
Manual for

BLUPF90 family of programs

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Introduction

BLUPF90 is a family of programs for mixed-model computations with focus 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 + for 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 and broiler chicken 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 1999 [paper](#) and as course notes. Nearly all programs are available in source code.

Online information about the programs is available at <http://nce.ads.uga.edu/wiki/doku.php> as wiki pages. There is discussion group blupf90 at groups.yahoo.com.




List of programs from Wiki page

Latest versions available from website at

http://nce.ads.uga.edu/wiki/doku.php?id=application_programs

(Use latest versions. All applications for Linux, Mac OSX, and Windows have been updated frequently)

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

- **BLUPF90** - BLUP in memory  [blupf90.pdf](#)
- **REMLF90** - accelerated EM REML  [remlf90.pdf](#)
- **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
- **CBLUP90THR** - as above but with thresholds computed and many linear traits (B. Auvray)
- **CBLUP90REML** - 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)
- **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)

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

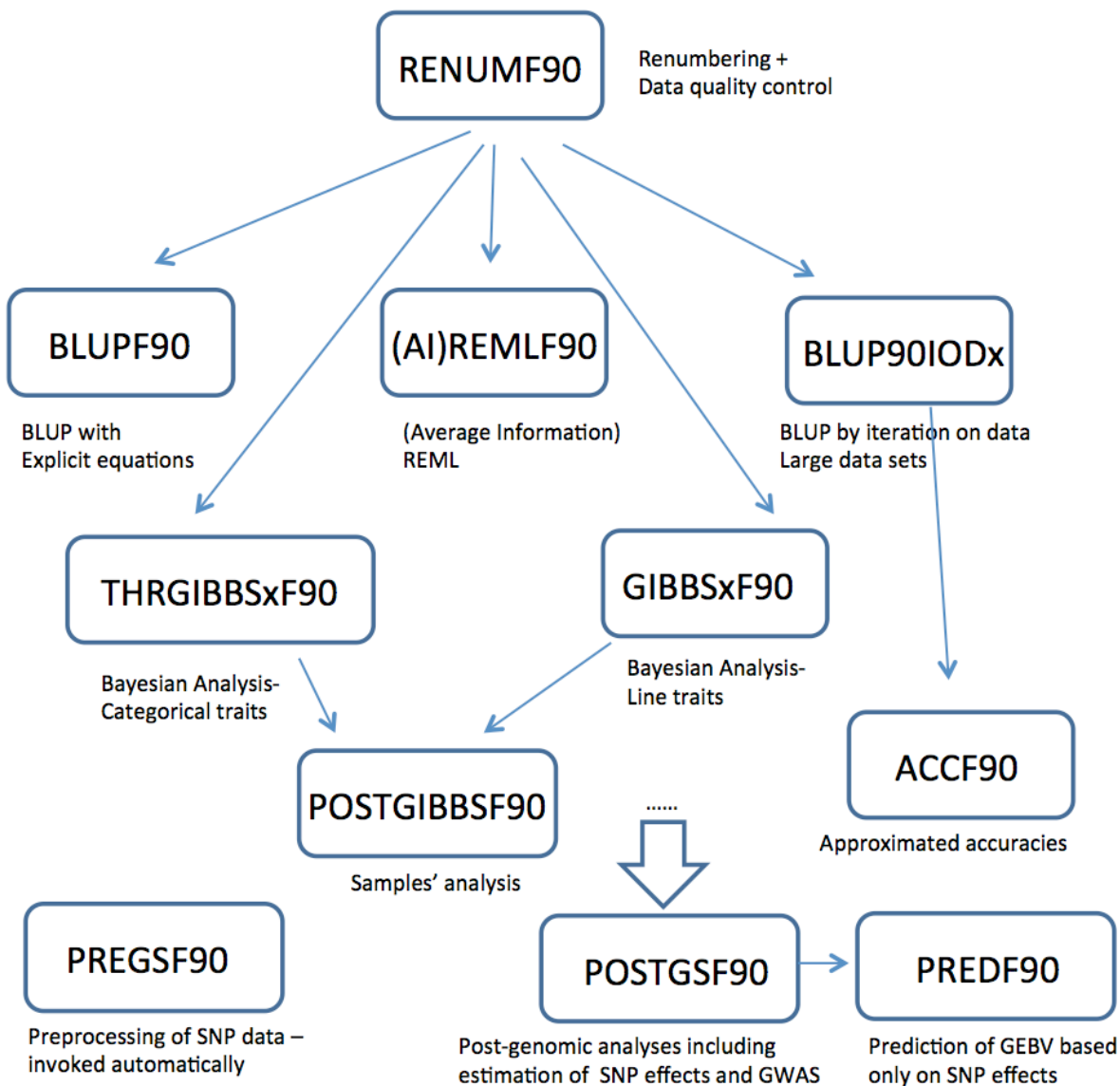
- **BLUP90IOD2** - BLUP by iteration on data with support for very large models (S. Tsuruta)
- **CBLUP90IOD** - BLUP by iteration on data for threshold-linear models
- **ACCF90** - approximation of accuracies for breeding values
- **BLUP90MBE** - BLUP by iteration on data with support for very large models for multi-breed evaluations
- **BLUP90ADJ** - BLUP data preadjustment tool

Included in application programs

- **PREGSF90** - genomic preprocessor that combines genomic and pedigree relationships (I. Aguilar)
- **POSTGSF90** - 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* and GIBBS*) are driven by parameter files and require data files with effects renumbered from 1 consecutively.

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:

Keywords*	Description
DATAFILE file.dat	Name of file with phenotypes; free fortran format (space-delimited file)
NUMBER OF TRAITS 2	Number of traits
NUMBER OF EFFECTS 6	Number of effects in a model except for residual
OBSERVATIONS(S) 1 2	Position(s) of observations in data file
WEIGHTS 2	Position of weight on observations if used; otherwise blank "2" means that residual variance (R) is set to R/2.
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]	
4 4 10 cross	4 4 = crossclassified effect positions in data file for 2 traits; 10 = levels
5 0 100 cross	5 0 = crossclassified effect, positions for 2 traits; 100 = levels
6 6 1 cov	6 6 = covariable positions in data file
7 7 10 cov 4 4	7 7 = covariable nested in effect position 4; 10 = levels
8 8 1000 cross	8 8 = crossclassified effect positions for 2 traits; 1000 = levels
0 9 1000 cross	0 9 = crossclassified effect positions for 2 traits; 1000 = levels
RANDOM_RESIDUAL_VALUES 10 1 1 10	Residual variance or residual covariance matrix For 2 trait model
RANDOM_GROUP 5 6	List of effect numbers that form a group For correlated random effects 5 6
RANDOM_TYPE add_animal	Type of random effect (distribution) diagonal, add_sire, add_an_upg, add_an_upginb, par_domin, or user_file
FILE file.ped	Pedigree file or other file associated with random effect; blank if none
(CO)VARIANCES 10 1 0 1 1 10 0 1 0 0 0 0 1 1 0 10	(Co)variance matrix for each random effect For 2 trait model

*Keywords need to be typed exactly (up to 20 characters). When preparing a new parameter file, consider modifying an existing file.

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
 - o crossclassified uses integer number from 1
 - o 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

Consider a data file (file.dat) with the following columns

<u>i</u>	<u>j</u>	<u>k</u>	<u>y1</u>	<u>y2</u>	<u>x1</u>
2	2	3	4.30	5.67	22.40
1	2	2	2.76	3.20	18.00
.....					
3	1	1	2.20	5.30	7.25

Let i go from 1 to 50, j from 1 to 80, and k from 1 to 200. The model:

$$y_{1ij} = a_j + b_i + cX + e_{ij}$$

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

1 50 cross # position 1, 50 levels

6 1 cov # covariable on position 6, one level

.....

By definition, a regular covariable has one level (i.e., a slope as regression).

For a similar model but with a nested covariable:

$$y_{1ij} = a_j + b_i + c_i X + e_{ij}$$

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:

$$y_{1ij} = a_{1j} + c_{1i} X + e_{1ij}$$

$$y_{2ij} = b_{2i} + c_{2i} X + e_{2ij}$$

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.

