

# MiX99

Solving Large Mixed Model Equations



MTT

## CLIM tutorial

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# Command Language Interface for MiX99

- Original MiX99 interface:
  - Directive file
  - Answers to questions
  - → not so easy for user
- CLIM:
  - Command driven
  - Order of commands flexible
  - Easy to read and change

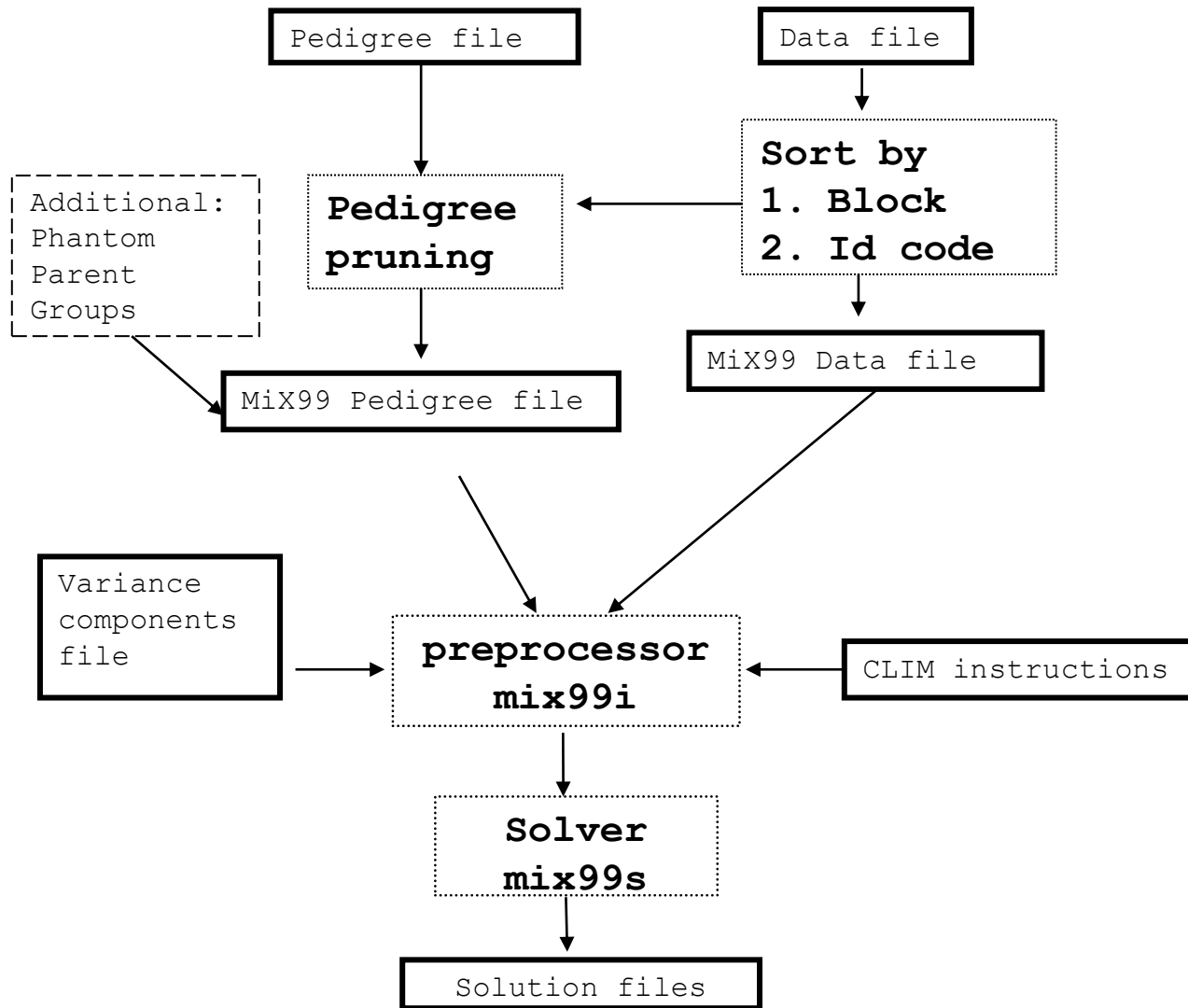
This presentation:

**WARNING: contains material from the CLIM manual**

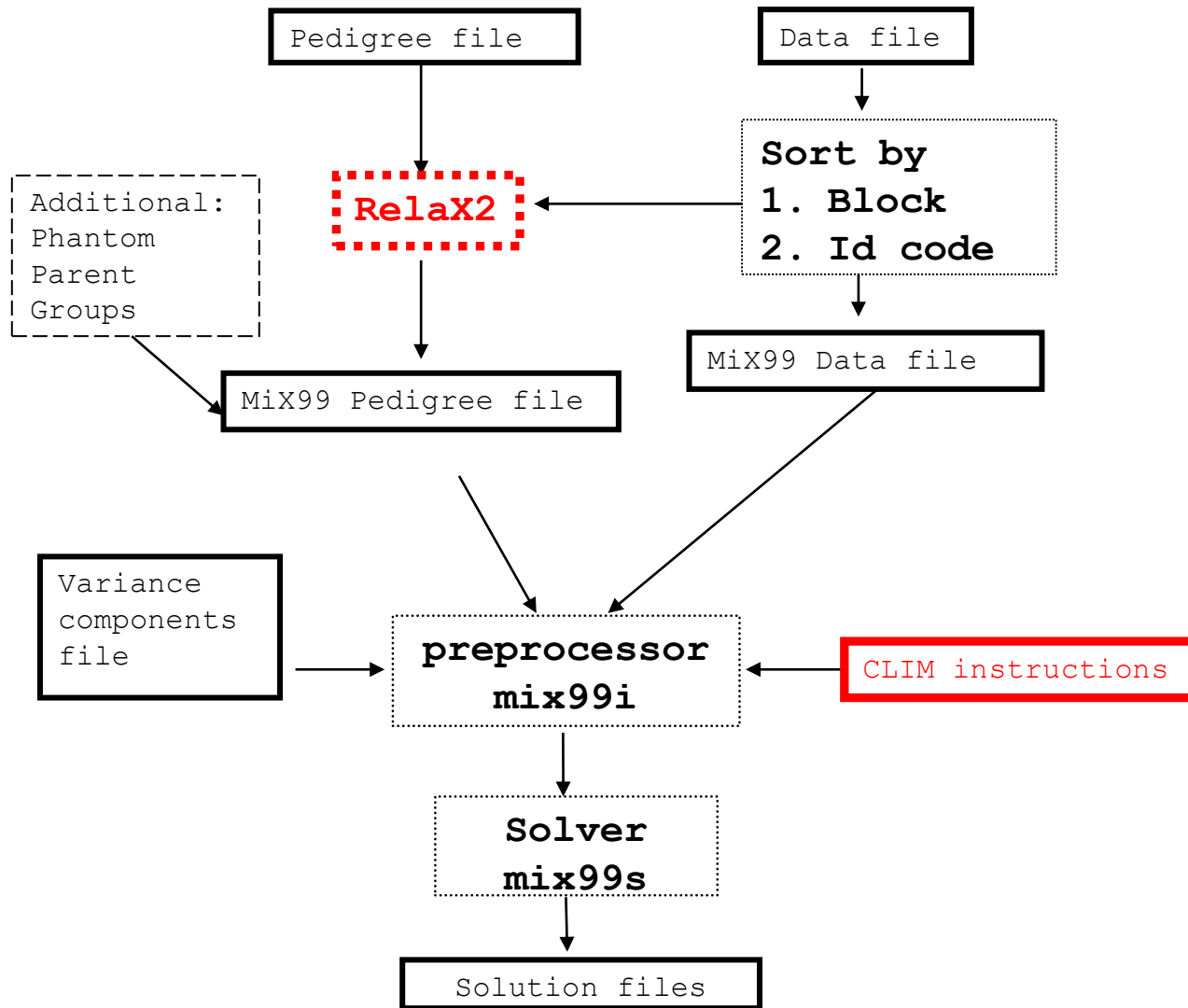
How to use MiX99 solver through CLIM

& pedigree for MiX99 through RelaX2

# MiX99 workflow



# MiX99 workflow



# RelaX2: Pedigree analysis program

1. Check pedigree for consistency, correct some errors
2. Prune pedigree
  - Different methods available
3. New pedigree
  - Pruned, corrected, formatted, ordered ...
4. Relationship information
  - Inbreeding coefficients, relationship matrix
5. Population statistics
  - Effective population size, generation interval
6. Breed proportions
7. ...

Command language driven



# Simple command file for RelaX2

```
# NOTE: no output to file is requested!

input pedigree          # Pedigree input
  file relaxc.ped       # This file has pedigree
  record id sire dam    # This input information

# Following are some additions that might be useful:
# output overwrite inbreeding simple.inbr # Inbreeding
# output overwrite cycles      simple.cycl # Cycles
# nopopulations # No calculation of number of populations
```

Execution of RelaX2 having commands in file `simple.dir`:  
`relax2 < simple.dir`

# Format for pedigree

Integer or character string in id code

Integers:

1. Record id 1 sire 2 dam 3
2. Record id sire dam
3. Record id 1:10 sire 50:59 dam 70:79

Character strings:

4. Record id \$ 1:10 sire \$ 50:59 dam \$ 70:79

Unknown parent can be space in 3. and 4.

# RelaX2: Pedigree

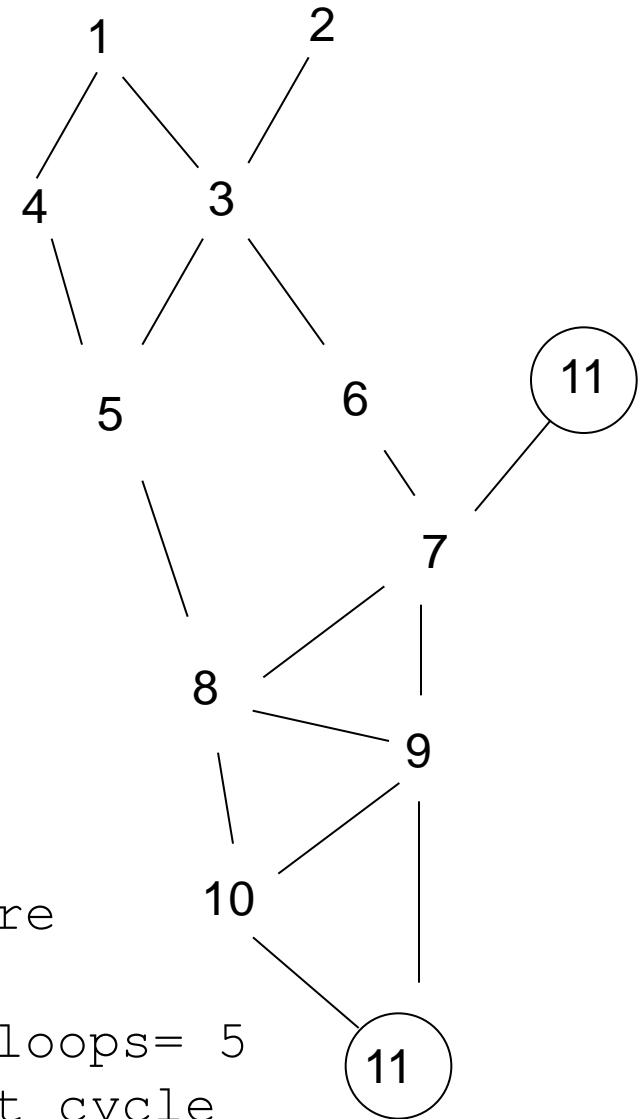
Some commands:

- `Input/Output pedigree`: animal model pedigree
- `Input/Output smpedigree`: sire model pedigree
- `Singlepopulation`
  - Chooses the largest pedigree among separate ones
- `Prune Some_Method`
  - Prunes pedigree of unnecessary animals.
- `Input select` (selecting for statistics calculations)
  - Chooses individuals according to some external information for calculation of statistics (mean generation interval, inbreeding coefficients etc.)
- `Output Amatrix`: relationship matrix



## RelaX2 example: pedigree loops

```
> cat relaxc.ped
1 0 0 10 01/1998
2 0 0 10 01/1999
3 1 2 10 01/2000
4 1 0 20 02/2000
5 4 3 20 01/2001
6 0 3 20 02/2001
7 6 11 30 01/2002
8 7 5 30 01/2003
9 7 8 30 01/2004
10 9 8 30 02/2005
11 9 10 30 01/2006
```



### RelaX2 says:

There are individual(s) that are parents for themselves.

