Manual for

BLUPF90 family of programs

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Introduction

BLUPF90 is a family of programs for mixed-model computations focusing on animal breeding applications. The programs can do data conditioning, estimate variances using several methods, calculate BLUP for very large data sets, calculate approximate accuracy, and use SNP information for improved accuracy of breeding values and genome-wide association studies (GWAS).

The programs have been designed with 3 goals in mind:

1. Flexibility to support a large set of models found in animal breeding applications.
2. Simplicity of software to minimize errors and facilitate modifications.
3. Efficiency at the algorithmic level.

Aside from being used in hundreds of studies, the programs are utilized for commercial genetic evaluation in dairy, beef, pigs, broiler chicken, and fish by major companies/institutions/associations in the US and beyond.

The programs are written in Fortran 90/95 and originated as exercises for a class taught by Ignacy Misztal at the University of Georgia. Over time, they have been upgraded and enhanced by many contributors. Details on programming and computing algorithms are available in an Interbull paper (Misztal, 1999) and as course notes. Old versions of source codes for nearly all programs are available here.

Additional information about the programs is available at http://nce.ads.uga.edu/wiki/doku.php as wiki pages. There is a BLUPF90 discussion group at groups.io.
List of programs from Wiki page

The latest binaries are available [here](#). All binaries for Linux, Mac OSX, and Windows are updated frequently. Always check for the most updated versions.

The programs support mixed models with multiple-correlated effects, multiple animal models and dominance.

- **BLUPF90** - BLUP in memory
- **REMLF90** - accelerated EM REML
- **QXPak** - joint analysis of QTL and polygenic effects (M. Perez-Enciso) [QxPak web page](#)
- **AIREMLF90** - Average Information REML with several options including EM-REML and heterogeneous residual variances (S. Tsuruta)
- **CBLUP90** - solutions for bivariate linear-threshold models
- **CBLUP90REMEL** - as above but with quasi REML (B. Auvray)
- **GIBBSF90** - simple block implementation of Gibbs sampling
- **GIBBS1F90** - as above but faster for creating mixed model equations only once
- **GIBBS2F90** - as above but with joint sampling of correlated effects
- **GIBBS3F90** - as above with support for heterogeneous residual variances
- **POSTGIBBSF90** - statistics and graphics for post-Gibbs analysis (S. Tsuruta)
- **THRGIBBSF90** - Gibbs sampling for any combination of categorical and linear traits (D. Lee)
- **THRGIBBS1F90** - as above but simplified with several options (S. Tsuruta)
- **THRGIBBS3F90** - as above with heterogeneous residual variances for linear traits
- **RENUMF90** - a renumbering program that also can check pedigrees and assign unknown parent groups; supports large data sets
- **INBUPGF90** - a program to calculate inbreeding coefficients with incomplete pedigree (I. Aguilar)
- **SEEKPARENTF90** - a program to verify paternity and parent discovery using SNP markers (I. Aguilar)
- **PREDICTF90** - a program to calculate adjusted $\hat{y}$, and residuals (I. Aguilar)
- **PREDF90** - a program to predict direct genomic value (DGV) for animals based on genotypes and SNP solution
- **QCF90** - a quality-control tool on genotypes and pedigree information (Y. Masuda)
- **BLUPF90+** - a combined program of blupf90, remif90, and airemlf90
- **GIBBSF90+** - a combined program of gibbs2f90, gibbs3f90, thrgibbs1f90, and thrgibbs3f90

Available by request
- **MRF90** - Method R program suitable for very large data sets; contact T. Druet.
- **COXF90** - Bayesian Cox model - contact J. P. Sanchez (JuanPablo.Sanchez@irta.cat)
- **BLUPF90HYP** – BLUPF90 with hypothesis testing (F and Chi2 tests) - contact J. P. Sanchez as above

Available only under research agreement
- **BLUP90IOD** - BLUP by iteration on data with support for very large models (S. Tsuruta)
- **CBLUP90IOD** - BLUP by iteration on data for threshold-linear models
- **ACCF90** - approximation of accuracies for breeding values
- **BLUP90ME** - BLUP by iteration on data with support for very large models for multi-breed evaluations
- **BLUP90ADJ** – BLUP with a data preadjustment tool

Included in application programs
- **PREGSF90** – genomic preprocessor that combines genomic and pedigree relationships (I. Aguilar)
- **POSTG SF90** – genomic postprocessor that extracts SNP solutions after genomic evaluations (single step, GBLUP) (I. Aguilar)

Other programming contributions were made by Miguel Perez-Enciso ([user file](#)) and François Guillaume (Jenkins hashing functions).
Programs in a chart

Application programs (BLUP*, *REMLF90, THRGIBBS*, GIBBS*, POSTGIBBSF90, PREGSF90, POSTGSF90, and PREDICTF90) are driven by parameter files and require data files with effects renumbered from 1 consecutively. Some programs (PREDF90, QCF90, and SEEKPARENTF90) use command line instead of a parameter file.

Renumbering and quality control can be done by RENUMF90, which is also driven by a parameter file. Separation of renumbering and application programs allows supporting complicated models.

Some models are not directly supported by RENUMF90 and require tweaking the parameter file in the application programs.
Parameter file for application programs

The parameter file has keywords that are fixed and cannot be changed followed by values, with the following structure (the following example comes from a 2-trait maternal model):

<table>
<thead>
<tr>
<th>Keywords*</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DATAFILE</td>
<td>Name of file with phenotypes; free Fortran format (space-delimited file)</td>
</tr>
<tr>
<td>file.dat</td>
<td></td>
</tr>
<tr>
<td>NUMBER OF PROGENY</td>
<td>Number of traits</td>
</tr>
<tr>
<td>2</td>
<td></td>
</tr>
<tr>
<td>NUMBER OF EFFECTS</td>
<td>Number of effects in a model except for residual</td>
</tr>
<tr>
<td>6</td>
<td></td>
</tr>
<tr>
<td>OBSERVATIONS(S)</td>
<td>Position(s) of observations in data file</td>
</tr>
<tr>
<td>1 2</td>
<td></td>
</tr>
<tr>
<td>WEIGHTS</td>
<td>Position of weight on observations if used; otherwise blank</td>
</tr>
<tr>
<td>2</td>
<td>means that the weight is in column 2, and residual variance (R) is set to R/weight.</td>
</tr>
<tr>
<td>EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>4 = crossclassified effect positions in data file for 2 traits; 10 = levels</td>
</tr>
<tr>
<td>5</td>
<td>5 = crossclassified effect, positions for 2 traits; 100 = levels</td>
</tr>
<tr>
<td>6</td>
<td>6 = covariable positions in data file</td>
</tr>
<tr>
<td>7</td>
<td>7 = covariable nested in effect position 4; 10 = levels</td>
</tr>
<tr>
<td>8</td>
<td>8 = crossclassified effect positions for 2 traits; 1000 = levels</td>
</tr>
<tr>
<td>0</td>
<td>0 = crossclassified effect positions for 2 traits; 1000 = levels</td>
</tr>
<tr>
<td>RANDOM RESIDUAL VALUES</td>
<td>Residual variance or residual covariance matrix</td>
</tr>
<tr>
<td>10 1</td>
<td>For 2 trait model</td>
</tr>
<tr>
<td>1 10</td>
<td></td>
</tr>
<tr>
<td>RANDOM_GROUP</td>
<td>List of effect numbers that form a group</td>
</tr>
<tr>
<td>5 6</td>
<td>For correlated random effects 5 6</td>
</tr>
<tr>
<td>RANDOM_TYPE</td>
<td>Type of random effect</td>
</tr>
<tr>
<td>add_animal</td>
<td>diagonal, add_sire, add_an_upg, add_an_upginb, par_dom, or user_file</td>
</tr>
<tr>
<td>FILE</td>
<td>Pedigree file or other file associated with random effect; blank if none</td>
</tr>
<tr>
<td>file.ped</td>
<td></td>
</tr>
<tr>
<td>(CO)VARIANCES</td>
<td>(Co)variance matrix for each random effect</td>
</tr>
<tr>
<td>10 1</td>
<td>For 2 trait, maternal model</td>
</tr>
<tr>
<td>1 10</td>
<td></td>
</tr>
</tbody>
</table>

*Keywords need to be typed exactly (up to 20 characters).

Hint: When preparing a new parameter file, consider modifying an existing file.

Note that this parameter file is for the application programs (BLUPF90, AIREMLF90, GIBBSF90, etc.) and not for RENUMF90. This program needs a different type of parameter file. See page 15 for details.
Description of effects

The effects are specified after the keyword:

**EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]**

Each line contains the following:
- Position(s) of each effect in the data file; t positions for t traits
- Number of levels (assumed consecutive from 1)
- Type of effect: “cross” for crossclassified, and “cov” for covariable
  - crossclassified uses integer number from 1
  - covariable uses integer or real numbers
- For nested covariables, the following number (or t numbers for t traits) indicates the position of nesting in the data file
- Text after # can be used as a comment

Data and pedigree file should not have header; columns should be separated by at least one space (no TAB); hash (#) is interpreted as a comment initiator and should not be present inside the data and pedigree files. See page 14 for further details.

Consider the following dataset (copied to file.dat without the header):

<table>
<thead>
<tr>
<th>i</th>
<th>j</th>
<th>k</th>
<th>y1</th>
<th>y2</th>
<th>x1</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>2</td>
<td>3</td>
<td>4.30</td>
<td>5.67</td>
<td>22.40</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>2</td>
<td>2.76</td>
<td>3.20</td>
<td>18.00</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1</td>
<td>2.20</td>
<td>5.30</td>
<td>7.25</td>
</tr>
</tbody>
</table>

Let i go from 1 to 50, j from 1 to 80, and k from 1 to 200. The model:
\[ y_{1ij} = a_i + b_j + cx1 + e_{ij} \]
will be specified in the parameter file as:

```
DATAFILE
file.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
3
OBSERVATIONS(S)
4
WEIGHTS

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 80 cross # position 2, 80 levels
```
By definition, a regular covariable has one level (i.e., a slope as regression).

For a similar model but with a nested covariable:

\[ y_{1ij} = a_j + b_i + c x_1 + e_{ij} \]

The description will change to:

```
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 80 cross # position 2, 80 levels
1 50 cross # position 1, 50 levels
6 50 cov 1 # covariable on position 6 nested in position 1; 50 levels
```

Assume a two-trait model:

\[ y_{1ij} = a_{1j} + c_1 x_1 + e_{1ij} \]
\[ y_{2ij} = b_2 + c_2 x_1 + e_{2ij} \]

This corresponds to:

```
......
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
3
......
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 0 80 cross # position 2 for trait 1 only, 80 levels
0 1 50 cross # position 1 for trait 2 only, 50 levels
6 6 50 cov 1 1 # covariable on position 6 for two traits nested in position 1
```

"0" in effect definitions means missing effect per trait.

The first two effects in the two-trait model above can be merged:

```
NUMBER_OF_EFFECTS
2
......
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 1 80 cross # positions 2 and 1 for traits 1 and 2, 80 is max(50,80) levels
6 6 50 cov 1 1 # covariable in position 6 for two traits nested in position 1
```
**Definition of random effects**

**RANDOM_GROUP** defines one group of random effects. A group is one effect or multiple (correlated) effects that share the same covariance structure, e.g., direct-maternal effect or random regressions.

The structure of **RANDOM GROUP** is:

```
RANDOM_GROUP
  5
```

Corresponding to the effect number specified above; “5” means that the 5th effect is random. Or “5 6” means that 5th and 6th are correlated random effects.

or

```
RANDOM_GROUP
  5  6
```

Corresponding to the effect number specified above; “5 6” means that 5th and 6th are correlated random effects.

**RANDOM_TYPE** defines a covariance structure: diagonal \( \text{var}(\cdot) = s \otimes I \) or \( G \) where \( s \) is a variance and \( G \) is a covariance matrix. For other types, see “Random effects and Pedigree files” on page 12.

Assume a model:

\[
y = \text{farm} + \text{animal}_\text{additive} + \text{permanent}_\text{environment} + \text{error}
\]

with \( \text{var(}\text{animal}_\text{additive}) = A \otimes 2.5 \), \( \text{var(}\text{permanent}_\text{environment}) = I \otimes 5.1 \), \( \text{var(}\text{error}) = I \otimes 13.7 \)

With these effects:

```
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
  3  100 cross  # effect 1: farm
  2  1000 cross  # effect 2: additive genetic
  2  1000 cross  # effect 3: permanent environment
RANDOM_RESIDUAL_VALUES
  13.7
RANDOM_GROUP
  2  # this is for effect 2 on the effect list
RANDOM_TYPE
  add_animal  # additive genetic
FILE
  file.ped  # name of pedigree file
(CO)VARIANCES
  2.5
RANDOM_GROUP
  3  # effect 3 on the effect list above
RANDOM_TYPE
  diagonal  # permanent environment
FILE
  # no file associated with diagonal structures
(CO)VARIANCES
  5.1
```
Correlated Effects

Assume a model:
\[ y = \text{farm} + \text{season} + \text{direct} + \text{maternal} + \text{error} \]

\[ \text{var(direct,maternal)} = \mathbf{A} \otimes \begin{bmatrix} \mathbf{5} & 1 \\ 1 & 6 \end{bmatrix} \]

with the effects as specified:

**EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]**

- 3 100 cross # effect 1: farm
- 4 4 cross # effect 2: season
- 2 1000 cross # effect 3: direct
- 2 1000 cross # effect 3: maternal

The distribution of the random effects is specified below:

Random regression models may have many correlated random effects. Assume a data file with the following positions:

1 to 4: polynomials
5: animal number (1000 levels)
6: herd year season (50 levels)

**EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]**

- 6 50 cross # herd year season
- 1 1000 cov 5 # first polynomial nested within the animal effect position 5
- 2 1000 cov 5 # second polynomial nested within the animal effect position 5
- 3 1000 cov 5 # third polynomial nested within the animal effect position 5
- 4 1000 cov 5 # fourth polynomial nested within the animal effect position 5

...
Random effects and Pedigree files

There are a few types of additive genetic effects, each with a different pedigree format.

a) additive sire (**add_sire**)
   The pedigree file has the following format:
   sire number, sire’s sire number, sire’s maternal grandsire (MGS) number
   where unknown sire’s sire and/or sire’s MGS numbers are replaced by 0.

b) additive animal (**add_animal**)
   The pedigree file has the following format:
   animal number, sire number, dam number
   where unknown sire and/or dam numbers are replaced by 0.

c) additive animal with unknown parent groups (**add_an_upg**)
   The pedigree file has the following format:
   animal number, sire number, dam number, parent code
   where sire and/or dam numbers can be replaced by unknown parent group numbers
   parent code = 3 - number of known parents:
   1 (both parents known)
   2 (one parent known)
   3 (both parents unknown)

b) additive animal with unknown parent groups and inbreeding (**add_an_upginb**)
   The pedigree file has the following format:
   animal number, sire number, dam number, inb/upg code
   where sire and/or dam numbers can be replaced by unknown parent group numbers
   inb/upg code = 4000 / [(1+ms)(1-Fs) + (1+md)(1-Fd)]
   where ms (md) is 0 whenever sire (dam) is known, and 1 otherwise, and Fs(Fd) is the coefficient of inbreeding of the sire (dam). For example, the inb/upg code for the animal with both parents known is 2000. The code should be an integer value.

e) user provided matrix (**user_file**)
   A file specified in FILE contains the inverse of a matrix in the following format:
   row col value
   as lower- or upper-triangular elements (but not full stored). The matrix is used directly by application programs. For example, to use a genomic relationship matrix \( G \), the file needs to contain \( G^{-1} \).

f) user provided matrix with inversion (**user_file_inv**)
   As above but the matrix in FILE is inverted by the application programs before being used. For example, to use a genomic relationship matrix \( G \), the file needs to contain \( G \). The inversion is by sparse matrix techniques so it is efficient for sparse matrices but slow for dense matrices.

f) additive animal with selfing (**add_an_self**)
   The pedigree file has the following format:
   animal number, sire number, dam number, number of selfing generations
   where unknown sire and/or dam numbers are replaced by 0.
   This option fits some breeding structures in plants.
e) parental dominance (*par_domin*)

The pedigree class file has the following format:

```
  s-d s-sd s-dd ss-d ds-dd ss-dd ds-dd ds-dd code
```

where x-y is a combination number of animals x and y, s is sire, d is dam, sd is sire of dam, etc.

Code is a number of 0 to 255 and refers to the combination of missing subclasses. If one line is:
```
p  s0  s1  s2  s3  s4  s5  s6  s7  code
```

then code = \( \sum_{i=0}^{7} (a_i \times 2^i) \) where \( a_i = 0 \) if \( s_i > 0 \), or \( a_i = 1 \) otherwise.

For example, the code for a line with all nonzero parental subclasses is 255. For a line with only zero parental subclasses, if classes are ordered so that lines with zero parental subclasses, code=0. If lines are ordered so that p for parental classes with code=0 are ordered last, they may be omitted and will added automatically. The parental dominance file can be created by program **RENDOMN**.
Data and Pedigree files

All files are free format, with fields separated by spaces. By default, 0 is a missing value for all effects, including covariables.

**Transferring a file from Windows (DOS) to Linux environment**

Use “dos2unix” to convert the DOS (Windows) format to the UNIX (Linux) format if the programs show an error message while reading a file (“flip –u” can be also used instead of “dos2unix”).

**Data file**

a. Space(s) is a delimiter. At least one space between columns is required.
b. Dot (.) is just one character but not a missing value (default missing value = 0).
c. Check the data again especially when converting from another format or software such as EXCEL, SAS, ...
d. For Gibbs sampling programs with “OPTION cont”, copy the previous output files somewhere else just in case making mistakes and replacing those files.

**Pedigree file**

a. An original pedigree file for RENUMF90 can include alpha-numeric characters with free format.
b. Remove duplicates.
c. Use 0 for unknown parent(s).

**Error messages in parameter file**

a. Wrong data file name
   Check outputs for the data file name and the number of records on the screen. The program will not stop if the wrong file name already exists.
b. Wrong pedigree file name
   Check output for the pedigree file name and the number of animals on the screen. The program will not stop if the wrong file name exists.
c. Wrong positions or formats for observations and effects
   Program may not stop and may get wrong results. Check outputs for the number of levels for each effect on the screen.
d. Missing or skipping one or more fixed lines in the parameter file
   Program may stop. Check the missing line.
e. Misspelling
   Program may stop. Correct the wrong spelling.
f. Missing an empty last line
   Program may not stop. Parameter, data, and pedigree files may need one more extra line at the end of the file.
g. (Co)variance matrix is not symmetric, not positive definite, not right sized, ...
   Program may not stop.
h. A good result does not mean that your parameter file is correct. Always double-check it!
RENUMF90 parameter file

Basic rules for RENUMF90 parameter file

RENUMF90 is a renumbering program to create input (data, pedigree, and parameter) files for BLUPF90 programs and provide basic statistics. Note that RENUMF90 uses a different type of parameter file as used in BLUPF90 or other programs. RENUMF90-specific parameter file should be prepared as follows.

- The file consists of pairs of **keyword** and the corresponding **value(s)**. The keyword is always capital.
- First 7 keywords are mandatory and must appear in the following order: **DATAFILE**, **TRAITS**, **FIELDS_PASSED TO OUTPUT**, **WEIGHT(S)**, **RESIDUAL_VARIANCE** and **EFFECT**. If you don’t actually need **FIELDS_PASSED TO OUTPUT** and **WEIGHT(S)**, simply leave an empty line.
- The remaining keywords are optional but appear in the specific order shown below. For example, the **FILE** keyword must be followed by **FILE_POS** (or by **SNP_FILE** if **FILE_POS** is omitted; or by **PED_DEPTH** if both **FILE_POS** and **SNP_FILE** are omitted, and so on).
- Several **OPTION** lines can be included. RENUMF90 interpret a few options. Other options are simply passed through the template parameter file for BLUPF90 (renf90.par).

**Parameter file**

**DATAFILE**

`f1`  # data file name – input files cannot contain character # because it is used as a comment.

**TRAITS**

`t1 t2 t3 ...`  # positions of traits in data file

**FIELDS_PASSED TO OUTPUT**

`p1 p2 .. pm`  # positions that are not renumbered; put empty line if not needed.

**WEIGHT(S)**

`w`  # position of weight - fraction to the residual variance; put empty line if not needed.

**RESIDUAL_VARIANCE**

`R`  # matrix of residual (co)variances

**EFFECT**

`e1 e2 e3 ... type form`  # `e1 e2 e3 ...` = position of this effect for each trait

- # type = 'cross' for crossclassified or 'cov' for covariables
- # form = 'alpha' for alphanumeric or 'numer' for numeric (form is only for cross)

**EFFECT**

`d1 d2 d3 ... cov`  # `d1 d2 d3 ...` = positions of covariables nested in the following cross-classified effects

**NESTED**

`e1 e2 e3 ... form`  # `e1 e2 e3 ...` = positions of cross-classified effects nested

- # form = 'alpha' for alphanumeric or 'numer' for numeric

**RANDOM**

`random_type`  # 'diagonal', 'sire' or 'animal' for random effect

**OPTIONAL**
01 02 03 ... # 'pe' for permanent environment, 'mat' for maternal, and 'mpe' for maternal
permanent environment

FILE
fped # pedigree file name

FILE_POS
animal sire dam alt_dam yob # positions of animal, sire, dam, alternate dam (recipient dam), and year
of birth in pedigree file (default 1 2 3 0 0).

SNP_FILE
fsnp # specify a SNP file with ID and SNP information; the relationship matrix will include the
genomic information; a fsnp file should start with ID with the same format as fped, and
SNP info needs to start from a fixed column and include digits 0, 1, 2 and 5 (5 is for
missing SNP);
ID and SNP info need to be separated by at least one space; see more information in

PED_DEPTH
p # depth of pedigree search (default 3); all pedigrees are loaded if p = 0.

GEN_INT
min avg max # minimum, average, and maximum generation interval; applicable only if year of birth
present in pedigree file; minimum and maximum used for pedigree checks; average
used to predict year of birth of parent with missing pedigree.

REC_SEX
sex # if only one sex has records, specifies which parent it is; used for pedigree checks.

UPG_TYPE
t # 'yob': based on year of birth.
# 'in_pedigrees': the value of a missing parent should be -x, where x is UPG number that
this missing parent should be allocated to; in this option, all known parents should have
pedigree lines, i.e., each parent field should contain either the ID of a real parent, or a
negative UPG number.
# 'group': it assigns the group using a user-defined group label in the pedigree file. The
field of the label should be specified as the 6th item in the FILE_POS entry.
# 'group': as above except assigning the same groups to sires and dams.
# 'internal', allocation is by a user-written function custom_upg (year_of_birth,sex,ID,
parent_code).

INBREEDING
s # use of inbreeding coefficients to compute inb/upg code in the 4th column of the
output pedigree file. Inbreeding calculation is default in RENUMF90 ≥ v1.157, even if
this keyword is not used.
# 'pedigree': the program computes inbreeding coefficients with Meuwissen and Luo
(1992) using the pedigree to be saved in renadxx.ped; calculated inbreeding
coefficients will be saved in a file "renf90.inb" with the original ID.
# 'file': the program reads inbreeding coefficients from an external file. You should put
the filename after 'file' e.g. 'file inbreeding.txt'. The file has at least 2 columns:
original ID and inbreeding value (from 0.0 to 1.0). The program skips unnecessary IDs.
# 'self x': Calculates inbreeding with selfing
x is the column in the pedigree file with the number of selfing generations
# 'no-inbreeding': turn inbreeding calculation off in RENUMF90 ≥ v1.157.

(CO)VARIANCES
G       # (co)variances for animal effects or animal + maternal effects
(CO)VARIANCES_PE
GPE      # (co)variances for the PE effect
(CO)VARIANCES_MPE
GMPE     # (co)variances for the MPE effect

Combining fields
How can we specify interactions? - Combining fields or interactions. Several fields in the data file can be
combined into one using a COMBINE keyword.
COMBINE a b c ....   # keywords COMBINE need to be on top of the parameter file (the first
keyword). It can be placed after comments.
For example:
COMBINE 2 3 4
combines content of fields 2 3 4 into field 7; the data file is not changed, only the program treats
field 7 as fields 2 3 4 put together (without spaces). The combined fields can be treated as
"numeric" with the total length is < 9 or "alpha". The keyword is optional but must be placed in
the top of the parameter file.

Hints: type renumf90 --show-template to have a template parameter file.
type renumf90 --version to see the version number.

Options
RENUMF90 parameter file can accept a few options. If the program detects non-RENUMF90 options,
such option lines are simply transferred to renf90.par.

OPTION alpha_size nn  # new size
Changes the maximum size of character fields (default 20 characters).

OPTION max_string_readline nn
Changes the maximum length of characters in a line (default 800 characters).

OPTION max_field_readline nn
Changes the maximum number of fields capable in a line (default 100 fields).

Output files
RENUMF90 generates several files.
- `renf90.par`: parameter template file for BLUPF90 and other application programs
- `renf90.tables`: table relating the original code and the renumbered code
- `renf90.dat`: data file for BLUPF90
- `renaddxx.ped`: pedigree file for BLUPF90; `xx` is an integer number that indicates the position of animal effect among all model effects in `renf90.par`. This file will be created only if `RANDOM animal` is specified.
- `SNPfile_XrefID`: cross-reference file for genomic analysis, which contains renumbered ID and original ID; `SNPfile` is the original SNP marker file. This file will be created only if `SNP_FILE` is specified.
- `renf90.inb`: inbreeding coefficients. This file will be created only if `INBREEDING pedigree` is specified.
- `renf90.fields`: has detailed information about the data fields.

