MiX99

Solving Large Mixed Model Equations

Release XI/2019

Command Language Interface Manual (CLIM)

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Preface

Development of MiX99 was initiated to allow more sophisticated models in estimation of breeding values for dairy cattle. In the first versions the emphasis was on computational efficiency and the target users were experts on genetic evaluations. Therefore the logic of model definitions were more from an animal breeding perspective. The foremost application of this software is solving of large-scale genetic and genomic evaluations for national dairy cattle evaluations. Nevertheless, we have tried to keep the software as a general tool, where many models can be used. As a result, besides cattle, MiX99 is used in genetic evaluation of other species like pig, horse, sheep, goats, fish, foxes, poultry, and for many types of research work.

Disclaimer

MiX99 software is owned by Natural Resources Institute Finland (Luke). When using this program you agree with the following terms. You are not allowed to distribute, copy, give or transfer MiX99, neither under the same nor under a different name. Any decisions based on information given by MiX99 are made at your own responsibility and risk. Only limited technical support can be provided, but vital questions on its use can be directed to the authors (mix99@luke.fi). Please report any bugs to the authors. MiX99 can be referenced by (MiX99 Development Team, 2019). If you would like to use MiX99, please contact Animal Genetics at Natural Resources Institute Finland[1].

MiX99 new (NEW) and development (DEV) features

New MiX99 features are indicated in the documentation by a colored vertical bar and note "NEW" on the right margin.   NEW

Some of the newest MiX99 features currently in development are not yet available in the official MiX99 release. These new MiX99 development features are indicated in the documentation by a colored vertical bar and note "DEV" on the right margin.   DEV

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Contents

1   Introduction

MiX99 is a software suite for breeding value evaluation. The set has three types of programs: preprocessor (`mix99i`), solver (`mix99s`, `mix99p`), and reliability calculator (`apax99`, `apax99p`). There are some other programs as well to assist use of these programs. For instance, `imake99` for the parallel computing programs `mix99p` and `apax99p`. The main purpose of this manual is to describe the command language interface (CLIM) to the preprocessor `mix99i`. Some use of `mix99s` is described as well.

The preprocessing program `mix99i` of MiX99 has two ways to give instructions: the original interface, and **command language interface**. In the original interface a **directive file** is given to `mix99i`. The directive file answers questions on data and statistical model. The **command language interface** for MiX99 is called **CLIM**. CLIM helps user in use of the MiX99 preprocessing program `mix99i`. CLIM has the following advantages over the directive file:

- Commands can be given in any order. Thus, the restriction on the strict order on giving commands has been lifted.

- Some commands have default values. Thus, not all commands need to be given.

- Commands have English language names. This makes the command instruction file somewhat easier to read than a directive file.

- All information on the statistical model are given in the same model area, not divided into several sections as in directive file.

Current version of CLIM assumes that model effects are given in the same order as explained for MiX99 directive file. Thus, fixed regression effects without nesting are given first, then fixed classification or nested fixed effects, and then random effect in order of their random effect number.

1.1   Supported statistical models and beta testing features

The MiX99 software can handle many kinds of statistical models. Many of the models have been implemented in CLIM, but not all. In general, the following models are in CLIM:

- linear mixed effect multiple trait model

- random regression (covariable table file)

- reduced rank (combining of traits)

- multiple residual variances

- weights

- least squares models

- large genome information models

There are some specific models, however, that have not been implemented into CLIM. For example, random regression model with both maternal and additive genetic effects has not been implemented. Currently **not implemented** in CLIM:

- random regression with multiple nesting in additive genetics

- MAS-BLUP (combining of effects)

- non-linear models: threshold and Gompertz models

In beta testing:

- order of effect on the model line is free unlike in a directive file.

1.2 Organization of the manual

This manual is organized in the following way.

- This chapter gives some introductory remarks on use of CLIM.

- The second chapter gives some theoretical background, and how it relates to the way models are presented in this manual. In addition, some remarks are given on computational implementation issues in MiX99 needed to understand some of the commands.

- MiX99 files are briefly described in the third chapter.

- The fourth chapter has brief description of the MiX99 solution files

- The fifth chapter has single trait examples. The section on basic models is required reading because basic concepts of the CLIM interface are explained.

- The sixth and seventh chapter gives multiple trait models, and some special topics.

- The last chapter has syntax of all commands.

The manual concentrates on how different statistical models are given to MiX99 using CLIM. However, some options are not much covered. Please study them in the Chapter 9 on summary of all commands. Some of these commands are quite important. For example, `MISSING` and `SCALE`. And, some options can be important when using the programs, such as `TMPDIR`, and `TITLE`. But, some are seldom needed, like `NORANSOL`.

1.3 Invoking CLIM and command line options

CLIM is called by the preprocessing program `mix99i`. CLIM reads a ***command file***, e.g., `mix99.clm`, and translates these instructions into a directive file `MiX99_-DIR.DIR` to be read by `mix99i`. CLIM is used by `mix99i` when an instruction file is given to it:

```
mix99i mix99.clm
```

Note that the old directive files are read from the standard input. Thus, executing

```
mix99i < mix99.dir
```

would expect the old `mix99i` directive file in the file `mix99.dir`.

It is possible to give some options on the command line of `mix99i` (see Table 1.1). When CLIM instruction information is used, the preprocessor program `mix99i` makes a file `MiX99_DIR.DIR`. This file has the old directive file format produced from the

Table 1.1: Command line options to CLIM, given on the `mix99i` command line.

Option	Effect
`-d`	CLIM is executed, no preprocessing part in `mix99i`. File `MiX99_DIR.DIR` is produced.
`-b`	allows use of beta version feature(s), see list above.
`-h`	help
`-l`	long listing option of `mix99i`.
`--nproc NPROC`	Number of parallel processes.
`--datafile DATAFILE`	Data file name.
`--pedfile PEDFILE`	Pedigree file name.
`--parfile PARFILE`	Variance file name.
`--checkdata`	Enhanced checking of data file.

CLIM instructions. Thus, if/when CLIM cannot make exactly the model you have in mind, a similar model may be feasible. Then, by using the '-d' option (Table 1.1), directive file is made, and this directive file can be used as a template:

```
mix99i -d mix99.clm
```

In any case, it is useful to check that the CLIM generated directive file is correct.

1.4 Simple example

Here is a simple example just to introduce CLIM. Some notes on the example:

- everything beyond '`#`' sign on a line is ignored and is considered as a comment.

- all command information are on a line which can be continued by a continuation symbol '`&`'.

- the parameter file has the old MiX99 format and assumes the same numbering. Because random effects of the given model are animal genetic and random residual, numbering is 1 for animal genetics and 2 for the residual.

A simple animal model with one fixed effect (`mean`) and random effect (`animal`):

```
DATAFILE    simple.dat   # Name of data file
INTEGER     animal mean  # Integer column names in the data file
REAL        y            # Real number column name in the data file

PEDFILE     simple.ped   # Name of pedigree file
PEDIGREE    animal am    # Genetics associated with animal code
                         # am=animal model
PARFILE     simple.var   # Name of variance components file
MODEL
  y = mean animal        # Model
```

The commands can be shortened from the full command names. In addition, the command names are not case sensitive, although in this manual all keywords will be written in capital letters. Thus, for example, the command `INTEGER` can be written `int`. However, all other names are case sensitive, e.g., `herd_year` name in the above example. Thus, the integer number column names must be written on the model lines exactly as they were given for the `INTEGER` command.

2 Theory and notation

Here we introduce some notation and theory for an animal model. The mixed model equations are not described in detail. In particular, differences in concepts such as animal and sire model, or maternal and paternal effects are not defined. For a clear presentation on these and many other models in animal breeding with examples, see Mrode and Thompson (2006). This manual uses examples from this book.

2.1 Single trait model

A simple single trait animal model has the form

$$y = Xb + Za + e$$

where

y is $n \times 1$ vector of observations,
b is $p \times 1$ vector of fixed effects,
X is $n \times p$ design matrix to link observations to appropriate fixed effects,
a is $q \times 1$ vector of random additive genetic effects,
Z is $n \times q$ design matrix to link observations to appropriate random effects,
e is $n \times 1$ random residual vector.

Hence, there are q animals with n observations, and there are p fixed effect.

In a simple animal model, the matrices X and Z are **incidence matrices**. In other words, these matrices have zeros and ones to indicate which effect corresponds to which observation. However, if model has regression coefficients, these matrices have regression coefficients. Thus, we call these matrices **design matrices** to indicate wider model possibilities.

In MiX99 it is possible to have both regression and classification variables (categories). Classification variables will be sometimes called class effects. For example, herd effect is a typical class effect, an observation belongs only to one herd, and observations with the same herd effect are predicted by the same estimate. Regression effects are not classification effects. For example, linear function has the linear coefficient in the design matrix. However, regression effect can be nested within classification. In practice, difference between regression and classification effects in MiX99 is that a class effect number is in integer number input column, but regression coefficient is in the real number input column of the data file.

Common linear mixed effects assumptions for the expectations are

$$
\begin{aligned}
\mathrm{E}(a) &= 0 & \mathrm{Var}(a) &= A\sigma_a^2 \\
\mathrm{E}(e) &= 0 & \mathrm{Var}(e) &= I\sigma_e^2 \\
\mathrm{E}(y) &= Xb & \mathrm{Cov}(a, e) &= 0
\end{aligned}
$$

where A is numerator relationship matrix.

For convenience of presentation, it is common to denote the residual covariance matrix by R. Also, it is common to denote the genetic covariance matrix by G. With this

notation, the ***mixed model equations*** to solve are

$$
\begin{bmatrix} \boldsymbol{X'R^{-1}X} & \boldsymbol{X'R^{-1}Z} \\ \boldsymbol{Z'R^{-1}X} & \boldsymbol{Z'R^{-1}Z + G^{-1}} \end{bmatrix} \begin{bmatrix} \widehat{\boldsymbol{b}} \\ \widehat{\boldsymbol{a}} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X'R^{-1}y} \\ \boldsymbol{Z'R^{-1}y} \end{bmatrix}
$$

where $'$ denotes transpose.

The model can be described by giving its effects. For example, if the above model had fixed herd effect ($herd$), and animal effect (a) for the additive genetic effects, then it can be written as

$$
y = herd + a + e
$$

where e is the residual term. This can be considered as model for one individual record, although subscripting to indicate this was not used.

2.2 Multiple trait model

The single trait model can be used to describe multiple trait model as well:

$$
\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Za} + \boldsymbol{e}
$$

However, for *T* traits the matrices and vectors have traitwise structure. Thus, we can write

$$
\boldsymbol{y'} = \begin{bmatrix} \boldsymbol{y'_1} & \boldsymbol{y'_2} & \cdots & \boldsymbol{y'_T} \end{bmatrix}
$$

$$
\boldsymbol{e'} = \begin{bmatrix} \boldsymbol{e'_1} & \boldsymbol{e'_2} & \cdots & \boldsymbol{e'_T} \end{bmatrix}
$$

$$
\boldsymbol{b} = \begin{bmatrix} \boldsymbol{b_1} \\ \boldsymbol{b_2} \\ \vdots \\ \boldsymbol{b_T} \end{bmatrix}, \quad \boldsymbol{X} = \begin{bmatrix} \boldsymbol{X_1} & \boldsymbol{0} & \cdots & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X_2} & \cdots & \boldsymbol{0} \\ \vdots & \vdots & \ddots & \vdots \\ \boldsymbol{0} & \boldsymbol{0} & \cdots & \boldsymbol{X_T} \end{bmatrix}
$$

$$
\boldsymbol{a} = \begin{bmatrix} \boldsymbol{a_1} \\ \boldsymbol{a_2} \\ \vdots \\ \boldsymbol{a_T} \end{bmatrix}, \quad \boldsymbol{Z} = \begin{bmatrix} \boldsymbol{Z_1} & \boldsymbol{0} & \cdots & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z_2} & \cdots & \boldsymbol{0} \\ \vdots & \vdots & \ddots & \vdots \\ \boldsymbol{0} & \boldsymbol{0} & \cdots & \boldsymbol{Z_T} \end{bmatrix}
$$

where the vectors and matrices have the same meaning as before and subscripts denote for appropriate trait.

Multiple trait linear mixed effects assumptions are

$$
\begin{array}{rclcrcl}
\mathrm{E}(\boldsymbol{a}) &=& \boldsymbol{0} & & \mathrm{Var}(\boldsymbol{a}) &=& \boldsymbol{G_0 \otimes A} \\
\mathrm{E}(\boldsymbol{e}) &=& \boldsymbol{0} & & \mathrm{Var}(\boldsymbol{e}) &=& \boldsymbol{R_0 \otimes I} \\
\mathrm{E}(\boldsymbol{y}) &=& \boldsymbol{Xb} & & \mathrm{Cov}(\boldsymbol{a}, \boldsymbol{e}) &=& \boldsymbol{0}
\end{array}
$$

where matrix $\boldsymbol{G_0}$ is T by T genetic covariance matrix, and $\boldsymbol{R_0}$ is T by T residual covariance matrix. The mixed model equations are

$$
\begin{bmatrix} \boldsymbol{X'R^{-1}X} & \boldsymbol{X'R^{-1}Z} \\ \boldsymbol{Z'R^{-1}X} & \boldsymbol{Z'R^{-1}Z + G_0^{-1} \otimes A^{-1}} \end{bmatrix} \begin{bmatrix} \widehat{\boldsymbol{b}} \\ \widehat{\boldsymbol{a}} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X'R^{-1}y} \\ \boldsymbol{Z'R^{-1}y} \end{bmatrix}
$$

2.3   Solving mixed model equations

MiX99 solves mixed model equations using preconditioned conjugate gradient (PCG) iteration. The following need to be considered when using the program:

- iterative method

- iteration on data

- ordering of equations by blocks

- preconditioner matrix

2.3.1   MiX99 solver: PCG

PCG is an iterative method to solve linear models. Thus, the coefficient matrix is not inverted or decomposed. In practice, iterative methods will solve the system of equations by updating the latest solutions by some procedure.

An **iterative solving method** continues updating solutions until convergence is determined. Convergence criteria value is given before starting iteration. Often this value is a small positive number. In addition, maximum number of iterations is set in order to ensure termination of the iterative method. It has been proved that number of iterations PCG needs is at most number of unknowns. This has no practical meaning for large problems, but for small problems it is good to know that this limit is used in MiX99.

It is not possible to give convergence criteria or maximum number of iterations by CLIM. This information is given to the solver program `mix99s` or `mix99p`, not the preprocessor (see Chapter 4).

2.3.2   Preconditioner

PCG iteration is a flexible method. The CG or **conjugate gradient** part of the algorithm is the same (with small variations) but the preconditioner part depends on implementation. Preconditioning usually means transforming the coefficient matrix to be as diagonal as possible. This is done by approximating inverse of the coefficient matrix. If the approximation is exact, PCG finds the correct solution in one step. Usually the approximation is not exact.

MiX99 has different preconditioners available. The reason for different preconditioners is memory and time. For very large systems of equations, it is not possible to use the most memory intensive preconditioners implemented. In addition, when only reliabilities are calculated, no preconditioner is needed. Making the preconditioner may take as much as half of the computing time in the preprocessing program.

2.3.3   Iteration on data

Iteration on data (IOD) means that MiX99 does not make or store the coefficient matrix of the mixed model equations to memory. PCG method needs the coefficient **matrix times a vector product**. This can be made using the model matrices X and Z, pedigree list, and the variance component information. In practice, IOD means that reliabilities must be calculated by a separate program because coefficient matrix is never made explicitly.

2.3.4   Ordering of equations by blocks

We described mixed model equations in a way that is typical in the literature. Equations are **ordered** by effect. This is convenient when presenting mixed model equations or theory. But, this is not always computationally optimal. It is better to order equations of animal and its herd close because IOD proceeds one records at a time with a record having animal and herd related classification information. In MiX99, equations can be ordered by common family blocks, e.g., herd. For more information see Chapter 3.2.3.

MiX99 orders equations in a different way than by effect even when block code has not been used to order equations. In multiple trait model, the different trait equations for an animal are always ordered next to each other. This will ensure efficient performance of the solver.

CLIM has command `WITHINBLOCKORDER` (Chapter 9.2.27). It can be used to indicate which effects are **within block equations**. For example, if herd is block code, then it is natural that animal effects (such as animal genetics and permanent environment), and herd contemporary effects (such as herd-year-season) are within block. This is not very important when solving the mixed model equations using `mix99s`. However, the parallel computing implementation (`mix99p`) depends on good block ordering. When reliabilities are estimated by ApaX (`apax99` or `apax99p`), block information is used to determine level of approximation. Only effects within blocks are considered in reliability calculations.

3   MiX99 files

Information on data, pedigree, and variance components for MiX99 are in files. Animals in the data and pedigree files must be in the same order. In other words, when data records have been sorted by animal id (or sire id for sire models), then individuals must be in the same order in the pedigree file. The pedigree can be ordered using RelaX2 program, a separate program for pedigree analysis from Luke (Strandén and Vuori, 2006).

The MiX99 input files have a certain quite simple format. In the following, formats of these files are described shortly. For a more complete explanation, see MiX99 pre-processor manual *Technical reference guide for MiX99 pre-processor*.

3.1   Data file

The data file has the observed data to be analyzed. This means observations, and model effect information such as of classification effect numbers and regression coefficients. The default format is 'text' which means **text format data file** where columns are separated by space. A rarely used alternative is **binary format data file**.

Each record, i.e., line in a free format file, has two parts:

- **Integer numbers** The integer number data part consists of positive integer numbers for all class variables in the model. In addition, it may contain sorting variables and indices such as index for heterogeneous residual variance.

- **Real numbers** These are observations, regression coefficients, and weights.

The data file can have columns that are not used in a particular run of MiX99. Because MiX99 accepts only numerical data, alphanumeric data are allowed on the record only after the real number columns in a free format text data file.

All integer numbers are coded using the default machine integer type. Hence, on 32-bit platforms the data file, integer numbers must be positive and at most 2.147.483.648. **Missing integer numbers** must be coded by number zero (0). **Missing real numbers** can be coded with an arbitrary real value which is specified to MiX99 by command MISSING.

3.1.1   Example: Multiple trait data

Consider a two trait data. The file has six columns: 4 integer number columns, and 2 real number columns. Note that the real number columns have integer values. Still, for MiX99 these are real number columns because observations can have any real values. The file named example.dat is:

animal$_1$	sire$_2$	herd$\times$year$_3$	ones$_4$	trait 1$_1$	trait 2$_2$
4	1	1	1	90	200
6	3	1	1	110	190
8	5	2	1	120	140
9	5	2	1	130	120
10	7	2	1	120	130

This data file can be described with the following CLIM commands:

```
DATAFILE   example.dat              # Name of the data file
INTEGER    animal sire season ones # Integer column names
REAL       tr1 tr2                  # Real column names
```

3.2   Pedigree file

All pedigree information is given in **pedigree file**. Each animal in the pedigree must have a record in the pedigree file with four integers of which the forth integer is optional. Columns of the pedigree file are

1	2	3	4
animal code	sire code	dam code (or maternal grand sire code in case of a sire model)	block code (optional)

The integers must be separated by at least one space.

When block code is given, the pedigree and observation files need to have the same order by blovk. The main sort key is block code (e.g., herd) within which sorting is by animal code. When animal has observations in several data file blocks, in pedigree file the animal must appear only in one of the blocks. This special case will be considered in a separate section on parallel computing.

