Reduced rank model

Model description

This example is from the old Finnish Ayrshire evaluation model for production. The example restricts to first lactation test day records for milk, protein and fat yields. Permanent environment and genetic lactation curves from the three traits have been combined, i.e., this is a reduced rank random regression test day model.

The model is

\[
\mathbf{y} = \mathbf{Xb} + f_1(\mathbf{lc}, \text{DIM}) + \mathbf{Zu} + f_2(\mathbf{pe}, \text{DIM}) + f_3(\mathbf{a}, \text{DIM}) + \mathbf{e},
\]

where,

- \(\mathbf{y}\) is vector of milk, protein and fat yield observations,
- \(\mathbf{b}\) is vector of fixed herd times year interaction effects,
- \(\mathbf{X}\) is design matrix to link observations to appropriate fixed effects,
- \(f_1(\mathbf{lc}, \text{DIM})\) is fixed lactation curve regression function,
- \(\mathbf{u}\) is vector of random herd times test-day interaction effects,
- \(\mathbf{Z}\) is design matrix to link observations to appropriate random effects,
- \(f_2(\mathbf{pe}, \text{DIM})\) is random permanent environment regression function,
- \(f_3(\mathbf{a}, \text{DIM})\) is random additive genetic regression function, and
- \(\mathbf{e}\) is random residual vector.

The fixed regression function for lactation curve of trait \(j\) has form

\[
f_1(\mathbf{lc}_j, \text{DIM}) = \sum_{r=0}^{3} \phi(\text{DIM})_r \mathbf{lc}_j r + \exp(-0.04 \cdot \text{DIM})\mathbf{lc}_j 4,
\]

where \(\phi(\text{DIM})_r\) contains Legendre polynomials. The random regression functions \(f_2\) for permanent environment effects and \(f_3\) for genetic animal effects has forms

\[
f_2(\mathbf{pe}, \text{DIM}) = \sum_{r=0}^{5} \phi(\text{DIM})_r \mathbf{pe}_r + \exp(-0.04 \cdot \text{DIM})\mathbf{pe}_6 \text{ and }
\]

\[
f_3(\mathbf{a}, \text{DIM}) = \sum_{r=0}^{5} \phi(\text{DIM})_r \mathbf{a}_r + \exp(-0.04 \cdot \text{DIM})\mathbf{a}_6.
\]

The coefficients differ by trait.

It is assumed that \(\text{var}(\mathbf{u}) = \mathbf{I} \otimes \mathbf{S}_0 = \mathbf{S}\), \(\text{var}(\mathbf{pe}) = \mathbf{I} \otimes \mathbf{P}_0 = \mathbf{P}\), \(\text{var}(\mathbf{a}) = \mathbf{A} \otimes \mathbf{G}_0 = \mathbf{G}\), \(\text{var}(\mathbf{e}) = \mathbf{I} \otimes \mathbf{R}_{0i} = \mathbf{R}\) and all random effects are non-correlated. Now, \(\mathbf{S}_0\) is \(3 \times 3\) -matrix of variance and covariance components for random herd \(x\) test-day effects, \(\mathbf{P}_0\) and \(\mathbf{G}_0\) are \(7 \times 7\) -matrices of variance and covariance components for random permanent environment and genetic animal effects, respectively, and \(\mathbf{R}_{0i}\) is \(3 \times 3\) -matrix of variance and covariance components for the random residual class \(i = 1, \ldots, 12\). \(\mathbf{A}\) is the numerator relationship matrix.

Variance-covariance matrices are

\[
\mathbf{S}_0 = \begin{bmatrix}
0.1615 & 0.1806 & 0.1146 \\
0.1806 & 0.2493 & 0.1424 \\
0.1146 & 0.1424 & 0.1925
\end{bmatrix}
\]

\[
\mathbf{P}_0 = \begin{bmatrix}
0.05567 & 0.07250 & 0.4089 \\
0.07250 & 1.4890 & 3.9420 \\
0.4089 & 3.9420 & 6.5690 \\
\end{bmatrix}
\]

\[
\mathbf{R}_0 = \begin{bmatrix}
87.5704
\end{bmatrix}
\]
\[
G_0 = \begin{bmatrix}
0.06547 \\
0.1136 \\
0.1438 \\
0.2139 \\
0.3464 \\
0.7556 \\
2.9177
\end{bmatrix}
\]

