Calculation of PBLUP reliabilities, ERCs and DRPs

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MiX99 course on genomic prediction

COURSE DAY 3, March 11th, 2026

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- Calculating deregressed proofs – Concept and MiX99 syntax
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Deregressed proofs

- Variable of choice in MACE evaluation, because often too difficult to provide daughter yield deviations
- Used for blending foreign information into national genetic evaluations
- Variable of choice for condensing information from non-genotyped animals into genotyped animals (e.g., multi-step genomic evaluation)
- Used for model validation purposes, GWAS studies, etc.

Deregressed proofs

Concept of deregressed genetic predictions or “deregressed poofs” (DRP)

- Making breeding values independent from genetic relationships and unknown parent groups
- Associating a weight to an animal’s DRP
- The applied weight depends on the purpose for which the DRP is used

  DRP as pseudo-phenotype: the weight reflects the animal’s own information that contributes to the evaluation, i.e., the effective record contribution (ERC)

- Evaluations based on proper DRPs and ERCs would give the same original EBVs as estimated from the original data

What is needed for calculating DRPs

- Breeding values
- Genetic relationships among the animals
- Variance components
- ERC (or EDC for MACE)
- Reliabilities of breeding values

Estimated breeding values and reliabilities from PBLUP

- Prediction of breeding values: see DAY1 and DAY2
- Breeding values and reliabilities from same evaluation
- Intended use of DRPs determines how accurate the reliability approximation needs to be

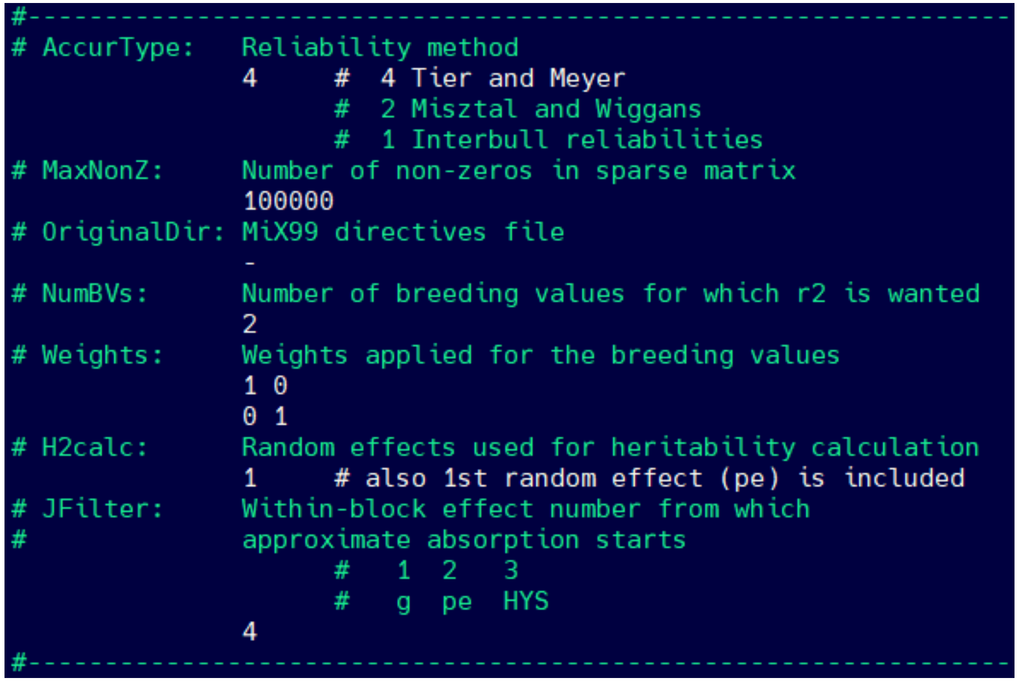
Some reliability options in MiX99

• Exact reliabilities:	for small models
• Tier and Meyer (2004):	multi-trait animal models
• Misztal and Wiggens (1988):	animal model
• Interbull reliabilities:	sire model

Absorbing within-block effects into animal genetic effects →

Exact absorption reduces (upwards) bias in reliabilities

Instruction file for apax99 (repeatability model, 2 traits)



```
#----------------------------------------------------------------
# AccurType:   Reliability method
               4     #  4 Tier and Meyer
                     #  2 Misztal and Wiggans
                     #  1 Interbull reliabilities
# MaxNonZ:     Number of non-zeros in sparse matrix
               100000
# OriginalDir: MiX99 directives file
               -
# NumBVs:      Number of breeding values for which r2 is wanted
               2
# Weights:     Weights applied for the breeding values
               1 0
               0 1
# H2calc:      Random effects used for heritability calculation
               1     # also 1st random effect (pe) is included
# JFilter:     Within-block effect number from which
#              approximate absorption starts
                     #    1  2   3
                     #    g  pe  HYS
               4
#----------------------------------------------------------------
```

Calculation of effective record contributions (ERC)

Reversed reliability approximation

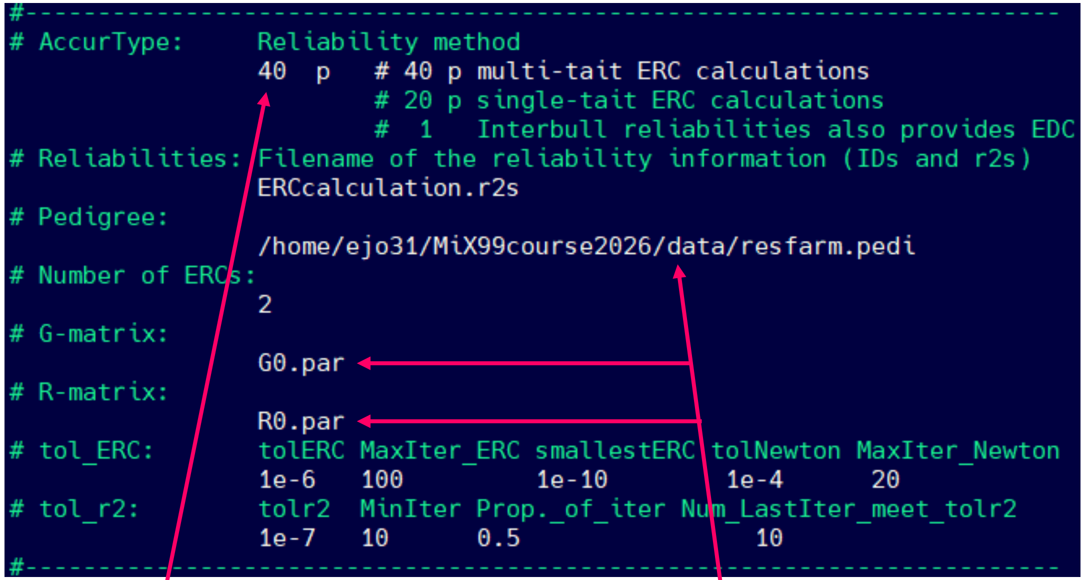
Idea: From given reliabilities such weights are approximated that lead back to the same reliabilities

- Weights are derived avoiding double counting of information → effective record contribution (ERC)
- Required information: reliabilities, pedigree, heritability
- Included reliabilities are only from those animals for which DRPs should be calculated

Approaches available in MiX99

Reverse Tier and Meyer (2004):	multi-trait ERC
Reverse Harris and Johnson (1998):	single-trait ERC
Interbull reliability:	EDCs for sires

Instruction file for apax99 (multi-trait ERC, 2 traits)



```
#-----------------------------------------------------------------------
# AccurType:     Reliability method
                 40  p   # 40 p multi-tait ERC calculations
                         # 20 p single-tait ERC calculations
                         #  1   Interbull reliabilities also provides EDC
# Reliabilities: Filename of the reliability information (IDs and r2s)
                 ERCcalculation.r2s
# Pedigree:
                 /home/ejo31/MiX99course2026/data/resfarm.pedi
# Number of ERCs:
                 2
# G-matrix:
                 G0.par
# R-matrix:
                 R0.par
# tol_ERC:       tolERC MaxIter_ERC smallestERC tolNewton MaxIter_Newton
                 1e-6   100         1e-10       1e-4      20
# tol_r2:        tolr2  MinIter Prop._of_iter Num_LastIter_meet_tolr2
                 1e-7   10      0.5           10
#-----------------------------------------------------------------------
```

For AccurType option “20 p” and “40 p” no mix99i pre-processing needed

Pedigree and variance component information

Calculation of deregressed proofs (DRP)

Solving a non-linear system of equations

- Solutions (breeding values) are known for individuals for which DRPs are wanted
- Other solutions are unknown (ancestors, unknown parent groups, general mean)

Deregression in MiX99 is based on Jairath et al. (1998) and Schaeffer (2001)

A two-step iteration procedure is applied:

1. Solve unknowns for ancestors and unknown parent group, given current solutions and know solutions of individuals
2. Calculate new estimate for general mean

Deregression options in MiX99

- Broyden method (default)
  - fast and most reliable
- Other methods
  - Secant, Gauss-Seidel, Bisection
- All methods should result same solutions

Important

- For some models, default convergence parameters need to be modified to achieve convergence
- Very small ERC values may cause convergence problems
- Unknown parent groups should be well defined