3.2.1   Example: Pedigree file for the data

Let pedigree file for the multiple trait model data in example Chapter 3.1.1 be

animal$_1$	sire$_2$	dam$_3$
1	0	0
2	0	0
3	1	2
4	1	2
5	3	4
6	3	4
7	5	6
8	5	6
9	5	6
10	7	8

3.2.2 Phantom parent groups

Missing parents can be replaced by phantom parent groups. Then, a ***phantom parent group*** code is in place of missing parent. This group code must be a <u>negative</u> integer number in order to distinguish it from an animal code. A phantom parent group code must not have an own record in the pedigree file.

For example, the pedigree above (Chapter 3.2.1) had two animals (1 and 2) that had unknown parents. The parents could be phantom parent groups (-1 for unknown sire, -2 for unknown dam). The pedigree file remains the same for all other animals. The changed part of the pedigree file is:

animal$_1$	sire$_2$	dam$_3$
1	−1	−2
2	−1	−2

3.2.3 Block code

There are some benefits from having a ***block code*** in the data and pedigree files. Block code is essential in calculation of reliabilities by ApaX, and when parallel computing is used by `mix99p`. Otherwise, block code brings very little benefit to computations, and can be omitted.

Block code of an animal is given on column 4 in the pedigree file. When the pedigree file has a block code column, then every animal must have a block code. In addition, the block code needs to be the same in the data file as well. Animals with records in different data blocks (e.g. in different herds) have to be coded with the code of one of the different data blocks where it has observations, e.g., block with most of its observations.

If animal does not have an observation, but is parent to an animal having observations in the data file (e.g. pedigree animal of a particular herd), then it is best that parent without observation and its offspring have the same block code. In dairy cattle, this is most suitable for a cow without observations. It should be assigned to a block having most of its daughters.

When an animal does not belong to any equation family (no observations to give block code), or it is in many different families through relationship information (e.g. dairy sires have progeny in many herds), an extra block code should be given. We recommend a separate block code for animals with links to many different equation family blocks.

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For example, sires in a dairy cattle population can be assigned to one group. Note that a group should never be too large. It is advisable to split a large block into several smaller blocks. The solver program reads as many animal blocks at a time as possible, and the largest animal block dictates memory requirements.

3.3 Variance components file

The ***variance components*** file has variances and covariances for all the random effects in the model. The matrices can be of different size depending on the model specification. The matrices are numbered in the same order as in the RANDOM command. However, no random command is needed when the only random effects in the model are animal genetics and residual effects. Residual effect has always the highest random effect number, and the additive genetic effect the second highest number.

The variance components file has a line for each (co)variance. Each line has 3 integers followed by a real number (the (co)variance value). The first integer is the random effect number followed by the row-column combination, and, finally, the (co)variance parameter. The row-column combination refers to the element position in the (co)variance matrix. Only the lower (or upper) triangle of the matrix needs to be given.

Order of lines in the file is irrelevant. It is easy to know the random effect number. Correct numbering of (co)variances, i.e., the row-column number, can be more difficult. For example, the row-column numbers have to be checked carefully when random regression effects are missing in a multiple trait random regression model. See examples on multiple trait random regression effects for better explanation (Chapter 5.2).

3.3.1 Example: Variance component file

We illustrate variance components file for the multiple trait model data in example Chapters 3.1.1 and 3.2.1. Let the genetic and residual (co)variance matrices be

$$\boldsymbol{G} = \left[\begin{array}{cc} 3.0 & 2.5 \\ 2.5 & 2.5 \end{array} \right]$$

and

$$\boldsymbol{R} = \left[\begin{array}{cc} 7.0 & 2.0 \\ 2.0 & 7.0 \end{array} \right],$$

respectively. Genetic correlation between the traits is about 91%, and residual correlation about 29%. Heritability of the first trait is 30%, and the second trait about 26%. The parameter file is

Random effect$_1$	Row$_2$	Column$_3$	Covariance$_1$
1	1	1	3.0
1	1	2	2.5
1	2	2	2.5
2	1	1	7.0
2	1	2	2.0
2	2	2	7.0

3.3.2 Multiple residual (co)variances

When multiple residual (co)variances are present, an ***additional residual (co)variance file*** has to be given. Format of this file is similar to the regular (co)variance file explained above. However, the first number on each line is not the random effect number but number of the residual variance class. Numbering of the residual (co)variance classes has to start from one (1), up to total number of residual (co)variance classes. Each observation has its residual (co)variance class number in the INTEGER column fields of the data file. Note that a residual (co)variance (matrix) has to be given in the variance components file. Values of residual (co)variance in the variance components file are ignored by the solver program (mix99s/mix99p) but used by the reliability calculation program (apax99/apax99p).

4 Using the MiX99 solver

The MiX99 ***solver*** (mix99s/mix99p) assumes user will give some instructions on some aspects of the iteration method, output files produced, and possible special computing to be made (see Chapter 8 on special topics). The instructions can be given either from the standard input or using the command line options.

In this manual, usually the command line option method has been used. This method is possible only when calculating breeding values. The easiest way to execute solver is to give option -s which uses default values in solving breeding values, and produces standard output files. Thus, you give mix99s -s. Examples in this manual have been produced with this option, if not otherwise mentioned.

The other command line options are

- -n or -N for number of iterations

- -ca or -Ca for Ca convergence criteria

- -cd or -Cd for Cd convergence criteria

- -cr or -Cr for Cr convergence criteria

- -cm or -Cm for Cm convergence criteria | NEW

For example, giving mix99s -n 100 -cr 1e-8 would limit maximum number of iterations to 100, and the Cr convergence criteria value to 10^{-8}.

Instructions can be given to the solver in the standard input. This allows much wider set of options and methods than available in the command line options. Note, however, that giving command line options will by default lead to not reading the standard input. It is sometimes more convenient to have the instructions in a file than type them every time to the program. This can be achieved by reading them from the standard input, e.g., mix99s < solver_option_file.slv. Again, giving command line options will by default lead to not reading the file. Thus, giving

```
mix99s -n 100 -cr 1e-8 < solver_option_file.slv
```

will not read commands from the file solver_option_file.slv but proceed with the command line options only.

By specifying command line option `-i` the solver option file (or standard input) is read first AND ***options from the command line override the corresponding solver option file values***:

```
mix99s -i -n 100 -cr 1e-8 < solver_option_file.slv
```

An example of instruction file for breeding value evaluation is

```
H        # RAM: RAM demand: L=large (mix99p only), H=high, M=medium, L=low
# Max. no. iter., Convergence_criterion, Criterion (A/R/M/D)
2000                     1.0e-8          R          F
N        # RESID: Calculate residuals? (Y/N)
N        # VALID: N=no
N        # VAROPT: adjust for HV? (N)o
Y        # SOLTYP: Solution files? (N)o, (Y)es
```

The first letter `H` requests high memory version which is usually used. The medium and low memory versions are rarely used because even the high memory version uses memory efficiently.

The most important line is the second line where PCG iteration information is given:

- number of iterations in the PCG method is limited to 2000 iterations

- convergence value is set to be 10^{-8}

- convergence criteria is set to "R"

- the above values are "F"orced to be used.

If "F" is not given then default values are used. Default values are

- limit to 5000 iterations in the PCG method

- convergence value is 10^{-4}

- convergence criteria is "D"

The three options after the PCG information are not that important for typical breeding value evaluation, and their values are "n" for no. The chapter on special topics (Chapter 8) will consider some of these options. The last "Y" is important. If the last letter is "N" then instead only binary format solution file is produced.

4.1   Solution files

The solver will write ***solution files*** depending on the model. Different types of solutions are written to different files. Different kinds of solution files are:

- `Solani`: Solutions for animal effects. (`Sol_mn` in case of a LS-model.)

- `Solfix`: Solutions for all across blocks fixed effects.

- `Solfnn`: Solutions for the nth within block fixed effect. For instance, `Solf02` is the solution file for the second within block fixed effect.

- `Solrnn`: Solutions for the nth random effect in the model. For example, `Solr03` is the solution file for the random effects with the random effect number 3.

- `Solreg`: Solutions for the regression effects of the first regression effect group (applied across all observations).

Structure of the text solution files depends on the model. General form of a particular solution file is the same. However, number of columns in a `Solani` file depends on the number of traits. Therefore, detailed explanation of the content of those files is given in the printout of the particular run of the program.

Below are descriptions of the two most common solution file formats. The other solution files have similar formats. Please check solver output for explanation. In this manual column titles are given for `Solani` although they are not present in the files.

In general, the `Solani` file has the following columns:

1) Animal ID

2) Number of offspring

3) Number of observations

4) Solution for trait 1

5) Solution for trait 2

6) . . .

When there are random regression effects, solutions are in the numbering order of the random regression effects.

In general, the `Solfix` file has the following columns

1) Factor number

2) Trait number

3) Level code

4) Number of observations

5) Solution

6) Name of factor (integer number column)

7) Name of trait

5 Single trait models

5.1 Naming of model components

Data file has integer and real number columns. Columns are given names by `INTEGER` and `REAL` commands. The names can have any alphanumeric characters, i.e., letters and numbers. Many other characters such as underscore (_) are allowed as well. However, there are some reserved characters not allowed in names: =, (,), @, |, !, <, & and #. These characters have special meaning. For example, # starts comment, and & marks for line continuation. Others are model component separators, and will be discussed in due course in this manual.

Statistical model has effects. The data column names can be used as effect names. If a data column name is an integer number column name, then it is assumed to be an effect with classes. If a data column name is a real number column name, then it

is assumed to be a regression effect. CLIM expects that all effect names are different on a model line. When some model effects refer to the same data column, component names can be used. See repeatability model example (Chapters 5.1.4 and 5.1.5).

5.1.1 Example: Animal model

We consider a simple animal model

$$tr1 = herd \times year + a + e$$

where

$herd \times year$	is fixed $herd$ times $year$ interaction effect,
a	is random additive genetic effect, and
e	is random residual.

CLIM (nor MiX99) does not make multiplication operations between effects in the model line. Thus, the $herd \times year$ interaction has to be coded in the data as a class effect.

Complete CLIM instruction file is (named `amodel.clm`)

```
DATAFILE   example.dat
INTEGER    animal sire herd_year ones
REAL       tr1 tr2

PEDFILE    AM.ped     # Pedigree file
PEDIGREE   animal am  # Genetics associated with animal code
                      # am=animal model
DATASORT PEDIGREECODE=animal

PARFILE    AM.var

MODEL
  tr1 = herd_year animal
```

The `example.dat` is the same as given earlier (Chapter 3.1.1). The `AM.ped` is the same as given earlier (Chapter 3.2.1). The variance components file (`AM.var`) is for the first trait:

Random effect$_1$	Row$_2$	Column$_3$	Variance$_1$
1	1	1	3.0
2	1	1	7.0

First the preprocessor is executed: `mix99i amodel.clm`. Next the solver is executed: `mix99s -s`. The solver will produce solution files `Solfix` having fixed effects, and `Solani` having the breeding values. The `Solfix` file is

```
Fact. Trt       Level    N-Obs  Solution         Factor Trait
1    1          1            2  99.538           herd_yea tr1
1    1          2            3  122.69           herd_yea tr1
```

The `Solani` file is (column names have been added)

```
  Animal N-Desc  N-Obs Solution
       1     2      0 -.18406E-14
       2     2      0 -.18406E-14
       3     2      0 0.92308
       4     2      1 -.92308
       5     3      0 -.37713E-14
       6     3      1  1.8462
       7     1      0 0.65421
       8     1      1 0.64447E-01
       9     0      1  2.0506
      10     0      1 -.17840
```

Solutions may differ somewhat due to computing precision when the example is tested in another computer. For instance, the solutions close to zero are likely to be different (breeding values for animals 1, 2, and 5).

5.1.2 Example: Phantom parent groups in animal model

Phantom parent groups are as easy to give in CLIM as in the MiX99 directive method. Phantom parent groups are signaled in the pedigree file by having them as negative numbers. In the CLIM file, a model with phantom parent groups is used when the PEDIGREE command has '+p' for phantom parent groups. For example, the previous CLIM instruction file needs only one change:

```
PEDIGREE   animal am+p
```

in order to have phantom parent groups. Note that the no space is allowed between the characters in am+p.

Notes:

- if the pedigree has negative parent numbers, and the model instruction file does not have '+p' then all negative parent numbers are considered to indicate an unknown parent, and are effectively same as zero.

- if '+p' was given but an animal has a zero (0) parent (instead of negative number), MiX99 assigns this parent to genetic group -99999999.

5.1.3 Example: Inbreeding in animal model

Relationship matrix in MiX99 does not account for non-zero inbreeding coefficients by default. However, it is possible to use precalculated inbreeding coefficients in the additive relationship matrix. MiX99 does not calculate inbreeding coefficients, a separate program such as RelaX2 (Strandén and Vuori, 2006) needs to be used.

Consider the example for animal model (Chapter 5.1.1). Inbreeding coefficients calculated using RelaX2 are (file AM.inbr):

```
 1  1 0.00000
 2  2 0.00000
 3  3 0.00000
 4  4 0.00000
 5  5 0.25000
 6  6 0.25000
 7  7 0.37500
 8  8 0.37500
 9  9 0.37500
10 10 0.50000
```

In order to read this file, two additional lines are needed in the CLIM code:
```
INBRFILE    AM.inbr
INBREEDING PEDIGREECODE=1 FINBR=3
```

The solutions will be slightly different. Fixed effect solutions in the `Solfix` file are

Fact. Trt		Level	N-Obs	Solution	Factor Trait
1	1	1	2	99.538	herd_yea tr1
1	1	2	3	122.61	herd_yea tr1

Breeding values in the `Solani` file are

Animal	N-Desc	N-Obs	Solution
1	2	0	-.13834E-13
2	2	0	-.13834E-13
3	2	0	0.92308
4	2	1	-.92308
5	3	0	-.12953E-13
6	3	1	1.8462
7	1	0	0.70457
8	1	1	0.24590
9	0	1	1.8188
10	0	1	0.11106

5.1.4 Example: Repeatability animal model

Repeatability animal model has usually two effects with the same incidence matrix but different covariance structure. Hence, in the model line the same integer number column in data file is referred by two different effects: permanent environment and direct genetic. However, the same name cannot appear twice on the model line. Because of this, component names can be used. Component names are user defined (renamed) names of one or more components in the model line. Basically, any classification effect can be renamed. For example, there is a column `id` but we want to rename this effect to be `animal`. This is achieved by giving `animal(id)` on the model line.

Consider a repeatability animal model

$$y = herd \times year + p + a + e$$

where $herd \times year$ is fixed $herd$ times $year$ interaction effect, p is random permanent environment effect, a is additive genetic effect, and e is random residual. Both $\boldsymbol{p}$ and $\boldsymbol{a}$ have the same design matrix relating observations to animals. However, they have different covariance structures. The usual repeatability model assumptions are

$$
\begin{array}{rclcrcl}
\mathrm{E}(\boldsymbol{p}) & = & \boldsymbol{0} & & \mathrm{Var}(\boldsymbol{p}) & = & \boldsymbol{I}\sigma_p^2 \\
\mathrm{E}(\boldsymbol{a}) & = & \boldsymbol{0} & & \mathrm{Var}(\boldsymbol{a}) & = & \boldsymbol{A}\sigma_a^2 \\
\mathrm{E}(\boldsymbol{e}) & = & \boldsymbol{0} & & \mathrm{Var}(\boldsymbol{e}) & = & \boldsymbol{I}\sigma_e^2
\end{array}
$$

where σ_p^2 is permanent environment variance, σ_a^2 is additive genetic variance, and σ_e^2 is residual variance.

The model has two random effects which refer to the same class name, named `animal`, that is present in the data file. The following model statement is unacceptable (note that only commands relevant to the model line are given):

```
INTEGER    animal sire herd_year ones
REAL       tr12

PEDIGREE   animal am
```

```
MODEL
  tr12 = herd_year animal animal
```

because `animal` appears twice as an effect.

An alternative would be to have two identical columns with animal id number in both of them. Thus, our model line would be

```
INTEGER     animal pe_animal sire herd_year ones
REAL        tr12

PEDIGREE    animal am # animal for animal genetic
RANDOM      pe_animal # permanent environment

MODEL
  tr12 = herd_year pe_animal animal
```

This model is correct. However, now the data file is larger, and it is necessary to remember to make two columns having the same content. Instead, component name can be used to name model effects.

The preferred way to give repeatability model in CLIM is to refer an effect by a component name. In the following, name 'G' was given to the animal genetic effect.

```
INTEGER     animal sire herd_year ones
REAL        tr12

PEDIGREE    G am    # G for animal genetics
RANDOM      animal # permanent environment

MODEL
  tr12 = herd_year animal G(animal)
```

This is just one way to give repeatability model. Two alternatives are (all other but the changed commands are given):

1:
```
PEDIGREE    G am #  G for animal genetics
RANDOM      PE   # PE for permanent environment
MODEL
  tr12 = herd_year PE(animal) G(animal)
```

2:
```
PEDIGREE    animal am # animal for animal genetics
RANDOM      PE        # PE      for permanent environment
MODEL
  tr12 = herd_year PE(animal) animal
```

All these versions will produce the same instructions for `mix99i`. Note that component names can be given to fixed effects as well. See the next chapter.

5.1.5   Example: Repeatability animal model in detail

We use the multiple trait model data already presented (Chapter 3.1.1) but modify it for repeatability model. The model is

$$tr_{12} = herd \times year + p + a + e$$

where $herd \times year$ is fixed herd-year effect, p is random permanent environment effect, a is random additive genetic effect, and e is random residual.

Variance components are: permanent environment $\sigma_p^2 = 2.0$, genetic $\sigma_a^2 = 3.0$, and residual $\sigma_e^2 = 5.0$. The parameter file `RM.var` is

Random effect$_1$	Row$_2$	Column$_3$	Covariance$_1$	Comment
1	1	1	2.0	permanent environment
2	1	1	3.0	additive genetic
3	1	1	5.0	residual variance

The multiple trait model data file is modified for the repeatability model:

animal$_1$	sire$_2$	herd×year$_3$	ones$_4$	tr12$_1$
4	1	11	1	90
4	1	21	1	200
6	3	11	1	110
6	3	21	1	190
8	5	12	1	120
8	5	22	1	140
9	5	12	1	130
9	5	22	1	120
10	7	12	1	120
10	7	22	1	130

```
DATAFILE   example_repeat.dat
INTEGER    animal sire herd_year ones
REAL       tr12

DATASORT PEDIGREECODE=animal

PEDFILE    AM.ped
PEDIGREE   G am   #  G for animal genetics
RANDOM     PE     # PE for permanent environment

PARFILE    rep.var

MODEL
  tr12 = herd_year PE(animal) G(animal)
```

The fixed effect solutions (`Solfix`) are

```
Fact. Trt       Level    N-Obs  Solution       Factor Trait
1    1          11          2  99.833          herd_yea tr12
1    1          12          3  123.01          herd_yea tr12
1    1          21          2  194.83          herd_yea tr12
1    1          22          3  129.68          herd_yea tr12
```

Permanent environment solutions (`Solr01`) are

```
  Animal      N-Obs Solution
       4        2 -.88889
       6        2 0.88889
       8        2  1.1867
       9        2 -.55846
      10        2 -.62828
```

The breeding values estimates (`Solani`) are

```
  Animal N-Desc  N-Obs Solution
       1      2      0 -.58526E-06
       2      2      0 -.58526E-06
       3      2      0 0.33333
```

```
         4        2        2 -.33333
         5        3        0 -.81159E-06
         6        3        2 0.66667
         7        1        0 0.97735E-01
         8        1        2 0.98778
         9        0        2 -.85516E-01
        10        0        2 0.71556E-01
```

5.1.6   Example: Simple sire model

We consider a simple sire model using the data introduced for animal model (Chapter 5.1.1). The sire model is

$$tr1 = herd \times year + s + e$$

where
$herd \times year$ is fixed herd-year effect,
s is random sire effect, and
e is random residual.

