.5000  0.5000
  7   2   3   1   5   0.0000  1.0000  1.0000  0.0000  0.0000  0.0000  1.0000
  8   2   4   3   5   0.5000  0.5000  1.0000  0.0000  0.5000  0.0000  0.5000
  9   2   5   5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000
 10  3   3   1   5   0.0000  1.0000  1.0000  0.0000  0.0000  0.0000  1.0000
 11  3   4   3   5   0.5000  0.5000  1.0000  0.0000  0.5000  0.0000  0.5000
 12  3   5   5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000
 13  4   4   3   5   0.5000  0.5000  1.0000  0.0000  0.5000  0.0000  0.5000
 14  4   5   5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000
 15  5   5   5   5   1.0000  0.0000  1.0000  0.0000  1.0000  0.0000  0.0000

=====
Parameter Estimates for set      1 MREMLEM iter      0
=====

=====
Additive Genetic Covariances for set      1 MREMLEM iter      0
=====

breed group combination 1 100B 00A x 100B 00A
  5.6460   1.6370  -0.2570   1.7750
  1.6370   67.5470   0.8530  -0.5750
  -0.2570   0.8530   6.2370   2.9480
   1.7750  -0.5750   2.9480  156.7180

breed group combination 2 100B 00A x 75B 25A

```

6.4451	2.9212	-0.2795	1.2891
2.9212	91.2669	1.1449	1.1546
-0.2795	1.1449	6.5790	2.5557
1.2891	1.1546	2.5557	149.0311
breed group combination	3 100B	00A x 50B	50A
6.7052	3.2985	-0.3068	0.9727
3.2985	98.4187	1.1970	0.6683
-0.3068	1.1970	6.6702	2.2060
0.9727	0.6683	2.2060	137.3628
breed group combination	4 100B	00A x 25B	75A
6.4266	2.7687	-0.3388	0.8259
2.7687	89.0026	1.0092	-2.0339
-0.3388	1.0092	6.5108	1.8987
0.8259	-2.0339	1.8987	121.7131
breed group combination	5 100B	00A x 00B	100A
5.6090	1.3320	-0.3755	0.8485
1.3320	63.0185	0.5815	-6.9520
-0.3755	0.5815	6.1005	1.6340
0.8485	-6.9520	1.6340	102.0820
breed group combination	6 75B	25A x 7B	25A
7.2441	4.2055	-0.3020	0.8032
4.2055	114.9868	1.4369	2.8841
-0.3020	1.4369	6.9210	2.1635
0.8032	2.8841	2.1635	141.3441
breed group combination	7 75B	25A x 50B	50A
7.5043	4.5827	-0.3293	0.4869
4.5827	122.1386	1.4889	2.3978
-0.3293	1.4889	7.0123	1.8137
0.4869	2.3978	1.8137	129.6758
breed group combination	8 75B	25A x 25B	75A
7.2256	4.0530	-0.3613	0.3400
4.0530	112.7225	1.3011	-0.3044
-0.3613	1.3011	6.8528	1.5065
0.3400	-0.3044	1.5065	114.0261
breed group combination	9 75B	25A x 00B	100A
6.4081	2.6162	-0.3980	0.3626
2.6162	86.7384	0.8734	-5.2224
-0.3980	0.8734	6.4425	1.2417
0.3626	-5.2224	1.2417	94.3951
breed group combination	10 50B	50A x 50B	50A
7.7645	4.9600	-0.3565	0.1705
4.9600	129.2905	1.5410	1.9115
-0.3565	1.5410	7.1035	1.4640
0.1705	1.9115	1.4640	118.0075
breed group combination	11 50B	50A x 25B	75A
7.4858	4.4303	-0.3885	0.0236
4.4303	119.8744	1.3532	-0.7907
-0.3885	1.3532	6.9440	1.1567
0.0236	-0.7907	1.1567	102.3578
breed group combination	12 50B	50A x 00B	100A
6.6683	2.9935	-0.4252	0.0462
2.9935	93.8903	0.9255	-5.7088
-0.4252	0.9255	6.5338	0.8920
0.0462	-5.7088	0.8920	82.7267
breed group combination	13 25B	75A x 25B	75A
7.2071	3.9005	-0.4205	-0.1233
3.9005	110.4583	1.1654	-3.4929
-0.4205	1.1654	6.7845	0.8495
-0.1233	-3.4929	0.8495	86.7081
breed group combination	14 25B	75A x 00B	100A
6.3896	2.4638	-0.4573	-0.1006
2.4638	84.4741	0.7377	-8.4109
-0.4573	0.7377	6.3743	0.5848
-0.1006	-8.4109	0.5848	67.0771
breed group combination	15 00B	100A x 00B	100A
5.5720	1.0270	-0.4940	-0.0780
1.0270	58.4900	0.3100	-13.3290
-0.4940	0.3100	5.9640	0.3200
-0.0780	-13.3290	0.3200	47.4460
<hr/>			
Nonadditive Genetic Covariances for set 1 MREMELM iter 0			
<hr/>			
breed group combination	1 100B	00A x 100B	00A
5.7580	1.1560	0.3460	0.1540
1.1560	83.6710	0.1260	2.4620
0.3460	0.1260	5.6190	0.5490
0.1540	2.4620	0.5490	53.6420

breed group combination 2 100B 00A x 75B 25A						
5.6558	1.2080	0.2945	0.2690			
1.2080	79.0263	0.2960	8.5275			
0.2945	0.2960	5.6188	0.7460			
0.2690	8.5275	0.7460	61.2388			
breed group combination 3 100B 00A x 50B 50A						
5.5535	1.2600	0.2430	0.3840			
1.2600	74.3815	0.4660	14.5930			
0.2430	0.4660	5.6185	0.9430			
0.3840	14.5930	0.9430	68.8355			
breed group combination 4 100B 00A x 25B 75A						
5.4512	1.3120	0.1915	0.4990			
1.3120	69.7368	0.6360	20.6585			
0.1915	0.6360	5.6182	1.1400			
0.4990	20.6585	1.1400	76.4322			
breed group combination 5 100B 00A x 00B 100A						
5.3490	1.3640	0.1400	0.6140			
1.3640	65.0920	0.8060	26.7240			
0.1400	0.8060	5.6180	1.3370			
0.6140	26.7240	1.3370	84.0290			
breed group combination 6 75B 25A x 7B 25A						
5.6168	1.2151	0.2592	0.3421			
1.2151	76.6056	0.4145	13.1836			
0.2592	0.4145	5.6626	0.8586			
0.3421	13.1836	0.8586	65.7729			
breed group combination 7 75B 25A x 50B 50A						
5.5779	1.2223	0.2240	0.4151			
1.2223	74.1850	0.5330	17.8396			
0.2240	0.5330	5.7065	0.9712			
0.4151	17.8396	0.9712	70.3070			
breed group combination 8 75B 25A x 25B 75A						
5.5389	1.2294	0.1888	0.4882			
1.2294	71.7644	0.6515	22.4957			
0.1888	0.6515	5.7504	1.0839			
0.4882	22.4957	1.0839	74.8411			
breed group combination 9 75B 25A x 00B 100A						
5.5000	1.2365	0.1535	0.5613			
1.2365	69.3438	0.7700	27.1517			
0.1535	0.7700	5.7942	1.1965			
0.5613	27.1517	1.1965	79.3752			
breed group combination 10 50B 50A x 50B 50A						
5.6022	1.1845	0.2050	0.4463			
1.1845	73.9885	0.6000	21.0862			
0.2050	0.6000	5.7945	0.9995			
0.4463	21.0862	0.9995	71.7785			
breed group combination 11 50B 50A x 25B 75A						
5.6266	1.1467	0.1860	0.4774			
1.1467	73.7920	0.6670	24.3329			
0.1860	0.6670	5.8825	1.0277			
0.4774	24.3329	1.0277	73.2500			
breed group combination 12 50B 50A x 00B 100A						
5.6510	1.1090	0.1670	0.5085			
1.1090	73.5955	0.7340	27.5795			
0.1670	0.7340	5.9705	1.0560			
0.5085	27.5795	1.0560	74.7215			
breed group combination 13 25B 75A x 25B 75A						
5.7143	1.0641	0.1833	0.4666			
1.0641	75.8196	0.6825	26.1701			
0.1833	0.6825	6.0146	0.9716			
0.4666	26.1701	0.9716	71.6589			
breed group combination 14 25B 75A x 00B 100A						
5.8020	0.9815	0.1805	0.4557			
0.9815	77.8473	0.6980	28.0072			
0.1805	0.6980	6.1468	0.9155			
0.4557	28.0072	0.9155	70.0678			
breed group combination 15 00B 100A x 00B 100A						
5.9530	0.8540	0.1940	0.4030			
0.8540	82.0990	0.6620	28.4350			
0.1940	0.6620	6.3230	0.7750			
0.4030	28.4350	0.7750	65.4140			

```
=====
Environmental Covariances for set 1 MREMLEM iter 0
=====
breed group combination 1 100B 00A x 100B 00A
13.5970 37.2540
37.2540 298.1820
breed group combination 2 100B 00A x 75B 25A
```

16.5570	40.3515				
40.3515	357.3839				
breed group combination	3 100B 00A x 50B 50A				
17.4230	40.8882				
40.8882	383.8590				
breed group combination	4 100B 00A x 25B 75A				
16.1950	38.8642				
38.8642	377.6074				
breed group combination	5 100B 00A x 00B 100A				
12.8730	34.2795				
34.2795	338.6290				
breed group combination	6 75B 25A x 7B 25A				
19.5170	43.4490				
43.4490	416.5858				
breed group combination	7 75B 25A x 50B 50A				
20.3830	43.9857				
43.9857	443.0609				
breed group combination	8 75B 25A x 25B 75A				
19.1550	41.9617				
41.9617	436.8093				
breed group combination	9 75B 25A x 00B 100A				
15.8330	37.3770				
37.3770	397.8309				
breed group combination	10 50B 50A x 50B 50A				
21.2490	44.5225				
44.5225	469.5360				
breed group combination	11 50B 50A x 25B 75A				
20.0210	42.4985				
42.4985	463.2844				
breed group combination	12 50B 50A x 00B 100A				
16.6990	37.9137				
37.9137	424.3060				
breed group combination	13 25B 75A x 25B 75A				
18.7930	40.4745				
40.4745	457.0328				
breed group combination	14 25B 75A x 00B 100A				
15.4710	35.8897				
35.8897	418.0544				
breed group combination	15 00B 100A x 00B 100A				
12.1490	31.3050				
31.3050	379.0760				
<hr/>					
Phenotypic Covariances for set 1 MREMLM iter 0					
<hr/>					
breed group combination	1 100B 00A x 100B 00A				
36.6000	46.1720				
46.1720	659.1850				
breed group combination	2 100B 00A x 75B 25A				
40.5761	50.2166				
50.2166	739.1014				
breed group combination	3 100B 00A x 50B 50A				
41.6637	50.7655				
50.7655	763.5258				
breed group combination	4 100B 00A x 25B 75A				
39.8631	47.8188				
47.8188	732.4581				
breed group combination	5 100B 00A x 00B 100A				
35.1740	41.3765				
41.3765	645.8985				
breed group combination	6 75B 25A x 7B 25A				
44.6596	54.1319				
54.1319	818.1793				
breed group combination	7 75B 25A x 50B 50A				
45.8547	54.5516				
54.5516	841.7651				
breed group combination	8 75B 25A x 25B 75A				
44.1614	51.4756				
51.4756	809.8590				
breed group combination	9 75B 25A x 00B 100A				
39.5798	44.9041				
44.9041	722.4609				
breed group combination	10 50B 50A x 50B 50A				
47.1573	54.8420				
54.8420	864.5125				
breed group combination	11 50B 50A x 25B 75A				
45.5714	51.6368				
51.6368	831.7679				

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breed group combination 12    50B   50A   x   00B   100A
  41.0972      44.9360
  44.9360      743.5312
breed group combination 13    25B   75A   x   25B   75A
  44.0931      48.3024
  48.3024      798.1848
breed group combination 14    25B   75A   x   00B   100A
  39.7263      41.4723
  41.4723      709.1096
breed group combination 15    00B   100A  x   00B   100A
  35.4670      34.5130
  34.5130      619.1960

=====
Heritabilities and Additive Genetic Correlations for set      1 MREMLEM iter      0
=====
breed group combination 1    100B   00A   x   100B   00A
  0.15      0.08      -0.04      0.06
  0.08      0.10      0.04      -0.01
  -0.04     0.04      0.17      0.09
  0.06     -0.01     0.09      0.24
breed group combination 2    100B   00A   x   75B   25A
  0.16      0.12      -0.04      0.04
  0.12      0.12      0.05      0.01
  -0.04     0.05      0.16      0.08
  0.04     0.01      0.08      0.20
breed group combination 3    100B   00A   x   50B   50A
  0.16      0.13      -0.05      0.03
  0.13      0.13      0.05      0.01
  -0.05     0.05      0.16      0.07
  0.03     0.01      0.07      0.18
breed group combination 4    100B   00A   x   25B   75A
  0.16      0.12      -0.05      0.03
  0.12      0.12      0.04      -0.02
  -0.05     0.04      0.16      0.07
  0.03     -0.02     0.07      0.17
breed group combination 5    100B   00A   x   00B   100A
  0.16      0.07      -0.06      0.04
  0.07      0.10      0.03      -0.09
  -0.06     0.03      0.17      0.07
  0.04     -0.09     0.07      0.16
breed group combination 6    75B   25A   x   7B    25A
  0.16      0.15      -0.04      0.03
  0.15      0.14      0.05      0.02
  -0.04     0.05      0.15      0.07
  0.03     0.02      0.07      0.17
breed group combination 7    75B   25A   x   50B   50A
  0.16      0.15      -0.05      0.02
  0.15      0.15      0.05      0.02
  -0.05     0.05      0.15      0.06
  0.02     0.02      0.06      0.15
breed group combination 8    75B   25A   x   25B   75A
  0.16      0.14      -0.05      0.01
  0.14      0.14      0.05      0.00
  -0.05     0.05      0.16      0.05
  0.01     0.00      0.05      0.14
breed group combination 9    75B   25A   x   00B   100A
  0.16      0.11      -0.06      0.01
  0.11      0.12      0.04      -0.06
  -0.06     0.04      0.16      0.05
  0.01     -0.06     0.05      0.13
breed group combination 10   50B   50A   x   50B   50A
  0.16      0.16      -0.05      0.01
  0.16      0.15      0.05      0.02
  -0.05     0.05      0.15      0.05
  0.01     0.02      0.05      0.14
breed group combination 11   50B   50A   x   25B   75A
  0.16      0.15      -0.05      0.00
  0.15      0.14      0.05      -0.01
  -0.05     0.05      0.15      0.04
  0.00     -0.01     0.04      0.12
breed group combination 12   50B   50A   x   00B   100A
  0.16      0.12      -0.06      0.00
  0.12      0.13      0.04      -0.06
  -0.06     0.04      0.16      0.04
  0.00     -0.06     0.04      0.11
breed group combination 13   25B   75A   x   25B   75A
  0.16      0.14      -0.06      0.00

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```

 0.14    0.14    0.04   -0.04
 -0.06    0.04    0.15    0.04
  0.00   -0.04    0.04    0.11
breed group combination 14  25B   75A   x   00B   100A
  0.16    0.11   -0.07    0.00
  0.11    0.12    0.03   -0.11
 -0.07    0.03    0.16    0.03
  0.00   -0.11    0.03    0.09
breed group combination 15  00B   100A   x   00B   100A
  0.16    0.06   -0.09    0.00
  0.06    0.09    0.02   -0.25
 -0.09    0.02    0.17    0.02
  0.00   -0.25    0.02    0.08

=====
Interactibilities and Nonadditive Genetic Correlations for set      1 MREMLM iter   0
=====
breed group combination 1  100B   00A   x  100B   00A
  0.16    0.05    0.06    0.01
  0.05    0.13    0.01    0.04
  0.06    0.01    0.15    0.03
  0.01    0.04    0.03    0.08
breed group combination 2  100B   00A   x   75B   25A
  0.14    0.06    0.05    0.01
  0.06    0.11    0.01    0.12
  0.05    0.01    0.14    0.04
  0.01    0.12    0.04    0.08
breed group combination 3  100B   00A   x   50B   50A
  0.13    0.06    0.04    0.02
  0.06    0.10    0.02    0.20
  0.04    0.02    0.13    0.05
  0.02    0.20    0.05    0.09
breed group combination 4  100B   00A   x   25B   75A
  0.14    0.07    0.03    0.02
  0.07    0.10    0.03    0.28
  0.03    0.03    0.14    0.06
  0.02    0.28    0.06    0.10
breed group combination 5  100B   00A   x   00B   100A
  0.15    0.07    0.03    0.03
  0.07    0.10    0.04    0.36
  0.03    0.04    0.16    0.06
  0.03    0.36    0.06    0.13
breed group combination 6  75B   25A   x   7B    25A
  0.13    0.06    0.05    0.02
  0.06    0.09    0.02    0.19
  0.05    0.02    0.13    0.04
  0.02    0.19    0.04    0.08
breed group combination 7  75B   25A   x   50B   50A
  0.12    0.06    0.04    0.02
  0.06    0.09    0.03    0.25
  0.04    0.03    0.12    0.05
  0.02    0.25    0.05    0.08
breed group combination 8  75B   25A   x   25B   75A
  0.13    0.06    0.03    0.02
  0.06    0.09    0.03    0.31
  0.03    0.03    0.13    0.05
  0.02    0.31    0.05    0.09
breed group combination 9  75B   25A   x   00B   100A
  0.14    0.06    0.03    0.03
  0.06    0.10    0.04    0.37
  0.03    0.04    0.15    0.06
  0.03    0.37    0.06    0.11
breed group combination 10  50B   50A   x   50B   50A
  0.12    0.06    0.04    0.02
  0.06    0.09    0.03    0.29
  0.04    0.03    0.12    0.05
  0.02    0.29    0.05    0.08
breed group combination 11  50B   50A   x   25B   75A
  0.12    0.06    0.03    0.02
  0.06    0.09    0.03    0.33
  0.03    0.03    0.13    0.05
  0.02    0.33    0.05    0.09
breed group combination 12  50B   50A   x   00B   100A
  0.14    0.05    0.03    0.02
  0.05    0.10    0.04    0.37
  0.03    0.04    0.15    0.05
  0.02    0.37    0.05    0.10
breed group combination 13  25B   75A   x   25B   75A

