


دانشگاه صنعتی اصفهان

## DMUv6 interface


$$\begin{bmatrix} X_1 e^{H_1} X_1 & X_1 e^{H_1} X_2 & X_1 e^{H_1} Z_1 & X_1 e^{H_1} Z_2 \\ X_2 e^{H_2} X_1 & X_2 e^{H_2} X_2 & X_2 e^{H_2} Z_1 & X_2 e^{H_2} Z_2 \\ Z_1 e^{H_3} X_1 & Z_1 e^{H_3} X_2 & Z_1 e^{H_3} Z_1 + e^{H_3} K^{-1} & Z_1 e^{H_3} Z_2 + e^{H_3} K^{-1} \\ Z_2 e^{H_4} X_1 & Z_2 e^{H_4} X_2 & Z_2 e^{H_4} Z_1 + e^{H_4} K^{-1} & Z_2 e^{H_4} Z_2 + e^{H_4} K^{-1} \end{bmatrix} \begin{bmatrix} y_1 \\ y_2 \\ a_1 \\ a_2 \end{bmatrix} = \begin{bmatrix} X_1 (e^{H_1} \gamma_1 + e^{H_1} \gamma_p) \\ X_2 (e^{H_2} \gamma_1 + e^{H_2} \gamma_p) \\ Z_1 (e^{H_3} \gamma_1 + e^{H_3} \gamma_p) \\ Z_2 (e^{H_4} \gamma_1 + e^{H_4} \gamma_p) \end{bmatrix}$$


## DMU - Version 6. - Status

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Module:

- dmu1 Prepare program
- dmuai AI-REML estimation of (co)variance comp
- dmu4 BLUE and BLUP in memory
- dmu5 BLUE and BLUP iteration on data
- rjmc Gibbs sampler




## DMUv6 - User interface

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Flexible "driver file"

- Data and pedigree information in separate files.
- Data and pedigree file can be in ASCII or BINARY format.
- Names for variables can be specified.
- The model is written using variable names in the output.
- More "simple statistics" for depended variables and for co-variables.