In sire model, records are associated with sire of the animal having record. The data file is the same as used for animal model `example.dat` in Chapter 3.1.1.

In this simple sire model, all sires are assumed to be unrelated. Thus, the pedigree file (`SM.ped`) is

animal₁	sire₂	maternal grand sire₃
1	0	0
3	0	0
5	0	0
7	0	0

Variance components file needs to be changed from the animal model to sire model. Sire genetics make only quarter of the additive genetics. Thus, the variance components file (`SM.var`) is

Random effect₁	Row₂	Column₃	Variance₁
1	1	1	0.75
2	1	1	9.25

CLIM code for the sire model is

```
DATAFILE   example.dat

INTEGER    animal sire herd_year ones
REAL       tr1 tr2

PEDFILE    SM.ped
PEDIGREE   G sm

PARFILE    SM.var

MODEL
  tr1 = herd_year G(sire)
```

The fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor Trait
1	1	1	2	100.00	herd_yea tr1
1	1	2	3	123.25	herd_yea tr1

The breeding values estimates (`Solani`) are

Bull	N-Desc	N-Obs	Solution
1	0	1	-.75000
3	0	1	0.75000
5	0	2	0.24390
7	0	1	-.24390

5.1.7 Example: Sire model

The previous sire model example can be analyzed by a sire model where a sire maternal grand sire relationship matrix is used. The command file does not change, but the pedigree file is different.

The pedigree file (`smgms.ped`) is

animal$_1$	sire$_2$	maternal grand sire$_3$
1	0	0
3	1	0
5	3	1
7	5	3

As before the solver will produce solution file `Solfix` having fixed effects

Fact.	Trt	Level	N-Obs	Solution	Factor Trait
1	1	1	2	99.976	herd_yea tr1
1	1	2	3	123.19	herd_yea tr1

The `Solani` file has breeding values for the sires is

Bull	N-Desc	N-Obs	Solution
1	2	1	-.35736
3	2	1	0.40621
5	1	2	0.20334
7	0	1	0.24076E-01

5.1.8 Example: Weights in a model

Weight can be used to indicate that an observation is actually mean from many records. Weight is a real number in the data file. It is indicated in CLIM to be weight by `WEIGHT` option in the model line. Model options for a trait come after "!" sign. For example, when column 'weight' has weights then option is '`!WEIGHT=weight`'.

Consider the previous chapter sire model example again but with weights. The data file (`example_w.dat`) is now:

animal$_1$	sire$_2$	herd×year$_3$	ones$_4$	trait 1$_1$	trait 2$_2$	weight$_3$
4	1	1	1	90	200	50
6	3	1	1	110	190	100
8	5	2	1	120	140	60
9	5	2	1	130	120	20
10	7	2	1	120	130	30

CLIM code for weighted sire model is

```
DATAFILE    example_w.dat

INTEGER     animal sire herd_year ones
REAL        tr1 tr2 weight

PEDFILE     smgs.ped
PEDIGREE    G sm

PARFILE     SM.var

MODEL
  tr1 = herd_year G(sire) ! WEIGHT=weight
```

Fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	2	100.68	herd_yea	tr1
1	1	2	3	119.33	herd_yea	tr1

Breeding value estimates (`Solani`) are

Bull	N-Desc	N-Obs	Solution
1	2	1	-7.0567
3	2	1	7.5018
5	1	2	2.8028
7	0	1	1.6447

5.2 Random regression and nested effects

Random regression models have regression effects nested within a classification effect. Typical random regression models are test-day models where lactation curve is fitted for test-day observations.

Class effect has an integer number column name or a component name (Chapter 5.1). In the following, we extend the use of component name as a class effect. Earlier we renamed a class effect such as the additive genetic effect G(animal) and G(sire). The same notation will be used for nested regression effects.

5.2.1 Nested regression effects

A regression effect can be nested within a class. This is similar to the component name concept introduced for repeatability model. However, we can go even further and combine several effects to a component with the same nesting class. For example, assume a fixed lactation curve is nested within season. The model could be

```
y = fixed_curve(1 linear quadratic cubic | season) animal
```

where `season` and `animal` are integer number column names in the data file, and `linear`, `quadratic`, and `cubic` are real number column names in the data file. The number 1 above means intercept term, i.e., season effect, in this example. The 'fixed_curve' is a component name with the common nesting class `season` applied to all its regression effects.

The intercept in the `fixed_curve` can be moved to be a separate class effect. Thus, the above model line can be written also as

```
y = season fixed_curve(linear quadratic cubic | season) animal
```

This moving of `season` effect to be a separate effect is fine for fixed effects. However, for a random effect this cannot be always done because component names are used

to distinguish correlated random regression effects. See below examples for random regression models.

5.2.2 Covariable tables

Regression models in dairy cattle are usually so called test-day models where repeated observations of a cow are modeled during lactation. The regression effects are functions of days in milk which can have only certain values, e.g., integer values from 1 (one) to 350. Because dairy cattle data sets can be very large, MiX99 allows reducing data file size by using days in milk as an index to a regression coefficient table.

Assume the same fixed effects regression curve as given above. A covariable table file can be given by command `TABLEFILE`. The data file must have an integer index column such as days in milk (`DIM`) which is used to indicate regression function coefficients in the table. In our example, the file will have five columns: DIM, intercept (just ones), linear (equals to DIM), quadratic (DIM^2), and cubic (DIM^3). The model line can now be written as

```
y = fixed_curve(t1 t2 t3 t4 | season) animal
```

where $t1$, $t2$, $t3$, $t4$ refer to columns two, three, four, five, respectively, in the coefficient table file. In the covariable table file, column one has the table index. Data file has an integer number column that has the index to pick the correct line in the coefficient table file. The input column in the data file is indicated by command `TABLEINDEX`. See example in Chapter 5.2.4.

5.2.3 Example: Random regression model

We consider a single trait random regression animal model. The example is from Schaeffer and Dekkers (1994).

Cows have repeated observations of milk yield. The model is

$$milk = DIM + log(305/DIM) + HTD + f(a, DIM) + e$$

where

$milk$	is milk yield observation,
DIM	is fixed days in milk linear regression effect,
$log(305/DIM)$	is fixed logarithm of days in milk regression effect,
HTD	is fixed herd test-day effect,
$f(a, DIM)$	is random additive genetic regression function, and
e	is random residual effect.

The random regression function f for animal i has form

$$f(\boldsymbol{a}, DIM) = a_{i,1} + DIM \cdot a_{i,2} + log(305/DIM) \cdot a_{i,3}$$

Thus, there are three random regression breeding values by animal.

Variance components are: residual variance $\sigma_e^2 = 100$, and random regression effect covariance matrix

$$\boldsymbol{G}_0 = \begin{bmatrix} 44.791 & -0.133 & 0.351 \\ -0.133 & 0.073 & -0.010 \\ 0.351 & -0.010 & 1.068 \end{bmatrix}$$

The parameter file `RRM.var` is

Random effect$_1$	Row$_2$	Column$_3$	Covariance$_1$	Comment
2	1	1	44.791	additive genetic: intercept
2	2	1	−0.133	intercept, DIM linear
2	3	1	0.351	intercept, ln(DIM/305)
2	2	2	0.073	DIM, DIM
2	2	3	−0.010	DIM, ln(DIM/305)
2	3	3	1.068	ln(DIM/305), ln(DIM/305)
3	1	1	100.000	residual variance

The pedigree and data files for the random regression model example:

pedigree file `RRM.ped`				data file `RRM.dat`					
animal$_1$	sire$_2$	dam$_3$	block$_4$	HTD$_1$	animal$_2$	block$_3$	DIM$_1$	ln(305/DIM)$_2$	milk$_3$
1	9	7	1	1	1	1	73.0	1.4298500	26.0
2	10	8	1	2	1	1	123.0	0.9081270	23.0
3	9	2	2	3	1	1	178.0	0.5385280	21.0
4	10	8	3	1	2	1	34.0	2.1939499	29.0
5	11	7	3	2	2	1	84.0	1.2894900	18.0
6	11	1	4	3	2	1	139.0	0.7858380	8.0
7	0	0	8	4	2	1	184.0	0.5053760	1.0
8	0	0	8	1	3	2	8.0	3.6408701	37.0
9	0	0	8	2	3	2	58.0	1.6598700	25.0
10	0	0	8	3	3	2	113.0	0.9929240	19.0
11	0	0	8	4	3	2	158.0	0.6577170	15.0
				5	3	2	218.0	0.3358170	11.0
				6	3	2	268.0	0.1293250	7.0
				2	4	3	5.0	4.1108699	44.0
				3	4	3	60.0	1.6259700	29.0
				4	4	3	105.0	1.0663500	22.0
				5	4	3	165.0	0.6143660	14.0
				6	4	3	215.0	0.3496740	8.0
				4	5	3	14.0	3.0812500	35.0
				5	5	3	74.0	1.4162500	23.0
				6	5	3	124.0	0.9000300	17.0
				5	6	4	31.0	2.2863200	28.0
				6	6	4	81.0	1.3258600	22.0

CLIM code for the random regression model is

```
DATAFILE   RRM.dat
INTEGER    HTD animal blk-var  # Integer column names
REAL       DIM  ln305DIM  &    # Covariables
           milk_yd              # Milk yield

PEDFILE    RRM.ped # Pedigree file
PEDIGREE   G am     # animal model

PARFILE    RRM.var

MODEL
  milk_yd = Lact_curve(DIM ln305DIM) HTD G(1 DIM ln305DIM| animal)
```

Note that the component name `Lact_curve` is informative for the user only, not

MiX99, because it is used for fixed regression effects and there is no nesting. Name `Lact_curve` will remind user that these regression effects model the lactation curve.

The fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	3	19.950	HTD	milk_yd
1	1	2	4	20.373	HTD	milk_yd
1	1	3	4	20.610	HTD	milk_yd
1	1	4	4	19.728	HTD	milk_yd
1	1	5	4	18.605	HTD	milk_yd
1	1	6	4	17.852	HTD	milk_yd

The `Lact_curve` regression effect solutions (`Solreg`) are

Trt	Reg-No	Solution	Trait	Covariable
1	1	-.49839E-01	milk_yd	DIM
1	2	5.2910	milk_yd	ln305DIM

The random regression effect estimates (`Solani`) for each animal are

Bull	N-Desc	N-Obs	Intercept	DIM	ln305DIM
1	1	3	-.44256	0.36869E-01	-.36961E-01
2	1	4	0.26977	-.66036E-01	0.32266E-01
3	0	6	-.72875	0.68317E-02	-.47899E-01
4	0	5	1.1019	-.53652E-02	0.76755E-01
5	0	3	-.16240	0.69360E-02	-.14924E-01
6	0	2	-.48256	0.16641E-01	-.37788E-01
7	2	0	-.98533E-01	0.13337E-01	-.10336E-01
8	2	0	0.45724	-.23800E-01	0.36344E-01
9	2	0	-.62847	0.35030E-01	-.47914E-01
10	2	0	0.45724	-.23800E-01	0.36344E-01
11	2	0	-.18720	-.76675E-03	-.14550E-01

5.2.4 Example: Covariable table and random regression model

MiX99 allows use of covariable table files. This means using an index in the data file that indicates a row in a covariable table file having regression coefficients. The table numbers in model lines refer to column numbers in this covariable table file instead of the data file. Note that the first column (index) is not counted as a column in the covariable table file. Use of covariable table file can reduce size of the data file. Typically covariable table files are small because number of possible indices is small. For example, days in milk in a data file can be from 1 to 350 days, and, so, only 350 different regression coefficients are needed for one regression effect in the covariable table file.

CLIM commands needed are `TABLEFILE` and `TABLEINDEX`. `TABLEFILE` indicates name of the covariable table file. `TABLEINDEX` has the integer number column name having the index in the data file. Only one table file and index is allowed. The indices must be positive numbers greater than zero, and be consecutively numbered. For example, the table file can have indices 1, 2, 3, 4, but having only 1, 2, 4 is unacceptable.

The covariable table file regression coefficients need to be referenced in the model differently from the other regression coefficients. The covariable table regression coefficients are referenced by letter *t* and a column number: `t`*n* where *n* is column number in the covariable table file. For example, `t3` means column 3 in the covariable table file.

We consider again the single trait random regression animal model example by Schaeffer and Dekkers (1994) (Chapter 5.2.3). We use the covariable table approach to reduce number of columns in the data file. The idea is that the data file has an index to indicate which regression coefficients are used. A natural indicator in dairy cattle test-day models is days in milk. For the purpose of this example, an artificial index was used instead. This was due to MiX99 requiring that the index is consecutively numbered. Thus, the covariable index table file has to have index numbers from some number, say 1, consecutively to a high number, say 305. This would give 305 lines.

Use of covariable table file leads to changes in the CLIM instruction file, and data file. In addition, there has to be a covariable table file.

The data file (RRM_table.dat) is

HTD$_1$	animal$_2$	block$_3$	index$_4$	milk$_1$
1	1	1	8	26.0
2	1	1	14	23.0
3	1	1	19	21.0
1	2	1	5	29.0
2	2	1	11	18.0
3	2	1	16	8.0
4	2	1	20	1.0
1	3	2	2	37.0
2	3	2	6	25.0
3	3	2	13	19.0
4	3	2	17	15.0
5	3	2	22	11.0
6	3	2	23	7.0
2	4	3	1	44.0
3	4	3	7	29.0
4	4	3	12	22.0
5	4	3	18	14.0
6	4	3	21	8.0
4	5	3	3	35.0
5	5	3	9	23.0
6	5	3	15	17.0
5	6	4	4	28.0
6	6	4	10	22.0

The covariable table file (RRM_table.cov) is

index$_1$	DIM$_1$	log(305/DIM)$_2$
1	5	4.1108699
2	8	3.6408701
3	14	3.0812500
4	31	2.2863200
5	34	2.1939499
6	58	1.6598700
7	60	1.6259700
8	73	1.4298500
9	74	1.4162500
10	81	1.3258600
11	84	1.2894900

```
   12    105    1.0663500
   13    113    0.9929240
   14    123    0.9081270
   15    124    0.9000300
   16    139    0.7858380
   17    158    0.6577170
   18    165    0.6143660
   19    178    0.5385280
   20    184    0.5053760
   21    215    0.3496740
   22    218    0.3358170
   23    268    0.1293250
```

```
DATAFILE   RRM_table.dat
INTEGER    HTD animal blk-var index
REAL       milk_yd

TABLEFILE  RRM_table.cov
TABLEINDEX index

PEDFILE    RRM.ped
PEDIGREE   G am

PARFILE    RRM.var

MODEL SCALE
  milk_yd = Lact_curve(t1 t2) HTD G(1 t1 t2| animal)
```

The solution files will be the same. However, there is small difference in the `Solreg` file. The file is now

```
Trt Reg-No  Solution     Trait   Covariable
  1   1 -.49839E-01   milk_yd    T1
  1   2  5.2910       milk_yd    T2
```

Thus, instead of the covariable names `DIM` and `ln305DIM`, there are the table covariable column names `T1` and `T2`.

5.2.5   Example: Heterogeneous residual variance in test day model

Consider the random regression model example by Schaeffer and Dekkers (1994) (Chapter 5.2.4). However, assume now that residual variance is different according to the block. There are four blocks. Let residual variance be 100, 110, 105, and 90 in blocks 1, 2, 3, and 4, respectively.

Important commands in CLIM for use of heterogeneous residual variance are `RESIDFILE` and `RESIDUAL`. Command `RESIDFILE` has the name of the residual variance file. Command `RESIDUAL` indicates the integer number column having the residual variance number in the data file.

Our example data stays the same. However, heterogeneous residual variance file (`RRM_res.var`) is needed:

```
1 1 1 100.0
2 1 1 110.0
3 1 1 105.0
4 1 1  90.0
```

The first column is the residual variance block number. The second and third column refer to matrix position, here scalar. Thus, in our example, matrix position is always (1,1). The last column has the variances.

CLIM code for analysis is

```
DATAFILE   RRM_table.dat
INTEGER    HTD animal blk-var index
REAL       milk_yd

TABLEFILE  RRM_table.cov
TABLEINDEX index

PEDFILE    RRM.ped
PEDIGREE   G am

PARFILE    RRM.var     # regular variance file
RESIDFILE  RRM_res.var # the residual variances
RESIDUAL   blk-var     # index for residual variance

MODEL SCALE
  milk_yd = Lact_curve(t1 t2) HTD G(1 t1 t2| animal)
```

Fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	3	19.954	HTD	milk_yd
1	1	2	4	20.369	HTD	milk_yd
1	1	3	4	20.589	HTD	milk_yd
1	1	4	4	19.689	HTD	milk_yd
1	1	5	4	18.484	HTD	milk_yd
1	1	6	4	17.755	HTD	milk_yd

Fixed regression effect solutions (`Solreg`) are

Trt	Reg-No	Solution	Trait	Covariable
1	1	−.49291E−01	milk_yd	T1
1	2	5.2951	milk_yd	T2

Random regression effect solutions (`Solani`) are

Bull	N-Desc	N-Obs	Intercept	DIM	ln305DIM
1	1	3	−.43705	0.36362E−01	−.36590E−01
2	1	4	0.26551	−.66395E−01	0.32095E−01
3	0	6	−.69442	0.64368E−02	−.45801E−01
4	0	5	1.0687	−.52282E−02	0.74740E−01
5	0	3	−.15415	0.72484E−02	−.14431E−01
6	0	2	−.48062	0.17272E−01	−.37930E−01
7	2	0	−.97642E−01	0.13161E−01	−.10194E−01
8	2	0	0.44474	−.23875E−01	0.35618E−01
9	2	0	−.60770	0.34699E−01	−.46705E−01
10	2	0	0.44474	−.23875E−01	0.35618E−01
11	2	0	−.18370	−.11773E−03	−.14523E−01

5.3 Maternal effect models

maternal effect model

The random regression effect models allow quite flexible model description. However, random regression effects have the same covariance structure, e.g., numerator relationship matrix. Random maternal and paternal effects with correlated animal effect

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have a different structure. Nesting within a component is now by different class variable. Thus, we have multiple correlated factors within genetic effect.

A random effect may have multiple class effects. For example, the genetic component has both a maternal and a direct genetic effect. Component name is again needed.

A simple model with a fixed herd effect, random maternal and animal effects is

```
PEDIGREE    G am
MODEL
        y = herd G(dam animal)
```

Although `G(dam animal)` looks similar to the random regression models, there is a notable difference. Here `dam` and `animal` are different class effects not regression coefficients by same class. This model specification requires a 2 by 2 genetic covariance matrix for the maternal and animal effect.

Note that the maternal genetic model is different from model

```
PEDIGREE    G am
RANDOM      dam
MODEL
        y = herd dam G(animal)
```

Here `dam` is a common dam environment effect for all of its progeny. There is no relationship matrix involved in this `dam` effect.

5.3.1 Example: Animal model for a maternal trait

Consider model

$$tr_1 = herd \times year + p_m + a_m + a_g + e$$

where $herd \times year$ is fixed herd-year effect, p_m is random common dam permanent environment effect, a_m is random additive maternal genetic effect, and a_g is random additive individual genetic effect, and e is random residual.