```

```

0.13    0.05    0.03    0.02
0.05    0.09    0.03    0.36
0.03    0.03    0.14    0.05
0.02    0.36    0.05    0.09
breed group combination 14    25B    75A    x    00B    100A
0.15    0.05    0.03    0.02
0.05    0.11    0.03    0.38
0.03    0.03    0.15    0.04
0.02    0.38    0.04    0.10
breed group combination 15    00B    100A    x    00B    100A
0.17    0.04    0.03    0.02
0.04    0.13    0.03    0.39
0.03    0.03    0.18    0.04
0.02    0.39    0.04    0.11

=====
Environmental Correlations for set      1 MREML EM iter      0
=====
breed group combination 1    100B    00A    x    100B    00A
1.00    0.59
0.59    1.00
breed group combination 2    100B    00A    x    75B    25A
1.00    0.52
0.52    1.00
breed group combination 3    100B    00A    x    50B    50A
1.00    0.50
0.50    1.00
breed group combination 4    100B    00A    x    25B    75A
1.00    0.50
0.50    1.00
breed group combination 5    100B    00A    x    00B    100A
1.00    0.52
0.52    1.00
breed group combination 6    75B    25A    x    7B    25A
1.00    0.48
0.48    1.00
breed group combination 7    75B    25A    x    50B    50A
1.00    0.46
0.46    1.00
breed group combination 8    75B    25A    x    25B    75A
1.00    0.46
0.46    1.00
breed group combination 9    75B    25A    x    00B    100A
1.00    0.47
0.47    1.00
breed group combination 10   50B    50A    x    50B    50A
1.00    0.45
0.45    1.00
breed group combination 11   50B    50A    x    25B    75A
1.00    0.44
0.44    1.00
breed group combination 12   50B    50A    x    00B    100A
1.00    0.45
0.45    1.00
breed group combination 13   25B    75A    x    25B    75A
1.00    0.44
0.44    1.00
breed group combination 14   25B    75A    x    00B    100A
1.00    0.45
0.45    1.00
breed group combination 15   00B    100A    x    00B    100A
1.00    0.46
0.46    1.00

=====
Phenotypic Correlations for set      1 MREML EM iter      0
=====
breed group combination 1    100B    00A    x    100B    00A
1.00    0.30
0.30    1.00
breed group combination 2    100B    00A    x    75B    25A
1.00    0.29
0.29    1.00
breed group combination 3    100B    00A    x    50B    50A
1.00    0.28
0.28    1.00
breed group combination 4    100B    00A    x    25B    75A
1.00    0.28

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0.28      1.00
breed group combination 5   100B    00A   x   00B   100A
  1.00      0.27
  0.27      1.00
breed group combination 6   75B     25A   x   7B    25A
  1.00      0.28
  0.28      1.00
breed group combination 7   75B     25A   x   50B   50A
  1.00      0.28
  0.28      1.00
breed group combination 8   75B     25A   x   25B   75A
  1.00      0.27
  0.27      1.00
breed group combination 9   75B     25A   x   00B   100A
  1.00      0.27
  0.27      1.00
breed group combination 10  50B     50A   x   50B   50A
  1.00      0.27
  0.27      1.00
breed group combination 11  50B     50A   x   25B   75A
  1.00      0.27
  0.27      1.00
breed group combination 12  50B     50A   x   00B   100A
  1.00      0.26
  0.26      1.00
breed group combination 13  25B     75A   x   25B   75A
  1.00      0.26
  0.26      1.00
breed group combination 14  25B     75A   x   00B   100A
  1.00      0.25
  0.25      1.00
breed group combination 15  00B   100A   x   00B   100A
  1.00      0.23
  0.23      1.00
=====
(mremlem_covest2b) [Add,Nad,Env] Covariance Estimates, set 1 MREMLEM iter 0
=====

(addwg2b) additive genetic weights of the 5 BASE breed group combinations
bgi bgs bgd      breed 11      breed 22      breed 12
  1   1   1   0.00000000   1.00000000   0.00000000
  2   1   3   0.25000000   0.75000000   0.25000000
  3   1   5   0.50000000   0.50000000   0.00000000
  4   5   3   0.75000000   0.25000000   0.25000000
  5   5   5   1.00000000   0.00000000   0.00000000

(addwg2b) additive genetic weights for the combination of 5 BASE breed group combinations
bgi bgs bgd      breed 11      breed 22      breed 12
  1   1   1   0.00000000   1.00000000   0.00000000
  2   1   2   0.12500000   0.87500000   0.18750000
  3   1   3   0.25000000   0.75000000   0.25000000
  4   1   4   0.37500000   0.62500000   0.18750000
  5   1   5   0.50000000   0.50000000   0.00000000
  6   2   2   0.25000000   0.75000000   0.37500000
  7   2   3   0.37500000   0.62500000   0.43750000
  8   2   4   0.50000000   0.50000000   0.37500000
  9   2   5   0.62500000   0.37500000   0.18750000
 10  3   3   0.50000000   0.50000000   0.50000000
 11  3   4   0.62500000   0.37500000   0.43750000
 12  3   5   0.75000000   0.25000000   0.25000000
 13  4   4   0.75000000   0.25000000   0.37500000
 14  4   5   0.87500000   0.12500000   0.18750000
 15  5   5   1.00000000   0.00000000   0.00000000

(nadcovwg2b) nonadditive genetic weights used to construct multibreed
covariances for nbgb2bcom mating combinations
i   j      nad 11      nad 12      nad 13
1   1   0.00000000   1.00000000   0.00000000
1   2   0.00000000   0.75000000   0.25000000
1   3   0.00000000   0.50000000   0.50000000
1   4   0.00000000   0.25000000   0.75000000
1   5   0.00000000   0.00000000   1.00000000
2   2   0.06250000   0.56250000   0.37500000
2   3   0.12500000   0.37500000   0.50000000
2   4   0.18750000   0.18750000   0.62500000
2   5   0.25000000   0.00000000   0.75000000
3   3   0.25000000   0.25000000   0.50000000

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3   4  0.37500000  0.12500000  0.50000000
3   5  0.50000000  0.00000000  0.50000000
4   4  0.56250000  0.06250000  0.37500000
4   5  0.75000000  0.00000000  0.25000000
5   5  1.00000000  0.00000000  0.00000000

(nadcovwg2bbasemat) nonadditive genetic weights used to construct
MATERNAL nonadditive covariances for nbg2b base breed group combinations
    i      j      nad 11      nad 12      nad 13
1   1  0.00000000  1.00000000  0.00000000
1   2  0.00000000  0.50000000  0.50000000
1   3  0.00000000  0.00000000  1.00000000
1   4  0.50000000  0.00000000  0.50000000
1   5  1.00000000  0.00000000  0.00000000
2   2  0.00000000  0.50000000  0.50000000
2   3  0.00000000  0.00000000  1.00000000
2   4  0.50000000  0.00000000  0.50000000
2   5  1.00000000  0.00000000  0.00000000
3   3  0.00000000  0.00000000  1.00000000
3   4  0.50000000  0.00000000  0.50000000
3   5  1.00000000  0.00000000  0.00000000
4   4  0.50000000  0.00000000  0.50000000
4   5  1.00000000  0.00000000  0.00000000
5   5  1.00000000  0.00000000  0.00000000

=====
(mremlem_covestmb) [Add,Nad,Env] Covariance Estimates, set 1 MREMLEM iter 0
=====

(gparemmitmb) additive genetic weights for the combination of 5 breed groups
bgi bgs bgd      breed 11      breed 22      breed 12
 1   1   1  0.00000000  1.00000000  0.00000000
 2   1   2  0.12500000  0.87500000  0.18750000
 3   1   3  0.25000000  0.75000000  0.25000000
 4   1   4  0.37500000  0.62500000  0.18750000
 5   1   5  0.50000000  0.50000000  0.00000000
 6   2   2  0.25000000  0.75000000  0.37500000
 7   2   3  0.37500000  0.62500000  0.43750000
 8   2   4  0.50000000  0.50000000  0.37500000
 9   2   5  0.62500000  0.37500000  0.18750000
10   3   3  0.50000000  0.50000000  0.50000000
11   3   4  0.62500000  0.37500000  0.43750000
12   3   5  0.75000000  0.25000000  0.25000000
13   4   4  0.75000000  0.25000000  0.37500000
14   4   5  0.87500000  0.12500000  0.18750000
15   5   5  1.00000000  0.00000000  0.00000000

(nadcovwgmbdir) nonadditive genetic weights used to construct multibreed
covariances for nbgbcom mating combinations
    i      ii      jj      nad 11      nad 12      nad 13
1   1     1     1  0.00000000  1.00000000  0.00000000
2   1     1     3  0.00000000  0.75000000  0.25000000
3   1     1     5  0.00000000  0.50000000  0.50000000
4   1     1     12 0.00000000  0.25000000  0.75000000
5   1     1     15 0.00000000  0.00000000  1.00000000
6   3     3     3  0.06250000  0.56250000  0.37500000
7   3     3     5  0.12500000  0.37500000  0.50000000
8   3     3     12 0.18750000  0.18750000  0.62500000
9   3     3     15 0.25000000  0.00000000  0.75000000
10   5     5     5  0.25000000  0.25000000  0.50000000
11   5     5     12 0.37500000  0.12500000  0.50000000
12   5     5     15 0.50000000  0.00000000  0.50000000
13   12    12    12 0.56250000  0.06250000  0.37500000
14   12    12    15 0.75000000  0.00000000  0.25000000
15   15    15    15 1.00000000  0.00000000  0.00000000

(nadcovwgmbmat) nonadditive genetic weights used to construct MATERNAL
nonadditive covariances for nbgbcom mating combinations
    i      ii      jj      nad 11      nad 12      nad 13
1   1     1     1  0.00000000  1.00000000  0.00000000
2   1     1     5  0.00000000  0.50000000  0.50000000
3   1     1     15 0.00000000  0.00000000  1.00000000
4   5     5     15 0.50000000  0.00000000  0.50000000
5   15    15    15 1.00000000  0.00000000  0.00000000
6   1     5     5  0.00000000  0.50000000  0.50000000
7   1     15    15 0.00000000  0.00000000  1.00000000
8   5     15    15 0.50000000  0.00000000  0.50000000
9   15    15    15 1.00000000  0.00000000  0.00000000

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```

10   1  15   0.00000000  0.00000000  1.00000000
11   5  15   0.50000000  0.00000000  0.50000000
12  15  15   1.00000000  0.00000000  0.00000000
13   5  15   0.50000000  0.00000000  0.50000000
14  15  15   1.00000000  0.00000000  0.00000000
15  15  15   1.00000000  0.00000000  0.00000000

(gparemitmb) DIRECT NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
  1   1   1   0.0000   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000
  2   1   3   0.0000   1.0000   0.2500   0.7500   0.0000   0.7500   0.2500
  3   1   5   0.0000   1.0000   0.5000   0.5000   0.0000   0.5000   0.5000
  4   1   12   0.0000   1.0000   0.7500   0.2500   0.0000   0.2500   0.7500
  5   1   15   0.0000   1.0000   1.0000   0.0000   0.0000   0.0000   1.0000
  6   3   3   0.2500   0.7500   0.2500   0.7500   0.0625   0.5625   0.3750
  7   3   5   0.2500   0.7500   0.5000   0.5000   0.1250   0.3750   0.5000
  8   3   12   0.2500   0.7500   0.7500   0.2500   0.1875   0.1875   0.6250
  9   3   15   0.2500   0.7500   1.0000   0.0000   0.2500   0.0000   0.7500
10   5   5   0.5000   0.5000   0.5000   0.5000   0.2500   0.2500   0.5000
11   5   12   0.5000   0.5000   0.7500   0.2500   0.3750   0.1250   0.5000
12   5   15   0.5000   0.5000   1.0000   0.0000   0.5000   0.0000   0.5000
13  12  12   0.7500   0.2500   0.7500   0.2500   0.5625   0.0625   0.3750
14  12  15   0.7500   0.2500   1.0000   0.0000   0.7500   0.0000   0.2500
15  15  15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000

(gparemitmb) MATERNAL NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd bgmgs bgmgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
  1   1   1   1   1   0.0000   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000
  2   1   3   1   5   0.0000   1.0000   0.5000   0.5000   0.0000   0.0000   1.0000
  3   1   5   1   15   0.0000   1.0000   1.0000   0.0000   1.0000   0.0000   0.0000
  4   1   12   5   15   0.5000   0.5000   1.0000   0.0000   1.0000   0.0000   0.0000
  5   1   15   15   15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000
  6   3   3   1   5   0.0000   1.0000   0.5000   0.5000   0.0000   0.0000   1.0000
  7   3   5   1   15   0.0000   1.0000   1.0000   0.0000   1.0000   0.0000   0.0000
  8   3   12   5   15   0.5000   0.5000   1.0000   0.0000   1.0000   0.0000   0.0000
  9   3   15   15   15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000
10   5   5   1   15   0.0000   1.0000   1.0000   0.0000   1.0000   0.0000   0.0000
11   5   12   5   15   0.5000   0.5000   1.0000   0.0000   1.0000   0.0000   0.0000
12   5   15   15   15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000
13  12  12   5   15   0.5000   0.5000   1.0000   0.0000   1.0000   0.0000   0.0000
14  12  15   15   15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000
15  15  15   15   15   1.0000   0.0000   1.0000   0.0000   1.0000   0.0000   0.0000

=====
Parameter Estimates for set      1 MREMLEM iter      0
=====

=====
Additive Genetic Covariances for set      1 MREMLEM iter      0
=====

CALF BG   1   0A  100B SIRE BG   1   0A  100B DAM BG   1   0A  100B
          MGS BG   1   0A  100B MGD BG   1   0A  100B
  5.6460   1.6370   -0.2570   1.7750
  1.6370   67.5470   0.8530   -0.5750
 -0.2570   0.8530   6.2370   2.9480
  1.7750   -0.5750   2.9480   156.7180
CALF BG   2   13A  88B SIRE BG   1   0A  100B DAM BG   3   25A   75B
          MGS BG   1   0A  100B MGD BG   5   50A   50B
  6.4451   2.9212   -0.2795   1.2891
  2.9212   91.2669   1.1449   1.1546
 -0.2795   1.1449   6.5790   2.5557
  1.2891   1.1546   2.5557   149.0311
CALF BG   3   25A   75B SIRE BG   1   0A  100B DAM BG   5   50A   50B
          MGS BG   1   0A  100B MGD BG  15  100A   0B
  6.7052   3.2985   -0.3068   0.9727
  3.2985   98.4187   1.1970   0.6683
 -0.3068   1.1970   6.6702   2.2060
  0.9727   0.6683   2.2060   137.3628
CALF BG   4   38A   63B SIRE BG   1   0A  100B DAM BG   12   75A   25B
          MGS BG   5   50A   50B MGD BG  15  100A   0B
  6.4266   2.7687   -0.3388   0.8259
  2.7687   89.0026   1.0092   -2.0339
 -0.3388   1.0092   6.5108   1.8987
  0.8259   -2.0339   1.8987   121.7131
CALF BG   5   50A   50B SIRE BG   1   0A  100B DAM BG   15  100A   0B
          MGS BG  15  100A   0B MGD BG  15  100A   0B
  5.6090   1.3320   -0.3755   0.8485
  1.3320   63.0185   0.5815   -6.9520

```

```

=====
Nonadditive Genetic Covariances for set      1 MREMLEM iter   0
=====
=====
```

CALF	BG	1	OA	100B	SIRE	BG	1	OA	100B	DAM	BG	1	OA	100B
					MGS	BG	1	OA	100B	MGD	BG	1	OA	100B
5.7580			1.1560		0.3460			0.1540						
1.1560			83.6710		0.1260			2.4620						
0.3460			0.1260		5.6190			0.5490						
0.1540			2.4620		0.5490			53.6420						
CALF	BG	2	13A	88B	SIRE	BG	1	OA	100B	DAM	BG	3	25A	75B
					MGS	BG	1	OA	100B	MGD	BG	5	50A	50B
5.6558			1.2080		0.2945			0.2690						
1.2080			79.0263		0.2960			8.5275						
0.2945			0.2960		5.6188			0.7460						
0.2690			8.5275		0.7460			61.2388						