Number of individuals in such loops= 5

Please rerun RelaX2 and request cycle output file (e.g., output cycles cycles.dat)

# Example on pruning for MiX99

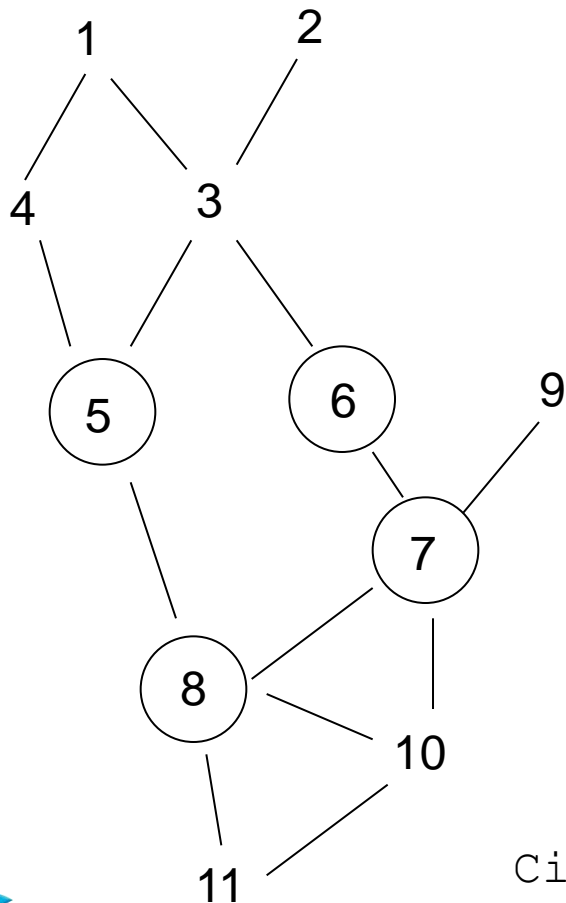
```
input pedigree
  file some.ped      # pedigree file
  record id sire dam group
  prune prediction # animals with data and their
                  # ancestors, only informative
                  # except always sire and dam

input data          # animals in data file have observ.
  file some.dat
  record id group  # id code and group/block code

mix99 keep # MiX99 format for output pedigree;
          # group in pedigree is kept if
          # animal has no observation

output overwrite pedigree pruned.ped
```

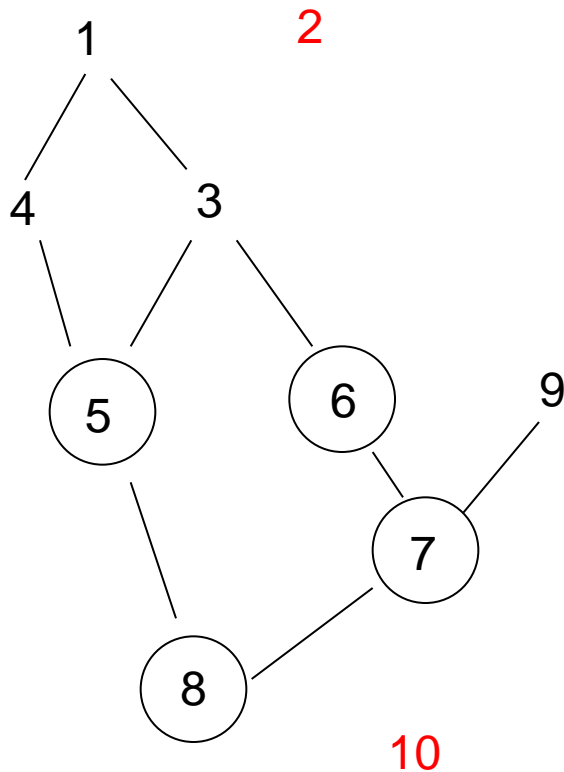
# Pruning: original pedigree



|    |    |    |    |
|----|----|----|----|
| 1  | -1 | -1 | 10 |
| 2  | -2 | -2 | 10 |
| 3  | 1  | 2  | 10 |
| 4  | 1  | -4 | 20 |
| 5  | 4  | 3  | 20 |
| 6  | -6 | 3  | 20 |
| 7  | 6  | 9  | 30 |
| 8  | 7  | 5  | 30 |
| 9  | -5 | -9 | 30 |
| 10 | 7  | 8  | 30 |
| 11 | 10 | 8  | 30 |