The variance components are: maternal permanent environment variance $\sigma_p^2 = 1$, residual variance $\sigma_e^2 = 7$, and genetic covariance matrix

$$\boldsymbol{G}_0 = \left[\begin{array}{cc} 2.0 & 1.0 \\ 1.0 & 3.0 \end{array} \right]$$

The parameter file `mat.var` is

Random effect₁	Row₂	Column₃	Covariance₁	Comment
1	1	1	1.0	maternal permanent env.
2	1	1	2.0	maternal genetic
2	1	2	1.0	cov(maternal, animal)
2	2	2	3.0	animal genetic
3	1	1	7.0	residual variance

We use the previously introduced data (Chapter 3). The pedigree file (Chapter 3.2.1) can be kept the same. For the purposes of this example, we modify the data (Chapter 3.1.1) to have the `dam` column instead of the `sire` column (`example_mat.dat`):

animal₁	dam₂	herd×year₃	ones₄	trait 1₁	trait 2₂
4	2	1	1	90	200
6	4	1	1	110	190

8	6	2	1	120	140
9	6	2	1	130	120
10	8	2	1	120	130

CLIM code is

```
DATAFILE   example_mat.dat

INTEGER    animal dam herd_year ones
REAL       tr1 tr2

PEDFILE    AM.ped
PEDIGREE   G  am
RANDOM     PE

PARFILE    mat.var

MODEL SCALE
 tr1 = herd_year PE(dam) G(dam animal)
```

The herd-year solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	2	99.338	herd_yea	tr1
1	1	2	3	121.71	herd_yea	tr1

The maternal permanent environment solutions (`Solr01`) are

2	1	-1.0095
4	1	1.0095
6	2	0.24829
8	1	-.24831

The maternal and animal genetic effect solutions (`Solani`) are

Animal id	N-Desc	N-Obs	Maternal	Animal
1	2	0	1.0095	0.50476
2	2	1	-1.0095	-.50475
3	2	0	0.25237	0.75717
4	2	1	0.75714	-.25240
5	3	0	0.38058	0.19030
6	3	2	1.1337	1.8287
7	1	0	0.69506	0.82321
8	1	1	0.22384	0.30441E-01
9	0	0	1.1042	2.0507
10	0	0	0.33530	0.54334E-01

Note that content of genetic effect solutions in the Solani file depends on the given order in the model line. In this example, we gave `G(dam animal)` with the maternal effect first, and direct animal effect second. Changing order of the effects changes order in the solution file as well.

6   Multiple trait models

Multiple traits are defined by separate model lines. Traits are numbered in MiX99. Trait number equals model line number. Thus, the first model line trait is trait number 1, the second is number 2 etc. This has to be kept in mind when making covariance matrix in `PARFILE`. Sometimes numbering of variance components can be difficult. In particular, when different traits have some (random regression or maternal) effects missing in another trait. The missing components are signaled by a dash (−) sign in

the model lines. In the following, we will consider this in animal models, but sire models work similarly.

6.1 All traits have the same effects

Simple multiple trait model has several traits that are equal in the sense of having the same effects. For example, both traits have herd-year effect and animal genetic effects. These effects have different solutions by trait. However, the important fact is that both traits refer to the same classification column in the data file.

6.1.1 Example: Simple multiple trait model

Consider the multiple trait model data presented in Chapter 3.1.1. First consider a simple model where both traits have the same effects:

$$tr_1 = herd \times year_1 + a_1 + e_1$$
$$tr_2 = herd \times year_2 + a_2 + e_2$$

where the subscripts 1 and 2 refer to traits 1 and 2. The variance components file (name `mt.var`) was already presented in Chapter 3.3.1. CLIM instruction file is:

```
DATAFILE   example.dat

INTEGER    animal sire herd_year ones
REAL       tr1 tr2

PEDFILE    AM.ped
PEDIGREE   animal am
DATASORT   PEDIGREECODE=animal

PARFILE    mt.var

MODEL SCALE
  tr1 = herd_year animal
  tr2 = herd_year animal
```

The fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	2	99.760	herd_yea	tr1
1	2	1	2	194.87	herd_yea	tr2
1	1	2	3	122.93	herd_yea	tr1
1	2	2	3	129.73	herd_yea	tr2

The breeding value estimates (`Solani`) are

Bull	N-Desc	N-Obs	tr1	tr2
1	2	0	0.44163E-04	0.10214E-04
2	2	0	0.44163E-04	0.10214E-04
3	2	0	0.47974	0.26924
4	2	1	-.47968	-.26923
5	3	0	-.31037E-04	-.40111E-04
6	3	1	0.95937	0.53844
7	1	0	0.23052	0.78139E-01
8	1	1	0.77389	0.86997
9	0	1	0.43458	-.14051
10	0	1	0.40098E-02	0.91964E-01

6.2 Traits have different effects

Multiple trait models having different effects can be easily handled by MiX99. However, there are some details that need to be remembered when using CLIM. The default CLIM model line works like the MiX99 directive file: an effects missing in a trait has to be indicated by a dash ('-') sign. Consequently, models are column restricted, i.e., each effect in the model has a column which is present (given model name) or missing (given dash sign) for each trait. Thus, it is important to give effects in a specific order. The beta testing version of CLIM lifts this restriction, and model effects can be given in any order without missing dash sign indicator. However, this may lead to models that are interpreted incorrectly. Thus, it is very important to check that the model generated by CLIM is correct in the `MiX99_DIR.DIR` file.

6.2.1 Example: Multiple trait model with different effects by trait

Consider the multiple trait model data as in Chapter 6.1.1 but use model

$$tr_1 = herd \times year + a_1 + e_1$$
$$tr_2 = \mu + a_2 + e_2$$

The variance components file is the same as before. CLIM instruction file is the same except for the model lines:

```
MODEL SCALE
  tr1 = -      herd_year animal
  tr2 = ones -          animal
```

The fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	2	1	5	160.28	ones	tr2
2	1	1	2	88.759	herd_yea	tr1
2	1	2	3	137.73	herd_yea	tr1

Breeding values estimates (`Solani`) are

Bull	N-Desc	N-Obs	tr1	tr2
1	2	0	-.43878E-05	0.21829E-05
2	2	0	-.43878E-05	0.21829E-05
3	2	0	-2.2842	-2.5112
4	2	1	2.2842	2.5112
5	3	0	-5.8968	-5.8969
6	3	1	1.3284	0.87453
7	1	0	-4.2748	-4.4635
8	1	1	-7.6804	-7.6190
9	0	1	-6.6912	-7.2448
10	0	1	-9.9586	-9.9459

6.2.2 Example: Different effects by trait using CLIM beta features

Order of effects is unimportant in the CLIM beta version. The model lines in example above in Chapter 6.2.1 can be given differently using the CLIM beta version (e.g., giving `mix99i -b model.clm`). A natural way of giving would be

```
MODEL SCALE
  tr1 =      herd_year animal
  tr2 = ones           animal
```

The additional space between the effect names is not important for CLIM, it is just to make the model easier to read. A perfectly acceptable model would be

```
MODEL SCALE
  tr1 = animal herd_year
  tr2 = ones animal
```

However, this is more difficult to read.

The breeding value estimates in the `Solani` solution file would be exactly the same as before. However, solutions in the `Solfix` file are printed in different order:

```
Fact. Trt      Level   N-Obs  Solution        Factor Trait
   1    1          1       2  88.759        herd_yea tr1
   1    1          2       3  137.73        herd_yea tr1
   2    2          1       5  160.28             ones tr2
```

The reason for different ordering is the `-b` option. The `-b` option leads to ordering by column number in the data file. Column `herd_year` is before `ones` in the data file. This can also be seen in the `MiX99_DIR.DIR` file.

6.3 Multiple trait random regression model

Multiple trait random regression models are a natural extension of the single trait ones. The model lines are as easy to give. However, it is important to get the numbering of random regression effects correct. Numbering is column-wise from first trait to second etc.

Consider quadratic random regression function of an animal for two traits:

$$\left[\begin{array}{c} f(\boldsymbol{a}_1, x_1) \\ f(\boldsymbol{a}_2, x_2) \end{array} \right] = \left[\begin{array}{ccc} 1 & x_1 & x_1^2 \\ 1 & x_2 & x_2^2 \end{array} \right] \left[\begin{array}{c} \boldsymbol{a}_1 \\ \boldsymbol{a}_2 \\ \boldsymbol{a}_3 \end{array} \right]$$

where subscripts 1 and 2 refer to trait number, x_1 and x_2 are regression coefficients, and a has random regression effects to be estimated. The functions can be written also

$$f(\boldsymbol{a}, x_1) = a_{1,1} + x_1 \cdot a_{1,2} + x_1^2 \cdot a_{1,3}$$
$$f(\boldsymbol{a}, x_2) = a_{2,1} + x_2 \cdot a_{2,2} + x_2^2 \cdot a_{2,3}$$

where the first subscript in a is trait number, and the second is random regression effect number. The random regression effects are numbered

$$\left[\begin{array}{ccc} a_{1,1} & a_{1,2} & a_{1,3} \\ a_{2,1} & a_{2,2} & a_{2,3} \end{array} \right] = \left[\begin{array}{ccc} (1) & (3) & (5) \\ (2) & (4) & (6) \end{array} \right]$$

where the numbers in parenthesis mean effect number.

The random regression effect numbers are used to identify variance components in the `PARFILE`. They also determine order of estimates in the solution files such as `Solani`.

6.3.1 Example: Multiple trait random regression model

Consider the single trait random regression test-day model data presented in Chapter 5.2.3. We expand the data by adding column of observations for a second trait. The observation column of the single trait is copied to this new column.

The two traits will have the same random regression function. Assume that within trait the genetic covariance matrix stays the same, and between the traits the correlation

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is 95 %. Remember that numbering of regression effects is column-wise. Thus, the genetic covariance matrix is

$$
\boldsymbol{G} =
\begin{bmatrix}
44.791 & 42.55145 & -0.133 & -0.12635 & 0.351 & 0.33345 \\
42.55145 & 44.791 & -0.12635 & -0.133 & 0.33345 & 0.351 \\
-0.133 & -0.12635 & 0.073 & 0.06935 & -0.010 & -0.0095 \\
-0.12635 & -0.133 & 0.06935 & 0.073 & -0.0095 & -0.010 \\
0.351 & 0.33345 & -0.010 & -0.0095 & 1.068 & 1.0146 \\
0.33345 & 0.351 & -0.0095 & -0.010 & 1.0146 & 1.068
\end{bmatrix}
\tag{1}
$$

and let the residual covariance matrix be

$$
\boldsymbol{R} =
\begin{bmatrix}
100.0 & 50.0 \\
50.0 & 100.0
\end{bmatrix}
\tag{2}
$$

Then, the variance parameter file (RRM_mt.var) is

```
1  1  1     44.791
1  2  2     44.791
1  1  2     42.55145
1  3  1     -0.133
1  4  2     -0.133
1  4  1     -0.12635
1  3  2     -0.12635
1  3  3      0.073
1  4  4      0.073
1  3  4      0.06935
1  3  5     -0.010
1  4  6     -0.010
1  3  6     -0.00950
1  4  5     -0.00950
1  5  1      0.351
1  6  2      0.351
1  5  2      0.33345
1  6  1      0.33345
1  5  5      1.068
1  6  6      1.068
1  5  6      1.01460
2  1  1    100.0
2  2  1     50.0
2  2  2    100.0
```

CLIM code is

```
DATAFILE   RRM_mt.dat
INTEGER    HTD animal blk-var
REAL       DIM  ln305DIM milk_1 milk_2

PEDFILE    ../data/RRM.ped
PEDIGREE   G am

PARFILE    RRM_mt.var

MODEL SCALE
  milk_1 = Lact_curve(DIM ln305DIM) HTD G(1 DIM ln305DIM| animal)
  milk_2 = Lact_curve(DIM ln305DIM) HTD G(1 DIM ln305DIM| animal)
```

Fixed effects solutions (Solfix) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	3	20.151	HTD	milk_1
1	2	1	3	20.151	HTD	milk_2
1	1	2	4	20.488	HTD	milk_1
1	2	2	4	20.488	HTD	milk_2
1	1	3	4	20.718	HTD	milk_1
1	2	3	4	20.718	HTD	milk_2
1	1	4	4	19.891	HTD	milk_1
1	2	4	4	19.891	HTD	milk_2
1	1	5	4	18.753	HTD	milk_1
1	2	5	4	18.753	HTD	milk_2
1	1	6	4	17.992	HTD	milk_1
1	2	6	4	17.992	HTD	milk_2

Fixed regression effects (`Solreg`) are

Trt	Reg-No	Solution	Trait	Covariable
1	1	-.50423E-01	milk_1	DIM
1	2	5.2367	milk_1	ln305DIM
2	1	-.50423E-01	milk_2	DIM
2	2	5.2367	milk_2	ln305DIM

Random regression breeding values (`Solani`) are

id			(1)	(2)	DIM(1)	DIM(2)	ln305DIM(1)	
1	1	3	-.54362	-.54362	0.37788E-01	0.37788E-01	-.43693E-01	...
2	1	4	0.34392	0.34392	-.67204E-01	-.67204E-01	0.37731E-01	...
3	0	6	-.85129	-.85129	0.75673E-02	0.75673E-02	-.54810E-01	...
4	0	5	1.2934	1.2934	-.65255E-02	-.65255E-02	0.89009E-01	...
5	0	3	-.18533	-.18533	0.70232E-02	0.70233E-02	-.17046E-01	...
6	0	2	-.57857	-.57857	0.17720E-01	0.17720E-01	-.44841E-01	...
7	2	0	-.12228	-.12228	0.13506E-01	0.13506E-01	-.12222E-01	...
8	2	0	0.54578	0.54579	-.24593E-01	-.24593E-01	0.42246E-01	...
9	2	0	-.75284	-.75284	0.36109E-01	0.36109E-01	-.55656E-01	...
10	2	0	0.54578	0.54579	-.24593E-01	-.24593E-01	0.42246E-01	...
11	2	0	-.21549	-.21549	-.46539E-03	-.46540E-03	-.17023E-01	...

The last column has been omitted due to page width restriction. It is equal to the second last column. Numbers in the parenthesis refer to the trait number of effect.

6.4 Combining of trait estimates

Combing of trait estimates means making effects of different traits to be the same. By default, it is assumed that effects in different traits will be different, and get separate estimated values. Combining of trait estimates or shortly combining of traits allows estimating the same solutions for effects in different traits. In practice, combining of traits is used in reduced rank random regression models. However, the concept is illustrated by a multiple trait model that is equivalent with repeatability model.

Combining of traits is indicated by the '@' sign in the model lines. After the '@' sign combining group name is given. The name can be any allowed name that has not already been used. Combining of traits can be instructed for any effects that have component name. Thus, it is not possible to use integer number column names when combining traits. The effect names have to be given a component name. For example, `G(animal)@fst`.

6.4.1 Example: Repeatability model by multiple trait model

Repeatability model is a multiple trait model where genetic correlation between traits is one, residual variances are equal, and residual covariances are equal. Residual correlations are equal to $\sigma_p^2 / \left(\sigma_p^2 + \sigma_e^2 \right)$ where σ_p^2 is permanent environment variance and σ_e^2 is residual variance. We consider the repeatability model example presented in Chapter 5.1.5.

An equivalent two trait animal model is

$$tr_1 = herd \times year + a + e_1$$
$$tr_2 = herd \times year + a + e_2$$

where the fixed effect $herd \times year$ and random animal genetic effect *a* are common to both traits. Genetic variance is as before $\sigma_a^2 = 2$. Residual covariance matrix is

$$\boldsymbol{R} = \left[\begin{array}{cc} 7.0 & 2.0 \\ 2.0 & 7.0 \end{array} \right] \tag{3}$$

Note that the residual variances equal sum of permanent environment and residual variances in the repeatability mode, and covariance equals repeatability variance.

The variance components file (`mt_repeat.var`) is

Random effect$_1$	Row$_2$	Column$_3$	Covariance$_1$	Comment
1	1	1	3.0	animal genetic
2	1	1	7.0	residual variance
2	1	2	2.0	permanent environment
2	2	2	7.0	residual variance

The repeatability data file changed to multiple trait format (`mt_repeat.dat`):

animal	sire	herd×year$_1$	herd×year$_2$	ones	trait 1	trait 2
4	1	11	21	1	90	200
6	3	11	21	1	110	190
8	5	12	22	1	120	140
9	5	12	22	1	130	120
10	7	12	22	1	120	130

CLIM code

```
DATAFILE   example_mt_repeat.dat

INTEGER    animal sire hy_1 hy_2 ones
REAL       tr1 tr2

PEDFILE    AM.ped
PEDIGREE   G am

PARFILE    mt_repeat.var

MODEL SCALE
  tr1 = hy_1 -     G(animal)@1
  tr2 = -     hy_2 G(animal)@1
```

Note that the animal genetic effect `animal` needs a name `G` for combining. Also, there has to be a dash (−) to indicate the use of separate integer columns for the herd-year effects.

Estimated herd-year solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	11	2	99.833	hy_1	tr1
1	1	12	3	123.01	hy_1	tr1
2	2	21	2	194.83	hy_2	tr2
2	2	22	3	129.68	hy_2	tr2

Estimated breeding values (`Solani`) are

Bull	N-Desc	N-Obs	tr12
1	2	0	-.34993E-13
2	2	0	-.34993E-13
3	2	0	0.33333
4	2	1	-.33333
5	3	0	-.76001E-13
6	3	1	0.66667
7	1	0	0.97731E-01
8	1	1	0.98778
9	0	1	-.85515E-01
10	0	1	0.71553E-01

The solutions are the same as by the repeatability model in Chapter 5.1.5. However, no solutions for permanent environment are calculated because no permanent environment effect was in this two trait model.

6.4.2   Example: Reduced rank random regression model

Rank reduction can be used to make covariance matrices of highly correlated random regression coefficients more independent. Consequently, size of the covariance matrix is reduced. Convergence of the iterative solver becomes faster for at least two reasons: equations become less correlated, and there are less unknowns to solve.

In a reduced rank model, coefficients from two or more traits multiply the same solutions. We consider the two trait random regression example in Chapter 6.3.1.

6.4.3   Example: Finnish test-day model

This example is not a complete presentation of the old Finnish test-day model. No data is given, and only the first lactation model. This illustrates potential of MiX99 for solving complex test-day models used currently to solve dairy cattle breeding values.

