Introduction to

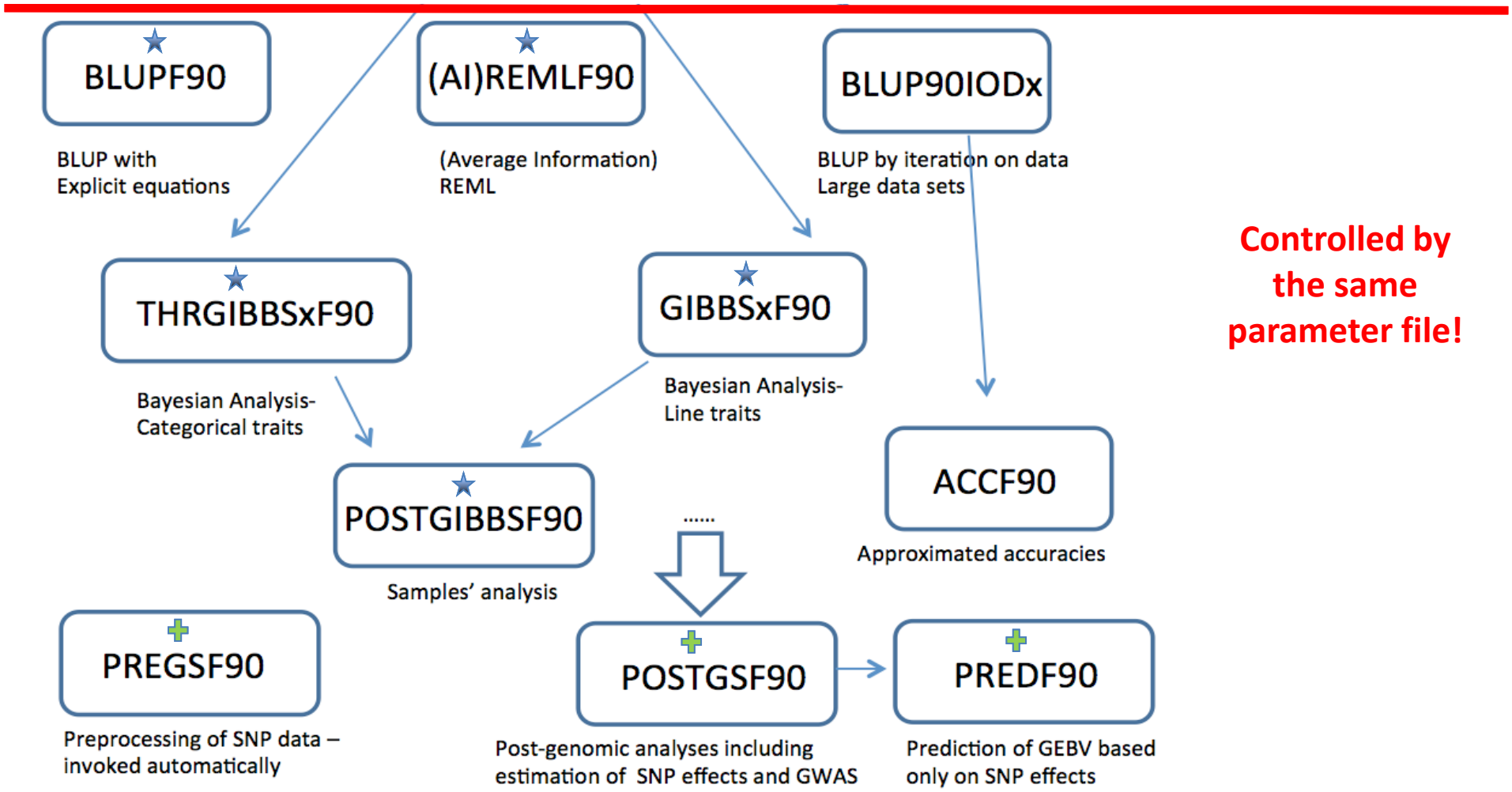
renumf90

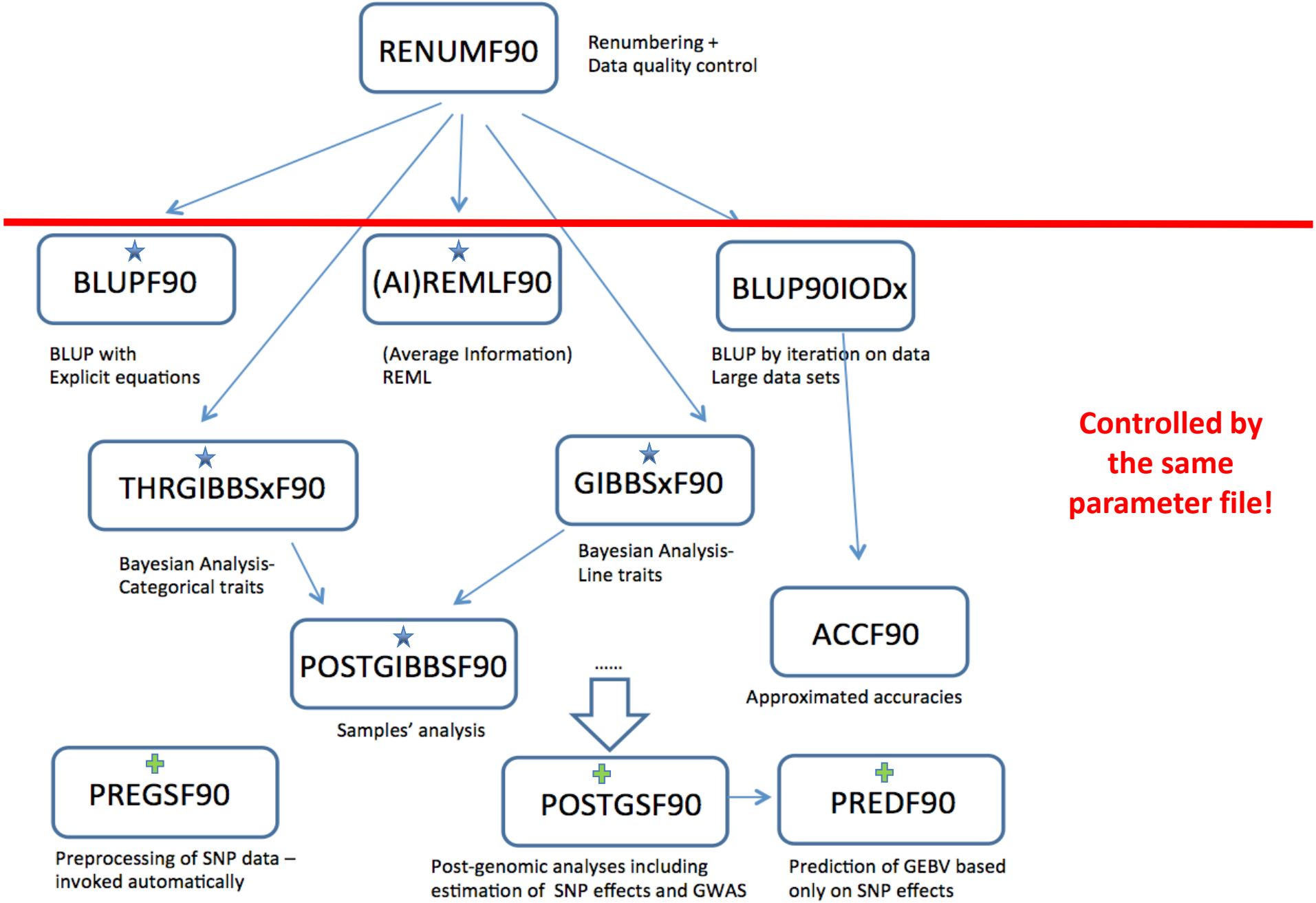
UGA – 05/2018

Data File for blupf90 family:

a) Only numbers – Integer or real

a) All effects need to be renumbered from 1 to N




RENUMF90
Renumbering +
Data quality control
BLUPF90
BLUP with
Explicit equations
(AI)REMLF90
(Average Information)
REML
BLUP90IODx
BLUP by iteration on data
Large data sets
THRGIBBSxF90
Bayesian Analysis-
Categorical traits
GIBBSxF90
Bayesian Analysis-
Line traits
POSTGIBBSF90
Samples' analysis
.....
ACCF90
Approximated accuracies
PREGSF90
Preprocessing of SNP data –
invoked automatically
POSTGSF90
Post-genomic analyses including
estimation of SNP effects and GWAS
PREDF90
Prediction of GEBV based
only on SNP effects
Controlled by
the same
parameter file!