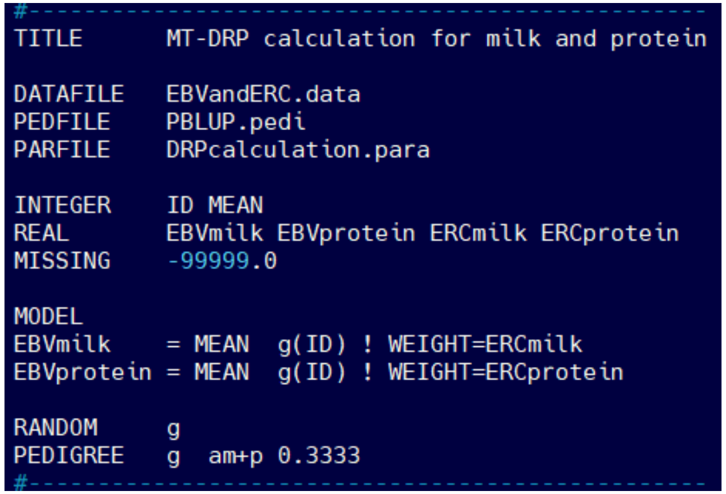
Calculation of deregressed proofs (DRP)

Basic model set-up for deregression

- Simple linear mixed model with a general mean as fixed effect, and one random animal effect
- Univariate and multivariate models are supported
- Weighted observations where:
  - breeding values are specified as observations
  - ERCs are the associated weights
- Observations are given only for individuals for which DRP should be calculated
- The unknown parent groups in the pedigree must be modelled as random effects

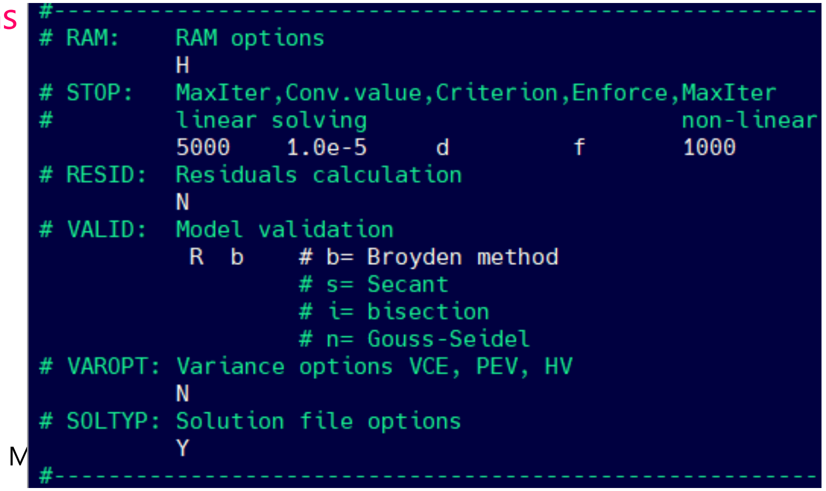
MiX99 instruction (bivariate model)

CLIM file



```
#-----------------------------------------------------
TITLE      MT-DRP calculation for milk and protein

DATAFILE   EBVandERC.data
PEDFILE    PBLUP.pedi
PARFILE    DRPcalculation.para

INTEGER    ID MEAN
REAL       EBVmilk EBVprotein ERCmilk ERCprotein
MISSING    -99999.0

MODEL
EBVmilk    = MEAN  g(ID) ! WEIGHT=ERCmilk
EBVprotein = MEAN  g(ID) ! WEIGHT=ERCprotein

RANDOM     g
PEDIGREE   g  am+p 0.3333
#-----------------------------------------------------
```

Solver options



```
#---------------------------------------------------------
# RAM:    RAM options
          H
# STOP:   MaxIter,Conv.value,Criterion,Enforce,MaxIter
#         linear solving                       non-linear
          5000    1.0e-5     d         f       1000
# RESID:  Residuals calculation
          N
# VALID:  Model validation
           R  b    # b= Broyden method
                   # s= Secant
                   # i= bisection
                   # n= Gouss-Seidel
# VAROPT: Variance options VCE, PEV, HV
          N
# SOLTYP: Solution file options
          Y
#---------------------------------------------------------
```

Example I: Multi-trait repeatability model

Data and Model

Example data

- First parity test-day milk and protein yields: 22,300 records from 607 cows and 1 herd
- Pedigree includes 2,751 animals and one unknow parent group

Bivariate repeatability model

$$milk_{ijk} = f_1(cage_i) + f_1\left(dim_{ij}\right) + HYS_{1:k} + pe_{1:i} + a_{1:i} + e_{1:ijk}$$

$$protein_{ijk} = f_2(cage_i) + f_2\left(dim_{ij}\right) + HYS_{2:k} + pe_{2:i} + a_{2:i} + e_{2:ijk}$$

where $f_*(cage_i)$ are functions for calving age effects,

and $f_*(dim)$ are functions for stage of lactation fixed effects,

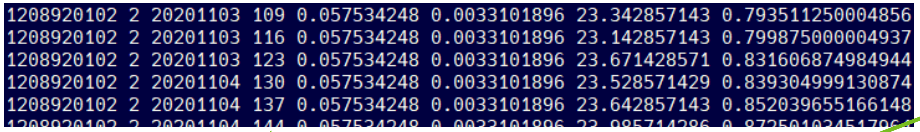
$HYS_{*:k}$ fixed herd year season effects

$pe_{*:i}$, $a_{*:i}$, and $e_{*:i}$ are random permanent environmental, additive genetic, and residual effects

Breeding value estimation

Data file

ID HERD HYD DIM age age2 milk protein

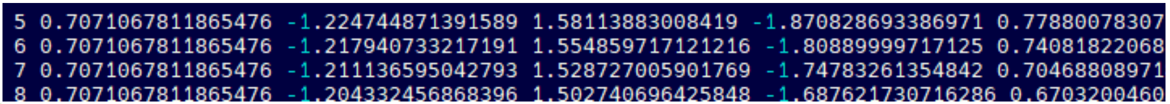


```
1208920102 2 20201103 109 0.057534248 0.0033101896 23.342857143 0.793511250004856
1208920102 2 20201103 116 0.057534248 0.0033101896 23.142857143 0.799875000004937
1208920102 2 20201103 123 0.057534248 0.0033101896 23.671428571 0.831606874984944
1208920102 2 20201104 130 0.057534248 0.0033101896 23.528571429 0.839304999130874
1208920102 2 20201104 137 0.057534248 0.0033101896 23.642857143 0.852039655166148
1208920102 2 20201104 144 0.057534248 0.0033101896 23.985714286 0.87250103451796
```

Table file

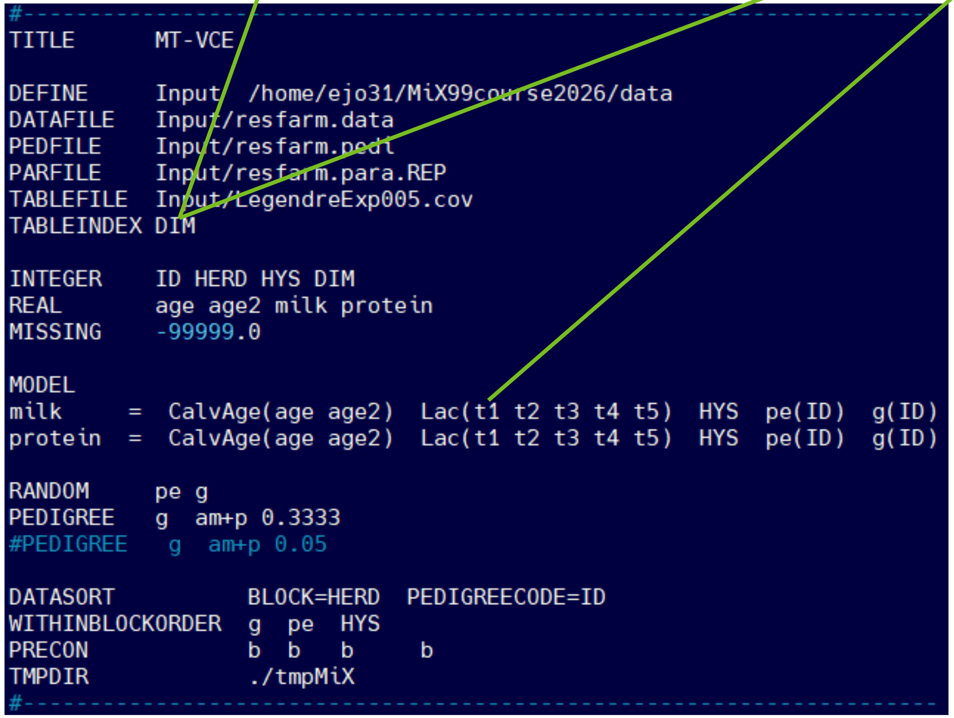
t1 t2 t3 t4 t5

DIM Leg_cov0 Leg_cov1 Leg_cov2 Leg_cov3 exp(-0.005*DIM)