CALF	BG	3	25A	75B	SIRE	BG	1	0A	100B	DAM	BG	5	50A	50B
					MGS	BG	1	0A	100B	MGD	BG	15	100A	0B
5.5535			1.2600		0.2430			0.3840						
1.2600			74.3815		0.4660			14.5930						
0.2430			0.4660		5.6185			0.9430						
0.3840			14.5930		0.9430			68.8355						
CALF	BG	4	38A	63B	SIRE	BG	1	0A	100B	DAM	BG	12	75A	25B
					MGS	BG	5	50A	50B	MGD	BG	15	100A	0B
5.4512			1.3120		0.1915			0.4990						
1.3120			69.7368		0.6360			20.6585						
0.1915			0.6360		5.6182			1.1400						
0.4990			20.6585		1.1400			76.4322						
CALF	BG	5	50A	50B	SIRE	BG	1	0A	100B	DAM	BG	15	100A	0B
					MGS	BG	15	100A	0B	MGD	BG	15	100A	0B
5.3490			1.3640		0.1400			0.6140						
1.3640			65.0920		0.8060			26.7240						
0.1400			0.8060		5.6180			1.3370						
0.6140			26.7240		1.3370			84.0290						
CALF	BG	6	25A	75B	SIRE	BG	3	25A	75B	DAM	BG	3	25A	75B
					MGS	BG	1	0A	100B	MGD	BG	5	50A	50B
5.6168			1.2151		0.2592			0.3421						
1.2151			76.6056		0.4145			13.1836						
0.2592			0.4145		5.6626			0.8586						
0.3421			13.1836		0.8586			65.7729						
CALF	BG	7	38A	63B	SIRE	BG	3	25A	75B	DAM	BG	5	50A	50B
					MGS	BG	1	0A	100B	MGD	BG	15	100A	0B
5.5779			1.2223		0.2240			0.4151						
1.2223			74.1850		0.5330			17.8396						
0.2240			0.5330		5.7065			0.9712						
0.4151			17.8396		0.9712			70.3070						
CALF	BG	8	50A	50B	SIRE	BG	3	25A	75B	DAM	BG	12	75A	25B
					MGS	BG	5	50A	50B	MGD	BG	15	100A	0B
5.5389			1.2294		0.1888			0.4882						
1.2294			71.7644		0.6515			22.4957						
0.1888			0.6515		5.7504			1.0839						
0.4882			22.4957		1.0839			74.8411						
CALF	BG	9	63A	38B	SIRE	BG	3	25A	75B	DAM	BG	15	100A	0B
					MGS	BG	15	100A	0B	MGD	BG	15	100A	0B
5.5000			1.2365		0.1535			0.5613						
1.2365			69.3438		0.7700			27.1517						
0.1535			0.7700		5.7942			1.1965						
0.5613			27.1517		1.1965			79.3752						
CALF	BG	10	50A	50B	SIRE	BG	5	50A	50B	DAM	BG	5	50A	50B
					MGS	BG	1	0A	100B	MGD	BG	15	100A	0B
5.6022			1.1845		0.2050			0.4463						
1.1845			73.9885		0.6000			21.0862						
0.2050			0.6000		5.7945			0.9995						
0.4463			21.0862		0.9995			71.7785						
CALF	BG	11	63A	38B	SIRE	BG	5	50A	50B	DAM	BG	12	75A	25B
					MGS	BG	5	50A	50B	MGD	BG	15	100A	0B
5.6266			1.1467		0.1860			0.4774						
1.1467			73.7920		0.6670			24.3329						
0.1860			0.6670		5.8825			1.0277						
0.4774			24.3329		1.0277			73.2500						
CALF	BG	12	75A	25B	SIRE	BG	5	50A	50B	DAM	BG	15	100A	0B
					MGS	BG	15	100A	0B	MGD	BG	15	100A	0B
5.6510			1.1090		0.1670			0.5085						
1.1090			73.5955		0.7340			27.5795						
0.1670			0.7340		5.9705			1.0560						
0.5085			27.5795		1.0560			74.7215						
CALF	BG	13	75A	25B	SIRE	BG	12	75A	25B	DAM	BG	12	75A	25B
					MGS	BG	5	50A	50B	MGD	BG	15	100A	0B
5.7143			1.0641		0.1833			0.4666						
1.0641			75.8196		0.6825			26.1701						
0.1833			0.6825		6.0146			0.9716						
0.4666			26.1701		0.9716			71.6589						
CALF	BG	14	88A	13B	SIRE	BG	12	75A	25B	DAM	BG	15	100A	0B
					MGS	BG	15	100A	0B	MGD	BG	15	100A	0B
5.8020			0.9815		0.1805			0.4557						
0.9815			77.8473		0.6980			28.0072						
0.1805			0.6980		6.1468			0.9155						
0.4557			28.0072		0.9155			70.0678						
CALF	BG	15	100A	0B	SIRE	BG	15	100A	0B	DAM	BG	15	100A	0B
					MGS	BG	15	100A	0B	MGD	BG	15	100A	0B
5.9530			0.8540		0.1940			0.4030						
0.8540			82.0990		0.6620			28.4350						
0.1940			0.6620		6.3230			0.7750						
0.4030			28.4350		0.7750			65.4140						

```
=====
Environmental Covariances for set 1 MREMMLM iter 0
=====
CALF BG 1 0A 100B SIRE BG 1 0A 100B DAM BG 1 0A 100B
          MGS BG 1 0A 100B MGD BG 1 0A 100B
13.5970 37.2540
37.2540 298.1820
CALF BG 2 13A 88B SIRE BG 1 0A 100B DAM BG 3 25A 75B
          MGS BG 1 0A 100B MGD BG 5 50A 50B
16.5570 40.3515
40.3515 357.3839
CALF BG 3 25A 75B SIRE BG 1 0A 100B DAM BG 5 50A 50B
          MGS BG 1 0A 100B MGD BG 15 100A 0B
17.4230 40.8882
40.8882 383.8590
CALF BG 4 38A 63B SIRE BG 1 0A 100B DAM BG 12 75A 25B
          MGS BG 5 50A 50B MGD BG 15 100A 0B
16.1950 38.8642
38.8642 377.6074
CALF BG 5 50A 50B SIRE BG 1 0A 100B DAM BG 15 100A 0B
          MGS BG 15 100A 0B MGD BG 15 100A 0B
12.8730 34.2795
34.2795 338.6290
CALF BG 6 25A 75B SIRE BG 3 25A 75B DAM BG 3 25A 75B
          MGS BG 1 0A 100B MGD BG 5 50A 50B
19.5170 43.4490
43.4490 416.5858
CALF BG 7 38A 63B SIRE BG 3 25A 75B DAM BG 5 50A 50B
          MGS BG 1 0A 100B MGD BG 15 100A 0B
20.3830 43.9857
43.9857 443.0609
CALF BG 8 50A 50B SIRE BG 3 25A 75B DAM BG 12 75A 25B
          MGS BG 5 50A 50B MGD BG 15 100A 0B
19.1550 41.9617
41.9617 436.8093
CALF BG 9 63A 38B SIRE BG 3 25A 75B DAM BG 15 100A 0B
          MGS BG 15 100A 0B MGD BG 15 100A 0B
15.8330 37.3770
37.3770 397.8309
CALF BG 10 50A 50B SIRE BG 5 50A 50B DAM BG 5 50A 50B
          MGS BG 1 0A 100B MGD BG 15 100A 0B
21.2490 44.5225
44.5225 469.5360
CALF BG 11 63A 38B SIRE BG 5 50A 50B DAM BG 12 75A 25B
          MGS BG 5 50A 50B MGD BG 15 100A 0B
20.0210 42.4985
42.4985 463.2844
CALF BG 12 75A 25B SIRE BG 5 50A 50B DAM BG 15 100A 0B
          MGS BG 15 100A 0B MGD BG 15 100A 0B
16.6990 37.9137
37.9137 424.3060
CALF BG 13 75A 25B SIRE BG 12 75A 25B DAM BG 12 75A 25B
          MGS BG 5 50A 50B MGD BG 15 100A 0B
18.7930 40.4745
40.4745 457.0328
CALF BG 14 88A 13B SIRE BG 12 75A 25B DAM BG 15 100A 0B
          MGS BG 15 100A 0B MGD BG 15 100A 0B
15.4710 35.8897
35.8897 418.0544
CALF BG 15 100A 0B SIRE BG 15 100A 0B DAM BG 15 100A 0B
          MGS BG 15 100A 0B MGD BG 15 100A 0B
12.1490 31.3050
31.3050 379.0760
=====

Phenotypic Covariances for set 1 MREMMLM iter 0
=====
CALF BG 1 0A 100B SIRE BG 1 0A 100B DAM BG 1 0A 100B
          MGS BG 1 0A 100B MGD BG 1 0A 100B
36.6000 46.1720
46.1720 659.1850
CALF BG 2 13A 88B SIRE BG 1 0A 100B DAM BG 3 25A 75B
          MGS BG 1 0A 100B MGD BG 5 50A 50B
40.5761 50.2166
50.2166 739.1014
CALF BG 3 25A 75B SIRE BG 1 0A 100B DAM BG 5 50A 50B
          MGS BG 1 0A 100B MGD BG 15 100A 0B
41.6637 50.7655
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=====
Heritabilities and Additive Genetic Correlations for set 1 MREMLM iter 0
=====
CALF BG   1   OA  100B  SIRE BG   1   OA  100B  DAM BG   1   OA  100B
                           MGS BG   1   OA  100B  MGD BG   1   OA  100B
    0.15      0.08     -0.04      0.06
    0.08      0.10     0.04     -0.01
   -0.04      0.04     0.17      0.09
    0.06     -0.01     0.09      0.24
CALF BG   2   13A  88B  SIRE BG   1   OA  100B  DAM BG   3   25A  75B
                           MGS BG   1   OA  100B  MGD BG   5   50A  50B
    0.16      0.12     -0.04      0.04
    0.12      0.12     0.05      0.01
   -0.04      0.05     0.16      0.08
    0.04     0.01     0.08      0.20
CALF BG   3   25A  75B  SIRE BG   1   OA  100B  DAM BG   5   50A  50B
                           MGS BG   1   OA  100B  MGD BG  15   100A   OB
    0.16      0.13     -0.05      0.03
    0.13      0.13     0.05      0.01
   -0.05      0.05     0.16      0.07
    0.03     0.01     0.07      0.18
CALF BG   4   38A  63B  SIRE BG   1   OA  100B  DAM BG   12   75A  25B
                           MGS BG   5   50A   50B  MGD BG  15   100A   OB
    0.16      0.12     -0.05      0.03
    0.12      0.12     0.04     -0.02
   -0.05      0.04     0.16      0.07
    0.03     -0.02     0.07      0.17
CALF BG   5   50A  50B  SIRE BG   1   OA  100B  DAM BG   15   100A   OB

```



0.06	0.11	0.01	0.12
0.05	0.01	0.14	0.04
0.01	0.12	0.04	0.08
CALF BG	3 25A	75B SIRE BG	1 0A 100B DAM BG 5 50A 50B
		MGS BG 1 0A 100B MGD BG 15 100A 0B	
0.13	0.06	0.04	0.02
0.06	0.10	0.02	0.20
0.04	0.02	0.13	0.05
0.02	0.20	0.05	0.09
CALF BG	4 38A	63B SIRE BG	1 0A 100B DAM BG 12 75A 25B
		MGS BG 5 50A 50B MGD BG 15 100A 0B	
0.14	0.07	0.03	0.02
0.07	0.10	0.03	0.28
0.03	0.03	0.14	0.06
0.02	0.28	0.06	0.10
CALF BG	5 50A	50B SIRE BG	1 0A 100B DAM BG 15 100A 0B
		MGS BG 15 100A 0B MGD BG 15 100A 0B	
0.15	0.07	0.03	0.03
0.07	0.10	0.04	0.36
0.03	0.04	0.16	0.06
0.03	0.36	0.06	0.13
CALF BG	6 25A	75B SIRE BG	3 25A 75B DAM BG 3 25A 75B
		MGS BG 1 0A 100B MGD BG 5 50A 50B	
0.13	0.06	0.05	0.02
0.06	0.09	0.02	0.19
0.05	0.02	0.13	0.04
0.02	0.19	0.04	0.08
CALF BG	7 38A	63B SIRE BG	3 25A 75B DAM BG 5 50A 50B
		MGS BG 1 0A 100B MGD BG 15 100A 0B	
0.12	0.06	0.04	0.02
0.06	0.09	0.03	0.25
0.04	0.03	0.12	0.05
0.02	0.25	0.05	0.08
CALF BG	8 50A	50B SIRE BG	3 25A 75B DAM BG 12 75A 25B
		MGS BG 5 50A 50B MGD BG 15 100A 0B	
0.13	0.06	0.03	0.02
0.06	0.09	0.03	0.31
0.03	0.03	0.13	0.05
0.02	0.31	0.05	0.09
CALF BG	9 63A	38B SIRE BG	3 25A 75B DAM BG 15 100A 0B
		MGS BG 15 100A 0B MGD BG 15 100A 0B	
0.14	0.06	0.03	0.03
0.06	0.10	0.04	0.37
0.03	0.04	0.15	0.06
0.03	0.37	0.06	0.11
CALF BG	10 50A	50B SIRE BG	5 50A 50B DAM BG 5 50A 50B
		MGS BG 1 0A 100B MGD BG 15 100A 0B	
0.12	0.06	0.04	0.02
0.06	0.09	0.03	0.29
0.04	0.03	0.12	0.05
0.02	0.29	0.05	0.08
CALF BG	11 63A	38B SIRE BG	5 50A 50B DAM BG 12 75A 25B
		MGS BG 5 50A 50B MGD BG 15 100A 0B	
0.12	0.06	0.03	0.02
0.06	0.09	0.03	0.33
0.03	0.03	0.13	0.05
0.02	0.33	0.05	0.09
CALF BG	12 75A	25B SIRE BG	5 50A 50B DAM BG 15 100A 0B
		MGS BG 15 100A 0B MGD BG 15 100A 0B	
0.14	0.05	0.03	0.02
0.05	0.10	0.04	0.37
0.03	0.04	0.15	0.05
0.02	0.37	0.05	0.10
CALF BG	13 75A	25B SIRE BG	12 75A 25B DAM BG 12 75A 25B
		MGS BG 5 50A 50B MGD BG 15 100A 0B	
0.13	0.05	0.03	0.02
0.05	0.09	0.03	0.36
0.03	0.03	0.14	0.05
0.02	0.36	0.05	0.09
CALF BG	14 88A	13B SIRE BG	12 75A 25B DAM BG 15 100A 0B
		MGS BG 15 100A 0B MGD BG 15 100A 0B	
0.15	0.05	0.03	0.02
0.05	0.11	0.03	0.38
0.03	0.03	0.15	0.04
0.02	0.38	0.04	0.10
CALF BG	15 100A	OB SIRE BG	15 100A 0B DAM BG 15 100A 0B
		MGS BG 15 100A 0B MGD BG 15 100A 0B	
0.17	0.04	0.03	0.02

0.04	0.13	0.03	0.39
0.03	0.03	0.18	0.04
0.02	0.39	0.04	0.11

```

=====
Environmental Correlations for set      1 MREMLEM iter   0
=====
CALF BG   1   OA  100B   SIRE BG   1   OA  100B   DAM BG   1   OA  100B
                           MGS BG   1   OA  100B   MGD BG   1   OA  100B
    1.00     0.59
    0.59     1.00
CALF BG   2   13A   88B   SIRE BG   1   OA  100B   DAM BG   3   25A   75B
                           MGS BG   1   OA  100B   MGD BG   5   50A   50B
    1.00     0.52
    0.52     1.00
CALF BG   3   25A   75B   SIRE BG   1   OA  100B   DAM BG   5   50A   50B
                           MGS BG   1   OA  100B   MGD BG   15  100A   OB
    1.00     0.50
    0.50     1.00
CALF BG   4   38A   63B   SIRE BG   1   OA  100B   DAM BG   12  75A   25B
                           MGS BG   5   50A   50B   MGD BG   15  100A   OB
    1.00     0.50
    0.50     1.00
CALF BG   5   50A   50B   SIRE BG   1   OA  100B   DAM BG   15  100A   OB
                           MGS BG   15  100A   OB   MGD BG   15  100A   OB
    1.00     0.52
    0.52     1.00
CALF BG   6   25A   75B   SIRE BG   3   25A   75B   DAM BG   3   25A   75B
                           MGS BG   1   OA  100B   MGD BG   5   50A   50B
    1.00     0.48
    0.48     1.00
CALF BG   7   38A   63B   SIRE BG   3   25A   75B   DAM BG   5   50A   50B
                           MGS BG   1   OA  100B   MGD BG   15  100A   OB
    1.00     0.46
    0.46     1.00
CALF BG   8   50A   50B   SIRE BG   3   25A   75B   DAM BG   12  75A   25B
                           MGS BG   5   50A   50B   MGD BG   15  100A   OB
    1.00     0.46
    0.46     1.00
CALF BG   9   63A   38B   SIRE BG   3   25A   75B   DAM BG   15  100A   OB
                           MGS BG   15  100A   OB   MGD BG   15  100A   OB
    1.00     0.47
    0.47     1.00
CALF BG  10   50A   50B   SIRE BG   5   50A   50B   DAM BG   5   50A   50B
                           MGS BG   1   OA  100B   MGD BG   15  100A   OB
    1.00     0.45
    0.45     1.00
CALF BG  11   63A   38B   SIRE BG   5   50A   50B   DAM BG   12  75A   25B
                           MGS BG   5   50A   50B   MGD BG   15  100A   OB
    1.00     0.44
    0.44     1.00
CALF BG  12   75A   25B   SIRE BG   5   50A   50B   DAM BG   15  100A   OB
                           MGS BG   15  100A   OB   MGD BG   15  100A   OB
    1.00     0.45
    0.45     1.00
CALF BG  13   75A   25B   SIRE BG   12  75A   25B   DAM BG   12  75A   25B
                           MGS BG   5   50A   50B   MGD BG   15  100A   OB
    1.00     0.44
    0.44     1.00
CALF BG  14   88A   13B   SIRE BG   12  75A   25B   DAM BG   15  100A   OB
                           MGS BG   15  100A   OB   MGD BG   15  100A   OB
    1.00     0.45
    0.45     1.00
CALF BG  15   100A   0B   SIRE BG   15  100A   0B   DAM BG   15  100A   OB
                           MGS BG   15  100A   0B   MGD BG   15  100A   OB
    1.00     0.46
    0.46     1.00

