Command Language Interface of MiX99 (CLIM)

Ismo Strandén

MiX99 course: test-day models and single step genomic prediction
COURSE DAY 1, April 10th, 2025

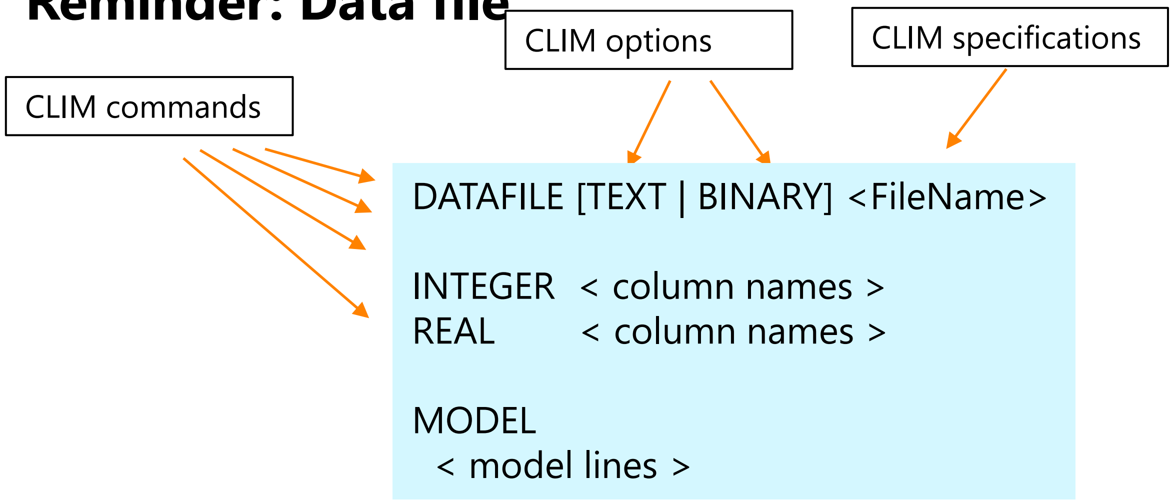
Introduction

Assumed that basic concepts of CLIM known

Contents

- Reminder: simplest CLIM
- GBLUP: many ways to achieve the same
- SNPBLUP and RegIndex to easy computations
- Giving variance components by CLIM
- Complex models and macros

Reminder: Data file



CLIM commands

CLIM options

CLIM specifications

```
DATAFILE [TEXT | BINARY] <FileName>

INTEGER  < column names >
REAL     < column names >

MODEL
  < model lines >
```

- Default format is “text format”, where columns are separated by space (alternative: binary format)
- There must not be a header in the file
- Sorting of records can reduce solving time
- **Example:**

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

A least squares model!

- The data file contains observations and model effect information (classification effects or regression coefficients)
- Each record ,i.e., line has two parts
  - 1st part: integer numbers (classification effects, sorting variables, index values)
  - 2nd part: real numbers (observations, covariables, weights)
- Integer numbers ≤ 0 are assumed as missing
- Missing real values are coded by a missing variable code (e.g. -9999.0)

id herd year xlin x2 pheno1 pheno2

```
1 1     1 0.17001745 0.028905933 -0.7079236 -0.7079236
2 1     2 0.81993105 0.672286934 25.1489620 25.1489620
3 1     1 0.10122364 0.010246224  1.3475760  1.3475760
4 1     2 0.89622887 0.803226186 27.0999594 27.0999594
5 1     1 0.33690867 0.113507451  2.7174209  2.7174209
…
```

Some ways to compute a simple two trait GBLUP model

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

PEDFILE LOWER iG.dat
PEDIGREE id FILE

RANDOM id

PARFILE vc_2tr.par

MODEL
    pheno1  = xlin x2 year herd id
    pheno2  = xlin x2 year herd id
```

Equivalent in MiX99

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

GBLUP id LOWER iG.dat

RANDOM id

PARFILE vc_2tr.par

MODEL
    pheno1  = xlin x2 year herd id
    pheno2  = xlin x2 year herd id
```

Different in MiX99

But results are the same

COVFILE approach

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

COVFILE id LOWER iG.dat

RANDOM id

PARFILE vc_2tr.par

MODEL
    pheno1  = xlin x2 year herd id
    pheno2  = xlin x2 year herd id
```

iG.dat

```
5 5
1 2 3 4 5
 27.5
-60.0 137.5
-15.0  35.0  10.0
 25.0 -57.5 -15.0  25.0
-47.5 107.5  27.5 -45.0  85.0
```

Solreg:

```
Trt Reg-No  Solution    Trait  Covariable
 1    1   9.6142      pheno1   xlin
 1    2   5.1683      pheno1   x2
 2    1   9.6142      pheno2   xlin
 2    2   5.1683      pheno2   x2
```

Solfix:

```
Fact. Trt       Level     N-Obs  Solution            Factor Trait
  1    1          1         10   -1.7419                year pheno1
  1    2          1         10   -1.7419                year pheno2
  1    1          2         10    13.427                year pheno1
  1    2          2         10    13.427                year pheno2
  2    1          1         10   0.49912                herd pheno1
  2    2          1         10   0.49912                herd pheno2
  2    1          2         10    11.186                herd pheno1
  2    2          2         10    11.186                herd pheno2
```

Solani:

```
1       1       4 -0.85062E-01 -0.85062E-01
2       1       4 -0.63589E-01 -0.63589E-01
3       1       4  0.37509E-01  0.37509E-01
4       1       4 -0.98786E-01 -0.98786E-01
5       1       4 -0.30458E-01 -0.30458E-01
```

← Genomic breeding values →

Solr01:

```
1          4 -0.85062E-01 -0.85062E-01
2          4 -0.63589E-01 -0.63589E-01
3          4  0.37509E-01  0.37509E-01
4          4 -0.98786E-01 -0.98786E-01
5          4 -0.30458E-01 -0.30458E-01
```

Note: different formats of inverse G in GBLUP can lead to same computations

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

GBLUP id LOWER iG.dat

RANDOM id

PARFILE vc_2tr.par

MODEL
    pheno1  = xlin x2 year herd id
    pheno2  = xlin x2 year herd id
```