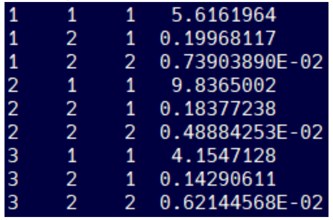
```
5 0.7071067811865476 -1.224744871391589 1.58113883008419 -1.870828693386971 0.77880078307
6 0.7071067811865476 -1.217940733217191 1.554859717121216 -1.80889999717125 0.74081822068
7 0.7071067811865476 -1.211136595042793 1.528727005901769 -1.74783261354842 0.70468808971
8 0.7071067811865476 -1.204332456868396 1.502740696425848 -1.687621730716286 0.6703200460
```

CLIM file



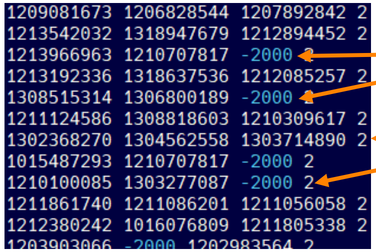
```
#---------------------------------------------------------------------
TITLE      MT-VCE

DEFINE     Input  /home/ejo31/MiX99course2026/data
DATAFILE   Input/resfarm.data
PEDFILE    Input/resfarm.pedt
PARFILE    Input/resfarm.para.REP
TABLEFILE  Input/LegendreExp005.cov
TABLEINDEX DIM

INTEGER    ID HERD HYS DIM
REAL       age age2 milk protein
MISSING    -99999.0

MODEL
milk     =  CalvAge(age age2)  Lac(t1 t2 t3 t4 t5)  HYS  pe(ID)  g(ID)
protein  =  CalvAge(age age2)  Lac(t1 t2 t3 t4 t5)  HYS  pe(ID)  g(ID)

RANDOM     pe g
PEDIGREE   g  am+p 0.3333
#PEDIGREE   g  am+p 0.05

DATASORT          BLOCK=HERD  PEDIGREECODE=ID
WITHINBLOCKORDER  g  pe  HYS
PRECON            b  b   b     b
TMPDIR            ./tmpMiX
#---------------------------------------------------------------------
```

VC parameter file



```
1     1     1   5.6161964
1     2     1  0.19968117
1     2     2  0.73903890E-02
2     1     1   9.8365002
2     2     1  0.18377238
2     2     2  0.48884253E-02
3     1     1   4.1547128
3     2     1  0.14290611
3     2     2  0.62144568E-02
```

Pedigree file

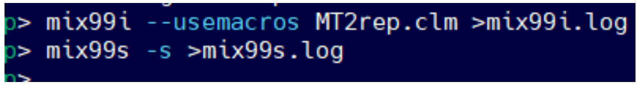


```
1209081673 1206828544 1207892842 2
1213542032 1318947679 1212894452 2
1213966963 1210707817 -2000 2
1213192336 1318637536 1212085257 2
1308515314 1306800189 -2000 2
1211124586 1308818603 1210309617 2
1302368270 1304562558 1303714890 2
1015487293 1210707817 -2000 2
1210100085 1303277087 -2000 2
1211861740 1211086201 1211056058 2
1212380242 1016076809 1211805338 2
1203903066 -2000 1202983564 2
```

Unknown parent group

Blocking code (HERD)

Solving the model…

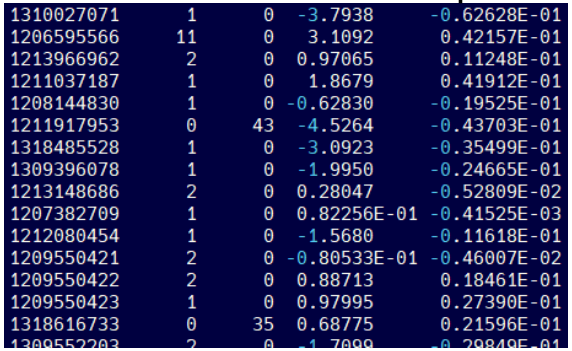


```
p> mix99i --usemacros MT2rep.clm >mix99i.log
p> mix99s -s >mix99s.log
p>
```

Breeding values

…Solani file

ID Desc Nrec milk protein

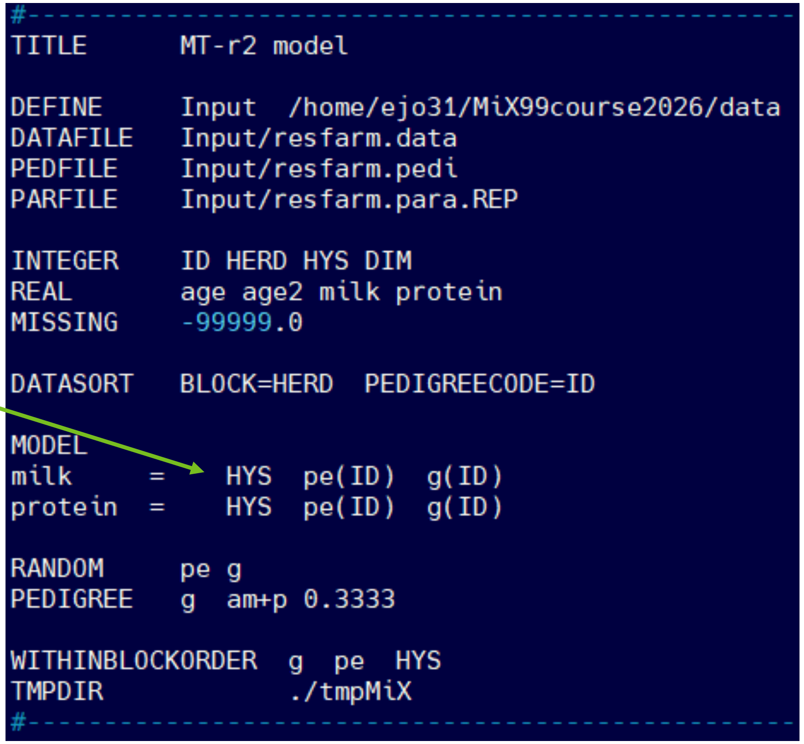


```
1310027071       1      0  -3.7938      -0.62628E-01
1206595566      11      0   3.1092       0.42157E-01
1213966962       2      0  0.97065       0.11248E-01
1211037187       1      0   1.8679       0.41912E-01
1208144830       1      0 -0.62830      -0.19525E-01
1211917953       0     43  -4.5264      -0.43703E-01
1318485528       1      0  -3.0923      -0.35499E-01
1309396078       1      0  -1.9950      -0.24665E-01
1213148686       2      0  0.28047      -0.52809E-02
1207382709       1      0  0.82256E-01 -0.41525E-03
1212080454       1      0  -1.5680      -0.11618E-01
1209550421       2      0 -0.80533E-01 -0.46007E-02
1209550422       2      0  0.88713       0.18461E-01
1209550423       1      0  0.97995       0.27390E-01
1318616733       0     35  0.68775       0.21596E-01
1309552203       2      0  -1.7099      -0.29849E-01
```

Approximation of reliabilities

- Records of input data are sorted by HERD and animal ID
- Only within-block effects are considered
- Order of effects within-block is important
  - animal genetic effect must be first
  - followed by other effects
  - the effect with least effect levels as last

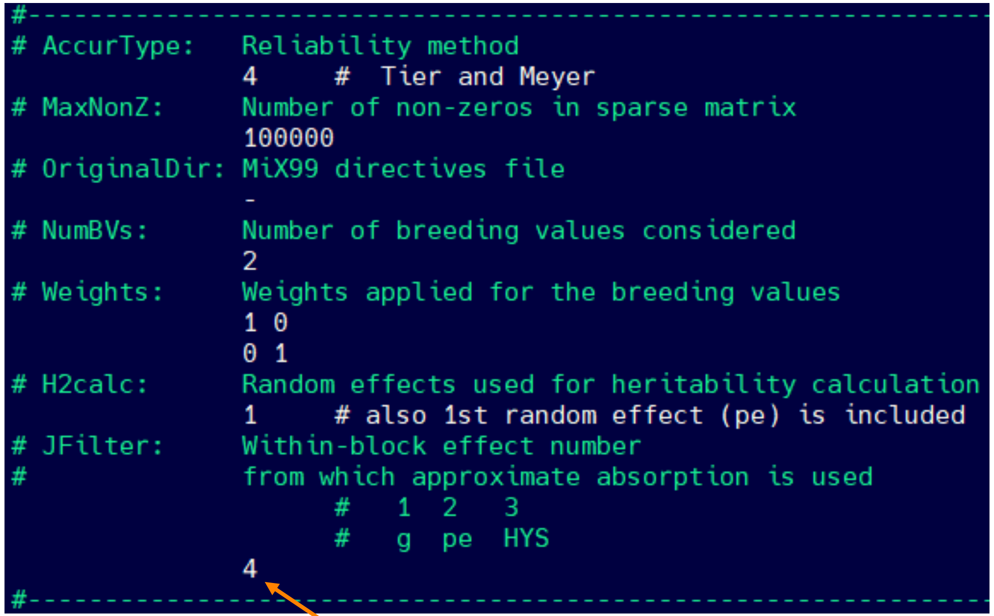
CLIM file



```
#--------------------------------------------------
TITLE      MT-r2 model

DEFINE     Input  /home/ejo31/MiX99course2026/data
DATAFILE   Input/resfarm.data
PEDFILE    Input/resfarm.pedi
PARFILE    Input/resfarm.para.REP

INTEGER    ID HERD HYS DIM
REAL       age age2 milk protein
MISSING    -99999.0

DATASORT   BLOCK=HERD  PEDIGREECODE=ID

MODEL
milk     =    HYS  pe(ID)  g(ID)
protein  =    HYS  pe(ID)  g(ID)

RANDOM     pe g
PEDIGREE   g  am+p 0.3333

WITHINBLOCKORDER  g  pe  HYS
TMPDIR            ./tmpMiX
#--------------------------------------------------
```

