Marker assisted BLUP model

Model description

Marker-assisted BLUP for a single trait using IBD-matrix.

The model is

$$\mathbf{y} = \mu + g_1 + g_2 + \mathbf{a} + \mathbf{e},$$

where

$\mathbf{y}$ is vector of phenotypes,
μ is mean,
g are random additive genotype effects,
$\mathbf{a}$ is vector of random additive polygenic effects, and
$\mathbf{e}$ is random residual vector.

It is assumed that $\mathrm{var}(\mathbf{g}) = \mathbf{IBD}\sigma_{\mathrm{g}}^2$, $\mathrm{var}(\mathbf{a}) = \mathbf{A}\sigma_{\mathrm{a}}^2$ and $\mathrm{var}(\mathbf{e}) = \mathbf{I}\sigma_{\mathrm{e}}^2$ and all random effects are non-correlated. The $\mathbf{IBD}$ is the IBD-matrix and $\mathbf{A}$ is the numerator relationship matrix.

The variance components are $\sigma_{\mathrm{g}}^2 = 0.0075$, $\sigma_{\mathrm{a}}^2 = 0.285$ and $\sigma_{\mathrm{e}}^2 = 0.70$.

Input files

Datafile:

The data file contains information on the data to be analyzed together with class and regression variables for the model. The data file can be in free format (columns are separated by at least one space) or in binary format.

Each record, i.e., line in a free format file, has been divided to two parts: 1) Integer number columns and 2) real number columns. Columns of real numbers are always after the integer number columns.

MAS.dat

```
  1     0     0     1     1     2    0.380925
  2     0     0     1     3     1    0.375538
  3     0     0     1     4     1    2.618100
  4     0     0     1     5     6    0.336157
  5     0     0     1     7     8    0.62505382
  6     0     0     1     1     1   -1.50472093
  7     1     3     1     1     9    0.40854526
  8     1     4     1     2    10   -0.64103413
  9     2     5     1     1    11   -0.17288433
 10     2     6     1     1     1   -0.64055294
```

Column 1: Animal (integer)
Column 2: Sire (integer)
Column 3: Dam (integer)
Column 4: Mean (integer)
Column 5: Haplotype 1 (integer)

Column 6: Haplotype 2 (integer)
Column 7: Phenotype (real)

Pedigree file:

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

MAS.ped

```
 1     0     0
 2     0     0
 3     0     0
 4     0     0
 5     0     0
 6     0     0
 7     1     3
 8     1     4
 9     2     5
10     2     6
```

Column 1: Animal ID
Column 2: Sire ID
Column 3: Dam ID

Variance component file:

The variance components file has variances and covariances for all the random effects in the model. The variance component file has a line for each (co)variance. Order of lines in the file is irrelevant.

MAS.var

```
1     1     1     0.0075       QTL effect
3     1     1     0.2850       polygenic effect
4     1     1     0.7000       residual effect
```

Column 1: Random effect number (integer)
Column 2: Row index (integer)
Column 3: Column index (integer)
Column 4: (Co)variance value (real)

External correlation matrix file:

The external correlation matrix file contains correlation structure for other than genetic effect, for example an inverse IBD matrix for the QTL effect. The size of the matrix is equal to the total number of different haplotypes present in the animals of the whole pedigree. The file contains the diagonal and the lower triangle of the inverse IBD matrix.

MAS.ibd

```
1    1     1.50000
2    2     5.69483
3    2    -0.92179
3    3     5.69483
4    1     0.50000
4    2    -0.92179
.    .     .
.    .     .
```

Column 1: Haplotype ID 1.
Column 2: Haplotype ID 2.
Column 3: Non-zero element

Command file:

Marker assisted BLUP model can be given to mix99i only using the old directive method; this model can not be given using CLIM instructions. Everything beyond '#' sign is considered as a comment.

MAS.dir

```
# TITLE:
          Marker-assisted BLUP for a single trait using an IBD-matrix
# INT-VAR:
          animal sire dam mean haploty1 haploty2
# REAL-VAR:
          phenoty
# TRAITS:
          1
# TRGRP:
          1 -
# SORT_R: Block_code, Relationship_code
          -           -
# FIXRAN: Fixed factors, Random factors, External correlation matrix
          1              3               1
# MODEL:  Traitgrp., Trait, Weight; mean haplotype1 haplotype2 animal
          1          1      -       4    5          6          1
# BLKORD: Order of effects within blocks, “<” combines allele effects
                                    -    -     <    -          1
# RANDOM: haplotype1 haplotype2 animal
          1          2          3
# PEDIGR: Number: animal
          1       1
# REGRES: Number: mean haplotype1 haplotype2 animal
          4       cl   cl         cl         cl
# COMBINE:
          n
# RELMET:
          am
# INPFIL:
          MAS.dat
# VAR:
          6   1   f
# MISSVA:
          0.0
# SCALE:
          n
# PEDFIL:
          MAS.ped
# CORRFIL: Random effect number, Filename
          1                      MAS.ibd
# PARFIL:
          MAS.var
# TMPDIR:
          .
# SOLFOR: animal haplotype1 haplotype2
          y      y          y
# SOLUNF:
          n
# PRECON: WpW, XpX
          b    d
# NPROC:  Number of processors used by the sover program
          1
# COMBLK: Number of blocks in common area when using parallel processing
          0
```

Solution files

Structure of the formatted solution files depends on the model. Therefore, explanation of the content of those files is given in the printout of the particular run of the program.

MiX99-solver program has been run by command `mix99s -s`, meaning that in all parts of the program default values are used.

"Solfix"-file contains solutions for fixed effects.

```
 Fact. Trt       Level     N-Obs   Solution                    Factor Trait
   1    1          1          10 0.21672                         mean phenoty
```

Column 1: Factor number
Column 2: Trait number
Column 3: Level code
Column 4: Number of observations
Column 5: Solution
Column 6: Name of factor
Column 7: Name of trait

"Solr01"-file contains solutions for random effect.

```
1   9 -0.15225E-01
2   2  0.12201E-01
3   1  0.13285E-01
4   1  0.15638E-01
5   1  0.12644E-01
6   1  0.12644E-01
7   1  0.13179E-01
8   1  0.13179E-01
9   1 -0.25214E-03
10  1  0.90256E-02
11  1  0.11458E-01
```

Column 1: Level code
Column 2: Number of observations
Column 3: Solution for trait 1 phenoty and factor haploty1

"Solani"-file contains solutions for genetic animal effect.

```
   1     2     1 -0.61707E-01
   2     2     1 -0.62435E-01
   3     1     1  0.68231
   4     1     1 -0.70471E-01
   5     1     1  0.64045E-01
   6     1     1 -0.55175
   7     0     1  0.29288
   8     0     1 -0.20358
   9     0     1 -0.64592E-01
  10     0     1 -0.39500
```

Column 1: Animal ID
Column 2: Number of descendants
Column 3: Number of observations
Column 4: Solution for trait 1 phenoty and factor animal