Inverse of G matrix in lower triangle dense format:

iG.dat

```
5 5
1 2 3 4 5
 27.5
-60.0 137.5
-15.0  35.0  10.0
 25.0 -57.5 -15.0  25.0
-47.5 107.5  27.5 -45.0  85.0
```

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

GBLUP id iGijv.dat

RANDOM id

PARFILE vc_2tr.par

MODEL
    pheno1  = xlin x2 year herd id
    pheno2  = xlin x2 year herd id
```

Inverse of G matrix in lower ijvalue format:
iGijv.dat

```
1  1  27.5
2  1 -60.0
3  1 -15.0
4  1  25.0
5  1 -47.5
2  2 137.5
3  2  35.0
4  2 -57.5
5  2 107.5
3  3  10.0
4  3 -15.0
5  3  27.5
4  4  25.0
5  4 -45.0
5  5  85.0
```

By default, the solver reads matrices to RAM
→ These formats lead to same computations.

Lower dense is more efficient (storage).

→ Some approaches may look different but solver may treat them the same.

For large models, “bin” or “raw” formats are more efficient.

We’ll cover that later.

Example: SNPBLUP model by REGMATRIX

SNPBLUP.clm:

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE    RM_geno.dat
REGMATRIX  Random SNP id=1 first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

This SNPBLUP model produces marker solutions, not directly breeding values.

Solreg:

```
Trt Reg-No  Solution     Trait   Covariable
 1    1    9.6142       pheno1    xlin
 1    2    5.1683       pheno1    x2
 2    1    9.6142       pheno2    xlin
 2    2    5.1683       pheno2    x2
```

Solfix:

```
Fact. Trt         Level     N-Obs  Solution                Factor Trait
  1    1            1         10  -1.7949                   year pheno1
  1    2            1         10  -1.7949                   year pheno2
  1    1            2         10   13.374                   year pheno1
  1    2            2         10   13.374                   year pheno2
```

Solf01:

```
 1          10  0.44614       0.44614
 2          10   11.133        11.133
```

Solreg_mat:

```
Trt  Matrix  Effect  Solution     Mat-Name
  1       1       1  0.59477E-01 SNP
  1       1       2  0.33264E-01 SNP
  1       1       3  0.89845E-02 SNP
  1       1       4  0.34570E-01 SNP
  1       1       5 -0.30324E-01 SNP
  2       1       1  0.59477E-01 SNP
  2       1       2  0.33264E-01 SNP
  2       1       3  0.89845E-02 SNP
  2       1       4  0.34570E-01 SNP
  2       1       5 -0.30324E-01 SNP
```

Solutions similar but
No breeding values directly
by this SNPBLUP model
and
preparing data is awkward.

GBLUP.clm

```
Trt Reg-No  Solution     Trait   Covariable
 1    1    9.6142       pheno1    xlin
 1    2    5.1683       pheno1    x2
 2    1    9.6142       pheno2    xlin
 2    2    5.1683       pheno2    x2
```

```
Fact. Trt         Level     N-Obs  Solution               Factor Trait
  1    1            1         10  -1.7419                   year pheno1
  1    2            1         10  -1.7419                   year pheno2
  1    1            2         10   13.427                   year pheno1
  1    2            2         10   13.427                   year pheno2
  2    1            1         10  0.49912                   herd pheno1
  2    2            1         10  0.49912                   herd pheno2
  2    1            2         10   11.186                   herd pheno1
  2    2            2         10   11.186                   herd pheno2
```

Solani:

```
1        1        4 -0.85062E-01 -0.85062E-01
2        1        4 -0.63589E-01 -0.63589E-01
3        1        4  0.37509E-01  0.37509E-01
4        1        4 -0.98786E-01 -0.98786E-01
5        1        4 -0.30458E-01 -0.30458E-01
```

© Luke

Example:
Using
REGINDEX in REGMATRIX

SNPBLUP.clm:

```
DATAFILE   data.dat

INTEGER    id herd year
REAL       xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE     RM_geno.dat
REGMATRIX  Random SNP id=1 first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

data_geno.dat

```
1 1    1 0.17001745 0.028905933 -0.7079236
2 1    2 0.81993105 0.672286934 25.1489620
3 1    1 0.10122364 0.010246224  1.3475760
4 1    2 0.89622887 0.803226186 27.0999594
5 1    1 0.33690867 0.113507451  2.7174209
1 1    2 0.07535836 0.005678883 14.0722251
2 1    1 0.24611983 0.060574969  0.7791845
3 1    2 0.08260870 0.006824198 15.0323770
4 1    1 0.80893255 0.654371868  9.1249718
5 1    2 0.61464561 0.377789222 22.3646796
1 2    1 0.99636615 0.992745498 25.7296024
2 2    2 0.68082035 0.463516349 35.1481721
3 2    1 0.55235644 0.305097638 16.8500291
4 2    2 0.78372758 0.614228920 35.3142666
5 2    1 0.92074811 0.847777080 22.2667699
1 2    2 0.34093483 0.116236556 28.2127363
2 2    1 0.83466677 0.696668623 20.1699458
3 2    2 0.90065598 0.811181186 35.3930001
4 2    1 0.25502135 0.065035889 11.9655357
5 2    2 0.58140852 0.338035871 31.7120296
```

RM_geno.dat

```
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
```

RegMatrix data and DataFile data must allign exactly!

→ When an individual has several observations, genotypes in the RegMatrix will be repeated.

1) In this case, a lot of repetition of the same data
2) REGFILE needs to be sorted in the same order as DATAFILE

It is simple to solve these using a **REGINDEX** in REGMATRIX.