Circled animals are in the data file

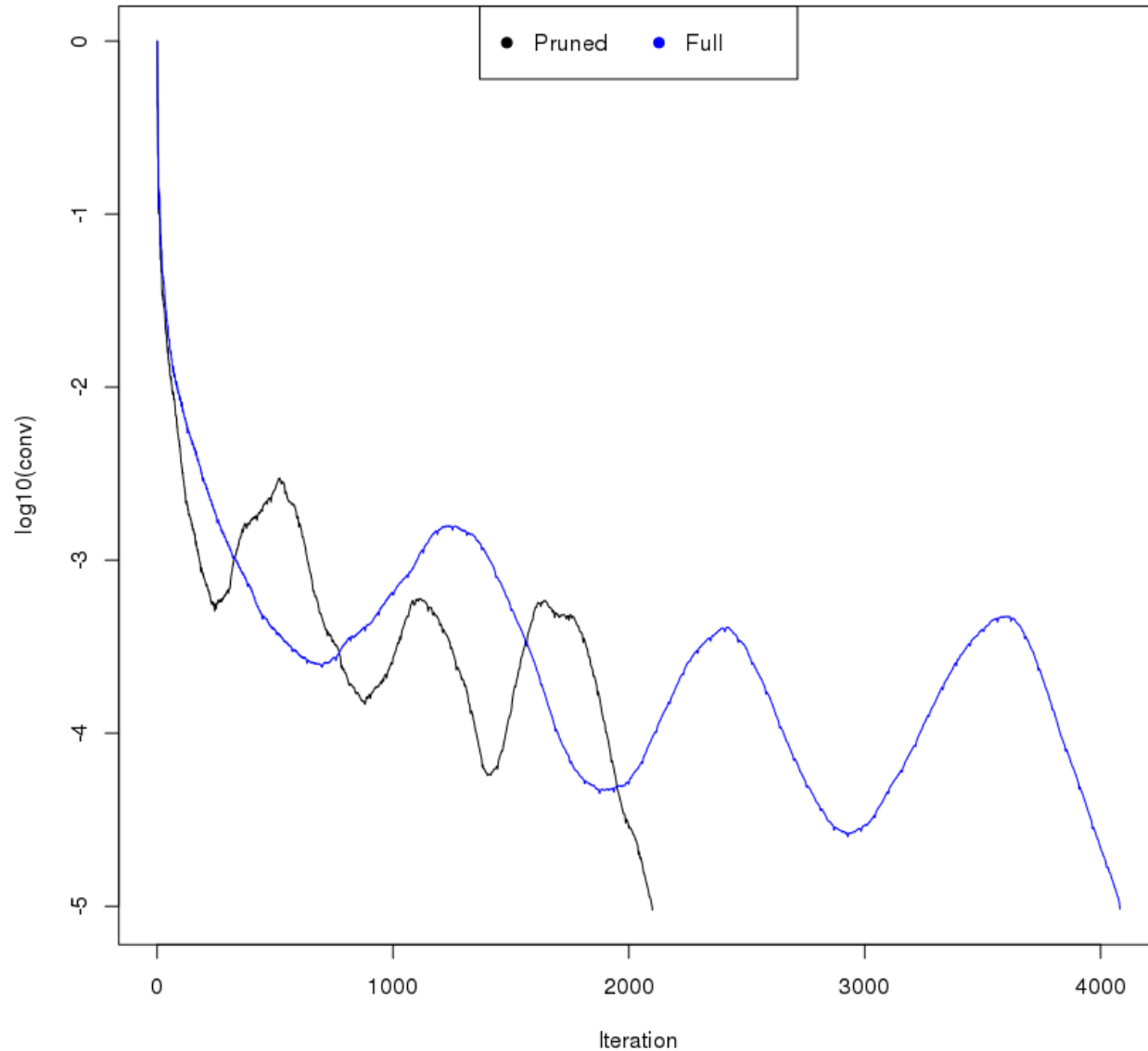
# Pruned pedigree



|    |    |          |    |
|----|----|----------|----|
| 1  | -1 | -1       | 10 |
| 2  | -2 | -2       | 10 |
| 3  | 1  | <b>0</b> | 10 |
| 4  | 1  | -4       | 20 |
| 5  | 4  | 3        | 20 |
| 6  | -6 | 3        | 20 |
| 7  | 6  | 9        | 30 |
| 8  | 7  | 5        | 30 |
| 9  | -5 | -9       | 30 |
| 10 | 7  | 8        | 30 |
| 11 | 10 | 8        | 30 |

**NOTE: Offspring of Dam 9 has observation but offspring of Dam 2 (animal 3) has no observation**

# Effect of pruning to convergence



# Short summary on RelaX2

1. Read pedigree and check its goodness
  - Need any corrections? Can use so called `errata` file
2. Prune pedigree, use data file
3. Output pedigree in MiX99 format
4. Other options of interest:
  - Calculate inbreeding coefficients (MiX99 cannot calculate)
  - Calculate relationship matrix (useful for single-step)
  - Calculate breed proportions

# CLIM by example

## Example: Single trait animal model

A simple single trait animal model has the form

$$y = Xb + Za + e$$

where

$y$  is  $n \times 1$  vector of observations,

$b$  is  $p \times 1$  vector of fixed effects,

$X$  is  $n \times p$  design matrix to link observations to appropriate fixed effects,

$a$  is  $q \times 1$  vector of random additive genetic effects,

$Z$  is  $n \times q$  design matrix to link observations to appropriate random effects,

$e$  is  $n \times 1$  random residual vector.

# Animal model example by CLIM:

R.Mrode. "Linear models for the Prediction of Animal Breeding Values". Ex. 3.1

Model:  $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$

$$\begin{array}{ll} E(\mathbf{a}) & = \mathbf{0} \\ E(\mathbf{e}) & = \mathbf{0} \\ E(\mathbf{y}) & = \mathbf{Xb} \end{array} \qquad \begin{array}{ll} \text{Var}(\mathbf{a}) & = \mathbf{A}\sigma_a^2 \\ \text{Var}(\mathbf{e}) & = \mathbf{I}\sigma_e^2 \\ \text{Cov}(\mathbf{a}, \mathbf{e}) & = \mathbf{0} \end{array}$$

Mixed model equations:

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

Example case:

Fixed effects: sex

Random effects: additive genetics and residual



# CLIM instruction file: AM.clm

```
herakles:~/MiX99/example/serial/animal_model> cat AM_example_3_1.clm
#-----
# R. Mrode: Linear Models for the Prediction of Animal Breeding Values
#
# A model for an animal evaluation (animal model)
# Example 3.1
#
# MODEL: Prewaning gain = sex + animal
#-----
```

```
DATAFILE AM_ex31.dat # Name of data file
INTEGER animal sex # Integer number column names
REAL weaningW # Real number column names
```

```
PEDFILE AM_ex31.ped # Name of Pedigree file
PEDIGREE animal am # Genetics associated with animal code
# am=animal model
```

```
PARFILE AM_ex31.var # Name of variance component file
```

```
MODEL
weaningW = sex animal # The model
```

```
herakles:~/clim_examples/animal_model_RMrode> cat AM_ex31.dat
4 1 4.5
5 2 2.9
6 2 3.9
7 1 3.5
8 1 5.0
```

sex  
weaningW  
animal

```
herakles:~/clim_examples/animal_model_RMrode> cat AM_ex31.ped
1 0 0
2 0 0
3 0 0
4 1 0
5 3 2
6 1 2
7 4 5
8 3 6
```

Sire and dam ID  
animal ID

```
herakles:~/clim_examples/animal_model_RMrode> cat AM_ex31.var
1 1 1 20.0 Genetic variance
2 1 1 40.0 Residual variance
```