This was Finnish test-day model for first lactation milk, protein, and fat yield. The full model had second, and third with later lactations as additional traits. In this subset model, both permanent environment and additive genetic effects are modeled by a curve with six coefficients. However, covariance matrices of both of these effects have size six because all traits are combined to one.

```
DATAFILE    Ter.dat
INTEGER     block animal HTM YM SEASON AGE DCC DIM
REAL        milk protein fat

PEDFILE     miniTDM.pedi
PARFILE     TDMpara.in
PEDIGREE    G am+p
RANDOM      HTM PE

TABLEFILE   finTDMpara.cov
TABLEINDEX  DIM
```

```
MODEL SCALE
  milk    = Curve(t1 t2 t3 t4 t96| SEASON) AGE DCC YM HTM &
            PE(t5 t6 t7 t8 t9 t10| animal)@1st          &
            G(t59 t60 t61 t62 t63 t64| animal)@FST

  protein = Curve(t1 t2 t3 t95 t97| SEASON) AGE DCC YM HTM &
            PE(t11 t12 t13 t14 t15 t16| animal)@1st       &
            G(t65 t66 t67 t68 t69 t70| animal)@FST

  fat     = Curve(t1 t2 t3 t95 t98| SEASON) AGE DCC YM HTM &
            PE(t17 t18 t19 t20 t21 t22| animal)@1st       &
            G(t71 t72 t73 t74 t75 t76| animal)@FST
```

Note that the model lines of the previous example can be shortened using CLIM macro and range abbreviations (command line option `--usemacros` is currently needed): **DEV**

```
DEFINE CurveMILK  Curve(t1:3 t4  t96 | SEASON)
DEFINE CurvePROT  Curve(t1:3 t95 t97 | SEASON)
DEFINE CurveFAT   Curve(t1:3 t95 t98 | SEASON)
DEFINE Common     AGE DCC YM HTM

MODEL SCALE
  milk    = CurveMILK Common PE( t5:10|animal)@1st G(t59:64|animal)@FST
  protein = CurvePROT Common PE(t11:16|animal)@1st G(t65:70|animal)@FST
  fat     = CurveFAT  Common PE(t17:22|animal)@1st G(t71:76|animal)@FST
```

6.5 Multiple trait maternal effects model

Consider three trait maternal effect model where the last trait does not have a maternal effect. In addition, some fixed effects are different by trait. Note that spaces between the effect names are only to help reading the model lines.

```
DATAFILE   Beef.dat
INTEGER    BREED HERD id dam sex twin dam_age &
           brth_mth HY_brth HY_200d HY_365d
REAL       Brth_w 200d_w 365d_w age_200d age_365d

PEDFILE    Beef.ped
PEDIGREE   G am+p

PARFILE    Beef.var

MODEL SCALE
  Brth_w =    -     twin sex    -     HY_brth -       -      G(dam id)
  200d_w = age_200d twin sex brth_mth  -     HY_200d -      G(dam id)
  365d_w = age_365d twin sex brth_mth  -       -     HY_365d G( -  id)

WITHINBLOCKORDER G HY_365d HY_200d HY_brth
```

Currently in beta testing (option `-b`) allows this model to be written without the dashes. Because effects are ordered by their column number, the resulting directive file is different from the example above. However, the analysis will be the same although effects are in different order on the model lines. It is still important to have `-` in the third trait `365d_w` within random effect in order to have correct numbering of variance components.

```
MODEL
  Brth_w =            twin sex            HY_brth  G(dam id)
  200d_w = age_200d twin sex brth_mth HY_200d  G(dam id)
  365d_w = age_365d twin sex brth_mth HY_365d  G( –  id)
```

7 Genomic data models

There are two commonly employed alternative ways to use genomic data in statistical models for animal breeding. One way has genomic marker effects directly in the model. The other way uses genomic data to build (co)variance structure such as genomic relationship matrix, and use it as a (co)variance structure to breeding values. Both kinds of models are supported in MiX99 using CLIM. The genomic marker effect model will be called SNP-BLUP model. Models using genomic relationship matrix include G-BLUP and the single-step method.

7.1 SNP-BLUP or genomic effect model

Statistical models for genomic selection have often several thousand SNP markers. In the SNP-BLUP model each marker is a regression effect. It would be tedious to write a model line which has several thousand regression coefficients. Instead, CLIM allows use of regression coefficient matrices in files by commands `REGMATRIX` and `REGFILE`. MiX99 allows use of several matrices but CLIM allows currently only one regression coefficient matrix.

The regression coefficients defined by the regression coefficient matrix can be either fixed (command `REGMATRIX FIXED` or random (command `REGMATRIX RANDOM`). If they are random, the marker effects in MiX99 can have either common variance or, alternatively, each marker can have its individual own variance.

Relevant commands for regression coefficient matrices are `REGFILE` for the name of the file having the regression coefficients, `REGMATRIX` for defining type of the matrix as well as coefficient columns, and `REGPARFILE` for variance component(s). For syntax and better explanation see Chapter 9.2.

All coefficients on a line in a regression coefficient matrix file belong to only one animal. Each line corresponds to a line in the data file defined by `DATAFILE`. It is important to have the lines in the regression coefficient file in the same order as corresponding observations in the data file. It is possible to instruct MiX99 to check that the files have lines in the same order by animal id code. Then, the genetic evaluation is not as error prone as when no animal id code has been given.

Animal id code can be on different columns in the regression coefficient file and the data file. Animal id code in the regression coefficient file is instructed by option `ID` in command `REGMATRIX RANDOM ID=value` where `value` is column number in the regression coefficient file. In the data file the command for animal id code is `DATASORT PEDIGREECODE=icol` where `icol` is integer number column name (or number) in the data file. If either one information is missing, order of lines cannot be checked, and order is assumed to be correct. Please check summary of commands for syntax and better explanation of these commands (Chapters 9.2.2 and 9.2.16).

Use of the `ID` option in `REGMATRIX` allows giving genotype files that have more genotyped animals than animals with observation. This is convenient when the genotype

data set has genotyped candidate animals without observation. Or, the same marker data is used in analysis of several traits where some animals do not have observations for some traits.

7.1.1 Example: simple genomic marker BLUP

Model is

$$y = \mu + \beta_1 g_1 + \beta_2 g_2 + \beta_3 g_3 + \beta_4 g_4 + \beta_5 g_5 + \beta_6 g_6 + e$$

where the βs are regression coefficients, the gs are random additive marker or allele effects, and e is random residual. There are six markers, numbered 1, 2, ..., 6. The markers have bi-allelic loci. For each marker, the genotypes are coded as 0 for homozygous first allele, 1 for heterozygote, and 2 for homozygous second allele. Marker effect is additive allele effect of the second allele. Thus, two times the marker effect solution gives difference between the homozygotes for the first and the second allele.

The variance components are: common SNP marker genetic variance $\sigma_g^2 = \frac{1}{6} = 0.166666666$, and residual variance $\sigma_e^2 = 1$. The variances are in two separate files. The file for the marker genotype variance (`gs_gen.par`) is

Matrix number$_1$	Row$_2$	Column$_3$	Covariance$_1$	
1	1	1	0.166666666	marker variance

The other parameter file (`gs_res.par`) has the residual variance:

Random effect$_1$	Row$_2$	Column$_3$	Covariance$_1$	
1	1	1	1.0	residual variance

The data has been divided into two separate files. The data file (command `DATAFILE`) is the standard MiX99 observation file having columns for animal id code, fixed effect (general mean), and observation. The other file (command `REGFILE`) has the genomic information, i.e., regression coefficients defined by genotype. As mentioned, records in these files must be in the same order. Thus, the first record in data file and in the regression coefficient file are from the same animal. It is assumed that all genotypes are known, and have been coded by user.

The data files are

data file `gs_obs.dat`			genotype file `gs_geno.dat`						
animal$_1$	mean$_2$	y$_1$	id$_1$	1	2	3	4	5	6
1	1	5	1	2	1	0	0	0	0
2	1	6	2	1	1	0	1	0	0
3	1	10	3	1	0	2	2	2	1
4	1	15	4	0	1	1	2	2	2
			5	0	0	2	1	1	1
			6	0	0	1	2	2	2

CLIM code is

```
DATAFILE   gs_obs.dat

INTEGER    animal mean
REAL       y
```

```
MISSING -99999.
DATASORT PEDIGREECODE=animal

PARFILE   gs_res.par # residual variance

REGMATRIX  RANDOM SNP ID=1 FIRST=2 LAST=7
REGFILE    gs_geno.dat
REGPARFILE gs_gen.par # snp variance

PRECON  d

MODEL
  y = mean
```

The fixed general mean solution (Solf01) is

```
         1          4  7.2604
```

The marker effect solutions (Solreg_mat) are

```
Trt  Matrix  Effect  Solution    Mat-Name
  1       1       1 -0.66624     SNP
  1       1       2  0.11015     SNP
  1       1       3  0.27294     SNP
  1       1       4  0.55610     SNP
  1       1       5  0.76616     SNP
  1       1       6  0.87631     SNP
```

Estimated genomic breeding values can be calculated as

$$\widehat{\boldsymbol{a}} = \mathbf{1}\hat{\mu} + \boldsymbol{Z}\widehat{\boldsymbol{g}} \tag{4}$$

where $\mathbf{1}$ is vector of ones, $\hat{\mu}$ is estimate of the general mean, $\boldsymbol{Z}$ is the regression coefficient matrix, and $\widehat{\boldsymbol{g}}$ is 6×1 vector of estimated marker effects. MiX99 (specifically mix99s) calculates genomic breeding values ($\widehat{\boldsymbol{a}}$) for this model when option -p is given. Thus, mix99s -p -s writes file yHat.data0 where each line has a breeding value for an animal. The values are in the same order as observations in the data file. Unix command paste gs_obs.dat yHat.data0 shows animal id numbers with their estimated genomic breeding values. Result is

```
1 1  5      6.0380783
2 1  6      7.2604141
3 1 10      10.660874
4 1 15      12.040634
```

Note that estimated genomic breeding value is not calculated to animals without observation using option -p.

7.1.2 Enhanced formatting of SNP marker information

SNP marker information is typically coded with values 0, 1, or 2, and optional missing marker value with some other one digit integer such as 3 or 9. The coding can also include separate centering and scaling information so that the possibly very large marker information can be kept in integer form to save disk space and memory.

REGMATRIX command has optional parameter IMPUTE for specifying **missing marker value**. For example:

```
  REGMATRIX ... IMPUTE=3
```

instructs to replace, or **impute**, all marker values 3 in the regression coefficient matrix by averages of the (non-missing) marker values.

The marker value ($\mathbf{Z}_{i,m}^{012}$) can be optionally centered and scaled by subtracting a center value (μ_m) from the marker value and multiplying this by a scaling value (s_m):

$$\mathbf{Z}_{i,m} = (\mathbf{Z}_{i,m}^{012} - \mu_m) * s_m$$

The centering can be specified with optional `CENTER` parameter of the `REGMATRIX` command. The centering value μ_m can be either average of the markers, a given constant for all markers, or separate value for each marker stored in a file. For example:

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 CENTER
```

centers the markers around the averages,

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 CENTER=1
```

uses "-1,0,1 coding" instead of the "0,1,2 coding", i.e. centers around one (1), and

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 CENTER=mu.dat
```

reads six (6 = 7-2+1) separate centering values from file `mu.dat`.

Similarly, optional scaling can be specified with `SCALE` parameter of the `REGMATRIX` command. The scaling value s_m can be either a given contant for all markers or separate value for each marker stored in a file. For example:

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 SCALE=0.5
```

scales all markers with a half (0.5) and

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 SCALE=s.dat
```

uses six separate scaling values stored in file `s.dat`.

By default, the general regression coefficient matrix values are **real valued numbers**. The SNP marker information is typically coded with **integer values** 0, 1, or 2, and optional missing marker value. In order to let MiX99 to check the allowed SNP marker integer values, the file format of the `REGFILE` file can be specified with optional `FORMAT` parameter of the `REGMATRIX` command. Default file format is "n" (or "normal") and the SNP marker information can be specified with format "m" (or "markers"):

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 FORMAT=markers
```

By default, the SNP marker values are assumed to be separated by spaces in the `REGFILE` file. The marker values (0, 1, and 2) are only one character wide. Thus, the spaces separating the markers effectively double the file size. The spaces between the marker values can be removed by specifying file format "s" (or "squeezed"). For example, file `gs_geno_nospaces.dat` could contain marker values without spaces as:

id$_1$	SNPs
1	210000
2	110100
3	102221
4	011222
5	002111
6	001222

and the file format can be specified with:

```
REGMATRIX RANDOM SNP ID=1 FIRST=2 LAST=7 FORMAT=squeezed
REGFILE    gs_geno_nospaces.dat
```

7.2   Example: simple G-BLUP

Consider the same data as in the previous example. The SNP-BLUP model using matrix notation is

$$\mathbf{y} = \mathbf{1}_4\mu + \mathbf{Z}\mathbf{g} + \mathbf{e}$$

where $\mathbf{y}$ is 4×1 vector of observations, $\mathbf{1}_4$ is 4×1 vector of ones, $\mathbf{Z}$ is 4×6 matrix of SNP marker genotypes, $\mathbf{g}$ is 6×1 vector of random marker effects, and $\mathbf{e}$ is random residual. An equivalent model or G-BLUP model solves breeding value vector $\mathbf{u} = \mathbf{Z}\mathbf{g}$ without need to solve the marker effects $\mathbf{g}$. The model is

$$\mathbf{y} = \mathbf{1}_4\mu + \mathbf{Z}_u\mathbf{u} + \mathbf{e}$$

where $\mathbf{Z}_u$ is 4×6 incidence matrix linking breeding values $\mathbf{u}$ to the observations. In our case, $\mathbf{Z}_u = [\ \mathbf{I}_4 \ \ \mathbf{0}\ ]$ where $\mathbf{0}$ is 4×2 matrix of zeros. In the SNP-BLUP model it was assumed that $\mathbf{g} \sim N(\mathbf{0}, \mathbf{I}_6\sigma_g^2)$. In the G-BLUP model, it is assumed that $\mathbf{u} \sim N(\mathbf{0}, \mathbf{G}\sigma_g^2)$ where $\mathbf{G} = \mathbf{Z}\mathbf{Z}'$ is a 6×6 matrix. Note that $\mathbf{Z}$ has marker coefficients of the candidate animals as well.

The $\mathbf{Z}$ matrix is

$$\mathbf{Z} = \begin{bmatrix} 2 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 2 & 2 & 2 & 1 \\ 0 & 1 & 1 & 2 & 2 & 2 \\ 0 & 0 & 2 & 1 & 1 & 1 \\ 0 & 0 & 1 & 2 & 2 & 2 \end{bmatrix}$$

and the covariance matrix is

$$\mathbf{G} = \mathbf{Z}\mathbf{Z}' = \begin{bmatrix} 5 & 3 & 2 & 1 & 0 & 0 \\ 3 & 3 & 3 & 3 & 1 & 2 \\ 2 & 3 & 14 & 12 & 9 & 12 \\ 1 & 3 & 12 & 14 & 8 & 13 \\ 0 & 1 & 9 & 8 & 7 & 8 \\ 0 & 2 & 12 & 13 & 8 & 13 \end{bmatrix}$$

Mixed model equations need inverse of covariance matrix of a random effect. In our case, $\mathbf{G}^{-1}$ is needed. MiX99 will not compute it: user has to calculate it. In our case the inverse is

$$\mathbf{G}^{-1} = \begin{bmatrix} 0.7500 & -0.5000 & -0.5000 & -0.2500 & 0.3333 & 0.5833 \\ -0.5000 & 2.0000 & -1.0000 & -1.5000 & 1.0000 & 1.5000 \\ -0.5000 & -1.0000 & 2.0000 & 1.5000 & -1.6666 & -2.1666 \\ -0.2500 & -1.5000 & 1.5000 & 2.7500 & -1.3333 & -3.0833 \\ 0.3333 & 1.0000 & -1.6666 & -1.3333 & 1.8888 & 1.5555 \\ 0.5833 & 1.5000 & -2.1666 & -3.0833 & 1.5555 & 3.9722 \end{bmatrix}$$

The inverse matrix is given to MiX99 in a file stored in either co-ordinate (Yale) sparse matrix format or lower triangle dense format.

The default inverse matrix format is the co-ordinate sparse matrix format, also called the Yale format. In this format, each element in the lower triangle of the matrix is given with its element position. In our case, the matrix in file `iG_raw.dat` is

```
1  1    0.75
2  1   -0.5
2  2    2
3  1   -0.5
3  2   -0.999999999999999
3  3    2
4  1   -0.25
4  2   -1.5
4  3    1.5
4  4    2.75
5  1    0.333333333333333
5  2    0.999999999999999
5  3   -1.66666666666667
5  4   -1.33333333333333
5  5    1.88888888888889
6  1    0.583333333333333
6  2    1.5
6  3   -2.16666666666667
6  4   -3.08333333333333
6  5    1.55555555555555
6  6    3.97222222222222
```

Note that the element positions are the animal id codes. In our case they are from one to six. In practice, the numbers need not be consecutive or in increasing order.

The inverse co-variance file `iG_raw.dat` is given by command `PEDFILE` as an inverse co-variance file to the breeding values. An important requirement is that all elements of the given matrix are from the lower triangle only. Option 'MIXED' can be used to read file that has both lower and upper triangle elements of a symmetric matrix, e.g.,

```
PEDFILE MIXED iG_raw.dat
```

The mixed option should be used with caution because MiX99 will not check if a matrix element appears as an upper and lower triangle element.

An altogether different matrix format is lower triangle dense matrix format. Command option 'LOWER' indicates it:

NEW

```
PEDFILE LOWER iG_raw.dat
```

In the lower triangle dense matrix format, all lower triangle elements of the matrix are in the file. There are two header rows having the size of the matrix and animal id codes. The previous matrix in a lower triangle dense format is

```
6 0
1 2 3 4 5 6
 0.75
-0.5   2
-0.5  -1    2
-0.25 -1.5  1.5   2.75
 0.33  1   -1.67 -1.33 1.89
 0.58  1.5 -2.17 -3.08 1.55 3.97
```

where the matrix values have been limited to two decimals for output reasons. Note that the order of id codes is irrelevant to MiX99, i.e., they do not have to be in increasing order as given here. However, the order of id codes on the second row gives order of rows below that. In other words, for MiX99 the previous matrix can be given as

```
6 0
3 1 2 4 5 6
 2
-0.5    0.75
-1      -0.5   2
-0.25  -1.5   1.5    2.75
 0.33   1    -1.67  -1.33 1.89
 0.58   1.5  -2.17  -3.08 1.55 3.97
```

Note that the first row has two number: 6 and 0. The second number (0) can be used to inform number of core animals when APY matrix is given. For example, core of 2 would mean matrix:

```
6 2
1 2 3 4 5 6
 0.75
-0.5    2
-0.5   -1      2
-0.25  -1.5   2.75
 0.33   1     1.89
 0.58   1.5   3.97
```

where the same values have been taken as above for presentation purposes. In practice, APY inverse matrix would have different values.

The variance components file (gs.par) is

Matrix number$_1$	Row$_2$	Column$_3$	Covariance$_1$	
1	1	1	0.166666666	marker variance
2	1	1	1.0	residual variance

Note that here $(\mathbf{Z}_u\mathbf{Z}'_u)^{-1}$ was used. This allowed using marker variance directly. Typically, genomic relationship matrix is build using some of the methods by VanRaden.

CLIM code for G-BLUP is

```
DATAFILE   gs_obs.dat

INTEGER    animal mean
REAL       y
MISSING -99999.
DATASORT PEDIGREECODE=animal

PARFILE    gs.par # parameters

PEDFILE   iG_raw.dat
PEDIGREE animal FILE

PRECON   d d

MODEL
  y = mean animal
```

Note how existence of the co-variance structure of animal genetic effect is indicated by the PEDIGREE command with option FILE.

The fixed general mean solution (Solfix) is

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	4	7.2604	mean	y

The breeding value solutions (Solani) are

```
         1       1       1 -1.2223
         2       2       1 -.11178E-05
         3       3       1  3.4005
         4       4       1  4.7802
         5       5       0  2.7444
         6       6       0  4.6701
```

Again giving Unix command `paste gs_obs.dat yHat.data0` associates animal id numbers to their estimated genomic breeding values. Result is

```
1 1  5      6.0380797
2 1  6      7.2604151
3 1 10      10.660873
4 1 15      12.040632
```

Note that these values can be calculated by adding the fixed general mean solution 7.2604 to the breeding value solutions in the `Solani` file.