Two effects 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 on 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 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.
5
or
5 6

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

Assume a model:

$$y = \text{farm} + \text{animal_additive} + \text{animal_environment} + \text{error}$$

with $\text{var}(\text{animal_additive}) = 2.5 \otimes \mathbf{A}$, $\text{var}(\text{animal_environment}) = 5.1 \otimes \mathbf{I}$, $\text{var}(\text{error}) = 13.7 \otimes \mathbf{I}$

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:

$$y = \text{farm} + \text{season} + \text{direct} + \text{maternal} + \text{error}$$

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

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 are specified below:

```
...
RANDOM_GROUP
3 4 # direct and maternal effects
RANDOM_TYPE
add_animal # additive genetic
FILE
file.ped # name of pedigree file
(CO)VARIANCES
5 1
1 6
...
```

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_GROUP
2 3 4 5 # all covariables are correlated (effects 2, 3, 4, and 5 on the list above)
RANDOM_TYPE
add_animal # additive genetic
FILE
file.ped # name of pedigree file
(CO)VARIANCES
(4 x 4 matrix)
```

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)

d) 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.

e) parental dominance (par_domin)

The pedigree class file has the following format:

s-d s-sd s-dd ss-d ds-d ss-sd ss-dd ds-sd 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 s8 s7 s6 s5 s4 s3 s2 s1 code

then code = $\sum(a_i 2^{**i})$, where $a_i=0$ if $s_i=1$ and 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.

Data file

- a. Space(s) is a delimiter. At least one character 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!

RENUMF90 parameter file

RENUMF90 is a renumbering program to create input (data and pedigree) files for BLUPF90 programs and provide basic statistics.

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

WEIGHT(S)

`w` # position of weight - fraction to the residual variance

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

EFFECT

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

NESTED

`e1 e2 e3 ... form` # `e1 e2 e3 ...` = positions of crossclassified effects nested
 # form = 'alpha' for alphanumeric or 'numer' for numeric

RANDOM

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

OPTIONAL

`o1 o2 o3 ...` # 'pe' for permanent environment, 'mat' for maternal, and 'mped' 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; ID and SNP info need to be separated by at least one space; see more information in **PREGSf90**.

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; if '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. If it is 'internal', allocation is by a user-written function custom_upg (year_of_birth,sex,ID, parent_code).

(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

The additive pedigree file built by RENUMF90 is renaddxx.ped and 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
- 5) known or estimated year of birth (0 if not provided)
- 6) number of known parents (if genotypes are used: 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

Can we change the maximum size of character fields?

OPTION alpha_size nn # new size (default 20 characters)

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, but possibly after comments.

For example:

COMBINE 7 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".

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
ii 0 0 2002
kk 0 0 2000
```

Parameter file - testpar1

Parameter file for program renf90; it is translated to parameter

file for BLUPF90 family f programs.

DATAFILE

data

TRAITS

3

FIELDS_PASSED TO OUTPUT

1

WEIGHT(S)

RESIDUAL_VARIANCE

1

EFFECT

2 cross num

EFFECT

1 cross alpha

RANDOM

animal

#OPTIONAL

#mat

FILE

ped
 FILE_POS
 1 2 3 0 4
 PED_DEPTH
 3
 GEN_INT
 1 2 10
 UPG_TYPE
 yob
 2002 2003

Output log

```

RENUMF90 version 1.73
name of parameter file?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 and yob 1 2 3 0 4
pedigree traced to generation 3
Minimum, average and maximum generation intervals: 1 2 10
Unknown parent groups separated by years:
  2002 2003

Maximum size of character fields: 20

hash tables for effects set up
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)
Pos  Min      Max      Mean      SD      N
  2   1.0000   2.0000   1.5714   0.53452  7
  3   10.0000  14.0000  12.286   1.4960   7

Correlation matrix
      2      3
2   1.00  0.80
3   0.80  1.00

Counts of nonzero values (order as above)
      7      7
      7      7

```



```

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

Equation	Group	#Animals	Years
10	1	0	0- 2001
11	2	8	2002- 2002
12	3	1	2003-

```

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"

```

Output data file - renf90.dat

observation, effect 1, effect 2, 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 - renadd03.ped

Animal, sire, dam, 3-#unknown parents, birth year, #known parents, #records, #progeny of sire, #progeny of dam, original animal ID

```

1 6 11 2 2002 1 1 0 1 ee
2 8 7 1 2004 2 1 0 0 bb
7 6 11 2 2002 1 0 0 1 gg
3 6 12 2 2004 1 1 0 0 dd
9 11 11 3 2002 0 0 0 1 ii
4 6 1 1 2004 2 2 0 0 aa
6 11 11 3 2002 0 0 4 0 ff
5 8 9 1 2004 2 2 0 0 cc
8 11 11 3 2002 0 0 2 0 hh

```

Output parameter file - renf90.par

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

1.000

RANDOM_GROUP

2

RANDOM_TYPE

add_an_upg

FILE

renadd02.ped

(CO)VARIANCES

1.000

Output tables after renumbering - renf90.tables

Effect group 1 of column 1 with 2 levels Value # consecutive number

1	3	1
2	4	2

When to use what program and computing limits

BLUP

BLUPF90 sets up equations in memory. It can support a few million equations with a simple model to much smaller with complicated models (multiple traits, maternal effects, random regression, etc). BLUPF90 uses three solvers, chosen with options. PCG is the default solver and is usually the fastest one. 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

Set convergence criteria (default 1e-10).

OPTION maxrounds 10000

Set maximum number of rounds (default 1000).

OPTION solv_method FSPAK

Selection of solving method: FSPAK, SOR or PCG (default PCG).

OPTION r_factor 1.6

Set relaxation factor for SOR (default 1.4).

OPTION sol se

Store solutions and s.e. If this option is used, the solving method will turn to FSPAK.

OPTION blksize 3

Set block size for preconditioner (default 1).

BLUP90IOD 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 with a research contract or for research at UGA. The following options are available:

OPTION conv_crit 1e-12

Set convergence criteria (deault 1e-12).

OPTION maxrounds 10000

Set maximum number of rounds (default 5000).

OPTION blksize 3

Set block size for preconditioner (default 1). Usually blksize will be the same number of traits.

OPTION init_eq 10

Set the number of effects to be solved directly (default 0).

OPTION solv_method FSPAK

Solving method for initial equations (default DIRECT).

OPTION tol 1d-12

Tolerance to get a positive definite matrix (default 1d-12).

OPTION residual

y-hat and residuals will be included in "yhat_residual".

OPTION avgeps 50

Using the last 50 average eps for convergence.

OPTION cont 1

To restart the program from the previous solutions.

OPTION missing -1

Set the missing value (default 0).

OPTION restart 100

Set the number of iteration to recompute residuals (default 100).

OPTION prior_solutions

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

OPTION random_upg 1 2

Set the UPG random. "1" the weight for random UPG = 1. If the second number exists, the weight will be inverted (e.g., 1/2=0.5).

OPTION SNP_file snp

Specify the SNP file name `snp` to use genotype data.

Variance component estimation

There is not a single-best choice for variance component estimation. Programs below offer choices for simple and complicated models. For advice on what works best under your circumstances, google a paper “[Reliable computing in estimation of variance components](#)”.

REMLF90 uses EM REML. For most problems it is the most reliable algorithm but can take hundreds of rounds of iteration. 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-10).

OPTION maxrounds 10000

Maximum rounds (default 5000).

OPTION sol se

Store solutions and se.

OPTION residual

y-hat and residuals will be included in “yhat_residual”.

OPTION missing -999

Specify missing observations (default 0).

OPTION use_yams

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

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

Specify the SNP file name snp to use genotype data.

AIREMLF90 uses Average Information 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-10).

OPTION maxrounds 500

Maximum rounds (default 5000). When it is negative, the program calculates BLUP without running REML.

OPTION EM-REML 10

Run 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

Store solutions and s.e.

OPTION missing -1

Set 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.

Heterogeneous residual variances for a single trait**OPTION hetres_pos 10 11**

Specify positions of covariables.

OPTION hetres_pol 4.0 0.1 0.1

Initial values of coefficients for heterogeneous residual variances. Use $\ln(a_0, a_1, a_2, \dots)$ 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**

Specify 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 $\ln(a_0, a_1, a_2, \dots)$ to make these values (trait first). "4.0 4.0" are 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 $\exp(a_0+a_1*X_1+a_2*X_2)$.

OPTION SNP_file snp

Specify the SNP file name **snp** to use genotype data.

GIBBSxF90 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 programs.

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.

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 **GIBBSx90**:

OPTION fixed_var all 1 2 3

Store all solutions and posterior means and SD for effects 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".

OPTION solution all 1 2 3

Store all solutions and posterior means and SD for effects 1, 2, and 3 are stored in "all_solutions" and in "final_solutions" every round. Without numbers, all solutions for all effects are stored.

OPTION solution mean 1 2 3

Posterior means and SD for effects 1, 2, and 3 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 effx correspond 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

Specify 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**.

THR**GIBBS1F90** is a Gibbs sampling program to analyze categorical and continuous traits simultaneously. The following options are available:

OPTION cat 0 0 2 5

“0” indicate 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 censored xx

Negative values of the last category in the data set indicate censored records. “xx” determines the lower and upper limit of the category + xx when sampling from the distribution.

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

POST**GIBBSF90** is a program to calculate posterior means and SD and diagnose the convergence. 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.

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, ...) to calculate posterior means and SD, and to create graphs.

postmean

Posterior means

postsd

Posterior standard deviations

postout

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

***** Posterior Standard Deviation *****

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

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

"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"

ratio between first half and second half of the samples should be < 1.0 , but it is not useful because it is < 1.0 most of the time.

"Autocorrelations"

autocorrelations between two lags. High correlation implies samples are not independent.

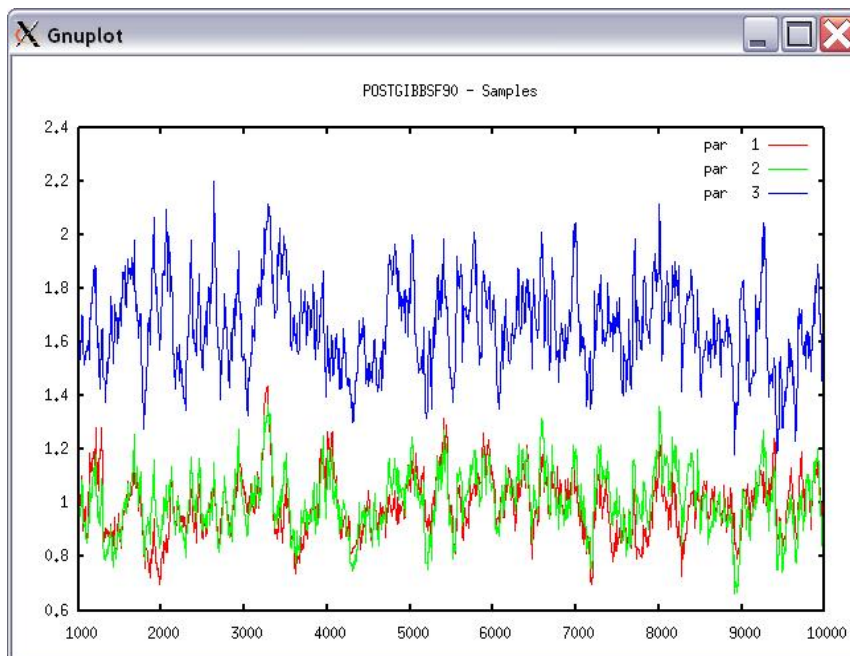
"Independent # batches"

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
```