\[
R_{0,1} = \begin{bmatrix}
0.09745 & -0.009369 & -0.01815 \\
-0.009369 & 0.1820 & -0.07951 \\
-0.01815 & -0.07951 & 1.5261
\end{bmatrix}
\]

\[
R_{0,2} = \begin{bmatrix}
0.4145 & 0.07455 & 0.05787 \\
0.07455 & 0.2191 & -0.1012 \\
0.05787 & -0.1012 & 1.8572
\end{bmatrix}
\]

\[
R_{0,3} = \begin{bmatrix}
1.4815 & 0.3577 & 0.2804 \\
0.3577 & 0.9098 & 0.4838 \\
0.2804 & 0.4838 & 2.0526
\end{bmatrix}
\]

\[
R_{0,4} = \begin{bmatrix}
1.1855 & 0.2629 & 0.2052 \\
0.2629 & 0.7765 & 0.4014 \\
0.2052 & 0.4014 & 1.8991
\end{bmatrix}
\]

\[
R_{0,5} = \begin{bmatrix}
1.0501 & 0.2454 & 0.1852 \\
0.2454 & 0.6911 & 0.3587 \\
0.1852 & 0.3587 & 1.6696
\end{bmatrix}
\]

\[
R_{0,6} = \begin{bmatrix}
1.1883 & 0.2817 & 0.2062 \\
0.2817 & 0.8215 & 0.4661 \\
0.2062 & 0.4661 & 1.5676
\end{bmatrix}
\]

\[
R_{0,7} = \begin{bmatrix}
1.1600 & 0.2789 & 0.1903 \\
0.2789 & 0.8418 & 0.4735 \\
0.1903 & 0.4735 & 1.2687
\end{bmatrix}
\]

\[
R_{0,8} = \begin{bmatrix}
1.0881 & 0.2731 & 0.1830 \\
0.2731 & 0.8270 & 0.4649 \\
0.1830 & 0.4649 & 1.1950
\end{bmatrix}
\]

\[
R_{0,9} = \begin{bmatrix}
1.1613 & 0.2807 & 0.1896 \\
0.2807 & 0.8570 & 0.5101 \\
0.1896 & 0.5101 & 1.0130
\end{bmatrix}
\]

\[
R_{0,10} = \begin{bmatrix}
1.4100 & 0.3756 & 0.2597 \\
0.3756 & 1.0649 & 0.6634 \\
0.2597 & 0.6634 & 1.1334
\end{bmatrix}
\]

\[
R_{0,11} = \begin{bmatrix}
1.6402 & 0.3637 & 0.2662 \\
0.3637 & 1.0388 & 0.6832 \\
0.2662 & 0.6832 & 1.1880
\end{bmatrix}
\]

\[
R_{0,12} = \begin{bmatrix}
1.4886 & 0.2991 & 0.2474 \\
0.2991 & 0.8203 & 0.5801 \\
0.2474 & 0.5801 & 1.1190
\end{bmatrix}
\]
Input files

Datafile:

The data file contains information on the data to be analyzed together with class and regression variables for the model. The data file can be in free format (columns are separated by at least one space) or in binary format.

Each record, i.e., line in a free format file, has been divided to two parts: 1) Integer number columns and 2) real number columns. Columns of real numbers are always after the integer number columns.

RRANK.dat

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</tbody>
</table>

Pedigree file:

All the pedigree information must be given in the pedigree file. Each animal in the pedigree must have a record with four integers of which the forth integer is optional.

RRANK.ped
The variance components file has variances and covariances for all the random effects in the model. The variance component file has a line for each (co)variance. Order of lines in the file is irrelevant.

Variance component file:

Column 1: Animal ID  
Column 2: Sire ID  
Column 3: Dam ID  
Column 4: Herd ID  

<table>
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<tr>
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<th>Column 3</th>
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</tbody>
</table>

RRANK.var
Column 1: Random effect number (integer)
Column 2: Row index (integer)
Column 3: Column index (integer)
Column 4: (Co)variance value (real)

Variance component file for multiple residuals:
The separate residual variance component file has variances and covariances for all the residual variance classes in the model. The file has a line for each (co)variance.