**Output pedigree file**
The additive pedigree file built by `RENUMF90` is `renaddxx.ped`. The pedigree file has the following structure:

1) animal number (from 1)
2) parent 1 number or unknown parent group number for parent 1
3) parent 2 number or unknown parent group number for parent 2
4) 3 minus number of known parents (this column is replaced by inbreeding code if `INBREEDING` is specified or by default in `RENUMF90 ≥ v1.157`)
5) known or estimated year of birth (0 if not provided)
6) number of known parents (for genotyped animals, if any: 10 + number of known parents)
7) number of records
8) number of progenies as parent 1
9) number of progenies as parent 2
10) original animal id

**Example**

**Input file - data**

```
aa 1 10
aa 2 12
bb 1 11
cc 1 12
cc 2 14
dd 2 13
ee 2 14
```

**Pedigree file - ped**

```
aa ff ee 2004
bb hh gg 2004
cc hh ii 2004
dd ff 0 2004
ee ff 0 2002
ff 0 0 2002
gg ff 0 2002
hh 0 0 2002
```
Parameter file - testpar1

# Parameter file for program renumf90; it is translated to parameter file for BLUPF90 family of programs.

DATASET

data

TRAITS
3

FIELDS_PASSED TO OUTPUT
1  #passing original ID to the renumbered data file

WEIGHT(S)

RESIDUAL_VARIANCE
1

EFFECT
2 cross num

EFFECT
1 cross alpha

RANDOM
animal

FILE
ped

FILE_POS
1 2 3 0 4

PED_DEPTH
3

GEN_INT
1 2 10

UPG_TYPE
yob

2002 2003

(CO)VARIANCES
1

Output log

RENUMF90 version 1.157 with zlib

testpar1
datafile:data
traits: 3
fields passed: 1
R 1.000

Processing effect 1 of type cross
item_kind=num

Processing effect 2 of type cross
item_kind=alpha
pedigree file name "ped"
positions of animal, sire, dam, alternate dam, yob, and group 1 2 3 0 4
0 0
pedigree traced to generation 3
Minimum, average and maximum generation intervals: 1 2 10
Unknown parent groups separated by years:
2002
2003
Reading (CO)VARIANCES: 1 x 1
Maximum size of character fields: 20
Maximum size of record (max_string_readline): 8000
Maximum number of fields for input file (max_field_readline): 100
Pedigree search method (ped_search): convention
Order of pedigree animals (animal_order): default
Order of UPG (upg_order): default
Missing observation code (missing): 0

Using prime hash function
hash tables for effects set up
first 3 lines of the data file (up to 70 characters)
  aa 1 10
  aa 2 12
  bb 1 11
read 7 records
table with 2 elements sorted
added count
Effect group 1 of column 1 with 2 levels
table expanded from 10000 to 10000 records
added count
Effect group 2 of column 1 with 5 levels
wrote statistics in file "renf90.tables"

Basic statistics for input data (missing value code is '0')
\[
\begin{array}{|c|c|c|c|c|}
\hline
\text{Pos} & \text{Min} & \text{Max} & \text{Mean} & \text{SD} & \text{N} \\
\hline
2 & 1.0000 & 2.0000 & 1.5714 & 0.53452 & 7 \\
3 & 10.0000 & 14.0000 & 12.286 & 1.4960 & 7 \\
\hline
\end{array}
\]

Correlation matrix
\[
\begin{pmatrix}
  2 & 3 \\
  2 & 1.00 & 0.80 \\
  3 & 0.80 & 1.00
\end{pmatrix}
\]
Counts of nonzero values (order as above)
\[
\begin{array}{|c|c|}
\hline
\text{Pos} & \text{N} \\
\hline
2 & 7 \\
3 & 7 \\
\hline
\end{array}
\]
random effect 2
type:animal
opened output pedigree file "renadd02.ped"
first 3 lines of the file (up to 70 characters)
  aa ff ee 2004
  bb hh gg 2004
  cc hh ii 2004
read 10 pedigree records
loaded 4 parent(s) in round 1

Pedigree checks
ee: younger than parent 1 by 0 years
gg: younger than parent 1 by 0 years
Unknown parent group allocation

<table>
<thead>
<tr>
<th>Equation</th>
<th>Group</th>
<th>#Animals</th>
<th>Years</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>1</td>
<td>0</td>
<td>0-2001</td>
</tr>
<tr>
<td>11</td>
<td>2</td>
<td>8</td>
<td>2002-2002</td>
</tr>
<tr>
<td>12</td>
<td>3</td>
<td>1</td>
<td>2003-</td>
</tr>
</tbody>
</table>

Max group = 3; Max UPG ID = 12

Computations for inbreeding coefficients

Tiny negative value will be replaced with 0 considered as numerical error.

Wrote inbreeding file "renf90.inb" with original id

Inbreeding statistics:

the maximum inbreeding coefficient = 0.2500
average inbreeding for inbred animals = 0.2500 n = 1
for all animals = 0.0278 n = 9

max upg 3

Number of animals with records = 5
Number of parents without records = 4
Total number of animals = 9

Wrote parameter file "renf90.par"
Wrote renumbered data "renf90.dat" 7 records
Wrote field information "renf90.fields" for 4 fields in data

Output data file - renf90.dat

#observation, effect 1, animal number, original animal ID
10 1 4 aa
12 2 4 aa
11 1 2 bb
12 1 5 cc
14 2 5 cc
13 2 3 dd
14 2 1 ee

Output pedigree file - renadd02.ped

Animal, sire, dam, inbreeding code (3-#unknown parents if no-inbreeding), birth year, #known parents, #records, #progeny of sire, # progeny of dam, original animal ID
1 6 11 1333 2002 1 1 0 1 ee
2 8 7 2000 2004 2 1 0 0 bb
7 6 11 1333 2002 1 0 0 1 gg
3 6 12 1333 2004 1 1 0 0 dd
9 11 11 1000 2002 0 0 0 1 ii
4 6 1 2000 2004 2 2 0 0 aa
6 11 11 1000 2002 0 0 4 0 ff
5 8 9 2000 2004 2 2 0 0 cc
8 11 11 1000 2002 0 0 2 0 hh

Output parameter file - renf90.par

# BLUPF90 parameter file created by RENUMF90

DATAFILE
renf90.dat
NUMBER_OF_TRAITS
1

NUMBER_OF_EFFECTS
2
OBSERVATION(S)
   1

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
   2     2 cross
   3     12 cross

RANDOM_RESIDUAL VALUES
   1.0000

RANDOM_GROUP
   2

RANDOM_TYPE
   add_an_upginb

FILE
   renadd02.ped

(CO)VARIANCES
   1.0000

Output tables after renumbering - renf90.tables
Effect group 1 of column 1 with 2 levels, effect # 1
   Value  #   consecutive number
   1  3 1
   2  4 2

Output tables after renumbering - renf90.fields

<table>
<thead>
<tr>
<th>field</th>
<th>variable</th>
<th>origfield</th>
<th>group</th>
<th>column</th>
<th>random</th>
<th>effect</th>
<th>file</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>trait</td>
<td></td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>*</td>
<td>cov</td>
</tr>
<tr>
<td>2</td>
<td>renumbered</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>*</td>
<td>cross</td>
<td>*</td>
</tr>
<tr>
<td>3</td>
<td>renumbered</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>animal</td>
<td>cross</td>
<td>renadd02.ped</td>
</tr>
<tr>
<td>4</td>
<td>passed</td>
<td></td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>*</td>
<td>cov</td>
</tr>
</tbody>
</table>

Output tables after renumbering - renf90.inb

<table>
<thead>
<tr>
<th>field</th>
<th>variable</th>
<th>origfield</th>
<th>group</th>
<th>column</th>
<th>random</th>
<th>effect</th>
<th>file</th>
</tr>
</thead>
<tbody>
<tr>
<td>ee</td>
<td>0.000000</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>bb</td>
<td>0.000000</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>gg</td>
<td>0.000000</td>
<td>7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>dd</td>
<td>0.000000</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ii</td>
<td>0.000000</td>
<td>9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>aa</td>
<td>0.250000</td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ff</td>
<td>0.000000</td>
<td>6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>cc</td>
<td>0.000000</td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hh</td>
<td>0.000000</td>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
When to use which program and computing limits

**BLUP**

**BLUPF90** sets up equations in memory. It can support a few million equations with a simple model but many fewer equations with complicated models (multiple traits, maternal effects, random regression, etc). BLUPF90 uses three solvers, chosen with options. Preconditioned conjugate gradient (PCG) is the default solver and is usually the fastest one. Successive over-relaxation (SOR) require less memory but usually converges slower. Sparse Cholesky (FSPAK) is usually the most accurate method but uses the most memory. The following options are available:

- **OPTION conv_crit 1e-12**
  Sets convergence criteria (default 1e-10).

- **OPTION maxrounds 10000**
  Sets maximum number of rounds (default 5000).

- **OPTION solv_method FSPAK**
  Selection of solving method: FSPAK, SOR, or PCG (default PCG).

- **OPTION r_factor 1.6**
  Sets relaxation factor for SOR (default 1.4). This factor helps speeding up convergence if the value is optimal; non-optimal values lead to poor convergence. It should be within [0,2].

- **OPTION store**
  Stores solutions and standard errors. If this option is used, the solving method will turn to FSPAK.

- **OPTION blksize 3**
  Sets block size for preconditioner (default 1) to accelerate convergence (usually 2 to 5 times faster). For a multiple-trait model, use the number of traits.

- **OPTION use_yams**
  Runs the program with YAMS (modified FSPAK). The computing time can be dramatically improved compared to when solv_method is FSPAK.

- **OPTION hetres_int 5 10**
  The position (5) to identify the interval in the data file and the number of intervals (10) for heterogeneous residual variances as used in GIBBS3F90.

- **OPTION fixed_var file**
  Combined with hetres_int, heterogeneous residual variances are read from file. The file has to contain residual (co)variances for each interval class.

- **OPTION snp_p_value**
  Computes the elements of the inverse of the Mixed Model Equations that are needed for exact GWAS with p-values using postGSf90. This requires quite a lot of memory and time.

**BLUP90IOD2** uses an iteration on data algorithm. It can handle hundreds of millions of equations with complicated models in a reasonable time. However, it is only available based on a research agreement with UGA. The following options are available:
OPTION conv_crit \texttt{1e-12}
Sets convergence criteria (default \texttt{1e-12}).

OPTION maxrounds \texttt{10000}
Sets maximum number of rounds (default \texttt{5000}).

OPTION blksize \texttt{3}
Sets block size for preconditioner (default \texttt{1}). Usually \texttt{blksize} number will be the same as the number of traits.

OPTION init_eq \texttt{10}
Sets the number of effects to be solved directly (default \texttt{0}).

OPTION solv_method \texttt{FSPAK}
Solving method for initial equations (default \texttt{DIRECT}).

OPTION tol \texttt{1d-12}
Tolerance to get a positive definite matrix (default \texttt{1d-12}).

OPTION residual
y-hat and residuals will be included in “\texttt{yhat_residual}”.

OPTION avgeps \texttt{50}
Using the last \texttt{50} average eps for convergence.

OPTION cont \texttt{1}
Restarts the program from the previous solutions.

OPTION missing \texttt{-1}
Sets the missing value (default \texttt{0}).

OPTION restart \texttt{100}
Sets the number of iteration to recompute residuals (default \texttt{100}).

OPTION prior_solutions
Using the previous solution file to start the iteration. Additional software is required to use this option.

OPTION random_upg \texttt{1 2}
Sets the UPG random. “\texttt{1}” is the computational algorithm used; only algorithm \texttt{1} is implemented. “\texttt{2}” is the weight (\(\gamma\)) for the group effects, the weight will be inverted (e.g., \(1/2=0.5\)).

OPTION SNP_file \texttt{snp}
Specifies the SNP file name \texttt{snp} to use genotype data.

OPTION origID
Stores solutions with the original ID. The output is \texttt{trait effect level original_id solution}, and is stored in \texttt{solutions.original}. 
Variance components estimation

There is not a single best choice for variance component estimation. The programs below offer choices for simple and complicated models. For advice on what works best under your circumstances, check this paper “Reliable computing in estimation of variance components”.

REMLF90 uses expectation maximization (EM) REML. It is the most reliable algorithm for most problems but can take hundreds of rounds of iterations. REMLF90 was found to have problems converging with random regression models. In this case, using starting variances that are too large than too small usually helps. Also, EM does not calculate standard errors for the estimates. The following options are available:

- **OPTION conv_crit 1d-12**
  Convergence criterion (default 1d-12).
- **OPTION maxrounds 10000**
  Maximum rounds (default 5000).
- **OPTION sol se**
  Stores solutions and standard errors (se).
- **OPTION residual**
  y-hat and residuals will be included in “yhat_residual”.
- **OPTION missing -999**
  Specifies missing observations (default 0). This is only for data, not pedigree (always 0 for missing pedigrees). There is no missing covariable, so 0 is treated as a level.
- **OPTION constant_var 5 1 2**
  5: effect number, 1: first trait number, 2: second trait number implying the covariance between traits 1 and 2 for effect 5 is fixed.
- **OPTION SNP_file snp**
  Specifies the SNP file name snp to use genotype data.
- **OPTION use_yams**
  Run the program with YAMS (modified FSPAK). The computing time can be dramatically improved.

AIREMLF90 uses Average Information (AI) REML. It usually converges much faster but sometimes does not converge. Very slow convergence usually indicates that the model is over parameterized, and there is insufficient information to estimate some variances. AI REML calculates standard errors for the estimates. The following options are available:

- **OPTION conv_crit 1d-12**
  Convergence criterion (default 1d-12).
- **OPTION maxrounds 500**
  Maximum rounds (default 5000). When it is zero, the program calculates BLUP without running REML.
OPTION EM-REML 10
Runs EM-REML for the first 10 rounds to get initial variances within the parameter space (default 0).

OPTION tol 1d-18
Tolerance (or precision) for positive definite matrix and G-inverse subroutines (default 1d-14).

OPTION sol se
Stores solutions and standard errors (se).

OPTION missing -1
Sets the missing observation (default 0).

OPTION constant_var 5 1 2
5: effect number, 1: first trait number, 2: second trait number implying the covariance between traits 1 and 2 for effect 5 is fixed.

OPTION use_yams
Runs the program with YAMS (modified FSPAK). The computing time can be dramatically improved.

OPTION fact_once memory
Saves the Cholesky factor of LHS in memory. It greatly improves the computing time instead of memory consumption.

OPTION fact_once file
Saves Cholesky factor of LHS in a temporary file. It improves the computing time without extra memory.

OPTION approx_loglike
Skips the exact computation of log-likelihood. It would improve the computing time.

Heterogeneous residual variances for a single trait
OPTION hetres_pos 10 11
Specifies the positions of covariables.

OPTION hetres_pol 4.0 0.1 0.1
Initial values of coefficients for heterogeneous residual variances. Use ln(a0, a1, a2, ...) to make these values. When the number of positions = the number of polynomials, the regressions do not include the intercept (e.g., linear spline).

Heterogeneous residual variances for multiple traits (the convergence will be very slow)
OPTION hetres_pos 10 10 11 11
Specifies positions of covariables (trait first).

OPTION hetres_pol 4.0 4.0 0.1 0.1 0.01 0.01
Initial values of coefficients for heterogeneous residual variances using ln(a0, a1, a2, ...) to make these values (trait first). “4.0 4.0” are the intercept for first and second traits. “0.1 0.1” could be linear and “0.01 0.01” could be quadratic. To transform back to the original scale, use exp(a0+a1*X1+a2*X2).

OPTION SNP_file snp
Specifies the SNP file name snp to use genotype data.

Standard deviations for (co)variance functions including heritability
OPTION se_covar_function label function
Calculates SD for (co)variance functions by repeated sampling of parameter estimates from their
asymptotic multivariate normal distribution, following idea presented by Meyer and Houle 2013. For details, see documentation at http://nce.ads.uga.edu/wiki/doku.php?id=readme aireml.

GIBBSx90 programs implement Bayesian methods. These methods potentially have better statistical properties. Also they are more stable and use less memory for complicated models. After running any of the Gibbs sampling programs, samples can be analyzed (posterior means, SD, and convergence parameters) with the POSTGIBBSF90 program. In practical cases, results from Gibbs samplers and REML are similar. Choose one or the other based on computing feasibility. If there are large differences beyond sampling errors, this indicates problems usually with the Gibbs sampler. Try longer chains or different priors.

Gibbs samplers may be slow to achieve convergence if initial values are far away from those at convergence, e.g., 100 times too low or too high. Before using more complicated models, Karin Meyer advocates using a series of simpler models.

GIBBS1F90 can run models with over 20 traits. However, if models are different per trait, the lines due to effects need to be modified. Also, with too many differences in models among traits, the program becomes increasingly slower.

GIBBS2F90 adds joint sampling of correlated effects. This results in faster mixing with random regression and maternal models. Memory requirements and CPU time per round are somewhat higher than in gibbs1f90.

Interactive inputs:

number of samples and length of burn-in?
In the first run, if you have no idea about the number of samples and burn-in, just type your guess (10000 or whatever) for samples and (0) for burn-in. You may need 2 or 3 runs to figure out the convergence.

Give n to store every n-th sample?
Gibbs samples are highly correlated, so you do not have to keep all samples (every 10th, 20th, 50th, ...).

The following options are available for GIBBSxF90:

OPTION fixed_var all 1 2 3
Stores all solutions and posterior means and SD for effects 1, 2, and 3 are stored in "all_solutions" and in "final_solutions" every round using fixed variances. Without numbers, all solutions for all effects are stored.

OPTION fixed_var mean 1 2 3
Posterior means and SD for effects 1, 2, and 3 in "final_solutions" using fixed (known) variances.

OPTION solution all 1 2 3
Stores all solutions and posterior means and SD for effects 1, 2, and 3 in "all_solutions" and in "final_solutions" every round. Without numbers, all solutions for all effects are stored.
Caution: this option will create a huge output solution file when you run many rounds and/or use a large model.

**OPTION solution mean 1 2 3**
Posterior means and SD for effects 1, 2, and 3 are stored in "final_solutions".

**OPTION cont 10000**
10000 is the number of samples run previously when restarting the program from the last run.

**OPTION prior 5 2 -1 5**
The (co)variance priors are specified in the parameter file. Degree of belief for all random effects should be specified using the following structure:

OPTION prior eff1 db1 eff2 db2 ... effn dbn -1 dbres; where effx corresponds to the effect number and dbx to the degree of belief for this random effect, -1 corresponds to the degree of belief of the residual variance. In this example, 2 is the degree of belief for the 5th effect, and 5 is the degree of belief for the residual.

**OPTION seed 123 321**
Two seeds for a random number generator can be specified.

**OPTION SNP_file snp**
Specifies the SNP file name snp to use genotype data.

**GIBBS3F90** adds estimation of heterogeneous residual covariances in classes. The computing costs usually increase with the number of classes.

**OPTION hetres_int 5 10**
The position (5) to identify the interval in the data file and the number of intervals (10) for heterogeneous residual variances.

Other options are the same as for **GIBBS1F90** and **GIBBS2F90**. For **fixed_var all** or **fixed_var mean**, heterogeneous residual variances are read from a file ‘hetres’. This file name cannot be changed.

**THRGIBBS1F90** is a Gibbs sampling program to analyze categorical and continuous traits simultaneously; categorical traits can be censored. The following options are available:

**OPTION cat 0 0 2 5**
“0” indicates that the first and second traits are linear. “2” and “5” indicate that the third and fourth traits are categorical with 2 (binary) and 5 categories.

**OPTION thresholds 0.0 1.0 2.0**
Set the fixed thresholds. No need to set 0 for binary traits.

**OPTION residual 1**
Set the residual variance = 1.

**OPTION save_halfway_samples 5000**
The program saves every “5000” samples to restart or recover the job right after the last saved samples. It is useful when the program accidentally stopped.
**OPTION censored 1 0**

Negative values of the last category in the data set indicate censored records. “1 0” determines that the first categorical trait is censored and the second categorical trait is uncensored.

Using the following options for ordered categorical data with right censored records:

**OPTION cat 0 0 2 5**

**OPTION censored 1 0**

The data file may look like:

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>1.71</td>
<td>11.1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2.22</td>
<td>15.2</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>3.29</td>
<td>16.4</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>1.95</td>
<td>14.7</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>2.25</td>
<td>20.8</td>
<td>-2</td>
<td>4</td>
</tr>
<tr>
<td>3.64</td>
<td>19.2</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>1.99</td>
<td>13.3</td>
<td>-1</td>
<td>2</td>
</tr>
</tbody>
</table>

Columns 1 and 2 are observations for linear traits and columns 3 and 4 are traits for 2 categories (binary) with censored records (negative values) and 5 categories.

Other options are the same as for **GIBBS1F90** and **GIBBS2F90**.

**THRGIBBS3F90** works as THRGIBBS1f90 but with the estimation of heterogeneous residual covariances in classes as described for GIBBS3F90.

**POSTGIBBSF90** is a program to calculate posterior means and SD and diagnose the convergence of the Gibbs chain. The program reads “gibbs_samples” and “fort.99” files from Gibbs sampling programs.

Read 1000 samples from round 10 to 10000

**Burn-in?**

1000 # in the first run, type 0 for burn-in to include all samples.

**Give n to read every n-th sample? (1 means read all samples)**

10 # Type the same number used with a Gibbs sampling program.

# You should not type 1 unless you have typed 1 in the Gibbs sampling program.

# samples after burn-in = 9000

**Input files:**

`gibbs_samples, fort.99, and other files used in a parameter file` from **(THR)GIBBSxF90**

**Output files:**
**postgibbs_samples, postout, postmean, postsd**

**postgibbs_samples**
A text file containing all Gibbs samples from gibbs_samples for other software (EXCEL, SAS, R, ...) to calculate posterior means and SD, and to create graphs.

**postmean**
Posterior means

**postsd**
Posterior standard deviations

**postout**

<table>
<thead>
<tr>
<th>Pos.</th>
<th>eff1</th>
<th>eff2</th>
<th>trt1</th>
<th>trt2</th>
<th>MCE</th>
<th>Mean</th>
<th>HPD Interval (95%)</th>
<th>Effective sample size</th>
<th>Median</th>
<th>Mode</th>
<th>Independent chain size</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4</td>
<td>4</td>
<td>1</td>
<td>1</td>
<td>1.362E-02</td>
<td>0.9889</td>
<td>0.7788 1.215</td>
<td>70.4 0.9844 0.9861</td>
<td></td>
<td></td>
<td>18</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>4</td>
<td>1</td>
<td>2</td>
<td>1.288E-02</td>
<td>1.006</td>
<td>0.777 1.219</td>
<td>84.1 1.006 0.952</td>
<td></td>
<td></td>
<td>18</td>
</tr>
<tr>
<td>3</td>
<td>4</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>1.847E-02</td>
<td>1.66</td>
<td>1.347 1.987</td>
<td>80.3 1.652 1.579</td>
<td></td>
<td></td>
<td>25</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>9.530E-03</td>
<td>24.47</td>
<td>24.07 24.84</td>
<td>425.6 24.47 24.53</td>
<td></td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2</td>
<td>8.253E-03</td>
<td>11.84</td>
<td>11.54 12.18</td>
<td>395.8 11.83 11.82</td>
<td></td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>6</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2</td>
<td>1.233E-02</td>
<td>30.1</td>
<td>29.65 30.58</td>
<td>387.8 30.09 29.97</td>
<td></td>
<td></td>
<td>5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Pos.</th>
<th>eff1</th>
<th>eff2</th>
<th>trt1</th>
<th>trt2</th>
<th>PSD</th>
<th>Mean</th>
<th>PSD Interval (95%)</th>
<th>Geweke diagnostic lag: 1 10 50</th>
<th>Autocorrelations</th>
<th>Independent # batches</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4</td>
<td>4</td>
<td>1</td>
<td>1</td>
<td>0.1144</td>
<td>0.9889</td>
<td>0.7648 1.213</td>
<td>-0.02 0.853 0.188 0.049</td>
<td></td>
<td>50</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>4</td>
<td>1</td>
<td>2</td>
<td>0.1182</td>
<td>1.006</td>
<td>0.7742 1.237</td>
<td>-0.11 0.828 0.111 -0.066</td>
<td></td>
<td>50</td>
</tr>
<tr>
<td>3</td>
<td>4</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>0.1656</td>
<td>1.66</td>
<td>1.335 1.984</td>
<td>0.06 0.828 0.108 -0.021</td>
<td></td>
<td>36</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0.1967</td>
<td>24.47</td>
<td>24.09 24.86</td>
<td>-0.01 0.034 0.029 -0.062</td>
<td></td>
<td>450</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2</td>
<td>0.1643</td>
<td>11.84</td>
<td>11.51 12.16</td>
<td>0.03 0.032 -0.006 -0.016</td>
<td></td>
<td>450</td>
</tr>
<tr>
<td>6</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2</td>
<td>0.2429</td>
<td>30.1</td>
<td>29.62 30.57</td>
<td>-0.02 0.07 -0.014 0.037</td>
<td></td>
<td>180</td>
</tr>
</tbody>
</table>

where

"Pos." position of each parameter in the parameter file.

"eff1" and "eff2" effect number in the parameter file.

"trt1" and "trt2" trait number in the parameter file (0 for residual).

"MCE" Monte Carlo Error.

"Mean" posterior means.

"HPD interval (95%)" 95% Highest Probability Density.
"Effective sample size"
   at least > 10 is recommended; > 30 may be better.
"Median"
   median of Gibbs samples.
"Mode"
   when the distribution of the samples is not normal, "Mean" and "Mode" could be different.
"Independent chain size"
   number of independent cycles of Gibbs samples.
"PSD"
   Posterior Standard Deviation.
"PSD interval (95%)"
   95% Posterior Standard Deviation interval.
"Geweke diagnostic"
   the ratio between the first and second halves of the samples should be < 1.0, but it may not be helpful because it is < 1.0 most of the time.
"Autocorrelations"
   autocorrelations between two lags. High correlation implies samples are not independent.
"Independent # batches"

Hint 1: when eff1, eff2, trt1, trt2 are all -1, the values presented are for thresholds (if THRGIBBSXF90 is used).

Choose a graph for samples (= 1) or histogram (= 2); or exit (= 0)
1 positions
1 2 3 # choose from the position numbers 1 through 6
If the graph is stable (not increasing or decreasing), the convergence is met. All samples before that point should be discarded as burn-in.

print = 1; other graphs = 2; or stop = 0

2

Choose a graph for samples (= 1) or histogram (= 2); or exit (= 0)

2

Type position and # bins

1 20

The distribution should be usually normal (Mean = Mode = Median).

print = 1; other graphs = 2; or stop = 0

0

*** Log Marginal Density for Bayes Factor ***

after 900 burn-in

log(p) = -179448.742766031

This value could be used when calculating Bayes Factor and/or DIC.
Combined programs

**BLUPF90+**
This software combines BLUPF90, REMLF90, and AIREMLF90. It has some new features such as the computation of accuracies of (G)EBV based on PEV, and the ability to save solutions with original ID. The default of this software is to run BLUP, unless variance components estimation options are used. Hint: type `blupf90+ --help` to see all the BLUPF90+ options or `blupf90+ --help-genomic` to see all the genomic options BLUPF90+ can take.

*Specific options*

**OPTION method VCE**
Runs AIREMLF90 for variance component estimation.

**OPTION EM-REML x**
Runs EM-REML (REMLF90) for first `x` rounds to get initial variances within the parameter space (default 0).

**OPTION store_accuracy eff**
Stores reliabilities based on PEV, where `eff` is the number of the animal effect. By default, it uses inbreeding (`F`) in the denominator of the reliability formula: reliability = 1−PEV/(\(\sigma_u^2(1+F)\)). It uses inbreeding based on the relationship matrix that is being used in the mixed model equations.

**OPTION acctype 1.0**
Select 1.0 for dairy cattle (Reliability) or 0.5 for beef cattle (BIF accuracy) (default 1.0).

**OPTION correct_accuracy_by_inbreeding filename**
`filename` is the name of the inbreeding file if other than renf90.inb

**OPTION correct_accuracy_by_inbreeding_direct 0**
This option turns off the inbreeding correction in the reliability formula.

**OPTION origID**
Stores solutions with the original ID. The output is *trait effect level original_id solution*, and is stored in `solutions.original`.