# MiX99 solving

- **MiX99 preprocessor:**

```
mix99i AM_example_3_1.clm >AM_mix99i.log
```

- Tmp-files
- Modlog, Parlog, Tralog
- Resid.List
- OK\_mix99i

- **MiX99 solver:** `mix99s -s > AM_mix99s.log`

- Conlog
- Solfix, Solani
- Solvec
- OK\_mix99s

# Repeatability animal model

- Consider model:
  - $y = \text{herd-year} + \text{permanent environment} + \text{add.genet.} + \text{residual}$
  - $\mathbf{y} = \mathbf{Xb} + \mathbf{Zp} + \mathbf{Za} + \mathbf{e}$ , with 
$$\begin{aligned}\text{Var}(\mathbf{p}) &= \mathbf{I}\sigma_p^2 \\ \text{Var}(\mathbf{a}) &= \mathbf{A}\sigma_a^2 \\ \text{Var}(\mathbf{e}) &= \mathbf{I}\sigma_e^2\end{aligned}$$
- When no permanent environment effect:
  - $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$

and CLIM instructions are previous example

# CLIM and repeatability model

- Problem: two effects use the same integer number column:  
animal
  - Which of the effects is additive genetic effect
  - How about number of random effect
  - Within block ordering?
- Solution: user defined component names

```
INTEGER  animal sire herd_year ones
REAL     tr12

PEDIGREE animal am
MODEL
tr12 = herd_year animal animal
```

**Not acceptable**

Model error: Same component name appears twice on the line.  
On line: 9  
Near token: animal  
Complete line information:  
tr12 = herd\_year animal animal

# Component names for repeatability model

$$tr_{12} = herd \times year + p + a + e$$

User defined component name: **G**

```
INTEGER  animal sire herd_year ones
REAL     tr12
PEDIGREE G am # G for animal genetics
RANDOM    animal # permanent environment
```

```
INTEGER MODEL
REAL     tr12 = herd_year animal G(animal)
```

```
PEDIGREE animal am
MODEL
tr12 = herd_year animal animal
```

Permanent environment is random

# Repeatability model: alternatives

```
INTEGER  animal sire herd_year ones
REAL     tr12

PEDIGREE  G am    # G for animal genetics
RANDOM    animal # permanent environment

MODEL
  tr12 = herd_year animal G(animal)
```

1:

```
PEDIGREE  G am # G for animal genetics
RANDOM    PE  # PE for permanent environment
MODEL
  tr12 = herd_year PE(animal) G(animal)
```

2:

```
PEDIGREE  animal am # animal for animal genetics
RANDOM    PE          # PE for permanent environment
MODEL
  tr12 = herd_year PE(animal) animal
```



# Component names

- Allows accessing the same integer column
- Can be used to combine effects for easier reading
- Can be used to group random effects with same variance-covariance structure:
  - Direct and maternal component
  - Random regression effects
- Note: unique name must be chosen, not used column name or reserved name

```
Improper pedigree effect name.
```

```
On line: 6
```

```
Near token: real
```

```
Complete line information:
```

```
PEDIGREE real am
```

```
Error: random effect can only be within integer class. Cannot be a random effect
```

```
On line: 7
```

```
Near token: block
```

```
Complete line information:
```

```
RANDOM block
```

# Solutions

MiX99 solver output:

Solutions for First 20 Levels of Across-Block Fixed Effect: 1 herd\_yea

```
-----
Fact.Trt ___Level___ N-Obs   Eq-No   Solution   Factor
  1  1   ___11___     2       11     99.8333   herd_yea
```

```
herakles:~/MiX99/example/serial/clim_examples/repeatability_model> cat Solfix
Fact. Trt   Level   N-Obs   Solution   Factor Trait
  1  1     11      2     99.833   herd_yea tr12
  1  1     12      3    123.01   herd_yea tr12
Fi  1  1     21      2    194.83   herd_yea tr12
--  1  1     22      3    129.68   herd_yea tr12
```

Fixed effects

```
Fact.Trt ___Level___ N-Obs   Eq-No   Solution   Factor
  1  1   ___4___     2       15    -0.888889  animal
```

Permanent environment

```
herakles:~/MiX99/example/serial/clim_examples/repeatability_model> cat Solr01
  1  1   ___4___     2    -0.88889
  1  1   ___6___     2     0.88889
  1  1   ___8___     2     1.1867
  1  1   ___9___     2    -0.55846
First 20 Ani  10     2    -0.62827
```

```
-----
Fact.Trt ___Animal-ID___ N-Desc  N-Obs   Eq-No   Solution   Factor
  1  1   ___1___         2      0        1    0.427759E-10 animal
  1  1   ___2___         2      0        2    0.427759E-10 animal
```

Animal genetics

```
herakles:~/MiX99/example/serial/clim_examples/repeatability_model> cat Solani
  1  1   ___1___         2     0.42776E-10
  1  1   ___2___         2     0.42776E-10
  1  1   ___3___         2     0.333333
  1  1   ___4___         2    -0.333333
  1  1   ___5___         3     0.38932E-10
  1  1   ___6___         3     0.66667
  1  1   ___7___         1     0.97731E-01
  1  1   ___8___         1     0.98778
  1  1   ___9___         0    -0.85515E-01
  1  1   ___10___        0     0.71553E-01
```