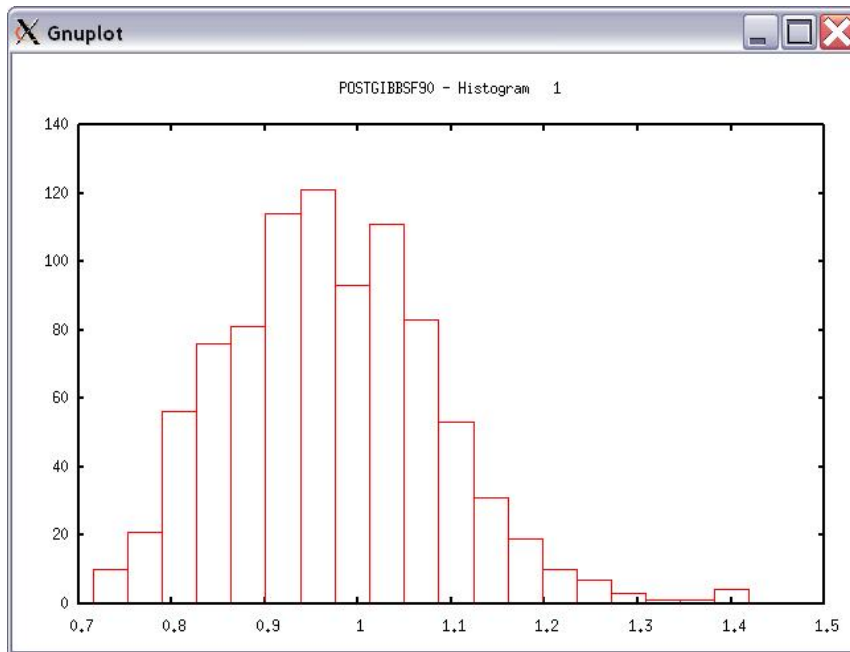
```
2
```

```
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.

Genomic programs

The **PREGSF90** program constructs a genomic relationship matrix **G** and a relationship matrix **A₂₂** for genotyped animals. The relationship matrix **A** based on the pedigree information in mixed model equations is replaced by matrix **H**, which combines the pedigree and genomic information. The main difference between **A⁻¹** and **H⁻¹** is structure of **G⁻¹ - A₂₂⁻¹**. Some of the options for **PREGSF90** can be also used with **BLUPF90**, **(AI)REMLF90**, **GIBBS1F90**, **GIBBS2F90**, **GIBBS3F90**, **THRGIBBS1F90**, and **BLUP90IOD2**.

OPTION SNP_file <file>

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 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 21101011002012011011010110111111211111210100
8014 21110101511101120221110111511112101112210100
516 21100101202252021120210121102111202212111101
181 21110111112201120550200020101022212211111100
```

The renumbered ID file for genotypes named as the genotype file **name.XrefID** is created by **RENUMF90** (using the SNP file), containing sequential ID renumbers and the original ID, which must be in the same order as in the SNP file as follows:

```
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
```

Several optional files are available:

Allele frequencies (**OPTION FreqFilev <file>**)

Map file (**OPTION chrinfo <file>**)

Weight file (**OPTION weightedG <file>**)

G or its inverse, **A₂₂** or its inverse, etc, as specified by respective **OPTIONS**.

OPTION chrinfo <file>: read SNP map information from the file.

These files are useful to check for Mendelian conflicts and HWE (with also **OPTION sex_chr**) and for **POSTGSF90** (ssGWAS).

Format = all numeric variables: SNP order, chromosome, position (bp): the SNP order corresponds to the index number of the SNP, in the sorted map by chromosome and the position.

The first line in the file corresponds to the first SNP in the genotype file, and so on. Other alphanumeric fields are optional.

By default, **PREGSf90** always create **GimA22i** in binary format for use by later programs specifying **OPTION readGimA22i**. With **OPTION saveAscii**, this file can be stored as ASCII format: $i, j, \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}$.
“freqdata.count” contains allele frequencies in the original genotype file with the format: SNP number (related to the genotype file) and allele frequency.
“freqdata.count.after.clean” contains allele frequencies as used in calculations with the format: SNP number (related to the genotype file), allele frequency, and code of exclusion.

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, **A₂₂** or its inverse, or other reports from QC as specified by their respective **OPTIONS**.

Options for creation of genomic relationship Matrix (**G**)

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

OPTION whichG x

Specify how **G** is created.

The variable **x** can be

- 1: $\mathbf{G} = \frac{\mathbf{ZZ}'}{k}$; VanRaden, 2008 (default)
- 2: $\mathbf{G} = \frac{\mathbf{ZDZ}'}{n}$; Amin et al., 2007; Leuttenger et al., 2003; where $\mathbf{D} = \frac{1}{2p(1-p)}$
- 3: As 2 with modification UAR from Yang et al 2010

OPTION whichfreq x

Specify what 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>

Read allele frequencies from a file. For example, based on allele frequencies calculated by estfreq.f90 (VanRaden, 2009) with format: SNP, frequency where SNP corresponds to the index of SNP based on the same order that are in the genotype file.

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

OPTION whichScale x

Specify how **G** is scaled.

The variable **x** can be

- 1: $2 \sum \{p(1-p)\}$; VanRaden 2008 (default)
- 2: $\frac{tr(ZZ')}{n}$; Legarra 2009, Hayes 2009
- 3: correction ; Gianola et al 2009

OPTION weightedG <file>

Read weights from a file to create weighted genomic relationship. Weighting $Z^* = Z \sqrt{D} \Rightarrow \mathbf{G} = Z^*Z^{*'} = ZDZ'$ (format: one column of weights in the same order as in the genotyped file). Weights can be extracted from output of the **POSTGSF90** program.

OPTION maxsnp x

Set 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

Ignore all SNP with MAF < x (default value = 0.05).

OPTION callrate x

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

OPTION callrateAnim x

Ignore genotypes with call rates < x (number of calls / number of SNPs). Default value is 0.90.

OPTION monomorphic x

Ignore monomorphic SNPs. Optional parameter **x** can be used to enable (1) or disable (0) the check, default value 1.

OPTION hwe x

Check 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

Check for high 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

Verify parent-progeny Mendelian conflicts and write report to a file “**Gen_conflicts**”. The optional parameter **x** can be

0: no action

1: only detect

2: detect and search for an alternate parent; no change to any file. Not yet implemented

3: detect and eliminate progenies with conflicts (default)

OPTION exclusion_threshold x

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

OPTION exclusion_threshold_snp x

Set 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

Set the number of minimum pair of parent-progeny evaluations to exclude SNP due to parent-progeny exclusion (default value = 100).

OPTION outparent_progeny x

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

OPTION excludeCHR n1 n2 n3 ...

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

OPTION sex_chr n

Set the chromosome number equal to or greater than **n** are not considered autosome. 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 chrinfo**).

OPTION threshold_duplicate_samples x

Set 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

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

OPTION plotca

Plot first two principal components to look for stratification in the population.