Approximation of reliabilities

Instruction file for apax99

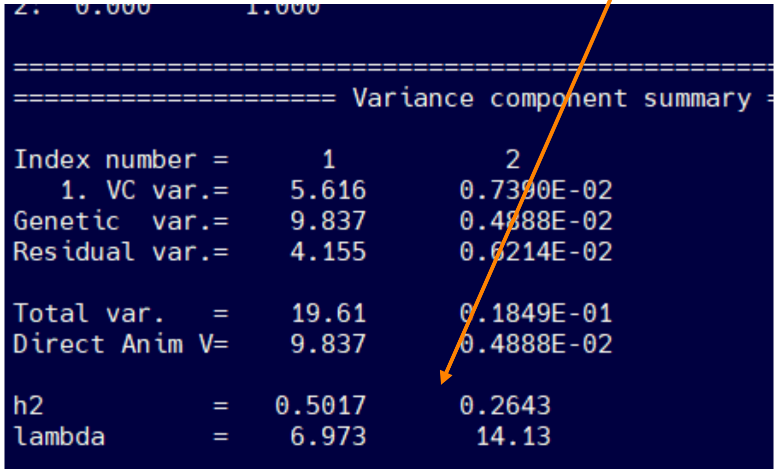


```
#---------------------------------------------------------------
# AccurType:    Reliability method
                4     #   Tier and Meyer
# MaxNonZ:      Number of non-zeros in sparse matrix
                100000
# OriginalDir: MiX99 directives file
                -
# NumBVs:       Number of breeding values considered
                2
# Weights:      Weights applied for the breeding values
                1 0
                0 1
# H2calc:       Random effects used for heritability calculation
                1      # also 1st random effect (pe) is included
# JFilter:      Within-block effect number
#               from which approximate absorption is used
                      #   1  2   3
                      #   g  pe  HYS
                4
#---------------------------------------------------------------
```

exact absorption of all within-block effects

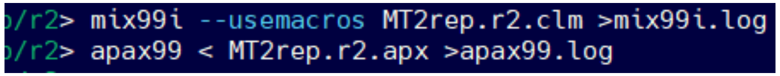
Inspect log file carefully! Is all as expected? Are h2s correct?

apax99.log file



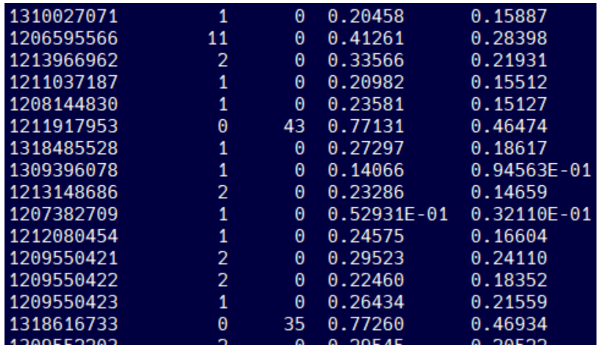
```
 2.   0.000       1.000

 ===========================================================
 ===================== Variance component summary =

 Index number =      1           2
    1. VC var.=    5.616      0.7390E-02
 Genetic  var.=    9.837      0.4888E-02
 Residual var.=    4.155      0.6214E-02

 Total var.   =    19.61      0.1849E-01
 Direct Anim V=    9.837      0.4888E-02

 h2           =   0.5017      0.2643
 lambda       =    6.973       14.13
```

Calculating reliabilities…



```
/r2> mix99i --usemacros MT2rep.r2.clm >mix99i.log
/r2> apax99 < MT2rep.r2.apx >apax99.log
```

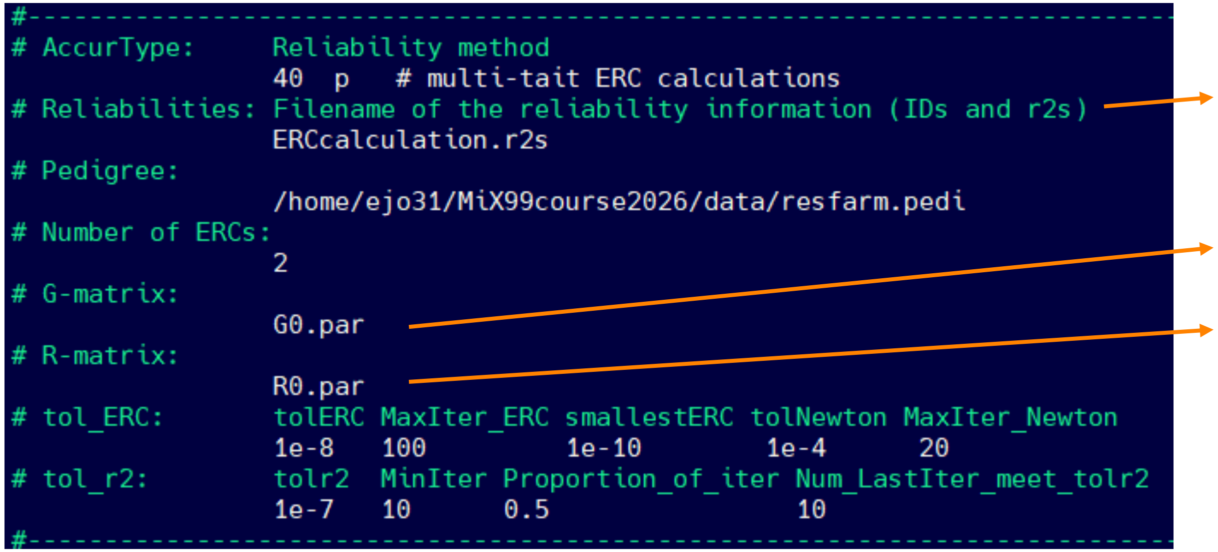
…PEVani file



```
    ID           Desc   Nrec  r2_milk      r2_protein
1310027071          1      0  0.20458      0.15887
1206595566         11      0  0.41261      0.28398
1213966962          2      0  0.33566      0.21931
1211037187          1      0  0.20982      0.15512
1208144830          1      0  0.23581      0.15127
1211917953          0     43  0.77131      0.46474
1318485528          1      0  0.27297      0.18617
1309396078          1      0  0.14066      0.94563E-01
1213148686          2      0  0.23286      0.14659
1207382709          1      0  0.52931E-01  0.32110E-01
1212080454          1      0  0.24575      0.16604
1209550421          2      0  0.29523      0.24110
1209550422          2      0  0.22460      0.18352
1209550423          1      0  0.26434      0.21559
1318616733          0     35  0.77260      0.46934
```

Effective record contributions (ERC) calculations

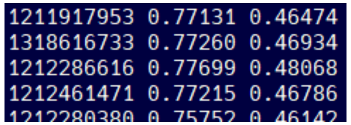
Instruction file for apax99



```
#-----------------------------------------------------------------------------
# AccurType:     Reliability method
                 40  p   # multi-tait ERC calculations
# Reliabilities: Filename of the reliability information (IDs and r2s)
                 ERCcalculation.r2s
# Pedigree:
                 /home/ejo31/MiX99course2026/data/resfarm.pedi
# Number of ERCs:
                 2
# G-matrix:
                 G0.par
# R-matrix:
                 R0.par
# tol_ERC:       tolERC MaxIter_ERC smallestERC tolNewton MaxIter_Newton
                 1e-8   100         1e-10       1e-4      20
# tol_r2:        tolr2  MinIter Proportion_of_iter Num_LastIter_meet_tolr2
                 1e-7   10      0.5                10
#-----------------------------------------------------------------------------
```

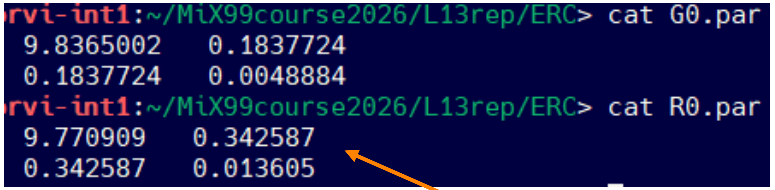
Input data file

ID r2_milk r2_protein



```
1211917953 0.77131 0.46474
1318616733 0.77260 0.46934
1212286616 0.77699 0.48068
1212461471 0.77215 0.46786
1212280380 0.75752 0.46142
```

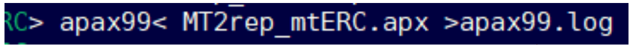
VC parameter file



```
rvi-int1:~/MiX99course2026/L13rep/ERC> cat G0.par
 9.8365002   0.1837724
 0.1837724   0.0048884
rvi-int1:~/MiX99course2026/L13rep/ERC> cat R0.par
 9.770909   0.342587
 0.342587   0.013605
```