```

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=====
Phenotypic Correlations for set      1 MREMLEM iter      0
=====
CALF BG   1   OA   100B   SIRE BG   1   OA   100B   DAM BG   1   OA   100B
                  MGS BG   1   OA   100B   MGD BG   1   OA   100B

    1.00      0.30
    0.30      1.00
CALF BG   2   13A   88B   SIRE BG   1   OA   100B   DAM BG   3   25A   75B
                  MGS BG   1   OA   100B   MGD BG   5   50A   50B

    1.00      0.29

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0.29	1.00										
CALF BG	3	25A	75B	SIRE BG	1	0A	100B	DAM BG	5	50A	50B
				MGS BG	1	0A	100B	MGD BG	15	100A	0B
1.00	0.28										
0.28	1.00										
CALF BG	4	38A	63B	SIRE BG	1	0A	100B	DAM BG	12	75A	25B
				MGS BG	5	50A	50B	MGD BG	15	100A	0B
1.00	0.28										
0.28	1.00										
CALF BG	5	50A	50B	SIRE BG	1	0A	100B	DAM BG	15	100A	0B
				MGS BG	15	100A	0B	MGD BG	15	100A	0B
1.00	0.27										
0.27	1.00										
CALF BG	6	25A	75B	SIRE BG	3	25A	75B	DAM BG	3	25A	75B
				MGS BG	1	0A	100B	MGD BG	5	50A	50B
1.00	0.28										
0.28	1.00										
CALF BG	7	38A	63B	SIRE BG	3	25A	75B	DAM BG	5	50A	50B
				MGS BG	1	0A	100B	MGD BG	15	100A	0B
1.00	0.28										
0.28	1.00										
CALF BG	8	50A	50B	SIRE BG	3	25A	75B	DAM BG	12	75A	25B
				MGS BG	5	50A	50B	MGD BG	15	100A	0B
1.00	0.27										
0.27	1.00										
CALF BG	9	63A	38B	SIRE BG	3	25A	75B	DAM BG	15	100A	0B
				MGS BG	15	100A	0B	MGD BG	15	100A	0B
1.00	0.27										
0.27	1.00										
CALF BG	10	50A	50B	SIRE BG	5	50A	50B	DAM BG	5	50A	50B
				MGS BG	1	0A	100B	MGD BG	15	100A	0B
1.00	0.27										
0.27	1.00										
CALF BG	11	63A	38B	SIRE BG	5	50A	50B	DAM BG	12	75A	25B
				MGS BG	5	50A	50B	MGD BG	15	100A	0B
1.00	0.27										
0.27	1.00										
CALF BG	12	75A	25B	SIRE BG	5	50A	50B	DAM BG	15	100A	0B
				MGS BG	15	100A	0B	MGD BG	15	100A	0B
1.00	0.26										
0.26	1.00										
CALF BG	13	75A	25B	SIRE BG	12	75A	25B	DAM BG	12	75A	25B
				MGS BG	5	50A	50B	MGD BG	15	100A	0B
1.00	0.26										
0.26	1.00										
CALF BG	14	88A	13B	SIRE BG	12	75A	25B	DAM BG	15	100A	0B
				MGS BG	15	100A	0B	MGD BG	15	100A	0B
1.00	0.25										
0.25	1.00										
CALF BG	15	100A	0B	SIRE BG	15	100A	0B	DAM BG	15	100A	0B
				MGS BG	15	100A	0B	MGD BG	15	100A	0B
1.00	0.23										
0.23	1.00										

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## File MBEOUT: Estimates of Environmental Fixed Effects.

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```
=====
(wrtsol) MME SOLUTIONS FOR EM ITER    1
=====
(wrtsol) SOLUTIONS FOR FIXED ENVIRONMENTAL EFFECTS AT EM ITER    1
=====
Cont Group l1eq lueq      BIRTH      WEANIN
=====
1       1   31   36.5713   191.6351
      se   0.9223   3.9117
2       2   32   33.9674   212.7774
      se   0.9404   3.8285
3       3   33   40.1313   196.9528
      se   0.8687   8.1060
4       4   34   37.5193   180.5609
      se   0.8799   3.6842
5       5   35   35.5417   185.3545
      se   0.8748   3.7193
6       6   36   35.1618   230.7143
      se   0.8780   16.5322
7       7   37   36.5740   239.9103
      se   0.8688   22.7808
```

8	8	38	33.2073	0.0000
		se	0.8732	0.0000
9	9	39	36.2292	239.8977
		se	0.8989	24.2412
10	10	40	33.4529	0.0000
		se	0.9224	0.0000
11	11	41	33.3825	198.7063
		se	0.9576	5.2922
12	12	42	31.3344	203.9823
		se	0.9190	8.0432
13	13	43	33.6570	213.1798
		se	0.9056	8.3254
14	14	44	33.9369	188.6365
		se	0.8981	6.8554
15	15	45	34.2046	194.2318
		se	0.8925	8.0865
16	16	46	30.9061	202.0579
		se	0.8751	6.2546
17	17	47	34.6950	194.8904
		se	0.8457	6.5989
18	18	48	32.3339	211.4429
		se	0.8807	5.3224
19	19	49	34.5466	221.1117
		se	0.8427	7.2475
20	20	50	33.1165	223.6701
		se	0.8553	7.8792
21	21	51	35.0699	207.4623
		se	0.8580	9.4317
22	22	52	32.0895	211.8294
		se	0.8724	7.8933
23	23	53	32.5860	213.6864
		se	0.8577	6.0533
24	24	54	30.4162	211.8313
		se	0.9232	6.4124
25	25	55	34.4939	223.0215
		se	0.9376	20.3768
26	26	56	31.3024	0.0000
		se	0.9094	0.0000
27	27	57	35.4332	0.0000
		se	1.1757	0.0000
28	28	58	34.4140	0.0000
		se	1.1234	0.0000
29	29	59	33.4638	240.4658
		se	0.9126	24.8042
30	30	60	31.5800	191.0947
		se	0.9457	5.5223

Age	Dam	Sex	Calf	F <sub>r</sub>	B <sub>r</sub>	D <sub>m</sub>	D <sub>a</sub>	I <sub>leq</sub>	I <sub>ueq</sub>	BIRTH	WEANIN
1	2		1	166	167	-0.0788	19.3093				
					se	1.0208	21.4484				
2	1		1	168	169	0.9814	15.8510				
					se	0.9101	16.8024				
2	2		1	170	171	-0.6619	12.2064				
					se	1.0044	16.6261				
3	1		1	172	173	2.9511	-61.5300				
					se	0.7269	32.4698				
3	2		1	174	175	1.0239	-33.0429				
					se	0.8766	22.9713				

## File MBEOUT: Estimates of Regression Group Genetic Effects.

