

Repeated Records Animal Model

1 Introduction

Animals are observed more than once for some traits, such as

- Fleece weight of sheep in different years.
- Calf records of a beef cow over time.
- Test day records within a lactation for a dairy cow.
- Litter size of sows over time.
- Antler size of deer in different seasons.
- Racing results of horses from several races.

Usually the trait is considered to be perfectly correlated over the ages of the animal. Besides an animal's additive genetic value for a trait, there is a common permanent environmental (PE) effect which is a non-genetic effect common to all observations on the same animal.

2 The Model

The model is written as

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \begin{pmatrix} \mathbf{0} & \mathbf{Z} \end{pmatrix} \begin{pmatrix} \mathbf{a}_0 \\ \mathbf{a}_r \end{pmatrix} + \mathbf{Z}\mathbf{p} + \mathbf{e},$$

where

$$\begin{aligned} \mathbf{b} &= \text{vector of fixed effects,} \\ \begin{pmatrix} \mathbf{a}_0 \\ \mathbf{a}_r \end{pmatrix} &= \begin{pmatrix} \text{animals without records} \\ \text{animals with records} \end{pmatrix}, \\ \mathbf{p} &= \text{vector of PE effects of length equal to } \mathbf{a}_r, \text{ and} \\ \mathbf{e} &= \text{vector of residual effects.} \end{aligned}$$

The matrices \mathbf{X} and \mathbf{Z} are design matrices that associate observations to particular levels of fixed effects and to additive genetic and PE effects, respectively. In a repeated records model,

\mathbf{Z} is not equal to an identity matrix. Also,

$$\begin{aligned} \mathbf{a} \mid \mathbf{A}, \sigma_a^2 &\sim N(\mathbf{0}, \mathbf{A}\sigma_a^2) \\ \mathbf{p} \mid \mathbf{I}, \sigma_p^2 &\sim N(\mathbf{0}, \mathbf{I}\sigma_p^2) \\ \mathbf{e} &\sim N(\mathbf{0}, \mathbf{I}\sigma_e^2) \\ \mathbf{G} &= \begin{pmatrix} \mathbf{A}\sigma_a^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_p^2 \end{pmatrix}. \end{aligned}$$

Repeatability is a measure of the average similarity of multiple records on animals across the population (part genetic and part environmental), and is defined as a ratio of variances as

$$r = \frac{\sigma_a^2 + \sigma_p^2}{\sigma_a^2 + \sigma_p^2 + \sigma_e^2},$$

which is always going to be greater than or equal to heritability, because

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_p^2 + \sigma_e^2}.$$

3 Simulation of Records

Simulating multiple records on animals may help to understand this type of model. Let

$$\begin{aligned} \sigma_a^2 &= 36 \\ \sigma_p^2 &= 16 \text{ and} \\ \sigma_e^2 &= 48 \end{aligned}$$

Thus,

$$h^2 = \frac{36}{36 + 16 + 48} = .36,$$

and

$$r = \frac{36 + 16}{36 + 16 + 48} = .52.$$

3.1 Data Structure

Animal	Sire	Dam	Year 1	Year 2	Year 3
7	1	2	✓	✓	✓
8	3	4	✓	✓	
9	5	6	✓		✓
10	1	4		✓	✓
11	3	6			✓
12	1	2		✓	

None of the animals are inbred, so that the inverse of the additive genetic relationship matrix is

$$\mathbf{A}^{-1} = \frac{1}{2} \begin{pmatrix} 5 & 2 & 0 & 1 & 0 & 0 & -2 & 0 & 0 & -2 & 0 & -2 \\ 2 & 4 & 0 & 0 & 0 & 0 & -2 & 0 & 0 & 0 & 0 & -2 \\ 0 & 0 & 4 & 1 & 0 & 1 & 0 & -2 & 0 & 0 & -2 & 0 \\ 1 & 0 & 1 & 4 & 0 & 0 & 0 & -2 & 0 & -2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 3 & 1 & 0 & 0 & -2 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 4 & 0 & 0 & -2 & 0 & -2 & 0 \\ -2 & -2 & 0 & 0 & 0 & 0 & 4 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -2 & -2 & 0 & 0 & 0 & 4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -2 & -2 & 0 & 0 & 4 & 0 & 0 & 0 \\ -2 & 0 & 0 & -2 & 0 & 0 & 0 & 0 & 0 & 4 & 0 & 0 \\ 0 & 0 & -2 & 0 & 0 & -2 & 0 & 0 & 0 & 0 & 4 & 0 \\ -2 & -2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 4 \end{pmatrix}.$$

3.2 Additive Genetic Values of Animals

The first six animals are assumed to be base generation animals, and should be generated first. Let RND represent a random normal deviate, and b_i is $0.5 - 0.25(F_s + F_d)$.