Click [here](#) for more details on BLUPF90+

**GIBBSF90+**
This software combines GIBBS1F90, GIBBS2F90, GIBBS3F90, THRGIBBS1F90, and THRGIBBS3F90. It takes any options from the above Gibbs programs.

Click [here](#) for more details on GIBBSF90+
Genomic programs

PREGSF90
PreGSF90 is an interface program to the genomic module to process the genomic information for the BLUPF90 family of programs. This software performs quality control of genomic data and constructs and inverts the genomic relationship matrix \((G)\) and the pedigree relationship matrix for genotyped animals \((A_{22}).\) When the inverse of the relationship matrix based on the pedigree information \((A)\) in the mixed model equations is replaced by the inverse of the realized relationship matrix \((H),\) which combines pedigree and genomic information, BLUP becomes single-step GBLUP \((ssGBLUP).\) The main difference between \(A^{-1}\) and \(H^{-1}\) is the structure of \(G^{-1} - A_{22}^{-1}\) added for the genotyped animals. Some of the options for PREGSF90 can be also used with BLUPF90, (AI)REMLF90, GIBBS1F90, GIBBS2F90, GIBBS3F90, THRGIBBS1F90, and BLUP90IOD2.

Input files

OPTION SNP_file <file>
This option invokes the genomic routine in the application programs. The SNP file should contain
Field 1 - animal ID with the same format as in pedigree file
Field 2 - genotypes with 0, 1, 2, and 5 (missing) or real values for gene content (or genotype probability) 0.12, ...

Two Fields (animal ID and SNP) need to be separated by at least one space, and Field 2 should have fixed format (i.e., all rows of genotypes should start at the same column number or position).

```
80   211101011002012011101101101111121111210100
8014 2111011511101202111115111121011221210100
516  21100102252021120121102111202212111101
181  21110111112201120550200020101222122111100
```

The renumbered ID file for genotypes named after the genotype file, e.g., file_XrefID, is created by RENUMF90 (using the SNP file), containing the renumbered ID and the original ID, which follows the same order as in the SNP file:

```
1732 80
8474 8014
406 516
9441 181
```

The pedigree file from RENUMF90 looks like

```
1732 11010 10584 1 3 12 1 0 0 80
8474 8691 9908 1 3 12 1 0 0 8014
406 8691 9825 1 3 12 1 0 2 516
9441 8691 8829 1 3 12 1 0 0 181
```

Map file for SNP can be used as optional:

OPTION map_file <file>: reads SNP map information from the file. The file should have a header with the following column names:

```
SNP_ID #identification of the SNP (alphanumeric)
```
CHR  #chromosome number (numeric), starting from 1
POS  #position bp (numeric)
Extra columns are possible (optional).
The first SNP in the Map file corresponds to the first SNP in the genotype file, and so on.
Example:

<table>
<thead>
<tr>
<th>SNP_ID</th>
<th>CHR</th>
<th>POS</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1201</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>8004</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>12006</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>16008</td>
</tr>
</tbody>
</table>

The map file is useful to check for Mendelian conflicts and HWE (with also OPTION sex_chr) and for POSTGSF90 (ssGWAS).

With other options, the program can read $G$ or its inverse, $A_{22}$ or its inverse, etc.

**Output files**

By default, PREGSf90 runs quality control and creates GimA22i in binary format for use by other application programs, specifying OPTION readGimA22i. With OPTION saveAscii, this file can be stored as ASCII format: $i, j, G^{-1} - A_{22}^{-1}$.

“freqdata.count” contains allele frequencies in the original genotype file with the format: SNP number (related to the genotype file) and allele frequency as mentioned above.

“freqdata.count.after.clean” contains allele frequencies as used in calculations with the format: SNP number (related to the genotype file), allele frequency, and exclusion code.

Exclusion codes:
1: Call Rate
2: MAF
3: Monomorphic
4: Excluded by request
5: Mendelian error
6: HWE
7: High Correlation with other(s) SNP

“Gen_call_rate” contains a list of animals excluded with call rate below the threshold.
“Gen_conflicts” contains a report of animals with Mendelian conflicts with their parents.

The program can store files such as $G$ or its inverse, $A_{22}$ or its inverse, or other reports from QC as specified by their respective OPTIONS.

**Options for creating the genomic relationship Matrix ($G$)**

The genomic relationship matrix, $G$, can be created in different ways.

**OPTION whichG x**

Specifies how $G$ is created.

The variable $x$ can be
1: \[ G = \frac{ZZ'}{k} \]; VanRaden, 2008 (default)

2: \[ G = \frac{ZDZ'}{n} \]; Amin et al., 2007; Leuttenger et al., 2003; where \[ D = \frac{1}{2p(1-p)} \]

3: As 2 with modification UAR from Yang et al., 2010

**OPTION whichfreq x**

Specifies which frequency is used to create \( G \).

The variable \( x \) can be

- 0: read from file “freqdata” or from the other file using **OPTION FreqFile**
- 1: 0.5
- 2: current calculated from genotypes (default)

**OPTION FreqFile <file>**

Reads allele frequencies from a file. For example, based on allele frequencies calculated by estfreq.f90 (VanRaden, 2009) with format:

Field 1 – SNP number (sequential marker number)
Field 2 – allele frequency as a real value from 0 to 1

Example:

<table>
<thead>
<tr>
<th>SNP</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.525333</td>
</tr>
<tr>
<td>2</td>
<td>0.293667</td>
</tr>
<tr>
<td>3</td>
<td>0.448333</td>
</tr>
<tr>
<td>4</td>
<td>0.510667</td>
</tr>
</tbody>
</table>

where SNP corresponds to the index of SNP based on the same order as in the genotype file.

If **whichfreq** is set to 0, the default file name is “freqdata”.

**OPTION whichScale x**

Specifies how \( G \) is scaled.

The variable \( x \) can be

- 1: \[ 2 \sum \{p(1-p)\} \]; VanRaden, 2008 (default)
- 2: \[ \frac{\text{tr}(ZZ')}{n} \]; Legarra, 2009, Hayes, 2009

3: correction; Gianola et al., 2009

**OPTION weightedG <file>**

Reads weights from a file to create weighted genomic relationships.

With weights, \( Z^* = Z \sqrt{D} \Rightarrow G = Z^*Z^*\' = ZDZ\'). Format:

Field 1 – weight

Example:

<table>
<thead>
<tr>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.7837836E-01</td>
</tr>
<tr>
<td>0.4900770E-01</td>
</tr>
<tr>
<td>0.7538282</td>
</tr>
<tr>
<td>1.0</td>
</tr>
</tbody>
</table>
Each weight corresponds to each SNP marker defined in the map file. Weights can be extracted from the output of POSTGSF90.

**OPTION maxsnp x**
Sets the maximum length of string to read marker data from a file. It is only necessary if greater than default (400,000).

**Quality Control (QC) for G**
By default the following QC can be run:
- MAF
- Call rate (SNPs and animals)
- Monomorphic
- Parent-progeny conflicts (SNPs and animals)

Parameters can be modified with the following options:
**OPTION minfreq x**
Ignores all SNP with MAF < x (default value = 0.05).

**OPTION callrate x**
Ignores SNP with call rates < x (number of calls / number of individuals with genotypes). The default value is 0.90.

**OPTION callrateAnim x**
Ignores genotypes with call rates < x (number of calls / number of SNPs). Default value is 0.90.

**OPTION monomorphic x**
Ignores monomorphic SNPs. Optional parameter x can be used to enable (1) or disable (0) the check. The default value is 1.

**OPTION hwe x**
Checks departure of heterozygous from Hardy-Weinberg equilibrium. By default, this QC is not run. The optional parameter x can be the maximum difference between observed and expected frequency (default value = 0.15) as used in Wiggans et al. (2009) in JDS.

**OPTION high_correlation x y**
Checks for highly correlated SNP. By default, this QC is not run. The optional parameter x can be the maximum difference in allele frequency to check a pair of locus. If no value is set, 0.025 is used. Decrease this value to speed up the calculation. A pair of loci is considered highly correlated if all genotypes are the same (0-0, 1-1, 2-2) or the opposite (0-2, 1-1, 2-0) (Wiggans et al., 2009. JDS). The optional parameter y can be used to set a threshold to check the number of identical samples out of the number of genotypes (default values: x=0.025, y=0.995).

**OPTION verify_parentage x**
Verifies parent-progeny Mendelian conflicts and writes a report into the “Gen_conflicts” file. The optional parameter x can be
- 0: no action
- 1: only detects
- 2: detects and searches for an alternate parent; no change to any file. This option is implemented in the
SeekParentF90 program.
3: detects and eliminates progenies with conflicts (default).

**OPTION exclusion_threshold** x
Sets the number of parent-progeny exclusions as percentage. All SNP are used to determine wrong relationships (default value = 2).

**OPTION exclusion_threshold_snp** x
Sets the number of parent-progeny exclusions for each locus as percentage. A pair of genotyped animals is evaluated to exclude SNP from the analysis (default value = 10).

**OPTION number_parent_progeny_evaluations** x
Sets the number of minimum pair of parent-progeny evaluations to exclude SNP due to parent-progeny exclusion (default value = 100).

**OPTION outparent_progeny** x
Creates a full log file “Gen_conflicts_all” with all pairs of parent-progeny tested for Mendelian conflicts.

**OPTION excludeCHR n1 n2 n3 ...**
Excludes all SNP from chromosomes n1, n2, n3, ... A map file must be provided (see **OPTION map_file**).

**OPTION sex_chr n**
Chromosomes with a number greater or equal to n are not considered as autosomes. If this option is used, sex chromosomes will not be used for checking parent-progeny, Mendelian conflicts, and HWE. A map file must be provided (see **OPTION map_file**).

**OPTION threshold_duplicate_samples** x
Sets the threshold to issue warning for possible duplicate samples if G(i,j) / sqrt(G(i,i) * G(j,j)) > x (default value = 0.9).

**OPTION threshold_diagonal_g** x
Checks for extremely large diagonals in the genomic relationship matrix. If optional x is present, the threshold will be set (default value = 1.6).

**OPTION plotpca**
Plots the first two principal components to look for stratification in the population.

**OPTION extra_info_pca <file> col**
Reads the column col to plot with different colors for different classes from the file. The file should contain at least one variable with different classes for each genotyped individual, and the order should match the order of the genotype file. Variables could be alphanumeric and separated by one or more spaces.

**OPTION calculate_LD**
Calculates LD as the squared correlation of allele counts for two SNP. Results are stored in “ld_results”, columns: snp_i, chr_i, pos_i, freq_i, snp_j, chr_j, pos_j, freq_j, dist_ij, Rsq_ij

**OPTION LD_by_chr**
Calculates LD within chromosome.

**OPTION LD_by_pos** x
Calculates LD within chromosome and windows of SNP based on position. Optional parameter x defines with windows size in Bp, default value 200000

**OPTION filter_by_LD**
Filters SNP with Rsq > threshold. Optional parameter x define the threshold. default value 0.8

**OPTION thr_output_LD x**
Threshold to print out Rsq between pair of SNP Optional parameter x define the threshold. default value 0.1

**OPTION saveCleanSNPs ***
Saves clean genotype data with excluded SNP and animals based on the OPTIONS specified.
*_clean files are created:
*  * gt_clean
  *  * gt_clean_XrefID

*_removed files are created:
*  * gt_SNPs_removed
  *  * gt_Animals_removed

where “gt” is the genotype file.

**OPTION no_quality_control**
Turns off all quality control. It speeds up computations when the QC was previously performed.

**OPTION outcallrate**
Prints all call rate information for SNP and individuals. The files “callrate” for SNP and “callrate_a” for individuals are created.

**Quality Control for Off-diagonal of \( A_{22} \) and \( G \)**

**OPTION thrWarnCorAG x**
Sets the threshold to issue warning if correlation between \( A_{22} \) and \( G < x \) (default value = 0.5).

**OPTION thrStopCorAG x**
Sets the threshold to stop the analysis if correlation between \( A_{22} \) and \( G < x \) (default value = 0.3).

**OPTION thrCorAG x**
Sets the threshold to calculate correlation between \( A_{22} \) and \( G \) for only \( A_{22} \geq x \) (default value = 0.02).

**Options for \( H \)**
The options include different weights to create \( G^{-1} - A_{22}^{-1} \) as
\[
\tau (\alpha G + \beta A_{22} + \gamma I + \delta 11')^{-1} - \omega A_{22}^{-1}
\]
where the parameters are to scale the genomic information to be compatible with the pedigree information, to make matrices invertible in the presence of clones, and to control bias. The default values are: \( \tau (\tau) = 1 \), alpha (\( \alpha \)) = 0.95, beta (\( \beta \)) = 0.05, gamma (\( \gamma \)) = 0, delta (\( \delta \)) = 0, and omega (\( \omega \)) = 1. Options to change these defaults are specified with:

**OPTION TauOmega tau omega**
**OPTION AlphaBeta alpha beta**
**OPTION GammaDelta gamma delta**

Hint: **OPTION TauOmega** was needed when inbreeding was not considered for \( A^{-1} \). Because inbreeding is now considered for \( A^{-1} \), we recommend not using this option anymore.
OPTION tunedG x
Scales G based on A_{22}. The variable x can be:
0: no scaling
1: mean(diag(G))=1 and mean(offdiag(G))=0
2: mean(diag(G))=mean(diag(A_{22})) and mean(offdiag(G))=mean(offdiag(A_{22})) (default)
3: mean(G)=mean(A_{22})
4: rescale G using the first adjustment as in Powell et al. (2010) or Vitezica et al. (2011).

General control of PREGSF90
OPTION num_threads_pregs n
Specifies number of threads to be used with MKL-OpenMP for creation and inversion of matrices.
OPTION num_theads_iod n
Specifies number of threads to be used with MKL-OpenMP in BLUP90IOD for matrix-vector multiplications in the PCG algorithm.
OPTION graphics s
Allows to generate plots with GNUPLOT. If optional parameter s is present, set the time in seconds to show the plot. Avoid using in batch programs!!!
OPTION msg x
Sets the level of verbose; 0 minimal; 1 prints lots of diagnostics on the screen.

Save and Read options:
OPTION saveAscii
Saves intermediate matrices (GimA22i, G, Gi, etc.) into files as ASCII (default = binary).
OPTION saveHinv
Saves H^{-1} in “Hinv.txt” (format: i, j, val; where i, j, are the index level for the additive genetic effect).
OPTION saveAinv
Saves A^{-1} in “Ainv.txt” (format: i, j, val; where i, j, are the index level for the additive genetic effect).

The following options use the information of the original ID (alphanumeric) stored in the 10th column of the “renaddxx.ped” file created by RENUMF90.
OPTION saveHinvOrig
Saves H^{-1} with original IDs
OPTION saveAinvOrig
Saves A^{-1} with original IDs
OPTION saveDiagGOrig
Saves diagonal of G in “DiagGOrig.txt” (format: id, val; where id is the original ID).
OPTION saveGOrig
Saves G in “G_Orig.txt” (format: id_i, id_j, val; where id_i and id_j are the original IDs).
OPTION saveA22Orig
Saves A_{22} in “A22_Orig.txt” (format: id_i, id_j, val; where id_i and id_j are the original IDs).
OPTION readOrigId
Reads information from “renaddxx.ped” file, original ID, and possibly year of birth for its use in parent-progeny conflict. Only needed if none of the previous “save*Orig” is present.

**OPTION saveGimA22iRen**
Saves GimA22i matrix in GimA22i_Ren.txt (format: id_i, id_j, val; where id_i and id_j are the IDs as read from the data/pedigree file).

**OPTION savePLINK**
Saves genotypes in PLINK format files: toPLINK.ped and toPLINK.map.

**OPTION no_full_binary**
Saves the elements of half-matrix instead of the full matrix. It is useful to keep the compatibility with the older versions of preGSf90. The newer versions save the matrix in a more efficient way, where reading the information from the binary file is not trivial (i.e., not as i, j, val anymore).

The following options are used to save and read intermediate files:

**OPTION readGimA22i <file>**
Reads $G^{-1} - A_{22}^{-\frac{1}{2}}$ from a file. This option can be used in the application programs (BLUPF90, REMLF90, etc.) to use the information already stored in the GimA22i file (default filename). In general, methods used to create and invert matrices in such programs do not use an optimized version. For a large number of genotyped animals, run first PREGSf90 and read stored matrices in the application programs. The optional file can be used to specify a different file name (other than GimA22i) or a path. For example,

**OPTION readGimA22i ../../pregsrun/GimA22i**

Other intermediate matrices files can be stored for inspection or for use in BLUPF90 programs as user_file type of random effect. See tricks and REMLF90 for details.

Individual output options:

**OPTION saveA22**
Saves $A_{22}$ in “A22”.

**OPTION saveA22Inverse**
Saves $A_{22}^{-\frac{1}{2}}$ in “A22i”.

**OPTION saveG all**
If optional all is present, all intermediate matrices for $G$ will be saved in separate files. If omitting all, only the final $G$ will be saved in “G”.

**OPTION saveGInverse**
Saves $G^{-1}$ in “Gi”.

**OPTION saveGmA22**
Saves $G - A_{22}$ in “GmA22”. This option is obsolete.

**OPTION readG <file>**
Reads $G$ from “G” by default, or from a user-supplied file.

**OPTION readGInverse <file>**
Reads $G^{-1}$ from “Gi” by default, or from a user-supplied file. See the caution below.

**OPTION readA22 <file>**
Reads $A_{22}$ from “A22” by default, or from a user-supplied file.
OPTION readA22Inverse <file>
Reads $A_{22}^{-1}$ from “A22” by default, or from a user-supplied file. See the caution below.

OPTION readGmA22 <file>
Reads $G - A_{22}$ from “GmA22” by default, or from user-supplied file. This option is obsolete.

Caution:
With the options readGInverse and readA22Inverse, the program applies $\tau$ to the loaded $G^{-1}$ and $\omega$ to the loaded $A_{22}^{-1}$ regardless of whether the matrices have been already scaled with $\tau$ or $\omega$. In other words, the loaded matrix could be scaled twice if the user used $\tau$ or $\omega$ both in saving and reading the matrix. Be careful to use the scaling factors combined with the input/output options.

Hint: OPTION TauOmega was needed when inbreeding was not considered for $A^{-1}$. Because inbreeding is now considered for $A^{-1}$, we recommend not using this option anymore.

POSTGSF90
Basic options
The program calculates SNP effects using the ssGBLUP framework (Wang et al., 2012). The program needs OPTION map_file to assign SNP to their location for Manhattan plots, so chromosomes are visualized in different colors. The following options for POSTGSF90 (ssGWAS) are available:

OPTION Manhattan_plot
Plots the Manhattan plot (SNP effects) for each trait and correlated effects using GNUPLT.

OPTION Manhattan_plot_R
Plots the Manhattan plot (SNP effects) for each trait and correlated effects using R. TIF images are created: manplot_Sft1e2.tif (note: t1e2 corresponds to trait 1, effect 2).

OPTION Manhattan_plot_R_format format
Controls the format type to create images in R. The format values accepted are: pdf (default), png, or tif.

OPTION plotsnp n
Controls the values of SNP effects to use in Manhattan plots
1: plots regular SNP effects: abs(val)
2: plots standardized SNP effects: abs(val/sd) (default)

OPTION SNP_moving_average n
Solutions for SNP effects will be by moving average of n adjacent SNPs.

OPTION windows_variance n
Calculates the variance explained by n adjacent SNPs.

Hint: When this option is used, the sum of variance explained by n adjacent SNPs (column 8 of snp_sol or column 3 of chrsnpvar) is not 100%. This is because moving variance is used. If windows size is 20, the proportion of variance assigned to SNP 1 is calculated from SNP 1 to 20, for SNP 2 it goes from 2 to 21, for SNP 3 it goes from 3 to 22, and so forth. A file called windows_variance has variance that sums to 100% in column 9.

OPTION windows_variance_mbp n
Calculates the variance explained by n Mb window of adjacent SNPs.
OPTION windows_variance_type n
Sets windows type for variances calculations
1: moving windows
2: exclusive windows

OPTION which_weight x
Generates a weight variable to construct a weighted genomic relationship matrix \( G = ZDZ' \)
1: \( w = y^2 \cdot (2(p(1-p))) \)
2: \( w = y^2 \)
3: experimental with the degree of brief
4: \( w = C^{\text{abs}(y_i)/\text{sqrt}(\text{var}(y))}-2 \) from VanRaden et al. (2009)
nonlinearA: same as 4
where \( y \) is the SNP solution, with scaled weight = \( w \cdot n\text{Snp}/\text{sum}(w) \); and \( C \) is 1.125 by default (enable to change it using the second argument of the option line (OPTION which_weight nonlinearA value), e.g.,
OPTION which_weight nonlinearA 1.2

OPTION solutions_postGS x
Sets the file name for the solutions file (default = solutions).

OPTION postgs_trt_eff x1 x2
Computes postGS solutions (SNP solutions, variance explained, etc.) for only trait: x1 and effect: x2

OPTION snp_p_value
Computes p-values for GWAS from elements of the inverse of the Mixed Model Equations previously obtained from blupf90. This requires quite a lot of memory and time. See Aguilar et al. (2019) for more details.

OPTION snp_var
Creates a file with prediction error covariance (PEC) for SNP to be used in PREDF90 to compute reliability for indirect predictions. This option works when OPTION snp_p_value is used in BLUPF90+.

Output files for POSTGSF90:
“snp_sol” contains solutions of SNP and weights
1: trait
2: effect
3: SNP
4: Chromosome
5: Position
6: SNP solution
7: weight (can be used as the weight to calculate the weighted G matrix)
8: variance explained by n adjacent SNP (if OPTION windows_variance is used)
9: variance of the SNP solution (used to compute the p-value if OPTION snp_p_value is used)

“chrsnp” contains data to create the plot by GNUPLOT
1: trait
2: effect
values of SNP effects to use in Manhattan plots, i.e., \((\text{abs}(\text{SNP}_i)/\text{var(SNP)})\)

**SNP**

**Chromosome**

**Position**

“chrsnpvar” contains data to create plot by GNUPLOT

**trait**

**effect**

**variance explained by n adjacent SNP**

**SNP**

**Chromosome**

**Position**

“windows_segment” contains information of windows segments used to get variance explained

**label**

**window size (number of SNP)**

**Start SNP number for the window**

**End SNP number for the window**

**identification of window: (ChrNumber)’_(startPositionMBP)**

**Start (ChrNumber)’_(startPositionMBP)**

**End (ChrNumber)’_(StartPositionMBP)**

“windows_variance” contains variance explained for the biggest non-overlapping windows segments

**trait**

**effect**

**Start SNP number or SNP name for the window**

**End SNP number or SNP name for the window**

**window size (number of SNP)**

**Start (ChrNumber)’_(Position) for the window**

**End (ChrNumber)’_(Position) for the window**

**identification of window: (ChrNumber)’_(startPositionMBP)**

**variance explained by n adjacent SNP**

“snp_pred” contains allele frequencies + SNP effects

**Graphic control files:**

Several files are created to generate graphics using either GNUPLOT or R.

File names rules

“Sft1e2.R”: The first letter indicates “S” for solutions of SNP, “V” for variance explained, and “P” for p-values.

“t1e2” indicates that the file is for the trait 1 and the effect 2.
PREDF90
Predicts direct genomic value (DGV) for young animals based on only genotypes i.e. \( \hat{u} = Z \hat{a} \), where \( \hat{u} \) is DGV and \( \hat{a} \) is the SNP effects. The prediction is based on SNP effects obtained from POSTGSF90. For young animals that were not included in the previous analysis, DGV can be calculated using the “snp_pred” file from POSTGSF90. PREDF90 requires some output files from POSTGSF90 and a genotype file for the animals to be predicted. It does not accept a parameter file but takes command-line options.

PREDF90 does not accept a parameter file but takes command-line options.

--snpfile name
Provides the SNP file for animals to be indirectly predicted. PREDF90 will ask for the SNP file name if this command is not present. The SNP file has the same format as for PREGSF90.

--acc
Computes reliability for indirect predictions. It requires OPTION snp_p_value in BLUPF90+ and OPTION snp_var in POSTGSF90. It reads “snp_var” created by POSTGSF90.

--acc_type
Select 1.0 for dairy cattle (Reliability) or 0.5 for beef cattle (BIF accuracy) (default 1.0).

--use_diagG_acc
Uses inbreeding (F) from G in the denominator of the reliability formula: reliability = 1-PEV/(\( \sigma_u^2(1+F) \)).

--use_mu_hat
Adds the base (\( \mu \)) for DGV so the values are comparable to GEBV. See Legarra et al. (2021) and Lourenco et al. (2018) for more details.

--use_var_mu_hat
Considers the variance of \( \hat{\mu} \) when calculating the reliability of DGV and is automatically turned on if --use_mu_hat and --acc are present.

--help
Shows the main options.

Usage:
predf90 --snpfile new_genotypes.txt --use_mu_hat --acc --use_diagG_acc
With these commands, predf90 will compute indirect predictions for the animals in new_genotypes.txt, including \( \hat{\mu} \) (i.e., DGV = \( \hat{\mu} + Z \hat{a} \)), computing reliabilities adjusted for inbreeding in G.
**Input files:**
This program automatically detects and read the following file.

```
"snp_pred"
- information about the random effect (number of traits + correlated effects)
- gene frequencies
- solutions of SNP effects
```

**SNP_file_for_animals_to_predict**
SNP file for animals to have DGV predicted. This file has the same format as used in PREGSF90 and POSTGSF90.

**Output file:**

```
"SNP_predictions"
- ID, call rate, DGV, reliability (if --acc is present)
```

Constant parameters that cannot be changed by the users:

1. alpha - fraction of G used (default=0.95); affects scale of prediction
2. callrate - to be used later for discarding genotypes with poor quality (default=0.7)

**PREDICTF90**
This is program is used to do cross-validations. It reads a blupf90 parameter file, a solutions file and a data file. It needs OPTION include_effects followed by a series of effects. It computes:

- $y_{\text{star}} = y - \text{corrected by the other (not included) effects}$
- $y_{\hat{}} = \text{sum of estimates of the included effects}$
- residual = $y - \text{included effects (not a true residual)}$

Example: $y = \text{herd} + \text{age} + \text{animal} + e$

If the parameter file has OPTION include_effects 3.

- $y_{\text{star}} = y - \text{herd}_{\hat{}} - \text{age}_{\hat{}} (y - \text{effects to be adjusted for})$
- $y_{\hat{}} = \text{animal}_{\hat{}} (\text{effect to keep})$

Which makes $\text{cor}(y_{\hat{}},y_{\text{star}}) = \text{cor}(ebv, \text{adjusted } y)$, in this example, which is a measure of accuracy.

It outputs the correlation between $y_{\hat{}}$ and $y_{\text{star}}$, for instance $\text{cor}(y_{\text{star}},y_{\hat{}}) = \text{cor}(u+e, u_{\hat{}})$ and outputs these columns into a file, together with animal id (if there is animal in the model) or record number (if not).

