Introduction to
blupf90
airemlf90

UGA – 05/2016
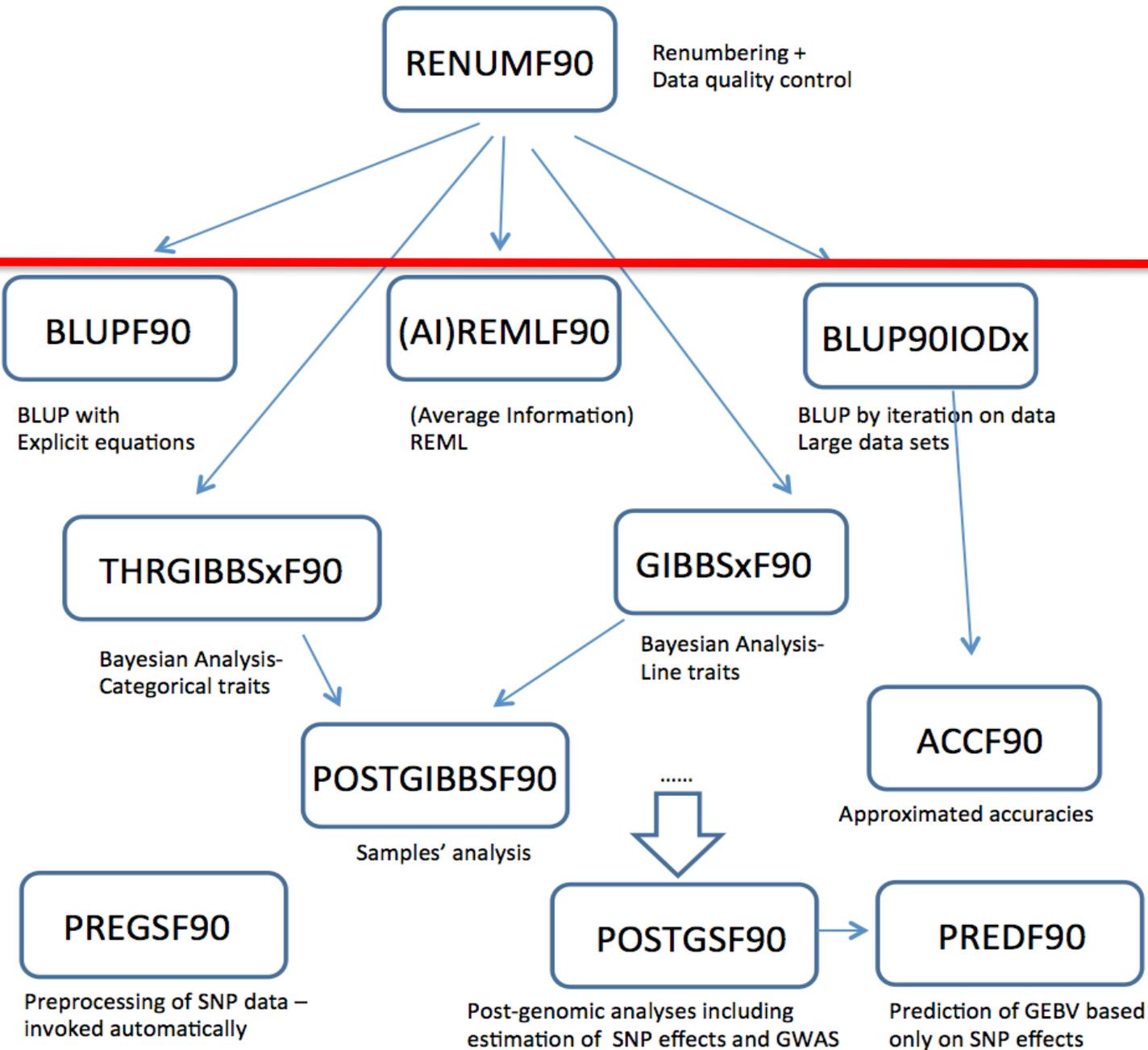
Each keyword can be preceded by comments, each starting with
#
DATAFILE
name of data file
NUMBER_OF_TRAITS
number of traits

NUMBER_OF_EFFECTS
number of effects
OBSERVATION(S)
position of observations in data file (one per trait)
WEIGHT(S)
*position of weight(s) in data file (one per trait); blank if
all weights equal*
**EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT
[EFFECT NESTED]**
one line per effect:
     position of effect (one per trait)
     number of levels
     type of effect (one of **cross** *for crossclassified or* **cov**
for covariable)
     position of effect where nested (one per trait, optional)