Example:
Using
REGINDEX in REGMATRIX

SNPBLUP.clm

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE     RM_geno.dat
REGMATRIX  Random SNP id=1 first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

SNPBLUPi.clm

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE     RMi_geno.dat
REGMATRIX  Random SNP id=1 RegIndex=id first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

data_geno.dat

```
1 1    1 0.17001745 0.028905933 -0.7079236
2 1    2 0.81993105 0.672286934 25.1489620
3 1    1 0.10122364 0.010246224  1.3475760
4 1    2 0.89622887 0.803226186 27.0999594
5 1    1 0.33690867 0.113507451  2.7174209
1 1    2 0.07535836 0.005678883 14.0722251
2 1    1 0.24611983 0.060574969  0.7791845
3 1    2 0.08260870 0.006824198 15.0323770
4 1    1 0.80893255 0.654371868  9.1249718
5 1    2 0.61464561 0.377789222 22.3646796
1 2    1 0.99636615 0.992745498 25.7296024
2 2    2 0.68082035 0.463516349 35.1481721
3 2    1 0.55235644 0.305097638 16.8500291
4 2    2 0.78372758 0.614228920 35.3142666
5 2    1 0.92074811 0.847777080 22.2667699
1 2    2 0.34093483 0.116236556 28.2127363
2 2    1 0.83466677 0.696668623 20.1699458
3 2    2 0.90065598 0.811181186 35.3930001
4 2    1 0.25502135 0.065035889 11.9655357
5 2    2 0.58140852 0.338035871 31.7120296
```

RM_geno.dat

```
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
```

RMi_geno.dat

```
1 0 1 2 0 1
2 1 0 1 1 2
3 1 2 1 2 2
4 0 1 0 1 2
5 0 2 1 0 0
```

RegIndex gives the owner of the row in the data file.

1) Each owner can have only one line in REGFILE

2) There is no need to sort the REGFILE file.

Example:
SNPBLUP model

SNPBLUPi.clm

```
DATAFILE  data.dat

INTEGER   id herd year
REAL      xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE    RMi_geno.dat
REGMATRIX  Random SNP id=1 RegIndex=id first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

Results remain the same!

Solreg:

```
Trt Reg-No  Solution     Trait  Covariable
  1    1   9.6142       pheno1   xlin
  1    2   5.1683       pheno1   x2
  2    1   9.6142       pheno2   xlin
  2    2   5.1683       pheno2   x2
```

Solfix:

```
Fact. Trt        Level    N-Obs  Solution              Factor Trait
  1    1            1       10  -1.7949                   year pheno1
  1    2            1       10  -1.7949                   year pheno2
  1    1            2       10   13.374                   year pheno1
  1    2            2       10   13.374                   year pheno2
```

Solf01:

```
 1         10  0.44614        0.44614
 2         10   11.133         11.133
```

Solreg_mat:

```
Trt  Matrix  Effect  Solution     Mat-Name
  1       1       1  0.59477E-01 SNP
  1       1       2  0.33264E-01 SNP
  1       1       3  0.89845E-02 SNP
  1       1       4  0.34570E-01 SNP
  1       1       5 -0.30324E-01 SNP
  2       1       1  0.59477E-01 SNP
  2       1       2  0.33264E-01 SNP
  2       1       3  0.89845E-02 SNP
  2       1       4  0.34570E-01 SNP
  2       1       5 -0.30324E-01 SNP
```

New:

SolDGV01:

```
1         8      0.20909E-01      0.20909E-01
2         8      0.42382E-01      0.42382E-01
3         8      0.14348          0.14348
4         8      0.71849E-02      0.71849E-02
5         8      0.75513E-01      0.75513E-01
```

GBLUP.clm

```
Trt Reg-No  Solution     Trait  Covariable
  1    1   9.6142       pheno1   xlin
  1    2   5.1683       pheno1   x2
  2    1   9.6142       pheno2   xlin
  2    2   5.1683       pheno2   x2
```

```
Fact. Trt        Level    N-Obs  Solution              Factor Trait
  1    1            1       10  -1.7419                   year pheno1
  1    2            1       10  -1.7419                   year pheno2
  1    1            2       10   13.427                   year pheno1
  1    2            2       10   13.427                   year pheno2
  2    1            1       10  0.49912                   herd pheno1
  2    2            1       10  0.49912                   herd pheno2
  2    1            2       10   11.186                   herd pheno1
  2    2            2       10   11.186                   herd pheno2
```

Solani:

```
1      1      4 -0.85062E-01 -0.85062E-01
2      1      4 -0.63589E-01 -0.63589E-01
3      1      4  0.37509E-01  0.37509E-01
4      1      4 -0.98786E-01 -0.98786E-01
5      1      4 -0.30458E-01 -0.30458E-01
```

Example:
SNPBLUP model

SNPBLUPi.clm

```
DATAFILE   data.dat

INTEGER    id herd year
REAL       xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE    RMi_geno.dat
REGMATRIX  Random SNP id=1 RegIndex=id first=2 last=6
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

SNPBLUPi.clm breeding values

SolDGV01:

```
1          8      0.20909E-01      0.20909E-01
2          8      0.42382E-01      0.42382E-01
3          8      0.14348          0.14348
4          8      0.71849E-02      0.71849E-02
5          8      0.75513E-01      0.75513E-01
```

GBLUP.clm breeding values

Solani:

```
1       1       4 -0.85062E-01 -0.85062E-01
2       1       4 -0.63589E-01 -0.63589E-01
3       1       4  0.37509E-01  0.37509E-01
4       1       4 -0.98786E-01 -0.98786E-01
5       1       4 -0.30458E-01 -0.30458E-01
```

Correlation is one but there is a level difference of 0.10597: SolDGV01 = Solani + 0.10597
This is due to not centering REGMATRIX as is done in the **G** matrix.

```
DATAFILE   data.dat

INTEGER    id herd year
REAL       xlin x2 pheno1 pheno2

DATASORT PEDIGREECODE=id

REGFILE    RMi_geno.dat
REGMATRIX  Random SNP id=1 RegIndex=id first=2 last=6 CENTER=1
REGPARFILE snp_2tr.par # snp variance

PARFILE res_2tr.par

MODEL
    pheno1  = xlin x2 year herd
    pheno2  = xlin x2 year herd
```