7.2.1 Example: G-BLUP with polygenic effect

Model is

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}_u\mathbf{u} + \mathbf{Z}_a\mathbf{a} + \mathbf{e}$$

where $\mathbf{u}$ is vector of random additive genetic effects from genomic data, vector $\mathbf{a}$ has random additive polygenic effect from pedigree information and vector $\mathbf{e}$ is random residual. Matrix $\mathbf{Z}_u$ is incidence matrix as in G-BLUP example, and matrix $\mathbf{Z}_a$ is incidence matrix relating observation in $\mathbf{y}$ to proper breeding value in $\mathbf{a}$. The model is the same as in the previous example except for the polygenic $\mathbf{a}$ effect.

The random effects have the following assumptions: $\mathbf{u} \sim N(\mathbf{0}, \mathbf{G}\sigma_g^2)$, $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$ where $\mathbf{G}$ is genomic co-variance matrix (see previous example), and $\mathbf{A}$ is pedigree based relationship matrix. The following pedigree for the relationship matrix $\mathbf{A}$ is in file (`gs_poly.ped`):

animal$_1$	sire$_2$	dam$_3$
1	2	3
2	4	3
3	5	6
4	5	6
5	0	0
6	0	0

This small pedigree has some non-zero inbreeding coefficients. We will account inbreeding coefficients in the building of the $\mathbf{A}^{-1}$ in MiX99 by an inbreeding coefficient file, named `gs_poly.inbr`. The file is

animal$_1$	number$_2$	F$_1$
5	1	0.00000
6	2	0.00000
3	3	0.00000
4	4	0.00000
2	5	0.25000
1	6	0.37500

where the first column has original animal id code, and the last column inbreeding coefficient. When no inbreeding coefficient file is given, MiX99 builds $\mathbf{A}^{-1}$ assuming all inbreeding coefficients are zero.

The variance components are: common SNP marker variance $\sigma_g^2 = \frac{1}{6}$, polygenic variance $\sigma_a^2 = 1$, and residual variance $\sigma_e^2 = 1$. The variances are in file `gs_poly.par`:

Random effect₁	Row₂	Column₃	Covariance₁	
1	1	1	0.166666666	SNP genetic variance
2	1	1	1.0	polygenic variance
3	1	1	1.0	residual variance

CLIM code is

```
DATAFILE   gs_obs.dat

INTEGER    animal mean
REAL       y
MISSING -99999.
DATASORT PEDIGREECODE=animal

PARFILE    gs_poly.par

COVFILE    animal iG_raw.dat

PEDFILE    gs_poly.ped
PEDIGREE   polygenic am

INBRFILE gs_poly.inbr
INBREEDING PEDIGREECODE=1 FINBR=3

RANDOM   genomic polygenic

MODEL
  y = mean genomic(animal) polygenic(animal)
```

Note that the RANDOM command gives numbering of the random effects (other than residual). The polygenic effect must be the last random effect in this statement. Note also that the words `genomic` and `polygenic` are NOT reserved names but names just to identify different random effects.

The fixed general mean solution (`Solfix`) is

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	4	7.9564	mean	y

The genomic breeding value estimates (`Solr01`) are

1	1	-.99014	
2	1	-.93297E-06	
3	1	3.0507	
4	1	4.0358	
5	0	2.4286	
6	0	3.9911	

The polygenic animal solutions (`Solani`) are

1	0	1	-1.1307
2	1	1	-.79141
3	2	1	-.73879
4	1	1	0.73879
5	2	0	0.12569E-12
6	2	0	0.12569E-12

Again giving Unix command `paste gs_obs.dat yHat.data0` associates animal

id numbers to their estimated complete breeding values. Result is

```
1 1  5      5.8356075
2 1  6      7.1650143
3 1 10      10.268371
4 1 15      12.731008
```

Note that in practice this model may have convergence problems because the polygenic and genomic breeding value effects try to estimate the same entity: genetics. Thus, this model must split genetic breeding value to its polygenic and marker components which may be sometimes difficult. In particular, the genomic breeding values have a genomic relationship matrix, and the polygenic effect has pedigree based relationship matrix. In this example, these matrices are very different but in practice they can be similar.

An alternative equivalent model to this model would be to make a relationship matrix that combines the genomic and pedigree relationship matrices. For example, let $\mathbf{G}_A = \mathbf{G} + \mathbf{A}\frac{\sigma_a^2}{\sigma_g^2}$. Then, instead of using $\mathbf{G}^{-1}$ in the G-BLUP model, use $\mathbf{G}_A^{-1}$. Thus, the instructions will be the same as for the G-BLUP model with the `PEDFILE` replaced by the new inverse covariance matrix $\mathbf{G}_A^{-1}$ where pedigree based relationship matrix and genomic information have been combined. This will yield the same estimated complete breeding values. However, in practice, convergence of the iterative method is likely to be better due to not having to estimate two genetic breeding values for every animal.

The equivalent G-BLUP model needs $\mathbf{G}_A^{-1}$ in a file. In our case, the $\mathbf{G}_A^{-1}$ matrix (lower triangle) in co-ordinate sparse matrix format is (file `iGa.dat`):

```
1  1    0.212360759655864
2  1   -0.173168009265463
2  2    0.302462455536769
3  1   -0.0820544909187614
3  2   -0.0175160071940054
3  3    0.284302642414021
4  1    0.0222724767716754
4  2   -0.10603222546145
4  3    0.0440272119204682
4  4    0.265976547255634
5  1    0.0343385639825208
5  2    0.0289958157919094
5  3   -0.169030129597629
5  4   -0.126868150312209
5  5    0.247839050926183
6  1    0.0436056268940923
6  2    0.0386568862841335
6  3   -0.172788965328849
6  4   -0.180933888034668
6  5    0.122875534464136
6  6    0.272614251165761
```

As mentioned, the CLIM-instructions will be the same as for the G-BLUP example with only one change: `PEDFILE iG_raw.dat` changed to `PEDFILE iGa.dat`. The predicted breeding values using this approach are as before

```
1 1  5      5.8356066
2 1  6      7.1650133
3 1 10      10.268371
```

```
4 1 15     12.731009
```

7.3 Example: single-step method

Model is

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}_a\mathbf{a}_g + \mathbf{e}$$

where $\mathbf{a}_g$ has random additive genetic effect using pedigree and genomic information, and $\mathbf{e}$ is random residual. Matrix $\mathbf{Z}_a$ is incidence matrix relating observation in $\mathbf{y}$ to correct breeding value in $\mathbf{a}$ as in previous example.

The random effects have the following assumptions: $\mathbf{a}_g \sim N(\mathbf{0}, \mathbf{H}\sigma_a^2)$, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$ where $\mathbf{H}$ is pedigree relationship matrix blended with genomic data. The $\mathbf{H}$ is not needed by MiX99 but its inverse $\mathbf{H}^{-1}$. The inverse is

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \end{bmatrix}$$

where $\mathbf{A}$ is the full pedigree based relationship matrix, $\mathbf{A}_{gg}$ is pedigree based relationship part for the genotyped animals, and $\mathbf{G}$ is genomic relationship matrix. User has to provide matrix $\mathbf{C}_{GA} = \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1}$ and the full pedigree used to calculate $\mathbf{A}$ to MiX99. In practice, the single-step method in MiX99 is similar to using animal model with an additional covariance matrix $\mathbf{C}_{GA}$ in lower triangle co-ordinate sparse matrix format (Yale format) by command `IGFILE`.

Let the full pedigree for relationship matrix $\mathbf{A}$ be in file `one_step.ped`:

animal$_1$	sire$_2$	dam$_3$
1	2	3
2	4	3
3	5	6
4	5	6
5	0	0
6	0	0
7	5	6
8	2	3

It is the same as in the previous example but with two added animals (numbers 7 and 8). Inbreeding coefficients are in file `full_one_step.inbr`:

animal$_1$	number$_2$	F$_1$
5	1	0.00000
6	2	0.00000
7	3	0.00000
3	4	0.00000
4	5	0.00000
2	6	0.25000
8	7	0.37500
1	8	0.37500

where the first column has original animal id code, and the last column inbreeding coefficient.

In the single-step method it is important to use properly made genomic relationship matrix $\mathbf{G}$ such that its scale is the same as the pedigree based relationship matrix $\mathbf{A}$.

A common approach is VanRaden method 1. In the example we will use this method, and add 20% of pedigree based relationship matrix $\mathbf{A}_{gg}$ to assume that the markers explain 80% of genetic variation, and 20% is polygenic variation not explained by the available markers. The same pedigree information will be used as in the previous example. The $\mathbf{C}_{GA} = \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1}$ matrix is provided in a file. As for the GBLUP model, the matrix can have either the co-ordinate sparse matrix format (default) or the lower triangle dense matrix format.

Assume the matrix has been stored in the default format, i.e., lower triangle co-ordinate sparse matrix format, in file `iH.dat`:

```
1   1   -0.263096445605446
2   1   -0.659942436053408
2   2    0.244046491072819
3   1    0.870441978527262
3   2    0.998787679967059
3   3   -1.40380798986209
4   1    0.526879611011652
4   2    0.476171586907099
4   3   -0.469768966568885
4   4   -0.0336084181419456
5   1    0.332614778332254
5   2   -0.119449290320484
5   3    0.469298887947602
5   4    1.10970591785976
5   5   -0.35147164842 8734
6   1    0.595748584829456
6   2    0.150394111665596
6   3    0.405173304876264
6   4   -0.697147095891039
6   5   -0.745222104850557
6   6    1.21570834901989
```

Command `IGFILE` is used to indicate single-step method. The command has option `MIXED` to allow giving mixed lower/upper triangle form matrix:

```
IGFILE MIXED iH.dat
```

The lower triangle dense matrix format has option `LOWER` and can be given as:

```
IGFILE LOWER iHL.dat
```

The `MIXED` option works as explained for the `PEDFILE` command earlier in G-BLUP example: mixed co-ordinate sparse matrix format file has both lower and upper triangle elements of a symmetric matrix but only one of them is assumed to be present. Thus, in a symmetric matrix it is assumed that only lower or upper triangle element is present in the file. The mixed option should be used with caution because MiX99 will not check if a matrix element given as an upper and lower triangle element.

Variance components are $\sigma_a^2 = 1$ and $\sigma_e^2 = 1$. These are in file `one_step.par`:

Random effect₁	Row₂	Column₃	Covariance₁	
1	1	1	1.0	polygenic variance
2	1	1	1.0	residual variance

CLIM code is

```
DATAFILE gs_obs.dat

INTEGER animal mean
REAL    y
MISSING -99999.
DATASORT PEDIGREECODE=animal

IGFILE   iH.dat
PEDFILE  one_step.ped
PEDIGREE animal am

INBRFILE full_one_step.inbr
INBREEDING PEDIGREECODE=1 FINBR=3

PARFILE  one_step.par

MODEL
  y = mean animal
```

The fixed general mean solution (`Solfix`) is

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	4	9.8195	mean	y

Estimated breeding values (`Solani`) are

1	0	1	-4.2873
2	2	1	-2.8378
3	3	1	0.85603
4	1	1	2.9909
5	3	0	0.32826
6	3	0	2.6379
7	0	0	1.4831
8	0	0	-.99089

Again giving Unix command `paste gs_obs.dat yHat.data0` associates animal id numbers to their estimated complete breeding values. Result is

1	1	5	5.5322323
2	1	6	6.9817309
3	1	10	10.675563
4	1	15	12.810474

It is possible to give the matrices $\mathbf{G}^{-1}$ and $\mathbf{A}_{gg}^{-1}$ that form the $\mathbf{C}_{GA}$ separately in different files by commands `IGFILE` and `IA22FILE`, respectively. In practice, it can be computationally more efficient to let the solver program to do the required computations to make $\mathbf{A}_{gg}^{-1}$ computations using pedigree information. Then, no $\mathbf{A}_{gg}^{-1}$ need to be computed before calling the preprocessor. This can be done by giving `PEDIGREE` as file name to `IA22FILE`.

NEW

An alternative command file to do single-step is

```
DATAFILE gs_obs.dat

INTEGER animal mean
REAL    y
MISSING -99999.
DATASORT PEDIGREECODE=animal

IGFILE   LOWER iGL.dat
IA22FILE PEDIGREE
PEDFILE  one_step.ped
```

```
PEDIGREE animal am

INBRFILE full_one_step.inbr
INBREEDING PEDIGREECODE=1 FINBR=3

PARFILE   one_step.par

MODEL
  y = mean animal
```

which will be more efficient than the former code when there are many genotyped animals. First, the $\mathbf{G}^{-1}$ matrix in file iGL.dat has been stored in the lower triangle dense format. Second, the $\mathbf{A}_{gg}^{-1}$ matrix is not precomputed but the computations are done using pedigree information by the solver.

8 Special topics

8.1 Trait groups for single trait analysis

8.1.1 Example: Multiple single trait analysis

It is common that several single trait analysis use the same pedigree and data file but observations are on different columns. Still, multiple trait model analysis is not wanted due to unknown variance components. Thus, although the data can be presented as for multiple trait analysis, all covariances between traits are zero. This can be analyzed as a multiple trait model by MiX99. However, this can be inefficient because the data file may have many missing observations, and the traits have different effects.

Trait groups can be used to make the analysis more efficient. Now, the data is given similarly to the repeatability model. However, instead of a repeatability model, there is a trait group indicator to indicate which model is used. In the example model, the trait group has observations from one trait.

We consider again the multiple trait model example with different effects by trait in Chapter6.2.1). The model is

$$
\begin{array}{rclcl}
tr1 & = & herd \times year & +a + e \\
tr2 & = & \mu & +a + e
\end{array}
$$

However, now the interest is in analyzing these two traits as separate independent evaluations in the same MiX99 solver run. The multiple trait model way would be to do as in Chapter 6.2.1 but with a parameter file where all covariances are zero.

Trait group way is to make the data to be similar to the repeatability data (Chapter 5.1.5) but with an additional column to indicate trait. The data file (example_-tr_group.dat) is

animal$_1$	sire$_2$	herd year$_3$	ones$_4$	trait$_5$	tr12$_1$
4	1	11	1	1	90
4	1	21	1	2	200
6	3	11	1	1	110
6	3	21	1	2	190
8	5	12	1	1	120
8	5	22	1	2	140

9	5	12	1	1	130
9	5	22	1	2	120
10	7	12	1	1	120
10	7	22	1	2	130

The parameter file (`mt_single.var`) is the same as would be for the multiple trait model analysis described above:

Random effect₁	Row₂	Column₃	Covariance₁
1	1	1	3.0
1	2	2	2.5
2	1	1	7.0
2	2	2	7.0

Column `trait` is used to indicate model of the trait. It is referenced by the trait group number in parenthesis on the model line. Command `TRAITGROUP` is needed to indicate which column is the trait group column in the data file. The CLIM file would be

```
DATAFILE   example_tr_group.dat

INTEGER    animal sire herd_year ones trait
REAL       tr

TRAITGROUP trait

PEDFILE    data/AM.ped
PEDIGREE   animal am

PARFILE    mt_single.var

MODEL SCALE
  tr(1) = -     herd_year animal
  tr(2) = ones  -         animal
```

Fixed effect solutions (`Solfix`) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	2	1	5	160.73	ones	tr
2	1	11	2	99.538	herd_yea	tr
2	1	12	3	122.69	herd_yea	tr

Breeding values estimates (`Solani`) are

Bull	N-Desc	N-Obs	tr1	tr2
1	2	0	-.29831E-05	0.29868E-05
2	2	0	-.29831E-05	0.29868E-05
3	2	0	0.92308	-3.2188
4	2	2	-.92308	3.2188
5	3	0	-.12098E-04	-5.8818
6	3	2	1.8462	-.55584
7	1	0	0.65422	-5.0727
8	1	2	0.64449E-01	-7.4451
9	0	2	2.0506	-8.9024
10	0	2	-.17839	-9.9667

Solutions can be compared with those for the `tr1` single trait evaluation in Chapter 5.1.1. Solutions are not exactly the same. The reason is that the multiple trait model analysis usually makes more iterations. For example, in the example above,

the multiple trait model analysis converged in 18 iterations but the single trait analysis converged in 12 iterations. There are 12 unknowns in the single trait model, and, in theory, only 12 iterations are needed. However, the multiple trait model has 24 unknowns, although in two separate blocks with 12 unknowns. The PCG method tries to solve the two separate systems at the same time. Solving and convergence in the separate blocks is compromised.

8.1.2 Example: MACE or Sire model with weights and trait groups

We consider a multiple trait sire model where yields of daughters in different countries are considered as different traits. This is MACE example as described in Schaeffer (1994). The model is

$$
\begin{aligned}
y_1 &= \mu_1 + g_1 + s_1 + e_1 \\
y_2 &= \mu_2 + g_2 + s_2 + e_2
\end{aligned}
$$

where subscript is for countries 1 and 2, μ is country genetic base, y is bull's daughter yield deviation (DYD), g is genetic group effect of phantom parents, s is sire transmitting ability by country, and e is residual.

The sire genetic effects and the residuals have the following assumptions:

$$
\begin{aligned}
\mathrm{E}(\boldsymbol{s}) &= \boldsymbol{0} & \mathrm{Var}(\boldsymbol{s}) &= \boldsymbol{G}_0 \otimes \boldsymbol{A} \\
\mathrm{E}(\boldsymbol{e}) &= \boldsymbol{0} & \mathrm{Var}(\boldsymbol{e}) &= \boldsymbol{R}
\end{aligned}
$$

These look similar to standard multiple trait model assumptions. However, in the MACE model the residual covariance matrix $\boldsymbol{R}$ is diagonal, i.e., residual correlations are zero, and varies by sire. Residual covariance matrix for sire i is

$$
\boldsymbol{R}_i = \left[\begin{array}{cc} d_{1_i} \sigma_{e_1}^2 & 0 \\ 0 & d_{2_i} \sigma_{e_2}^2 \end{array} \right] \tag{5}
$$

where d equals one over the number of daughters in a bull's DYD, and $\sigma_{e_j}^2$ is residual variance for country j. The d_i values in residual covariance matrix can be considered as weights. Weights can be defined for each trait separately by option `weight` after the model line. In Schaeffer (1994), the genetic covariance matrix is

$$
\boldsymbol{G}_0 = \left[\begin{array}{cc} 100 & 20 \\ 20 & 5 \end{array} \right]
$$

The residual variances are $\sigma_{e_1}^2$ = 1000, and $\sigma_{e_2}^2$ = 80.

Trait group has one or more traits that can be observed together from an individual but cannot be observed with any trait belonging to another trait group. Residual correlation between trait groups is zero. This definition of trait group matches with the MACE model where country is trait group. In practice, observation belongs to a trait group specified by an integer number column. The appropriate trait group number is given in parenthesis after the observation name. For example, trait `protein` in trait group 1 is `protein(1)`, but in group 2, `protein(2)`.