```
(wrtsol) SOLUTIONS FOR REGRESSION GENETIC GROUP EFFECTS AT EM ITER      1
=====
name effect      regr #    BIRTH_D WEANIN_D    BIRTH_M WEANIN_M
=====
intrabr addmgd   1   -0.0607   -9.9020
                  se   0.5716   8.3305
intrabr adddm    2   -5.2474  -10.2166    3.0768   1.0811
                  se   0.6023   2.3393   0.7362   3.0980
interbr naddm    3   2.6738   19.1847   0.6903   28.9559
                  se   0.6327   2.6065   0.4987   2.1064
=====
```

**File MBEOU: Sample of Sire Genetic Predictions.**

(wrtsol) BULL PREDICTIONS AT EM ITER 1										
sqnum	bullid	iig	ibg	geneff	geneval	BIRTH_D	WEANIN_D	BIRTH_M	WEANIN_M	
1	6834245	15	15	add	12	pgv	-5.3123	-10.5272	2.7911	1.3800
1	6834245	15	15	add	12	sep	1.2874	4.4137	1.3892	4.5879
1	6834245	15	15	add	12	sol/gsd	-4.5010	-2.7530	2.2858	0.4007
1	6834245	15	15	add	12	sep/gsd	109	115	114	133
1	6834245	15	15	add	12	bifacc	-9	-15	-14	-33
<hr/>										
1	6834245	15	15	nad	12	pgv	1.3142	8.7213	0.3113	14.6003
1	6834245	15	15	nad	12	sep	1.3534	5.0712	1.3359	4.1488
1	6834245	15	15	nad	12	sol/gsd	0.9829	1.7593	0.2335	3.6080
1	6834245	15	15	nad	12	sep/gsd	101	102	100	103
1	6834245	15	15	nad	12	bifacc	-1	-2	0	-3
<hr/>										
1	6834245	15	15	tot	12	pgv	-3.9981	-1.8059	3.1024	15.9803
1	6834245	15	15	tot	12	sep	2.1815	7.6703	2.2803	7.1746
1	6834245	15	15	tot	12	sol/gsd	-2.2418	-0.2885	1.7160	3.0073
1	6834245	15	15	tot	12	sep/gsd	122	123	126	135
1	6834245	15	15	tot	12	bifacc	-22	-23	-26	-35
<hr/>										
2	10362604	15	15	add	12	pgv	-5.3351	-11.4822	2.6917	1.3041
2	10362604	15	15	add	12	sep	1.2694	4.3750	1.3845	4.5830
2	10362604	15	15	add	12	sol/gsd	-4.5203	-3.0027	2.2044	0.3787
2	10362604	15	15	add	12	sep/gsd	108	114	113	133
2	10362604	15	15	add	12	bifacc	-8	-14	-13	-33
<hr/>										
2	10362604	15	15	nad	12	pgv	1.2658	7.5122	0.1834	14.3007
2	10362604	15	15	nad	12	sep	1.3271	4.9883	1.3189	4.1214
2	10362604	15	15	nad	12	sol/gsd	0.9467	1.5154	0.1376	3.5339
2	10362604	15	15	nad	12	sep/gsd	99	101	99	102
2	10362604	15	15	nad	12	bifacc	1	-1	1	-2
<hr/>										
2	10362604	15	15	tot	12	pgv	-4.0693	-3.9701	2.8751	15.6049
2	10362604	15	15	tot	12	sep	2.1438	7.5710	2.2646	7.1525
2	10362604	15	15	tot	12	sol/gsd	-2.2817	-0.6341	1.5903	2.9366
2	10362604	15	15	tot	12	sep/gsd	120	121	125	135
2	10362604	15	15	tot	12	bifacc	-20	-21	-25	-35
<hr/>										
3	9000014	13	13	add	12	pgv	-3.9588	-7.2931	2.2414	1.4685
3	9000014	13	13	add	12	sep	1.4098	5.5181	1.3851	5.1359
3	9000014	13	13	add	12	sol/gsd	-2.9492	-1.3878	1.7210	0.3154
3	9000014	13	13	add	12	sep/gsd	105	105	106	110
3	9000014	13	13	add	12	bifacc	-5	-5	-6	-10
<hr/>										
3	9000014	13	13	nad	12	pgv	1.3288	9.7650	0.2852	14.9571
3	9000014	13	13	nad	12	sep	1.3868	5.3079	1.3398	4.3094
3	9000014	13	13	nad	12	sol/gsd	0.9837	1.8969	0.2130	3.5425
3	9000014	13	13	nad	12	sep/gsd	103	103	100	102
3	9000014	13	13	nad	12	bifacc	-3	-3	0	-2
<hr/>										
3	9000014	13	13	tot	12	pgv	-2.6300	2.4719	2.5265	16.4256
3	9000014	13	13	tot	12	sep	2.2376	8.6867	2.1695	7.6686
3	9000014	13	13	tot	12	sol/gsd	-1.3810	0.3360	1.3527	2.6134
3	9000014	13	13	tot	12	sep/gsd	118	118	116	122
3	9000014	13	13	tot	12	bifacc	-18	-18	-16	-22
<hr/>										
4	8442952	15	15	add	12	pgv	-6.1298	-8.8626	2.9218	1.2297
4	8442952	15	15	add	12	sep	1.2393	4.3083	1.3861	4.5768
4	8442952	15	15	add	12	sol/gsd	-5.1937	-2.3177	2.3929	0.3571
4	8442952	15	15	add	12	sep/gsd	105	113	114	133
4	8442952	15	15	add	12	bifacc	-5	-13	-14	-33
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4	8442952	15	15	nad	12	pgv	0.8957	10.2694	0.2676	14.5522
4	8442952	15	15	nad	12	sep	1.3604	5.1074	1.3468	4.1692
4	8442952	15	15	nad	12	sol/gsd	0.6699	2.0716	0.2007	3.5961
4	8442952	15	15	nad	12	sep/gsd	102	103	101	103
4	8442952	15	15	nad	12	bifacc	-2	-3	-1	-3
<hr/>										
4	8442952	15	15	tot	12	pgv	-5.2341	1.4067	3.1895	15.7820
4	8442952	15	15	tot	12	sep	2.1378	7.5999	2.2838	7.1758
4	8442952	15	15	tot	12	sol/gsd	-2.9348	0.2247	1.7642	2.9699

4	8442952	15	15	tot	12	sep/gsd	120	121	126	135
4	8442952	15	15	tot	12	bifacc	-20	-21	-26	-35
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5	7640000	1	1	add	12	pgv	0.3699	1.3263	-0.1333	-0.6149
5	7640000	1	1	add	12	sep	1.0890	3.8401	1.1592	5.5013
5	7640000	1	1	add	12	sol/gsd	0.3114	0.3228	-0.1067	-0.0982
5	7640000	1	1	add	12	sep/gsd	92	93	93	88
5	7640000	1	1	add	12	bifacc	8	7	7	12
<hr/>										
5	7640000	1	1	nad	12	pgv	2.1793	13.1541	0.1762	14.1309
5	7640000	1	1	nad	12	sep	1.4764	5.6304	1.5225	5.1632
5	7640000	1	1	nad	12	sol/gsd	1.2737	2.0433	0.1020	2.5901
5	7640000	1	1	nad	12	sep/gsd	86	87	88	95
5	7640000	1	1	nad	12	bifacc	14	13	12	5
<hr/>										
5	7640000	1	1	tot	12	pgv	2.5493	14.4805	0.0429	13.5160
5	7640000	1	1	tot	12	sep	1.6003	6.1293	1.6968	6.6863
5	7640000	1	1	tot	12	sol/gsd	1.2238	1.8960	0.0201	1.6278
5	7640000	1	1	tot	12	sep/gsd	77	80	80	81
5	7640000	1	1	tot	12	bifacc	23	20	20	19
<hr/>										
6	5670200	1	1	add	12	pgv	-0.0287	0.7090	-0.1329	3.4802
6	5670200	1	1	add	12	sep	1.1754	4.0731	1.1779	5.6999
6	5670200	1	1	add	12	sol/gsd	-0.0241	0.1725	-0.1064	0.5560
6	5670200	1	1	add	12	sep/gsd	99	99	94	91
6	5670200	1	1	add	12	bifacc	1	1	6	9
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6	5670200	1	1	nad	12	pgv	1.3201	9.6974	-0.0173	16.9177
6	5670200	1	1	nad	12	sep	1.7394	6.5677	1.5640	5.2598
6	5670200	1	1	nad	12	sol/gsd	0.7715	1.5064	-0.0100	3.1009
6	5670200	1	1	nad	12	sep/gsd	102	102	91	96
6	5670200	1	1	nad	12	bifacc	-2	-2	9	4
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6	5670200	1	1	tot	12	pgv	1.2915	10.4064	-0.1502	20.3979
6	5670200	1	1	tot	12	sep	2.0996	7.7301	1.7873	7.1347
6	5670200	1	1	tot	12	sol/gsd	0.6200	1.3626	-0.0704	2.4566
6	5670200	1	1	tot	12	sep/gsd	101	101	84	86
6	5670200	1	1	tot	12	bifacc	-1	-1	16	14
<hr/>										
7	5150000	1	1	add	12	pgv	-0.1132	-0.3632	0.2102	-2.8406
7	5150000	1	1	add	12	sep	1.1048	3.8958	1.1697	5.6404
7	5150000	1	1	add	12	sol/gsd	-0.0952	-0.0884	0.1683	-0.4538
7	5150000	1	1	add	12	sep/gsd	93	95	94	90
7	5150000	1	1	add	12	bifacc	7	5	6	10
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7	5150000	1	1	nad	12	pgv	1.0011	10.0377	0.7861	12.5121
7	5150000	1	1	nad	12	sep	1.5227	5.8384	1.5473	5.2319
7	5150000	1	1	nad	12	sol/gsd	0.5851	1.5592	0.4550	2.2934
7	5150000	1	1	nad	12	sep/gsd	89	91	90	96
7	5150000	1	1	nad	12	bifacc	11	9	10	4
<hr/>										
7	5150000	1	1	tot	12	pgv	0.8879	9.6745	0.9963	9.6716
7	5150000	1	1	tot	12	sep	1.6891	6.4882	1.7506	7.0051
7	5150000	1	1	tot	12	sol/gsd	0.4263	1.2667	0.4673	1.1648
7	5150000	1	1	tot	12	sep/gsd	81	85	82	84
7	5150000	1	1	tot	12	bifacc	19	15	18	16
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8	5111000	13	13	add	12	pgv	-4.6837	-9.8136	1.6133	-3.1786
8	5111000	13	13	add	12	sep	1.1948	4.7483	1.2629	4.7856
8	5111000	13	13	add	12	sol/gsd	-3.4893	-1.8675	1.2388	-0.6827
8	5111000	13	13	add	12	sep/gsd	89	90	97	103
8	5111000	13	13	add	12	bifacc	11	10	3	-3
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8	5111000	13	13	nad	12	pgv	0.8995	8.8553	-0.2565	11.6104
8	5111000	13	13	nad	12	sep	1.2595	4.8681	1.2586	4.1254
8	5111000	13	13	nad	12	sol/gsd	0.6659	1.7202	-0.1916	2.7498
8	5111000	13	13	nad	12	sep/gsd	93	95	94	98
8	5111000	13	13	nad	12	bifacc	7	5	6	2
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8	5111000	13	13	tot	12	pgv	-3.7843	-0.9583	1.3568	8.4318
8	5111000	13	13	tot	12	sep	1.8044	7.1620	1.9122	7.0265
8	5111000	13	13	tot	12	sol/gsd	-1.9872	-0.1303	0.7264	1.3415
8	5111000	13	13	tot	12	sep/gsd	95	97	102	112
8	5111000	13	13	tot	12	bifacc	5	3	-2	-12
<hr/>										
9	5000000	13	13	add	12	pgv	-3.9044	-7.6717	2.5954	1.1505
9	5000000	13	13	add	12	sep	1.3128	5.2084	1.3107	4.9391
9	5000000	13	13	add	12	sol/gsd	-2.9087	-1.4599	1.9928	0.2471

9	5000000	13	13	add	12	sep/gsd	98	99	101	106
9	5000000	13	13	add	12	bifacc	2	1	-1	-6
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9	5000000	13	13	nad	12	pgv	1.3021	9.5234	0.5792	14.6877
9	5000000	13	13	nad	12	sep	1.3328	5.1406	1.2904	4.1997
9	5000000	13	13	nad	12	sol/gsd	0.9639	1.8500	0.4326	3.4787
9	5000000	13	13	nad	12	sep/gsd	99	100	96	99
9	5000000	13	13	nad	12	bifacc	1	0	4	1
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9	5000000	13	13	tot	12	pgv	-2.6023	1.8517	3.1746	15.8382
9	5000000	13	13	tot	12	sep	2.0515	8.0969	2.0135	7.2954
9	5000000	13	13	tot	12	sol/gsd	-1.3665	0.2517	1.6996	2.5199
9	5000000	13	13	tot	12	sep/gsd	108	110	108	116
9	5000000	13	13	tot	12	bifacc	-8	-10	-8	-16
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10	4520000	13	13	add	12	pgv	-3.4167	6.0525	3.2848	3.8850
10	4520000	13	13	add	12	sep	1.2037	4.7584	1.2634	4.7192
10	4520000	13	13	add	12	sol/gsd	-2.5454	1.1518	2.5222	0.8344
10	4520000	13	13	add	12	sep/gsd	90	91	97	101
10	4520000	13	13	add	12	bifacc	10	9	3	-1
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10	4520000	13	13	nad	12	pgv	1.4287	18.4248	1.0445	18.0648
10	4520000	13	13	nad	12	sep	1.2990	4.9995	1.2715	4.1055
10	4520000	13	13	nad	12	sol/gsd	1.0576	3.5791	0.7801	4.2785
10	4520000	13	13	nad	12	sep/gsd	96	97	95	97
10	4520000	13	13	nad	12	bifacc	4	3	5	3
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10	4520000	13	13	tot	12	pgv	-1.9880	24.4773	4.3292	21.9498
10	4520000	13	13	tot	12	sep	1.8798	7.3814	1.9301	6.9148
10	4520000	13	13	tot	12	sol/gsd	-1.0439	3.3274	2.3178	3.4923
10	4520000	13	13	tot	12	sep/gsd	99	100	103	110
10	4520000	13	13	tot	12	bifacc	1	0	-3	-10
<hr/>										
11	4400000	1	1	add	12	pgv	-0.1997	0.2678	0.2844	0.1010
11	4400000	1	1	add	12	sep	1.0770	3.7956	1.1273	5.1046
11	4400000	1	1	add	12	sol/gsd	-0.1681	0.0652	0.2277	0.0161
11	4400000	1	1	add	12	sep/gsd	91	92	90	82
11	4400000	1	1	add	12	bifacc	9	8	10	18
<hr/>										
11	4400000	1	1	nad	12	pgv	0.7632	11.3417	0.7345	15.0995
11	4400000	1	1	nad	12	sep	1.4594	5.5458	1.4502	4.9760
11	4400000	1	1	nad	12	sol/gsd	0.4460	1.7618	0.4251	2.7677
11	4400000	1	1	nad	12	sep/gsd	85	86	84	91
11	4400000	1	1	nad	12	bifacc	15	14	16	9
<hr/>										
11	4400000	1	1	tot	12	pgv	0.5635	11.6095	1.0188	15.2005
11	4400000	1	1	tot	12	sep	1.5644	5.9705	1.5347	5.7541
11	4400000	1	1	tot	12	sol/gsd	0.2705	1.5201	0.4779	1.8307
11	4400000	1	1	tot	12	sep/gsd	75	78	72	69
11	4400000	1	1	tot	12	bifacc	25	22	28	31
<hr/>										
12	4285112	15	15	add	12	pgv	-4.9906	-8.9398	3.1746	0.5329
12	4285112	15	15	add	12	sep	1.2676	4.3668	1.3992	4.5972
12	4285112	15	15	add	12	sol/gsd	-4.2284	-2.3378	2.5999	0.1547
12	4285112	15	15	add	12	sep/gsd	107	114	115	133
12	4285112	15	15	add	12	bifacc	-7	-14	-15	-33
<hr/>										
12	4285112	15	15	nad	12	pgv	1.4653	10.2308	0.3940	14.2039
12	4285112	15	15	nad	12	sep	1.3604	5.1005	1.3494	4.1718
12	4285112	15	15	nad	12	sol/gsd	1.0959	2.0638	0.2956	3.5100
12	4285112	15	15	nad	12	sep/gsd	102	103	101	103
12	4285112	15	15	nad	12	bifacc	-2	-3	-1	-3
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12	4285112	15	15	tot	12	pgv	-3.5253	1.2910	3.5687	14.7368
12	4285112	15	15	tot	12	sep	2.1625	7.6360	2.3004	7.1998
12	4285112	15	15	tot	12	sol/gsd	-1.9766	0.2062	1.9739	2.7733
12	4285112	15	15	tot	12	sep/gsd	121	122	127	135
12	4285112	15	15	tot	12	bifacc	-21	-22	-27	-35
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13	4000000	13	13	add	12	pgv	-4.2550	-11.5926	2.2779	0.9351
13	4000000	13	13	add	12	sep	1.2588	4.9927	1.4137	5.2029
13	4000000	13	13	add	12	sol/gsd	-3.1699	-2.2060	1.7491	0.2008
13	4000000	13	13	add	12	sep/gsd	94	95	109	112
13	4000000	13	13	add	12	bifacc	6	5	-9	-12
<hr/>										
13	4000000	13	13	nad	12	pgv	1.1312	6.6993	0.3240	14.1998
13	4000000	13	13	nad	12	sep	1.2958	5.0156	1.3618	4.3479
13	4000000	13	13	nad	12	sol/gsd	0.8374	1.3014	0.2420	3.3631

13	4000000	13	13	nad	12	sep/gsd	96	97	102	103
13	4000000	13	13	nad	12	bifacc	4	3	-2	-3
<hr/>										
13	4000000	13	13	tot	12	pgv	-3.1238	-4.8932	2.6019	15.1349
13	4000000	13	13	tot	12	sep	1.9309	7.6614	2.2326	7.8001
13	4000000	13	13	tot	12	sol/gsd	-1.6404	-0.6652	1.3930	2.4080
13	4000000	13	13	tot	12	sep/gsd	101	104	120	124
13	4000000	13	13	tot	12	bifacc	-1	-4	-20	-24
<hr/>										
14	3870140	15	15	add	12	pgv	-5.2250	-10.0622	3.1272	1.4619
14	3870140	15	15	add	12	sep	1.3175	4.4761	1.3624	4.5474
14	3870140	15	15	add	12	sol/gsd	-4.4270	-2.6314	2.5610	0.4245
14	3870140	15	15	add	12	sep/gsd	112	117	112	132
14	3870140	15	15	add	12	bifacc	-12	-17	-12	-32
<hr/>										
14	3870140	15	15	nad	12	pgv	1.3481	9.6695	0.3703	14.6683
14	3870140	15	15	nad	12	sep	1.3724	5.1245	1.3424	4.1646
14	3870140	15	15	nad	12	sol/gsd	1.0083	1.9506	0.2778	3.6248
14	3870140	15	15	nad	12	sep/gsd	103	103	101	103
14	3870140	15	15	nad	12	bifacc	-3	-3	-1	-3
<hr/>										
14	3870140	15	15	tot	12	pgv	-3.8769	-0.3927	3.4975	16.1303
14	3870140	15	15	tot	12	sep	2.2290	7.7779	2.2545	7.1397
14	3870140	15	15	tot	12	sol/gsd	-2.1738	-0.0627	1.9345	3.0355
14	3870140	15	15	tot	12	sep/gsd	125	124	125	134
14	3870140	15	15	tot	12	bifacc	-25	-24	-25	-34
<hr/>										
15	3800047	15	15	add	12	pgv	-5.5935	-10.3161	2.5980	1.3556
15	3800047	15	15	add	12	sep	1.2916	4.4295	1.2638	4.3825
15	3800047	15	15	add	12	sol/gsd	-4.7392	-2.6978	2.1277	0.3936
15	3800047	15	15	add	12	sep/gsd	109	116	103	127
15	3800047	15	15	add	12	bifacc	-9	-16	-3	-27
<hr/>										
15	3800047	15	15	nad	12	pgv	1.1421	9.4829	0.3259	14.6546
15	3800047	15	15	nad	12	sep	1.3601	5.0941	1.3150	4.1191
15	3800047	15	15	nad	12	sol/gsd	0.8542	1.9130	0.2444	3.6214
15	3800047	15	15	nad	12	sep/gsd	102	103	99	102
15	3800047	15	15	nad	12	bifacc	-2	-3	1	-2
<hr/>										
15	3800047	15	15	tot	12	pgv	-4.4514	-0.8332	2.9239	16.0102
15	3800047	15	15	tot	12	sep	2.1917	7.7071	2.1234	6.9148
15	3800047	15	15	tot	12	sol/gsd	-2.4959	-0.1331	1.6173	3.0129
15	3800047	15	15	tot	12	sep/gsd	123	123	117	130
15	3800047	15	15	tot	12	bifacc	-23	-23	-17	-30
<hr/>										
16	3856515	1	1	add	12	pgv	0.3484	-0.1246	0.2095	-1.0744
16	3856515	1	1	add	12	sep	1.0952	3.8660	1.1845	5.7861
16	3856515	1	1	add	12	sol/gsd	0.2933	-0.0303	0.1678	-0.1717
16	3856515	1	1	add	12	sep/gsd	92	94	95	92
16	3856515	1	1	add	12	bifacc	8	6	5	8
<hr/>										
16	3856515	1	1	nad	12	pgv	1.9035	9.6924	0.8280	13.6364
16	3856515	1	1	nad	12	sep	1.4863	5.6806	1.5845	5.3062
16	3856515	1	1	nad	12	sol/gsd	1.1125	1.5056	0.4792	2.4995
16	3856515	1	1	nad	12	sep/gsd	87	88	92	97
16	3856515	1	1	nad	12	bifacc	13	12	8	3
<hr/>										
16	3856515	1	1	tot	12	pgv	2.2519	9.5678	1.0375	12.5620
16	3856515	1	1	tot	12	sep	1.6219	6.2256	1.8284	7.3351
16	3856515	1	1	tot	12	sol/gsd	1.0810	1.2528	0.4867	1.5129
16	3856515	1	1	tot	12	sep/gsd	78	82	86	88
16	3856515	1	1	tot	12	bifacc	22	18	14	12
<hr/>										
17	3850506	1	1	add	12	pgv	0.2034	-2.0176	0.1009	-2.5847
17	3850506	1	1	add	12	sep	1.0888	3.8437	1.1702	5.6409
17	3850506	1	1	add	12	sol/gsd	0.1712	-0.4910	0.0808	-0.4129
17	3850506	1	1	add	12	sep/gsd	92	94	94	90
17	3850506	1	1	add	12	bifacc	8	6	6	10
<hr/>										
17	3850506	1	1	nad	12	pgv	1.7226	5.7843	0.6944	12.5032
17	3850506	1	1	nad	12	sep	1.4707	5.6119	1.5491	5.2326
17	3850506	1	1	nad	12	sol/gsd	1.0067	0.8985	0.4019	2.2918
17	3850506	1	1	nad	12	sep/gsd	86	87	90	96
17	3850506	1	1	nad	12	bifacc	14	13	10	4
<hr/>										
17	3850506	1	1	tot	12	pgv	1.9260	3.7667	0.7954	9.9185
17	3850506	1	1	tot	12	sep	1.5920	6.1100	1.7542	7.0074
17	3850506	1	1	tot	12	sol/gsd	0.9246	0.4932	0.3731	1.1945

17	3850506	1	1	tot	12	sep/gsd	76	80	82	84
17	3850506	1	1	tot	12	bifacc	24	20	18	16
<hr/>										
18	3840047	15	15	add	12	pgv	-5.2115	-10.3163	3.1709	0.7944
18	3840047	15	15	add	12	sep	1.3087	4.4674	1.3051	4.4734
18	3840047	15	15	add	12	sol/gsd	-4.4156	-2.6978	2.5968	0.2307
18	3840047	15	15	add	12	sep/gsd	111	117	107	130
18	3840047	15	15	add	12	bifacc	-11	-17	-7	-30
<hr/>										
18	3840047	15	15	nad	12	pgv	1.3549	9.5425	0.3922	14.3346
18	3840047	15	15	nad	12	sep	1.3699	5.1222	1.3295	4.1481
18	3840047	15	15	nad	12	sol/gsd	1.0133	1.9250	0.2941	3.5423
18	3840047	15	15	nad	12	sep/gsd	102	103	100	103
18	3840047	15	15	nad	12	bifacc	-2	-3	0	-3
<hr/>										
18	3840047	15	15	tot	12	pgv	-3.8566	-0.7738	3.5631	15.1290
18	3840047	15	15	tot	12	sep	2.2167	7.7657	2.1795	7.0399
18	3840047	15	15	tot	12	sol/gsd	-2.1624	-0.1236	1.9708	2.8471
18	3840047	15	15	tot	12	sep/gsd	124	124	121	132
18	3840047	15	15	tot	12	bifacc	-24	-24	-21	-32
<hr/>										
19	3830394	1	1	add	12	pgv	-0.0662	0.4241	-0.1991	2.1632
19	3830394	1	1	add	12	sep	1.1796	4.0862	1.2012	5.9039
19	3830394	1	1	add	12	sol/gsd	-0.0557	0.1032	-0.1594	0.3456
19	3830394	1	1	add	12	sep/gsd	99	99	96	94
19	3830394	1	1	add	12	bifacc	1	1	4	6
<hr/>										
19	3830394	1	1	nad	12	pgv	1.3132	9.6551	-0.0969	16.0241
19	3830394	1	1	nad	12	sep	1.7396	6.5679	1.6239	5.3657
19	3830394	1	1	nad	12	sol/gsd	0.7675	1.4998	-0.0561	2.9372
19	3830394	1	1	nad	12	sep/gsd	102	102	94	98
19	3830394	1	1	nad	12	bifacc	-2	-2	6	2
<hr/>										
19	3830394	1	1	tot	12	pgv	1.2470	10.0792	-0.2960	18.1873
19	3830394	1	1	tot	12	sep	2.1014	7.7338	1.9093	7.5930
19	3830394	1	1	tot	12	sol/gsd	0.5986	1.3197	-0.1389	2.1904
19	3830394	1	1	tot	12	sep/gsd	101	101	90	91
19	3830394	1	1	tot	12	bifacc	-1	-1	10	9
<hr/>										
20	3830378	1	1	add	12	pgv	0.1141	2.4742	0.2680	0.1048
20	3830378	1	1	add	12	sep	1.0983	3.8643	1.1296	5.1005
20	3830378	1	1	add	12	sol/gsd	0.0961	0.6021	0.2147	0.0167
20	3830378	1	1	add	12	sep/gsd	92	94	90	81
20	3830378	1	1	add	12	bifacc	8	6	10	19
<hr/>										
20	3830378	1	1	nad	12	pgv	1.4889	15.5493	0.7901	14.6901
20	3830378	1	1	nad	12	sep	1.5243	5.8385	1.4501	4.9690
20	3830378	1	1	nad	12	sol/gsd	0.8702	2.4154	0.4573	2.6926
20	3830378	1	1	nad	12	sep/gsd	89	91	84	91
20	3830378	1	1	nad	12	bifacc	11	9	16	9
<hr/>										
20	3830378	1	1	tot	12	pgv	1.6031	18.0234	1.0582	14.7949
20	3830378	1	1	tot	12	sep	1.6932	6.4888	1.5350	5.7193
20	3830378	1	1	tot	12	sol/gsd	0.7696	2.3599	0.4964	1.7818
20	3830378	1	1	tot	12	sep/gsd	81	85	72	69
20	3830378	1	1	tot	12	bifacc	19	15	28	31
<hr/>										

## OUTPUT FILE 2 = covariances and genetic parameter estimates (RESULTS)

Contains:

- 1) MREML covariance and genetic parameter estimates computed at convergence, or
  - 2) MREML covariances and genetic parameters computed based on input covariances, as indicated by parameter mxiter.
- mxiter = maximum number of mreml iterations, and indicator to compute genetic parameters and genetic predictions only  
= -1 => compute genetic parameters (herit, interact, corr) \*\*ONLY\*\*  
= 0 => compute genetic parameters \*\*AND\*\* genetic predictions  
= 1 or larger => compute MREML covariances, gen par, and gen pred