OPTION extra_info_pca <file> col

Read 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 saveCleanSNPs *

Save 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 is useful to speed up computation when the QC was performed previously.

OPTION outcallrate

Print 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 \mathbf{A}_{22} and \mathbf{G}

OPTION thrWarnCorAG x

Set the threshold to issue warning if correlation between \mathbf{A}_{22} and $\mathbf{G} < \mathbf{x}$ (default value = 0.5).

OPTION thrStopCorAG x

Set the threshold to stop the analysis if correlation between \mathbf{A}_{22} and $\mathbf{G} < \mathbf{x}$ (default values = 0.3).

OPTION thrCorAG x

Set the threshold to calculate correlation between \mathbf{A}_{22} and \mathbf{G} for only $\mathbf{A}_{22} \geq \mathbf{x}$ (default values = 0.02).

Options for \mathbf{H} including different weights to create $\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}$ as

$(\alpha \mathbf{G} + \beta \mathbf{A}_{22} + \gamma \mathbf{I} + \delta \mathbf{A}_{22}^{-1})^{-1} - \omega \mathbf{A}_{22}^{-1}$

where the parameters are to scale the genomic info to be compatible with the pedigree information, to make matrices invertible in the presence of clones, and to control bias.

The defaults values are:

tau=1 alpha =0.95 beta = 0.05 gamma=0 delta=0 omega=1

Options to change these defaults are specified with:

OPTION TauOmega tau omega

OPTION AlphaBeta alpha beta

OPTION GammaDelta gamma delta

OPTION tunedG x

Scale **G** based on \mathbf{A}_{22} . The variable **x** can be:

0: no scaling

1: $\text{mean}(\text{diag}(\mathbf{G}))=1$, $\text{mean}(\text{offdiag}(\mathbf{G}))=0$

2: $\text{mean}(\text{diag}(\mathbf{G}))=\text{mean}(\text{diag}(\mathbf{A}_{22}))$, $\text{mean}(\text{offdiag}(\mathbf{G}))=\text{mean}(\text{offdiag}(\mathbf{A}_{22}))$ (default)

3: $\text{mean}(\mathbf{G})=\text{mean}(\mathbf{A}_{22})$

4: rescale **G** using the first adjustment as in Powell et al. (2010) or Vitezica et al. (2011).

OPTION nthreads n

Specify number of threads to be used with MKL-OpenMP for creation and inversion of matrices.

OPTION ntheadsiod n

Specify 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

Set the level of verbose; 0 minimal; 1 gives lots of diagnostics.

Save and Read options:

OPTION saveAscii

Save intermediate matrices (GimA22i, G, Gi, etc.) files as ASCII (default = binary).

OPTION saveHinv

Save \mathbf{H}^{-1} in "Hinv.txt" (format: i, j, val with i, j, the index level for the additive genetic effect).

OPTION saveAinv

Save \mathbf{A}^{-1} in "Ainv.txt" (format: i, j, val with i, j, 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

Save \mathbf{H}^{-1} with original IDs

OPTION saveAinvOrig

Save \mathbf{A}^{-1} with original IDs

OPTION saveDiagGOrig

Save diagonal of **G** in "DiagGOrig.txt" (format: id, val with id, original IDs).

OPTION saveGOrig

Save **G** in "G_Orig.txt" (format: id_i, id_j, val with id_i and id_j, the original IDs).

OPTION saveA22Orig

Save A_{22} in "A22_Orig.txt" (format: id_i, id_j, val with id_i and id_j, the original IDs).

OPTION readOrigId

Read information from "renaddxx.ped" file, original ID and possibly year of birth for its use in parent-progeny conflict. Only need unless the previous "save*Orig" is present.

OPTION savePLINK

Save genotypes in PLINK format files: [toPLINK.ped](#) and [toPLINK.map](#).

Save and Read intermediate files:

OPTION readGimA22i <file>

This option can be used in analysis programs (BLUPF90, REMLF90, etc.) in order to use matrices stored in [GimA22i](#) file (default filename). In general, methods used to create and invert matrices in such programs do not use optimized version. For large number of genotyped animals, run first PREGSf90 and read stored matrices in analysis programs.

The optional file can be used to specify the other file name or 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.

OPTION saveA22**OPTION saveA22Inverse****OPTION saveG all**

If optional `all` is present, all intermediate matrices for **G** will be saved.

OPTION saveGInverse**OPTION saveGmA22****OPTION readG <file>****OPTION readGInverse <file>****OPTION readA22 <file>****OPTION readA22Inverse <file>****OPTION readGmA22 <file>****POSTGSF90**

The following options for **POSTGSF90** (ssGWAS) are available:

OPTION Manhattan_plot

Plot using **GNU PLOT** the Manhattan plot (SNP effects) for each trait and correlated effect.

OPTION Manhattan_plot_R

Plot 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). **CAIRO** packaged is required.

OPTION plotsnp n

Control the values of SNP effects to use in Manhattan plots

1: plot regular SNP effects: abs(val)

2: plot 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

Calculate the variance explained by n adjacent SNPs.

OPTION windows_variance_mbp n

Calculate the variance explained by n Mb window of adjacent SNPs.

OPTION windows_variance_type n

Set windows type for variances calculations

- 1: moving windows
- 2: exclusive windows

OPTION which_weight x

Generate a weight variable to be used in the creation of a weighted genomic relationship matrix $G=ZDZ'$

$$1: w = y^2 * (2(p(1-p)))$$

$$2: w = y^2$$

with scaled weight = $w * nSnp / \sum(w)$

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 if **OPTION windows_variance** is used
- 8: variance explained by n adjacent SNP.

“**chrnsp**” contains data to create plot by GNUPLOT

- 1: trait
- 2: effect
- 3: values of SNP effects to use in Manhattan plots
- 4: SNP
- 5: Chromosome
- 6: Position

“**chrnspvar**” contains data to create plot by GNUPLOT

- 1: trait
- 2: effect
- 3: variance explained by n adjacent SNP
- 4: SNP
- 5: Chromosome
- 6: Position

“[snp_pred](#)” contains gene 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 and “[V](#)” for variance explained.

“[t1e2](#)” indicates that the file is for the trait 1 and the effect 2.

Filename extension

[xxx.gnuplot](#) => GNUPLOT

[xxx.R](#) => R programs

[xxx.tif](#) => image

PREDF90 predicts GEBV for young animals based on only genotypes. The prediction is based on SNP effects obtained from **POSTGSF90**. For young animals that were not included in the previous analysis, GEBV can be calculated using the “[snp_pred](#)” file from **POSTGSF90**.

Input files:

“[snp_pred](#)”

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

Prepare an updated genotype file in the same format as used in POSTGSf90.

Output file:

“[SNP_predictions](#)”

- ID, calling rate, and GEBV

Parameters:

1. α - 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)

Sample run using example from our website

“[renum.par](#)” for **RENUMF90**

DATAFILE

[phenotypes.txt](#)

TRAITS

3

FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE # variances are from airemf90 results

0.9038

EFFECT

1 cross alpha

EFFECT

2 cross alpha #animal

RANDOM

animal

FILE

pedigree

SNP_FILE

marker.geno.clean

(CO)VARIANCES

0.9951E-01

Run RENUMF90

RENUMF90 version 1.94

name of parameter file?renum.par

.....

Number of animals with records: 15800

Number of animals with genotypes: 1500

.....

Wrote renumbered data "renf90.dat"

"renf90.par" from RENUMF90

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

```

Run BLUPF90

```

name of parameter file?renf90.par
.....
round          67      convergence= 1.259204136398044E-012
round          68      convergence= 9.025592858512443E-013
          68 iterations, convergence criterion= 9.025592858512443E-013
solutions stored in file: "solutions"

```

```

$a/postGSf90
name of parameter file?renf90.par

      postGS 1.11
.....
Solutions read from file: "solutions"
.....
Files for predictions by SNP effects in file: "snp_pred"

```

```

$head -5 snp_pred
      3000      1      0      15800
0.751 0.382 0.569 0.680 0.184 0.298 0.392 0.380 0.597 0.352
0.514 0.717 0.464 0.502 0.639 0.773 0.364 0.645 0.566 0.514
0.622 0.673 0.238 0.556 0.606 0.590 0.477 0.341 0.523 0.525
0.660 0.439 0.609 0.418 0.572 0.401 0.490 0.608 0.454 0.589

```

Run PREDF90

```

Predf90 1.00
Predicts EBVs from genotypes based on results from single-step evaluation
name of genotype file?
marker.geno.clean
Number of SNP:      3000
Number of traits:   1
number of correlated traits: 1
      3000 SNP
The genotype file contains 3000 SNP starting from position 7
      8002 0.1186204
      8014 -0.1033363
      8016 0.1308713
      8018 -0.1905423
      8024 -0.3675095
      8038 0.1939673
      8041 -0.1284970
      8063 -0.1314869
      8065 -2.8898019E-02
Processed 1500 genotypes

```

Average calling rate: 1.00