Centering as for **G** in $\mathbf{G}^{-1}$ of iG.dat gives SolDGV01:

```
1          8     -0.85062E-01     -0.85062E-01
2          8     -0.63589E-01     -0.63589E-01
3          8      0.37509E-01      0.37509E-01
4          8     -0.98786E-01     -0.98786E-01
5          8     -0.30458E-01     -0.30458E-01
```

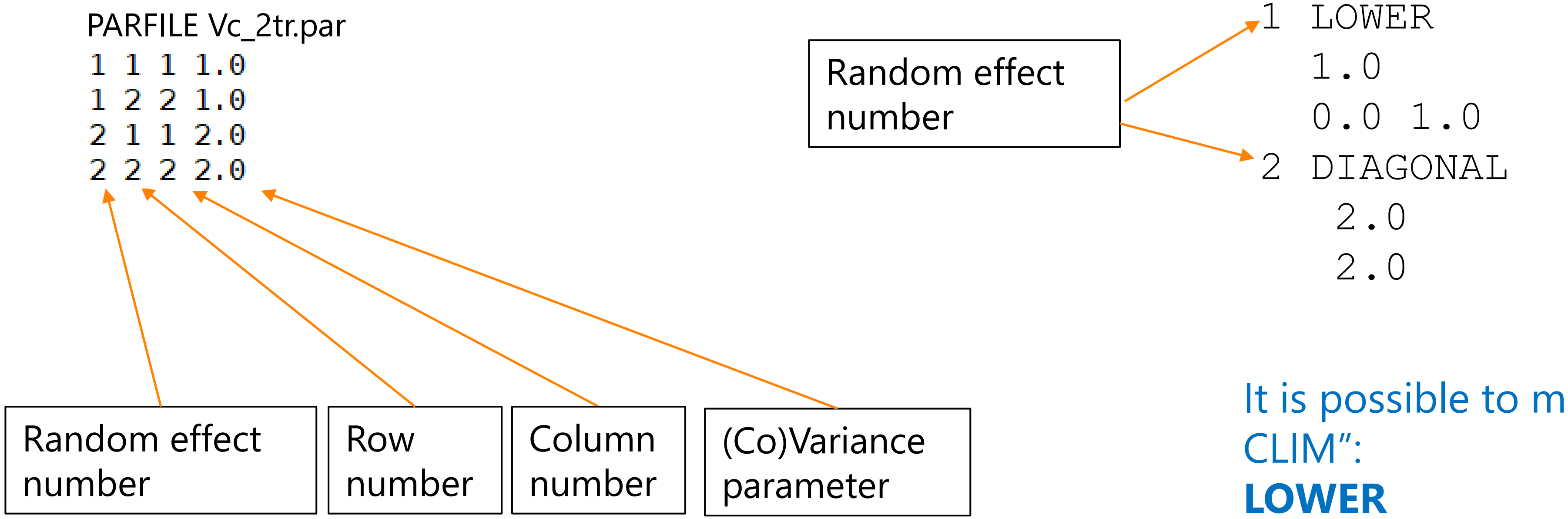
Other useful options in REGMATRIX: SCALE & FORMAT

SCALE: allows using the same variances as for GBLUP model as scaling done like for the G matrix
FORMAT: allows SNP marker packing (FORMAT=m) or not space separated SNPs (FORMAT=s)

Similar options for single-step SNPBLUP considered later.

Variance component parameter file

GBLUP model



```
PARFILE Vc_2tr.par
1 1 1 1.0
1 2 2 1.0
2 1 1 2.0
2 2 2 2.0
```

→ Genetic variance is 1.0
→ Residual variance is 2.0

Alternatively (in new MiX99)

```
PARFILE CLIM
1 LOWER
  1.0
  0.0 1.0
2 DIAGONAL
   2.0
   2.0
```

It is possible to mix formats after “PARFILE CLIM”:

LOWER	**Lower dense matrix**
DIAGONAL	**A diagonal matrix**
IDENTITY	**Identity matrix**
SPARSE	**The typical parfile format**

Special option 1: PARFILE IDENTITY → all variance matrices set to identity matrices

Special option 2: PARFILE MIXED <parfile> → parfile has the LOWER/DIAGONAL … commands