```
=====
(gparemit2b) DIRECT NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
 1 1 1 0.0000 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000
 2 1 2 0.0000 1.0000 0.2500 0.7500 0.0000 0.7500 0.2500
 3 1 3 0.0000 1.0000 0.5000 0.5000 0.0000 0.5000 0.5000
 4 1 4 0.0000 1.0000 0.7500 0.2500 0.0000 0.2500 0.7500
 5 1 5 0.0000 1.0000 1.0000 0.0000 0.0000 0.0000 1.0000
 6 2 2 0.2500 0.7500 0.2500 0.7500 0.0625 0.5625 0.3750
 7 2 3 0.2500 0.7500 0.5000 0.5000 0.1250 0.3750 0.5000
 8 2 4 0.2500 0.7500 0.7500 0.2500 0.1875 0.1875 0.6250
 9 2 5 0.2500 0.7500 1.0000 0.0000 0.2500 0.0000 0.7500
10 3 3 0.5000 0.5000 0.5000 0.5000 0.2500 0.2500 0.5000
11 3 4 0.5000 0.5000 0.7500 0.2500 0.3750 0.1250 0.5000
12 3 5 0.5000 0.5000 1.0000 0.0000 0.5000 0.0000 0.5000
13 4 4 0.7500 0.2500 0.7500 0.2500 0.5625 0.0625 0.3750
14 4 5 0.7500 0.2500 1.0000 0.0000 0.7500 0.0000 0.2500
15 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000

(gparemit2b) MATERNAL NONADDITIVE GENETIC COEFFICIENTS
bgi bgs bgd bgmgs bgmgd wgbases1 wgbases2 wgbased1 wgbased2 nad 11 nad 12 nad 13
 1 1 1 1 1 0.0000 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000
 2 1 2 1 3 0.0000 1.0000 0.5000 0.5000 0.0000 0.5000 0.5000
 3 1 3 1 5 0.0000 1.0000 1.0000 0.0000 0.0000 0.0000 1.0000
 4 1 4 3 5 0.5000 0.5000 1.0000 0.0000 0.5000 0.0000 0.5000
 5 1 5 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000
 6 2 2 1 3 0.0000 1.0000 0.5000 0.5000 0.0000 0.5000 0.5000
 7 2 3 1 5 0.0000 1.0000 1.0000 0.0000 0.0000 0.0000 1.0000
 8 2 4 3 5 0.5000 0.5000 1.0000 0.0000 0.5000 0.0000 0.5000
 9 2 5 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000
10 3 3 1 5 0.0000 1.0000 1.0000 0.0000 0.0000 0.0000 1.0000
11 3 4 3 5 0.5000 0.5000 1.0000 0.0000 0.5000 0.0000 0.5000
12 3 5 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000
13 4 4 3 5 0.5000 0.5000 1.0000 0.0000 0.5000 0.0000 0.5000
14 4 5 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000
15 5 5 5 5 1.0000 0.0000 1.0000 0.0000 1.0000 0.0000 0.0000

=====
Parameter Estimates for set 1 MREMLEM iter 0
=====

=====
Additive Genetic Covariances for set 1 MREMLEM iter 0
=====

breed group combination 1 100B 00A x 100B 00A
 5.6460 1.6370 -0.2570 1.7750
 1.6370 67.5470 0.8530 -0.5750
 -0.2570 0.8530 6.2370 2.9480
 1.7750 -0.5750 2.9480 156.7180

breed group combination 2 100B 00A x 75B 25A
 6.4451 2.9212 -0.2795 1.2891
 2.9212 91.2669 1.1449 1.1546
 -0.2795 1.1449 6.5790 2.5557
 1.2891 1.1546 2.5557 149.0311

breed group combination 3 100B 00A x 50B 50A
 6.7052 3.2985 -0.3068 0.9727
 3.2985 98.4187 1.1970 0.6683
 -0.3068 1.1970 6.6702 2.2060
 0.9727 0.6683 2.2060 137.3628

breed group combination 4 100B 00A x 25B 75A
 6.4266 2.7687 -0.3388 0.8259
 2.7687 89.0026 1.0092 -2.0339
 -0.3388 1.0092 6.5108 1.8987
 0.8259 -2.0339 1.8987 121.7131

breed group combination 5 100B 00A x 00B 100A
 5.6090 1.3320 -0.3755 0.8485
 1.3320 63.0185 0.5815 -6.9520
 -0.3755 0.5815 6.1005 1.6340
 0.8485 -6.9520 1.6340 102.0820

breed group combination 6 75B 25A x 7B 25A
 7.2441 4.2055 -0.3020 0.8032
 4.2055 114.9868 1.4369 2.8841
 -0.3020 1.4369 6.9210 2.1635
 0.8032 2.8841 2.1635 141.3441

breed group combination 7 75B 25A x 50B 50A
 7.5043 4.5827 -0.3293 0.4869
 4.5827 122.1386 1.4889 2.3978
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-0.3293    1.4889    7.0123    1.8137
 0.4869    2.3978    1.8137   129.6758
breed group combination 8    75B    25A x 25B    75A
 7.2256    4.0530   -0.3613    0.3400
 4.0530   112.7225   1.3011   -0.3044
 -0.3613    1.3011    6.8528    1.5065
 0.3400   -0.3044   1.5065   114.0261
breed group combination 9    75B    25A x 00B   100A
 6.4081    2.6162   -0.3980    0.3626
 2.6162   86.7384   0.8734   -5.2224
 -0.3980    0.8734   6.4425   1.2417
 0.3626   -5.2224   1.2417   94.3951
breed group combination 10   50B    50A x 50B    50A
 7.7645    4.9600   -0.3565    0.1705
 4.9600  129.2905   1.5410   1.9115
 -0.3565    1.5410   7.1035   1.4640
 0.1705    1.9115   1.4640   118.0075
breed group combination 11   50B    50A x 25B    75A
 7.4858    4.4303   -0.3885    0.0236
 4.4303  119.8744   1.3532   -0.7907
 -0.3885    1.3532   6.9440   1.1567
 0.0236   -0.7907   1.1567   102.3578
breed group combination 12   50B    50A x 00B   100A
 6.6683    2.9935   -0.4252    0.0462
 2.9935  93.8903   0.9255   -5.7088
 -0.4252    0.9255   6.5338   0.8920
 0.0462   -5.7088   0.8920   82.7267
breed group combination 13   25B    75A x 25B    75A
 7.2071    3.9005   -0.4205   -0.1233
 3.9005  110.4583   1.1654   -3.4929
 -0.4205    1.1654   6.7845   0.8495
 -0.1233   -3.4929   0.8495   86.7081
breed group combination 14   25B    75A x 00B   100A
 6.3896    2.4638   -0.4573   -0.1006
 2.4638  84.4741   0.7377   -8.4109
 -0.4573    0.7377   6.3743   0.5848
 -0.1006   -8.4109   0.5848   67.0771
breed group combination 15   00B   100A x 00B   100A
 5.5720    1.0270   -0.4940   -0.0780
 1.0270   58.4900   0.3100   -13.3290
 -0.4940    0.3100   5.9640   0.3200
 -0.0780   -13.3290   0.3200   47.4460
=====
Nonadditive Genetic Covariances for set 1 MREMLEM iter 0
=====
breed group combination 1  100B   00A x 100B   00A
 5.7580    1.1560   0.3460    0.1540
 1.1560   83.6710   0.1260   2.4620
 0.3460   0.1260   5.6190    0.5490
 0.1540   2.4620   0.5490   53.6420
breed group combination 2  100B   00A x 75B    25A
 5.6558    1.2080   0.2945    0.2690
 1.2080   79.0263   0.2960   8.5275
 0.2945   0.2960   5.6188    0.7460
 0.2690   8.5275   0.7460   61.2388
breed group combination 3  100B   00A x 50B    50A
 5.5535    1.2600   0.2430    0.3840
 1.2600   74.3815   0.4660  14.5930
 0.2430   0.4660   5.6185    0.9430
 0.3840   14.5930   0.9430   68.8355
breed group combination 4  100B   00A x 25B    75A
 5.4512    1.3120   0.1915    0.4990
 1.3120   69.7368   0.6360  20.6585
 0.1915   0.6360   5.6182    1.1400
 0.4990   20.6585   1.1400   76.4322
breed group combination 5  100B   00A x 00B   100A
 5.3490    1.3640   0.1400    0.6140
 1.3640   65.0920   0.8060  26.7240
 0.1400   0.8060   5.6180    1.3370
 0.6140   26.7240   1.3370   84.0290
breed group combination 6   75B   25A x 7B     25A
 5.6168    1.2151   0.2592    0.3421
 1.2151   76.6056   0.4145  13.1836
 0.2592   0.4145   5.6626    0.8586
 0.3421   13.1836   0.8586   65.7729
breed group combination 7   75B   25A x 50B   50A
 5.5779    1.2223   0.2240    0.4151

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1.2223	74.1850	0.5330	17.8396
0.2240	0.5330	5.7065	0.9712
0.4151	17.8396	0.9712	70.3070
breed group combination	8	75B	25A x 25B 75A
5.5389	1.2294	0.1888	0.4882
1.2294	71.7644	0.6515	22.4957
0.1888	0.6515	5.7504	1.0839
0.4882	22.4957	1.0839	74.8411
breed group combination	9	75B	25A x 00B 100A
5.5000	1.2365	0.1535	0.5613
1.2365	69.3438	0.7700	27.1517
0.1535	0.7700	5.7942	1.1965
0.5613	27.1517	1.1965	79.3752
breed group combination	10	50B	50A x 50B 50A
5.6022	1.1845	0.2050	0.4463
1.1845	73.9885	0.6000	21.0862
0.2050	0.6000	5.7945	0.9995
0.4463	21.0862	0.9995	71.7785
breed group combination	11	50B	50A x 25B 75A
5.6266	1.1467	0.1860	0.4774
1.1467	73.7920	0.6670	24.3329
0.1860	0.6670	5.8825	1.0277
0.4774	24.3329	1.0277	73.2500
breed group combination	12	50B	50A x 00B 100A
5.6510	1.1090	0.1670	0.5085
1.1090	73.5955	0.7340	27.5795
0.1670	0.7340	5.9705	1.0560
0.5085	27.5795	1.0560	74.7215
breed group combination	13	25B	75A x 25B 75A
5.7143	1.0641	0.1833	0.4666
1.0641	75.8196	0.6825	26.1701
0.1833	0.6825	6.0146	0.9716
0.4666	26.1701	0.9716	71.6589
breed group combination	14	25B	75A x 00B 100A
5.8020	0.9815	0.1805	0.4557
0.9815	77.8473	0.6980	28.0072
0.1805	0.6980	6.1468	0.9155
0.4557	28.0072	0.9155	70.0678
breed group combination	15	00B	100A x 00B 100A
5.9530	0.8540	0.1940	0.4030
0.8540	82.0990	0.6620	28.4350
0.1940	0.6620	6.3230	0.7750
0.4030	28.4350	0.7750	65.4140

=====

Environmental Covariances for set 1 MREMLM iter 0

=====

breed group combination	1	100B	00A x 100B 00A
13.5970	37.2540		
37.2540	298.1820		
breed group combination	2	100B	00A x 75B 25A
16.5570	40.3515		
40.3515	357.3839		
breed group combination	3	100B	00A x 50B 50A
17.4230	40.8882		
40.8882	383.8590		
breed group combination	4	100B	00A x 25B 75A
16.1950	38.8642		
38.8642	377.6074		
breed group combination	5	100B	00A x 00B 100A
12.8730	34.2795		
34.2795	338.6290		
breed group combination	6	75B	25A x 7B 25A
19.5170	43.4490		
43.4490	416.5858		
breed group combination	7	75B	25A x 50B 50A
20.3830	43.9857		
43.9857	443.0609		
breed group combination	8	75B	25A x 25B 75A
19.1550	41.9617		
41.9617	436.8093		
breed group combination	9	75B	25A x 00B 100A
15.8330	37.3770		
37.3770	397.8309		
breed group combination	10	50B	50A x 50B 50A
21.2490	44.5225		
44.5225	469.5360		
breed group combination	11	50B	50A x 25B 75A

```

20.0210    42.4985
42.4985    463.2844
breed group combination 12    50B    50A   x   00B   100A
  16.6990    37.9137
  37.9137    424.3060
breed group combination 13    25B    75A   x   25B   75A
  18.7930    40.4745
  40.4745    457.0328
breed group combination 14    25B    75A   x   00B   100A
  15.4710    35.8897
  35.8897    418.0544
breed group combination 15    00B   100A   x   00B   100A
  12.1490    31.3050
  31.3050    379.0760
=====
Phenotypic Covariances for set      1 MREMLEM iter      0
=====
breed group combination 1    100B   00A   x   100B   00A
  36.6000    46.1720
  46.1720    659.1850
breed group combination 2    100B   00A   x   75B   25A
  40.5761    50.2166
  50.2166    739.1014
breed group combination 3    100B   00A   x   50B   50A
  41.6637    50.7655
  50.7655    763.5258
breed group combination 4    100B   00A   x   25B   75A
  39.8631    47.8188
  47.8188    732.4581
breed group combination 5    100B   00A   x   00B   100A
  35.1740    41.3765
  41.3765    645.8985
breed group combination 6    75B   25A   x   7B   25A
  44.6596    54.1319
  54.1319    818.1793
breed group combination 7    75B   25A   x   50B   50A
  45.8547    54.5516
  54.5516    841.7651
breed group combination 8    75B   25A   x   25B   75A
  44.1614    51.4756
  51.4756    809.8590
breed group combination 9    75B   25A   x   00B   100A
  39.5798    44.9041
  44.9041    722.4609
breed group combination 10   50B   50A   x   50B   50A
  47.1573    54.8420
  54.8420    864.5125
breed group combination 11   50B   50A   x   25B   75A
  45.5714    51.6368
  51.6368    831.7679
breed group combination 12   50B   50A   x   00B   100A
  41.0972    44.9360
  44.9360    743.5312
breed group combination 13   25B   75A   x   25B   75A
  44.0931    48.3024
  48.3024    798.1848
breed group combination 14   25B   75A   x   00B   100A
  39.7263    41.4723
  41.4723    709.1096
breed group combination 15   00B   100A   x   00B   100A
  35.4670    34.5130
  34.5130    619.1960
=====
Heritabilities and Additive Genetic Correlations for set      1 MREMLEM iter      0
=====
breed group combination 1    100B   00A   x   100B   00A
  0.15      0.08    -0.04    0.06
  0.08      0.10    0.04     -0.01
  -0.04     0.04    0.17     0.09
  0.06     -0.01    0.09     0.24
breed group combination 2    100B   00A   x   75B   25A
  0.16      0.12    -0.04    0.04
  0.12      0.12    0.05     0.01
  -0.04     0.05    0.16     0.08
  0.04     0.01     0.08     0.20
breed group combination 3    100B   00A   x   50B   50A