The parameter file `MACE.var` is

Random effect₁	Row₂	Column₃	Covariance₁	Variance
1	1	1	100.0	genetic

Table 8.1: The pedigree and data files for the MACE model example.

pedigree file MACE.ped Table 2 in Schaeffer (1994)				data file MACE.dat Table 1 in Schaeffer (1994)			
$bull_1$	$sire_2$	$MGS^1{}_3$	$MGD^2{}_4$	$bull_1$	$country_2$	$protein_1$	$weight^3{}_2$
1	6	7	−5	1	1	56.0	10.0
2	8	9	−5	2	1	−23.0	20.0
3	10	8	−5	3	1	8.0	50.0
4	10	11	−6	1	2	9.0	100.0
5	2	6	−6	4	2	3.0	40.0
6	−1	−2	−6	5	2	−11.0	20.0
7	−1	−2	−6				
8	−1	−2	−6				
9	−3	−4	−6				
10	−3	−4	−6				
11	−3	−4	−6				

[1]maternal grandsire
[2]maternal grandam
[3]daughter yield deviation (DYD)

1	2	1	20.0	genetic
1	2	2	5.0	genetic
2	1	1	1000.0	residual
2	2	2	80.0	residual

```
TITLE      MACE, L.Schaeffer (1994)

DATAFILE   MACE.dat
INTEGER    bull country
REAL       protein weight

TRAITGROUP country

PEDFILE    MACE.ped
PEDIGREE   bull sm+p 1.0 # sm=sire model

PARFILE    MACE.var

MISSING   -8192.0

MODEL
  protein(1) = country bull ! WEIGHT=weight
  protein(2) = country bull ! WEIGHT=weight
```

Estimates of the country means (Solfix) are

Fact.	Trt	Level	N-Obs	Solution	Factor	Trait
1	1	1	3	10.497	country	protein
1	2	2	3	1.2141	country	protein

Breeding values estimates (Solani) by country are

```
                        Country
   Bull  N-Desc  N-Obs     1              2
      1       0      2   31.132        7.0211
      2       1      1  -26.538       -5.9504
      3       0      1  -2.4056       -.47722
      4       0      1   4.3014        1.1245
      5       0      1  -29.221       -7.0674
      6       2      0   10.936        2.3169
      7       1      0   8.9970        2.0117
      8       2      0  -12.881       -2.9245
      9       1      0  -8.3029       -1.8438
     10       2      0   1.4727        0.43745
     11       1      0  0.46456E-01   0.69527E-01
     -4       3      0  -.49058       -.76316E-01
     -3       3      0  -.98117       -.15263
     -2       3      0   1.2948        0.27736
     -1       3      0   2.5895        0.55472
     -5       3      0   1.5631        0.39077
     -6       8      0  -3.9756       -.99390
```

8.2 Deregression

Deregression in MiX99 is based on Jairath et al. (1998) and Schaeffer (2001). Calculation of deregressed proofs means solving a non-linear system of equations. The system of equations looks the same as regular mixed model equations. However, it is assumed that solutions for some animals (for which deregressed proofs are needed) are known but solutions of their ancestors, phantom parent groups, and general mean in the model are unknown. In addition, the deregressed proofs are unknown. In the mixed model equations, the deregressed proofs are in the right hand side of the equation.

In MiX99 (or `mix99s`), the non-linear deregression problem is solved by a two step iterative process:

1) solve ancestral and phantom parent group unknowns given current solution for mean estimate, and known proofs.

2) calculate new general mean estimate

In practice, the first step means solving mixed model equations which is the core work done in MiX99. The model used to solve ancestral and phantom groups has only one fixed effect: general mean. Another important aspect of deregression model is that the phantom parent groups are random.

Many methods can be used in solving non-linear systems. MiX99 has the following methods

- Gauss-Seidel

- Bisection

- Secant

- Broyden

Default method is Broyden method which is often the fastest and most reliable of the implemented methods. Secant method, however, can be better when solving many

single trait models.

Deregression using `mix99s` needs to be specifically requested. A directive file for the program is convenient to make as was described in Chapter 4. Let the directive file (`dereg.slv`) be

```
H # RAM: RAM demand: H=high, M=medium, L=low
# Max. no. iterations, Stopping criterion, Criterion (A/R/M/D)
5000                    1.0e-3                D  F 1000
N # RESID: Calculate residuals? (Y/N)
R b # R=deregression
    # b= Broyden method
    # s= Secant method
    # i= bisection
    # n= Gauss-Seidel
N # adjust for HV?  No
Y # Solution files? Yes
```

There are some most important difference to the regular breeding value estimation. Deregression is requested (letter 'R') with Broyden method (letter 'b'). In addition, an additional number `1000` on the line for maximum number of iterations and convergence criteria. The additional number is maximum number of iterations for the non-linear solving method, which is Broyden method in this example. Deregression is a non-linear problem. Consequently, two iterative methods are used: PCG iteration to solve a linear problem, and Broyden method for the non-linear problem. In case the Broyden method does not converge, the maximum number of iterations is reached. Then, another method (e.g. secant method) can be used, or the problem needs reformulation (e.g. new definition of genetic groups, or different random genetic group value).

8.2.1 Example: Single trait deregression

Pedigree earlier used for the animal and sire model examples are used. However, it is modified for deregression purposes. The sire model pedigree (`sm_dereg.ped`) is

bull$_1$	sire$_2$	maternal grand sire$_3$	maternal grand dam group$_4$
1	−2	−2	−10
3	1	−2	−10
5	3	1	−11
7	5	3	−11

There is a fourth column for maternal grand dam group. This pedigree for animal model (`am_dereg.ped`) is

animal$_1$	sire$_2$	dam$_3$
1	−2	11
3	1	2
5	3	4
7	5	6
2	−2	−10
4	1	−11
6	3	−11
11	−2	−10

The data is (dereg.dat)

sire$_1$	ones$_2$	proof$_1$	EDC$_2$
1	1	−.35736	50
3	1	0.40621	100
5	1	0.20334	80
7	1	0.24076E−01	20

The variance components file (SM.var) is the same as before

Random effect$_1$	Row$_2$	Column$_3$	Variance$_1$
1	1	1	0.75
2	1	1	9.25

Sire model   The model for deregression is very simple: only general mean and the sire effect. It is important to use random phantom parent groups. CLIM code for deregression (sm_dereg.clm) is

```
DATAFILE   dereg.dat

INTEGER    sire ones
REAL       ebv EDC

PEDFILE    smgs.ped
PEDIGREE   sire sm+p 1.0

PARFILE    SM.var

MODEL
  ebv = ones sire ! WEIGHT=EDC
```

Calculating deregressed proofs (mix99s < dereg.slv) will give solution for the general mean (Solfix)

```
Fact. Trt      Level    N-Obs  Solution                 Factor Trait
   1   1          1          4 0.18958E-01                 ones ebv
```

and the deregressed proofs (Solani):

```
      sire N-Desc  N-Obs deregressed proof
         1      2      1 −.54488
         3      2      1 0.49919
         5      1      1 0.24384
         7      0      1 −.13403
       −11      2      0  0.0000
       −10      2      0  0.0000
        −2      3      0  0.0000
```

Solutions for the phantom parent groups (negative id code) can be ignored because these solutions have been set to zero by MiX99. In general, deregressed proofs are those in the Solani file that have an observation, i.e., N-Obs is one.

Animal model   CLIM code for animal model is very similar to the sire model case above:

```
DATAFILE   dereg.dat
```

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```
INTEGER    animal ones
REAL       ebv EDC

PEDFILE    am_dereg.ped
PEDIGREE   animal am+p 1.0

PARFILE    SM.var

MODEL SCALE
  ebv = ones animal ! WEIGHT=EDC
```

General mean solution (`Solfix`) is exactly the same as before. Solutions are the same (`Solani`):

```
    animal N-Desc  N-Obs deregressed proof
         1      2      1 -.54488
         3      2      1 0.49919
         5      1      1 0.24384
         7      0      1 -.13403
         2      1      0  0.0000
         4      1      0  0.0000
         6      1      0  0.0000
        11      1      0  0.0000
       -11      2      0  0.0000
       -10      2      0  0.0000
        -2      3      0  0.0000
```

Naturally there are now more solutions because the pedigree had more animals. As before, only solutions with observations (`N-Obs` equal to one) are relevant.

8.2.2   Example: Multiple trait deregression

Multiple trait deregression is done the same way as single trait deregression. We illustrate multiple trait deregression by example given in Schaeffer (2001) where detailed explanation can be found. The example is on multiple trait sire model deregression for international bull evaluation. We consider only the example data for country A. Country B proceeds similarly.

Sire model pedigree (`sch_sm.ped`) is

bull$_1$	sire$_2$	maternal grand sire$_3$	maternal grand dam group$_4$
1	-22	-23	-24
2	-22	-23	-24
3	-22	-23	-24
4	-22	-23	-24
5	-22	-23	-24
6	-25	-26	-27
7	-25	-26	-27
8	-25	-26	-27
9	-25	-26	-27
10	-25	-26	-27
11	-25	-26	-27
12	1	2	-28
13	3	4	-28
14	3	5	-28
15	6	2	-28

```
16      6       7           -29
17      3       8           -29
18      3       9           -29
19      3      10           -29
20     11       8           -29
21     11       3           -29
```

As before, there is a fourth column for maternal grand dam group. The data (`sch_-cntry_A.dat`) has three lactations:

		Lactation 1		Lactation 2		Lactation 3	
$ones_1$	$sire_2$	$Progeny_1$	EBV_2	$Progeny_3$	EBV_4	$Progeny_5$	EBV_6
1	12	126	23	0	-999	0	-999
1	12	43	23	43	34	0	-999
1	12	36	23	36	34	36	38
1	13	18	36	0	-999	0	-999
1	13	5	36	5	21	0	-999
1	13	6	36	6	21	6	17
1	14	55	-14	0	-999	0	-999
1	14	21	-14	21	-26	0	-999
1	14	17	-14	17	-26	17	-49
1	15	17	48	0	-999	0	-999
1	15	7	48	7	66	0	-999
1	15	5	48	5	66	5	59
1	16	120	30	0	-999	0	-999
1	16	44	30	44	27	0	-999
1	16	39	30	39	27	39	3

The data has been constructed such that number of progeny in the third lactation also were observed for first and second lactation. Consequently, number of progeny is the same in all lactations when third lactation is observed. Similarly, the number of progeny observed for second lactations were assumed to also be observed for first lactation. This data structure is described in Schaeffer (2001).

The variance components file (`sch_cntry_A.var`) is

Random effect$_1$	Row$_2$	Column$_3$	Variance$_1$	
1	1	1	96	Lact. 1 genetic
1	1	2	68	Lact. 1,2 genetic
1	1	3	62	Lact. 1,3 genetic
1	2	2	160	Lact. 2 genetic
1	2	3	110	Lact. 2,3 genetic
1	3	3	190	Lact. 3 genetic
2	1	1	1018	Lact. 1 residual
2	1	2	128	Lact. 1,2 residual
2	1	3	67	Lact. 1,3 residual
2	2	2	1625	Lact. 2 residual
2	2	3	170	Lact. 2,3 residual
2	3	3	1792	Lact. 3 residual

As for the single trait model, the model for deregression is very simple: only general mean and the sire effect. It is important to use random phantom parent groups. CLIM code for deregression (`sch_sm.clm`) is

```
TITLE      Multiple trait model

DATAFILE   sch_cntry_A_2.dat # Data file
INTEGER    ones sire          # Integer column names
REAL       w_1 e_1 w_2 e_2 w_3 e_3

DATASORT   PEDIGREECODE=sire
MISSING    -999

PEDFILE    sch_sm.ped
PEDIGREE   sire sm+p 1.0

PARFILE    sch_cntry_A.var

PRECON     b f # Preconditioner: b=block

MODEL
  e_1 = ones sire ! weight=w_1
  e_2 = ones sire ! weight=w_2
  e_3 = ones sire ! weight=w_3
```

Calculating deregressed proofs (`mix99s < dereg.slv`) will give solution for the general mean (`Solfix`)

Fact.	Trt	Level	N-Obs	Solution	Factor Trait
1	1	1	15	25.011	mean e_1
1	2	1	10	24.971	mean e_2
1	3	1	5	13.586	mean e_3

and the deregressed proofs (`Solani`):

```
      sire N-Desc  N-Obs deregressed proof
...
        12       0      3   22.510       34.257       45.390
        13       0      3   45.149        9.6328      38.644
        14       0      3  -17.035      -29.146      -75.258
        15       0      3   50.363       85.822      118.94
        16       0      3   30.240       26.829       -3.4327
...
```

Solutions were given above for only those animals that have an observations, i.e., `N-Obs` more than zero. All other solutions have been set to zero by MiX99.

9 Summary of all commands

CLIM has optional commands, and options to the required commands. If an optional command is not given then default values are used for this command. In general, the commands are quite self explanatory. Below they are divided into groups. There are chapter numbers after the short description. Required commands are explained in Chapter 9.1 and optional commands in Chapter 9.2.

Data file commands	
DATAFILE	name of data file, 3.1
DATASORT	information on how the data file was sorted, 9.2.2 (optional)
INTEGER	integer number column names in the data file, 9.1.2
MISSING	code for missing observations, 9.2.9 (optional)
REAL	real number column names in the data file, 9.1.6
REGFILE	regression coefficient matrix file, 9.2.15 (optional)
TABLEFILE	name of the separate covariable table file, 9.2.20 (optional)
TABLEINDEX	integer number column name of the covariable table file number in the data file, 9.2.21 (optional)
TRAITGROUP	integer number column name of the trait group number, 9.2.26 (optional)

Pedigree file commands	
PEDFILE	name of pedigree file, 3.2
PEDIGREE	effect/component name in the model to which the pedigree is attached. Also, type of pedigree information, i.e., model type (animal or sire model). If random genetic groups, then coefficient value as well, 9.1.5 (optional)

Variance component information	
PARFILE	MiX99 variance components file, 3.3
RESIDFILE	name of residual (co)variance parameter file, 9.2.18 (optional)
RESIDUAL	integer number column name of the residual (co)variance number, 9.2.19 (optional)
REGPARFILE	name of random regression matrix parameter file, 9.2.17 (optional)

Model commands	
MODEL	statistical model
RANDOM	random effects in the model, 9.2.14 (optional if additive genetic and residual effects are the only random effects)
REGMATRIX	regression coefficient matrix information, 9.2.16 (optional)

Solving	
NORANSOL	random effects for which no solution files are to be written, 9.2.8 (optional)
PARALLEL	number of processors used in parallel computing, 9.2.12 (optional)
PRECON	preconditioning information, 9.2.13
TITLE	title of the analysis, 9.2.24 (optional)
TMPDIR	directory for the MiX99 temporary files, 9.2.25 (optional)
WITHINBLOCKORDER	ordering of effects in the blocks, 9.2.27 (optional)

Macros and range abbreviations	
DEFINE	defines a text macro replacement

9.1 Required commands

Following are explanation and syntax of all commands except MODEL which is considered in Chapters 5, 6, 7 and 8.

9.1.1 DATAFILE

Name of data file. Optional information: file type of text or binary can be given. Default is text file. So, for a binary file, file type has to be always specified.

Syntax:
```
DATAFILE [TEXT/BINARY] <filename>}
```
Example. Data file Beef_MiX.dat has standard text data.
```
DATAFILE ../data/Beef_MiX.dat
```

9.1.2 INTEGER

Names of integer number columns in the data file. These are used to give names to data file columns.

Syntax:
```
INTEGER <names of integer variables>
```
Example. Data file having 8 columns of integer data information. The first column is named block, second is id, the third is trt_group etc.
```
INTEGER block id trt_group HTM AGE DCC DIM
```

9.1.3 PARFILE

Name of (co)variance parameter file. Information in the file has the same format as described in the MiX99 manual for mix99i *Technical reference guide for MiX99 pre-processor*.

Syntax:
```
PARFILE <filename>
```
Example. Name of the parameter file is Beef.par.

```
PARFILE ../data/Beef.par
```

9.1.4 **PEDFILE**

Name of pedigree file. This pedigree file is read by `mix99i`. When type of pedigree is `FILE` in command `PEDIGREE`, the file has inverse of the co-variance matrix for breeding values. Default format for the matrix is lower triangle co-ordinate sparse matrix format (see Ch. 7.2). Option `MIXED` can be used to relax requirement of lower triangle matrix (see Ch. 7.2). However, this means that there can be element (1,2) of matrix, i.e., upper triangle element, but there cannot be corresponding lower triangle element (2,1) in the file. Another optional format is lower triangle dense matrix or `LOWER` (see Ch. 7.2).   **NEW**

Syntax:
```
PEDFILE [LOWER | MIXED] <filename>
```
Example 1. Name of the pedigree file is `Beef_phantom.ped`.
```
PEDFILE ../data/Beef_phantom.ped
```
Example 2. Name of co-ordinate format matrix with upper and lower triangle elements:
```
PEDFILE MIXED ../data/iG_matrix.dat
```
Example 3. Name of lower triangel dense matrix: **NEW**
```
PEDFILE LOWER ../data/iGL_matrix.dat
```

9.1.5 **PEDIGREE**

Pedigree type and other information. See MiX99 manual *Technical reference guide for MiX99 pre-processor* for the pedigree types. Common pedigree types are `am` for animal model and `sm` for sire model. Autoregressive model has type `ar`. Genetic groups are indicated by suffix `+p`, e.g., `am+p` for animal model with phantom genetic groups. Pedigree has been stored in file given by command `PEDFILE`.

When pedigree type is `FILE`, the inverse of the relationship co-variance structure (e.g. G^{-1} in G-BLUP) is in file specified by `PEDFILE` command. See example in Ch. 7.2.

Syntax:
```
PEDIGREE <effect name> <pedigree type> &
         [<optional number for random genetic groups>]
```
Example 1. Pedigree is for an animal model with random genetic groups. Pedigree is associated with model effect name `G`. The phantom parent groups are random with genetic variance coefficient 1.0.
```
PEDIGREE G am+p 1.0
```
Example 2. GBLUP model where the inverse of the genomic relationship matrix G^{-1} **NEW**
is in file iGL.dat stored in lower triangle dense matrix format.
```
PEDFILE  LOWER iGL.dat
PEDIGREE G FILE
```

9.1.6 **REAL**

Names of real number columns in the data file. Integer number columns are always before real number columns. See MiX99 manual *Technical reference guide for MiX99 pre-processor* for more information.

Syntax:

```
REAL <names of real variables>
```

Example. There are 3 real number columns (after the integer number columns) in the data file. The first is B_WEIGHT, the second is W_WEIGHT, and the third is W_AGE.