# Multiple traits

- Repeatability model:
- Two trait model:

$$tr_{12} = herd \times year + p + a + e$$

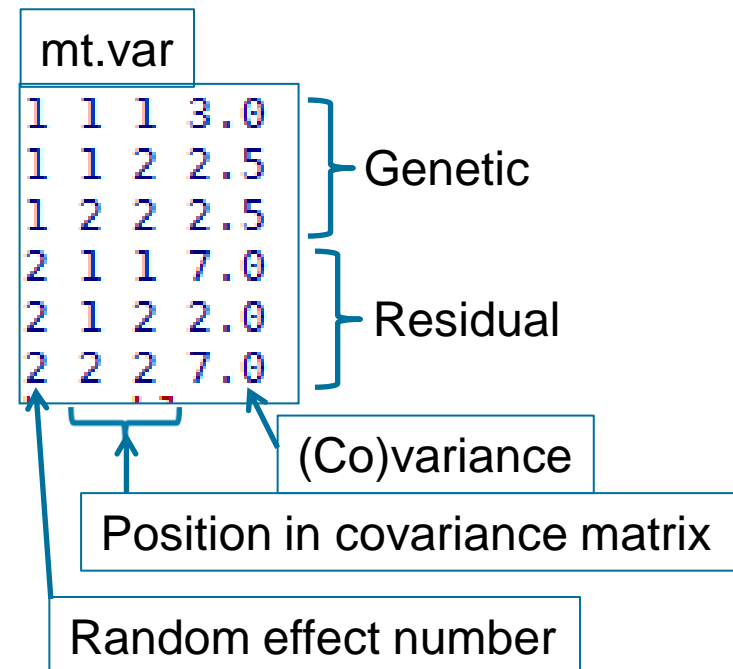
$$tr_1 = herd \times year + a_1 + e_1$$

$$tr_2 = \mu + a_2 + e_2$$

two\_tr.clm

```
DATAFILE example.dat
INTEGER animal sire herd_year ones
REAL    tr1 tr2
PEDFILE AM.ped
PEDIGREE animal am
DATASORT PEDIGREECODE=animal
PARFILE mt.var
MODEL SCALE
  tr1 = - herd_year animal
  tr2 = ones - animal
```

Important indicators



# Two trait model solutions

Solutions for First 20 Levels of Across-Block Fixed Effect: 1 ones

| Fact.Trt | Level | N-Obs | Eq-No | Solution | Factor       |
|----------|-------|-------|-------|----------|--------------|
| 1 2      | 1     | 5     | 21    | 160.285  | ones         |
| 1 2      | 1     | 5     | 5     | 160.28   | ones tr2     |
| 2 1      | 1     | 2     | 2     | 88.759   | herd_yea tr1 |
| 2 1      | 2     | 3     | 3     | 137.73   | herd_yea tr1 |
| 2 1      | 1     | 2     | 22    | 88.7587  | herd_yea     |
| 2 1      | 2     | 3     | 23    | 137.733  | herd_yea     |

Fixed effects

Solfix

First 20 Animal Solutions

| Fact.Trt | Animal-ID | N-Desc | N-Obs | Eq-No | Solution     | Factor |
|----------|-----------|--------|-------|-------|--------------|--------|
| 1 1      | 1         | 2      | 0     | 1     | 0.142930E-05 | animal |
| 2 2      | 1         | 2      | 0     | 2     | 0.609187E-06 | animal |
| 1 1      | 2         | 2      | 0     | 3     | 0.142930E-05 | animal |
| 2 2      | 2         | 2      | 0     | 4     | 0.609187E-06 | animal |
| 1 1      | 3         | 2      | 0     | 5     | -2.28421     | animal |
| 2 2      | 3         | 2      | 0     | 6     | -2.51119     | animal |
| 1 1      | 4         | 2      | 1     | 7     | 2.28422      | animal |
| 2 2      | 4         | 2      | 1     | 8     | 2.51119      | animal |
| 1 1      | 5         | 3      | 0     | 9     | -5.89685     | animal |
| 2 2      | 5         | 3      | 0     | 10    | -5.89685     | animal |
| 1 1      | 6         | 3      | 1     | 11    | 1.32842      | animal |
| 2 2      | 6         | 3      | 1     | 12    | 0.874481     | animal |
| 1 1      | 7         | 1      | 0     | 13    | -4.27474     | animal |
| 2 2      | 7         | 1      | 0     | 14    | -4.46353     | animal |
| 1 1      | 8         | 1      | 1     | 15    | -7.68036     | animal |
| 2 2      | 8         | 1      | 1     | 16    | -7.61893     | animal |
| 1 1      | 9         | 0      | 1     | 17    | -6.69126     | animal |
| 2 2      | 9         | 0      | 1     | 18    | -7.24481     | animal |
| 1 1      | 10        | 0      | 1     | 19    | -9.95859     | animal |
| 2 2      | 10        | 0      | 1     | 20    | -9.94590     | animal |

Animal genetics

Solani

| Fact.Trt | Animal-ID | N-Desc | N-Obs | Eq-No | Solution    | Factor      |
|----------|-----------|--------|-------|-------|-------------|-------------|
| 1 2      | 0         | 0      | 0     | 1     | 0.14293E-05 | 0.60919E-06 |
| 2 2      | 0         | 0      | 0     | 2     | 0.14293E-05 | 0.60919E-06 |
| 3 2      | 0         | 0      | 0     | 3     | -2.2842     | -2.5112     |
| 4 2      | 1         | 1      | 1     | 4     | 2.2842      | 2.5112      |
| 5 3      | 0         | 0      | 0     | 5     | -5.8969     | -5.8969     |
| 6 3      | 1         | 1      | 1     | 6     | 1.3284      | 0.87448     |
| 7 1      | 0         | 0      | 0     | 7     | -4.2747     | -4.4635     |
| 8 1      | 1         | 1      | 1     | 8     | -7.6804     | -7.6189     |
| 9 0      | 1         | 1      | 1     | 9     | -6.6913     | -7.2448     |
| 10 0     | 1         | 1      | 1     | 10    | -9.9586     | -9.9459     |



N-Desc= Number of progeny  
N-Obs= number of records

# Maternal effects example

```

DATAFILE  maternal_2.dat

INTEGER  calf sire dam herd sex
REAL     B_weight B2

DATASORT  PEDIGREECODE=calf

PEDFILE   data/maternal.ped
PEDIGREE  G am
RANDOM     PE

PARFILE   maternal_2.var      # Variance co

WITHINBLOCK G PE herd

MODEL
  B_weight = herd sex PE(dam) G(calf dam)
  B2       = herd sex PE(dam) G(calf -)
  
```

Numbering of genetic effects!

|   |   |   |     |                         |
|---|---|---|-----|-------------------------|
| 1 | 1 | 1 | 40  | permanent environment   |
| 1 | 2 | 2 | 40  | permanent environment   |
| 2 | 1 | 1 | 150 | additive genetic 1      |
| 2 | 1 | 3 | -40 | cov (genetic, maternal) |
| 2 | 3 | 3 | 90  | maternal genetic 1      |
| 2 | 2 | 2 | 150 | additive genetic 2      |
| 3 | 1 | 1 | 350 |                         |
| 3 | 2 | 2 | 350 |                         |

Genetics has 2 class effects

Missing maternal needs to be indicated

# Combining of effects: repeatability model by two trait model

Consider two trait model:  $tr_1 = herd \times year_1 + a_1 + e_1$   
 $tr_2 = herd \times year_2 + a_2 + e_2$

Repeatability model has genetic correlatin of one.