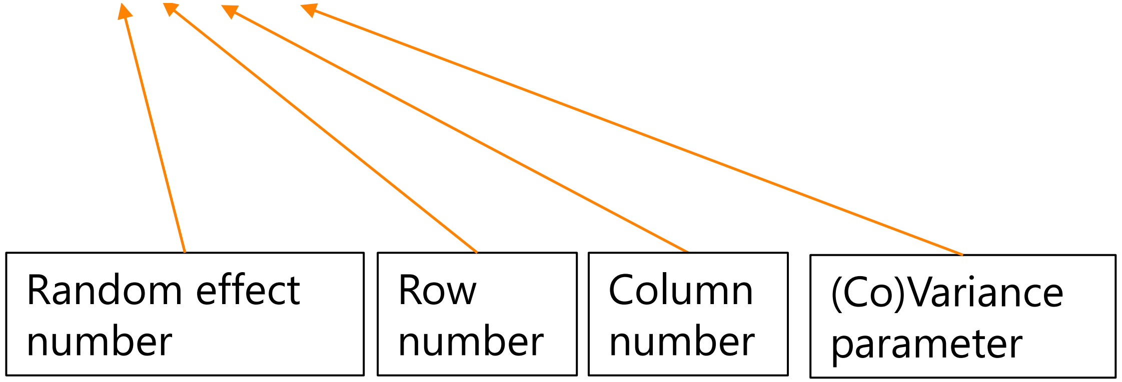
Variance component parameter file

GBLUP model

PARFILE vc_2tr.par

vc_2tr.par:

```
1 1 1 1.0
1 2 2 1.0
2 1 1 2.0
2 2 2 2.0
```



Random effect number

Row number

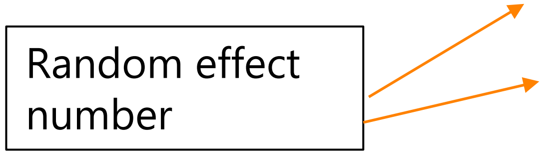
Column number

(Co)Variance parameter

→ Genetic variance is 1.0

→ Residual variance is 2.0

```
PARFILE MIXED vc_2tr.mix
```



Random effect number

```
vc_2tr.mix:
1 IDENTITY
2 DIAGONAL
   2.0
   2.0
```

Or in CLIM equivalently:

```
PARFILE CLIM
1 IDENTITY
2 DIAGONAL
   2.0
   2.0
```

Reminder: MODEL instructions with component names

Single trait repeatability model with a fixed regression function

$$milk = c_1*cov1 + c_2*cov2 + c_3*cov3 + c_4*cov4 + HYS + p + a + e$$

- p = nonhereditary animal effect
- a = random additive genetic effect
- where the regression function could be a 3rd order Legendre on days in milk

```
DATAFILE  RM.dat   # Data file
PEDFILE   RM.ped   # Pedigree file
PARFILE   RM.var   # Variance component file

INTEGER   animal HYS DIM                # Integer column names
REAL      milk cov1 cov2 cov3 cov4    # Real column names

MODEL
  milk = cov1 cov2 cov3 cov4  HYS  P(animal) G(animal) # The model

PEDIGREE  G am     # Genetics associated with animal code: am=animal model
RANDOM    P        # Random nonhereditary animal effect

WITHINBLOCKORDER G P HYS # Random effects are within block effects
```

- General regression effects are always given at the beginning of the model line
- Only the covariables are specified

User-defined component names: P and G

Example: two trait GBLUP model (PARFILE CLIM available in new MiX99)

```
DATAFILE small_GBLUP_with_misses.dat

INTEGER ID ones HerdYear
REAL    Cov1 Y1 Y2

MISSING -99999.
DATASORT PEDIGREECODE=ID

GBLUP DGV LOWER iGL.dat

PARFILE CLIM
1 DIAGONAL
  2.0
  2.1
2 LOWER
  1.0
  0.5 0.8
  0.1 0.01 0.2
3 LOWER
  3.0
  0.8 3.1

RANDOM PE DGV

MODEL
  Y1 = HerdYear    -   PE(ID) DGV(1 Cov1 | ID)
  Y2 =    -       ones PE(ID) DGV(1 -     | ID)
```

PE

DGV

Residual

Tmpfile.par

1 1 1 2.0	
1 2 2 2.1	
2 1 1 1.0	**DGV variance of trait 1, component 1**
2 2 1 0.5	**DGV covariance between 1st components in traits 1 & 2**
2 2 2 0.8	**DGV variance of trait 2**
2 3 1 0.1	**DGV covariance of trait 1 components 1 and Cov1**
2 3 2 0.01	**DGV covariance of Cov1 of trait 1 and trait 2**
2 3 3 0.2	**DGV variance of Cov1 of trait 1**
3 1 1 3.0	
3 2 1 0.8	
3 2 2 3.1	

Variance counting is column down from left to right

Macros can simplify models

- Some model parts are replaced by a short name
- Less errors because same macro used in different traits
- Large models look simpler

Example model:

- 6 trait model with maternal and direct effects
- Showing the model is not possible
- Following are given steps to simpler macro based model

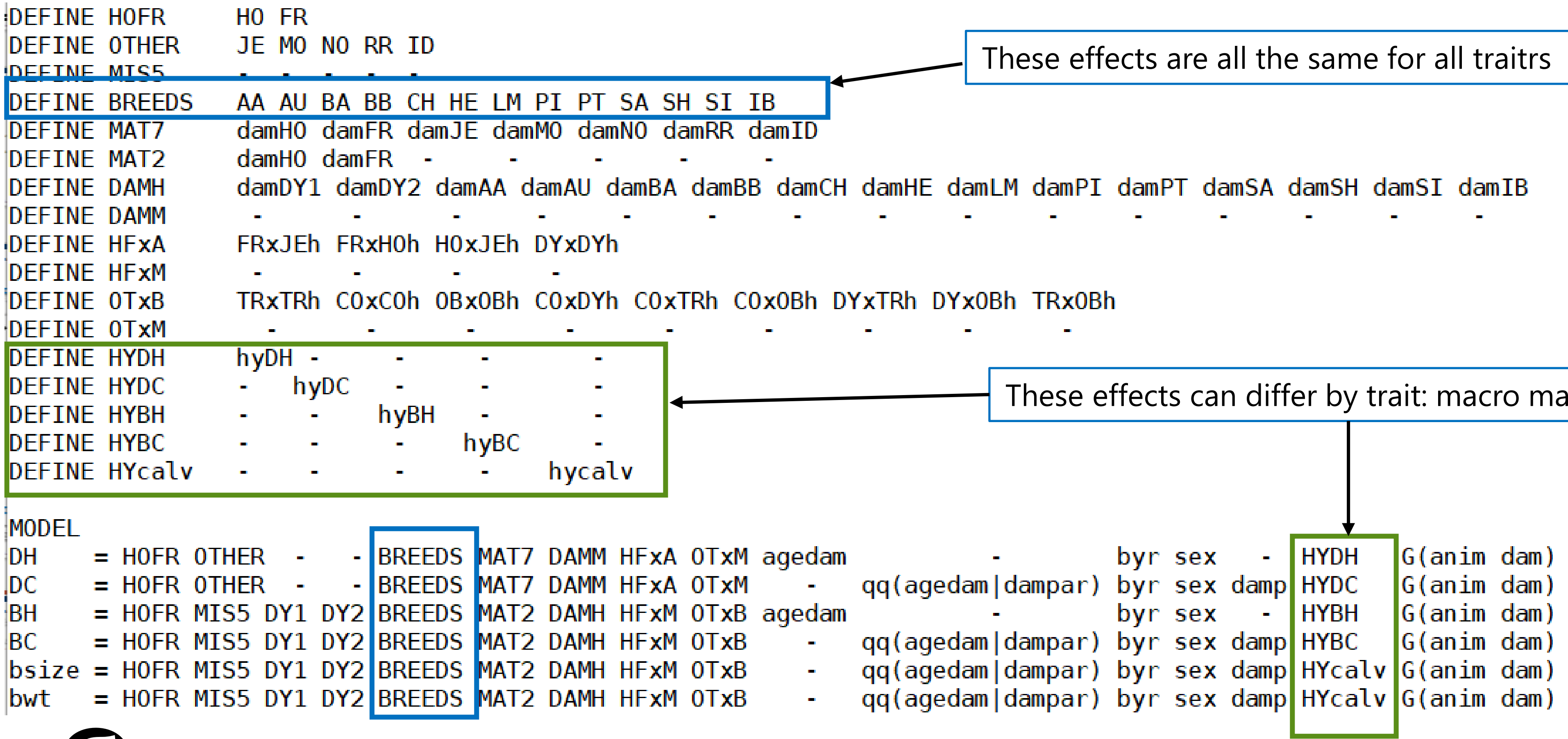
Macro: DEFINE <name> <what this name means>