RENUMF90

A **renumbering program** for the BLUPF90 family of programs

RENUMF90

- **Renumbers data and pedigree**
- **Traces back pedigree for individuals in data file**
- **Performs comprehensive pedigree checking**
- **Provides data statistics**

RENUMF90

- **Supports**
  - virtually any dataset
  - multiple traits
  - different effects per trait
  - alphanumeric and numeric fields
  - unknown parent groups
  - covariates for random regression models

RENUMF90 – Input files

- **Data file and pedigree file as flat files**
  - Columns separated by at least one SPACE
  - No TABS !!!! (current version checks for it)
  - Input files cannot contain character #
  - Missing sire/dams must have code 0
  - code 00 is treated as a known animal

- **Parameter file for renumf90**
  - Has its own parameter file!!!!
  - Not the same for other programs!!!!

RENUMF90 – Output files

- **Create files to be used by BLUPF90 family**
  - renf90.dat - data recoded
  - renaddxx.ped - renumbered pedigree + statistics
  - renf90.tables - cross reference file with renumbered and original effects
  - renf90.par - parameter file

RENUMF90 parameter file

- Based on keywords in capital followed by a line(s) with the corresponding data item
- Keywords need to be typed exactly
- Keywords need to be in sequential order!!!
- Lines starting with # are treated as comments and are ignored

RENUMF90 parameter file

MANDATORY

Keyword	possible value	description
DATAFILE	character	The name of data file to be processed
TRAITS	integer	Position for observation (trait) in the data file
FIELDS_PASSED TO OUTPUT	integer	Position for the columns in the original data that will be passed to the renumbered data without changes Keep empty if not needed
WEIGHT(S)	integer	The position(s) for weight in the data file Keep empty if not needed
RESIDUAL_VARIANCE	real value(s)	Residual (co)variance
EFFECT	(next slide …)	Description of an effect Repeatable

RENUMF90 parameter file

Effects

Keyword	Possible value	effect type	form
EFFECT	integer	cross	alpha
			numer
		cov	

Keyword (only for covariables)	Possible value	form
NESTED	integer	alpha
		numer

RENUMF90 parameter file

Model: $y = herd + sex + \beta\ age + e$

DATAFILE

TRAITS

FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE

EFFECT

data1.txt

ID	herd	sex	age	phen
ID006	A	1	1.0	3.0
ID009	A	2	1.0	2.0
ID012	A	1	2.0	4.0
ID007	B	2	2.0	6.0
ID010	B	1	1.0	3.0
ID013	B	2	2.0	6.0
ID008	C	1	2.0	6.0
ID011	C	2	1.0	6.0
ID014	C	1	1.0	8.0
ID015	C	2	2.0	4.0

RENUMF90 parameter file

Model: $y = herd + sex + \beta\ age + e$

```
DATAFILE
data1.txt
TRAITS
5
FIELDS_PASSED TO OUTPUT
2
WEIGHT(S)

RESIDUAL_VARIANCE
1.0
EFFECT        #1st effect
2 cross alpha
EFFECT        #2nd effect
3 cross numer
EFFECT        #3rd effect
4 cov
```

Fixed model

data1.txt

ID	herd	sex	age	phen
ID006	A	1	1.0	3.0
ID009	A	2	1.0	2.0
ID012	A	1	2.0	4.0
ID007	B	2	2.0	6.0
ID010	B	1	1.0	3.0
ID013	B	2	2.0	6.0
ID008	C	1	2.0	6.0
ID011	C	2	1.0	6.0
ID014	C	1	1.0	8.0
ID015	C	2	2.0	4.0

RENUMF90 parameter file

Random Effects

Keyword after EFFECT	possible value	description
RANDOM	diagonal	Non-correlated
	animal	Correlation structure among animals
	sire	Not implemented!!!