OR: the two trait model:  $tr_1 = herd \times year + a + e_1$   
 $tr_2 = herd \times year + a + e_2$

where herd x year is by trait.

```
DATAFILE example_mt_repeat.dat
INTEGER animal sire hy_1 hy_2 ones
REAL tr1 tr2

PEDFILE AM.ped
PEDIGREE G am

PARFILE mt_repeat.var

MODEL SCALE
tr1 = hy_1 - G(animal)@fst
tr2 = - hy_2 G(animal)@fst
```

Effects combined

# Random regression model

Consider model (Schaeffer & Dekkers, 1994, WCGALP):

$$milk = DIM + \log(305/DIM) + HTD + f(a, DIM) + e$$

where random regression function is

$$f(a, DIM) = a_{i,1} + DIM \cdot a_{i,2} + \log(305/DIM) \cdot a_{i,3}$$

Fixed regression function

Herd test day effect

CLIM model line:

MODEL

```
milk_yd = Lact_curve(DIM ln305DIM) HTD G(1 DIM ln305DIM| animal)
```

# Random regression model data can be large

data file RRM.dat

| HTD <sub>1</sub> | animal <sub>2</sub> | block <sub>3</sub> | DIM <sub>1</sub> | ln(305/DIM) <sub>2</sub> | milk <sub>3</sub> |
|------------------|---------------------|--------------------|------------------|--------------------------|-------------------|
| 1                | 1                   | 1                  | 73.0             | 1.4298500                | 26.0              |
| 2                | 1                   | 1                  | 123.0            | 0.9081270                | 23.0              |
| 3                | 1                   | 1                  | 178.0            | 0.5385280                | 21.0              |
| 1                | 2                   | 1                  | 34.0             | 2.1939499                | 29.0              |
| 2                | 2                   | 1                  | 84.0             | 1.2894900                | 18.0              |
| 3                | 2                   | 1                  | 139.0            | 0.7858380                | 8.0               |
| 4                | 2                   | 1                  | 184.0            | 0.5053760                | 1.0               |
| 1                | 3                   | 2                  | 8.0              | 3.6408701                | 37.0              |
| 2                | 3                   | 2                  | 58.0             | 1.6598700                | 25.0              |
| 3                | 3                   | 2                  | 113.0            | 0.9929240                | 19.0              |
| 4                | 3                   | 2                  | 158.0            | 0.6577170                | 15.0              |
| 5                | 3                   | 2                  | 218.0            | 0.3358170                | 11.0              |
| 6                | 3                   | 2                  | 268.0            | 0.1293250                | 7.0               |
| 2                | 4                   | 3                  | 5.0              | 4.1108699                | 44.0              |
| 3                | 4                   | 3                  | 60.0             | 1.6259700                | 29.0              |
| 4                | 4                   | 3                  | 105.0            | 1.0663500                | 22.0              |
| 5                | 4                   | 3                  | 165.0            | 0.6143660                | 14.0              |
| 6                | 4                   | 3                  | 215.0            | 0.3496740                | 8.0               |
| 4                | 5                   | 3                  | 14.0             | 3.0812500                | 35.0              |

Limited number of different numbers



# Covariable tables with index in data

| HTD <sub>1</sub> | animal <sub>2</sub> | block <sub>3</sub> | index <sub>4</sub> | milk <sub>1</sub> |
|------------------|---------------------|--------------------|--------------------|-------------------|
| 1                | 1                   | 1                  | 8                  | 26.0              |
| 2                | 1                   | 1                  | 14                 | 23.0              |
| 3                | 1                   | 1                  | 19                 | 21.0              |
| 1                | 2                   | 1                  | 5                  | 29.0              |
| 2                | 2                   | 1                  | 11                 | 18.0              |
| 3                | 2                   | 1                  | 16                 | 8.0               |
| 4                | 2                   | 1                  | 20                 | 1.0               |
| 1                | 3                   | 2                  | 2                  | 37.0              |
| 2                | 3                   | 2                  | 6                  | 25.0              |
| 3                | 3                   | 2                  | 13                 | 19.0              |
| 4                | 3                   | 2                  | 17                 | 15.0              |
| 5                | 3                   | 2                  | 22                 | 11.0              |
| 6                | 3                   | 2                  | 23                 | 7.0               |
| 2                | 4                   | 3                  | 1                  | 44.0              |
| 3                | 4                   | 3                  | 7                  | 29.0              |
| 4                | 4                   | 3                  | 12                 | 22.0              |
| 5                | 4                   | 3                  | 18                 | 14.0              |
| 6                | 4                   | 3                  | 21                 | 8.0               |

| index <sub>1</sub> | DIM <sub>1</sub> | log(305/DIM) <sub>2</sub> |
|--------------------|------------------|---------------------------|
| 1                  | 5                | 4.1108699                 |
| 2                  | 8                | 3.6408701                 |
| 3                  | 14               | 3.0812500                 |
| 4                  | 31               | 2.2863200                 |
| 5                  | 34               | 2.1939499                 |
| 6                  | 58               | 1.6598700                 |
| 7                  | 60               | 1.6259700                 |
| 8                  | 73               | 1.4298500                 |
| 9                  | 74               | 1.4162500                 |
| 10                 | 81               | 1.3258600                 |
| 11                 | 84               | 1.2894900                 |
| 12                 | 105              | 1.0663500                 |
| 13                 | 113              | 0.9929240                 |
| 14                 | 123              | 0.9081270                 |
| 15                 | 124              | 0.9000300                 |
| 16                 | 139              | 0.7858380                 |
| 17                 | 158              | 0.6577170                 |
| 18                 | 165              | 0.6142660                 |