NOTE: macro name should not be the same as an already used CLIM command or column name or component name.
Depending on where macro has been defined, this rule may be broken (not recommended!)

Using CLIM having macros:

mix99i --usemacros AMBLUP_macros.clm

Where AMBLUP_macros.clm has the CLIM file.



```
DEFINE HOFR     HO FR
DEFINE OTHER    JE MO NO RR ID
DEFINE MIS5     -  -  -  -  -
DEFINE BREEDS   AA AU BA BB CH HE LM PI PT SA SH SI IB
DEFINE MAT7     damHO damFR damJE damMO damNO damRR damID
DEFINE MAT2     damHO damFR  -     -     -     -     -
DEFINE DAMH     damDY1 damDY2 damAA damAU damBA damBB damCH damHE damLM damPI damPT damSA damSH damSI damIB
DEFINE DAMM      -      -      -     -     -     -     -     -     -     -     -     -     -     -     -
DEFINE HFxA     FRxJEh FRxHOh HOxJEh DYxDYh
DEFINE HFxM      -      -      -      -
DEFINE OTxB     TRxTRh COxCOh OBxOBh COxDYh COxTRh COxOBh DYxTRh DYxOBh TRxOBh
DEFINE OTxM       -      -      -      -      -      -      -      -      -
DEFINE HYDH     hyDH -     -     -       -
DEFINE HYDC     -   hyDC   -     -       -
DEFINE HYBH     -    -    hyBH   -       -
DEFINE HYBC     -    -     -    hyBC     -
DEFINE HYcalv   -    -     -     -    hycalv

MODEL
DH    = HOFR OTHER  -   - BREEDS MAT7 DAMM HFxA OTxM agedam          -        byr sex   -  HYDH   G(anim dam)
DC    = HOFR OTHER  -   - BREEDS MAT7 DAMM HFxA OTxM   -   qq(agedam|dampar) byr sex damp HYDC   G(anim dam)
BH    = HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB agedam          -        byr sex   -  HYBH   G(anim dam)
BC    = HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB   -   qq(agedam|dampar) byr sex damp HYBC   G(anim dam)
bsize = HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB   -   qq(agedam|dampar) byr sex damp HYcalv G(anim dam)
bwt   = HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB   -   qq(agedam|dampar) byr sex damp HYcalv G(anim dam)
```

These effects are all the same for all traitrs

These effects can differ by trait: macro makes a substitution

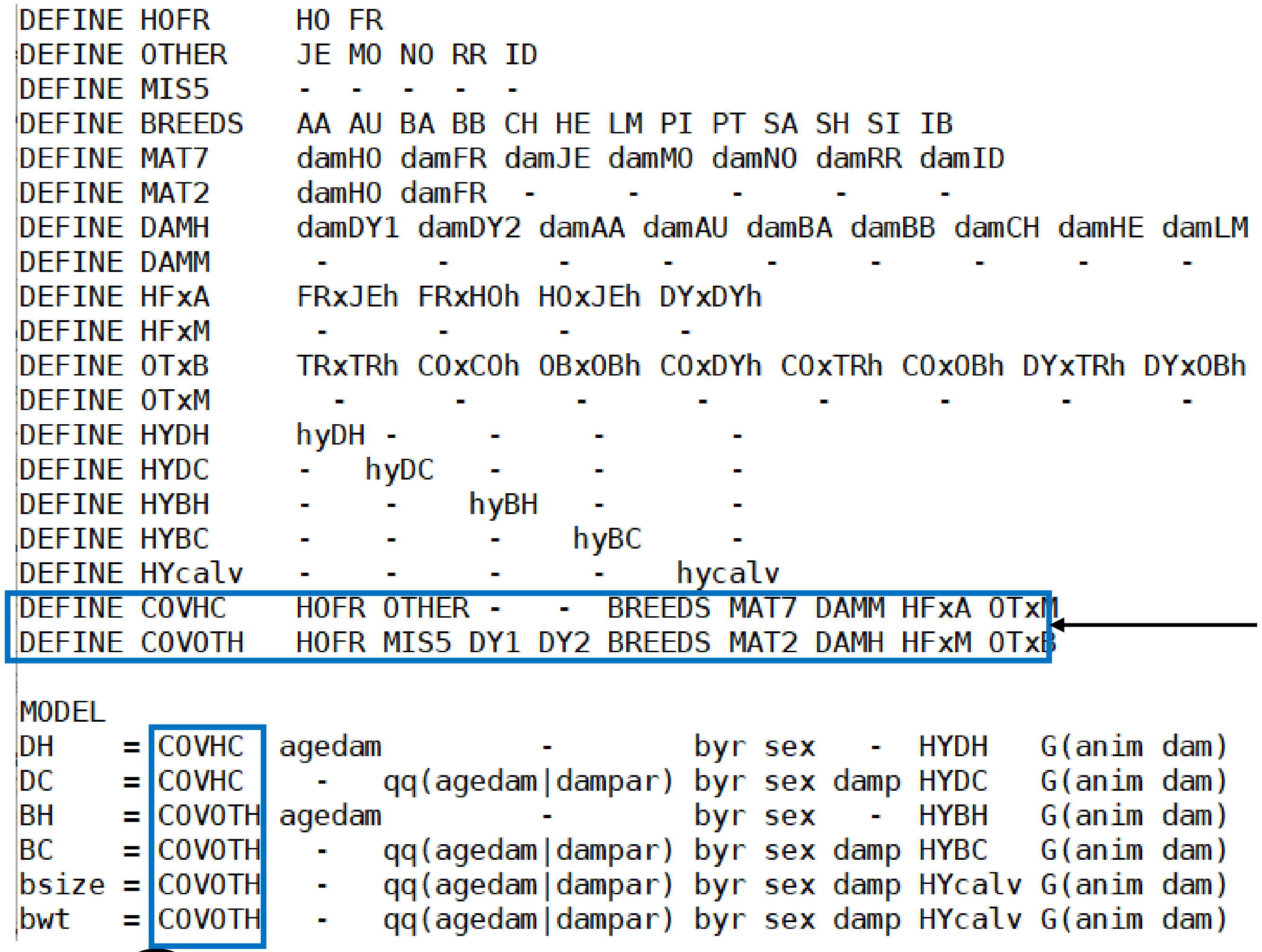
Remember: Order of effects have to follow the required order: regression, fixed class effects, random effects, additive genetics