Keyword	possible value	description
OPTIONAL	pe	Permanent environmental
	mat	Maternal
	mpe	Permanent environmental maternal (only if mat is used)

RENUMF90 parameter file

Random effects file section

Keyword after RANDOM (animal or sire only)	possible value	description
FILE	character	Name of the pedigree file for animal or sire models only

Keyword after FILE (for RANDOM animal only)	possible value	description
FILE_POS	integer	Specifies positions in the pedigree for ani sire dam alternate_dam yob Default: 1 2 3 0 0 If maternal effect alternate_dam

Keyword (for RANDOM animal only)	possible value	description
SNP_FILE	character	Optional: If genomic info is to be used Name of the SNP file Format: ID 011122211155152222

RENUMF90 parameter file

Pedigree options

Keyword **(for RANDOM animal only)**	**possible value**	**description**
PED_DEPTH	Integer	Optional Specifies the depth of pedigree search Default = 3 All pedigree = 0

Keyword **(for RANDOM animal only)**	**possible value**	**description**
GEN_INT	Integer min avg max	Optional Specifies min, avg, max generation interval; if yob is present Average used to predict yob of parents

Keyword **(for RANDOM animal only)**	**possible value**	**description**
REC_SEX	Integer	Optional Specifies which parent has records Checks if records are found in specific sex

RENUMF90 parameter file

Unknown Parent Group options

Keyword **(for RANDOM animal only)**	**possible value**	**description**
UPG_TYPE		Optional
	yob 1990 1992 …	UPG assigned based on yob
	in_pedigrees	Missing parent receives -x x is the UPG number
	internal	UPG assigned by a user-written function (not implemented yet)

RENUMF90 parameter file

Inbreeding option

Keyword **(for RANDOM animal only)**	**possible value**	**description**
INBREEDING		Optional
	pedigree	Calculates inbreeding and saves in the renumbered pedigree file
	file	Reads inbreeding from an external file format: original_ID inbreeding (0 to 1)

RENUMF90 parameter file

Random Regression options

Keyword	possible value	description
RANDOM_REGRESSION		Specifies that random regression should be applied to the random effects
	data	If covariables are in the data
	legendre	Generates legendre polynomials (not implemented)

Keyword	possible value	description
RR_POSITON	Integer	Specifies positions of covariables if RANDOM_REGRESSION type is data

RENUMF90 parameter file

(CO)VARIANCES for Random effects

Keyword	possible value	description
(CO)VARIANCES	real	(co)variance for the animal effect dimension should account for number of traits and random correlated effects

DIRECT	32.79	-7.22	-11.07	-8.59	-0.35	-0.68
	-7.22	258.06	87.66	4.55	21.57	29.92
	-11.07	87.66	194.34	4.54	23.12	26.67
COV DIRRECT,MAT	-8.59	4.55	4.54	46.91	0.6	-0.08
	-0.35	21.57	23.12	0.6	132.24	29.95
	-0.68	29.92	26.67	-0.08	29.95	132.65

MATERNAL

RENUMF90 parameter file

(CO)VARIANCES structure

- 3 trait (T1-T3) and 2 correlated effects (E1-E2)

		E1			E2		
		T1	T2	T3	T1	T2	T3
E1	T1						
	T2						
	T3						
E2	T1						
	T2						
	T3						

RENUMF90 parameter file

(CO)VARIANCES for Random effects

Keyword	possible value	description
(CO)VARIANCES	real	(co)variance for non-correlated random effects

Keyword	possible value	description
(CO)VARIANCES_PE	real	(co)variance for the PE effect if present

Keyword	possible value	description
(CO)VARIANCES_MPE	real	(co)variance for the MPE effect if present

RENUMF90 parameter file

Creating interaction between effects

Keyword	possible value	description
COMBINE	integer	Should come before DATAFILE COMBINE 7 2 3 4 Columns 2, 3, 4 are combined into 7 They can be numer or alpha