In addition, if animal effect is in the model, it produces a file with ebvs from the solutions file.
Output file: “yhat_residual”
The main file is yhat_residual, which has corrected phenotypes and predicted residuals. The number of columns in this file depend on the number of traits (N).

Column 1: Animal ID (renumbered i.e., same as the 1st column in renaddxx.ped)
Column 2 to N+1: “y_star” explained above
Column N+2 to 2N+1: “y_hat” explained above
Column 2N+2 to 3N+1: “residual” explained above

Demonstration for genomic analysis
Data were simulated by D. Lourenco and the files are available here:
https://github.com/danielall/Data_ssGBLUP

Preparation with RENUMF90
“renum.par” for RENUMF90

```
# Parameter file for renumf90
# Data file = phenotypes.txt
#  1  2  3  4  5
#  animal, sex, phenotype, TBV, generation
# Pedigree file = pedigree.txt
#  1  2  3
#  animal sire dam
# SNP file = genotypes.txt
# SNP map file = gen_map.txt
DATAFILE
phenotypes.txt
TRAITS
3
FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE
0.60
EFFECT
2 cross alpha #sex
EFFECT
1 cross alpha #animal
RANDOM
animal
FILE
pedigree.txt
SNP_FILE
genotypes.txt
(CO)VARIANCES
```
Run RENUMF90
RENUMF90 version 1.157 with zlib
renum.par

Inbreeding statistics:
the maximum inbreeding coefficient = 0.3125
average inbreeding for inbred animals = 0.0621  n = 1292
for all animals = 0.0067  n = 12010

Number of animals with records = 10000
Number of animals with genotypes = 2024
Number of animals with records or genotypes = 10000
Number of animals with genotypes and no records = 0
Number of parents without records or genotypes = 2010
Total number of animals = 12010

Wrote cross reference IDs for SNP file "genotypes.txt_XrefID"

Wrote parameter file "renf90.par"
Wrote renumbered data "renf90.dat" 10000 records
Wrote field information "renf90.fields" for 3 fields in data

"renf90.par" from RENUMF90
# BLUPF90 parameter file created by RENUMF90
DATAFILE
renf90.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2   2 cross
3  12010 cross
RANDOM_RESIDUAL VALUES
0.60000
RANDOM_GROUP
2
RANDOM_TYPE
add_an_upginb
FILE
renadd02.ped
(CO)VARIANCES
0.40000
OPTION SNP_file genotypes.txt
OPTION map_file gen_map.txt
Analysis with BLUPF90

Run BLUPF90

BLUPF90 ver. 1.71

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weights 0
Value of Missing Trait/Observation 0

name of parameter file? renf90.par

*-------------------------------------------------------------*
* Genomic Library: Version 1.308                             *
* Optimized OpenMP Version - 4 threads                       *
* Modified relationship matrix (H) created for effect: 2    *
*-------------------------------------------------------------*

Read 12010 animals from pedigree file: "renadd02.ped"
Number of Genotyped Animals: 2024

round = 55 convergence = 0.1126E-11
round = 56 convergence = 0.5045E-12
56 iterations, convergence criterion= 0.5045E-12
solutions stored in file: "solutions"

Analysis with POSTGSF90

Run POSTGSF90

name of parameter file? renf90.par

postGSf90 ver. 1.77

Solutions read from file: "solutions"
Solutions for SNPs in file: "snp_sol"
Files for predictions by SNP effects in file: "snp_pred"

Indirect Predictions with PREDF90

Run PREDF90

predf90 1.13
Predicts EBVs from genotypes based on results from single-step evaluation

Number of SNP: 4500
Number of traits: 1
number of correlated traits: 1

MU_hat to adjust Za
Trait: 1
Correlated effect: 1
mu_hat: 0.1443

3000 SNP
The genotype file contains 45000 SNP starting from position 14
First 10 genotypes: Id, EBV
UGA42014       0.4649608
UGA42019       0.6343889
UGA42029       -0.1096066
UGA42039       0.9360114
UGA42047       0.6454658
UGA42051       0.5041275
UGA42052       1.7737031E-02
UGA42056       0.9935431
UGA42057       0.2609830

Processed 2024 genotypes
Average calling rate: 1.00

$head -5 SNP_predictions
UGA42014       1.00       0.46496075
UGA42019       1.00       0.63438886
UGA42029       1.00       -0.10960658
UGA42039       1.00       0.93601137
UGA42047       1.00       0.64546579

**Computing adjusted phenotypes with PREDICTF90**

Run PREDICTF90

This program is used to calculate adjusted y, ŷ, and residuals using the same parameter file and “solutions” as BLUPF90.

Output files:
“yhat_residual”
Format: record #, adjusted y, ŷ, residual
“bvs.dat”
The same format as “solutions” including (G)EBV.

# BLUPF90 parameter file created by RENF90 and extended to work with PREDICTF90
DATAFILE renf90.dat
NUMBER_OF_TRAITS
  1
NUMBER_OF_EFFECTS
  2
OBSERVATION(S)
  1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
  2   2 cross
  3   12010 cross
RANDOM_RESIDUAL VALUES
  0.60000
RANDOM_GROUP
  2
RANDOM_TYPE
add_an_upginnb
FILE
renadd02.ped
(CO)VARIANCES
0.40000
OPTION SNP_file genotypes.txt
OPTION map_file gen_map.txt
OPTION include_effects 2  #phenotypes will be adjusted for all effects but effect number 2 (animal)

Run PREDICTF90
name of parameter file?
pred.par

*** include effects to predict Yhat n, effects    1    2

PREDICTF90 ver. 1.6
.
.
.
.
Animal Effect:    2
Y(s), yhat(s), residual(s) in written in "yhat_residual" file
10000 records read
Trait:    1    10000
          mean Y  8.66251402103672E-002  var Y  0.93465837702133
          mean Yhat  8.662514367382973E-002  var Yhat  0.181142370417667
          cov (Y,Yhat)  0.344475853966058  corr (Y,Yhat)  0.837272925060839
wrote bvs for animals in data in file "bvs.dat"

Hints:
1) The effect that goes into OPTION include_effects (e.g., OPTION include_effects 2) is included in the Yhat. In this small example with 1 trait, the format of yhat_residual is: Animal_id, Y, Yhat, residual
Where: Y = Phenotype – 𝜇
       Yhat = EBV (or animal effect)
       Residual = Phenotype - EBV

2) When 2 traits are used in the model, the format of yhat_residual is:
   Animal_id, Y1, Y2, Yhat1, Yhat2, residual1, residual2

3) corr (Y,Yhat) should not be used as a measure of predictivity because it uses adjusted phenotypes and EBVs from the same dataset. Usually, predictivity requires phenotypes adjusted for fixed effects in the complete data (benchmark) and (G)EBVs calculated from the reduced data (without records for validation animals). The regular predictivity measure is: corr[Y_from_PREDICTF90, (G)EBV_reduced]

For this small example with 1 trait, a general Linux bash code is:
$ awk '{print $1,$2}' ebv_complete/yhat_residual | sort +0 -1 > Y
$ awk '{if ($2==2) print $3,$4}' ebv_reduced/solutions | sort +0 -1 > evb.temp
$ awk '{if ($2==2) print $3,$4}' gebv_reduced/solutions | sort +0 -1 > gebv.temp
$join -1 +1 -2 +1 Y validation_animals > file1.temp
$join -1 +1 -2 +1 file1.temp evb.temp > file2.temp
$join -l +1 -2 +1 file2.temp gebv.temp > Y_ebv_gebv

#obs: validation_animals is a file that contains sorted ids for validation animals

An R code to calculate correlations is:
```r
pred <- read.table("Y_ebv_gebv",header=F)
ebv_predictivity <- cor(pred[,2],pred[,3]); ebv_predictivity
gebv_predictivity <- cor(pred[,2],pred[,4]); gebv_predictivity
```

Examples of parameter files

**Sire model without A matrix**

DATAFILE
test.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
2 3 cross
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
2
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1

**Sire model with A matrix**

DATAFILE
test.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3
WEIGHT(S)
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
2 3 cross
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
2
RANDOM_TYPE
add_sire
FILE
sire.ped
(CO)VARIANCES
1

Two-trait sire model
DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3 4
WEIGHT(S)
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
2 2 3 cross
RANDOM_RESIDUAL VALUES
10 1
1 5
RANDOM_GROUP
2
RANDOM_TYPE
add_sire
FILE
sire.ped
(CO)VARIANCES
1 0.1
0.1 1

Animal model
DATAFILE
test.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
5 10 cross
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
2
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1

Multiple trait animal model
# Example 1: two-trait animal model
DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
5 5 10 cross
RANDOM_RESIDUAL VALUES
10 1
1 5
RANDOM_GROUP
2
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1 0.1
0.1 1

# Example 2: different model for each trait
DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
Animal model with UPG

DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
5 5 13 cross
RANDOM_RESIDUAL VALUES
10 1
1 5
RANDOM_GROUP
2
RANDOM_TYPE
add_an_upg
FILE
animal.ped
(CO)VARIANCES
 1 0.1
 0.1 1

Animal model with inbreeding
DATAFILE
test.dat
NUMBER_OF_TRAITS
 2
NUMBER_OF_EFFECTS
 2
OBSERVATION(S)
 3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
 1 1 2 cross
 5 5 13 cross
RANDOM_RESIDUAL VALUES
 10 1
 1 5
RANDOM_GROUP
 2
RANDOM_TYPE
add_an_upginb
FILE
animal.ped
(CO)VARIANCES
 1 0.1
 0.1 1

Repeatability model – single trait
DATAFILE
test.dat
NUMBER_OF_TRAITS
 1
NUMBER_OF_EFFECTS
 3
OBSERVATION(S)
 3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
 1 2 cross
 5 5 cross
 5 5 cross
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
2
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1
RANDOM_GROUP
3
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1

Repeatability model – two traits
DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
3
OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
5 5 5 cross
5 5 5 cross
RANDOM_RESIDUAL VALUES
10 1
1 5
RANDOM_GROUP
2
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1 0.1
0.1 1
RANDOM_GROUP
3
RANDOM_TYPE
diagonal
(CO)VARIANCES
1 0.1
0.1 1

Maternal effect model
DATAFILE
maternal.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
4
OBSERVATION(S)
4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
3 946 cross
1 22473 cross
2 22473 cross
2 22473 cross
RANDOM_RESIDUAL VALUES
1050
RANDOM_GROUP
2 3
RANDOM_TYPE
add_animal
FILE
maternal.ped

(CO)VARIANCES
450 -100
-100 340
RANDOM_GROUP
4
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
370

# For (THR)GIBBSxF90
# Example 1 – declaring the random, diagonal effect separately for effects 4 and 5.
DATAFILE
test.dat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
5
OBSERVATION(S)
3 4

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 0 2 cross
0 2 2 cross
5 5 10 cross
6 0 30 cross
0 7 20 cross

RANDOM_RESIDUAL VALUES
10 1
1 5

RANDOM_GROUP
3

RANDOM_TYPE
add_animal

FILE
animal.ped

(CO)VARIANCES
1 0.1
0.1 1

RANDOM_GROUP
4

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
1 0
0 0

RANDOM_GROUP
5

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
0 0
0 1

# Example 2 – joint declaration for the random, diagonal effects 4 and 5.

DATAFILE
test.dat

NUMBER_OF_TRAITS
2

NUMBER_OF_EFFECTS
5

OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 0 2 cross
0 2 2 cross
5 5 10 cross
6 0 30 cross
0 7 30 cross

RANDOM_RESIDUAL VALUES
10 1
1 5

RANDOM_GROUP
3

RANDOM_TYPE
add_animal

FILE
animal.ped

(CO)VARIANCES
1 0 0 0
0 0 0 0
0 0 0 0
0 0 0 1

# Dominance model

DATAFILE
dom.dat

NUMBER_OF_TRAITS
1

NUMBER_OF_EFFECTS
4

OBSERVATION(S)
3

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 cross
4 1 cov
2 30001 cross
5 10412 cross

RANDOM_RESIDUAL VALUES
100
Random regression model

# Single trait

DATAFILE
data_score
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
10
OBSERVATION(S)
9
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 788 cross
2 32 cross
5 1 cov
6 1 cov
3 15097 cross
5 15097 cov 3
6 15097 cov 3
3 81883 cross
5 81883 cov 3
6 81883 cov 3
RANDOM_RESIDUAL VALUES
100
RANDOM_GROUP
5 6 7
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
100 1 1
# Two traits

DATAFILE
test.dat1
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
9
OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
6 6 1 cov
7 7 1 cov
2 2 5 cross
6 6 5 cov 2 2
7 7 5 cov 2 2
2 2 10 cross
6 6 10 cov 2 2
7 7 10 cov 2 2

RANDOM_RESIDUAL VALUES
10 1
1 5

RANDOM_GROUP
1 5

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
1.0 0.1 0.1 0.1 0.1 0.1
0.1 0.1 0.1 0.1 0.1 0.1
0.1 0.1 0.1 0.1 0.1 0.1
0.1 0.1 0.1 0.1 0.1 0.1
0.1 0.1 0.1 0.1 0.1 0.1
RANDOM_GROUP
7 8 9
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1 0.1 0.1 0.1 0.1 0.1
0.1 1 0.1 0.1 0.1 0.1
0.1 0.1 1 0.1 0.1 0.1
0.1 0.1 0.1 1 0.1 0.1
0.1 0.1 0.1 0.1 1 0.1
0.1 0.1 0.1 0.1 0.1 1

# Example 3
DATAFILE
test.dat2
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
10
OBSERVATION(S)
3 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 1 2 cross
6 6 1 cov
7 7 1 cov
8 8 1 cov
6 6 5 cov 2 2
7 7 5 cov 2 2
8 8 5 cov 2 2
6 6 10 cov 2 2
7 7 10 cov 2 2
8 8 10 cov 2 2
RANDOM_RESIDUAL VALUES
10 1
1 5
RANDOM_GROUP
5 6 7
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1 0.1 0.1 0.1 0.1 0.1
0.1 1 0.1 0.1 0.1 0.1
0.1 0.1 1 0.1 0.1 0.1
0.1 0.1 0.1 1 0.1 0.1
0.1 0.1 0.1 0.1 1 0.1
Random regression model with heterogeneous residual variances
### using airemlf90

# Example 1: with intercept
DATAFILE
test.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
9
OBSERVATION(S)
3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
6 1 cov
7 1 cov
5 5 cross
6 5 cov 5
7 5 cov 5
5 10 cross
6 10 cov 5
7 10 cov 5
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
4 5 6
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1 0.1 0.1

RANDOM_GROUP 7 8 9
RANDOM_TYPE add_animal
FILE animal.ped
(CO)VARIANCES 1 0.1 0.1 0.1 1 0.1 0.1 0.1 0.1 1
OPTION hetres_pos 6 7
OPTION hetres_pol 4.0 1.0 0.1

# Example 2: with no intercept
DATAFILE test.dat
NUMBER_OF_TRAITS 1
NUMBER_OF_EFFECTS 7
OBSERVATION(S) 3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
6 1 cov
7 1 cov
6 5 cov 5
7 5 cov 5
6 10 cov 5
7 10 cov 5
RANDOM_RESIDUAL VALUES 10
RANDOM_GROUP 4 5
RANDOM_TYPE diagonal
FILE

(CO)VARIANCES 1 0.1 0.1 1
RANDOM_GROUP 6 7
RANDOM_TYPE add_animal
FILE
animal.ped
(CO)VARIANCES
1 0.1
0.1 1
OPTION hetres_pos 6 7
OPTION hetres_pol 1.0 0.1

### using GIBBS3F90
DATAFILE
test.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
9
OBSERVATION(S)
3
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 cross
6 1 cov
7 1 cov
5 5 cross
6 5 cov 5
7 5 cov 5
5 10 cross
6 10 cov 5
7 10 cov 5
RANDOM_RESIDUAL VALUES
10
RANDOM_GROUP
4 5 6
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1 0.1 0.1
0.1 1 0.1
0.1 0.1 1
RANDOM_GROUP
7 8 9
RANDOM_TYPE
add_animal
FILE
animal.ped
(CO)VARIANCES
1 0.1 0.1
0.1 1 0.1
0.1 0.1 1
OPTION hetres_int 8 5

**Competitive model (i.e., social interaction effects)**

<table>
<thead>
<tr>
<th>DATAFILE</th>
<th>competition.dat</th>
</tr>
</thead>
<tbody>
<tr>
<td>NUMBER_OF_TRAITS</td>
<td>1</td>
</tr>
<tr>
<td>NUMBER_OF_EFFECTS</td>
<td>19</td>
</tr>
<tr>
<td>OBSERVATION(S)</td>
<td>24</td>
</tr>
</tbody>
</table>

**WEIGHT(S)**

**EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]**

<table>
<thead>
<tr>
<th>EFFECT</th>
<th>POSITIONS_IN_DATAFILE</th>
<th>NUMBER_OF_LEVELS</th>
<th>TYPE_OF_EFFECT</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>88</td>
<td>8</td>
<td>cross</td>
</tr>
<tr>
<td>3</td>
<td>362</td>
<td>8</td>
<td>cross</td>
</tr>
<tr>
<td>21</td>
<td>2409</td>
<td>8</td>
<td>cross</td>
</tr>
<tr>
<td>4</td>
<td>8004</td>
<td>8</td>
<td>cross</td>
</tr>
<tr>
<td>22</td>
<td>0 cov 5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 7</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 10</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 11</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 12</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 13</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 14</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 16</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 17</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>0 cov 18</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>8004 cov 19</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**RANDOM_RESIDUAL VALUES**

<table>
<thead>
<tr>
<th>VALUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>1225.8</td>
</tr>
</tbody>
</table>

**RANDOM_GROUP**

<table>
<thead>
<tr>
<th>GROUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>4 5</td>
</tr>
</tbody>
</table>

**RANDOM_TYPE**

<table>
<thead>
<tr>
<th>TYPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>add_animal</td>
</tr>
</tbody>
</table>

**FILE**

renadd04.ped

**(CO)VARIANCES**

<table>
<thead>
<tr>
<th>VALUE 1</th>
<th>VALUE 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>267.03</td>
<td>25.313</td>
</tr>
<tr>
<td>25.313</td>
<td>104.44</td>
</tr>
</tbody>
</table>

**RANDOM_GROUP**

<table>
<thead>
<tr>
<th>GROUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
</tr>
</tbody>
</table>

**RANDOM_TYPE**

<table>
<thead>
<tr>
<th>TYPE</th>
</tr>
</thead>
<tbody>
<tr>
<td>diagonal</td>
</tr>
</tbody>
</table>

**FILE**

...
(CO)VARIANCES
89.187
RANDOM_GROUP
3
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
167.34
Appendix A (single trait animal model)

Single trait “USDA-type” animal model. The files used in this example are available here.

\[ y_{ijkl} = hys_i + hs_{ij} + p_k + a_k + e_{ijkl} \]

where

\[ y_{ijkl} \] - production yield

\[ hys_i \] - fixed herd year season

\[ hs_{ij} \] - random herd x sire interaction

\[ p_k \] - random permanent environment

\[ a_k \] - random animal

and

\[ \text{var}(hs_{ij}) = .05, \text{var}(p_k) = .1, \text{var}(a_k) = .5, \text{var}(e_{ijkl}) = 1 \]

Data file (ic)
Format: animal/hys/p/hs/y

1 1 1 1 10
2 1 2 1 11
3 2 3 2 15
4 2 4 3 13
5 3 5 4 14
6 3 6 3 12

Pedigree file (is)
Format: animal/dam/sire/code

1 12 8 2
2 1 8 1
3 2 9 1
4 7 10 1
5 12 11 2
6 1 10 1
7 13 14 3
8 5 11 1
9 13 8 2
10 7 14 2
11 13 14 3

Parameter file
# Example of single-trait animal model with one fixed effect
DATAFILE
ic
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
4
OBSERVATION(S)
5
WEIGHT(S)
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 3 cross
3 6 cross
4 4 cross
1 14 cross

RANDOM_RESIDUAL VALUES
1

RANDOM_GROUP
2

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
0.1

RANDOM_GROUP
3

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
0.05

RANDOM_GROUP
4

RANDOM_TYPE
add_an_upg

FILE
is

(CO)VARIANCES
0.5

Execution
name of parameter file?exiap

    BLUPF90 1.00

Parameter file:    exiap
Data file:        ic
Number of Traits  1
Number of Effects 4
Position of Observations 5
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
#  type                position (2)        levels   [positions for nested]
1  cross-classified      2                     3
2  cross-classified      3                     6
3  cross-classified      4                     4
4  cross-classified      1                     14
Residual (co)variance Matrix

1.000

Random Effect 2
Type of Random Effect: diagonal
trait effect (CO)VARIANCES
1 2 0.100

Random Effect 3
Type of Random Effect: diagonal
trait effect (CO)VARIANCES
1 3 0.050

Random Effect 4
Type of Random Effect: additive animal
Pedigree File: is
trait effect (CO)VARIANCES
1 4 0.500

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 5
original G
0.10
inverted G
10.00
original G
0.05
inverted G
20.00
original G
0.50
inverted G
2.00
solutions stored in file: "solutions"

trait/effect level solution
1 1 1 11.8589
1 1 2 13.7539
1 1 3 14.7086
1 2 1 -0.0088
1 2 2 0.0088
1 2 3 -0.0159
1 2 4 0.0159
1 2 5 0.0321
1 2 6 -0.0321
1 3 1 0.0000
1 3 2 -0.0079
1 3 3 -0.0081
1 3 4 0.0161
1 4 1 -1.7627
1 4 2 -0.9553
1 4 3 1.4288
1 4 4 -0.9206
1 4 5 -1.0781
1 4 6 -2.3474
1 4 7 0.8511
1 4 8 -0.1521
1 4 9 3.8926
1 4 10 -2.7717
<table>
<thead>
<tr>
<th>1</th>
<th>4</th>
<th>11</th>
<th>0.8528</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4</td>
<td>12</td>
<td>-3.1911</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>13</td>
<td>7.9976</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>14</td>
<td>-6.3340</td>
</tr>
</tbody>
</table>
Appendix B (multiple trait sire model)

Example of multiple trait sire model (from L.R. Schaeffer notes of 1985).

Models

Trait 1: \( y_{1i} = h_i + s_{1j} + e_{1ijk} \)

Trait 2: \( y_{2i} = \mu + s_{2j} + e_{2jk} \)

where

- \( h \) - fixed herd
- \( s \) - random sire

and

\[
\text{var}(s) = A[8 \ 6; 6 \ 17], \text{var}(e) = I[10 \ 10; 10 \ 20]
\]

Data file (lrsdat)
Format: h/\mu/s/y_1/y_2
\[
\begin{align*}
1 & 0 & 1 & 3 & .4 & 0 \\
2 & 0 & 2 & 1 & .3 & 0 \\
1 & 1 & 3 & .8 & 50 & .3 \\
2 & 1 & 4 & 4 & .5 & 52 & .6 \\
0 & 1 & 5 & 0 & 55 & .0
\end{align*}
\]

Pedigree file (lrsrel)
Format: bull/sire/MGS
\[
\begin{align*}
1 & 3 & 0 \\
2 & 0 & 5 \\
3 & 0 & 0 \\
4 & 0 & 0 \\
5 & 0 & 0
\end{align*}
\]

Parameter file (lrsex)
# Example of two trait sire model with unequal models
DATAFILE
lrsdat
NUMBER_OF_TRAITS
2
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
4 5
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 2 cross
3 3 5 cross
RANDOM RESIDUAL VALUES
10 10
10 20

RANDOM_GROUP
2

RANDOM_TYPE
add sire

FILE
lrsrel

(CO)VARIANCES
8 6
6 17

Execution
name of parameter file? lrsex

BLUPF90 1.00

Parameter file: lrsex
Data file: lrsdat
Number of Traits 2
Number of Effects 2
Position of Observations 4 5
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
#  type                position (2)        levels  [positions for nested]
1  cross-classified      1  2                  2
2  cross-classified      3  3                  5

Residual (co)variance Matrix
10.000  10.000
10.000  20.000

Random Effect 1
Type of Random Effect: additive sire
Pedigree File: lrsrel

trait  effect  (CO)VARIANCES
1  2  8.000   6.000
2  2  6.000  17.000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 5
original G
 8.00  6.00
 6.00 17.00
inverted G
 0.17 -0.06
-0.06  0.08

solutions stored in file: "solutions"
<table>
<thead>
<tr>
<th>trait/effect level</th>
<th>solution</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 1</td>
<td>2.3877</td>
</tr>
<tr>
<td>2 1</td>
<td>52.4449</td>
</tr>
<tr>
<td>1 1</td>
<td>3.2180</td>
</tr>
<tr>
<td>2 1</td>
<td>0.0000</td>
</tr>
<tr>
<td>1 2</td>
<td>0.2243</td>
</tr>
<tr>
<td>2 2</td>
<td>-0.0210</td>
</tr>
<tr>
<td>1 2</td>
<td>-0.8217</td>
</tr>
<tr>
<td>2 2</td>
<td>-0.3866</td>
</tr>
<tr>
<td>1 2</td>
<td>-0.4969</td>
</tr>
<tr>
<td>2 2</td>
<td>-0.7512</td>
</tr>
<tr>
<td>1 2</td>
<td>0.6178</td>
</tr>
<tr>
<td>2 2</td>
<td>-0.0769</td>
</tr>
<tr>
<td>1 2</td>
<td>0.2217</td>
</tr>
<tr>
<td>2 2</td>
<td>1.0851</td>
</tr>
</tbody>
</table>
Appendix C (test-day model)

This test-day model example comes from the paper of Schaeffer and Dekkers (WCGALP94 18:443). The files used in this example are available here.