RANDOM_RESIDUAL VALUES
residual variance covariance matrix (full stored)
RANDOM_GROUP
*number of one random effect or list of correlated effects
(order as in EFFECTS above); correlated effects must be
consecutive*
RANDOM_TYPE
type of random effect: *one of* **diagonal, add_animal,add_sire,
add_an_upg, add_an_upginb, user_file,
user_file_i** *or* **par_domin**
FILE
relationship file; blank line if file unnecessary
(CO)VARIANCES
*variance covariance matrix for given correlated effects and
traits(full stored)*

parameter file - testpar1

```
# Parameter file for program renf90; it is translated to parameter
# file for BLUPF90 family programs.
DATAFILE
data.test
TRAITS
3 4
FIELDS_PASSED TO OUTPUT
2 1 # passing alphanumeric
WEIGHT(S)

RESIDUAL_VARIANCE
5 2
2 4
EFFECT
1 1 cross alpha
EFFECT
2 2 cross alpha
RANDOM
animal
OPTIONAL
mat mpe pe
FILE
test.ped
(CO)VARIANCES
10 3 2 1
3 11 4 5
2 4 12 6
1 5 6 13.01
(CO)VARIANCES_PE
5.3 2.1
2.1 4.85
(CO)VARIANCES_MPE
1.03 .27
.27 .85
EFFECT
5 0 cov
NESTED
 1 0 alpha
EFFECT
6 6 cross alpha
RANDOM
diagonal
```

new parameter file - renf90.par

```
# BLUPF90 parameter file created by RENF90
DATAFILE
 renf90.dat
NUMBER_OF_TRAITS
          2
NUMBER_OF_EFFECTS
          7
OBSERVATION(S)
    1    2
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
    3   3        4 cross
    4   4        7 cross
    5   5        7 cross
    5   5        7 cross
    4   4        7 cross
    6   0        4 cov   7   0
    8   8        3 cross
RANDOM_RESIDUAL VALUES
    5.000       2.000
    2.000       4.000
 RANDOM_GROUP
     2      3
 RANDOM_TYPE
 add_animal
 FILE
renadd02.ped
 (CO)VARIANCES
    10.00       3.000       2.000       1.000
    3.000       11.00       4.000       5.000
    2.000       4.000       12.00       6.000
    1.000       5.000       6.000       13.01
 RANDOM_GROUP
     4
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    1.030       0.2700
    0.2700      0.8500
 RANDOM_GROUP
     5
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    5.300       2.100
    2.100       4.850
 RANDOM_GROUP
     7
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    1.000       0.1000
    0.1000      1.000
```

Options for blupf90

```
OPTION conv_crit 1e-12
```

Set convergence criteria (deault 1e-12).

```
OPTION maxrounds 10000
```

Set maximum number of rounds (default 1000).

```
OPTION solv_method FSPAK
```

Selection solutions by 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.

Options for blupf90

←

OPTION missing -999

Specify missing observations (default 0).

OPTION residual

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

OPTION blksize 3

Set block size for preconditioner (default 1).

OPTION SNP_file snp

Specify the SNP file name to use genotype data.

blupf90 family

renf90.par

```
# BLUPF90 parameter file created by RENF90
DATAFILE
 renf90.dat
NUMBER_OF_TRAITS
          2
NUMBER_OF_EFFECTS
          7
OBSERVATION(S)
    1    2
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECT[EFFECT NESTED]
   3  3          4 cross
   4  4          7 cross
   5  5          7 cross
   5  5          7 cross
   4  4          7 cross
   6  0          4 cov   7  0
   8  8          3 cross
RANDOM_RESIDUAL VALUES
    5.000        2.000
    2.000        4.000
 RANDOM_GROUP
    2    3
 RANDOM_TYPE
  add_animal
 FILE
 renadd02.ped
 (CO)VARIANCES
    10.00       3.000       2.000       1.000
    3.000       11.00       4.000       5.000
    2.000       4.000       12.00       6.000
    1.000       5.000       6.000       13.01
 RANDOM_GROUP
    4
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    1.030       0.2700
    0.2700      0.8500
 RANDOM_GROUP
    5
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    5.300       2.100
    2.100       4.850
 RANDOM_GROUP
    7
 RANDOM_TYPE
 diagonal
 FILE

 (CO)VARIANCES
    1.000       0.1000
    0.1000      1.000
```

RANDOM_TYPE	Type of random effect (distribution)
add_animal	diagonal, add_sire, add_an_upg, add_an_upginb, par_domin, or user_file

blupf90 family

renf90.par

- *user_file*
  - a matrix is read from file
  - Matrix is stored only upper- or lower-triangular
  - Matrix file:
    - `row, col, value`

- *user_file_i*
  - As before but the matrix will be inverted

- *par_domin*
  - A parental dominance file created by program RENDOM

Options for airemlf90

```
OPTION conv_crit 1d-12
```

Convergence criterion (default 1d-10).

```
OPTION maxrounds 1000
```

Maximum rounds (default 5000). When the number = 0, the program calculates BLUP without iterating REML

```
OPTION EM-REML 10
```