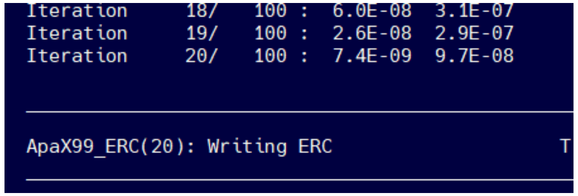
VC for pe and residual effects are combined

Calculating ERCs…



```
RC> apax99< MT2rep_mtERC.apx >apax99.log
```

…check convergence information in apax99.log

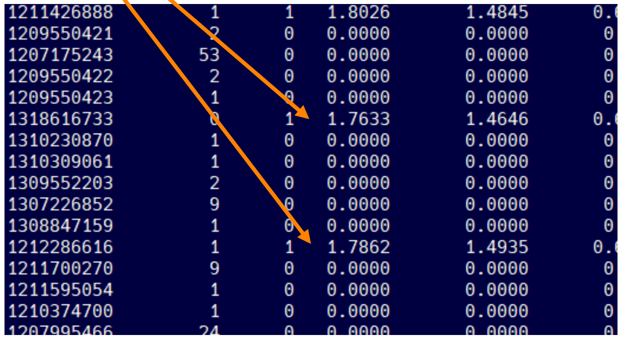


```
 Iteration      18/    100 :  6.0E-08  3.1E-07
 Iteration      19/    100 :  2.6E-08  2.9E-07
 Iteration      20/    100 :  7.4E-09  9.7E-08

 ------------------------------------------------------

 ApaX99_ERC(20): Writing ERC                          T
 ------------------------------------------------------
```

…only individuals included in input data file receive ERCs

…PEVani file

ID Desc Nrec ERCmilk ERCprotein



```
1211426888        1     1   1.8026       1.4845      0.
1209550421        2     0   0.0000       0.0000      0
1207175243       53     0   0.0000       0.0000      0
1209550422        2     0   0.0000       0.0000      0
1209550423        1     0   0.0000       0.0000      0
1318616733        0     1   1.7633       1.4646      0.
1310230870        1     0   0.0000       0.0000      0
1310309061        1     0   0.0000       0.0000      0
1309552203        2     0   0.0000       0.0000      0
1307226852        9     0   0.0000       0.0000      0
1308847159        1     0   0.0000       0.0000      0
1212286616        1     1   1.7862       1.4935      0.
1211700270        9     0   0.0000       0.0000      0
1211595054        1     0   0.0000       0.0000      0
1210374700        1     0   0.0000       0.0000      0
1207995466       24     0   0.0000       0.0000      0
```

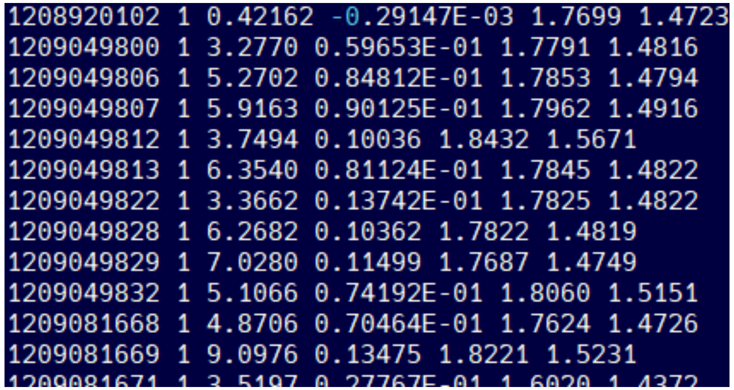
Deregression of proofs

Input data file

- Input data file includes the following columns:

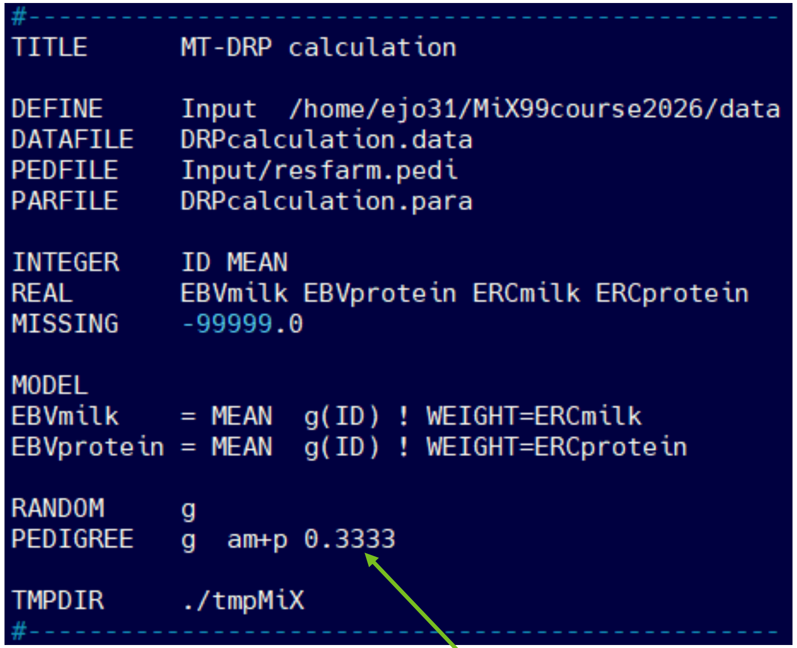
  ID, 1, EBV columns, ERC columns
- Only individuals with ERCs are included
- If ERC is very small, EBV should be set missing

ID MN EBVmilk EBVprotein ERCmilk ERCprotein



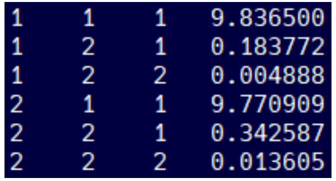
```
1208920102 1 0.42162 -0.29147E-03 1.7699 1.4723
1209049800 1 3.2770 0.59653E-01 1.7791 1.4816
1209049806 1 5.2702 0.84812E-01 1.7853 1.4794
1209049807 1 5.9163 0.90125E-01 1.7962 1.4916
1209049812 1 3.7494 0.10036 1.8432 1.5671
1209049813 1 6.3540 0.81124E-01 1.7845 1.4822
1209049822 1 3.3662 0.13742E-01 1.7825 1.4822
1209049828 1 6.2682 0.10362 1.7822 1.4819
1209049829 1 7.0280 0.11499 1.7687 1.4749
1209049832 1 5.1066 0.74192E-01 1.8060 1.5151
1209081668 1 4.8706 0.70464E-01 1.7624 1.4726
1209081669 1 9.0976 0.13475 1.8221 1.5231
1209081671 1 3.5197 0.27767E-01 1.6020 1.4372
```

CLIM file



```
#-------------------------------------------------
TITLE      MT-DRP calculation

DEFINE     Input  /home/ejo31/MiX99course2026/data
DATAFILE   DRPcalculation.data
PEDFILE    Input/resfarm.pedi
PARFILE    DRPcalculation.para

INTEGER    ID MEAN
REAL       EBVmilk EBVprotein ERCmilk ERCprotein
MISSING    -99999.0

MODEL
EBVmilk    = MEAN  g(ID) ! WEIGHT=ERCmilk
EBVprotein = MEAN  g(ID) ! WEIGHT=ERCprotein

RANDOM     g
PEDIGREE   g  am+p 0.3333

TMPDIR     ./tmpMiX
#-------------------------------------------------
```

VC parameter file



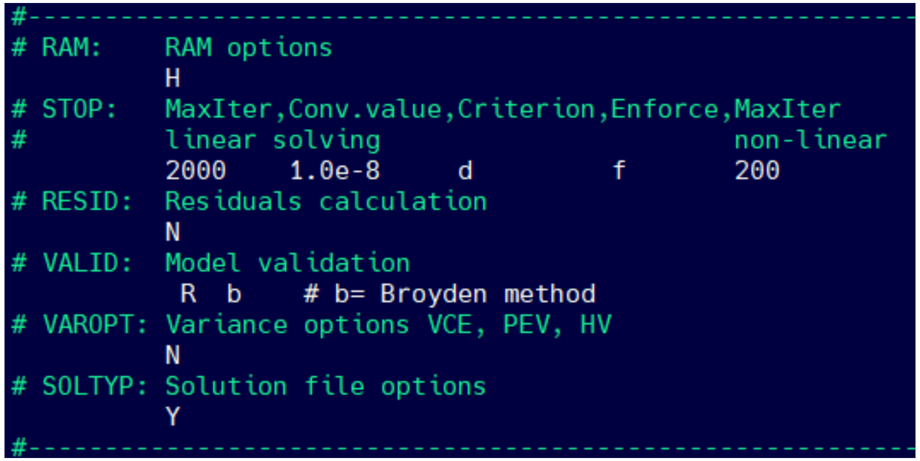
```
1    1    1    9.836500
1    2    1    0.183772
1    2    2    0.004888
2    1    1    9.770909
2    2    1    0.342587
2    2    2    0.013605
```

Same parameters as used for the ERC calculation!

Unknown parent groups must be defined to be random!