Model

\[ y_{ijkl} = h_i + \beta_1 X_{1j} + \beta_2 X_{2j} + a_k + \gamma_1 X_{1j} + \gamma_2 X_{2j} + e_{ijkl} \]

where

- \( y_{ijkl} \) - yield of test day
- \( h_i \) - test day effect
- \( X_{1j} \) - days in milk
- \( X_{2j} \) - log(days in milk)
- \( \beta_1, \beta_2 \) - fixed regressions
- \( a_k \) - random animal
- \( \gamma_1, \gamma_2 \) - random regressions for each animal

and

\[ \text{var}(e_{ijkl}) = 1; \text{var}(a_k, \gamma_1 k, \gamma_2 k) = \begin{bmatrix} 2.25 & 4 & -0.7 & 4 & 1375 & 12 & -0.7 & 12 & 94 \end{bmatrix} \]

Data file (lrsrrdat)

Format: h/a/X1/X2/y

<table>
<thead>
<tr>
<th>h</th>
<th>a</th>
<th>X1</th>
<th>X2</th>
<th>y</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>73</td>
<td>1.42985</td>
<td>26</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>34</td>
<td>2.19395</td>
<td>29</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>8</td>
<td>3.64087</td>
<td>37</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>123</td>
<td>0.908127</td>
<td>23</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>84</td>
<td>1.28949</td>
<td>18</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>58</td>
<td>1.65987</td>
<td>25</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>5</td>
<td>4.11087</td>
<td>44</td>
</tr>
<tr>
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<td>178</td>
<td>0.538528</td>
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<td>2</td>
<td>139</td>
<td>0.785838</td>
<td>8</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>113</td>
<td>0.992924</td>
<td>19</td>
</tr>
<tr>
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<td>4</td>
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<td>1.62597</td>
<td>29</td>
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<td>3</td>
<td>158</td>
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<td>15</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>105</td>
<td>1.06635</td>
<td>22</td>
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<tr>
<td>4</td>
<td>5</td>
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<td>3.08125</td>
<td>35</td>
</tr>
<tr>
<td>5</td>
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<td>218</td>
<td>0.335817</td>
<td>11</td>
</tr>
<tr>
<td>5</td>
<td>4</td>
<td>165</td>
<td>0.614366</td>
<td>14</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
<td>74</td>
<td>1.41625</td>
<td>23</td>
</tr>
<tr>
<td>5</td>
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<td>31</td>
<td>2.28632</td>
<td>28</td>
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<tr>
<td>6</td>
<td>3</td>
<td>268</td>
<td>0.129325</td>
<td>7</td>
</tr>
<tr>
<td>6</td>
<td>4</td>
<td>215</td>
<td>0.349674</td>
<td>8</td>
</tr>
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<td>6</td>
<td>5</td>
<td>124</td>
<td>0.90003</td>
<td>17</td>
</tr>
<tr>
<td>6</td>
<td>6</td>
<td>81</td>
<td>1.32586</td>
<td>22</td>
</tr>
</tbody>
</table>

Pedigree file (lrsrrrel)

Format: animal/sire/dam

<table>
<thead>
<tr>
<th>animal</th>
<th>sire</th>
<th>dam</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>9</td>
<td>7</td>
</tr>
<tr>
<td>2</td>
<td>10</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>9</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>10</td>
<td>8</td>
</tr>
</tbody>
</table>
Parameter file (exlrsrr)

# Example of single-trait random-regression model

DATAFILE
lrsrdat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
6
OBSERVATION(S)
5
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 6 cross
3 1 cov
4 1 cov
2 11 cross
3 11 cov 2
4 11 cov 2

RANDOM_RESIDUAL VALUES
1
RANDOM_GROUP
4 5 6
RANDOM_TYPE
add_animal
FILE
lrsrrrel

(CO)VARIANCES
.447906 -0.001334 0.003506
-0.001334 0.000732 -0.000103
0.003506 -0.000103 0.010678

Execution
name of parameter file?exlrsrr

BLUPF90 1.00

Parameter file: exlrsrr
Data file: lrsrdat
Number of Traits 1
Number of Effects 6
Position of Observations 5
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type                position (2)        levels   [positions for nested]
1  cross-classified      1                     6
2  covariable            3                     1
3  covariable            4                     1
4  cross-classified      2                    11
5  covariable            3                    11     2
6  covariable            4                    11     2

Residual (co)variance Matrix
1.000

correlated random effects     4  5  6
Type of Random Effect:      additive animal
Pedigree File:              lrsrrrel

trait   effect    (CO)VARIANCES
1       4       0.448   -0.001   0.004
1       5      -0.001   0.001   0.000
1       6       0.004   0.000   0.011

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 5
original G
0.45   0.00   0.00
0.00   0.00   0.00
0.00   0.00   0.01
inverted G
2.25   4.00   -0.70
4.001375.09  11.95
-0.70  11.95  94.00
solutions stored in file: "solutions"

trait/effect level  solution
1  1       1     19.9496
1  1       2     20.3729
1  1       3     20.6095
1  1       4     19.7278
1  1       5     18.6035
1  1       6     17.8500
1  2       1     0.0498
1  3       1     5.2912
1  4       1     -0.4430
1  4       2     0.2704
1  4       3     -0.7288
1  4       4     1.1019
1  4       5     -0.1626
1  4       6     -0.4828
1  4       7     -0.0988
1  4       8     0.4574
1  4       9     -0.6288
1  4      10     0.4574
1  4      11     -0.1872
1  5       1     0.0369
1  5       2     -0.0661
1  5       3     0.0068
1  5       4     -0.0054
1  5       5     0.0069
1  5       6     0.0167
1  5       7     0.0133
<p>| | | | |</p>
<table>
<thead>
<tr>
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<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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<td>8</td>
<td>-0.0238</td>
</tr>
<tr>
<td>1</td>
<td>5</td>
<td>9</td>
<td>0.0350</td>
</tr>
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<td>5</td>
<td>10</td>
<td>-0.0238</td>
</tr>
<tr>
<td>1</td>
<td>5</td>
<td>11</td>
<td>-0.0008</td>
</tr>
<tr>
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<td>6</td>
<td>1</td>
<td>-0.0370</td>
</tr>
<tr>
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<td>6</td>
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<td>0.0325</td>
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<td>6</td>
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<td>6</td>
<td>5</td>
<td>-0.0149</td>
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<td>6</td>
<td>6</td>
<td>-0.0377</td>
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<tr>
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<td>6</td>
<td>7</td>
<td>-0.0103</td>
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<tr>
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<td>6</td>
<td>8</td>
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</tr>
<tr>
<td>1</td>
<td>6</td>
<td>10</td>
<td>0.0364</td>
</tr>
<tr>
<td>1</td>
<td>6</td>
<td>11</td>
<td>-0.0145</td>
</tr>
</tbody>
</table>
Appendix D (multibreed maternal effect model)

This model was used for studies on multibreed evaluation in beef cattle. It is provided as an example of a model with maternal effect and different models per trait.

Model (in concise form, with most indices omitted)

\[
\begin{align*}
y_1 &= c_{g1} + bt + mbt + a + M + e \\
y_2 &= c_{g2} + bt + mbt + a + M + pe + e \\
y_3 &= c_{g3} + bt + mbt + a + e
\end{align*}
\]

where

- \(y_{1:3}\) - birth weight, weaning weight, and gain
- \(c_{g1:3}\) - contemporary groups separate for each trait
- \(br\) - breed type
- \(mbt\) - maternal breed type
- \(a\) - additive effect
- \(m\) - maternal effect
- \(pe\) - permanent environmental effect of the dam

Data file (data.out)
Format:
1. contemporary group for trait 1
2. contemporary group for trait 2
3. contemporary group for trait 3
4. animal breed type
5. maternal breed type
6. animal id
7. dam id
8. birth weight
9. weaning weight
10. gain

Pedigree file (pedi.outok)
Format:

- animal
- sire or unknown parent group
- dam or unknown parent group
- “1 + number of missing parents”

Parameter file (param.out)
DATAFILE
data.out

NUMBER_OF_TRAITS
3

NUMBER_OF_EFFECTS
6

OBSERVATION(S)
8 9 10

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 3  133085 cross
4 4 4  181 cross
5 5 0  165 cross
6 6 6  1724112 cross
7 7 0  1724112 cross
0 7 0  1724112 cross

RANDOM RESIDUAL VALUES
26.3  40.7  20.3
40.7  1312.9  141.9
20.3  141.9  1246.3

RANDOM_GROUP
4 5

RANDOM_TYPE
add_an_upg

FILE
pedi.outok

(CO)VARIANCES
22.9  36.3  18.6  -4.6  0.0  0.0
36.6  500.2  110.8  0.0  -91.6  0.0
18.6  110.8  313.0  0.0  0.0  0.0
-4.6  0.0  0.0  10.1  0.0  0.0
0.0  -91.6  0.0  0.0  419.1  0.0
0.0  0.0  0.0  0.0  0.0  0.0

RANDOM_GROUP
2

RANDOM_TYPE
diagonal

FILE

(CO)VARIANCES
0.263  0.0  0.0
0.0  13.129  0.0
0.0  0.0  12.463

RANDOM_GROUP
3

RANDOM_TYPE
diagonal

FILE
<table>
<thead>
<tr>
<th>(CO)VARIANCES</th>
<th>0.263</th>
<th>0.0</th>
<th>0.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0</td>
<td>13.129</td>
<td>0.0</td>
<td></td>
</tr>
<tr>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
<td></td>
</tr>
</tbody>
</table>

RANDOM_GROUP
6

RANDOM_TYPE
diagonal

FILE

<table>
<thead>
<tr>
<th>(CO)VARIANCES</th>
<th>0.0</th>
<th>0.0</th>
<th>0.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0</td>
<td>45.5</td>
<td>0.0</td>
<td></td>
</tr>
<tr>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
<td></td>
</tr>
</tbody>
</table>
Appendix E (random regression model)

A single-trait random regression model for test-day milk is using cubic Legendre polynomials.

Model

\[ y_{ijkl} = hym_{ij} + \sum_{m=1}^{4} \alpha_m(l) h_{im} + \sum_{m=1}^{4} \alpha_m(l) u_{km} + \sum_{m=1}^{4} \alpha_m(l) pe_{im} + e_{ijkl} \]

where

- \( y_{ijkl} \) - test day milk
- \( hym_{ij} \) - hear-year-test for herd i and year-test j
- \( h_i \) - effects of herd i
- \( \alpha_m(l) \) - value of m-th Legendre polynomial at point corresponding to DIM=l
- \( u \) - additive effects
- \( pe \) - permanent environmental effects

Data file (datarr)

Format:
1. herd
2. hear-year-test
3-6. values of Legendre polynomials
7. weight for residuals: 100/var(e_{ijkl})
8. test day
9. animal

Relationship file (pedirr)

Format:
- animal
- sire
- dam

Parameter file (exrr3)

DATAFILE
datarr
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
13
OBSERVATION(S)
8
WEIGHT(S)  
7  
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT  
2 3726 cross #herd-year-test  
3 84 cov 1 #herd  
4 84 cov 1  
5 84 cov 1  
6 84 cov 1  
3 21874 cov 9 #additive  
4 21874 cov 9  
5 21874 cov 9  
6 21874 cov 9  
3 21874 cov 9 #pe  
4 21874 cov 9  
5 21874 cov 9  
6 21874 cov 9  
RANDOM_RESIDUAL_VALUES  
100  
RANDOM_GROUP  
6 7 8 9  
RANDOM_TYPE  
add_animal  
FILE  
pedirr  
(CO)VARIANCES  
(4 x 4 matrix)  
RANDOM_GROUP  
10 11 12 13  
RANDOM_TYPE  
diagonal  
FILE  
(CO)VARIANCES  
(4 x 4 matrix)
Appendix F (terminal cross model)

A terminal cross model by Fernando et al. and Lo et al.

breed A: \[ y_a = c_g a + u_a + e_a \]
breed B: \[ y_b = c_g b + u_b + e_b \]
cross: \[ y_{ab} = c_g a b + u_{aab} + u_{bab} + e_{ab} \]

Data file (data_cross)
1. cg A (85 levels)
2. cg B (110 levels)
3. cg crossbred (87 levels)
4. animal - breed A (2400 animals) or parent from breed A
5. animal - breed B (3000 animals) or parent from breed B
6. ya
7. yb
8. yc

Pedigree files: pedig_A for breed A and pedig_B for breed B

Parameter file

# Example of a terminal-cross model
DATAFILE
data-cross
NUMBER_OF_TRAITS
3
NUMBER_OF_EFFECTS
3
OBSERVATION(S)
6 7 8
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 3 110 cross
4 0 4 2400 cross
0 5 5 3000 cross

RANDOM_RESIDUAL_VALUES
100 0 0
0 100 0
0 0 100

RANDOM_GROUP
2

FILE
pedig_A
(CO)VARIANCES
(3 x 3 matrix)
RANDOM_GROUP
3
RANDOM_TYPE
add_animal
FILE
pedig_B
(CO)VARIANCES
(3 x 3 matrix)
Appendix G (competitive model)

Example of a competitive model (a la Muir and Schinkel)

\[ y = cg + a + c_1 + c_2 + \ldots + c_5 + e \]

ci is the effect of the i-th competitor; assumed pen size of up to 6.

Datafile (data_comp)
1. y
2. cg (max 120)
3. animal (max 3000)
4. competitor 1
5. c 2
   ...
8. c 5

If pen size is less than 6, unused fields set to 0.

Parameter file
# Example of a competitive model
DATAFILE
data_comp
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
7
OBSERVATION(S)
1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
2 120 cross
3 3000 cross
4 0 cross
5 0 cross
6 0 cross
7 0 cross
8 3000 cross
RANDOM_RESIDUAL VALUES
50
RANDOM_GROUP
2 3
RANDOM_TYPE
add_animal
FILE

The 2nd effect (position 3 in the data) is additive direct effect and 3rd to 7th effects (positions 4 to 8 in the data) are competitive effects (animal ID for competitors).
The covariance matrix contains variance for the second effect, variance for effects 3 to 7 (accumulated to 7), and covariance between direct and competitive effects.
Appendix H (genomic model)

Example of evaluation /variance component estimation using phenotypic, pedigree and genomic information in single-step evaluation

Files simulated by Huiyu Wang using program QMSim by Mehdi Sargolzaei & Flavio Schenkel.

**Parameter file for renumbering program RENUMF90**

<table>
<thead>
<tr>
<th>DATAFILE</th>
<th>phenotypes.txt</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRAITS</td>
<td>3</td>
</tr>
<tr>
<td>FIELDS_PASSED TO OUTPUT</td>
<td></td>
</tr>
<tr>
<td>WEIGHT(S)</td>
<td></td>
</tr>
<tr>
<td>RESIDUAL_VARIANCE</td>
<td>0.9038</td>
</tr>
<tr>
<td>EFFECT</td>
<td>1 cross alpha #fixed effect</td>
</tr>
<tr>
<td>EFFECT</td>
<td>2 cross alpha #animal</td>
</tr>
<tr>
<td>RANDOM</td>
<td>animal</td>
</tr>
<tr>
<td>FILE</td>
<td>pedigree</td>
</tr>
<tr>
<td>SNP_FILE</td>
<td>marker.geno.clean</td>
</tr>
<tr>
<td>(CO)VARIANCES</td>
<td>0.9951E-01</td>
</tr>
</tbody>
</table>

**Phenotypes.txt – phenotype file**

- Single trait in position 3
- Fixed effect in position 1 read as alphanumeric
- Random animal effect in position 3

**Phenotypes.txt**

- Pedigree file pedigrees
- SNP file marker.geno.clean

**Phenotype file**

**phenotypes.txt**

```
1 1 4.16 0
1 2 3.47 0
1 3 4.5 0
1 4 4.97 0
1 5 5.98 0
1 6 6.63 0
1 7 3.32 0
1 8 5.85 0
1 9 4.77 0
1 10 4.22 0
```

**Pedigree file**

```
pedigree
1 0 0 0
2 0 0 0
3 0 0 0
4 0 0 0
5 0 0 0
```
SNP file for the first 50 SNP

$cut -c1-50 marker.geno.clean|head -10

8002 21101011002012011011011011111211111210100
8014 2111010111110112201101111111210112210100
8016 211001012022021120211211211012112212111101
8018 21110111122011201201020102221221111100
8024 211101022012011122010111021220122111111
8038 111100000210012120112111211121121121111
8041 22210000120112112111012112010212001110012
8063 201101012022022211110110112022012120021
8065 2111011111121112111101011022012001110012
8083 1011101111001111111111012101121011010121

Run RENUMF90

RENUMF90 version 1.86
name of parameter file?renum.par
renum.par
datafile:phenotypes.txt
traits:           3
fields passed:           4
R 0.9038
Processing effect 1 of type cross
item_kind=alpha

Processing effect 2 of type cross
item_kind=alpha
pedigree file name "pedigree"
positions of animal, sire, dam, alternate dam and yob 1 2 0 3
SNP file name "marker.geno.clean"
all pedigrees to be included
Reading (CO)VARIANCES: 1 x 1

Maximum size of character fields: 20

Maximum size of record (max_string_readline): 800

Maximum number of fields input file (max_field_readline): 100

hash tables for effects set up
table expanded from 10000 to 20000 records
read 15800 records
table with 1 elements sorted
added count
Effect group 1 of column 1 with 1 levels
table expanded from 10000 to 10000 records
added count
Effect group 2 of column 1 with 15800 levels
wrote statistics in file "renf90.tables"

Basic statistics for input data (missing value code is 0)
<table>
<thead>
<tr>
<th>Pos</th>
<th>Min</th>
<th>Max</th>
<th>Mean</th>
<th>SD</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>0.73000</td>
<td>8.8300</td>
<td>4.9793</td>
<td>1.0069</td>
<td>15800</td>
</tr>
</tbody>
</table>
random effect with SNPs 2
type: animal
file: marker.geno.clean
read SNPs 1500 records
Effect group 2 of column 1 with 15800 levels

random effect 2
type: animal
opened output pedigree file "renadd02.ped"
read 15800 pedigree records

Pedigree checks
Number of animals with records: 15800
Number of animals with genotypes: 1500
Number of animals with records or genotypes: 15800
Number of animals with genotypes and no records 0
Number of parents without records or genotypes: 0
Total number of animals: 15800

Wrote cross reference IDs for SNP file "marker.geno.clean_XrefID"

Wrote parameter file "renf90.par"
Wrote renumbered data "renf90.dat"

Parameter file for application programs with renumbered fields

renf90.par

# BLUPF90 parameter file created by RENF90
DATAFILE
renf90.dat
NUMBER_OF_TRAITS 1
NUMBER_OF_EFFECTS 2
OBSERVATION(S) 1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2 1 cross
3 15800 cross
RANDOM_RESIDUAL VALUES
0.9038
RANDOM_GROUP
2
RANDOM_TYPE add_animal
FILE
renadd02.ped
(CO)VARIANCES
0.9951E-01
OPTION SNP_file marker.geno.clean

renf90.dat – phenotype file
Single trait in position 1
Two effects in model
Fixed effect in position 1 cross-classified with 1 level (μ)
Animal effect in position 3
Second effect (Random Group 2) is additive-animal with
renadd02.ped – pedigree file
SNP file marker.geno.clean

Renumbered pedigree file

renadd02.ped
name of parameter file? renf90.par

* SNP file: marker.geno.clean
* SNP Xref file: marker.geno.clean_XrefID
* Frequency to Center Z=M-p to create G=ZZ'/k (default whichfreq = 2):
  2
BLUPF90 1.42

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type                position (2)        levels [positions for nested]
1  cross-classified          2             1
2  cross-classified          3     1
Residual (co)variance Matrix
0.90380

Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such effects are missing for specified traits
read 15800 records in 3.5994001E-02 s, 31601 nonzeroes
read 15800 additive pedigrees

*------------------------------------------------------------------------*
* Setup Genomic: Version 1.76 *
* Modified relationship matrix (H) created for effect: 2 *
*----------------------------------------------------------------------*

Read 15800 animals from pedigree file
Pedigree was in not chronological order (parent first format), reordering will be performed!!!

Current OPTIONS

Genomic Matrix
Make/Read Which Save Test File StorageType
Make 1 F F G densem

Rel. Matrix A22
Make/Read Which Save Test File StorageType
Make 4 F F A22 densem

Inv. Genomic Matrix
Make/Read Which Save Test File StorageType
Make 9 F F Gi densem

Inv. Rel. Matrix A22
Make/Read Which Save Test File StorageType
Make 9 F F A22i densem

Genomic - A22 Matrix
Make/Read Which Save Test File StorageType
None 9 F F GmA22 densem

Inv. Genomic- A22 Matrix
Make/Read Which Save Test File StorageType
Make 0 F F GimA22i densem

Other options
Allele Frequency file: freqdata
Center Allele Frequency: 2
Scale Allele Frequency: 2
Scale Method: 1
Regression G on A: F
Tuned G Method: 2

Creation of GimA22i
tau inv(alpha G + beta A22 + gamma I + delta) - omega inv(A22)
alpha,beta 0.950 0.050
gamma,delta 0.000 0.000
tau,omega 1.000 1.000

Number of Genotyped Animals 1500

Creating A22
Extracting subset of: 3432 pedigrees from: 15800 elapsed time: 0.0000
Calculating Inbreeding by M&L function.. elapsed time 1.0000020E-03
Calculating A22 Matrix by Colleau .. elapsed time 0.3299500

Statistics for A22

<table>
<thead>
<tr>
<th>Statistic of Rel. Matrix A22</th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>1.001</td>
<td>1.000</td>
<td>1.250</td>
<td>0.000</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>0.003</td>
<td>0.000</td>
<td>0.750</td>
<td>0.001</td>
</tr>
</tbody>
</table>

Reading SNP file
Column position in file for the first marker: 7
Format to read SNP file: (6x,400000i1)
Number of SNPs: 3000
Number of Genotyped animals: 1500
Reading SNP file elapsed time 0.4639290

Statistics of alleles frequencies in the current population
N: 3000
Mean: 0.501
Min: 0.132
Max: 0.890
Var: 0.014

Quality Control - Check call rate for animals

Quality Control - Check Parent-Progeny Mendelian conflicts
Total animals: 15800 - Genotyped animals: 1500
Number of Individual - Sire pairs: 470
Number of Individual - Dams pairs: 256
Number of Individual - Sire - Dam trios: 152

Checking SNPs for Mendelian conflicts
Total number of parent-progeny evaluations: 726
Number of SNPs with Mendelian conflicts: 0

Checking Animals for Mendelian conflicts

Statistics of alleles frequencies in the current population after Quality Control (MAF, monomorphic, call rate)
N: 3000
Mean: 0.501
Min: 0.132
Max: 0.890
Var: 0.014

<table>
<thead>
<tr>
<th>Locus</th>
<th>Freq</th>
<th>0-2p</th>
<th>1-2p</th>
<th>2-2p</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.751333</td>
<td>-1.502667</td>
<td>-0.502667</td>
<td>0.497333</td>
</tr>
<tr>
<td>2</td>
<td>0.382333</td>
<td>-0.764667</td>
<td>0.235333</td>
<td>1.235333</td>
</tr>
<tr>
<td>3</td>
<td>0.568667</td>
<td>-1.137333</td>
<td>-0.137333</td>
<td>0.862667</td>
</tr>
<tr>
<td>4</td>
<td>0.680000</td>
<td>-1.360000</td>
<td>-0.360000</td>
<td>0.640000</td>
</tr>
<tr>
<td>5</td>
<td>0.184333</td>
<td>-0.368667</td>
<td>0.631333</td>
<td>1.631333</td>
</tr>
<tr>
<td>6</td>
<td>0.298333</td>
<td>-0.596667</td>
<td>0.403333</td>
<td>1.403333</td>
</tr>
<tr>
<td>7</td>
<td>0.392000</td>
<td>-0.784000</td>
<td>0.216000</td>
<td>1.216000</td>
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<tr>
<td>8</td>
<td>0.379667</td>
<td>-0.759333</td>
<td>0.240667</td>
<td>1.240667</td>
</tr>
<tr>
<td>9</td>
<td>0.596667</td>
<td>-1.193333</td>
<td>-0.193333</td>
<td>0.806667</td>
</tr>
<tr>
<td>10</td>
<td>0.352333</td>
<td>-0.704667</td>
<td>0.295333</td>
<td>1.295333</td>
</tr>
</tbody>
</table>

Genotypes missings (%): 0.0000000E+00
Average denom. (scale): 1415.90178466665
Center Matrix elapsed: 8.3986998E-02

Creating G Matrix

Calculating G Matrix
- Wall time: 08-05-2011 16h 57m 34s 213
- MMP - OPTML
- Elapsed time 18.47419
- Wall time: 08-05-2011 16h 58m 09s 371

Statistics of G calculated assuming current allele frequencies

<table>
<thead>
<tr>
<th>Statistic of Genomic Matrix</th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>0.999</td>
<td>0.889</td>
<td>1.463</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>-0.001</td>
<td>-0.147</td>
<td>0.830</td>
<td>0.002</td>
</tr>
</tbody>
</table>

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Several quality checks performed; no error messages as all files for this example have been simulated
Correlation: 0.3220

All elements - Diagonal / Off-Diagonal
Estimating Regression Coefficients \[ G = b_0 11' + b_1 A + e \]
Regression coefficients \[ b_0, b_1 = -0.004, 0.997 \]
Correlation all elements \( G \& A \) 0.644

Off-Diagonal
Using 70386 elements from \( A^{22} \) >= 0.02000

Estimating Regression Coefficients \[ G = b_0 11' + b_1 A + e \]
Regression coefficients \[ b_0, b_1 = -0.006, 1.000 \]
Correlation Off-Diagonal elements \( G \& A \) 0.660

Blend \( G \) as \( \alpha^*G + \beta^*A^{22} \): (\( \alpha, \beta \)) 0.950 0.050

Statistic of Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>0.999</td>
<td>0.894</td>
<td>1.446</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>0.000</td>
<td>-0.139</td>
<td>0.820</td>
<td>0.002</td>
</tr>
</tbody>
</table>

Frequency - Diagonal of \( G \)

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min.</th>
<th>Max.</th>
<th>Range</th>
<th>Class</th>
</tr>
</thead>
<tbody>
<tr>
<td>1500</td>
<td>0.999</td>
<td>0.894</td>
<td>1.446</td>
<td>0.028</td>
<td>20</td>
</tr>
</tbody>
</table>

#Class | Class | Count |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.8942</td>
<td>9</td>
</tr>
<tr>
<td>2</td>
<td>0.9218</td>
<td>86</td>
</tr>
<tr>
<td>3</td>
<td>0.9494</td>
<td>343</td>
</tr>
<tr>
<td>4</td>
<td>0.9770</td>
<td>480</td>
</tr>
<tr>
<td>5</td>
<td>1.005</td>
<td>361</td>
</tr>
<tr>
<td>6</td>
<td>1.032</td>
<td>139</td>
</tr>
<tr>
<td>7</td>
<td>1.060</td>
<td>51</td>
</tr>
<tr>
<td>8</td>
<td>1.087</td>
<td>16</td>
</tr>
<tr>
<td>9</td>
<td>1.115</td>
<td>6</td>
</tr>
<tr>
<td>10</td>
<td>1.142</td>
<td>2</td>
</tr>
<tr>
<td>11</td>
<td>1.170</td>
<td>1</td>
</tr>
<tr>
<td>12</td>
<td>1.198</td>
<td>1</td>
</tr>
<tr>
<td>13</td>
<td>1.225</td>
<td>1</td>
</tr>
<tr>
<td>14</td>
<td>1.253</td>
<td>1</td>
</tr>
<tr>
<td>15</td>
<td>1.280</td>
<td>0</td>
</tr>
<tr>
<td>16</td>
<td>1.308</td>
<td>0</td>
</tr>
<tr>
<td>17</td>
<td>1.336</td>
<td>0</td>
</tr>
<tr>
<td>18</td>
<td>1.363</td>
<td>2</td>
</tr>
<tr>
<td>19</td>
<td>1.391</td>
<td>0</td>
</tr>
<tr>
<td>20</td>
<td>1.418</td>
<td>1</td>
</tr>
<tr>
<td>21</td>
<td>1.446</td>
<td>0</td>
</tr>
</tbody>
</table>