Animal	Parent Ave.	RND	$(36 * b_i)^{.5}$	TBV
1	0.0	-2.5038	6.0	-15.0228
2	0.0	-.3490	6.0	-2.0940
3	0.0	-.2265	6.0	-1.3590
4	0.0	-.3938	6.0	-2.3628
5	0.0	1.4786	6.0	8.8716
6	0.0	2.3750	6.0	14.2500
7	-8.5584	-.8166	4.2426	-12.0229
8	-1.8609	1.0993	4.2426	2.8030
9	11.5608	1.5388	4.2426	18.0893
10	-8.6928	.0936	4.2426	-8.2957
11	6.4455	1.3805	4.2426	12.3024
12	-8.5584	-1.2754	4.2426	-13.9694

3.3 Permanent Environmental Effects

Each animal has a PE effect that is common to each of its own records, but is not transmitted to progeny. Genetic relationships have no bearing on PE effects. Generate a RND and multiply by $\sigma_p = 4$. These are shown in the table below.

Animal	TBV	PE
1	-15.02	2.97
2	-2.09	-9.04
3	-1.36	4.44
4	-2.36	-4.16
5	8.87	-5.68
6	14.25	6.85
7	-12.02	1.38
8	2.80	7.02
9	18.09	5.94
10	-8.30	-5.03
11	12.30	-1.06
12	-13.97	-2.69

3.4 Records

Records are generated according to the model equation,

$$y_{ijk} = t_i + a_j + p_j + e_{ijk},$$

where t_i is a year effect. Let $t_1 = 53$, $t_2 = 59$, and $t_3 = 65$. Note that $\sigma_p = 4$, and $\sigma_e = 6.9282$. Residual values are generated for each observation as $RND * \sigma_e$. Add together the pieces and round to the nearest whole number.

Animal	TBV	PE	Year 1	Year 2	Year 3
			y_{1jk}	y_{2jk}	y_{3jk}
1	-15.02	2.97			
2	-2.09	-9.04			
3	-1.36	4.44			
4	-2.36	-4.16			
5	8.87	-5.68			
6	14.25	6.85			
7	-12.02	1.38	39	51	62
8	2.80	7.02	48	72	
9	18.09	5.94	71		96
10	-8.30	-5.03		56	47
11	12.30	-1.06			86
12	-13.97	-2.69		46	

An interesting point to observe from the simulation is that the PE effects are present even for animals with only one record. Also, the same PE value is present in all records of one animal.

Another assumption is that the records have a genetic correlation of one, which is true in the way that the above records were simulated because the same TBV was used for each record. In real life, genes affecting a trait might change as the animal ages, and therefore, the genetic correlation between successive records could be less than unity.

4 Mixed Model Equations

Let

$$\mathbf{W} = \begin{bmatrix} \mathbf{X} & \begin{pmatrix} \mathbf{0} & \mathbf{Z} \end{pmatrix} & \mathbf{Z} \end{bmatrix},$$

then

$$\mathbf{W}'\mathbf{W} = \begin{pmatrix} \mathbf{X}'\mathbf{X} & \mathbf{0} & \mathbf{X}'\mathbf{Z} & \mathbf{X}'\mathbf{Z} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{Z}'\mathbf{X} & \mathbf{0} & \mathbf{Z}'\mathbf{Z} & \mathbf{Z}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{0} & \mathbf{Z}'\mathbf{Z} & \mathbf{Z}'\mathbf{Z} \end{pmatrix}, \quad \mathbf{W}'\mathbf{y} = \begin{pmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{0} \\ \mathbf{Z}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{pmatrix},$$

and

$$\Sigma = \begin{pmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{A}^{00}k_a & \mathbf{A}^{0r}k_a & \mathbf{0} \\ \mathbf{0} & \mathbf{A}^{r0}k_a & \mathbf{A}^{rr}k_a & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}k_p \end{pmatrix},$$

where \mathbf{A}^{ij} are corresponding elements of the inverse of the additive genetic relationship matrix (given earlier) partitioned according to animals without and with records. In this example, each submatrix is of order 6. Also,

$$k_a = \sigma_e^2/\sigma_a^2 = 1.33333, \quad \text{and } k_p = \sigma_e^2/\sigma_p^2 = 3.$$

MME are therefore,

$$\begin{aligned} (\mathbf{W}'\mathbf{W} + \Sigma)\beta &= \mathbf{W}'\mathbf{y} \\ (\mathbf{W}'\mathbf{W} + \Sigma)\beta &= \begin{pmatrix} \mathbf{X}'\mathbf{X} & \mathbf{0} & \mathbf{X}'\mathbf{Z} & \mathbf{X}'\mathbf{Z} \\ \mathbf{0} & \mathbf{A}^{00}k_a & \mathbf{A}^{0r}k_a & \mathbf{0} \\ \mathbf{Z}'\mathbf{X} & \mathbf{A}^{r0}k_a & \mathbf{Z}'\mathbf{Z} + \mathbf{A}^{rr}k_a & \mathbf{Z}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{0} & \mathbf{Z}'\mathbf{Z} & \mathbf{Z}'\mathbf{Z} + \mathbf{I}k_p \end{pmatrix} \begin{pmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}}_0 \\ \hat{\mathbf{a}}_r \\ \hat{\mathbf{p}} \end{pmatrix}. \end{aligned}$$

