



aska

British Columbia Alberta Saskatchewan Manitoba Nunavut Newfoundland and Labrador

Québec

Ontario

Washington Montana Minnesota Michigan Maine

Oregon Idaho Wyoming Nebraska Iowa New York New Jersey

Nevada Utah Colorado Kansas Missouri Ohio Virginia

California New Mexico Oklahoma Kentucky North Carolina

Texas Louisiana **Athens**

Florida

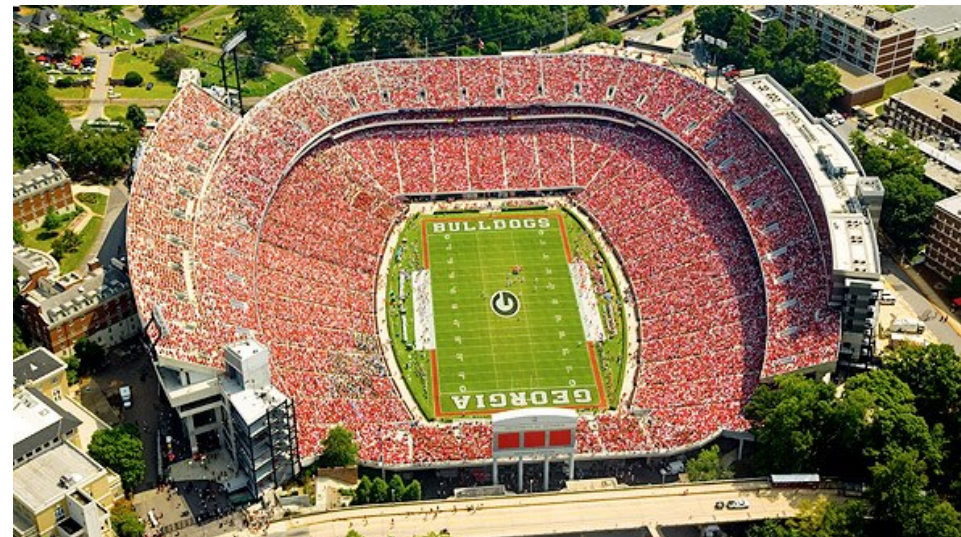
Mexico





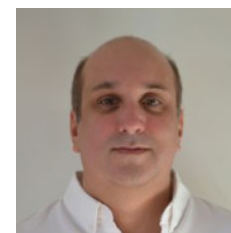
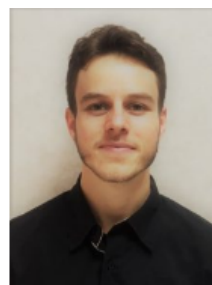
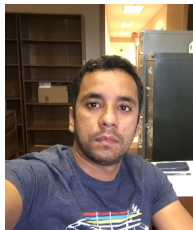
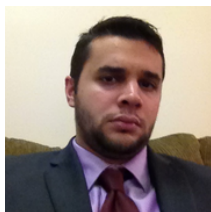
- U pública mais antiga dos EUA: 1785
- Top 16 nos EUA
- 29k graduandos
- 9k pós-graduandos
- *Tuition*: 26k – 46k

- Estádio para 92k pessoas
- Jogos Olímpicos de 1996 (Atlanta)
- Futebol Americano
- Salário do Reitor?
- Salário do Treinador?