RENUMF90 parameter file

Keyword	optional	possible values
COMBINE	optional	definition of new field as a combination of existing fields
DATAFILE	mandatory	name of raw data file
TRAITS	mandatory	positions of observations in the raw data file
FIELDS_PASSED	mandatory	positions of items in the raw data file to be passed to renf90.dat
WEIGHT(S)	mandatory	positions of weights in the raw data file
RESIDUAL_VARIANCE	mandatory	residual covariance matrix
EFFECT	mandatory	effect description
NESTED	optional	positions of nested covatiates
RANDOM	optional	declaration of random effect
OPTIONAL	optional	declaration of MAT, PE, MPE
FILE	optional	name of raw pedigree file
FILE_POS	optional	positions of animal ID, sire ID and dam ID
SNP_FILE	optional	name of SNP marker file
PED_DEPTH	optional	the maximum generation back from animals with phenotype or genotype
GEN_INT	optional	generation interval to set unknown parent groups (UPG)
REC_SEX	optional	check if records are found in specific sex
UPG_TYPE	optional	UPG specification
INBREEDING	optional	create pedigree file with inbreeding
RANDOM_REGRESSION	optional	put covariates for random regressions
RR_POSITION	optional	positions of covariates for random regrtessions
(CO)VARIANCES	optional	covariance components
(CO)VARIANCES_PE	optional	covariance components for animal's PE effects
(CO)VARIANCES_MPE	optional	covariance components for maternal PE effects
OPTION	optional	option parameters

RENUMF90 parameter file

Options passed to blupf90

- All lines that begin with keyword OPTION are passed to parameter file `renf90.par`

- This allows automatization of process by using scripts

- For example:
  - `OPTION sol se`

RENUMF90 parameter file

Extra options

The following options can added at the end of the parameter file to redefine parameters used to read the input file:

– the default size of character fields (maximum number of letters in a column)

```
OPTION alpha_size nn
```

where *nn* is the new size.

– the size of th record length (maximum number of letters in a line)

```
OPTION max_string_readline nn
```

where *nn* is the new size.

– the maximun number of fields (maximum number of columns in a line)

```
OPTION max_field_readline nn
```

where *nn* is the number of fields.

RENUMF90 parameter file

Hints

- Keyword EFFECT is repeated as many time as effects in the model
- If (CO)VARIANCES for any effect are missing, default matrix with 1.0 in diagonal and 0.1 on off-diagonal will be used
  - WARNING: for EM-REML convergence rate is improved if starting values are too large rather than too small !!!

RENUMF90 parameter file

Model: $y = herd + sex + \beta\ age + e$

```
DATAFILE
data1.txt
TRAITS
5
FIELDS_PASSED TO OUTPUT
2
WEIGHT(S)

RESIDUAL_VARIANCE
1.0
EFFECT        #1st effect
2 cross alpha
RANDOM
diagonal
(CO)VARIANCES
0.5
EFFECT        #2nd effect
3 cross numer
EFFECT        #3rd effect
4 cov
```

What if we want to consider herd as random?

data1.txt

ID	herd	sex	age	phen
ID006	A	1	1.0	3.0
ID009	A	2	1.0	2.0
ID012	A	1	2.0	4.0
ID007	B	2	2.0	6.0
ID010	B	1	1.0	3.0
ID013	B	2	2.0	6.0
ID008	C	1	2.0	6.0
ID011	C	2	1.0	6.0
ID014	C	1	1.0	8.0
ID015	C	2	2.0	4.0

RENUMF90 parameter file

Model: $y = herd + sex + \beta\ age + animal + e$

```
DATAFILE
data1.txt
TRAITS
5
FIELDS_PASSED TO OUTPUT
2
WEIGHT(S)

RESIDUAL_VARIANCE
1.0
EFFECT        #1st effect
2 cross alpha
EFFECT        #2nd effect
3 cross numer
EFFECT        #3rd effect
4 cov
EFFECT        #4th effect
1 cross alpha
RANDOM
animal
FILE
ped1.txt
FILE_POS
1 2 3 0 0
(CO)VARIANCES
0.5
```

What if we want to consider animal effect as random?