Scale \( G \) matrix according to \( A^{22} \) - Method: 2
Diagonal \( A \): 1.001 Offdiagonal \( A \): 0.003 All \( A \): 0.004 Difference: 0.998
Diagonal \( G \): 0.999 Offdiagonal \( G \): 0.000 All \( G \): 0.000 Difference: 0.999
Diff \( G \) Diag - G OffDiag: 0.999 \( (d_a-o_a)/(d_g-o_g) \): 0.998
Diff \( A \) OffDiag - G OffDiag: 0.004
Diff \( A \) all - G all: 0.004
New Alpha: 0.948 New Beta: 0.050 :New Delta 0.004

Final Pedigree-Based Matrix

Statistic of Rel. Matrix \( A^{22} \)
### Final Genomic Matrix

#### Statistic of Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>1.001</td>
<td>0.896</td>
<td>1.447</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>0.003</td>
<td>-0.134</td>
<td>0.822</td>
<td>0.002</td>
</tr>
</tbody>
</table>

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.3363

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 \mathbf{1}' + b_1 \mathbf{A} + e$

Regression coefficients $b_0 \ b_1$ =

- $b_0$ = 0.000
- $b_1$ = 0.995

Correlation all elements $G$ & $A$ = 0.663

Off-Diagonal

Using 70386 elements from $A_{22} >= 0.02000$

Estimating Regression Coefficients $G = b_0 \mathbf{1}' + b_1 \mathbf{A} + e$

Regression coefficients $b_0 \ b_1$ =

- $b_0$ = -0.001
- $b_1$ = 0.998

Correlation Off-Diagonal elements $G$ & $A$ = 0.679

Creating $A_{22}^{-1}$

Wall time: 08-05-2011 16h 58m 10s 866

Inverse using ginv2

elapsed time 3.54446100000000

Wall time: 08-05-2011 16h 58m 17s 691

#### Statistics of $A_{22}^{-1}$

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>1.607</td>
<td>1.056</td>
<td>9.221</td>
<td>0.575</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>-0.001</td>
<td>-1.067</td>
<td>0.533</td>
<td>0.001</td>
</tr>
</tbody>
</table>

Creating $G^{-1}$

Wall time: 08-05-2011 16h 58m 17s 987

Inverse using ginv2

elapsed time 4.24635400000000

Wall time: 08-05-2011 16h 58m 26s 044

#### Statistics of $G^{-1}$

$2 \times \text{diag}(G^{-1} \cdot A_{22}^{-1})$ is approx. measure of extra genomic info in terms of effective daughters

#### Statistic of Inv. Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>8.007</td>
<td>3.597</td>
<td>64.893</td>
<td>21.055</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>-0.005</td>
<td>-12.697</td>
<td>6.632</td>
<td>0.056</td>
</tr>
</tbody>
</table>

Creating GimA22i in file: "GimA22i"

Calculating GmA22/GimA22i Matrix Densem storage

Calculating GmA22/GimA22i Matrix...elapsed time 0.1269817
Setup Genomic Done.

hash matrix increased from 100000 to 150000 % filled: 0.9000
hash matrix increased from 150000 to 225000 % filled: 0.9000
hash matrix increased from 225000 to 337500 % filled: 0.9000
hash matrix increased from 337500 to 506250 % filled: 0.9000
hash matrix increased from 506250 to 759375 % filled: 0.9000
hash matrix increased from 759375 to 1139062 % filled: 0.9000

finished peds in 30.68333 s, 1193064 nonzeroes

round 1 convergence= 3.234776127905992E-004
round 2 convergence= 1.615955145159698E-005
round 3 convergence= 9.675137058360991E-006
round 4 convergence= 6.533482675941447E-006
round 5 convergence= 2.711751165983321E-006

round 64 convergence= 2.721030958617683E-012
round 65 convergence= 1.9310295785311E-012
round 66 convergence= 1.610472992188148E-012
round 67 convergence= 1.259204136643006E-012
round 68 convergence= 9.025592862452768E-013

68 iterations, convergence criterion= 9.025592862452768E-013
solutions stored in file: "solutions"

---

Solution file

solutions

trait/effect level solution
1 1 1 4.97591211
1 2 1 0.10194865
1 2 2 0.33749439
1 2 3 0.04475742
1 2 4 -0.31055520
1 2 5 0.22368631
1 2 6 -0.09454804
1 2 7 -0.03186435
1 2 8 0.18033163

---

Variance component estimation by AIREMLF90

name of parameter file?renf90.par

* SNP file: marker.geno.clean
* SNP Xref file: marker.geno.clean_XrefID
* Frequency to Center Z=M to create G=ZZ'/k (default whichfreq = 2):
  2

AI-REMLF90 ver. 1.96

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

---

Statistic of Inv. Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1500</td>
<td>8.007</td>
<td>3.597</td>
<td>64.893</td>
<td>21.055</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>2248500</td>
<td>-0.005</td>
<td>-12.697</td>
<td>6.632</td>
<td>0.056</td>
</tr>
</tbody>
</table>

Creating GimA22i in file: "GimA22i"
Calculating GmA22/GimA22i Matrix Densem storage
Calculating GmA22/GimA22i Matrix...elapsed time 0.1089821
Setup Genomic Done.
wGimA22i  1.00000000000000
hash matrix increased from 85428 to 128142 % filled: 0.9000
hash matrix increased from 128142 to 192213 % filled: 0.9000
hash matrix increased from 192213 to 288319 % filled: 0.9000
hash matrix increased from 288319 to 432478 % filled: 0.9000
hash matrix increased from 432478 to 648717 % filled: 0.9000
hash matrix increased from 648717 to 973075 % filled: 0.9000
hash matrix increased from 973075 to 1459612 % filled: 0.9000
hash matrix increased from 85428 to 128142 % filled: 0.9000
hash matrix increased from 128142 to 192213 % filled: 0.9000
hash matrix increased from 192213 to 288319 % filled: 0.9000
hash matrix increased from 288319 to 432478 % filled: 0.9000
hash matrix increased from 432478 to 648717 % filled: 0.9000
hash matrix increased from 648717 to 973075 % filled: 0.9000
hash matrix increased from 973075 to 1459612 % filled: 0.9000
finished peds in 32.01313 s, 1193064 nonzeroes
rank= 15801
*************
***** FSPAK *****
*************
MPE / IM / MAE
Jun 1994

SPARSE STATISTICS
DIMENSION OF MATRIX = 15801
RANK = 15801
STORAGE AVAILABLE = 7061497
MAXIMUM NEEDED = 7061497
NZE IN UPPER TRIANGULAR = 1208865
NZE IN FACTOR = 1521480
NO. OF CALLS NUM FACT = 1
NO. OF CALLS SOLVE = 1
NO. OF CALLS SPARS SOLV = 0
NO. OF CALLS DET / LDET = 1
NO. OF CALLS SPARS INV = 1
TOTAL CPU TIME IN FSPAK = 9.465561
TIME FOR FINDING ORDER = 2.568611
TIME FOR SYMBOLIC FAC = 0.676899
TIME FOR NUMERICAL FAC = 2.017693
TIME FOR SOLVE = 0.008995
TIME FOR SPARSE SOLVE = 0.000000
TIME FOR SPARSE INVERSE = 4.147369

-2logL = 43515.7413644011 : AIC = 43519.7413644011
In round 1 convergence= 0.423851780381002
delta convergence= 0.252173522062583
new R 0.58510
new G 0.28516
-2logL = 53013.2734486053 : AIC = 53017.2734486053
In round 2 convergence= 0.141351613622645
delta convergence= 0.117430758820623
new R 0.52205
new G 0.45696
-2logL = 52800.6601605267 : AIC = 52804.6601605267
In round 3 convergence= 0.12141351613622645
delta convergence= 0.117430758820623
new R 0.49575
new G 0.49400
new G
0.53164
-2logL = 52785.1635385807 : AIC = 52789.1635385807
In round 5 convergence = 2.804695847240073E-009
delta convergence = 1.777604045032979E-005
new R
0.49400
new G
0.53167

Estimates of variance components

Final Estimates
Genetic variance(s) for effect 2
0.53167
Residual variance(s)
0.49400
inverse of AI matrix (Sampling Variance)
0.40448E-03 -0.17367E-03
-0.17367E-03 0.14702E-03
Correlations from inverse of AI matrix
1.0000 -0.71219
-0.71219 1.0000
SE for R
0.12125E-01
SE for G
0.20112E-01
solutions stored in file: "solutions"
Appendix I (complete genomic analysis)


Using RENUMF90, PREGSF90, BLUPF90 (BLUP), BLUPF90 (ssGBLUP), PREDICTF90, POSTGSF90 (ssGWAS)

Simulated data

Single trait with heritability of 0.30 and phenotypic variance = 1.0

Five generations

Total of 994 parents from generations 1 to 4 were genotyped

Three hundred progeny from 5\textsuperscript{th} generation had genotypes and pedigree, but phenotypes were removed for traditional and genomic evaluations

Data Structure:

<table>
<thead>
<tr>
<th>#Animal</th>
<th>Generation</th>
<th>Sex</th>
<th>Mu</th>
<th>QTL</th>
<th>Residual</th>
<th>Phenotype</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>1</td>
<td>-0.826104</td>
<td>1.586661</td>
<td>1.76056</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>1</td>
<td>-1.093034</td>
<td>-0.451821</td>
<td>-0.544855</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>1</td>
<td>-0.135824</td>
<td>0.984936</td>
<td>1.84911</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>1</td>
<td>0.044242</td>
<td>-0.802145</td>
<td>0.242097</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>1</td>
<td>0.342068</td>
<td>0.028434</td>
<td>1.3705</td>
<td></td>
</tr>
</tbody>
</table>

Pedigree: 6100 animals

<table>
<thead>
<tr>
<th>#Animal</th>
<th>Sire</th>
<th>Dam</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>6095</td>
<td>4576</td>
<td>4403</td>
</tr>
<tr>
<td>6096</td>
<td>4576</td>
<td>4065</td>
</tr>
<tr>
<td>6097</td>
<td>4576</td>
<td>2263</td>
</tr>
<tr>
<td>6098</td>
<td>4576</td>
<td>4150</td>
</tr>
<tr>
<td>6099</td>
<td>4576</td>
<td>3690</td>
</tr>
<tr>
<td>6100</td>
<td>4576</td>
<td>4311</td>
</tr>
</tbody>
</table>

Genotypes: 1294 animals genotyped for 1000 SNP across 5 chromosomes

<table>
<thead>
<tr>
<th># Animal</th>
<th>SNP\textsubscript{1}SNP\textsubscript{2}SNP\textsubscript{3}SNP\textsubscript{4}SNP\textsubscript{5}...SNP\textsubscript{1000}</th>
</tr>
</thead>
<tbody>
<tr>
<td>6100</td>
<td>22212...1</td>
</tr>
</tbody>
</table>
Map:
#SNP order chromosome position
1 1 10010
2 1 16722
3 1 33444
4 1 50166
5 1 66888
.
1000 5 299878

**Parameter file for RENUMF90**

DATAFILE
newdata.txt
TRAITS
7
FIELDS_PASSED TO OUTPUT
2
WEIGHT(S)

RESIDUAL_VARIANCE
0.70
EFFECT
4 cross alpha #mu
EFFECT
1 cross alpha #animal
RANDOM
animal
FILE
ped.txt
FILE_POS
1 2 3 0 0
SNP_FILE
snp.txt
PED_DEPTH
0
(CO)VARIANCES
0.30
OPTION chrinfo map.txt

**Log file for RENUMF90**

RENUMF90 version 1.104
name of parameter file? renum.par
datafile:newdata.txt
traits: 7
fields passed: 2
R
0.7000

Processing effect 1 of type cross
item_kind=alpha

Processing effect 2 of type cross
item_kind=alpha
pedigree file name "ped.txt"
positions of animal, sire, dam, alternate dam and yob 1 2 3 0 0
SNP file name "snp.txt"
all pedigrees to be included
Reading (CO)VARIANCES: 1 x 1

Maximum size of character fields: 20
Maximum size of record (max_string_readline): 800
Maximum number of fields for input file (max_field_readline): 100

hash tables for effects set up
read 6100 records
table with 1 elements sorted
added count
Effect group 1 of column 1 with 1 levels
table expanded from 10000 to 10000 records
added count
Effect group 2 of column 1 with 6100 levels
wrote statistics in file "renf90.tables"

Basic statistics for input data (missing value code is 0)
Pos Min  Max  Mean  SD  N
7 -2.8883 5.0863 1.0042 0.99034 6100

random effect with SNPs 2
type: animal
file: snp.txt
read SNPs 1294 records
Effect group 2 of column 1 with 6100 levels

random effect 2
type: animal
opened output pedigree file "renadd02.ped"
read 6100 pedigree records

Pedigree checks
Number of animals with records: 6100
Number of animals with genotypes: 1294
Number of animals with records or genotypes: 6100
Number of animals with genotypes and no records 0
Number of parents without records or genotypes: 0
Total number of animals: 6100

Wrote cross reference IDs for SNP file "snp.txt_XrefID"
Wrote parameter file "renf90.par"
Wrote renumbered data "renf90.dat"

Parameter file for PREGSF90 without quality control

DATAFILE
renf90.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
1

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2 1 cross
3 6100 cross

RANDOM_RESIDUAL VALUES
0.70000

RANDOM_GROUP
2

RANDOM_TYPE
add_animal

FILE
renadd02.ped

(CO)VARIANCES
0.30000

OPTION SNP_file snp.txt
OPTION chrinfo map.txt
OPTION no_quality_control

Log file for PREGSF90 without quality control
name of parameter file?
renf90.par

  preGS 1.10

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
#  type                position (2)        levels   [positions for nested]
1  cross-classified 2 1
2  cross-classified 3 6100

Residual (co)variance Matrix
0.70000

Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped

trait  effect  (CO)VARIANCES
1  2  0.30000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Options read from parameter file:

* SNP file: snp.txt
* SNP Xref file: snp.txt_XrefID
* Map file: map.txt
* No Quality Control Checks !!!!! (default .false.): T

*-------------------------------------------------------------------*
* Genomic Library: Version 1.164
* Optimized OpenMP Version
* Modified relationship matrix (H) created for effect: 2
*-------------------------------------------------------------------*

Read 6100 animals from pedigree file: "renadd02.ped"
Number of Genotyped Animals: 1294

Creating A22
Extracting subset of: 2312 pedigrees from: 6100 elapsed time: 0.0150
Calculating A22 Matrix by Colleau OpenMP...elapsed time: .0190
Numbers of threads=8 16

Reading SNP file
Column position in file for the first marker: 8
Format to read SNP file: (7x,400000i1)
Number of SNPs: 1000
Number of Genotyped animals: 1294
Reading SNP file elapsed time: .06

Statistics of alleles frequencies in the current population
N: 1000
Mean: 0.504
Min: 0.043
Max: 0.929
Var: 0.032

Reading MAP file: "map.txt" - 1000 SNPs out of 1000
Min and max # of chromosome: 1 5
Min and max # of SNP: 1 1000
Genotypes missings (%): 0.000

Calculating G Matrix
Dgemm MKL #threads= 8 16 Elapsed omp_get_time: 0.7359

Scale by Sum(2pq). Average: 435.221580281360

Blend G as alpha*G + beta*A22: (alpha,beta) 0.950 0.050

Frequency - Diagonal of G
N: 1294
Mean: 0.999
Min: 0.895
Max: 1.468
Range: 0.029
Class: 20

#Class  Class  Count
1 0.8949 27
2 0.9236 109
3 0.9523 300
4 0.9810 380
Check for diagonal of genomic relationship matrix

Check for diagonal of genomic relationship matrix, genotypes not removed: 0

--------------------------
----

Final Pedigree-Based Matrix

Statistic of Rel. Matrix A22

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>1.000</td>
<td>1.250</td>
<td>0.000</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>0.000</td>
<td>0.750</td>
<td>0.001</td>
</tr>
</tbody>
</table>

----------------------

Final Genomic Matrix

Statistic of Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>0.898</td>
<td>1.469</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>-0.158</td>
<td>0.791</td>
<td>0.002</td>
</tr>
</tbody>
</table>

Correlation of Genomic Inbreeding and Pedigree Inbreeding
Correlation: 0.2177

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients \( G = b_0 \ 11' + b_1 \ A + e \)
Regression coefficients \( b_0 \ b_1 = \)

Correlation all elements \( G \ & \ A \) 0.717

Off-Diagonal

Using 83426 elements from A22 >= .02000

Estimating Regression Coefficients \( G = b_0 \ 11' + b_1 \ A + e \)
Regression coefficients \( b_0 \ b_1 = \)

Correlation Off-Diagonal elements \( G \ & \ A \) 0.777

Creating A22-inverse

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1071

----------------------
Final A22 Inv Matrix
------------------------

Statistic of Inv. Rel. Matrix A22

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.851</td>
<td>1.067</td>
<td>5.812</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.001</td>
<td>-1.200</td>
<td>0.600</td>
</tr>
</tbody>
</table>

Creating G-inverse
Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1050

------------------------
Final Genomic Inv Matrix
------------------------

Statistic of Inv. Genomic Matrix

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>13.457</td>
<td>5.827</td>
<td>45.588</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.010</td>
<td>-13.500</td>
<td>6.896</td>
</tr>
</tbody>
</table>

Check for diagonal of Inverse Genomic - Inverse of pedigree relationship matrix

Saving GimA22i in file: "GimA22i"

------------------------
Final G Inv - A22 Inv Matrix
------------------------

Statistic of Inv. Genomic- A22 Matrix

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>11.606</td>
<td>4.746</td>
<td>40.310</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.009</td>
<td>-12.500</td>
<td>6.396</td>
</tr>
</tbody>
</table>

*------------------------*  
* Setup Genomic Done !!! *  
*------------------------*  

Parameter file for PREGSF90 with quality control

DATAFILE
renf90.dat

NUMBER_OF_TRAITS
1

NUMBER_OF_EFFECTS
2

OBSERVATION(S)
2

WEIGHT(S)
1

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2 1 cross
3 6100 cross

RANDOM_RESIDUAL VALUES
0.70000

RANDOM_GROUP
2

RANDOM_TYPE
add_animal
FILE
renadd02.ped

(CO)VARIANCES
0.30000
OPTION SNP_file snp.txt
OPTION chrinfo map.txt

Log file for PREGSF90 with quality control
name of parameter file?
renf90.par

preGS 1.10

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type position (2) levels [positions for nested]
1 cross-classified 2 1
2 cross-classified 3 6100

Residual (co)variance Matrix
0.70000

Type of Random Effect: additive animal
Pedigree File: renadd02.ped

trait effect (CO)VARIANCES
1 2 0.3000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Options read from parameter file:

* SNP file: snp.txt
* SNP Xref file: snp.txt_XrefID
* Map file: map.txt

*---------------------------------------------------------------*
*     Genomic Library: Version 1.164                           *
*     Optimized OpenMP Version                           *
*     Modified relationship matrix (H) created for effect: 2 *
*---------------------------------------------------------------*

Read 6100 animals from pedigree file: "renadd02.ped"
Number of Genotyped Animals: 1294

Creating A22
Extracting subset of: 2312 pedigrees from: 6100 elapsed time: 0.0160
Calculating A22 Matrix by Colleau OpenMP...elapsed time: .0189
Numbers of threads=8 16

Reading SNP file
Column position in file for the first marker: 8
Format to read SNP file: (7x,400000i1)
Number of SNPs: 1000
Number of Genotyped animals: 1294
Reading SNP file elapsed time: .06

Statistics of alleles frequencies in the current population
N: 1000
Mean: 0.504
Min: 0.043
Max: 0.929
Var: 0.032

Reading MAP file: "map.txt" - 1000 SNPs out of 1000
Min and max # of chromosome: 1 5
Min and max # of SNP: 1 1000

Quality Control - SNPs with Call Rate < callrate (0.90) will removed: 0
Quality Control - SNPs with MAF < minfreq (0.05) will removed: 1
Quality Control - Monomorphic SNPs will be removed: 0
Quality Control - Removed Animals with Call rate < callrate (0.90): 0

Quality Control - Check Parent-Progeny Mendelian conflicts
Total animals: 6100 - Genotyped animals: 1294 - Effective: 1294

Number of pairs Individual - Sire: 450
Number of pairs Individual - Dam: 440
Number of trios Individual - Sire - Dam: 206

No sex Chromosome information is available
Parent-progeny conflicts or HWE could eliminate SNPs in sex Chr
Provide map information and sex Chr to checks using autosomes

Checking SNPs for Mendelian conflicts

Total number of effective SNP: 999
Total number of parent-progeny evaluations: 890
Number of SNPs with Mendelian conflicts: 0

Checking Animals for Mendelian conflicts

Total number of effective SNP for checks on Animals: 999
Number of Parent-Progeny Mendelian Conflicts: 0

Number of effective SNPs (after QC): 999
Number of effective Individuals (after QC): 1294

Statistics of alleles frequencies in the current population after Quality Control (MAF, monomorphic, call rate, HWE, Mendelian conflicts)
N:            999
Mean:       0.504
Min:        0.051
Max:        0.929
Var:        0.032

Genotypes missings (%):  0.100

Calculating G Matrix

Dgemm MKL #threads=     8   16 Elapsed omp_get_time:     0.9840

Scale by Sum(2pq). Average:   435.140185710293

Blend G as alpha*G + beta*A22: (alpha,beta)     0.950     0.050

Frequency - Diagonal of G

N:        1294
Mean:        0.999
Min:         0.895
Max:         1.469
Range:       0.029
Class:     20

#Class       Class   Count
  1  0.8951          27
  2  0.9238         109
  3  0.9524         304
  4  0.9811         379
  5  1.010          285
  6  1.038          137
  7  1.067           32
  8  1.096           14
  9  1.125            3
 10  1.153            1
 11  1.182            0
 12  1.211            2
 13  1.239            0
 14  1.268            0
 15  1.297            0
 16  1.325            0
 17  1.354            0
 18  1.383            0
 19  1.411            0
 20  1.440            1
 21  1.469            0

Check for diagonal of genomic relationship matrix

Check for diagonal of genomic relationship matrix, genotypes not removed: 0

------------------------------------------

Final Pedigree-Based Matrix

------------------------------------------

Statistic of Rel. Matrix A22

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>1.000</td>
<td>1.250</td>
<td>0.000</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>0.000</td>
<td>0.750</td>
<td>0.001</td>
</tr>
</tbody>
</table>

------------------------------------------
Final Genomic Matrix

Statistic of Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>0.898</td>
<td>1.470</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>-0.158</td>
<td>0.791</td>
<td>0.002</td>
</tr>
</tbody>
</table>

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.2180

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b0 \cdot 11' + b1 \cdot A + e$

Regression coefficients $b0$, $b1$ = 0.000, 0.991

Correlation all elements $G$ & $A$ 0.717

Off-Diagonal

Using 83426 elements from $A22 >= 0.02000$

Estimating Regression Coefficients $G = b0 \cdot 11' + b1 \cdot A + e$

Regression coefficients $b0$, $b1$ = -0.003, 0.999

Correlation Off-Diagonal elements $G$ & $A$ 0.777

Creating $A22$-inverse

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1068

Final $A22$ Inv Matrix

Statistic of Inv. Rel. Matrix $A22$

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.851</td>
<td>1.067</td>
<td>5.812</td>
<td>0.431</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.001</td>
<td>-1.200</td>
<td>0.600</td>
<td>0.001</td>
</tr>
</tbody>
</table>

Creating $G$-inverse

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1047

Final Genomic Inv Matrix

Statistic of Inv. Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>13.466</td>
<td>5.863</td>
<td>45.587</td>
<td>28.023</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.010</td>
<td>-13.521</td>
<td>6.897</td>
<td>0.227</td>
</tr>
</tbody>
</table>

Check for diagonal of Inverse Genomic - Inverse of pedigree relationship matrix

Saving $GimA22i$ in file: "GimA22i"

Final G Inv - $A22$ Inv Matrix

Statistic of Inv. Genomic- $A22$ Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>11.615</td>
<td>4.782</td>
<td>40.309</td>
<td>21.740</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.009</td>
<td>-12.521</td>
<td>6.397</td>
<td>0.211</td>
</tr>
</tbody>
</table>

*------------------------*
Parameter file for PREGSF90 with quality control, removing SNP from chromosome 5 and saving the clean SNP file

DATAFILE renf90.dat
NUMBER_OF_TRAITS 1
NUMBER_OF_EFFECTS 2
OBSERVATION(S) 1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFEKT NESTED]
2 1 cross
3 6100 cross

RANDOM_RESIDUAL VALUES
0.70000
RANDOM_GROUP 2
RANDOM_TYPE add_animal
FILE renadd02.ped
(CO)VARIANCES 0.30000
OPTION SNP_file snp.txt
OPTION chrinfo map.txt
OPTION excludeCHR 5
OPTION saveCleanSNPs

Log file for PREGSF90 with quality control, removing SNP from chromosome 5 and saving the clean SNP file
name of parameter file?
renf90.par

preGS 1.10

Parameter file: renf90.par
Data file: renf90.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type position (2) levels [positions for nested]
1 cross-classified 2 1
2 cross-classified 3 6100
Residual (co)variance Matrix
0.70000

Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped

trait | effect | (CO)VARIANCES
1 | 2 | 0.3000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such effects are missing for specified traits

Options read from parameter file:
* SNP file: snp.txt
* SNP Xref file: snp.txt_XrefID
* Map file: map.txt
* Save Clean SNP data to (SNP_file)_clean file (default .false.)
* Exclude Chromosomes (default .false.): 5

*---------------------------------------------------------------*
* Genomic Library: Version 1.164 *
* Optimized OpenMP Version *
* Modified relationship matrix (H) created for effect: 2 *
*---------------------------------------------------------------*

Read 6100 animals from pedigree file: "renadd02.ped"
Number of Genotyped Animals: 1294

Creating A22
Extracting subset of: 2312 pedigrees from: 6100 elapsed time: 0.0150
Calculating A22 Matrix by Colleau OpenMP...elapsed time: .0190
Numbers of threads=8 16

Reading SNP file
Column position in file for the first marker: 8
Format to read SNP file: (7x,400000i1)
Number of SNPs: 1000
Number of Genotyped animals: 1294
Reading SNP file elapsed time: .06

Statistics of alleles frequencies in the current population
N: 1000
Mean: 0.504
Min: 0.043
Max: 0.929
Var: 0.032

Reading MAP file: "map.txt" - 1000 SNPs out of 1000

Min and max # of chromosome: 1 5
Min and max # of SNP: 1 1000
Excluded 199 SNPs from 1 chromosomes: 5

Quality Control - SNPs with Call Rate < callrate (0.90) will removed: 199
Quality Control - SNPs with MAF < minfreq (0.05) will removed: 1

Quality Control - Monomorphic SNPs will be removed: 0

Quality Control - Removed Animals with Call rate < callrate (0.90): 0

Quality Control - Check Parent-Progeny Mendelian conflicts

Total animals: 6100 - Genotyped animals: 1294 - Effective: 1294

Number of pairs Individual - Sire: 450
Number of pairs Individual - Dam: 440
Number of trios Individual - Sire - Dam: 206