# Using covariable table files

## MODEL

```
milk_yd = Lact_curve(DIM ln305DIM) HTD G(1 DIM ln305DIM| animal)
```

With table files:

```
DATAFILE RRM_table.dat
```

```
INTEGER HTD animal blk-var index
```

```
REAL milk_yd
```

```
TABLEFILE RRM_table.cov
```

```
TABLEINDEX index
```

```
PEDFILE RRM.ped
```

```
PEDIGREE G am
```

```
PARFILE RRM.var
```

## MODEL SCALE

```
milk_yd = Lact_curve(t1 t2) HTD G(1 t1 t2 animal)
```



# Multiple trait random regression model

```
DATAFILE RRM_table.dat2
INTEGER HTD animal blk-var index
REAL milk_yd milk_yd2

TABLEFILE RRM_table.cov
TABLEINDEX index

PEDFILE RRM.ped
PEDIGREE G am

PARFILE RRM.var2

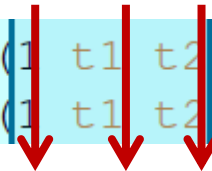
MODEL SCALE
milk_yd = Lact_curve(t1 t2) HTD G(1 t1 t2 | animal)
milk_yd2= Lact_curve(t1 t2) HTD G(1 t1 t2 | animal)
```

Numbering in PARFILE?

# Numbering of variance components within random effect

```

milk_yd = Lact_curve (t1 t2) HTD G (1 t1 t2 | animal)
milk_yd2= Lact_curve (t1 t2) HTD G (1 t1 t2 | animal)
    
```



- (1,1) = 1st trait animal variance
- (2,2) = 2nd trait animal variance
- (3,3) = 1st trait t1 variance
- (4,4) = 2nd trait t1 variance
- (5,5) = 1st trait t2 variance
- (6,6) = 2nd trait t2 variance

|   |   |   |         |             |
|---|---|---|---------|-------------|
| 1 | 1 | 1 | 44.791  | } 1st trait |
| 1 | 3 | 1 | -0.133  |             |
| 1 | 5 | 1 | 0.351   |             |
| 1 | 3 | 3 | 0.073   |             |
| 1 | 3 | 5 | -0.010  |             |
| 1 | 5 | 5 | 1.068   |             |
| 1 | 2 | 2 | 4.4791  | } 2nd trait |
| 1 | 4 | 2 | -0.0133 |             |
| 1 | 4 | 2 | 0.0351  |             |
| 1 | 4 | 2 | 0.0073  |             |
| 1 | 4 | 6 | -0.0010 |             |
| 1 | 6 | 6 | 0.1068  |             |
| 2 | 1 | 1 | 100.000 | } residuals |
| 2 | 2 | 2 | 10.000  |             |

# Reduced rank models

- Use:
  - Multiple traits
  - Random regression effects
  - Combining of random effects
- Large models with many effects
  - Easy to make errors in model description

# Part of Nordic test-day model for production

Random regression effects with combining of effects and covariable table

|  |                   |  |       |
|--|-------------------|--|-------|
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD) -      | FIPE( t9 t10 t11 t12 t13 t14 t15 t16 t17   ANI)  | @pef1 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD) -      | FIPE( t18 t19 t20 t21 t22 t23 t24 t25 t26   ANI) | @pef1 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD) -      | FIPE( t27 t28 t29 t30 t31 t32 t33 t34 t35   ANI) | @pef1 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)      | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)      | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)      | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)      | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)      | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t36 t37 t38 t39 t40 t41 t42 t43 t44   ANI) | @pef2 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t45 t46 t47 t48 t49 t50 t51 t52 t53   ANI) | @pef2 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t54 t55 t56 t57 t58 t59 t60 t61 t62   ANI) | @pef2 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t63 t64 t65 t66 t67 t68 t69 t70 t71   ANI) | @pef3 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t72 t73 t74 t75 t76 t77 t78 t79 t80   ANI) | @pef3 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | FIHTD(HTD)@fhtd - | FIPE( t81 t82 t83 t84 t85 t86 t87 t88 t89   ANI) | @pef3 |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |
| REC( rec1 rec2 rec3 rec4 rec5   HETCL) | - SDHTD(HTD)@shtd | - - - - -  |       |

REC, FIHTD, SDHTD and FIPE are all random effects

Combining indicated by symbol @



# Multiple single trait analysis

- Want to analyze several models simultaneously
- Can do: multiple trait analysis with zero correlations
  - But data may be very sparse and computations very inefficient
- Instead: trait groups
  - Zero correlation between trait groups
  - Own model and variance component information
  - Trait (or model) recognized by trait group number

Warning: May have sometimes convergence issues!

# Two single trait analyses by trait groups

```
INTEGER  animal sire herd_year ones trait
REAL     tr
```

```
TRAITGROUP trait
```

Trait group number in data selects model and variance components

```
PEDFILE  data/AM.ped
PEDIGREE animal am
```

```
PARFILE  mt_single.var
```

```
MODEL SCALE
```

```
tr(1) = -      herd_year animal
tr(2) = ones -      animal
```

# Trait groups and models: 8 separate model analysis

```
INTEGER  I1 I2 I3 I4 I5 I6 I7 I8 I9 I10
REAL     R1 R2 R3
```

TRAITGROUP I3

MODEL

```
R1(1) = I4 I5 I6 I7 - LITTER(I1) I9 I1
R1(2) = I4 I5 I6 I7 - - I9 I1
R1(3) = I4 I5 I6 I7 - - I9 I1
R1(4) = I4 I5 I6 I7 - - I9 I1
R1(5) = I4 I5 I6 I7 - - I9 I1
R1(6) = I4 I5 I6 I7 - - I9 I1
R1(7) = I4 I5 I6 I7 - - I9 I1
R1(8) = I4 I5 I6 I7 I8 - I9 I1
R2(8) = I4 - I6 I7 - - I9 I1
R3(8) = I4 I5 - I7 - - I9 I1
```

} 3 trait model for group 8

Models for trait groups

# Summary on CLIM

- Standard single and multiple trait models
- Many random effects
- Maternal effects
- Random regression models
- Combining of effects (Reduced rank models)

and many more ... during this workshop and in the manual