ped1.txt

ID	Sire	Dam
ID006	ID001	ID003
ID009	ID001	ID004
ID012	ID001	ID005
ID007	ID001	ID003
ID010	ID001	ID004
ID013	ID002	ID005
ID008	ID002	ID003
ID011	ID002	ID004
ID014	ID002	ID005
ID015	ID002	ID003

data1.txt

ID	herd	sex	age	phen
ID006	A	1	1.0	3.0
ID009	A	2	1.0	2.0
ID012	A	1	2.0	4.0
ID007	B	2	2.0	6.0
ID010	B	1	1.0	3.0
ID013	B	2	2.0	6.0
ID008	C	1	2.0	6.0
ID011	C	2	1.0	6.0
ID014	C	1	1.0	8.0
ID015	C	2	2.0	4.0

RENUMF90 output files

Pedigree file: `renaddxx.ped`

Data file: `renf90.dat`

Parameter file: `renf90.par`

Renumbering table: `renf90.table`

RENUMF90 output files
Pedigree file: `renaddxx.ped`

- Structure:
  1. Animal ID (from 1)
  2. Parent 1 ID or UPG number for parent 1
  3. Parent 2 ID or UPG 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 animal has genotype: 10+number of known parents
  7. Number of records
  8. Number of progeny as parent 1
  9. Number of progeny as parent 2
  10. Original animal ID

RENUMF90 output files
Pedigree file: renaddxx.ped

- If option for inbreeding is used:

  Column 4:

  inb/upg code = 4000 / [(1+ms)(1-Fs) + (1+md)(1-Fd)]

  ms (md) is 0 if sire (dam) is known, and 1 otherwise

  Fs (Fd) is the coefficient of inbreeding of sire (dam)

  Ex: inb/upg code for the animal with both parents F=0

RENUMF90 output files renumbering tables: `renf90.tables`

- For each cross-classified effects
  - Original ID, count, consecutive number

- Useful
  - To translate solutions from BLUPF90 program into original alphanumeric values
  - Check counts of records by level

Example of RENUMF90 parameter file

```
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
```

data file – data.test

```
1 aa 34.5 11 12 zz
3 bb 21.333 22 23 xx
8 cc 23.666 33 34 yy
1 dd 29 44 45 xx
3 aa  30 55 56 yy
5 bb 1234567.890 66 67 zz
```

pedigree file – test.ped

```
qq 0 0
aa 0 0
bb qq aa
cc qq 0
dd 0 aa
```

RENUMF90 Printout

```
RENUMF90 version 1.93
name of parameter file? testpar1
datafile:data.test
traits:           3           4
fields passed:           2           1
R
  5.000       2.000
  2.000       4.000

Processing effect  1 of type cross
item_kind=alpha

Processing effect  2 of type cross
item_kind=alpha
Optional maternal effect
Optional maternal permanent environment
Optional permanent environment
pedigree file name  "test.ped"
positions of animal, sire, dam, alternate dam and yob    1    2    3    0    0
Reading (CO)VARIANCES:           4 x           4
Reading (CO)VARIANCES_PE:           2 x           2
Reading (CO)VARIANCES_MPE:           2 x           2

Processing effect  3 of type cov
item_kind=alpha

Processing effect  4 of type cross
item_kind=alpha

Maximum size of character fields: 20

Maximum size of record (max_string_readline): 800

Maximum number of fields innput file (max_field_readline): 100
```

RENUMF90 Printout

```
hash tables for effects set up
read            6  records
table with            4  elements sorted
added count
Effect group            1  of column            1  with            4  levels
table expanded from        10000  to        10000  records
added count
Effect group            2  of column            1  with            4  levels
table with            4  elements sorted
added count
Effect group            3  of column            1  with            4  levels
table expanded from        10000  to        10000  records
table with            3  elements sorted
added count
Effect group            4  of column            1  with            3  levels
table expanded from        10000  to        10000  records
wrote statistics in file "renf90.tables"

Basic statistics for input data  (missing value code is 0)
Pos  Min         Max         Mean        SD                 N
  3    21.333     0.12346E+07 0.20578E+06 0.50400E+06       6
  4    11.000      66.000      38.500      20.579           6
  5    12.000      67.000      39.500      20.579           6

Correlation matrix
       3     4     5
 3   1.00  0.65  0.65
 4   0.65  1.00  1.00
 5   0.65  1.00  1.00

Counts of nonzero values (order as above)
         6         6         6
         6         6         6
         6         6         6
```