```
head -5 SNP_predictions
8002  1.00    0.1156
8014  1.00   -0.1007
8016  1.00    0.1276
8018  1.00   -0.1857
8024  1.00   -0.3582
```

PREDICTF90 is to calculate \hat{y} and residuals using the same parameter file and “[solutions](#)” and can be used to calculate predictive ability $r(y, \hat{y})$.

Output files:

“[yhat_residual](#)”

Format: record #, original y , \hat{y} , residual

“[bvs.dat](#)”

The same format as “[solutions](#)” including (G)EBV.

Examples for parameter files

Sire model without A

```

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

```

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

```


Multiple (2) 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: 2 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
3
OBSERVATION(S)
3 4
WEIGHT(S)
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT [EFFECT NESTED]
1 2 2 cross
5 5 10 cross
6 7 30 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
FILE

```

```

(CO)VARIANCES
1 0
0 1

```

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 1

```

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 10 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 2

```

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 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
RANDOM_GROUP
3
RANDOM_TYPE
diagonal
FILE

(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

```

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

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 0.1
0.1 1
RANDOM_GROUP
4 5
RANDOM_TYPE

diagonal
FILE

(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_GROUP
3

RANDOM_TYPE
add_an_upginb
FILE

add.ped
(CO)VARIANCES
10

RANDOM_GROUP
4

RANDOM_TYPE
par_dom
FILE

dom.ped
(CO)VARIANCES
2

Random regression model

Example 1

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

1 10 1

1 1 10

RANDOM_GROUP

8 9 10

RANDOM_TYPE

add_an_upg

FILE

ped_score

(CO)VARIANCES

100 1 1

1 10 1

1 1 10

Example 2

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

4 5 6

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

0.1 0.1 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 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

0.1 0.1 0.1 0.1 0.1 1

RANDOM_GROUP

8 9 10

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

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
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_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

DATAFILE

competition.dat

NUMBER_OF_TRAITS

1

NUMBER_OF_EFFECTS

19

OBSERVATION(S)

24

WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]

2 88 cross

3 362 cross

21 2409 cross

4 8004 cross

22 0 cov 5

22 0 cov 6

22 0 cov 7

22 0 cov 8

22 0 cov 9

22 0 cov 10

22 0 cov 11

22 0 cov 12

22 0 cov 13

22 0 cov 14

22 0 cov 15
22 0 cov 16
22 0 cov 17
22 0 cov 18
22 8004 cov 19
RANDOM_RESIDUAL VALUES
1225.8
RANDOM_GROUP
4 5
RANDOM_TYPE
add_animal
FILE
renadd04.ped
(CO)VARIANCES
267.03 25.313
25.313 104.44
RANDOM_GROUP
2
RANDOM_TYPE
diagonal
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. This example is from the documentation of program JAA20.

$$y_{ijkl} = hys_i + hs_{ij} + p_k + a_k + e_{ijkl}$$

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
```

Relationship 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

.1

RANDOM_GROUP

3

RANDOM_TYPE

diagonal

FILE

(CO)VARIANCES

.05

RANDOM_GROUP

4

RANDOM_TYPE

add_an_upg

FILE

is

(CO)VARIANCES

.5

Execution

/home/ignacy/f90/examples blupf90
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"

/home/ignacy/f90/examples cat 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
1	4	11	0.8528
1	4	12	-3.1911
1	4	13	7.9976
1	4	14	-6.3340

Appendix B (multiple trait sire model)

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

Models

$$\text{Trait 1: } y_{1i} = h_i + s_{1j} + e_{1ijk}$$

$$\text{Trait 2: } y_{2i} = \mu + s_{2j} + e_{2jk}$$

where

h - fixed herd

s - random sire

and

$$\text{var}(s) = A \begin{bmatrix} 8 & 6 \\ 6 & 17 \end{bmatrix}, \text{var}(e) = I \begin{bmatrix} 10 & 10 \\ 10 & 20 \end{bmatrix}$$

Data file (Irsdat)

Format: h/ μ /s/ y_1 / y_2

```
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
```

Pedigree file (Irsrel)

Format: bull/sire/MGS

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

Parameter file (Irssex)

Example of two trait sire model with unequal models

DATAFILE

Irsdat

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

/home/ignacy/f90/examples blupf90
 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"

/home/ignacy/f90/examples cat solutions

trait/effect	level	solution
1 1	1	2.3877
2 1	1	52.4449
1 1	2	3.2180
2 1	2	0.0000
1 2	1	0.2243
2 2	1	-0.0210
1 2	2	-0.8217
2 2	2	-0.3866
1 2	3	-0.4969
2 2	3	-0.7512
1 2	4	0.6178
2 2	4	-0.0769
1 2	5	0.2217
2 2	5	1.0851

Appendix C (test-day model)

This test-day model example comes from the paper of Schaeffer and Dekkers (WCGALP94 18:443)

Model

$$y_{ijkl} = h_i + \beta_1 X_{1j} + \beta_2 X_{2j} + a_k + \gamma_{1k} X_{1j} + \gamma_{2k} X_{2j} + e_{ijkl}$$

where

y_{ijkl} - yield of test day

h_i - test day effect

X_{1j} - days in milk

X_{2j} - log(days in milk)

β_1, β_2 - fixed regressions

a_k - random animal

γ_{1k}, γ_{2k} - random regressions for each animal

and

$$\text{var}(e_{ijkl}) = 1; \text{var}(a_k, \gamma_{1k}, \gamma_{2k}) = \begin{bmatrix} 2.25 & 4 & -.7 \\ 4 & 1375 & 12 \\ -.7 & 12 & 94 \end{bmatrix}^{-1}$$

Data file (Irsrrdat)

Format: h/a/ X_1 / X_2 / y

```
1 1 73 1.42985 26
1 2 34 2.19395 29
1 3 8 3.64087 37
2 1 123 0.908127 23
2 2 84 1.28949 18
2 3 58 1.65987 25
2 4 5 4.11087 44
3 1 178 0.538528 21
3 2 139 0.785838 8
3 3 113 0.992924 19
3 4 60 1.62597 29
4 2 184 0.505376 1
4 3 158 0.657717 15
4 4 105 1.06635 22
4 5 14 3.08125 35
5 3 218 0.335817 11
5 4 165 0.614366 14
5 5 74 1.41625 23
5 6 31 2.28632 28
6 3 268 0.129325 7
6 4 215 0.349674 8
6 5 124 0.90003 17
6 6 81 1.32586 22
```

Relationship file (Irsrrrel)

Format: animal/sire/dam

```
1 9 7
2 10 8
3 9 2
4 10 8
```

```

5 11 7
6 11 1
7 0 0
8 0 0
9 0 0
10 0 0
11 0 0

```

Parameter file (exlrsrr)

Example of single-trait random-regression model

DATAFILE

lrsrrdat

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 .010678

Execution

/home/ignacy/f90/examples blupf90

name of parameter file?exlrsrr

BLUPF90 1.00

```

Parameter file:          exlrsrr
Data file:              lrsrrdat
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	0.09	11.95
-0.70	11.95	94.00

solutions stored in file: "solutions"

/home/ignacy/f90/examples cat 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
1	5	8	-0.0238
1	5	9	0.0350
1	5	10	-0.0238
1	5	11	-0.0008
1	6	1	-0.0370
1	6	2	0.0325
1	6	3	-0.0479
1	6	4	0.0767
1	6	5	-0.0149
1	6	6	-0.0377
1	6	7	-0.0103
1	6	8	0.0364
1	6	9	-0.0480
1	6	10	0.0364
1	6	11	-0.0145

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)

$$y_1 = cg_1 + bt + mbt + a + M + e$$

$$y_2 = cg_2 + bt + mbt + a + M + pe + e$$

$$y_3 = cg_3 + bt + mbt + a + e$$

where

y_{1-3} - birth weight, weaning weight, and gain

cg_{1-3} - 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

Relationship file (pedi.outok)

Format:

animal
 sire or unknown parent group
 dam or unknown parent group
 "1 + number of missing parents"

Parameter file (exlrsrr)

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

(CO)VARIANCES

0.263	0.0	0.0
0.0	13.129	0.0
0.0	0.0	0.0

RANDOM_GROUP

6

RANDOM_TYPE

diagonal

FILE

(CO)VARIANCES

0.0	0.0	0.0
0.0	45.5	0.0
0.0	0.0	0.0

Appendix E (random regression model)

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

Model

```
func{
y_ijkl = hym_ij+sum from {m=1} to 4 alpha_m(l) h_im+
sum from {m=1} to 4 alpha_m(l) u_km+
sum from {m=1} to 4 alpha_m(l) p_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: $100/\text{var}(e_{ijkl})$
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:      ya=cga +      ua      + ea
breed B:      yb=cgb+      ub      +eb
cross:  yab=cgab+      uaab + ubab  +eab
```

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

RANDOM_TYPE

add_animal

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)

$$y = cg + a + c_1 + c_2 + \dots + c_5 + e$$

c_i 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

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).

add_animal
FILE
pedig
(CO)VARIANCES
40 -10
-10 10

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.