No sex Chromosome information is available
Parent-progeny conflicts or HWE could eliminate SNPs in sex Chr
Provide map information and sex Chr to checks using autosomes

Checking SNPs for Mendelian conflicts

Total number of effective SNF: 801
Total number of parent-progeny evaluations: 890
Number of SNPs with Mendelian conflicts: 0

Checking Animals for Mendelian conflicts

Total number of effective SNF for checks on Animals: 801
Number of Parent-Progeny Mendelian Conflicts: 0

Number of effective SNPs (after QC): 801
Number of effective Individuals (after QC): 1294

Statistics of alleles frequencies in the current population after Quality Control (MAF, monomorphic, call rate, HWE, Mendelian conflicts)
N: 801
Mean: 0.503
Min: 0.051
Max: 0.928
Var: 0.032

List of SNPs removed in: "snp.txt_SNPs_removed"

Clean genotype file was created: "snp.txt_clean"

Cross reference ID file was created: "snp.txt_clean_XrefID"

Genotypes missings (%): 19.900
Genotypes missings after cleaning (%): 0.000

Calculating G Matrix
Dgemm MKL #threads= 8   16 Elapsed omp_get_time: 0.8764
Scale by Sum(2pq). Average: 349.571560214902
Blend G as alpha*G + beta*A22: (alpha,beta) 0.950 0.050

Number of effective SNP was reduced to 801 after removing chromosome 5

New files with clean genotypes
Min: 0.874
Max: 1.593
Range: 0.036
Class: 20

#Class    Class    Count
  1  0.8741          17
  2  0.9100         107
  3  0.9460         341
  4  0.9819         419
  5  1.018          281
  6  1.054          98
  7  1.090           20
  8  1.126           4
  9  1.162           4
10  1.198           1
11  1.234           0
12  1.270           1
13  1.306           0
14  1.342           0
15  1.377           0
16  1.413           0
17  1.449           0
18  1.485           0
19  1.521           0
20  1.557           1
21  1.593           0

Check for diagonal of genomic relationship matrix

Check for diagonal of genomic relationship matrix, genotypes not removed: 0

----------------------------------
Final Pedigree-Based Matrix
----------------------------------

Statistic of Rel. Matrix A22

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>1.000</td>
<td>1.250</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>0.000</td>
<td>0.750</td>
</tr>
</tbody>
</table>

----------------------------------
Final Genomic Matrix
----------------------------------

Statistic of Genomic Matrix

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>0.876</td>
<td>1.593</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>-0.169</td>
<td>0.861</td>
</tr>
</tbody>
</table>

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.2092

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients \( G = b_0 \mathbf{1}' + b_1 \mathbf{A} + e \)

Regression coefficients \( b_0 \) \( b_1 \) = 0.000 0.991

Correlation all elements \( G \& A \) 0.677

Off-Diagonal

Using 83426 elements from A22 >= .02000
Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$

Regression coefficients $b_0, b_1 = -0.002, 0.996$

Correlation Off-Diagonal elements $G \& A = 0.742$

Creating $A22$-inverse

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1409

Final $A22$ Inv Matrix

Statistic of Inv. Rel. Matrix $A22$

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.851</td>
<td>1.067</td>
<td>5.812</td>
<td>0.431</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.001</td>
<td>-1.200</td>
<td>0.600</td>
<td>0.001</td>
</tr>
</tbody>
</table>

Creating $G$-inverse

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1370

Final Genomic Inv Matrix

Statistic of Inv. Genomic Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>17.075</td>
<td>7.840</td>
<td>56.092</td>
<td>43.645</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.013</td>
<td>-16.499</td>
<td>8.893</td>
<td>0.309</td>
</tr>
</tbody>
</table>

Check for diagonal of Inverse Genomic - Inverse of pedigree relationship matrix

Saving GimA22i in file: "GimA22i"

Final G Inv - $A22$ Inv Matrix

Statistic of Inv. Genomic- $A22$ Matrix

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>15.223</td>
<td>6.759</td>
<td>51.043</td>
<td>35.648</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.012</td>
<td>-15.499</td>
<td>8.393</td>
<td>0.289</td>
</tr>
</tbody>
</table>

* Setup Genomic Done !!! *

Parameter file for PREGSF90 with quality control and PCA analysis

Include extra option: OPTION plotpca
Parameter file for BLUPF90 without genomic information

DATAFILE
renf90_5.dat

NUMBER_OF_TRAITS 1
NUMBER_OF_EFFECTS 2

OBSERVATION(S) 1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2 1 cross
3 6100 cross

RANDOM_RESIDUAL VALUES
0.70000

RANDOM_GROUP
2

RANDOM_TYPE
add_animal

FILE
renadd02.ped

(CO)VARIANCES
0.30000

OPTION conv_crit 1e-15

Default convergence criteria = 1e-12

Log file for BLUPF90 without genomic information

name of parameter file?

renf90_5.dat has phenotypes for all animals, but generation 5

Linux code to remove phenotypes for those animals:

```bash
$awk '{ if ($4==5) print 0,$2,$3,$4; else print $1,$2,$3,$4}' renf90.dat > renf90_5.dat
```
renf90.par
* convergence criterion (default=1e-12):  1.0000000E-15

BLUPF90 1.48

Parameter file: renf90.par
Data file: renf90_5.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type position (2) levels [positions for nested]
1  cross-classified  2 1
2  cross-classified  3 6100

Residual (co)variance Matrix
0.70000

Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped

trait effect (CO)VARIANCES
1 2 0.3000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 3
# equations = 6101
G 0.30000
read 6100 records in 1.4997000E-02 s,
nonzeroes
read 6100 additive pedigrees
finished peds in 1.9996000E-02 s, 27178 nonzeroes
round = 1 convergence = 0.1730E-03
round = 2 convergence = 0.7971E-03
round = 3 convergence = 0.5923E-04
round = 4 convergence = 0.6219E-04
round = 5 convergence = 0.2122E-04
.
round = 40 convergence = 0.1230E-13
round = 41 convergence = 0.3164E-14
round = 42 convergence = 0.2804E-14
round = 43 convergence = 0.1081E-14
round = 44 convergence = 0.5761E-15
44 iterations, convergence criterion= 0.5761E-15
solutions stored in file: "solutions"

Solutions for BLUPF90 without genomic information

<table>
<thead>
<tr>
<th>trait/effect level</th>
<th>solution</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 1 1</td>
<td>1.02176505</td>
</tr>
<tr>
<td>1 2 1</td>
<td>-0.24665178</td>
</tr>
</tbody>
</table>
The solution file (solutions) has 4 columns:
1) Trait [only 1 trait in this example]
2) Effect [we have 2 effects: overall mean (effect 1) and additive genetic direct (effect 2)]
3) Level [number of the level for each effect in the model]
4) Solution

**EBV accuracy**

If accuracy of EBV is desired, it can be calculated based on standard errors (se) for EBV.

**BLUPF90** has an option for calculating se:

**OPTION sol se**

### Solutions for BLUPF90 with option to calculate se

<table>
<thead>
<tr>
<th>trait/effect level</th>
<th>solution</th>
<th>s.e.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 1</td>
<td>1.02176504</td>
<td>0.02496866</td>
</tr>
<tr>
<td>1 2</td>
<td>-0.24665117</td>
<td>0.39158195</td>
</tr>
<tr>
<td>1 2</td>
<td>0.16421026</td>
<td>0.40488662</td>
</tr>
<tr>
<td>1 2</td>
<td>0.32371755</td>
<td>0.29405286</td>
</tr>
<tr>
<td>1 2</td>
<td>0.00318218</td>
<td>0.38229658</td>
</tr>
<tr>
<td>1 2</td>
<td>-0.13277154</td>
<td>0.46566701</td>
</tr>
</tbody>
</table>

### Parameter file for BLUPF90 with genomic information (ssGBLUP)

**DATAFILE**
renf90_5.dat

**NUMBER_OF_TRAITS**
1

**NUMBER_OF_EFFECTS**
2

**OBSERVATION(S)**
1

**WEIGHT(S)**

**EFFECTS:** POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECKT NESTED]

| 2 1 cross |
| 3 6100 cross |

**RANDOM_RESIDUAL VALUES**
0.70000

**RANDOM_GROUP**
2

**RANDOM_TYPE**
add_animal

**FILE**
renadd02.ped

**(CO)VARIANCES**
0.30000

**OPTION SNP_file snp.txt**

**OPTION chrinfo map.txt**

**OPTION conv_crit 1e-15**
Log file for BLUPF90 with genomic information (ssGBLUP)

name of parameter file?
renf90.par

* convergence criterion (default=1e-12): 1.0000000E-15

Options read from parameter file:

* SNP file: snp.txt
* SNP Xref file: snp.txt_XrefID
* Map file: map.txt

BLUPF90 1.48

Parameter file: renf90.par
Data file: renf90_5.dat

Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0

Value of Missing Trait/Observation 0

EFFECTS

<table>
<thead>
<tr>
<th>#</th>
<th>type</th>
<th>position (2)</th>
<th>levels</th>
<th>[positions for nested]</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>cross-classified</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>cross-classified</td>
<td>3</td>
<td></td>
<td>6100</td>
</tr>
</tbody>
</table>

Residual (co)variance Matrix

0.70000

Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped

trait effect (CO)VARIANCES

1 2 0.3000

REMARKS

(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such effects are missing for specified traits

Data record length = 3
# equations = 6101

G

0.30000

read 6100 records in 0.1499770 s, 12201
nonzeroes

read 6100 additive pedigrees

*-------------------------------------------------------------*
* Genomic Library: Version 1.164 *
* Optimized OpenMP Version *
* Modified relationship matrix (H) created for effect: 2 *
*-------------------------------------------------------------*

Read 6100 animals from pedigree file: "renadd02.ped"
Number of Genotyped Animals: 1294

Creating A22
Extracting subset of: 2312 pedigrees from: 6100 elapsed time: 0.0150
Calculating A22 Matrix by Colleau OpenMP...elapsed time: 0.0346
Numbers of threads=8 16

Reading SNP file
- Column position in file for the first marker: 8
- Format to read SNP file: (7x,400000i1)
- Number of SNPs: 1000
- Number of Genotyped animals: 1294
- Reading SNP file elapsed time: .06

Statistics of alleles frequencies in the current population
- N: 1000
- Mean: 0.504
- Min: 0.043
- Max: 0.929
- Var: 0.032

Reading MAP file: "map.txt" - 1000 SNPs out of 1000
- Min and max # of chromosome: 1 5
- Min and max # of SNP: 1 1000

Quality Control - SNPs with Call Rate < callrate (0.90) will removed: 0
Quality Control - SNPs with MAF < minfreq (0.05) will removed: 1
Quality Control - Monomorphic SNPs will be removed: 0
Quality Control - Removed Animals with Call rate < callrate (0.90): 0
Quality Control - Check Parent-Progeny Mendelian conflicts

Total animals: 6100 - Genotyped animals: 1294 - Effective: 1294
- Number of pairs Individual - Sire: 450
- Number of pairs Individual - Dam: 440
- Number of trios Individual - Sire - Dam: 206

No sex Chromosome information is available
Parent-progeny conflicts or HWE could eliminate SNPs in sex Chr
Provide map information and sex Chr to checks using autosomes

Checking SNPs for Mendelian conflicts
- Total number of effective SNP: 999
- Total number of parent-progeny evaluations: 890
- Number of SNPs with Mendelian conflicts: 0

Checking Animals for Mendelian conflicts
- Total number of effective SNP for checks on Animals: 999
- Number of Parent-Progeny Mendelian Conflicts: 0

Number of effective SNPs (after QC): 999
Number of effective Individuals (after QC): 1294

Statistics of alleles frequencies in the current population after Quality Control (MAF, monomorphic, call rate, HWE, Mendelian conflicts)
N: 999
Mean: 0.504
Min: 0.051
Max: 0.929
Var: 0.032

Genotypes missings (%): 0.100
Genotypes missings after cleaning (%): 0.000

Calculating G Matrix

Dgemm MKL #threads= 8 16 Elapsed omp_get_time: 1.0240

Scale by Sum(2pq). Average: 435.140185710293

Blend G as alpha*G + beta*A22: (alpha, beta) 0.950 0.050

Frequency - Diagonal of G
N: 1294
Mean: 0.999
Min: 0.895
Max: 1.469
Range: 0.029
Class: 20

#Class  Class  Count
1  0.8951  27
2  0.9238  109
3  0.9524  304
4  0.9811  379
5  1.010  285
6  1.038  137
7  1.067  32
8  1.096  14
9  1.125  3
10  1.153  1
11  1.182  0
12  1.211  2
13  1.239  0
14  1.268  0
15  1.297  0
16  1.325  0
17  1.354  0
18  1.383  0
19  1.411  0
20  1.440  1
21  1.469  0

Check for diagonal of genomic relationship matrix

Check for diagonal of genomic relationship matrix, genotypes not removed: 0

---------------------------------
Final Pedigree-Based Matrix
---------------------------------

Statistic of Rel. Matrix A22

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>1.000</td>
<td>1.250</td>
<td>0.000</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>0.000</td>
<td>0.750</td>
<td>0.001</td>
</tr>
</tbody>
</table>
---

**Final Genomic Matrix**

---

**Statistic of Genomic Matrix**

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.001</td>
<td>0.898</td>
<td>1.470</td>
<td>0.002</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>0.005</td>
<td>-0.158</td>
<td>0.791</td>
<td>0.002</td>
</tr>
</tbody>
</table>

**Correlation of Genomic Inbreeding and Pedigree Inbreeding**

**Correlation:** 0.2180

**All elements - Diagonal / Off-Diagonal**

Estimating Regression Coefficients $G = b0 \ 11' + b1 \ A + e$

Regression coefficients $b0$ $b1$ = 0.000 0.991

Correlation all elements $G \ & \ A$ 0.717

**Off-Diagonal**

Using 83426 elements from $A22 \ >= \ .02000$

Estimating Regression Coefficients $G = b0 \ 11' + b1 \ A + e$

Regression coefficients $b0$ $b1$ = -0.003 0.999

Correlation Off-Diagonal elements $G \ & \ A$ 0.777

**Creating A22-inverse**

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1059

---

**Final A22 Inv Matrix**

---

**Statistic of Inv. Rel. Matrix A22**

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>1.851</td>
<td>1.067</td>
<td>5.812</td>
<td>0.431</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.001</td>
<td>-1.200</td>
<td>0.600</td>
<td>0.001</td>
</tr>
</tbody>
</table>

**Creating G-inverse**

Inverse LAPACK MKL dpotrf/i #threads= 8 16 Elapsed omp_get_time: 0.1093

---

**Final Genomic Inv Matrix**

---

**Statistic of Inv. Genomic Matrix**

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>13.466</td>
<td>5.863</td>
<td>45.587</td>
<td>28.023</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.010</td>
<td>-13.521</td>
<td>6.897</td>
<td>0.227</td>
</tr>
</tbody>
</table>

**Check for diagonal of Inverse Genomic - Inverse of pedigree relationship matrix**

---

**Final G Inv - A22 Inv Matrix**

---

**Statistic of Inv. Genomic- A22 Matrix**
<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Min</th>
<th>Max</th>
<th>Var</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diagonal</td>
<td>1294</td>
<td>11.615</td>
<td>4.782</td>
<td>40.309</td>
</tr>
<tr>
<td>Off-diagonal</td>
<td>1673142</td>
<td>-0.009</td>
<td>-12.521</td>
<td>6.397</td>
</tr>
</tbody>
</table>

*------------------------*
* Setup Genomic Done !!! *
*------------------------*

hash matrix increased from 131072 to 262144 % filled: 0.8000
hash matrix increased from 262144 to 524288 % filled: 0.8000
hash matrix increased from 524288 to 1048576 % filled: 0.8000
hash matrix increased from 1048576 to 2097152 % filled: 0.8000

finished peds in 25.61810 s, 861721 nonzeroes

round = 1  convergence = 0.6397E-03
round = 2  convergence = 0.4280E-03
round = 3  convergence = 0.3112E-03
round = 4  convergence = 0.9994E-04
round = 5  convergence = 0.8129E-04

round = 90  convergence = 0.3590E-14
round = 91  convergence = 0.2549E-14
round = 92  convergence = 0.2022E-14
round = 93  convergence = 0.1453E-14
round = 94  convergence = 0.9599E-15

94 iterations, convergence criterion= 0.9599E-15
solutions stored in file: "solutions"

Solutions for BLUPF90 with genomic information (ssGBLUP)
The solution file has the same format as in blupf90 without genomic information. The option for calculating se for EBV can also be used here.

Parameter file for PREDICTF90
Predictivity can be measured as correlation between adjusted phenotypes and (G)EBV. In this example we show how to use PREDICTF90 to adjust phenotypes for genotyped animals in the validation population.

1) Adjusting phenotypes
As this program needs solution file, it can be run in the same folder as BLUP with complete data

Parameter file:
DATAFILE
pred.dat
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
2
OBSERVATION(S)
1
WEIGHT(S)

* pred.dat is the data file only for genotyped animals in the 5th generation (validation animals). Lines can be extracted from renf90.dat*
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
2  1 cross
3  6100 cross
RANDOM_RESIDUAL VALUES
0.70000
RANDOM_GROUP
2
RANDOM_TYPE
add_animal
FILE
renadd02.ped
(CO)VARIANCES
0.30000
OPTION include_effects 2

Log file for adjusting phenotypes for genotyped animals in 5th generation
name of parameter file?
pred.par

*** include effects to predict $Y_{hat}$, effects 1 2
PREDICTF90 1.3

Parameter file: gen.par
Data file: pred.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type                position (2)        levels   [positions for nested]
1  cross-classified  2                           1
2  cross-classified  3                        6100

Residual (co)variance Matrix
0.70000
Random Effect(s) 2
Type of Random Effect: additive animal
Pedigree File: renadd02.ped
trait  effect    (CO)VARIANCES
1  2    0.3000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 3
# equations = 6101
*** effets to include in Yhat (T/F): F T
solutions read from file: soltutions
Animal Effect: 2
$y(s)$, $yhat(s)$, residual(s) in written in "yhat_residual" file
300 records read
Trait: 1 300
mean $Y$ -5.204056186291079E-002 var $Y$ 0.979795877964320
mean Yhat  -1.187536126623551E-002 var Yhat  7.349890384221654E-002
cov (Y,Yhat)  8.232182257800019E-002 corr (Y,Yhat)  0.306765659847626
wrote bvs for animals in data in file “bvs.dat”

Output files from PREDICTF90

yhat_residual

<table>
<thead>
<tr>
<th>yhat_residual has 4 columns: animal</th>
<th>y</th>
<th>yhat</th>
<th>residual</th>
</tr>
</thead>
<tbody>
<tr>
<td>4644 -0.266520 0.415535 0.339710</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2176 -0.418925 0.094263 0.508577</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

bvs.dat

<table>
<thead>
<tr>
<th>bvs.dat has 4 columns: trait</th>
<th>effect</th>
<th>Animal</th>
<th>solution (EBV)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 2 4644 0.415535</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1 2 2176 0.094263</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Hint: corr (Y,Yhat) from the output of PREDICTF90 (corr (Y,Yhat)  0.306765659847626) should not be used as a measure of predictivity because it uses adjusted phenotypes and EBVs from the same dataset. Usually, predictivity requires phenotypes adjusted for fixed effects in the complete data (benchmark) and (G)EBVs calculated from the reduced data (without records for validation animals). The regular predictivity measure is: corr[Y_from_PREDICTf90, (G)EBV_reduced]

For this small example with 1 trait, a general Linux code to merge files is:

```
$ awk '{print $1,$2}' ebv_complete/yhat_residual | sort +0 -1 > Y
$ awk '{if ($2==2) print $3,$4}' ebv_reduced/solutions | sort +0 -1 > ebv.temp
$ awk '{if ($2==2) print $3,$4}' gebv_reduced/solutions | sort +0 -1 > gebv.temp
$join -1 +1 -2 +1 Y ebv.temp > file1.temp
$join -1 +1 -2 +1 file1.temp gebv.temp > Y_ebv_gebv
```

An R code to calculate correlations is:

```
pred <- read.table("Y_ebv_gebv",header=F)
ebv_predictivity <- cor(pred[,2],pred[,3]); ebv_predictivity
gebv_predictivity <- cor(pred[,2],pred[,4]); gebv_predictivity
```

Parameter files for GWAS using ssGBLUP (ssGWAS)

Run BLUPF90 with genomic information and salve G^{-1} and A_{22}^{-1}

DATAFILE
renf90.dat
NUMBER_OF_TRAITS
Weights for SNP can be updated by an iterative process, where the initial weights are all equal to 1.

Linux code to get initial weights for 1000 SNP:
```bash
$ awk 'BEGIN { for (i==1;i<1000;i++) print 1}' > wei
```

Run POSTGSF90 and read $G^{-1}$ and $A_{22}^{-1}$

```bash
DATAFILE renf90.dat
NUMBER_OF_TRAITS 1
NUMBER_OF_EFFECTS 2
OBSERVATION(S) 1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
  2 1 cross
  3 6100 cross
RANDOM_RESIDUAL VALUES
  0.70000
RANDOM_GROUP
  2
RANDOM_TYPE
  add_animal
FILE renadd02.ped
(CO)VARIANCES
  0.30000
```

```bash
OPTION SNP_file snp.txt
OPTION chrinfo map.txt
OPTION no_quality_control
OPTION saveGInverse
OPTION saveA22Inverse
OPTION weightedG wei
```
OPTION SNP_file snp.txt
OPTION chrinfo map.txt
OPTION no_quality_control
OPTION Manhattan_plot
OPTION readGInverse
OPTION readA22Inverse
OPTION weightedG wei
OPTION windows_variance 5

Moving average of SNP effects can be obtained by using the following option:
OPTION SNP_moving_average n
where n is the number of SNP

Manhattan plots for SNP windows variance

Manhattan plots for SNP effect using moving average of 2 SNP
Output files for ssGWAS

snp_sol

<table>
<thead>
<tr>
<th>SNP</th>
<th>chromosome</th>
<th>position</th>
<th>SNP_solution</th>
<th>weight</th>
<th>% of variance explained by n adjacent SNP</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0.7001368E-02</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0.2209213</td>
<td>0.1119293</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>0.1359349E-01</td>
<td>0.5065436</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>0.8714214E-02</td>
<td>0.3917027</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>4</td>
<td>0.4223401E-02</td>
<td>0.6873333E-01</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>5</td>
<td>0.5471629E-03</td>
<td>0.1539137E-02</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>5</td>
<td>1</td>
<td>0.1269296E-02</td>
<td>0.1269296E-02</td>
</tr>
</tbody>
</table>

snp_sol has 9 columns because “OPTION windows_variance” was used:

trait | effect | SNP | chromosome | position | SNP_solution | weight | % of variance explained by n adjacent SNP

chrsnpvar

<table>
<thead>
<tr>
<th>SNP</th>
<th>chromosome</th>
<th>position</th>
<th>SNP</th>
<th>% of variance explained by n adjacent SNP</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0.1119293459</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>0.2104747339</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>0.7757968029</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>4</td>
<td>1.2711127978</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>5</td>
<td>1.2610103595</td>
</tr>
</tbody>
</table>

chrsnpvar has 6 columns:

trait | effect | % of variance explained by n adjacent SNP | SNP | chromosome | position

This file is used by POSTGSF90 for Manhattan plots
Appendix J (custom relationship matrices)

When a relationship (or dispersion) matrix cannot be created within the application programs, it can be prepared separately and then included as a custom relationship matrix. Two options exist for inclusion of such a matrix. Option user_file incorporates this matrix directly. Option user_file_inv incorporates the inverse of this matrix.

The example below presents a model from the previous Appendix with matrix $H^{-1}$ created externally and then read as a custom matrix. The custom matrix (Hinverse.txt) is stored as below, with each line containing: row, column and value.

```
1   1   3.0000
1   422  -1.0000
1   870   0.5000
1   4326  -1.0000
1   4612  -1.0000
   .   .   
   .   .   
6096 6100  -0.0527
6097 6097   2.5000
6098 6098  11.0000
6099 6099   2.0000
6100 6100  12.0236
```

Parameter file for BLUPF90 with a custom relationship matrix

```
DATAFILE
  renf90_5.dat
NUMBER_OF_TRAITS
  1
NUMBER_OF_EFFECTS
  2
OBSERVATION(S)
  1
WEIGHT(S)
  1

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFE
CT NESTED]
  2   1 cross
  3   6100 cross
RANDOM_RESIDUAL VALUES
  0.70000
RANDOM_GROUP
  2
RANDOM_TYPE
  user_file
FILE
  Hinverse.txt
(CO)VARIANCES
  0.30000
OPTION conv_crit 1e-15
```
Log file for BLUPF90 with a custom relationship matrix

name of parameter file?
user.par

* convergence criterion (default=1e-12):  1.0000000E-15

BLUPF90 1.48

Parameter file: user.par
Data file: renf90_5.dat
Number of Traits 1
Number of Effects 2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

EFFECTS
# type position (2) levels [positions for nested]
1 cross-classified 2 1
2 cross-classified 3 6100

Residual (co)variance Matrix
0.70000

Random Effect(s) 2
Type of Random Effect: user defined from file
User File: Hinverse.txt

trait effect (CO)VARIANCES
1 2 0.3000

REMARKS
(1) Weight position 0 means no weights utilized
(2) Effect positions of 0 for some effects and traits means that such
effects are missing for specified traits

Data record length = 3
# equations = 6101
G
0.30000
read 6100 records in 4.7991998E-02 s, 12201 nonzeros
...
g_usr_inv: read 855620 elements
largest row, column, diagonal: 6100 6100 6100
...
finished peds in 1.776729 s, 861721 nonzeros
round = 1 convergence = 0.5737E-03
...
round = 80 convergence = 0.9128E-15
80 iterations, convergence criterion=0.9128E-15
solutions stored in file: "solutions"
Appendix K (selected programming details)

This section provides some programming insights into an early version of the blupf90 program. The model is completely described in the module MODEL.

module model
implicit none
!
! Types of effects
integer, parameter :: effcross=0, & ! effects can be cross-classified
   effcov=1 ! or covariables
+
!
! Types of random effects
integer, parameter ::
   g_fixed=1, & ! fixed effect
   g_diag=2, & ! diagonal
   g_A=3, & ! additive animal
   g_A_UPG=4, & ! additive animal with unknown
   ! parent groups
   & g_A_UPG_INB=5, & ! additive animal with unknown
   ! parent groups and inbreeding
   & g_AS=6, & ! additive size
   g_PD =7, & ! parental dominance
   g_last=8 ! last type
character (40) :: parfile, & ! name of parameter file
datafile ! name of data set
integer :: ntrait,& ! number of traits
neff,& ! number of effects
miss=0 ! value of missing trait/effect
integer, allocatable :: pos_y(:) ! positions of observations
integer :: pos_weight ! position of weight of records; zero if none
integer, allocatable :: pos_eff(:,,:),& ! positions of effects for each trait
   nlev(:,),& ! number of levels
   effecttype(:,),& ! type of effects
   nestedcov(:,,:),& ! position of nesting effect for each trait
   ! if the effect is nested covariable
   & randomtype(:,),& ! status of each effect, as above
   randomnumb(:) ! number of consecutive correlated effects
character (40), allocatable :: randomfile(:) ! name of file associated with given
! effect
real, allocatable :: r(:,,:),& ! residual (co)variance matrix
   rinv(:,,:),& ! and its inverse
   g(:,,:) ! The random (co)variance matrix for each trait
end module model

The core of the program is presented below.

program BLUPF90
use model; use sparsem; use sparseop
implicit none
real, allocatable :: y(:,:),& ! observation value
   indata(:) ! one line of input data
real :: weight_y ! weight for records
type (sparse_hashm):: xx ! X'X in sparse hash form
type (sparse_ija):: xx_ija
! X'X in IJA form, for use with FSPAK only
real, allocatable:: xy(:),sol(:)
! X'Y and solutions
real, allocatable :: weight_cov(:,:)
integer, allocatable:: address(:,:)
! start and address of each effect
integer :: neq,io,&
data_len,&
i,j,k,l
! number of equations and io-status
! length of data record to read
! extra variables
real:: val, dat_eff
!
call read_parameters
call print_parameters
neq=ntrait*sum(nlev)
allocate (xy(neq), sol(neq), address(neff,ntrait),&
    weight_cov(neff,ntrait), y(ntrait), indata(data_len))
call zerom(xx,neq); xy=0
!
call setup_g
! invert R matrices
!
open(50,file=datafile)
!
! Contributions from records
do
    read(50,*),iostat=io)indata
    if (io.ne.0) exit
    call decode_record
call find_addresses
call find_rinv
do i=1,neff
    do j=1,neff
    do k=1,ntrait
        do l=1,ntrait
            val=weight_cov(i,k)*weight_cov(j,l)*weight_y*rinv(k,l)
call addm(val,address(i,k),address(j,l),xx)
        enddo
    enddo
enddo
!
call setup_g
! invert R matrices
!
open(50,file=datafile)
!
! Random effects' contributions
do i=1,neff
select case (randomtype(i))
  case (g_fixed)
      continue
  case (g_diag)
      call add_g_diag(i)
  case (g_A, g_As, g_A_UPG, g_A_UPG_INB)
      call add_g_add(randomtype(i),i)
  case (g_PD)
      call add_g_domin(i)
  case default
      print*,'unimplemented random type',randomtype(i)
endselect
enddo
!
if (neq < 15) then
    print*, 'left hand side'
call printm(xx)
    print '(('' right hand side:'',100f8.1)'',xy
endif
call solve_iterm(xx,xy,sol)

! Comment the line above and uncomment the lines below only if
! solutions by FSPAK are desired
!xx_ija=xx;
!call fspak90('solve',xx_ija,xy,sol)

if (neq <15) print '( '' solution:' ,100f7.3)',sol

call store_solutions
Modules and Libraries

Module DENSEOP
Subroutines and functions for dense matrix manipulation in Fortran 90.
Uses F90 LAPACK implementation by Alan Miller for some low level routines.