```

0.16	0.13	-0.05	0.03
0.13	0.13	0.05	0.01
-0.05	0.05	0.16	0.07
0.03	0.01	0.07	0.18
breed group combination 4 100B 00A x 25B 75A			
0.16	0.12	-0.05	0.03
0.12	0.12	0.04	-0.02
-0.05	0.04	0.16	0.07
0.03	-0.02	0.07	0.17
breed group combination 5 100B 00A x 00B 100A			
0.16	0.07	-0.06	0.04
0.07	0.10	0.03	-0.09
-0.06	0.03	0.17	0.07
0.04	-0.09	0.07	0.16
breed group combination 6 75B 25A x 7B 25A			
0.16	0.15	-0.04	0.03
0.15	0.14	0.05	0.02
-0.04	0.05	0.15	0.07
0.03	0.02	0.07	0.17
breed group combination 7 75B 25A x 50B 50A			
0.16	0.15	-0.05	0.02
0.15	0.15	0.05	0.02
-0.05	0.05	0.15	0.06
0.02	0.02	0.06	0.15
breed group combination 8 75B 25A x 25B 75A			
0.16	0.14	-0.05	0.01
0.14	0.14	0.05	0.00
-0.05	0.05	0.16	0.05
0.01	0.00	0.05	0.14
breed group combination 9 75B 25A x 00B 100A			
0.16	0.11	-0.06	0.01
0.11	0.12	0.04	-0.06
-0.06	0.04	0.16	0.05
0.01	-0.06	0.05	0.13
breed group combination 10 50B 50A x 50B 50A			
0.16	0.16	-0.05	0.01
0.16	0.15	0.05	0.02
-0.05	0.05	0.15	0.05
0.01	0.02	0.05	0.14
breed group combination 11 50B 50A x 25B 75A			
0.16	0.15	-0.05	0.00
0.15	0.14	0.05	-0.01
-0.05	0.05	0.15	0.04
0.00	-0.01	0.04	0.12
breed group combination 12 50B 50A x 00B 100A			
0.16	0.12	-0.06	0.00
0.12	0.13	0.04	-0.06
-0.06	0.04	0.16	0.04
0.00	-0.06	0.04	0.11
breed group combination 13 25B 75A x 25B 75A			
0.16	0.14	-0.06	0.00
0.14	0.14	0.04	-0.04
-0.06	0.04	0.15	0.04
0.00	-0.04	0.04	0.11
breed group combination 14 25B 75A x 00B 100A			
0.16	0.11	-0.07	0.00
0.11	0.12	0.03	-0.11
-0.07	0.03	0.16	0.03
0.00	-0.11	0.03	0.09
breed group combination 15 00B 100A x 00B 100A			
0.16	0.06	-0.09	0.00
0.06	0.09	0.02	-0.25
-0.09	0.02	0.17	0.02
0.00	-0.25	0.02	0.08

=====
Interactibilities and Nonadditive Genetic Correlations for set 1 MREMLM iter 0
=====

breed group combination 1 100B 00A x 100B 00A			
0.16	0.05	0.06	0.01
0.05	0.13	0.01	0.04
0.06	0.01	0.15	0.03
0.01	0.04	0.03	0.08
breed group combination 2 100B 00A x 75B 25A			
0.14	0.06	0.05	0.01
0.06	0.11	0.01	0.12
0.05	0.01	0.14	0.04
0.01	0.12	0.04	0.08

```

breed group combination 3 100B 00A x 50B 50A
  0.13  0.06  0.04  0.02
  0.06  0.10  0.02  0.20
  0.04  0.02  0.13  0.05
  0.02  0.20  0.05  0.09
breed group combination 4 100B 00A x 25B 75A
  0.14  0.07  0.03  0.02
  0.07  0.10  0.03  0.28
  0.03  0.03  0.14  0.06
  0.02  0.28  0.06  0.10
breed group combination 5 100B 00A x 00B 100A
  0.15  0.07  0.03  0.03
  0.07  0.10  0.04  0.36
  0.03  0.04  0.16  0.06
  0.03  0.36  0.06  0.13
breed group combination 6 75B 25A x 7B 25A
  0.13  0.06  0.05  0.02
  0.06  0.09  0.02  0.19
  0.05  0.02  0.13  0.04
  0.02  0.19  0.04  0.08
breed group combination 7 75B 25A x 50B 50A
  0.12  0.06  0.04  0.02
  0.06  0.09  0.03  0.25
  0.04  0.03  0.12  0.05
  0.02  0.25  0.05  0.08
breed group combination 8 75B 25A x 25B 75A
  0.13  0.06  0.03  0.02
  0.06  0.09  0.03  0.31
  0.03  0.03  0.13  0.05
  0.02  0.31  0.05  0.09
breed group combination 9 75B 25A x 00B 100A
  0.14  0.06  0.03  0.03
  0.06  0.10  0.04  0.37
  0.03  0.04  0.15  0.06
  0.03  0.37  0.06  0.11
breed group combination 10 50B 50A x 50B 50A
  0.12  0.06  0.04  0.02
  0.06  0.09  0.03  0.29
  0.04  0.03  0.12  0.05
  0.02  0.29  0.05  0.08
breed group combination 11 50B 50A x 25B 75A
  0.12  0.06  0.03  0.02
  0.06  0.09  0.03  0.33
  0.03  0.03  0.13  0.05
  0.02  0.33  0.05  0.09
breed group combination 12 50B 50A x 00B 100A
  0.14  0.05  0.03  0.02
  0.05  0.10  0.04  0.37
  0.03  0.04  0.15  0.05
  0.02  0.37  0.05  0.10
breed group combination 13 25B 75A x 25B 75A
  0.13  0.05  0.03  0.02
  0.05  0.09  0.03  0.36
  0.03  0.03  0.14  0.05
  0.02  0.36  0.05  0.09
breed group combination 14 25B 75A x 00B 100A
  0.15  0.05  0.03  0.02
  0.05  0.11  0.03  0.38
  0.03  0.03  0.15  0.04
  0.02  0.38  0.04  0.10
breed group combination 15 00B 100A x 00B 100A
  0.17  0.04  0.03  0.02
  0.04  0.13  0.03  0.39
  0.03  0.03  0.18  0.04
  0.02  0.39  0.04  0.11

=====
Environmental Correlations for set 1 MREMLM iter 0
=====
breed group combination 1 100B 00A x 100B 00A
  1.00  0.59
  0.59  1.00
breed group combination 2 100B 00A x 75B 25A
  1.00  0.52
  0.52  1.00
breed group combination 3 100B 00A x 50B 50A
  1.00  0.50
  0.50  1.00

```

```

breed group combination 4 100B 00A x 25B 75A
  1.00 0.50
  0.50 1.00
breed group combination 5 100B 00A x 00B 100A
  1.00 0.52
  0.52 1.00
breed group combination 6 75B 25A x 7B 25A
  1.00 0.48
  0.48 1.00
breed group combination 7 75B 25A x 50B 50A
  1.00 0.46
  0.46 1.00
breed group combination 8 75B 25A x 25B 75A
  1.00 0.46
  0.46 1.00
breed group combination 9 75B 25A x 00B 100A
  1.00 0.47
  0.47 1.00
breed group combination 10 50B 50A x 50B 50A
  1.00 0.45
  0.45 1.00
breed group combination 11 50B 50A x 25B 75A
  1.00 0.44
  0.44 1.00
breed group combination 12 50B 50A x 00B 100A
  1.00 0.45
  0.45 1.00
breed group combination 13 25B 75A x 25B 75A
  1.00 0.44
  0.44 1.00
breed group combination 14 25B 75A x 00B 100A
  1.00 0.45
  0.45 1.00
breed group combination 15 00B 100A x 00B 100A
  1.00 0.46
  0.46 1.00

=====
Phenotypic Correlations for set 1 MREML EM iter 0
=====
breed group combination 1 100B 00A x 100B 00A
  1.00 0.30
  0.30 1.00
breed group combination 2 100B 00A x 75B 25A
  1.00 0.29
  0.29 1.00
breed group combination 3 100B 00A x 50B 50A
  1.00 0.28
  0.28 1.00
breed group combination 4 100B 00A x 25B 75A
  1.00 0.28
  0.28 1.00
breed group combination 5 100B 00A x 00B 100A
  1.00 0.27
  0.27 1.00
breed group combination 6 75B 25A x 7B 25A
  1.00 0.28
  0.28 1.00
breed group combination 7 75B 25A x 50B 50A
  1.00 0.28
  0.28 1.00
breed group combination 8 75B 25A x 25B 75A
  1.00 0.27
  0.27 1.00
breed group combination 9 75B 25A x 00B 100A
  1.00 0.27
  0.27 1.00
breed group combination 10 50B 50A x 50B 50A
  1.00 0.27
  0.27 1.00
breed group combination 11 50B 50A x 25B 75A
  1.00 0.27
  0.27 1.00
breed group combination 12 50B 50A x 00B 100A
  1.00 0.26
  0.26 1.00
breed group combination 13 25B 75A x 25B 75A
  1.00 0.26

```

```

0.26      1.00
breed group combination 14    25B    75A   x  00B   100A
 1.00      0.25
 0.25      1.00
breed group combination 15    00B   100A   x  00B   100A
 1.00      0.23
 0.23      1.00
=====
=====
```

## OUTPUT FILE 3 = genetic predictions file (WRTSOL)

### File WRTSOL: Sample of Sire Genetic Predictions.

sqnum	bullid	iig	ibg	geneff	geneval	BIRTH_D	WEANIN_D	BIRTH_M	WEANIN_M
1	6834245	15	15	add 12	pgv	-5.3123	-10.5272	2.7911	1.3800
1	6834245	15	15	add 12	sep	1.2874	4.4137	1.3892	4.5879
1	6834245	15	15	add 12	sol/gsd	-4.5010	-2.7530	2.2858	0.4007
1	6834245	15	15	add 12	sep/gsd	109	115	114	133
1	6834245	15	15	add 12	bifacc	-9	-15	-14	-33
1	6834245	15	15	nad 12	pgv	1.3142	8.7213	0.3113	14.6003
1	6834245	15	15	nad 12	sep	1.3534	5.0712	1.3359	4.1488
1	6834245	15	15	nad 12	sol/gsd	0.9829	1.7593	0.2335	3.6080
1	6834245	15	15	nad 12	sep/gsd	101	102	100	103
1	6834245	15	15	nad 12	bifacc	-1	-2	0	-3
1	6834245	15	15	tot 12	pgv	-3.9981	-1.8059	3.1024	15.9803
1	6834245	15	15	tot 12	sep	2.1815	7.6703	2.2803	7.1746
1	6834245	15	15	tot 12	sol/gsd	-2.2418	-0.2885	1.7160	3.0073
1	6834245	15	15	tot 12	sep/gsd	122	123	126	135
1	6834245	15	15	tot 12	bifacc	-22	-23	-26	-35
2	10362604	15	15	add 12	pgv	-5.3351	-11.4822	2.6917	1.3041
2	10362604	15	15	add 12	sep	1.2694	4.3750	1.3845	4.5830
2	10362604	15	15	add 12	sol/gsd	-4.5203	-3.0027	2.2044	0.3787
2	10362604	15	15	add 12	sep/gsd	108	114	113	133
2	10362604	15	15	add 12	bifacc	-8	-14	-13	-33
2	10362604	15	15	nad 12	pgv	1.2658	7.5122	0.1834	14.3007
2	10362604	15	15	nad 12	sep	1.3271	4.9883	1.3189	4.1214
2	10362604	15	15	nad 12	sol/gsd	0.9467	1.5154	0.1376	3.5339
2	10362604	15	15	nad 12	sep/gsd	99	101	99	102
2	10362604	15	15	nad 12	bifacc	1	-1	1	-2
2	10362604	15	15	tot 12	pgv	-4.0693	-3.9701	2.8751	15.6049
2	10362604	15	15	tot 12	sep	2.1438	7.5710	2.2646	7.1525
2	10362604	15	15	tot 12	sol/gsd	-2.2817	-0.6341	1.5903	2.9366
2	10362604	15	15	tot 12	sep/gsd	120	121	125	135
2	10362604	15	15	tot 12	bifacc	-20	-21	-25	-35
3	9000014	13	13	add 12	pgv	-3.9588	-7.2931	2.2414	1.4685
3	9000014	13	13	add 12	sep	1.4098	5.5181	1.3851	5.1359
3	9000014	13	13	add 12	sol/gsd	-2.9492	-1.3878	1.7210	0.3154
3	9000014	13	13	add 12	sep/gsd	105	105	106	110
3	9000014	13	13	add 12	bifacc	-5	-5	-6	-10
3	9000014	13	13	nad 12	pgv	1.3288	9.7650	0.2852	14.9571
3	9000014	13	13	nad 12	sep	1.3868	5.3079	1.3398	4.3094
3	9000014	13	13	nad 12	sol/gsd	0.9837	1.8969	0.2130	3.5425
3	9000014	13	13	nad 12	sep/gsd	103	103	100	102
3	9000014	13	13	nad 12	bifacc	-3	-3	0	-2
3	9000014	13	13	tot 12	pgv	-2.6300	2.4719	2.5265	16.4256
3	9000014	13	13	tot 12	sep	2.2376	8.6867	2.1695	7.6686
3	9000014	13	13	tot 12	sol/gsd	-1.3810	0.3360	1.3527	2.6134
3	9000014	13	13	tot 12	sep/gsd	118	118	116	122
3	9000014	13	13	tot 12	bifacc	-18	-18	-16	-22
4	8442952	15	15	add 12	pgv	-6.1298	-8.8626	2.9218	1.2297
4	8442952	15	15	add 12	sep	1.2393	4.3083	1.3861	4.5768
4	8442952	15	15	add 12	sol/gsd	-5.1937	-2.3177	2.3929	0.3571
4	8442952	15	15	add 12	sep/gsd	105	113	114	133
4	8442952	15	15	add 12	bifacc	-5	-13	-14	-33
4	8442952	15	15	nad 12	pgv	0.8957	10.2694	0.2676	14.5522
4	8442952	15	15	nad 12	sep	1.3604	5.1074	1.3468	4.1692
4	8442952	15	15	nad 12	sol/gsd	0.6699	2.0716	0.2007	3.5961
4	8442952	15	15	nad 12	sep/gsd	102	103	101	103
4	8442952	15	15	nad 12	bifacc	-2	-3	-1	-3
4	8442952	15	15	tot 12	pgv	-5.2341	1.4067	3.1895	15.7820
4	8442952	15	15	tot 12	sep	2.1378	7.5999	2.2838	7.1758
4	8442952	15	15	tot 12	sol/gsd	-2.9348	0.2247	1.7642	2.9699
4	8442952	15	15	tot 12	sep/gsd	120	121	126	135
4	8442952	15	15	tot 12	bifacc	-20	-21	-26	-35

5	7640000	1	1	add	12	pgv	0.3699	1.3263	-0.1333	-0.6149
5	7640000	1	1	add	12	sep	1.0890	3.8401	1.1592	5.5013
5	7640000	1	1	add	12	sol/gsd	0.3114	0.3228	-0.1067	-0.0982
5	7640000	1	1	add	12	sep/gsd	92	93	93	88
5	7640000	1	1	add	12	bifacc	8	7	7	12
5	7640000	1	1	nad	12	pgv	2.1793	13.1541	0.1762	14.1309
5	7640000	1	1	nad	12	sep	1.4764	5.6304	1.5225	5.1632
5	7640000	1	1	nad	12	sol/gsd	1.2737	2.0433	0.1020	2.5901
5	7640000	1	1	nad	12	sep/gsd	86	87	88	95
5	7640000	1	1	nad	12	bifacc	14	13	12	5
5	7640000	1	1	tot	12	pgv	2.5493	14.4805	0.0429	13.5160
5	7640000	1	1	tot	12	sep	1.6003	6.1293	1.6968	6.6863
5	7640000	1	1	tot	12	sol/gsd	1.2238	1.8960	0.0201	1.6278
5	7640000	1	1	tot	12	sep/gsd	77	80	80	81
5	7640000	1	1	tot	12	bifacc	23	20	20	19
6	5670200	1	1	add	12	pgv	-0.0287	0.7090	-0.1329	3.4802
6	5670200	1	1	add	12	sep	1.1754	4.0731	1.1779	5.6999
6	5670200	1	1	add	12	sol/gsd	-0.0241	0.1725	-0.1064	0.5560
6	5670200	1	1	add	12	sep/gsd	99	99	94	91
6	5670200	1	1	add	12	bifacc	1	1	6	9
6	5670200	1	1	nad	12	pgv	1.3201	9.6974	-0.0173	16.9177
6	5670200	1	1	nad	12	sep	1.7394	6.5677	1.5640	5.2598
6	5670200	1	1	nad	12	sol/gsd	0.7715	1.5064	-0.0100	3.1009
6	5670200	1	1	nad	12	sep/gsd	102	102	91	96
6	5670200	1	1	nad	12	bifacc	-2	-2	9	4
6	5670200	1	1	tot	12	pgv	1.2915	10.4064	-0.1502	20.3979
6	5670200	1	1	tot	12	sep	2.0996	7.7301	1.7873	7.1347
6	5670200	1	1	tot	12	sol/gsd	0.6200	1.3626	-0.0704	2.4566
6	5670200	1	1	tot	12	sep/gsd	101	101	84	86
6	5670200	1	1	tot	12	bifacc	-1	-1	16	14
7	5150000	1	1	add	12	pgv	-0.1132	-0.3632	0.2102	-2.8406
7	5150000	1	1	add	12	sep	1.1048	3.8958	1.1697	5.6404
7	5150000	1	1	add	12	sol/gsd	-0.0952	-0.0884	0.1683	-0.4538
7	5150000	1	1	add	12	sep/gsd	93	95	94	90
7	5150000	1	1	add	12	bifacc	7	5	6	10
7	5150000	1	1	nad	12	pgv	1.0011	10.0377	0.7861	12.5121
7	5150000	1	1	nad	12	sep	1.5227	5.8384	1.5473	5.2319
7	5150000	1	1	nad	12	sol/gsd	0.5851	1.5592	0.4550	2.2934
7	5150000	1	1	nad	12	sep/gsd	89	91	90	96
7	5150000	1	1	nad	12	bifacc	11	9	10	4
7	5150000	1	1	tot	12	pgv	0.8879	9.6745	0.9963	9.6716
7	5150000	1	1	tot	12	sep	1.6891	6.4882	1.7506	7.0051
7	5150000	1	1	tot	12	sol/gsd	0.4263	1.2667	0.4673	1.1648
7	5150000	1	1	tot	12	sep/gsd	81	85	82	84
7	5150000	1	1	tot	12	bifacc	19	15	18	16
8	5111000	13	13	add	12	pgv	-4.6837	-9.8136	1.6133	-3.1786
8	5111000	13	13	add	12	sep	1.1948	4.7483	1.2629	4.7856
8	5111000	13	13	add	12	sol/gsd	-3.4893	-1.8675	1.2388	-0.6827
8	5111000	13	13	add	12	sep/gsd	89	90	97	103
8	5111000	13	13	add	12	bifacc	11	10	3	-3
8	5111000	13	13	nad	12	pgv	0.8995	8.8553	-0.2565	11.6104
8	5111000	13	13	nad	12	sep	1.2595	4.8681	1.2586	4.1254
8	5111000	13	13	nad	12	sol/gsd	0.6659	1.7202	-0.1916	2.7498
8	5111000	13	13	nad	12	sep/gsd	93	95	94	98
8	5111000	13	13	nad	12	bifacc	7	5	6	2
8	5111000	13	13	tot	12	pgv	-3.7843	-0.9583	1.3568	8.4318
8	5111000	13	13	tot	12	sep	1.8044	7.1620	1.9122	7.0265
8	5111000	13	13	tot	12	sol/gsd	-1.9872	-0.1303	0.7264	1.3415
8	5111000	13	13	tot	12	sep/gsd	95	97	102	112
8	5111000	13	13	tot	12	bifacc	5	3	-2	-12
9	5000000	13	13	add	12	pgv	-3.9044	-7.6717	2.5954	1.1505
9	5000000	13	13	add	12	sep	1.3128	5.2084	1.3107	4.9391
9	5000000	13	13	add	12	sol/gsd	-2.9087	-1.4599	1.9928	0.2471
9	5000000	13	13	add	12	sep/gsd	98	99	101	106
9	5000000	13	13	add	12	bifacc	2	1	-1	-6
9	5000000	13	13	nad	12	pgv	1.3021	9.5234	0.5792	14.6877
9	5000000	13	13	nad	12	sep	1.3328	5.1406	1.2904	4.1997
9	5000000	13	13	nad	12	sol/gsd	0.9639	1.8500	0.4326	3.4787
9	5000000	13	13	nad	12	sep/gsd	99	100	96	99
9	5000000	13	13	nad	12	bifacc	1	0	4	1
9	5000000	13	13	tot	12	pgv	-2.6023	1.8517	3.1746	15.8382
9	5000000	13	13	tot	12	sep	2.0515	8.0969	2.0135	7.2954
9	5000000	13	13	tot	12	sol/gsd	-1.3665	0.2517	1.6996	2.5199
9	5000000	13	13	tot	12	sep/gsd	108	110	108	116
9	5000000	13	13	tot	12	bifacc	-8	-10	-8	-16
10	4520000	13	13	add	12	pgv	-3.4167	6.0525	3.2848	3.8850
10	4520000	13	13	add	12	sep	1.2037	4.7584	1.2634	4.7192
10	4520000	13	13	add	12	sol/gsd	-2.5454	1.1518	2.5222	0.8344