RENUMF90 Printout

```
random effect   2
type:animal
opened output pedigree file "renadd02.ped"
read            5  pedigree records
loaded            3  parent(s) in round            1

Pedigree checks

Number of animals with records:           4
Number of parents without records:           1
Number of phantom dams:           2
Total number of animals:           7

random effect   4
type:diag

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

RENUMF90 output files

data file – renf90.dat

```
34.5 11 1 3 5 12 1 3 aa 1
21.333 22 2 1 3 23 2 1 bb 3
23.666 33 4 4 7 34 4 2 cc 8
29 44 1 2 3 45 1 1 dd 1
30 55 2 3 5 56 2 2 aa 3
1234567.890 66 3 1 3 67 3 3 bb 5
```

Pedigree file – renadd02.ped

```
1 6 3 1 0 2 2 0 0 bb
6 0 0 1 0 0 0 2 0 qq
2 0 3 1 0 1 1 0 0 dd
7 0 0 1 0 0 0 0 1 D@@0000002
5 0 0 1 0 0 0 0 1 D@@0000001
3 0 5 1 0 1 2 0 2 aa
4 6 7 1 0 2 1 0 0 cc
```

renumbering tables - renf90.tables

```
 Effect group 1 of column 1 with 4 levels
 Value    #    consecutive number
1 2 1
3 2 2
5 1 3
8 1 4
 Effect group 3 of column 1 with 4 levels
 Value    #    consecutive number
1 2 1
3 2 2
5 1 3
8 1 4
 Effect group 4 of column 1 with 3 levels
 Value    #    consecutive number
xx 2 1
yy 2 2
zz 2 3
```

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
```

renumf90 FAQ

1) renumf90 cannot find the data file — Check for typos

2) How to include quadratic covariable? — Column in data file

3) Error when trying to use covariable — 2 cov numer

4) I want to have original IDs in renf90.dat — FIELDS_PASSED TO OUTPUT

5) Fixed effects in renf90.dat are different from original — renf90.tables

6) Why solutions are not with original ID? — ask Ignacy Misztal

7) How to match solutions with original ID? — Bash scripting

For trait 1 when animal is effect number 2

```
$awk '{ if ($1==1 && $2==2) print $3,$4}' solutions | sort +0 -1 > sol.temp
$awk '{print $1,$10}' renadd02.ped | sort +0 -1 > ids.temp
$join -1 +1 -2 +1 ids.temp sol.temp > renumbered_original_EBV
```

renumf90 FAQ

8) When to run renumf90?

a) Objective to compare models

Run renumf90 ONCE with the most complete model

Remove effects from renf90.par

b) Objective to mask phenotypes for some animals for validation

Run renumf90 ONCE with the complete data

Remove animals from renf90.dat

c) Objective to compare non-genomic vs genomic model

Run renumf90 ONCE with SNP file

For non-genomic: Remove option for SNP file from renf90.par

blupf90 family

renf90.par

RANDOM_TYPE

add_animal

Type of random effect (distribution)

diagonal, **add_sire**, **add_an_upg**, **add_an_upginb**, **par_domin**, or **user_file**

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
```

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 blupf90

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

Set convergence criteria (deault 1e-12).

```
OPTION maxrounds 10000
```

Set maximum number of rounds (default 5000).

```
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 standard errors.

Options for blupf90

Missing data
Not pedigree!

```
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.

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.

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

Options for aiemlf90

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

```
(G_eff1_eff2_trt1_trt2)

R_trt1_trt1
```

Examples:

```
OPTION se_covar_function P 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 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).

log-residual function (Foulley and Quaas, 1995)

Common problems for blupf90 family

- Wrong data file and pedigree name
  - Program does not stop if wrong file name does 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 form blupf90 family

- Output printed on the screen is not saved in 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 airemlf.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 bash by sh
```

```
$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
```