```
REAL       B_WEIGHT W_WEIGHT W_AGE
```

9.2 Optional commands

The following commands have default values that are used if command is not given.

9.2.1 AR

Define the autoregressive values for each trait in autoregressive model. When this command is given, the PEDIGREE type must be ar. Default is no autoregressive model.

Syntax:

```
AR <values for each trait>
```

Example. Autoregressive values for 2 traits

```
AR 0.8 0.9
```

9.2.2 DATASORT

Names of the integer number columns for the block sorting variable (BLOCK), and the animal sorting variable (PEDIGREECODE). See MiX99 manual *Technical reference guide for MiX99 pre-processor* for more explanation. By default none are needed.

Syntax:

```
DATASORT BLOCK        =<block in INTEGER column> &
         PEDIGREECODE=<code  in INTEGER column>
```

Example. The block code is integer number column block, and the pedigree code is column animal in the data file

```
DATASORT BLOCK=block PEDIGREECODE=animal
```

9.2.3 IA22FILE

Gives file having matrix $\mathbf{A}_{gg}^{-1}$ used in the single-step method. In the single-step method, matrix $\mathbf{C}_{GA} = \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1}$ is needed. The two matrices can be given in a single file using the IGFILE command, or in two separate files giving $\mathbf{G}^{-1}$ to the IGFILE and $\mathbf{A}_{gg}^{-1}$ to the IA22FILE.

NEW

This approach of giving two separate filenames for the components of $\mathbf{C}_{GA}$ allows separation of the needed computations for the two matrices. In particular, giving file name PEDIGREE for IA22FILE indicates MiX99 that the computations for $\mathbf{A}_{gg}^{-1}$ are done using pedigree information without need to give this matrix explicitly in a file.

Default format is the co-ordinate (Yale) sparse matrix format. The preprocessor checks that each row is in lower triangle part of the matrix. This check is simple (the second column value (j) must be less or equal to the first column value (i)), and not all programs produce this format. Thus, option MIXED allows reading the file without the check. Another format allowed is the lower triangle dense format (see Ch. 7.2). which can be prepared using hginv program. For this matrix option LOWER need to be used.

Syntax:
```
IA22FILE [LOWER | MIXED] <filename>
```
If the filename is `PEDIGREE` then no file of that name is read but instead the solver will use pedigree information to do the required computations.

Example. Matrix $\mathbf{A}_{gg}^{-1}$ is in file `iA22L.dat`
```
IA22FILE LOWER iA22L.dat
```

9.2.4 IGFILE

Gives file having matrix $\mathbf{C}_{GA} = \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1}$ used by the single-step method. In case `IA22FILE` is given as well, then the file given by `IGFILE` contains $\mathbf{G}^{-1}$ for the single-step and `IA22FILE` has $\mathbf{A}_{gg}^{-1}$.

Default matrix format is the co-ordinate (Yale) sparse matrix format. The preprocessor checks that each row is a lower triangle part of the matrix. This check is simple (the second column value (j) must be less or equal to the first column value (i)), and not all programs produce this format. Thus, option `MIXED` allows reading the file without the check. Another format allowed is the lower triangle dense format (see Ch. 7.2). which can be prepared using hginv program. For this matrix option `LOWER` need to be used.

Syntax:
```
IGFILE [LOWER | MIXED] <filename>
```
Example. Matrix $\mathbf{C}_{GA}$ is in file `iH.dat`
```
IGFILE iH.dat
```

9.2.5 IHPRECON

Gives file having changes to the preconditioner matrix in the diagonal of inverse relationship matrix. For example, consider inverse relationship matrix for the single-step method: $\mathbf{H}^{-1} = \mathbf{A}^{-1} - \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{gg}^{-1} \end{bmatrix}$ where $\mathbf{A}^{-1}$ is inverse of pedigree relationship matrix for all animals, $\mathbf{G}^{-1}$ is inverse genomic relationship matrix, and $\mathbf{A}_{gg}^{-1}$ is inverse pedigree relationship matrix of genotyped animals. When command `IA22FILE` is used with the `PEDIGREE` option, no precalculated diagonal element values of $\mathbf{A}_{gg}^{-1}$ are available for the preconditioner. These values can be given using `IHPRECON` in a file. One diagonal element of $-\mathbf{A}_{gg}^{-1}$ is given on a line: <ID code> <value>. Note that these are <u>NOT</u> diagonal elements of $\mathbf{A}_{gg}$ nor $\mathbf{A}_{gg}^{-1}$ but diagonal elements of $-\mathbf{A}_{gg}^{-1}$.

NEW

Syntax:
```
IHPRECON <filename>
```
Example. Diagonal of matrix $-\mathbf{A}_{gg}$ is in file `minus_diA_genotyped.dat`
```
IHPRECON minus_diA_genotyped.dat
```

9.2.6 INBREEDING

Column numbers of individual id code and inbreeding coefficient in the inbreeding coefficient file (see 9.2.7). Default is that inbreeding coefficients are all zero. Column number of the individual id code must be before the inbreeding coefficient.

Syntax:
```
INBREEDING PEDIGREECODE=<individual id code column> &
           FINBR=<inbreeding coefficient column>
```

Example. The first column has the individual id code, and the third column has the inbreeding coefficient.

```
INBREEDING PEDIGREECODE=1 FINBR=3
```

9.2.7 INBRFILE

Name of inbreeding coefficient file. Default is that all inbreeding coefficients are zero, and, thus, no inbreeding coefficient file is read.

Syntax:

```
INBRFILE <filename>
```

Example. Inbreeding coefficient file is AM.inbr.

```
INBRFILE AM.inbr
```

9.2.8 NORANSOL

Give random effects for which no solution files are made. Default is that solutions are written for all random effects.

Syntax:

```
NORANSOL <random effects>
```

Example. No solutions are written of effects HTM and PE.

```
NORANSOL HTM PE
```

9.2.9 MISSING

Number indicating missing information for data in the real number columns. Default is zero.

Syntax:

```
MISSING <number for missing>
```

Example. Set missing value to -99999.0

```
MISSING        -99999.0
```

9.2.10 RESTARTSOL

Make restart solution file. The restart solution file allows the solver mix99s to start iteration using old solutions. Default is no file is written. Command RESTARTSOL is an option within MODEL command. The option is given on the same line as command MODEL.

Syntax:

```
MODEL RESTARTSOL
```

Example. Restart solution files requested.

```
MODEL RESTARTSOL
```

9.2.11 SCALE

Scaling of observation by residual standard deviation. Scaling of observations by the residual standard deviation can be important for multiple trait models. Scaling makes observations from different traits to be on the same residual scale which may lead to numerically better behaving computations. Before any output is generated, all solutions are scaled back to the original units. Default is no scaling. Command SCALE is

an option within `MODEL` command. The option is given on the same line as command `MODEL`.

Syntax:
```
MODEL SCALE
```
Example. Scaling is requested.
```
MODEL SCALE
```

9.2.12 **PARALLEL**

Information on parallel computing: number of processors and number of common area blocks. Alternatively, common area blocks can be defined by specifying the block code of the first common area block instead and adding option `FIRST` after it.

Optional additional information is method of the work load division, and total maximum size of I/O buffers. Default is no parallel computing, i.e., number of processors is zero. Work division is either by number of records (default), or number of equations. Giving letter E or e will use number of equations in work division to the processors. Total size of I/O buffers is given as an integer number in megabytes but by default is determined by the preprocessor program. See PARALLEL in MiX99 manual *Technical reference guide for MiX99 pre-processor* for more information.

Syntax:
```
PARALLEL <N processors> <N common blocks> [<work division> <buffer size>]
PARALLEL <N processors> <first common block> FIRST [...]
```
Example. Parallel computing with 6 processors. The last 10 blocks in the data file belong to the common area blocks.
```
PARALLEL       6    10
```

9.2.13 **PRECON**

Information on the preconditioning. Format is the same as given in MiX99 manual for `mix99i` *Technical reference guide for MiX99 pre-processor*. Thus, first characters (one for each effect) are for the within block effects, and then one common for all across blocks effects. Default is block diagonal preconditioner for all effects.

effect type	available preconditioners
within block	d=diagonal, b=block diagonal.
across blocks fixed	d=diagonal, b=block diagonal,
	f= full block, m=mixed block

Note that giving `PRECON n` will lead to use of no preconditioner. See MiX99 manual for details.

Syntax:
```
PRECON <preconditioning information>
```
Example. Block diagonal preconditioner is used for the 4 within block effects. The across blocks fixed effects have mixed block preconditioner where the first effect is in block of its own and the others are in another block.
```
PRECON b b b b   m
```

9.2.14 `RANDOM`

Random effect names other than the additive genetic effect associated to pedigree. If command is not given, the only random effects are additive genetic and residual effects. Order of the effects give numbering of the random effects.

Syntax:

```
RANDOM <effect names>
```

Example. There are four random effects: `HTM`, `PE`, additive genetic, and residual. Thus, `HTM` is random effect number 1, `PE` is number 2, additive genetics is number 3, and residual is number 4. These numbers are used in the (co)variance file defined by `PARFILE`.

```
RANDOM HTM PE
```

or alternatively

```
RANDOM HTM PE animal
```

9.2.15 `REGFILE`

Regression matrix coefficient file. Commonly SNP coefficient matrix is given as a regression coefficient matrix file. See also commands `REGPARFILE` and `REGMATRIX`.

Syntax:

```
REGFILE <filename>
```

Example. Regression matrix in file `snp.dat`

```
REGFILE snp.dat
```

9.2.16 `REGMATRIX`

Regression matrix information. The information given:

- type:

    FIXED Fixed coefficient matrix,

    RANDOM Random effects with single common variance,

    HETEROGENEOUS Each effect has its own variance

- name: name of the effect

- column number information:

    ID = a Column number of individual code is *a* (optional),

    FIRST = b First column of regression coefficients is *b*,

    LAST = c Last column number is *c*.

- SNP marker information (optional):   NEW

    – Imputation:

        IMPUTE = i Missing (integer) marker value *i* to be imputed.

    – Centering:

        CENTER Average marker value.

CENTER = **r** Constant real value *r*.

CENTER = **f** Separate centering for markers in file *f*.

– Scaling:

SCALE = **r** Constant real value *r*.

SCALE = **f** Separate scaling for markers in file *f*.

– File format:

FORMAT = **n|m|s** File format is *n* (or *normal*) for normal real valued regression coefficients with spaces separating columns, *m* (or *markers*) for SNP markers of integer values '0', '1', '2' and optional missing value of IMPUTE (with spaces separating columns), or *s* (*squeezed*) for "squeezed" SNP marker values without separating spaces.

• preconditioner type (optional):

PRECON = **n|d|b** Preconditioner type is *n* for none, *d* for diagonal (default), or *b* for block diagonal. Block diagonal means trait block by regression coefficient.

See also commands REGFILE and REGPARFILE.

Syntax:
```
REGMATRIX <type> <name> [ID=<column>] FIRST=<column> LAST=<column>
          [IMPUTE=<missing>] [CENTER[={<real value>|<filename>}]]
          [SCALE={<real value>|<filename>}] [FORMAT=<file format>]
          [PRECON=<preconditioner>]
```
Example. Regression matrix information: common random variance, name of effects is snp, regression coefficients in columns 3 to 10. No column for id code. Block diagonal preconditioner.
```
REGMATRIX RANDOM snp FIRST=3 LAST=10 PRECON=b
```

9.2.17 REGPARFILE

Variance components for a random regression matrix. See also commands REGFILE and REGMATRIX.

Syntax:
```
REGPARFILE <filename>
```
Example. Variance components in file reg.par
```
REGPARFILE rep.par
```

9.2.18 RESIDFILE

Residual variance covariance matrix file in case of different residuals for different observations. If residual file is given then data file must have an integer number column associated with the residual matrix number. See command RESIDUAL. Default is that no additional residual variance file is used, i.e., the same residual (co)variance defined in PARFILE is used for all observations.

Syntax:

```
RESIDFILE <filename>
```

Example. Residuals are in file `mix99pat.respar`

```
RESIDFILE ./data/mix99par.respar
```

9.2.19 RESIDUAL

Name of integer number column in the data file indicating number of residual variance used for this observation (see RESIDFILE). Default is that same residual (co)variance is used for all observations.

Syntax:

```
RESIDUAL <integer column name>
```

Example. Residual variance number is on integer data column `ResidualNumber`.

```
RESIDUAL ResidualNumber
```

9.2.20 TABLEFILE

Name of covariable table file. See TABLEINDEX command. Default is no table index file is needed.

Syntax:

```
TABLEFILE <filename>
```

Example. Covariable table file is `FinTDMpara.cov`.

```
TABLEFILE FinTDMpara.cov
```

9.2.21 TABLEINDEX

Name of integer number column in the data file indicating column for table index. Default is no table index. See TABLEFILE.

Syntax:

```
TABLEINDEX <integer column name>
```

Example. Index for the covariable table file is on the integer number column `DIM`. in the data file.

```
TABLEINDEX DIM
```

9.2.22 TAFILE

Gives file having the $\mathbf{T}_A$ matrix in $\mathbf{G}^{-1} = ((1-w)\mathbf{Z}\mathbf{Z}' + w\mathbf{A}_{gg})^{-1} = \frac{1}{w}\mathbf{A}_{gg}^{-1} - \mathbf{T}'_A\mathbf{T}_A$ used by the single-step method where w is the residual polygenic proportion. The approach requires the $\mathbf{A}_{gg}^{-1}$ matrix to be given separately using the command IA22FILE, or by option PEDIGREE.   DEV

Format of the $\mathbf{T}_A$ matrix file is similar to the lower triangle dense format. However, the $\mathbf{T}_A$ matrix is a rectangular matrix. The $\mathbf{T}_A$ matrix file needs to be made by a special preprocessing program.

Syntax:

```
TAFILE   <filename>
```

Example. Matrix $\mathbf{T}_A$ is in file `TA.dat`

```
TAFILE TA.dat
```

9.2.23 **TEFILE**

Gives file having the $\mathbf{T}_e$ matrix in $\mathbf{G}^{-1} = (\mathbf{Z}\mathbf{Z}' + \epsilon\mathbf{I})^{-1} = \frac{1}{\epsilon}\mathbf{I} - \mathbf{T}_e'\mathbf{T}_e$ used by the single-step method where ϵ is a small number such as 0.01. The approach requires the $\mathbf{A}_{gg}^{-1}$ matrix to be given separately using the command `IA22FILE`, or by option PEDIGREE.

NEW

Format of the $\mathbf{T}_e$ matrix file is similar to the lower triangle dense format. However, the $\mathbf{T}_e$ matrix is a rectangular matrix. The $\mathbf{T}_e$ matrix file needs to be made by a special preprocessing program such as Teig_make.

Syntax:
```
TEFILE   <filename>
```
Example. Matrix $\mathbf{T}_e$ is in file `Te.dat`
```
TEFILE Te.dat
```

9.2.24 **TITLE**

Line for title of the analysis. Default title is:
```
MiX99 analysis time: <current time and date>
```

Syntax:
```
TITLE <Title of the analysis>
```
Example.
```
TITLE New model for Simmental birth weight
```

9.2.25 **TMPDIR**

Directory for temporary files. Default is current directory.

Syntax:
```
TMPDIR <directory>
```
Example.
```
TMPDIR ./tmpMiX
```

9.2.26 **TRAITGROUP**

Name of integer number column for the trait group.

Syntax:
```
TRAITGROUP <integer column name>
```
Example. Trait group is in integer number column `trait`.
```
TRAITGROUP trait
```

9.2.27 **WITHINBLOCKORDER**

Ordering of effects within block. Order of effect after the command name gives the ordering. Default is that only animal genetic effect is within block.

Syntax:
```
WITHINBLOCKORDER <effect names>
```
Example. There are three effects within block. Order of effects within block: 1=`G`, 2=`PE`, 3=`HerdYear`.
```
WITHINBLOCKORDER G PE HerdYear
```

9.2.28 `DEFINE`

Defines a ***macro*** identifier to be used as an abbreviation for its replacement text: DEV

```
DEFINE <macro name> <replacement text>
```

Instructs to replace all successive occurrences of the identifier with the replacement. Allows to shorten repeatedly occuring text, for example, directory names and common effects in complex CLIM models.

In addition to macros, a ***range expansion*** can be used as an abbreviation. Every occurence of

```
<identifier><N>:<M>
```

is replaced by a space separated list of

```
<identifier><N> <identifier><N+1> ... <identifier><M-1>  <identifier><M>
```

where the identifier is replicated M-N+1 times with integers from N to M. For example `het1:5` is replaced by

```
het1 het2 het3 het4 het5
```

Range expansion can be used, for example, to name INTEGER and REAL columns, or to specify covariable table columns in complex models.

Example:

```
DEFINE HomeDIR /home/user
DEFINE WorkDIR .

DATAFILE HomeDIR/mydata.dat
PEDFILE  HomeDIR/mydata.ped

REAL  milk protein fat x1:2 het1:5

DEFINE CurveMILK  Curve(t1:3 t4  t96 | SEASON)
DEFINE CurvePROT  Curve(t1:3 t95 t97 | SEASON)
DEFINE CurveFAT   Curve(t1:3 t95 t98 | SEASON)
DEFINE Common     AGE DCC YM HTM

MODEL SCALE
  milk    = CurveMILK Common PE( t5:10|animal)@1st G(t59:64|animal)@FST
  protein = CurvePROT Common PE(t11:16|animal)@1st G(t65:70|animal)@FST
  fat     = CurveFAT  Common PE(t17:22|animal)@1st G(t71:76|animal)@FST

TMPDIR WorkDIR/tmpMiX
```

is replaced by

```
DATAFILE /home/user/mydata.dat
PEDFILE  /home/user/mydata.ped

REAL  milk protein fat x1 x2 het1 het2 het3 het4 het5

MODEL SCALE
  milk    = Curve(t1  t2  t3  t4  t96      | SEASON)     AGE DCC YM HTM &
            PE(t5  t6  t7  t8  t9  t10 | animal)@1st                    &
             G(t59 t60 t61 t62 t63 t64 | animal)@FST
  protein = Curve(t1  t2  t3  t95 t97      | SEASON)     AGE DCC YM HTM &
            PE(t11 t12 t13 t14 t15 t16 | animal)@1st                   &
             G(t65 t66 t67 t68 t69 t70 | animal)@FST
  fat     = Curve(t1  t2  t3  t95 t98      | SEASON)     AGE DCC YM HTM &
```

```
                  PE(t17 t18 t19 t20 t21 t22 | animal)@1st                    &
                   G(t71 t72 t73 t74 t75 t76 | animal)@FST

TMPDIR ./tmpMiX
```

Currently, preprocessor (`mix99i`) command line option `--usemacros` is needed to activate the CLIM macro and range expansion.

```
                  PE(t17 t18 t19 t20 t21 t22 | animal)@1st                    &
                   G(t71 t72 t73 t74 t75 t76 | animal)@FST

TMPDIR ./tmpMiX
```

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10 Appendix: Quick reference card

The following commands are necessary. Options are in square brackets [ ]. Syntax and short explanation of the required commands are in Chapter 9.1 except for command MODEL which is considered separately in Chapters 5, 6, 7 and 8. Note that in CLIM and in the following, symbol '&' is continuation to the next line.

```
DATAFILE [TEXT | BINARY] <FileName>
INTEGER   <column names>
REAL      <column names>


PARFILE   <FileName>


PEDFILE   <FileName>
PEDIGREE <Effect name> [ FILE | <type of relationship matrix>  &
                  [<coefficient for random genetic group>] ]


MODEL [SCALE] [RESTARTSOL]
  <model lines>
```

Optional commands (see "Optional commands" for more details):

```
DATASORT    BLOCK=<block in INTEGER> PEDIGREECODE=<code in INTEGER>
IGFILE      [LOWER|MIXED] <filename>
IA22FILE    [LOWER|MIXED] <filename>
MISSING     <value for missing real number data>
NORANSOL    <random effect numbers without solution file>
PARALLEL    <number of processors> <number/first of common blocks> [FIRST]
PRECON      <preconditioning information>
RANDOM      <random effect names>
REGFILE     <filename>
REGPARFILE <filename>
REGMATRIX   <type> <name> [ID=<column>] FIRST=<column> LAST=<column>
            [IMPUTE=<missing>] [CENTER[={<real value>|<filename>}]]
            [SCALE={<real value>|<filename>}] [FORMAT=<file format>]
            [PRECON=<preconditioner>]
RESIDFILE   <filename>
RESIDUAL    <INTEGER column name of the residual variance number>
TABLEFILE   <filename>
TABLEINDEX <table index INTEGER column name>
TITLE       <title of analysis>
TMPDIR      <directory>
TRAITGROUP <trait group INTEGER column name>
WITHINBLOCKORDER <Effect names in the order>
DEFINE      <macro name> <replacement text>
```

Special symbols that cannot be used in user defined names like data file column names:

```
#    start for comment
&    symbol for line continuation
" "  string in between the apostrophes is read un-
     changed
!    options follow (on the model line)
( )  parenthesis used on model line(s)
```

11 References

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