Written by: Tomasz Strabel & Ignacy Misztal, University of Georgia e-mail: strabel@au.poznan.pl, ignacy@uga.edu, Oct/5/98-June 8, 2006

The module implements matrix operations on dense general and symmetric matrices. Each subroutine/function is overloaded to work with several types of arguments. The module is primarily designed for matrix operations where timing and memory requirements are not critical.

Symmetric matrices
Each of the functions/subroutines works with full-stored and packed (half-stored) matrices. Each matrix or vector can be single or double precision. However, in one function/subroutine, all arguments should be of the same precision, and all matrices should be stored the same way.

Subroutines

call chol(a, rank) - Cholesky decomposition

call inverse_s(A, rank) - Generalized inverse: \( A^I = A^{-1} \)

call eigen(A, d, V) - Eigenvalues and eigenvectors: \( A = V \text{diag}(d) V' \)

call solve_s(A, b, x) - Generalized solutions: \( A x = b \)

The optional variable rank returns the rank of the matrix.

Functions

fchol(A) - Cholesky decomposition

finverse_s(A) - Generalized inverse

fsolve_s(A, b) - Generalized solve

fdet_s(A) - Determinant of A

Procedures for symmetric matrices work with generalized matrices. Redundant rows/columns equations are determined by operational zero, which is kept in global variable denseop_tol with default value is 10^-10. To change the limit, change the value of the variable in the application program, e.g., denseop_tol=1d-12

Conversions
Let A be a square matrix and AP be a packed matrix
call packit(A,AP) - Conversion from square to packed form; only lower-diagonal elements are used.
call unpackit(AP,A) - Conversion from packed to square form; the matrix is assumed symmetric.

**General matrices**
Each matrix or vector can be single or double precision. However, in one function/subroutine, all arguments should be of the same precision. All matrices are assumed full-rank.

**Subroutines**
call inverse(A) - Inverse: AI = A^(-1)  
call solve(A,b,x) - Solutions: x: Ax=b

**Functions**
AI=finverse(A) - Returns inverse: AI = Ax=f{solve(A,b)} - Computes solutions: x: Ax=b

**Printing**
call printmat(matrix, text, fmt, un) - print any type of matrix using the specified format fmt and preceded by text. Both text and fmt are optional. If optional un is present, the output is send to file with unit un.  
Warning: The printmat function prints the symmetric packed matrices in full. If a half-stored matrix is in packed form, it will be printed as full-stored matrix.

**Additional subroutines and functions**
The subroutine(s) and functions below work only with double precision arguments (r8) and fullstored matrices.
call pos_def(x,text,min_eig,stat) - Corrects X if it is not “sufficiently” positive-definite; ignores rows/columns with 0 elements only.
    X - real (r8) symmetric square matrix
    text - optional character variable that is printed if X is corrected
    min_eig - optional real (r8) variable that sets the minimum relative eigenvalue in X; if min_eig is missing, 1e-5 is used.
    stat - optional logical variable that is set to .true. if X was corrected and .false. if not.
A = diag(b) - creates square diagonal real (r8) matrix with values of real (r8) vector b on diagonal
b = diag(A) - creates real (r8) vector b containing diagonals of real (r8) matrix A
A=kron(B,C) - A = B “Kronecker product” C; works with real(r4) and real (r8) matrices

**Technical details**
The basic operations are done in full storage and double precision. Operations with other formats and precision are obtained by conversions. Computing of eigenvalues/eigenevectors and general matrix
operations use parts of LAPACK subroutines as converted by Alan Miller. These subroutines may contain many more functionality than necessary and may be trimmed to reduce size of the object code.

The modules consist of two files:
lapack90r.f90 - Part of LAPACK denseop.f90 - Interfaces, subroutines, functions and conversion codes.

For compilation, module kind in file kind.f90 that contains definitions of single and double precision is also needed.

In the BLUPF90 distribution, these files are included in directory libs and are compiled as denseop.a. One way to use the denseop module is via a Makefile from an application program in the blupf90 package.

Example (exdense.f90)
Program Example:

```fortran
use kinds; use denseop
real (r4):: xpacked4(3)=(/1,3,10/) ! Symmetric packed single precision
real (r4)::x4(2,2) ! Full single precision
real (r8)::x8(2,2) ! Full double precision
call printmat(xpacked4, ' X ')
call printmat(fchol(xpacked4), ' Cholesky(X) ','(10(f10.2))')
x4=xpacked4
x8=x4
print*, ' Determinant(xpacked4)=',fdet_s(xpacked4)
print*, ' Determinant(x8)=',fdet_s(x8)
print*, ' Determinant(x4)=',fdet_s(x4)
end
```

Compilation
To compile standalone:
```
f90 kind.f90 lapack90r.f90 denseop.f90 exdense.f90
```
This assumes that all files are in the same directory.

To compile in subdirectory of the blupf90 distribution under Linux/Absoft,
```
f90 -p ../libs exdense.f90 ../libs/denseop.a
```
where option -p specifies library directory. This option (-p) is different under different platforms. See documentation on blupf90 distribution for details.
Module SPARSEM
Collection of sparse matrix modules for Fortran 90 useful in animal breeding problems

Written by: Ignacy Misztal, University of Georgia e-mail: ignacy@uga.edu, 9/4/1997 - 5/25/2007

Introduction
Traditionally, programming in animal breeding is done in 2 stages: in a matrix language and in a regular programming language. Programs in a matrix language such as IML SAS, Matlab, Mathematica or APL are reasonably simple and useful for creating examples but inefficient for large problems. Programs in a regular programming language such as Fortran or C/C++ are much more efficient but could take much longer to write and require substantial training.

Matrix languages are easy to deal with matrices partly because usually only one format is usually supported: dense rectangular. Operations on such matrices are easy to specify and program, but large matrices require large memory and long running time. Also, memory and computations are equal whether matrices are sparse (contain very few nonzero elements) or not. In animal breeding, many matrices are sparse. If that sparsity is taken into account, the memory requirements and computations can decrease dramatically. Unfortunately, there is more than one format for storing sparse matrices, and some computations are fast with one format and but not with another one. Also, the storage formats and operations are considerably more complicated than dense rectangular matrices. A library to handle multiple matrix formats and multiple operations would contain many subroutines, each with a long list of arguments. Such a library would involve considerable learning, and many details associated with the library would create many opportunities for making a mistake.

One matrix package, Matlab, has some forms of sparse-matrix storage and operations included.

Modern programming languages with “object-oriented” features, such as C++ or Fortran 90, have abilities to create classes/modules, where many implementation details on specific data structures can be hidden. A technique called overloading allows single function/subroutine to work with different formats of its arguments. Therefore, the number of details to remember can be drastically reduced. Subsequently, programming can be done much easier and quicker.

SPARSEM is a module for Fortran 90 that enables programming common sparse matrix operations almost as easily as with dense matrices. It supports two dense matrix formats, useful for testing, and two sparse matrix formats. Changing a program from dense to sparse-matrix format using DENSEM can be as simple as changing one declaration line. SPARSEM incorporates an interface to FSPAK, which enables efficient sparse matrix factorization, solving, sparse inversion and calculation of determinant on matrices much larger than possible with dense matrix structures.
**Matrix formats**

Four matrix formats are available.

DENSEM - dense square matrix.

DENSE_SYMM - dense symmetric upper-stored.

   It has approximately only half memory requirements of the dense square matrix.

SPARSE_HASHM - sparse triple accessed by hash algorithm.

   This is a very efficient format for set-up and for iterative-solving of sparse matrices.

SPARSE_IJA - Sparse IJA.

   This is a memory-efficient format for sparse matrices used by sparse matrix packages. Format IJA cannot easily be set up directly but can be derived by conversion from the hash format.

For more information on all these formats see Duff et al, George and Liu, or my class notes.

A popular format that is not included here is linked list. That format is reasonably efficient for creating and computing with sparse matrices if the number of nonzero elements per row is not too high and the matrix is not too large. However, the combination of hash plus ija is generally more efficient.

**Matrix operations**

The following subroutines/functions are supported. All real scalars and vectors are single precision unless indicated otherwise.

<table>
<thead>
<tr>
<th>Operation</th>
<th>Description</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>call init(x)</td>
<td>Initialize x</td>
<td>Required by standard but usually not necessary because on most systems pointers are initialized automatically</td>
</tr>
<tr>
<td>call zerom(x,n)</td>
<td>Allocate storage for x as an n*n matrix and zero it</td>
<td>If x was set before, it is reallocated¹</td>
</tr>
<tr>
<td>call reset(x)</td>
<td>Deallocates storage</td>
<td></td>
</tr>
</tbody>
</table>
call addm(a,i,j,x) \quad \text{Add to matrix: } x(i,j)=x(i,j)+a \quad \text{Does not work on SPARSE_IJA}

call setm(a,i,j,x) \quad \text{sets element of matrix: } x(i,j)=a \quad \text{Does not work on SPARSE_IJA}

y=getm(i,j,x) \quad \text{find element of matrix: } y=x(i,j) \quad \text{real(4) function; returns lower-diagonal elements of upper-stored matrix}

x=y \quad \text{Conversion between formats} \quad \text{Conversion from sparse to dense formats may require too much storage}

call printm(x) \quad \text{Prints } x \text{ as square matrix} \quad \text{print(x,'internal') prints sparse matrices in internal format}

call solve_iterm(x,rs,sol) \quad \text{Solves: } x \text{ sol=rs iteratively by SOR}

call default_iter \quad \text{Changes default iteration parameters} \quad \text{All parameters are optional; default values are: conv(ergence criterion)=1e-10, max round(s)=1000, relax(ation factor)=1.0, zerosol(utions ar beginning of iteration) = .true.}

x=block(y,i1,i2,j1,j2) \quad \text{Selects block from y: } x=y(i1:i1,j1:j2) \quad \text{does not work on dense_symm format; may not work with unsymmetric blocks from symmetric matrices}

q=quadrf(u,x,v) \quad q=u'Xv \quad \text{real(8) function; does not work on dense_symm format}

tr=trace(x,y) \quad \text{Self explanatory} \quad \text{real(8) function; } x \text{ and } y \text{ must be in same formats; works on dense and sparse_iia formats only}

tr=traceblock(x,y,i1,i2,j1,j2) \quad \text{tr=trace(xy(i1:i2,j1:j2))} \quad \text{Works as a block-trace combination; produces correct results when blocks of } y \text{ are nonsymmetric}
1The hash matrix is allocated for a default number of elements. If the default is too small, the hash matrix is enlarged automatically. To change the default p elements, use call zerom(x,n,p). One matrix element in hash format takes 12 bytes, and for efficient operation there should be at least 10% more nonzero elements available than used.

All operations assume that the densem type is general while all the other types are upperstored.

Operations tr, quadf work with both upper- and full-stored matrices but the block operation works literally, i.e., selecting a lower block would return an empty matrix and selecting an upper block would return only an upper-stored matrix. This could be a source of incompatibility between densem and other formats that use the block operation without taking its limitations into consideration. Potential problems can be noticed in examples by printing matrices of interest.

**Storage type**
Matrices in the hash or ija format are half-stored by default. To change the storage type to full, add the option ‘f’ to the addm subroutine: call addm(a,i,j,x,’f’)
The subsequent conversion to the ija format will also be full-stored. For conversion from half-stored hash matrix to full-stored ija, please see a documentation for the GIBBS module.

The printing and other functions/subroutines have been designed for half-stored hash and ija matrices. Results may not be correct with full-stored matrices.

**Numerical accuracy**
Module KINDS defines precision r4 to be equivalent to real*4, and r8 to be equivalent to r8. Precision rh can be set up to r4 or r8 dependent on whether memory or precision is more important.

Formats DENSEM, DENSE_SYMM, and SPARSE_IJA use precision r8. Format SPARSE_HASHM uses precision rh. Whenever the precision of numbers in SPARSEM functions/subroutines is not specified, it is of type rh. Setting rh to r4 is useful when memory usage needs to be reduced, e.g., for large BLUP programs. Setting rh to r8 is necessary when numerical accuracy is important, e.g., in variance component programs, and is usually a safer choice.

**Diagnostics**
Printing of some diagnostic messages depends on the value of an integer variable sparsem_msg. The value of 3 means maximum diagnostic messages while the value of 0 means no diagnostic messages. The default is 2. This variable can be set in any part of the application program using the module SPARSEM.
**FSPAK90**

FSPAK is a sparse matrix package written in F77 that performs operations on sparse matrices in format SPARSE_IJA. Operations include solving a system of linear equations by factorization, calculating a (log) determinant or finding a sparse inverse of a matrix. A sparse inverse is such a matrix that contains inverse values only for those elements that were nonzero in the original matrix. For sparse matrices, FSPAK is very efficient computationally.

FSPAK90 is a F90 interface written to simplify the use of FSPAK.

A complete call to FSPAK90 is:

```fortran
call fspak90(operation, ija, rs, sol, det, msglev, maxmem, rank)
```

where

- `operation` =  
  - “factorize” - calculate sparse factorization
  - “invert” - calculate sparse inverse
  - “solve” - solve a system of equation
  - “reset” - reset the storage
  - “det” - calculate determinant
  - “stat” - print statistics
  - “fact_mult” - multiplication by Cholesky factor of the reordered matrix (if LL=IJA; sol=L*rs)
  - “inv_fact_mult” - solve the system formed by the Cholesky factor of the reordered matrix (sol: L*sol=rs)

- `ija` = matrix in SPARSE_IJA form
- `rs` = real (r4) or (r8) vector of right hand side,
- `sol` = real (r4) or (r8), identical to precision of `rs`, vector of solutions
- `det` = real (r8) determinant or log-determinant
- `msglev`= message level from 0 (minimum) to 3 (maximum); default=0
- `maxmem`=maximum memory available in the system; default=infinite
- `rank`=rank of matrix

All the arguments of `fspak90` except “operation” and “ija” are optional except when they are needed in a specific “operation”. Thus, `rs` and `sol` are needed for solving and `det` for “det” or “ldet”.

**Examples:**

To solve:

```fortran
call fspak90(’solve’, ija, rs, sol)
```
for both `rs` and `sol` either in single or double precision; all. Preceding steps are done automatically.

To solve using double precision right hand side and solutions:

```fortran
call fspak90(’solve’, ija, rs8=rs, sol8=sol)
```

To sparse invert:
call fspak90('invert',ija)

To obtain the determinant $d$:
call fspak90('det',ija,det=d)

To obtain the log determinant $ld$:
call fspak90('ldet',ija,det=ld)

To obtain rank $r$ with any operation:
call fspak90(......,rank=r)

To force new factorization, when the input matrix has changed: call fspak90('factor',ija)

To deallocate the internal memory:
call fspak90('reset')

To limit memory to a maximum of maxmem, e.g., 20,000k, with any operation call fspak90(.................,maxmem=20000)

Note that only relevant arguments for each step need to be included in calling FSPAK90. Reordering is performed the first time when FSPAK90 is called. Subsequent factorization except after the option “reset” will reuse the ordering. Subsequent solves will reuse the factorization.

Additionally:

To sample $y$ from $N(0,A)$ where $x\sim N(0,1)$
call fspak90('fact_mult',A,rs8=x,sol8=y)

To sample $y$ from $N(0,A^{-1})$ where $x\sim N(0,1)$
call fspak90('inv_fact_mult',A,rs8=x,sol8=y)

For details of the last operations, see Appendix S2

Additional subroutines and functions:

Function

\[
\begin{align*}
y &= \text{mult}(A, x) \\
y &= \text{mult}(x, A)
\end{align*}
\]

Implements the matrix by vector multiplication for all matrix formats except dense_symm, and for double precision $x$ and $y$.

Subroutine

\[
\text{call multmatscal}(A, x)
\]

Implements $A=A\times x$ for all matrix formats except dense_symm, and for double precision $x$.

Hints on using SPARSEM

Initially all the matrices can be implemented in DENSEM format. After the program works well with an example, convert all data structures for potentially large matrices to sparse formats and verify that same results are obtained.
Compiling
Matrix types and functions subroutine are defined in module sparsem. Subroutine fspak90 is in module sparseop. Program xx.f90 can be compiled as

```
f90 -Maa xx.f90 aa/sparsem.a
```

where aa is the directory containing the modules and the library, and M is the option to include module directory.

Beginning in May, 1999, SPARSEM is part of a programming package that includes BLUPF90, REMLF90, GIBSF90 etc. Compilation for several Unix environments is automated by makefiles. To find details, read Readme and Installation files in the package distributions. To create application with SPARSEM and possibly other modules, create a subdirectory in the main directory of the package, and adapt a makefile from the existing directory, e.g., blup.

Sample Programs

Dense matrix solution program

```
program test_sparse_structures use sparsem; use kinds type (densem)::x
integer,parameter ::n=5
integer :: i,j
real (rh):: rs(n),sol(n),val

call init(x)
call zerom(x,n)

! set up a sample matrix do
i=1,n
   rs(i)=n+1-i
   val=10.0*i/i
   call addm(val,i,i,x)
do j=i+1,n
   val=10.0*i/j
   call addm(val,i,j,x); call addm(val,j,i,x)
endo
dendo

print*,'rs: ',rs print*,'matrix' ; call printm(y) call solve_iterm(y,rs,sol) !solve iteratively
print*,'sol: ',sol
end
```

Triangular dense matrix iterative-solution program
Sparse hash matrix iterative-solution program

....

Sparse IJA matrix iterative-solution program

Matrix in ija form cannot be set up directly but can be converted from hash form.

....

type (sparse_hashm)::x type
(sparse_ija)::y
...

end

Sparse IJA matrix finite-solution and inversion program with FSPACK90

... use sparsem use sparseop !fspak90 is in module sparseop ..... call fspak90('solve',y,rs,sol) ....
!now invert call fspak90('invert',y)
call printm(y)
end

References

Appendix S1
Definitions of structure (type)

type densem     !traditional dense square matrix
  integer :: n
  real(8) ,pointer::x(:, :)
end type densem

type dense_symm       !upper stored symmetric dense matrix
  integer :: n
  real(8) ,pointer::x(:)
end type dense_symm

type sparse_hashm
  integer:: n, &           ! for compatibility mainly
  nel, &                   ! number of elements
  filled, &                ! number of filled elements
  status                   ! 1 if ready to hash, 2 if in sorted
  ! order
  real (rh) , pointer :: x(:, :)
end type sparse_hashm

type sparse_ija
  integer :: n, &           ! number of equations
  nel                      ! number of nonzeros
  integer, pointer::ia(:), ja(:)       ! will be ia(n+1), ja(m)
  real (8), pointer::a(:)         ! will be a(m)
end type

Accessing structures
Structures can be accessed within the application program using the “%” symbol. This is useful, e.g., when using Fortran 77 programs. The example below shows how to use a determinant program written in F77.

type (densem):: z
integer::i, j
real (rh)::value

call init(z)
call zerom(x, 2)

! initialize z
do i=1, 2
  do j=1, 2
    value=i**j/10.
    call addm(value, i, j, z)
  enddo
enddo
print*, det(z%n,z%x)
end

function det(n,x)
!calculate determinant for a 2x2 matrix
integer n
real (r8):: x(n,n), det !
det= x(1,1)*x(2,2)/x(1,2)/x(2,1)
end

Library
The following files are compiled into the library:

kind.f90 - definitions of precisions
sparse.f90 - type definitions + main subroutines,
sparse2.f - supporting subroutines (in f77),
fspak.f90 - f90 interface to fspak
fspak.f - main fspak subroutine (in f77),
fspaksub.f - supporting fspak subroutines (in f77),
sparssub.f - low-level subroutines from the book of George and Liu (in f77),
second.f - timing subroutine specific to each computer (in f77).

Subroutines second() specific to other computers can be found in the FSPAK manual.

Appendix S2

Multiplication and solving using factors
Let A be a matrix. Factorization produced by FSPAK is L:
\[ A=P'LL'P \]
where P is a reordering matrix chosen to minimize the size of L:
\[ PP'=P'P=I \]
Operation “fact_mult” multiplies the factor by a vector:
\[ y=P' L P x \]
Operation “inv_fact_mult” solves the system of equation:
\[ P'L' Py=x \]
This is equivalent to:
\[ y= P' (L^{-1}) P x \]
Both operations were programmed by Juan Pablo Sanchez. The operations are useful for generation of large random samples from a multivariate normal distribution. They may be useful in Gibbs sampler algorithms when setting up and factorization of the system of equations in each round are feasible.
Module Prob

Probability routines for use in threshold models and Gibbs sampling

Written by: Ignacy Misztal and Deukhwan Lee, University of Georgia e-mail: ignacy@uga.edu, 04/29/99-04/19/2001

Module Prob is a collection of random number generators / probabilities / truncated distributions useful for Gibbs sampling and for threshold models. The module uses features of Fortran 90 to simplify programming and high-level optimization to reduce running time, with simplicity being as important as efficiency. To understand the module fully, please read the documentation on SPARSEM and on BLUPF90.

Module prob uses high-quality generators from public domain package RANLIB for random number generators. Some low level code is from Luis Varona.

Subroutines/functions

call set_seed(n)
Sets seed for random number generator to integer n. If this subroutine is not called, the seed will be selected by the system.

\[ x = \text{gen_uniform}(a,b) \]
\[ a,b \text{ - both real (r*) or both integers or both missing.} \]
If a, b are missing, generates samples from uniform(0,1) distribution
If a, b are real (r8), generates samples from uniform(a,b) distribution
If a, b are integers, generates random integer between a and b

\[ x = \text{gen_normal}(\text{mean}, \text{var}) \]
\[ \text{mean} \text{ - (r8) scalar or vector} \]
\[ \text{var} \text{ - (r8) scalar or square matrix} \]
\[ x \text{ - (r8) scalar or square matrix} \]
Generates \( x = \text{N(\text{mean}, \text{Var})} \) when mean and var are scalars, or \( x = \text{MVN(\text{mean}, \text{Var})} \) when mean is a vector and Var is a matrix. Arguments mean and var are optional. If they are missing, sampling is from \( \text{N(0,1)} \)

\[ x = \text{gen_invwishart}(\text{inv_q_form}, \text{df}) \]
\[ \text{inv_q_form} \text{ - (r8) scalar or square matrix containing inverse of quadratic form} \]
\[ \text{df} \text{ - an integer containing degrees of freedom} \]
Generates samples from inverted chi square or inverted Wishart distributions.
\[ y = \text{normal}(x) \]
\[ x - \text{real}(r8) \text{ scalar} \]
\[ y - \text{real} (r8) \text{ contains density}(X) \text{ for } N(0,1) \]

\[ y = \text{normal}_\text{cdf}(x) \]
\[ x - \text{real} (r8) \text{ scalar} \]
\[ y - \text{real} (r8) \text{ cumulative distribution function for } N(0,1) \]

\[ y = \text{normal}_\text{invcdf}(x) \]
\[ x - \text{real} (r8) \text{ scalar in the range of } <0,1> \]
\[ y - \text{real} (r8) \text{ as in: } x = \text{normal}_\text{cdf}(y) \]

\[ y = \text{generate}_\text{trunc}\_\text{normal}(a, b, \text{mean}, \text{var}) \]
\[ y - \text{real} (r8) \text{ scalar or vector} \]
\[ a, b - \text{real} (r8) \text{ lower and upper bound of random samples} \]
\[ \text{mean} - \text{real}(r8) \text{ scalar or vectors of mean, optional if scalar} \]
\[ \text{var} - \text{real}(r8) \text{ variance or covariance matrix, optional if scalar} \]

If mean and var are missing, generates random samples from \( N(0,1) \) distribution truncated to interval \(<a,b>\).

If mean and var are scalars, generates random samples from \( N(\text{mean},\text{var}) \) distribution truncated to interval \(<a,b>\).
If mean is a vector and var is a matrix, generates random samples from MVN(\text{mean},\text{var}) distribution with first dimension truncated to interval \(<a,b>\).

**Other functions/subroutines**

New functions/subroutines are added to Module prob periodically. Please see program prob.f90 for details.