10	4520000	13	13	add	12	sep/gsd	90	91	97	101
10	4520000	13	13	add	12	bifacc	10	9	3	-1
10	4520000	13	13	nad	12	pgv	1.4287	18.4248	1.0445	18.0648
10	4520000	13	13	nad	12	sep	1.2990	4.9995	1.2715	4.1055
10	4520000	13	13	nad	12	sol/gsd	1.0576	3.5791	0.7801	4.2785
10	4520000	13	13	nad	12	sep/gsd	96	97	95	97
10	4520000	13	13	nad	12	bifacc	4	3	5	3
10	4520000	13	13	tot	12	pgv	-1.9880	24.4773	4.3292	21.9498
10	4520000	13	13	tot	12	sep	1.8798	7.3814	1.9301	6.9148
10	4520000	13	13	tot	12	sol/gsd	-1.0439	3.3274	2.3178	3.4923
10	4520000	13	13	tot	12	sep/gsd	99	100	103	110
10	4520000	13	13	tot	12	bifacc	1	0	-3	-10
11	4400000	1	1	add	12	pgv	-0.1997	0.2678	0.2844	0.1010
11	4400000	1	1	add	12	sep	1.0770	3.7956	1.1273	5.1046
11	4400000	1	1	add	12	sol/gsd	-0.1681	0.0652	0.2277	0.0161
11	4400000	1	1	add	12	sep/gsd	91	92	90	82
11	4400000	1	1	add	12	bifacc	9	8	10	18
11	4400000	1	1	nad	12	pgv	0.7632	11.3417	0.7345	15.0995
11	4400000	1	1	nad	12	sep	1.4594	5.5458	1.4502	4.9760
11	4400000	1	1	nad	12	sol/gsd	0.4460	1.7618	0.4251	2.7677
11	4400000	1	1	nad	12	sep/gsd	85	86	84	91
11	4400000	1	1	nad	12	bifacc	15	14	16	9
11	4400000	1	1	tot	12	pgv	0.5635	11.6095	1.0188	15.2005
11	4400000	1	1	tot	12	sep	1.5644	5.9705	1.5347	5.7541
11	4400000	1	1	tot	12	sol/gsd	0.2705	1.5201	0.4779	1.8307
11	4400000	1	1	tot	12	sep/gsd	75	78	72	69
11	4400000	1	1	tot	12	bifacc	25	22	28	31
12	4285112	15	15	add	12	pgv	-4.9906	-8.9398	3.1746	0.5329
12	4285112	15	15	add	12	sep	1.2676	4.3668	1.3992	4.5972
12	4285112	15	15	add	12	sol/gsd	-4.2284	-2.3378	2.5999	0.1547
12	4285112	15	15	add	12	sep/gsd	107	114	115	133
12	4285112	15	15	add	12	bifacc	-7	-14	-15	-33
12	4285112	15	15	nad	12	pgv	1.4653	10.2308	0.3940	14.2039
12	4285112	15	15	nad	12	sep	1.3604	5.1005	1.3494	4.1718
12	4285112	15	15	nad	12	sol/gsd	1.0959	2.0638	0.2956	3.5100
12	4285112	15	15	nad	12	sep/gsd	102	103	101	103
12	4285112	15	15	nad	12	bifacc	-2	-3	-1	-3
12	4285112	15	15	tot	12	pgv	-3.5253	1.2910	3.5687	14.7368
12	4285112	15	15	tot	12	sep	2.1625	7.6360	2.3004	7.1998
12	4285112	15	15	tot	12	sol/gsd	-1.9766	0.2062	1.9739	2.7733
12	4285112	15	15	tot	12	sep/gsd	121	122	127	135
12	4285112	15	15	tot	12	bifacc	-21	-22	-27	-35
13	4000000	13	13	add	12	pgv	-4.2550	-11.5926	2.2779	0.9351
13	4000000	13	13	add	12	sep	1.2588	4.9927	1.4137	5.2029
13	4000000	13	13	add	12	sol/gsd	-3.1699	-2.2060	1.7491	0.2008
13	4000000	13	13	add	12	sep/gsd	94	95	109	112
13	4000000	13	13	add	12	bifacc	6	5	-9	-12
13	4000000	13	13	nad	12	pgv	1.1312	6.6993	0.3240	14.1998
13	4000000	13	13	nad	12	sep	1.2958	5.0156	1.3618	4.3479
13	4000000	13	13	nad	12	sol/gsd	0.8374	1.3014	0.2420	3.3631
13	4000000	13	13	nad	12	sep/gsd	96	97	102	103
13	4000000	13	13	nad	12	bifacc	4	3	-2	-3
13	4000000	13	13	tot	12	pgv	-3.1238	-4.8932	2.6019	15.1349
13	4000000	13	13	tot	12	sep	1.9309	7.6614	2.2326	7.8001
13	4000000	13	13	tot	12	sol/gsd	-1.6404	-0.6652	1.3930	2.4080
13	4000000	13	13	tot	12	sep/gsd	101	104	120	124
13	4000000	13	13	tot	12	bifacc	-1	-4	-20	-24
14	3870140	15	15	add	12	pgv	-5.2250	-10.0622	3.1272	1.4619
14	3870140	15	15	add	12	sep	1.3175	4.4761	1.3624	4.5474
14	3870140	15	15	add	12	sol/gsd	-4.4270	-2.6314	2.5610	0.4245
14	3870140	15	15	add	12	sep/gsd	112	117	112	132
14	3870140	15	15	add	12	bifacc	-12	-17	-12	-32
14	3870140	15	15	nad	12	pgv	1.3481	9.6695	0.3703	14.6683
14	3870140	15	15	nad	12	sep	1.3724	5.1245	1.3424	4.1646
14	3870140	15	15	nad	12	sol/gsd	1.0083	1.9506	0.2778	3.6248
14	3870140	15	15	nad	12	sep/gsd	103	103	101	103
14	3870140	15	15	nad	12	bifacc	-3	-3	-1	-3
14	3870140	15	15	tot	12	pgv	-3.8769	-0.3927	3.4975	16.1303
14	3870140	15	15	tot	12	sep	2.2290	7.7779	2.2545	7.1397
14	3870140	15	15	tot	12	sol/gsd	-2.1738	-0.0627	1.9345	3.0355
14	3870140	15	15	tot	12	sep/gsd	125	124	125	134
14	3870140	15	15	tot	12	bifacc	-25	-24	-25	-34
15	3800047	15	15	add	12	pgv	-5.5935	-10.3161	2.5980	1.3556
15	3800047	15	15	add	12	sep	1.2916	4.4295	1.2638	4.3825
15	3800047	15	15	add	12	sol/gsd	-4.7392	-2.6978	2.1277	0.3936
15	3800047	15	15	add	12	sep/gsd	109	116	103	127
15	3800047	15	15	add	12	bifacc	-9	-16	-3	-27
15	3800047	15	15	nad	12	pgv	1.1421	9.4829	0.3259	14.6546

15	3800047	15	15	nad	12	sep	1.3601	5.0941	1.3150	4.1191
15	3800047	15	15	nad	12	sol/gsd	0.8542	1.9130	0.2444	3.6214
15	3800047	15	15	nad	12	sep/gsd	102	103	99	102
15	3800047	15	15	nad	12	bifacc	-2	-3	1	-2
15	3800047	15	15	tot	12	pgv	-4.4514	-0.8332	2.9239	16.0102
15	3800047	15	15	tot	12	sep	2.1917	7.7071	2.1234	6.9148
15	3800047	15	15	tot	12	sol/gsd	-2.4959	-0.1331	1.6173	3.0129
15	3800047	15	15	tot	12	sep/gsd	123	123	117	130
15	3800047	15	15	tot	12	bifacc	-23	-23	-17	-30
16	3856515	1	1	add	12	pgv	0.3484	-0.1246	0.2095	-1.0744
16	3856515	1	1	add	12	sep	1.0952	3.8660	1.1845	5.7861
16	3856515	1	1	add	12	sol/gsd	0.2933	-0.0303	0.1678	-0.1717
16	3856515	1	1	add	12	sep/gsd	92	94	95	92
16	3856515	1	1	add	12	bifacc	8	6	5	8
16	3856515	1	1	nad	12	pgv	1.9035	9.6924	0.8280	13.6364
16	3856515	1	1	nad	12	sep	1.4863	5.6806	1.5845	5.3062
16	3856515	1	1	nad	12	sol/gsd	1.1125	1.5056	0.4792	2.4995
16	3856515	1	1	nad	12	sep/gsd	87	88	92	97
16	3856515	1	1	nad	12	bifacc	13	12	8	3
16	3856515	1	1	tot	12	pgv	2.2519	9.5678	1.0375	12.5620
16	3856515	1	1	tot	12	sep	1.6219	6.2256	1.8284	7.3351
16	3856515	1	1	tot	12	sol/gsd	1.0810	1.2528	0.4867	1.5129
16	3856515	1	1	tot	12	sep/gsd	78	82	86	88
16	3856515	1	1	tot	12	bifacc	22	18	14	12
17	3850506	1	1	add	12	pgv	0.2034	-2.0176	0.1009	-2.5847
17	3850506	1	1	add	12	sep	1.0888	3.8437	1.1702	5.6409
17	3850506	1	1	add	12	sol/gsd	0.1712	-0.4910	0.0808	-0.4129
17	3850506	1	1	add	12	sep/gsd	92	94	94	90
17	3850506	1	1	add	12	bifacc	8	6	6	10
17	3850506	1	1	nad	12	pgv	1.7226	5.7843	0.6944	12.5032
17	3850506	1	1	nad	12	sep	1.4707	5.6119	1.5491	5.2326
17	3850506	1	1	nad	12	sol/gsd	1.0067	0.8985	0.4019	2.2918
17	3850506	1	1	nad	12	sep/gsd	86	87	90	96
17	3850506	1	1	nad	12	bifacc	14	13	10	4
17	3850506	1	1	tot	12	pgv	1.9260	3.7667	0.7954	9.9185
17	3850506	1	1	tot	12	sep	1.5920	6.1100	1.7542	7.0074
17	3850506	1	1	tot	12	sol/gsd	0.9246	0.4932	0.3731	1.1945
17	3850506	1	1	tot	12	sep/gsd	76	80	82	84
17	3850506	1	1	tot	12	bifacc	24	20	18	16
18	3840047	15	15	add	12	pgv	-5.2115	-10.3163	3.1709	0.7944
18	3840047	15	15	add	12	sep	1.3087	4.4674	1.3051	4.4734
18	3840047	15	15	add	12	sol/gsd	-4.4156	-2.6978	2.5968	0.2307
18	3840047	15	15	add	12	sep/gsd	111	117	107	130
18	3840047	15	15	add	12	bifacc	-11	-17	-7	-30
18	3840047	15	15	nad	12	pgv	1.3549	9.5425	0.3922	14.3346
18	3840047	15	15	nad	12	sep	1.3699	5.1222	1.3295	4.1481
18	3840047	15	15	nad	12	sol/gsd	1.0133	1.9250	0.2941	3.5423
18	3840047	15	15	nad	12	sep/gsd	102	103	100	103
18	3840047	15	15	nad	12	bifacc	-2	-3	0	-3
18	3840047	15	15	tot	12	pgv	-3.8566	-0.7738	3.5631	15.1290
18	3840047	15	15	tot	12	sep	2.2167	7.7657	2.1795	7.0399
18	3840047	15	15	tot	12	sol/gsd	-2.1624	-0.1236	1.9708	2.8471
18	3840047	15	15	tot	12	sep/gsd	124	124	121	132
18	3840047	15	15	tot	12	bifacc	-24	-24	-21	-32
19	3830394	1	1	add	12	pgv	-0.0662	0.4241	-0.1991	2.1632
19	3830394	1	1	add	12	sep	1.1796	4.0862	1.2012	5.9039
19	3830394	1	1	add	12	sol/gsd	-0.0557	0.1032	-0.1594	0.3456
19	3830394	1	1	add	12	sep/gsd	99	99	96	94
19	3830394	1	1	add	12	bifacc	1	1	4	6
19	3830394	1	1	nad	12	pgv	1.3132	9.6551	-0.0969	16.0241
19	3830394	1	1	nad	12	sep	1.7396	6.5679	1.6239	5.3657
19	3830394	1	1	nad	12	sol/gsd	0.7675	1.4998	-0.0561	2.9372
19	3830394	1	1	nad	12	sep/gsd	102	102	94	98
19	3830394	1	1	nad	12	bifacc	-2	-2	6	2
19	3830394	1	1	tot	12	pgv	1.2470	10.0792	-0.2960	18.1873
19	3830394	1	1	tot	12	sep	2.1014	7.7338	1.9093	7.5930
19	3830394	1	1	tot	12	sol/gsd	0.5986	1.3197	-0.1389	2.1904
19	3830394	1	1	tot	12	sep/gsd	101	101	90	91
19	3830394	1	1	tot	12	bifacc	-1	-1	10	9
20	3830378	1	1	add	12	pgv	0.1141	2.4742	0.2680	0.1048
20	3830378	1	1	add	12	sep	1.0983	3.8643	1.1296	5.1005
20	3830378	1	1	add	12	sol/gsd	0.0961	0.6021	0.2147	0.0167
20	3830378	1	1	add	12	sep/gsd	92	94	90	81
20	3830378	1	1	add	12	bifacc	8	6	10	19
20	3830378	1	1	nad	12	pgv	1.4889	15.5493	0.7901	14.6901
20	3830378	1	1	nad	12	sep	1.5243	5.8385	1.4501	4.9690
20	3830378	1	1	nad	12	sol/gsd	0.8702	2.4154	0.4573	2.6926
20	3830378	1	1	nad	12	sep/gsd	89	91	84	91

20	3830378	1	1	nad	12	bifacc	11	9	16	9
20	3830378	1	1	tot	12	pgv	1.6031	18.0234	1.0582	14.7949
20	3830378	1	1	tot	12	sep	1.6932	6.4888	1.5350	5.7193
20	3830378	1	1	tot	12	sol/gsd	0.7696	2.3599	0.4964	1.7818
20	3830378	1	1	tot	12	sep/gsd	81	85	72	69
20	3830378	1	1	tot	12	bifacc	19	15	28	31

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