Parameter file for renumbering program RENUMF90

```
DATAFILE
phenotypes.txt
TRAITS
3
FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE
0.9038
EFFECT
1 cross alpha #fixed effect
EFFECT
2 cross alpha #animal
RANDOM
animal
FILE
pedigree
SNP_FILE
marker.geno.clean
(CO)VARIANCES
0.9951E-01
```

```
Phenotypes.txt – phenotype file
Single trait in position 3
Fixed effect in position 1 read as alphanumeric
Random animal effect in position 3
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
```

```

6 0 0 0
7 0 0 0
8 0 0 0
9 0 0 0
10 0 0 0

```

SNP file for the first 50 SNP

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

```

8002 21101011002012011011010110111111211111210100
8014 21110101111101120221110111111112101112210100
8016 21100101202202021120210121102111202212111101
8018 21110111112201120210200020101022212211111100
8024 21110102201201111220210111102122201221111111
8038 11110000102100120201211121201022112111121111
8041 22210001201201121110210121202111102102121001
8063 20110101202202020212211101101120222012120021
8065 21110101111112111221110101010220212001110012
8083 1011101111001011111110112100111121011010121

```

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
3 0 0
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 innput file (max_field_readline): 100

hash tables for effects set up
table expanded from 10000 to 20000 records
table expanded from 20000 to 40000 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)
Pos Min Max Mean SD N
3 0.73000 8.8300 4.9793 1.0069 15800

```

```

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
```

```

1 5742 14705 1 0 2 1 0 0 14670
2 2302 1384 1 0 2 1 0 0 12367
3 4248 15309 1 0 12 1 0 2 9123
4 4241 3492 1 0 2 1 0 0 7455
5 14459 14202 1 0 2 1 0 0 5736
6 1029 1292 1 0 2 1 0 3 5877
7 10876 7596 1 0 2 1 0 0 9638
8 13589 12642 1 0 2 1 0 0 14136
9 7070 11562 1 0 2 1 0 0 6010
10 6449 2448 1 0 2 1 0 0 15498

```

Renumbered phenotype file

renf90.dat

```

4.16 1 5903 0
3.47 1 3628 0
4.5 1 1329 0
4.97 1 14808 0
5.98 1 12481 0
6.63 1 10205 0
3.32 1 7935 0
5.85 1 5639 0
4.77 1 3348 0
4.22 1 1951 0

```

Run BLUPF90

```

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
2 cross-classified    3                                1
                                                15800

Residual (co)variance Matrix
0.90380

Random Effect(s)      2
Type of Random Effect: additive animal
Pedigree File:        renadd02.ped
trait  effect  (CO)VARIANCES
1      2      0.9951E-01

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 =          15801
G
0.99510E-01

```

read 15800 records in 3.5994001E-02 s, 31601 nonzeros
 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

$\tau \text{ inv}(\alpha G + \beta A22 + \gamma I + \delta) - \omega \text{ inv}(A22)$
 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

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	1.000	1.250	0.000
Off-diagonal	2248500	0.003	0.000	0.750	0.001

Statistics for SNP file

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

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

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

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

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

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	0.999	0.889	1.463	0.002
Off-diagonal	2248500	-0.001	-0.147	0.830	0.002

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.3220

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 b_1 = -0.004 \quad 0.997$

Correlation all elements G & A 0.644

Correlations of off-diagonal elements of G and A22 is 0.660; low numbers indicated genotyped mistakes or poor pedigrees

Off-Diagonal

Using 70386 elements from A22 ≥ 0.02000

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 b_1 = -0.006 \quad 1.000$

Correlation Off-Diagonal elements G & A 0.660

Blend G as $\alpha * G + \beta * A22$: (α, β) 0.950 0.050

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	0.999	0.894	1.446	0.002
Off-diagonal	2248500	0.000	-0.139	0.820	0.002

Frequency - Diagonal of G

N: 1500
 Mean: 0.999
 Min: 0.894
 Max: 1.446
 Range: 0.028
 Class: 20

Diagonal elements of G should be 1 ± 0.2 . Too large or too small elements indicate:
 Genotyping mistakes
 Mixed lines
 See Simeone et al. (2011)

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

Scale G matrix according to A22 - 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	(da-oa)/(dg-og):	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 Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	1.000	1.250	0.000
Off-diagonal	2248500	0.003	0.000	0.750	0.001

Statistics of G after scaling as in Chen et al (2011) or Vitezica et al. (2011)
 Statistics should be same as for A22.

 Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	0.896	1.447	0.002
Off-diagonal	2248500	0.003	-0.134	0.822	0.002

Correlation of Genomic Inbreeding and Pedigree Inbreeding
 Correlation: 0.3363

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad 0.000 \quad 0.995$

Correlation all elements G & A 0.663

Off-Diagonal

Using 70386 elements from A22 ≥ 0.02000

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad -0.001 \quad 0.998$

Correlation Off-Diagonal elements G & A 0.679

Creating A22-inverse

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}

Statistic of Inv. Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.607	1.056	9.221	0.575
Off-diagonal	2248500	-0.001	-1.067	0.533	0.001

Creating G-inverse

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}

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

Statistic of Inv. Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	8.007	3.597	64.893	21.055
Off-diagonal	2248500	-0.005	-12.697	6.632	0.056

Creating GimA22i in file: "GimA22i"

Calculating GmA22/GimA22i Matrix Densem storage

Calculating GmA22/GimA22i Matrix...elapsed time 0.1269817

```

Setup Genomic Done.
wGimA22i 1.0000000000000000
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
hash matrix increased from 1139062 to 1708593 % filled: 0.9000
finished peds in 30.68333 s, 1193064 nonzeros
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= 1.931029578758311E-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-p 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
          N      Mean      Min      Max      Var
Diagonal 1500    8.007    3.597    64.893    21.055
Off-diagonal 2248500 -0.005   -12.697    6.632    0.056

```

Creating GimA22i in file: "GimA22i"

```

Calculating GmA22/GimA22i Matrix Densem storage
Calculating GmA22/GimA22i Matrix...elapsed time 0.1089821
Setup Genomic Done.
wGimA22i 1.000000000000000
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 nonzeros
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 = 1521840
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= 1.725330565925358E-002
delta convergence= 4.769938966058494E-002
new R
0.49575
new G
0.52606
-2logL = 52785.2479463395 : AIC = 52789.2479463395
In round 4 convergence= 1.101891763451498E-004
delta convergence= 3.662497104484009E-003
new R
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)

Data files are available at http://nce.ads.uga.edu/wiki/doku.php?id=course_materials_-_from_uga_2014

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 5th generation had genotypes and pedigree, but phenotypes were removed for traditional and genomic evaluations

Data Structure:

#Animal Generation Sex Mu QTL Residual Phenotype (Phenotype = Mu + QTL + Residual)

```
1 0 1 1 -0.826104 1.586661 1.76056
2 0 1 1 -1.093034 -0.451821 -0.544855
3 0 1 1 -0.135824 0.984936 1.84911
4 0 1 1 0.044242 -0.802145 0.242097
5 0 1 1 0.342068 0.028434 1.3705
.
.
6095 5 1 1 1.801324 -0.494822 2.3065
6096 5 2 1 0.772964 0.791936 2.5649
6097 5 2 1 0.748241 0.285815 2.03406
6098 5 1 1 1.042522 -1.606656 0.435866
6099 5 1 1 0.891319 0.179843 2.07116
6100 5 1 1 0.745873 0.034715 1.78059
```

Pedigree: 6100 animals

#Animal Sire Dam

```
1 0 0
2 0 0
3 0 0
4 0 0
5 0 0
.
.
6095 4576 4403
6096 4576 4065
6097 4576 2263
6098 4576 4150
6099 4576 3690
6100 4576 4311
```

Genotypes: 1294 animals genotyped for 1000 SNP across 5 chromosomes

```
# Animal SNP1SNP2SNP3SNP4SNP5...SNP1000
6100 22212...1
```

Map:

#SNP order chromosome position

```
1 1 0.00000
2 1 0.16722
3 1 0.33444
4 1 0.50166
5 1 0.66888
.
.
1000 5 49.99878
```