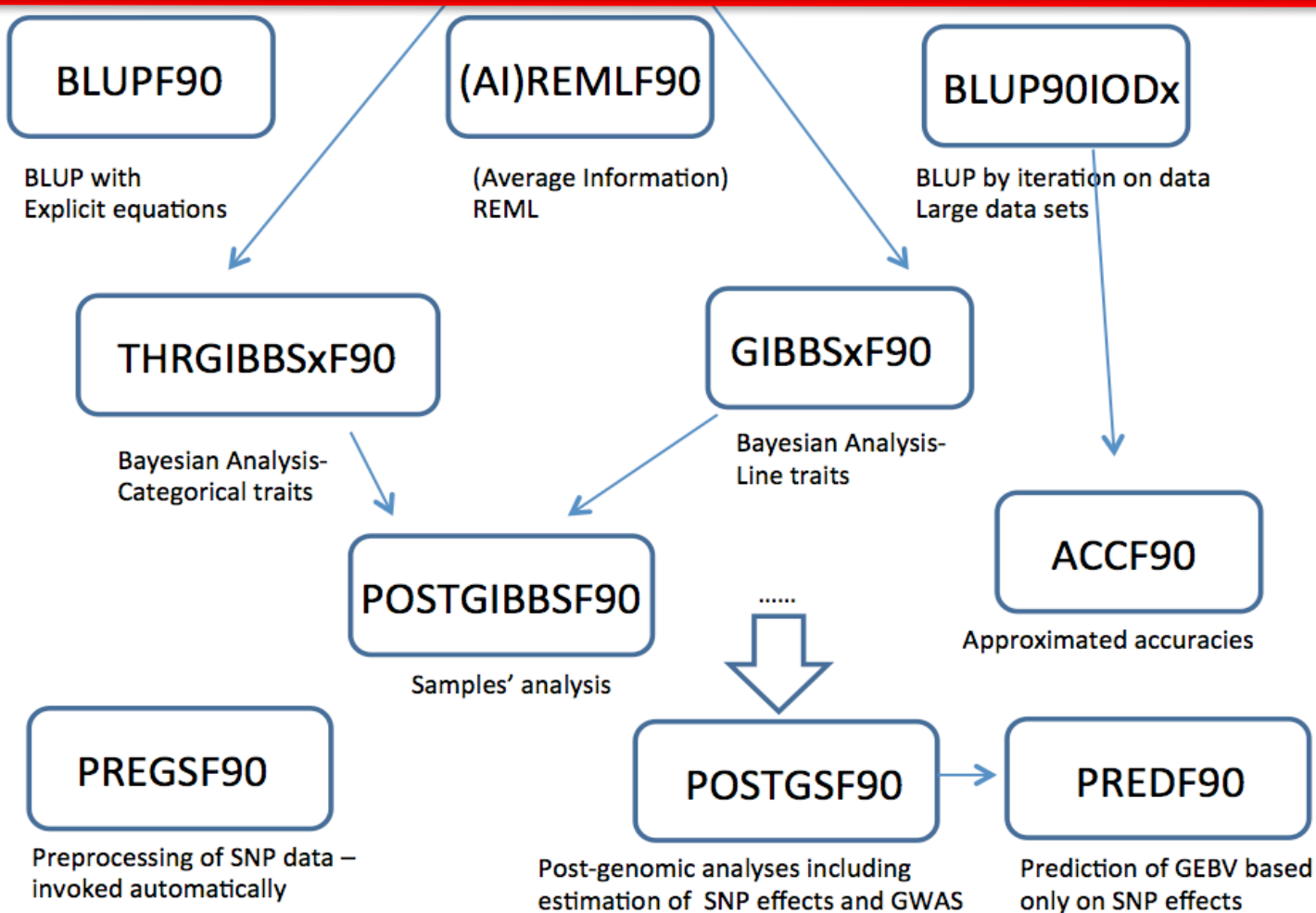
Grupo de Melhoramento Genético Animal



Data File for blupf90 family:

a) Only numbers – Integer or real

a) All effects need to be renumbered from 1 consecutively



**Controlled by
the same
parameter file!**

Introduction to **renumf90**

UGA – 05/2016

RENUMF90

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

RENUMF90

- **Supports**
 - multiple traits
 - different effects per trait
 - alphanumeric and numeric fields
 - unknown parent groups
 - covariates for random regression models
- **Traces back pedigree for individuals in data file**
- **Performs comprehensive pedigree checking**
- **Provides data statistics**

RENUMF90 – Output files

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

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 parameter file

- Based on keywords in capital following by a line(s) with the corresponding data item
- Keywords need to be typed exactly
- Keywords need to occur 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: $y = \textit{herd} + \textit{sex} + \beta \textit{age} + e$

DATAFILE

data1.txt

TRAITS

FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE

EFFECT

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 yet

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 and sire 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 and sire 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 and sire only)	possible value	description
PED_DEPTH	Integer	Optional Specifies the depth of pedigree search Default = 3 All pedigree = 0
Keyword (for RANDOM animal and sire only)	possible value	description
GEN_INT	Integer min avg max	Optional Specifies min, avg, max generation interval; if job is present Avg used to predict job of parents
Keyword (for RANDOM animal and sire 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 and sire only)	possible value	description
UPG_TYPE	yob 1990 1992 ... in_pedigrees internal	Optional UPG assigned based on yob Missing parent receives -x x is the UPG number UPG assigned by a user-written function (not implemented yet)

RENUMF90 parameter file

Inbreeding option

Keyword (for RANDOM animal and sire only)	possible value	description
INBREEDING	pedigree file	Optional Calculates inbreeding and saves in the renumbered pedigree 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 yet)

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	MATERNAL
	-0.35	21.57	23.12	0.6	132.24	29.95	
	-0.68	29.92	26.67	-0.08	29.95	132.65	

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

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

Hints

- Keyword EFFECT is repeated as many times 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: $y = \text{herd} + \text{sex} + \beta \text{ age} + e$

```
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
RANDOM
diagonal
(CO)VARIANCES
0.5
EFFECT      #3rd effect
4 cov
```

*What if we want to
consider sex 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: $y = \text{herd} + \text{sex} + \text{animal} + \beta \text{ age} + e$

```
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
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			data1.txt				
ID	Sire	Dam	ID	herd	sex	age	phen
ID006	ID001	ID003	ID006	A	1	1.0	3.0
ID009	ID001	ID004	ID009	A	2	1.0	2.0
ID012	ID001	ID005	ID012	A	1	2.0	4.0
ID007	ID001	ID003	ID007	B	2	2.0	6.0
ID010	ID001	ID004	ID010	B	1	1.0	3.0
ID013	ID002	ID005	ID013	B	2	2.0	6.0
ID008	ID002	ID003	ID008	C	1	2.0	6.0
ID011	ID002	ID004	ID011	C	2	1.0	6.0
ID014	ID002	ID005	ID014	C	1	1.0	8.0
ID015	ID002	ID003	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`

Inbreeding coeff: `renf90.inb`

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:

$$\text{inb/upg code} = 4000 / [(1+m_s)(1-F_s) + (1+m_d)(1-F_d)]$$

m_s (m_d) is 0 if sire (dam) is known, and 1 otherwise

F_s (F_d) 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

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
```

```
# 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

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
```