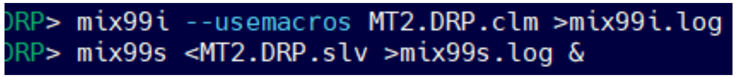
Deregression of proofs

Solver option file



```
#-----------------------------------------------------------
# RAM:    RAM options
          H
# STOP:   MaxIter,Conv.value,Criterion,Enforce,MaxIter
#         linear solving                       non-linear
          2000     1.0e-8      d          f        200
# RESID:  Residuals calculation
          N
# VALID:  Model validation
           R  b     # b= Broyden method
# VAROPT: Variance options VCE, PEV, HV
          N
# SOLTYP: Solution file options
          Y
#-----------------------------------------------------------
```

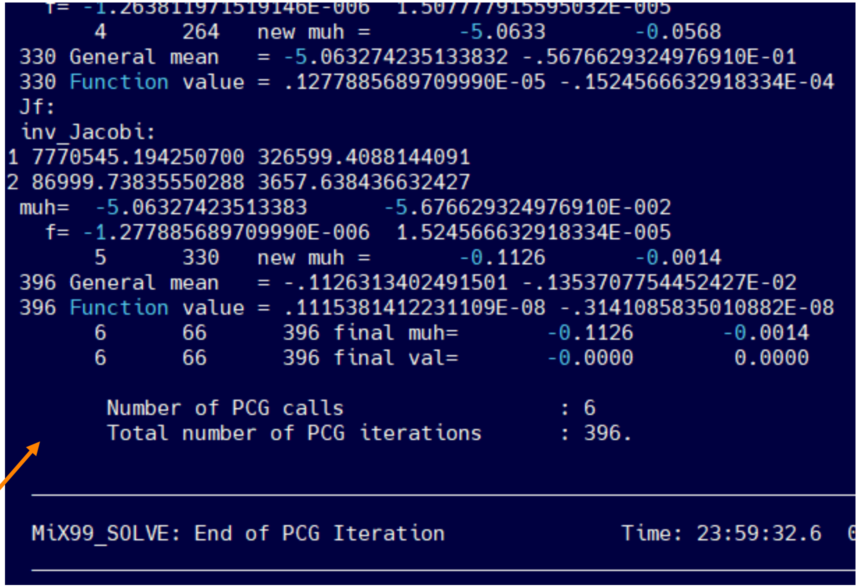
Calculating deregressed proofs…



```
DRP> mix99i --usemacros MT2.DRP.clm >mix99i.log
DRP> mix99s <MT2.DRP.slv >mix99s.log &
```

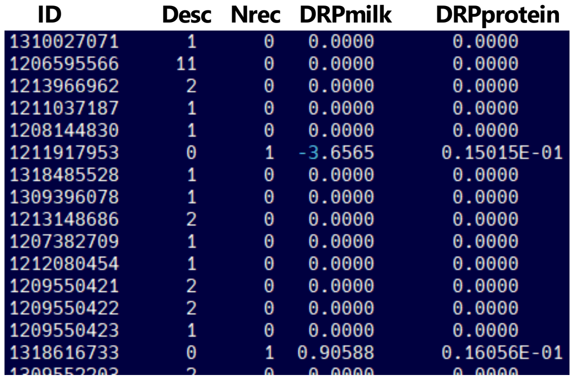
…check convergence information in mix99s.log

mix99s.log



```
   f= -1.263811971519146E-006  1.507777915595032E-005
      4       264    new muh =         -5.0633         -0.0568
 330 General mean    = -5.063274235133832 -.5676629324976910E-01
 330 Function value = .1277885689709990E-05 -.1524566632918334E-04
 Jf:
 inv_Jacobi:
1 7770545.194250700 326599.4088144091
2 86999.73835550288 3657.638436632427
 muh=  -5.06327423513383       -5.676629324976910E-002
   f= -1.277885689709990E-006  1.524566632918334E-005
      5       330    new muh =         -0.1126         -0.0014
 396 General mean    = -.1126313402491501 -.1353707754452427E-02
 396 Function value = .1115381412231109E-08 -.3141085835010882E-08
      6       66      396 final muh=       -0.1126         -0.0014
      6       66      396 final val=       -0.0000          0.0000

       Number of PCG calls                  : 6
       Total number of PCG iterations       : 396.


  ------------------------------------------------------------------

  MiX99_SOLVE: End of PCG Iteration               Time: 23:59:32.6  0
  ------------------------------------------------------------------
```

…Solani file



```
ID                Desc  Nrec  DRPmilk     DRPprotein
1310027071          1      0   0.0000       0.0000
1206595566         11      0   0.0000       0.0000
1213966962          2      0   0.0000       0.0000
1211037187          1      0   0.0000       0.0000
1208144830          1      0   0.0000       0.0000
1211917953          0      1  -3.6565      0.15015E-01
1318485528          1      0   0.0000       0.0000
1309396078          1      0   0.0000       0.0000
1213148686          2      0   0.0000       0.0000
1207382709          1      0   0.0000       0.0000
1212080454          1      0   0.0000       0.0000
1209550421          2      0   0.0000       0.0000
1209550422          2      0   0.0000       0.0000
1209550423          1      0   0.0000       0.0000
1318616733          0      1  0.90588      0.16056E-01
1209552203          2      0   0.0000       0.0000
```

Validation

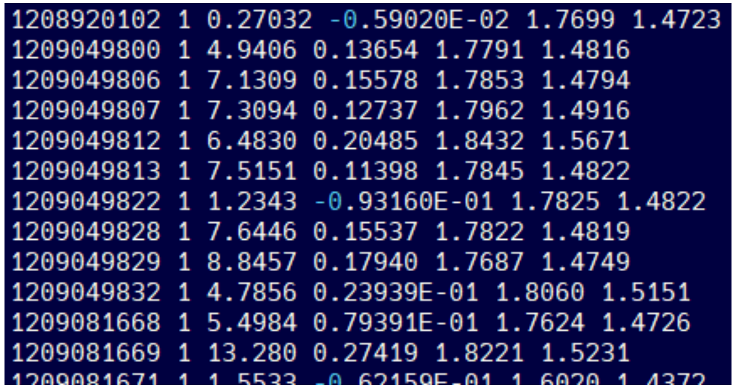
Estimating breeding values using DRPs and ERCs should result same EBVs as the original ones

Estimation approach

- Input data includes DRPs and ERCs
- Same VC parameters and model as used for DRP calculation

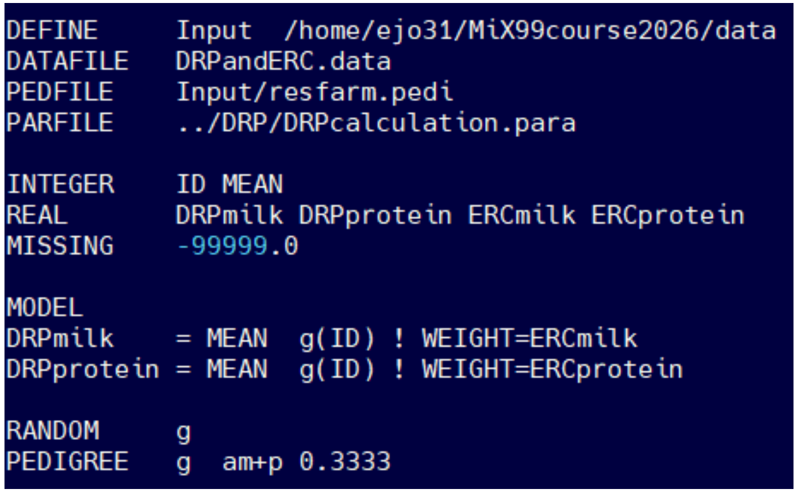
Input data file

ID MN DRPmilk DRPprotein ERCmilk ERCprotein



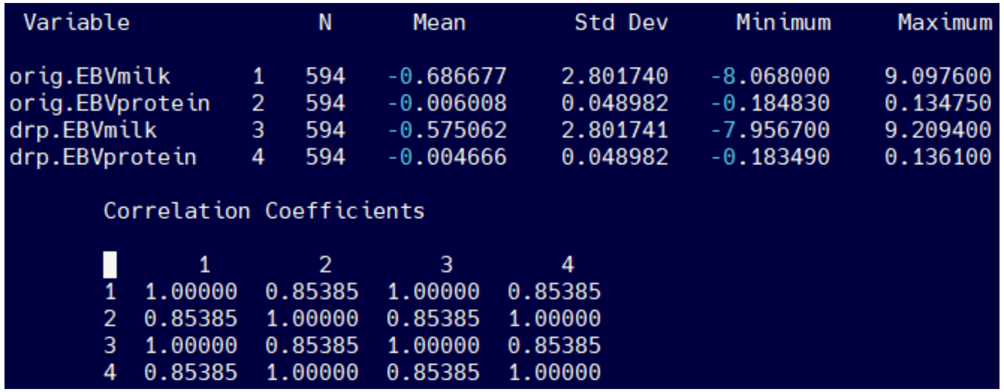
```
1208920102 1 0.27032 -0.59020E-02 1.7699 1.4723
1209049800 1 4.9406 0.13654 1.7791 1.4816
1209049806 1 7.1309 0.15578 1.7853 1.4794
1209049807 1 7.3094 0.12737 1.7962 1.4916
1209049812 1 6.4830 0.20485 1.8432 1.5671
1209049813 1 7.5151 0.11398 1.7845 1.4822
1209049822 1 1.2343 -0.93160E-01 1.7825 1.4822
1209049828 1 7.6446 0.15537 1.7822 1.4819
1209049829 1 8.8457 0.17940 1.7687 1.4749
1209049832 1 4.7856 0.23939E-01 1.8060 1.5151
1209081668 1 5.4984 0.79391E-01 1.7624 1.4726
1209081669 1 13.280 0.27419 1.8221 1.5231
1209081671 1 1.5533 -0.62159E-01 1.6020 1.4372
```