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 0.3000

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
* 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

```

5	1.010	287
6	1.038	137
7	1.067	33
8	1.096	14
9	1.124	3
10	1.153	1
11	1.182	0
12	1.210	2
13	1.239	0
14	1.268	0
15	1.296	0
16	1.325	0
17	1.354	0
18	1.382	0
19	1.411	0
20	1.440	1
21	1.468	0

Check for diagonal of genomic relationship matrix

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

Final Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	1.000	1.250	0.000
Off-diagonal	1673142	0.005	0.000	0.750	0.001

Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	0.898	1.469	0.002
Off-diagonal	1673142	0.005	-0.158	0.791	0.002

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 $b_0 b_1 = 0.000 \quad 0.991$

Correlation all elements G & A 0.717

Off-Diagonal

Using 83426 elements from A22 $\geq .02000$

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$

Regression coefficients $b_0 b_1 = -0.003 \quad 0.999$

Correlation Off-Diagonal elements G & A 0.777

Creating A22-inverse

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

Final A22 Inv Matrix

Statistic of Inv. Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1294	1.851	1.067	5.812	0.431
Off-diagonal	1673142	-0.001	-1.200	0.600	0.001

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

	N	Mean	Min	Max	Var
Diagonal	1294	13.457	5.827	45.588	27.985
Off-diagonal	1673142	-0.010	-13.500	6.896	0.226

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

	N	Mean	Min	Max	Var
Diagonal	1294	11.606	4.746	40.310	21.707
Off-diagonal	1673142	-0.009	-12.500	6.396	0.211

* Setup Genomic Done !!! *

Parameter file for PREGSF90 with 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

```

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

```

```

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

```

```

*-----*
*              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

Genotypes missings after cleannig (%): 0.000

Calculating G Matrix

Dgemm MKL #threads= 8 16 Elapsed omp_get_time: 0.9840

Scale by Sum(2pq) . Average: 435.140185710293

Blend G as $\alpha G + \beta A_{22}$: (α, β) 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 Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	1.000	1.250	0.000
Off-diagonal	1673142	0.005	0.000	0.750	0.001

Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	0.898	1.470	0.002
Off-diagonal	1673142	0.005	-0.158	0.791	0.002

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.2180

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad 0.000 \quad 0.991$

Correlation all elements G & A 0.717

Off-Diagonal

Using 83426 elements from A22 $\geq .02000$

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad -0.003 \quad 0.999$

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

	N	Mean	Min	Max	Var
Diagonal	1294	1.851	1.067	5.812	0.431
Off-diagonal	1673142	-0.001	-1.200	0.600	0.001

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

	N	Mean	Min	Max	Var
Diagonal	1294	13.466	5.863	45.587	28.023
Off-diagonal	1673142	-0.010	-13.521	6.897	0.227

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

	N	Mean	Min	Max	Var
Diagonal	1294	11.615	4.782	40.309	21.740
Off-diagonal	1673142	-0.009	-12.521	6.397	0.211

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

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[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 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
2 cross-classified    3                                1
                                                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 SNP: 801
 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: 801

Number of Parent-Progeny Mendelian Conflicts: 0

Number of effective SNPs (after QC): 801

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

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"

New files with clean genotypes

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

Genotypes missings (%): 19.900

Genotypes missings after cleannig (%): 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

Frequency - Diagonal of G

N: 1294
 Mean: 1.000

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 Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	1.000	1.250	0.000
Off-diagonal	1673142	0.005	0.000	0.750	0.001

 Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	0.876	1.593	0.002
Off-diagonal	1673142	0.005	-0.169	0.861	0.003

Correlation of Genomic Inbreeding and Pedigree Inbreeding
 Correlation: 0.2092

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad 0.000 \quad 0.991$

Correlation all elements G & A 0.677

Off-Diagonal

Using 83426 elements from A22 $\geq .02000$

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$
 Regression coefficients $b_0 \ b_1 = \quad -0.002 \quad 0.996$

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

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

	N	Mean	Min	Max	Var
Diagonal	1294	1.851	1.067	5.812	0.431
Off-diagonal	1673142	-0.001	-1.200	0.600	0.001

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

	N	Mean	Min	Max	Var
Diagonal	1294	17.075	7.840	56.092	43.645
Off-diagonal	1673142	-0.013	-16.499	8.893	0.309

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

Saving GimA22i in file: "GimA22i"

 Final G Inv - A22 Inv Matrix

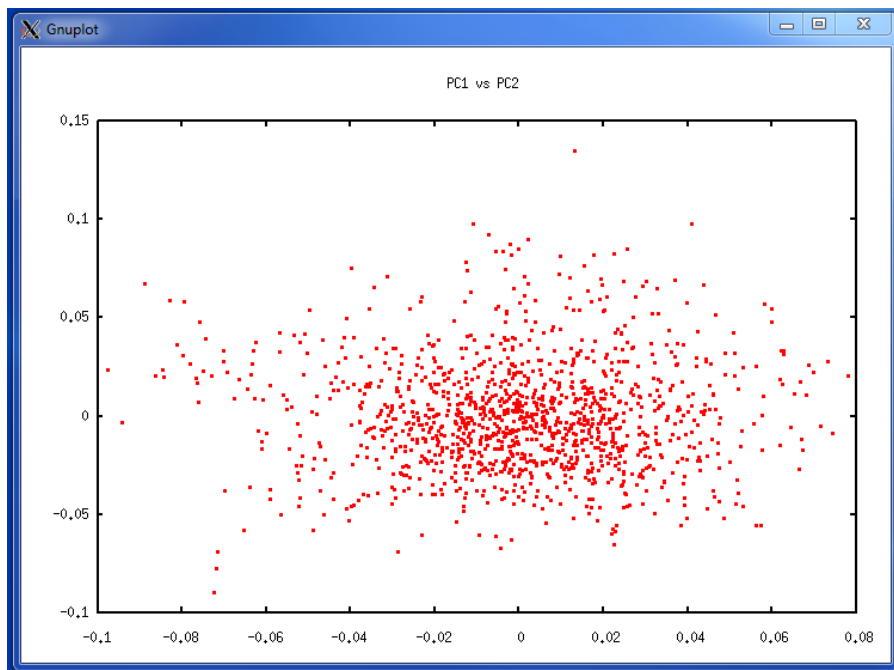
Statistic of Inv. Genomic- A22 Matrix

	N	Mean	Min	Max	Var
Diagonal	1294	15.223	6.759	51.043	35.648
Off-diagonal	1673142	-0.012	-15.499	8.393	0.289

 * 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

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

Linux code to remove phenotypes for those animals:

```
awk '{ if ($4==5) print 0,$2,$3,$4; else print $1,$2,$3,$4}' renf90.dat > renf90_5.dat
```

Default convergence criteria = 1e-12

Log file for BLUPF90 without genomic information

name of parameter file?

```

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,          12201
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

```

trait/effect level  solution
1 1 1 1.02176505
1 2 1 -0.24665178

```


1	2	2	0.16420973
1	2	3	0.32371581
1	2	4	0.00318130
1	2	5	-0.13277100

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

trait/effect	level	solution	s.e.	
1	1	1	0.02496866	
1.02176504				
1	2	1	-0.24665117	0.39158195
1	2	2	0.16421026	0.40488662
1	2	3	0.32371755	0.29405286
1	2	4	0.00318218	0.38229658
1	2	5	-0.13277154	0.46566701

The solution file now includes a 5th column with EBV standard errors

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[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 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

#	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 0.1499770 s, 12201
 nonzeros
 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: .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 cleannig (%): 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 $\alpha * G + \beta * A22$: (α, β) 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 Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	1.000	1.250	0.000
Off-diagonal	1673142	0.005	0.000	0.750	0.001

Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1294	1.001	0.898	1.470	0.002
Off-diagonal	1673142	0.005	-0.158	0.791	0.002

Correlation of Genomic Inbreeding and Pedigree Inbreeding

Correlation: 0.2180

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$ Regression coefficients $b_0 \ b_1 = \quad 0.000 \quad 0.991$

Correlation all elements G & A 0.717

Off-Diagonal

Using 83426 elements from A22 $\geq .02000$ Estimating Regression Coefficients $G = b_0 11' + b_1 A + e$ Regression coefficients $b_0 \ b_1 = \quad -0.003 \quad 0.999$

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

	N	Mean	Min	Max	Var
Diagonal	1294	1.851	1.067	5.812	0.431
Off-diagonal	1673142	-0.001	-1.200	0.600	0.001

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

	N	Mean	Min	Max	Var
Diagonal	1294	13.466	5.863	45.587	28.023
Off-diagonal	1673142	-0.010	-13.521	6.897	0.227

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

Final G Inv - A22 Inv Matrix

```

-----
Statistic of Inv. Genomic- A22 Matrix
      N      Mean      Min      Max      Var
Diagonal      1294      11.615      4.782      40.309      21.740
Off-diagonal  1673142      -0.009     -12.521      6.397      0.211

*-----*
* 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 nonzeros

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 corrected phenotypes and (G)EBV. In this example we show predictivity for all young animals and for all young genotyped animals.