## DMUv6 - Driver file

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```

$COMMENT
$ANALYSE
$DATA
$VARIABLE
$MODEL
$VAR_STR
$PRIOR
$VAR_REST
$RESIDUALS
$REDUCE
$GLMM
$MIXTURE
$DMUAI
$DMU4
$DMU5
$RJMC

```




## \$COMMENT

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**\$COMMENT**

Users own comments, which are written in the output file.

The comments can be up to 10 lines each up to 80 characters.



## \$ANALYSE

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**\$ANALYSE** Task Method Scaling Test\_prt

Where

Task = type of analyses: 1 = REML, 2 = RJMC,  
11 = BLUP in core 12 = BLUP IOD

Method = method to use if more then one exist for this Task

Scaling = 1 => scaling to residual variance equal to 1 based on the priors for residual variance

Test\_prt = option for amount of print out:

- 0 => normal output
- 1 => limited amount of extra output
- 2 => extensive amount of test print

## \$DATA



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**\$DATA** FMT (#int, #real, miss ) fn [fn2]

where

FMT = ASCII or BINARY

#int = no. of integer variable

#real = no. of real variable

miss = code for missing real variable

fn = file name

fn2 = file name for real part, if data is split  
in an integer and a real part

## \$VARIABLE



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### \$VARIABLE

hys year mth y\_mth animal lact  
milk fat protein age

\_\_\_\_\_  
Name max. 8 characters long

## \$MODEL



**\$MODEL**  
**\$MODEL** [fn]

The model description consists of the following lines:

• TRAIT (one line)

• ABSORB (one line per trait)

• CLASS (one line per trait)

• RANDOM (one line per trait)

• REGRES (one line per trait)

• NOCOV (number of non existing residual co-variances, followed by  
NOCOV lines with row, column for non existing residual  
co-variances)

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## \$MODEL – The TRAIT line



The line contains 5 integer values:

# traits # Gaussian # right Censored # categorical #  
binary

Example:

4 2 0 0 2

This defines a 4 trait analysis of 2 Gaussian and 2 binary  
traits

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## \$MODEL – The ABSORB line(s)



One line for each trait indicating an integer value

- The ABSORB lines are used to specify a fixed effect to be treated block-diagonal when forming the preconditioned in DMU5
- For DMUAI, DMU4 and RJMC the line(s) must contain a null (0)

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## \$MODEL – The Trait, weight and Class effect(s) lines(s)



One line for each trait containing several integers.

- 1st value is real input number for the trait
- 2nd value is real input number for a weight variable. If no weight variable is used specify zero (0)
- 3rd value is the number of class variables (fixed and random) in the model for this trait
- On the rest of the line integer input numbers for each class variable in the model is specified (fixed effect before random)
- If a class effect is needed for nesting of regressions, but the effect itself should not be included, append (0) to the integer input number

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## \$MODEL – The RANDOM lines(s)



One line per trait in the same sequence as in the TRAIT line(s)

- The first value is the number of random effects in the model for this trait, followed by a numbering of the random factors
- This numbering is used to find random effects that might be correlated such as maternal and direct genetic effects, which must be specified as two effects on the model line. It is also used to group effects, that are correlated across traits, and factors with same effect (eg. Sire-Dam models)

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## \$MODEL – The REGRESS lines(s)



One line per trait in the same order as in the TRAIT line(S)

- The 1st value is the number of regressions for this trait. If no covariables are desired for this trait, a zero must be specified
- On the rest of the line the real input numbers for the covariables must be specified
- Overall regressions can be specified as a single integer number (the real input number for the covariable)
- Nested regressions are specified as covariable number followed by the effect number in the TRAIT line for nesting in brackets

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## \$MODEL – The REGRESS lines(s) Nesting



Nesting is specified in a bracket after the covariable input number

- The effect for nesting is specified by the effects position in the TRAIT line
- If the model includes more than one regression on the same covariable (i.e. overall and nested regressions or nesting within several effects), it can be put into one set of brackets separated by blanks
- The following three specifications are treated identically
  - 7 1 2 2(3) 2(4) 3 4 4(3)
  - 7 1 2 2(3 4) 3 4 4(3)
  - 7 1 2(0 3 4) 3 4(0 3)
- Nesting within effect 0 is the same as an overall regression

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## \$MODEL – The NOCOV line



A line specifying the number of non-existing residual covariances

- Such a situation can occur if the traits in question are measured on different animals or experimental units
- If the value on the NOCOV line  $\neq 0$ , a line for each non-existing residual covariance's must be specified
- The format is:  
row column  
where row and column are the position in the residual co-variance matrix

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## \$MODEL – Putting it together



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```
$VARIABLE
# 1 2 3 4 5 6
  hys year mth y_mth animal lact
# 1 2 3 4
  milk fat protein age
```

```
Protein =      hys +
               year +
               mth +
               y_mth +
               lact +
               b*age +
               b*age(lact) +
               pe +
               animal +
               e
```

```
$MODEL
1 1 0 0 0
0
3 0 7 1 2 3 4 6 5 5
2 1 2
2 4 4(5)   [or 2 4 (0 5) ]
0
```

## \$VAR\_STR



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\$VAR\_STR r\_factor type <options>

where:  
r\_factor = structure number, used to associate (co)variance structure to random effects in the model section

type = PED, DOM, ABS\_QTL or GROUP

options depends on type of structure.

**\$VAR\_STR – type =PED**

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**\$VAR\_STR** r\_factor PED method FMT fn

Where

r\_factor = random factor no. from the random lines in the \$MODEL section

method = 1 -> Sire – Dam, incl. inbreeding  
 2 -> Sire – Dam, excl. inbreeding  
 3 -> Sire – MGS, incl. inbreeding  
 4 -> Sire – MGS, excl. inbreeding  
 6 -> Sire – Dam, Genetic groups (PHG's), excl. inbreeding

FMT = ASCII or BINARY

fn = file name for the pedigree file.

If method = 6, PHG's can be treated as fixed or random

**\$VAR\_STR** r\_factor PED 6 RANDOM x.z FMT fn**\$PRIOR**

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**\$PRIOR** fn**\$PRIOR**

1 1 1 7.5

2 1 1 15.0

3 1 1 27.5

**\$RESIDUALS**

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**\$RESIDUALS** FMT

where: FMT = ASCII or BINARY

**\$DMUAI**

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**\$DMUAI** fn**\$DMUAI**

10 ! Emstep = Number of steps before full weight on EM

1.0d-7 ! Conv\_ndelta = Conv. criteria for norm of the update vector

1.0d-6 ! Conv\_gnorm = Conv. criteria for norm of the gradient vector (AI)

1 ! Printout = 1 -&gt; Solution vector is printed/written to file SOL

0 ! Fspopt = 0 -&gt; time = 1 memory optimized FSPAK

**\$DMU4**

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**\$DMU4** fn**\$DMU4**

18 ! Compute s.e for equation 18

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**\$DMU5**

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**\$DMU5** fn**\$DMU5**

1000 0.0e-7! Max no. of iteration Converges criteria

512 ! Amount of available memory (in MB)