CLIM file



```
DEFINE     Input  /home/ejo31/MiX99course2026/data
DATAFILE   DRPandERC.data
PEDFILE    Input/resfarm.pedi
PARFILE    ../DRP/DRPcalculation.para

INTEGER    ID MEAN
REAL       DRPmilk DRPprotein ERCmilk ERCprotein
MISSING    -99999.0

MODEL
DRPmilk    = MEAN  g(ID) ! WEIGHT=ERCmilk
DRPprotein = MEAN  g(ID) ! WEIGHT=ERCprotein

RANDOM     g
PEDIGREE   g  am+p 0.3333
```

Simple statistics for breeding values



```
 Variable            N      Mean        Std Dev      Minimum       Maximum

orig.EBVmilk     1   594   -0.686677    2.801740   -8.068000    9.097600
orig.EBVprotein  2   594   -0.006008    0.048982   -0.184830    0.134750
drp.EBVmilk      3   594   -0.575062    2.801741   -7.956700    9.209400
drp.EBVprotein   4   594   -0.004666    0.048982   -0.183490    0.136100

       Correlation Coefficients

       █     1        2        3        4
       1  1.00000  0.85385  1.00000  0.85385
       2  0.85385  1.00000  0.85385  1.00000
       3  1.00000  0.85385  1.00000  0.85385
       4  0.85385  1.00000  0.85385  1.00000
```

Example II: Multi-trait random regression model

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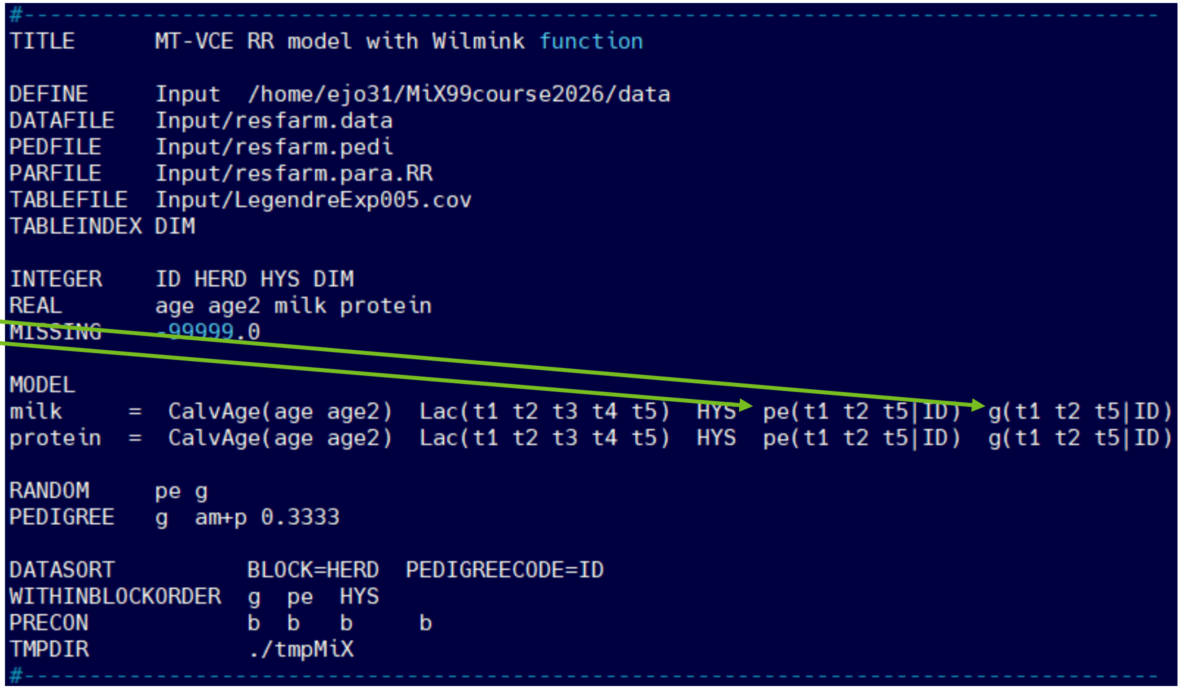
Breeding value estimation

- Same data are used as for Example I
- Same traits and model effects as in model for Example I

Only difference

Here, the permanent environmental and additive genetic effects are modelled by a Wilmink function

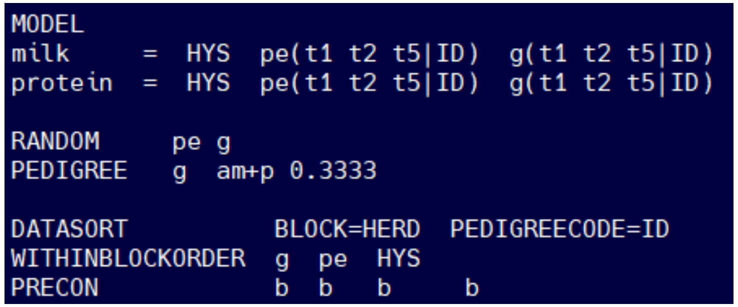
CLIM file



```
#----------------------------------------------------------------------------
TITLE      MT-VCE RR model with Wilmink function

DEFINE     Input  /home/ejo31/MiX99course2026/data
DATAFILE   Input/resfarm.data
PEDFILE    Input/resfarm.pedi
PARFILE    Input/resfarm.para.RR
TABLEFILE  Input/LegendreExp005.cov
TABLEINDEX DIM

INTEGER    ID HERD HYS DIM
REAL       age age2 milk protein
MISSING    -99999.0

MODEL
milk     =  CalvAge(age age2)  Lac(t1 t2 t3 t4 t5)  HYS  pe(t1 t2 t5|ID)  g(t1 t2 t5|ID)
protein  =  CalvAge(age age2)  Lac(t1 t2 t3 t4 t5)  HYS  pe(t1 t2 t5|ID)  g(t1 t2 t5|ID)

RANDOM     pe g
PEDIGREE   g  am+p 0.3333

DATASORT           BLOCK=HERD  PEDIGREECODE=ID
WITHINBLOCKORDER   g  pe  HYS
PRECON             b  b   b     b
TMPDIR             ./tmpMiX
#----------------------------------------------------------------------------
```

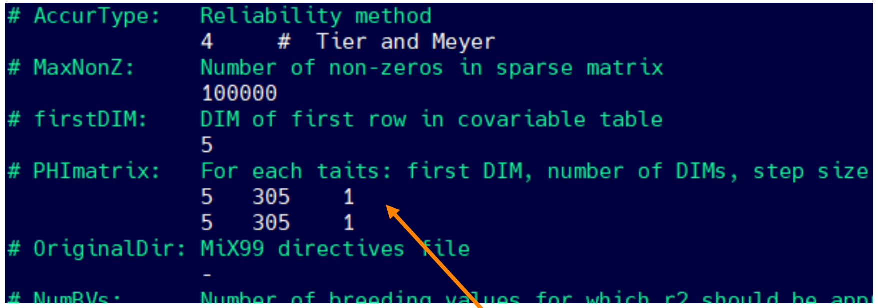
Approximation of reliabilities

CLIM file has same setup as for Example I



```
MODEL
milk      =  HYS  pe(t1 t2 t5|ID)  g(t1 t2 t5|ID)
protein   =  HYS  pe(t1 t2 t5|ID)  g(t1 t2 t5|ID)

RANDOM      pe g
PEDIGREE    g  am+p 0.3333

DATASORT           BLOCK=HERD  PEDIGREECODE=ID
WITHINBLOCKORDER   g  pe   HYS
PRECON             b  b    b      b
```

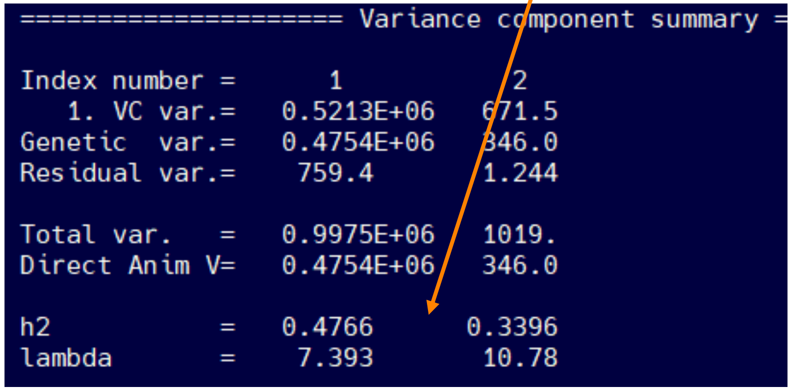
Instruction file for apax99



```
# AccurType:   Reliability method
               4     #  Tier and Meyer
# MaxNonZ:     Number of non-zeros in sparse matrix
               100000
# firstDIM:    DIM of first row in covariable table
               5
# PHImatrix:   For each taits: first DIM, number of DIMs, step size
               5   305     1
               5   305     1
# OriginalDir: MiX99 directives file
               -
# NumBVs:      Number of breeding values for which r2 should be app
```