1) Predictivity for traditional BLUP

As this program needs solution file, it can be run in the same folder as BLUP

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 animals in 5th generation

Linux code to create pred.dat:

```
awk '$4==5' renf90.dat > pred.dat
```

For creating pred.dat only for genotyped animals in 5th generation:

```
awk 'BEGIN { for (i=0;i<1000;i++) print i+1}' > ind
```

```
paste -d " " pred.dat ind | sort +2 -3 > dat1.temp
```

```
awk '{print $1}' snp.txt_XrefID | sort +0 -1 > dat2.temp
```

```
join -1 +1 -2 +3 dat2.temp dat1.temp | sort -n +4 -5 | awk '{print $2,$3,$1,$4}' >
gen.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 predicting all animals in 5th generation:

name of parameter file?

pred.par

*** include effects to predict Yhat n, effects 1 2
PREDICTF90 1.3

Parameter file: pred.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
*** effects to include in Yhat (T/F): F T
solutions read from file: solutions
Animal Effect: 2
y(s), yhat(s), residual(s) in written in "yhat_residual" file
1000 records read
Trait: 1 1000

```

mean Y          2.803014134522528E-003  var Y          0.982498631522066
mean Yhat      -1.204401846975088E-002  var Yhat       7.851567205278141E-002
cov (Y,Yhat)   8.256236151221331E-002  corr (Y,Yhat)  0.297261012857303
wrote bvs for animals in data in file "bvs.dat"

```

Predictivity

Output files from PREDICTF90

yhat_residual

yhat_residual has 4 columns: animal | y | yhat | residual

4644	-0.266520	0.415535	0.339710
2176	-0.418925	0.094263	0.508577
2934	2.154195	0.157782	3.018178
797	1.226565	0.328604	1.919726
6021	1.143225	0.430780	1.734210

Because **OPTION include_effects 2** was used:
y is phenotype minus all effects other than animal
yhat receives the second effect, which is the animal effect
residual is phenotype minus animal effect

bvs.dat

bvs.dat has 4 columns: trait | effect | Animal | solution (EBV)

1	2	4644	0.415535
1	2	2176	0.094263
1	2	2934	0.157782
1	2	797	0.328604
1	2	6021	0.430780

Log file for predicting genotyped animals in 5th generation

```

name of parameter file?
pred.par

```

```

*** include effets to predict Yhat n, effects          1          2
    PREDICTF90 1.3

```

```

Parameter file:          gen.par
Data file:              gen.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"

```

Predictivity

2) Predictivity for ssGBLUP

Parameter file:

DATAFILE

pred.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 include_effects 2

Log file for predicting all animals in 5th generation

name of parameter file?

pred.par

```

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

```

PREDICTF90 1.3

```

Parameter file:      pred.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
*** effects to include in Yhat (T/F): F T
solutions read from file: solutions
Animal Effect: 2
y(s), yhat(s), residual(s) in written in "yhat_residual" file
1000 records read
Trait: 1 1000
mean Y 1.729620725009590E-002 var Y 0.982498616557168
mean Yhat -1.458232188504189E-002 var Yhat 8.642763611542703E-002
cov (Y,Yhat) 9.189071888926587E-002 corr (Y,Yhat) 0.315340214001692

```

Predictivity

Output files from PREDICTF90

Output files for predictf90 follow the same pattern whether using genomic information or not.

Log file for predicting genotyped animals in 5th generation

```

name of parameter file?
pred.par

```

```

*** include effects to predict Yhat n, effects 1 2
PREDICTF90 1.3

```

```

Parameter file:      gen.par
Data file:          gen.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
*** effects 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      -3.754737233898292E-002  var Y          0.979795861954017
  mean Yhat   -1.863066248595715E-002  var Yhat       0.119326686734040
  cov (Y,Yhat) 0.117365728215231      corr (Y,Yhat) 0.343245384612940
wrote bvs for animals in data in file "bvs.dat"

```

Predictivity

Parameter files for GWAS using ssGBLUP (ssGWAS)

Run BLUPF90 with genomic information and solve G^{-1} and A_{22}^{-1}

```

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
OPTION saveGInverse
OPTION saveA22Inverse
OPTION weightedG wei

```

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:
`awk 'BEGIN { for (i=1;i<1000;i++) print 1}' > wei`

Run POSTGSF90 and solve G^{-1} and A_{22}^{-1}

```

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]

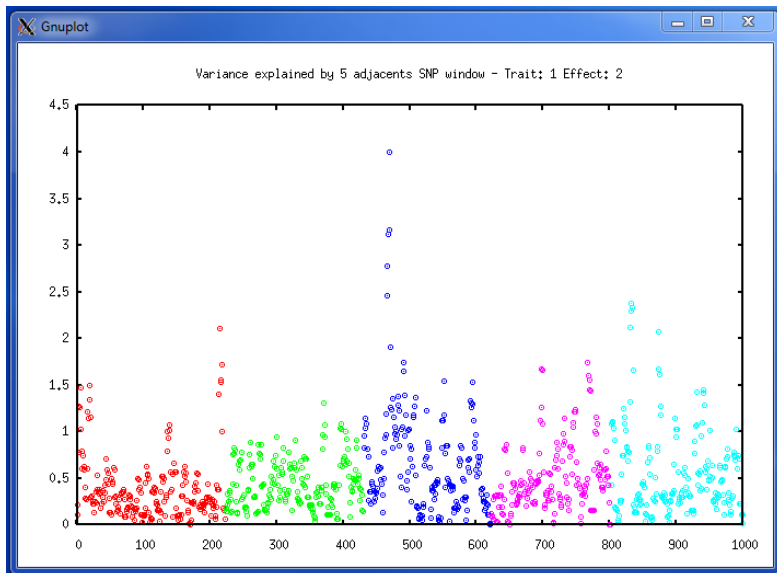
```

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
OPTION Manhattan_plot
OPTION readGInverse
OPTION readA22Inverse
OPTION weightedG wei
OPTION windows_variance 5

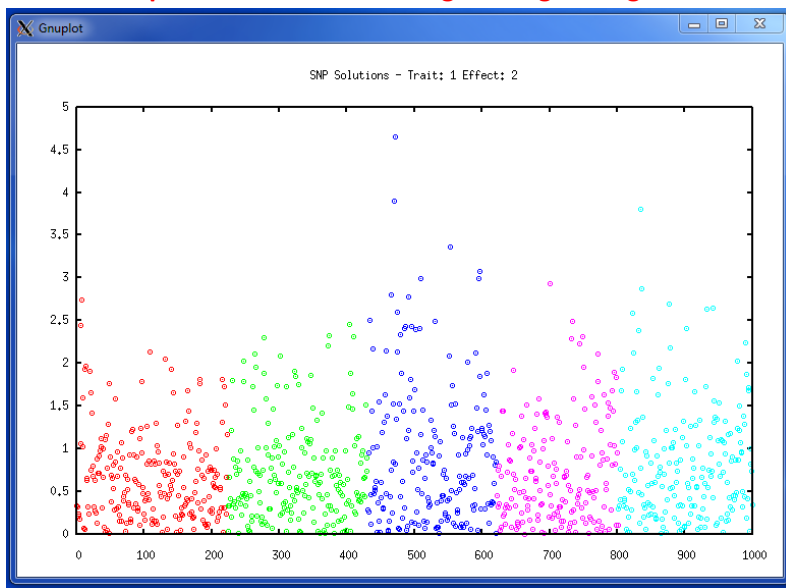
```

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

1	2	1	1	0	0.7001368E-02	0.2209213	0.1119293	0.1126648E-03
1	2	2	1	0	-0.1359349E-01	0.5065436	0.2104747	0.2118577E-03
1	2	3	1	0	0.8714214E-02	0.3917027	0.7757968	0.7808942E-03
1	2	4	1	0	-0.4223401E-02	0.6873333E-01	1.271113	0.1279465E-02
1	2	5	1	0	0.5471629E-03	0.1539137E-02	1.261010	0.1269296E-02

snp_sol has 9 columns:
 trait | effect | SNP | chromosome | position | SNP_solution | weight | % of variance explained by n adjacent SNP | variance explained by n adjacent SNP

chrnpvar

1	2	0.1119293459	1	1	0
1	2	0.2104747339	2	1	0
1	2	0.7757968029	3	1	0
1	2	1.2711127978	4	1	0
1	2	1.2610103595	5	1	0

chrnpvar 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 (selected programming details)

This section provides some programming insight 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 sire
                    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,&                       ! number of equations and io-status
          data_len,&                       ! length of data record to read
          i,j,k,l                          ! extra variables
real:: val, dat_eff

!
call read_parameters
call print_parameters
neq=ntrait*sum(nlev)
data_len=max(pos_weight,maxval(pos_y),maxval(pos_eff))
print*,'Data record length = ',data_len
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)                !data file

! 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
    do k=1,ntrait
      do l=1,ntrait
        xy(address(i,k))=xy(address(i,k))+rinv(k,l)*y(l)*weight_cov(i,k) &
          *weight_y
      enddo
    enddo
  enddo
enddo
!
! Random effects' contributions
do i=1,neff
  select case (randomtype(i))
    case (g_fixed)
      continue                          ! fixed effect, do nothing
    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 uncomments 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
```