Run EM-REML (REMLF90) for first 10 rounds to get initial variances within the parameter space (default 0).

```
OPTION use_yams
```

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

Options for airemlf90

```
OPTION se_covar_function <label> <function>
```

```
OPTION se_covar_function H2d G_2_2_1_1/(G_2_2_1_1+G_2_3_1_1+G_3_3_1_1+G_4_4_1_1+R_1_1)
```

```
OPTION se_covar_function rg12 G_2_2_1_2/(G_2_2_1_1*G_2_2_2_2)**0.5
```

Options for airemlf90

Heterogeneous residual variances for a single trait

```
OPTION hetres_pos 10 11
```

Specify the position of covariables.

```
OPTION hetres_pol 4.0 0.1 0.1
```

Initial values of coefficients for heterogeneous residual variances using ln(a0, a1, a2, …) to make these values.

Heterogeneous residual variances for multiple traits
Convergence will be very slow with multiple trait heterogeneous residual variances

```
OPTION hetres_pos 10 10 11 11
```

or

```
OPTION hetres_pos 10 11 12 13
```

Specify the position of covariables (trait first). "10 10" or "10 11" could be linear for first and second traits.
"11 11" or "12 13" could be quadratic.

```
OPTION hetres_pol 4.0 4.0 0.1 0.1 0.01 0.01
```

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

Common problems for blupf90 family

- Wrong data file and pedigree name
  - Program does not stop if wrong file name not exist
  - Check outputs for data file name and number of records and pedigree read

```
round =  4995  convergence =          NaN
round =  4996  convergence =          NaN
round =  4997  convergence =          NaN
round =  4998  convergence =          NaN
round =  4999  convergence =          NaN
round =  5000  convergence =          NaN
 5001 iterations,    convergence criterion=          NaN
 solutions stored in file: "solutions"
```

Common problems for blupf90 family

- Wrong position or formats for observation and effects

- Misspelling of Keywords
  - Program may stop

- (Co)variance matrices not symmetric, not positive definite
  - Program may not stop

- Large numbers (e.g. 305-day milk yield 10,000 kg)
  - Scale down i.e. 10,000 /1,000 = 10

General output from blupf90 family

```
 name of parameter file?
exmr99s

      BLUPF90 1.46

 Parameter file:                 exmr99s
 Data file:                      renco99s
 Number of Traits                   3
 Number of Effects                  3
 Position of Observations      3   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   1   1                                    51
 2   cross-classified      2   2   2                                  2147
 3   cross-classified      2   2   2                                  2699
```

Check file names

Check model

General output form blupf90 family

```
Residual (co)variance Matrix
  1825.3       909.82       842.39
  909.82       2057.0       1309.8
  842.39       1309.8       1716.4

Random Effect(s)    2
Type of Random Effect:        diagonal
trait    effect    (CO)VARIANCES
  1        2       2523.       1901.       1885.
  2        2       1901.       1965.       1809.
  3        2       1885.       1809.       1926.

Random Effect(s)    3
Type of Random Effect:        additive animal with unknown parent groups
Pedigree File:               renpe99s
trait    effect    (CO)VARIANCES
  1        3       613.7      -360.9       80.93
  2        3      -360.9       475.2       319.5
  3        3       80.93       319.5       666.6

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
# equations =        14691
G
  2522.6       1901.4       1885.4
  1901.4       1965.3       1808.9
  1885.4       1808.9       1925.9
G
  613.75      -360.90       80.927
 -360.90       475.23       319.52
  80.927       319.52       666.60
hash matrix increased from          131072 to          262144 % filled:      0.8000
 read            4539  records in    0.1445990       s,          127095  nonzeroes
  read           2697  additive pedigrees
 finished peds in    0.2006180       s,          191175  nonzeroes
```

Check (co)variances

Check maximum
number of columns
to read

Check number of records
And pedigree read

General output from blupf90 family

- Output printed on the screen is not saved to any file!

- Should use redirection or pipes to store output

renumf90

```
echo renum.par | renumf90 | tee renum.log
```

blupf90

```
echo renf90.par | blupf90 | tee blup.log
```

airemlf90

```
echo renf90.par | remlf90 | tee aireml.log
```

Run in background + Save output

```
$vi ai.sh
```
#type the following commands inside ai.sh
```
        blupf90 <<AA > blup.log
        renf90.par
        AA
```
#save and exit
```
$bash ai.sh &
```
    #can replace sh by bash

```
$vi gibbs.sh
```
#type the following commands inside ai.sh
```
        gibbs2f90 <<AA > gibbs.log
        renf90.par
        1000 0
        10
        AA
```
#save and exit
```
$bash gibbs.sh &
```
#can replace bash by sh