Information about setting up covariable matrix
for 305d breeding value calculation

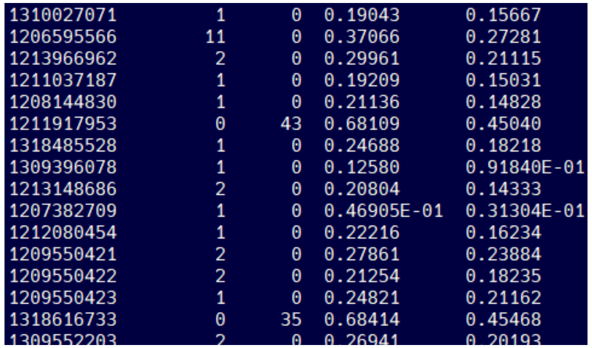
- apax99.log file shows the applied 305d heritabilities



```
==================== Variance component summary =

Index number =       1           2
   1. VC var.=   0.5213E+06   671.5
Genetic   var.=   0.4754E+06   346.0
Residual var.=     759.4       1.244

Total var.    =   0.9975E+06   1019.
Direct Anim V=   0.4754E+06   346.0

h2            =   0.4766       0.3396
lambda        =    7.393        10.78
```

- PEVani gives reliabilities for 305d breeding values

…PEVani file

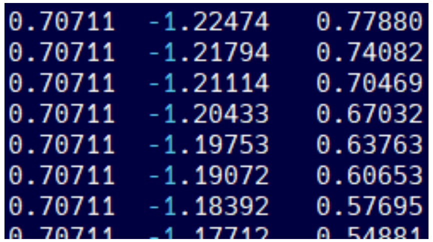


```
    ID           Desc   Nrec  r2_milk        r2_protein
1310027071         1      0  0.19043       0.15667
1206595566        11      0  0.37066       0.27281
1213966962         2      0  0.29961       0.21115
1211037187         1      0  0.19209       0.15031
1208144830         1      0  0.21136       0.14828
1211917953         0     43  0.68109       0.45040
1318485528         1      0  0.24688       0.18218
1309396078         1      0  0.12580       0.91840E-01
1213148686         2      0  0.20804       0.14333
1207382709         1      0  0.46905E-01   0.31304E-01
1212080454         1      0  0.22216       0.16234
1209550421         2      0  0.27861       0.23884
1209550422         2      0  0.21254       0.18235
1209550423         1      0  0.24821       0.21162
1318616733         0     35  0.68414       0.45468
1309552203         2      0  0.26941       0.20193
```

Calculation of ERCs and DRPs

- Exactly the same models and procedures are applied as for Example I
- However, applied variance components must be for 305d breeding values

$$\mathbf{\Phi}_0 =$$



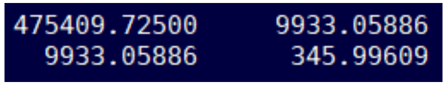
```
0.70711   -1.22474    0.77880
0.70711   -1.21794    0.74082
0.70711   -1.21114    0.70469
0.70711   -1.20433    0.67032
0.70711   -1.19753    0.63763
0.70711   -1.19072    0.60653
0.70711   -1.18392    0.57695
0.70711   -1.17712    0.54881
```

$$\mathbf{\Phi}_{305} = [215.7 \quad -58.1 \quad 16.0]$$

$$\mathbf{S} = \begin{bmatrix} 215.7 & 0 & -58.1 & 0 & 16.0 & 0 \\ 0 & 215.7 & 0 & -58.1 & 0 & 16.0 \end{bmatrix}$$

305d variance components

- $\mathbf{G}_{305} = \mathbf{S}\mathbf{K}_{\mathrm{a}}\mathbf{S}' =$



```
475409.72500      9933.05886
  9933.05886       345.99609
```

- $\mathbf{R}_{305} = \mathbf{S}\mathbf{K}_{\mathrm{p}}\mathbf{S}' + 305 \times \mathbf{K}_{\mathrm{e}} =$

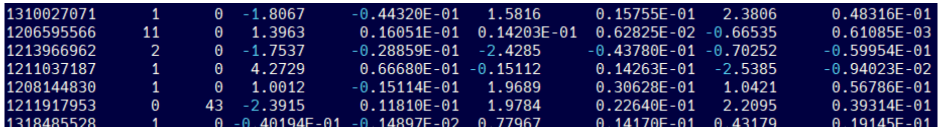
```
522059.61397     18225.04345
 18225.04345       672.78187
```

Validation

305d breeding values from original RR model

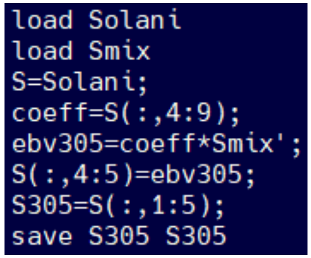
We can use the previous summing matrix **S**

Solani file from random regression model



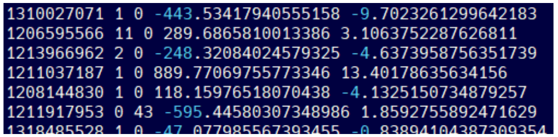
```
1310027071       1       0  -1.8067      -0.44320E-01    1.5816       0.15755E-01    2.3806        0.48316E-01
1206595566      11       0   1.3963       0.16051E-01  0.14203E-01  0.62825E-02  -0.66535        0.61085E-03
1213966962       2       0  -1.7537      -0.28859E-01   -2.4285      -0.43780E-01  -0.70252       -0.59954E-01
1211037187       1       0   4.2729       0.66680E-01  -0.15112      0.14263E-01   -2.5385       -0.94023E-02
1208144830       1       0   1.0012      -0.15114E-01    1.9689       0.30628E-01    1.0421        0.56786E-01
1211917953       0      43  -2.3915       0.11810E-01    1.9784       0.22640E-01    2.2095        0.39314E-01
1318485528       1       0 -0.40194E-01 -0.14897E-02   0.77967      0.14170E-01    0.43179       0.19145E-01
```

Octave script



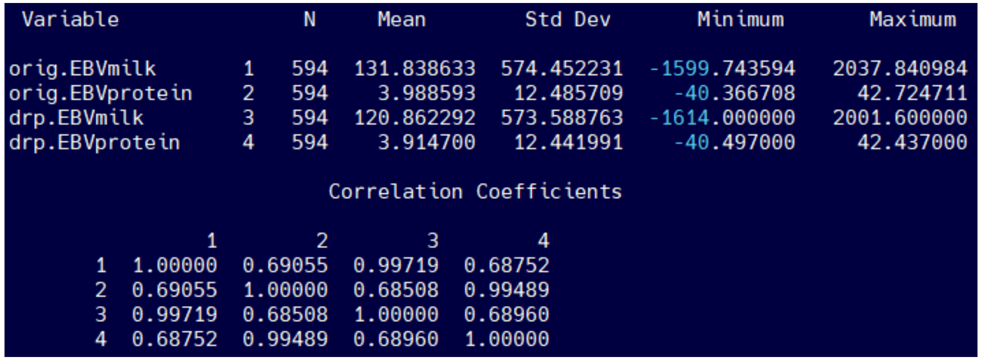
```
load Solani
load Smix
S=Solani;
coeff=S(:,4:9);
ebv305=coeff*Smix';
S(:,4:5)=ebv305;
S305=S(:,1:5);
save S305 S305
```

Solani305 file



```
1310027071 1 0 -443.53417940555158 -9.7023261299642183
1206595566 11 0 289.6865810013386 3.1063752287626811
1213966962 2 0 -248.32084024579325 -4.6373958756351739
1211037187 1 0 889.77069755773346 13.40178635634156
1208144830 1 0 118.15976518070438 -4.1325150734879257
1211917953 0 43 -595.44580307348986 1.8592755892471629
1318485528 1 0 -47.077985567393455 -0.83894104387309354
```

Simple statistics for breeding values



```
 Variable                  N     Mean       Std Dev       Minimum       Maximum

orig.EBVmilk       1    594   131.838633  574.452231  -1599.743594   2037.840984
orig.EBVprotein    2    594     3.988593   12.485709    -40.366708     42.724711
drp.EBVmilk        3    594   120.862292  573.588763  -1614.000000   2001.600000
drp.EBVprotein     4    594     3.914700   12.441991    -40.497000     42.437000

                              Correlation Coefficients

                 1        2        3        4
        1  1.00000  0.69055  0.99719  0.68752
        2  0.69055  1.00000  0.68508  0.99489
        3  0.99719  0.68508  1.00000  0.68960
        4  0.68752  0.99489  0.68960  1.00000
```

Thank you!

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