Macros using macros possible

Using CLIM having macros:

mix99i --usemacros AMBLUP_macros2.clm

Where AMBLUP_macros2.clm has the CLIM file.



```
DEFINE HOFR     HO FR
DEFINE OTHER    JE MO NO RR ID
DEFINE MIS5     -  -  -  -  -
DEFINE BREEDS   AA AU BA BB CH HE LM PI PT SA SH SI IB
DEFINE MAT7     damHO damFR damJE damMO damNO damRR damID
DEFINE MAT2     damHO damFR  -     -     -     -     -
DEFINE DAMH     damDY1 damDY2 damAA damAU damBA damBB damCH damHE damLM damPI damPT damSA damSH damSI damIB
DEFINE DAMM      -      -      -     -     -     -     -     -     -     -     -     -     -     -     -
DEFINE HFxA     FRxJEh FRxHOh HOxJEh DYxDYh
DEFINE HFxM      -      -      -      -
DEFINE OTxB     TRxTRh COxCOh OBxOBh COxDYh COxTRh COxOBh DYxTRh DYxOBh TRxOBh
DEFINE OTxM       -      -      -      -      -      -      -      -      -
DEFINE HYDH     hyDH -     -     -       -
DEFINE HYDC     -   hyDC   -     -       -
DEFINE HYBH     -    -    hyBH   -       -
DEFINE HYBC     -    -     -    hyBC     -
DEFINE HYcalv   -    -     -     -    hycalv
DEFINE COVHC    HOFR OTHER -   -  BREEDS MAT7 DAMM HFxA OTxM
DEFINE COVOTH   HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB

MODEL
DH    = COVHC  agedam         -        byr sex  -   HYDH   G(anim dam)
DC    = COVHC    -    qq(agedam|dampar) byr sex damp HYDC   G(anim dam)
BH    = COVOTH agedam         -        byr sex  -   HYBH   G(anim dam)
BC    = COVOTH   -    qq(agedam|dampar) byr sex damp HYBC   G(anim dam)
bsize = COVOTH   -    qq(agedam|dampar) byr sex damp HYcalv G(anim dam)
bwt   = COVOTH   -    qq(agedam|dampar) byr sex damp HYcalv G(anim dam)
```

Macros having macros are defined after the macros they include

A simplified model

Using CLIM having macros:

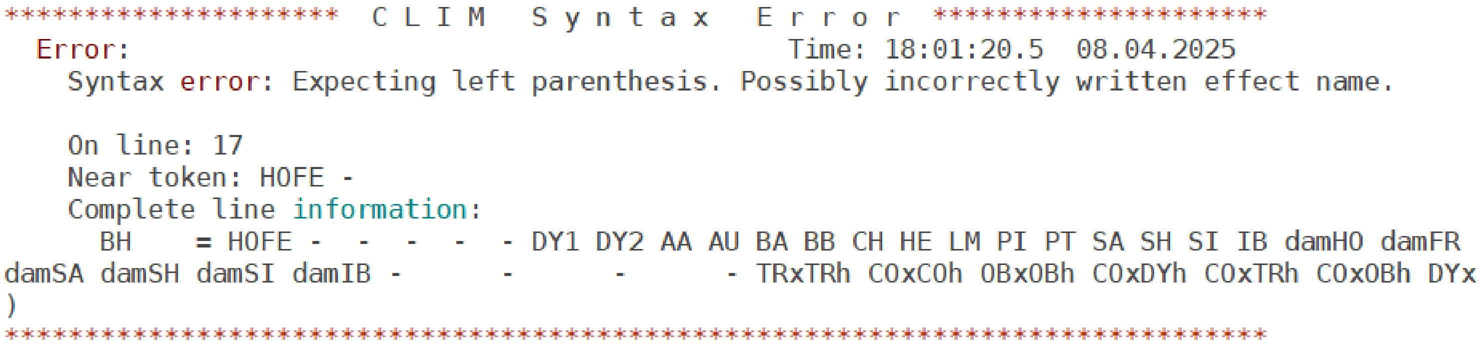
mix99i --usemacros AMBLUP_macros2.clm

Where AMBLUP_macros2.clm has the CLIM file.

```
DEFINE HOFR     HO FR
DEFINE OTHER    JE MO NO RR ID
DEFINE MIS5     -  -  -  -  -
DEFINE BREEDS   AA AU BA BB CH HE LM PI PT SA SH SI IB
DEFINE MAT7     damHO damFR damJE damMO damNO damRR damID
DEFINE MAT2     damHO damFR  -     -     -     -     -
DEFINE DAMH     damDY1 damDY2 damAA damAU damBA damBB damCH damHE damLM damPI damPT damSA damSH damSI damIB
DEFINE DAMM      -      -      -     -     -     -     -     -     -     -     -     -     -     -     -
DEFINE HFxA     FRxJEh FRxHOh HOxJEh DYxDYh
DEFINE HFxM      -      -      -      -
DEFINE OTxB     TRxTRh COxCOh OBxOBh COxDYh COxTRh COxOBh DYxTRh DYxOBh TRxOBh
DEFINE OTxM       -      -      -      -      -      -      -      -      -
DEFINE HYDH     hyDH -     -     -       -
DEFINE HYDC     -   hyDC   -     -       -
DEFINE HYBH     -    -    hyBH   -       -
DEFINE HYBC     -    -     -    hyBC     -
DEFINE HYcalv   -    -     -     -    hycalv
DEFINE COVHC    HOFR OTHER -   -  BREEDS MAT7 DAMM HFxA OTxM
DEFINE COVOTH   HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB
DEFINE FIXC1    agedam         -        byr sex   -
DEFINE FIXC2      -   qq(agedam|dampar) byr sex damp
DEFINE GENETIC  G(anim dam)


MODEL
DH    = COVHC  FIXC1 HYDH   GENETIC
DC    = COVHC  FIXC2 HYDC   GENETIC
BH    = COVOTH FIXC1 HYBH   GENETIC
BC    = COVOTH FIXC2 HYBC   GENETIC
bsize = COVOTH FIXC2 HYcalv GENETIC
bwt   = COVOTH FIXC2 HYcalv GENETIC
```

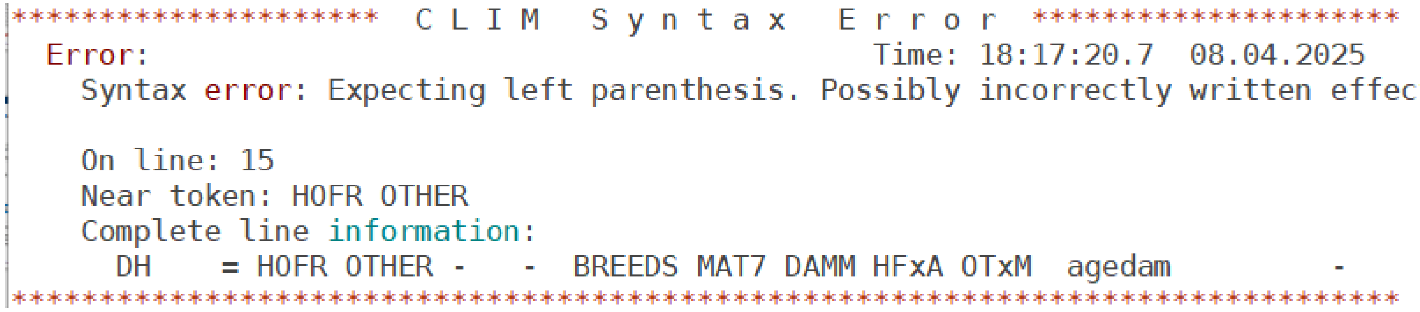
Using macros may give uninformative error messages



```
********************* C L I M   S y n t a x   E r r o r *********************
  Error:                                          Time: 18:01:20.5  08.04.2025
    Syntax error: Expecting left parenthesis. Possibly incorrectly written effect name.

    On line: 17
    Near token: HOFE -
    Complete line information:
      BH    = HOFE -   -   -   -   - DY1 DY2 AA AU BA BB CH HE LM PI PT SA SH SI IB damHO damFR
damSA damSH damSI damIB -       -       -       - TRxTRh COxCOh OBxOBh COxDYh COxTRh COxOBh DYx
)
*******************************************************************************
```

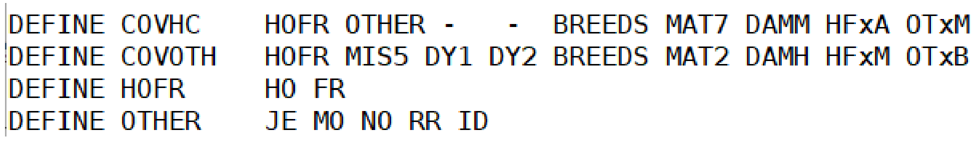
Should have used HOFR



```
********************* C L I M   S y n t a x   E r r o r *********************
  Error:                                          Time: 18:17:20.7   08.04.2025
    Syntax error: Expecting left parenthesis. Possibly incorrectly written effect name.

    On line: 15
    Near token: HOFR OTHER
    Complete line information:
      DH    = HOFR OTHER -    -   BREEDS MAT7 DAMM HFxA OTxM   agedam          -
*******************************************************************************
```

Should define macros using macros later



```
DEFINE COVHC     HOFR OTHER -    -  BREEDS MAT7 DAMM HFxA OTxM
DEFINE COVOTH    HOFR MIS5 DY1 DY2 BREEDS MAT2 DAMH HFxM OTxB
DEFINE HOFR      HO FR
DEFINE OTHER     JE MO NO RR ID
```

Error message usually looks like this and seem not very informative!
Here OTHER is not present in the original DATAFILE columns suggesting macro was not replaced by the string intended.

DEFINE MODEL   HO FR ⟶ MODEL command is changed to be ‘HO FR’ → ERROR: Syntax error or unknown command.

Questions?

Luke