RRANK.res

<table>
<thead>
<tr>
<th>Column 1</th>
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</table>

Column 1: Residual variance class number (integer)
Column 2: Row index (integer)
Column 3: Column index (integer)
Column 4: (Co)variance value (real)

Covariable table file:
The covariable table file has covariables for regression effects in the model. First column contains the index that connects an observation in the data file to the corresponding set of covariables in the table. The rows have to be sorted in ascending order by the covariable index. Within the smallest and largest index line, index lines must not be missing.

RRANK.cov

<table>
<thead>
<tr>
<th>Column 1</th>
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</tbody>
</table>

Column 1: Days in milk (integer)
Column 2: Intercept term of 3th order Legendre polynomial for fixed lactation curve (real)
Column 3: Slope term of 3th order Legendre polynomial for fixed lactation curve (real)
Column 4: Quadratic term of 3th order Legendre polynomial for fixed lactation curve (real)
Column 5: Cubic term of 3rd order Legendre polynomial for fixed lactation curve (real)
Column 6: Wilmink term \(e^{-0.04t}\) for fixed lactation curve (real)
Column 2: Intercept term of 5th order Legendre polynomial for permanent environment random regression effect of milk yield (real)
Column 3: Slope term of 5th order Legendre polynomial for permanent environment random regression effect of milk yield (real)
Column 4: Quadratic term of 5th order Legendre polynomial for permanent environment random regression effect of milk yield (real)

Command file:

CLIM instructions for a reduced rank model analysis. Everything beyond `#` sign is considered as a comment.

RRANK.clm

```
TITLE 3 Ayrshire herds, first lactation, milk protein fat, rank 7
DATAFILE RRANK.dat
INTEGER herd animal LAC ANIxLAC HY HTD Hslope YM & MThx4YR AGEclass DCC DDRY DIM residual_num
REAL milk protein fat
DATASORT BLOCK=herd PEDIGREECODE=animal
PEDFILE RRANK.ped       # Pedigree file
PEDIGREE G am+p 0.3333333 # am=animal model, random genetic groups
RANDOM HTD PE
NORANSOL HTD PE
PARFILE RRANK.var        # Variance component file
RESIDFILE RRANK.res      # Multiple residuals
TABLEFILE RRANK.cov      # Covariable table information
RESIDUAL residual_num
TABLEINDEX DIM
MISSING -9.
PRECON d d d d d b
WITHINBLOCKORDER G PE HTD HY
MODEL
milk  =  HY fix_curve(t1 t2 t3 t4 t5 | LAC) HTD & PE(t6 t7 t8 t9 t10 t11 t12| animal)@fst & G(t27 t28 t29 t30 t31 t32 t33| animal)@fst
protein =  HY fix_curve(t1 t2 t3 t4 t5 | LAC) HTD & PE(t13 t14 t15 t16 t17 t18 t19| animal)@fst & G(t34 t35 t36 t37 t38 t39 t40| animal)@fst
fat      =  HY fix_curve(t1 t2 t3 t4 t5 | LAC) HTD & PE(t20 t21 t22 t23 t24 t25 t26| animal)@fst & G(t41 t42 t43 t44 t45 t46 t47| animal)@fst
```
Solution files

Structure of the formatted solution files depends on the model. Therefore, explanation of the content of those files is given in the printout of the particular run of the program.

MiX99-solver program has been run by command \texttt{mix99 -s}, meaning that in all parts of the program default values are used.

"Solfix"-file contains solutions for fixed effects.

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<th>Solution</th>
<th>Factor Trait</th>
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Column 1: Factor number  
Column 2: Trait number  
Column 3: Level code  
Column 4: Number of observations  
Column 5: Solution  
Column 6: Name of factor  
Column 7: Name of trait

"Solf01"-file contains solutions for first within-block fixed effect.

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<th>Level</th>
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Column 1: Level code  
Column 2: Number of observations  
Column 3: Solution for trait 1 milk and factor HY  
Column 4: Solution for trait 2 protein and factor HY  
Column 5: Solution for trait 3 fat and factor HY

"Solani"-file contains solutions for genetic animal effects.
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<th>Animal ID</th>
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<th>Number of observations</th>
<th>Solution for trait 1 milk and factor T27 (animal)</th>
<th>Solution for trait 1 milk and factor T28 (animal)</th>
<th>Solution for trait 1 milk and factor T29 (animal)</th>
<th>Solution for trait 1 milk and factor T30 (animal)</th>
<th>Solution for trait 1 milk and factor T31 (animal)</th>
<th>Solution for trait 1 milk and factor T32 (animal)</th>
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