Let a generalized inverse of the coefficient matrix be represented as

$$(\mathbf{W}'\mathbf{W} + \Sigma)^- = \begin{pmatrix} - & - & - \\ - & \mathbf{C}_{aa} & - \\ - & - & \mathbf{C}_{pp} \end{pmatrix},$$

where \mathbf{C}_{aa} is of order 12 in this case, and \mathbf{C}_{pp} is of order 6.

The full HMME are too large to present here as a whole, so parts of the matrix are given as follows.

$$\mathbf{X}'\mathbf{X} = \begin{pmatrix} 3 & 0 & 0 \\ 0 & 4 & 0 \\ 0 & 0 & 4 \end{pmatrix}, \quad \mathbf{X}'\mathbf{y} = \begin{pmatrix} 158 \\ 225 \\ 291 \end{pmatrix},$$

$$\mathbf{X}'\mathbf{Z} = \begin{pmatrix} 1 & 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 & 1 & 0 \end{pmatrix},$$

$$\mathbf{Z}'\mathbf{Z} = \text{diag}(3 \ 2 \ 2 \ 2 \ 1 \ 1),$$

and

$$\mathbf{Z}'\mathbf{y} = \begin{pmatrix} 152 \\ 120 \\ 167 \\ 103 \\ 86 \\ 46 \end{pmatrix}.$$

The solutions for animals are given in the table below. Solutions for year effects were

$$\hat{t}_1 = 50.0858,$$

$$\hat{t}_2 = 63.9612,$$

$$\hat{t}_3 = 72.0582.$$

Animal	TBV	PE	$\hat{\mathbf{a}}$	$\hat{\mathbf{p}}$
1	-15.02	2.97	-7.9356	
2	-2.09	-9.04	-4.4473	
3	-1.36	4.44	2.8573	
4	-2.36	-4.16	-2.6039	
5	8.87	-5.68	5.0783	
6	14.25	6.85	7.0512	
7	-12.02	1.38	-8.0551	-1.6566
8	2.80	7.02	1.0111	0.7861
9	18.09	5.94	11.1430	4.5140
10	-8.30	-5.03	-8.7580	-3.1007
11	12.30	-1.06	6.9271	1.7537
12	-13.97	-2.69	-8.7750	-2.2965

The correlation between $\hat{\mathbf{a}}$ and TBV was .9637, and between $\hat{\mathbf{p}}$ and true PE was .7215.

5 Reliability of EBVs

Owners of animals are very interested in Estimated Breeding Values (EBVs), and the main question is about its reliability or accuracy. The variance-covariance matrix of prediction errors is given by $\mathbf{C}_{aa}\sigma_e^2$. Reliability, R , of the i^{th} animal is defined as

$$R = (a_{ii}\sigma_a^2 - c_{ii}\sigma_e^2)/\sigma_a^2,$$

where a_{ii} is the diagonal of \mathbf{A} for animal i , and c_{ii} is the diagonal of \mathbf{C}_{aa} for animal i . Note that this is equivalent to

$$R = a_{ii} - c_{ii}k_a.$$

This procedure does not work when phantom groups are included in the formation of \mathbf{A}^{-1} because then it is possible that

$$c_{ii}k_a > a_{ii}$$

for some situations. Below is a table of the reliabilities for the twelve animals in the example analysis.

Animal	$\hat{\mathbf{a}}$	c_{ii}	R
1	-7.9285	.6472	.1371
2	-4.4339	.6524	.1301
3	2.8289	.6476	.1365
4	-2.6365	.6398	.1469
5	5.0996	.6807	.0924
6	7.0703	.6653	.1129
7	-8.0155	.4740	.3680
8	.9544	.5012	.3317
9	11.1845	.4985	.3353
10	-8.7771	.5180	.3093
11	6.9204	.5656	.2459
12	-8.7807	.5592	.2544

Animals with records have a higher reliability than animals that have only progeny. Also, animal 7 had a higher reliability because it had three records while animals 11 and 12 had only one record. Reliability reflects the years in which the records were made and the number of contemporaries within a year, and specifically who the contemporaries actually were. Reliability also includes the fact that animals were related.

In the analysis of very large numbers of animals, the calculation of \mathbf{C}_{aa} is virtually impossible. Thus, animal breeders have devised many ways of approximating the diagonals of \mathbf{C}_{aa} . The following method is due to Schaeffer and Jansen (1997).

Step 1 Account for contemporary group size and PE effects. Take animal 7 as an example.

Animal 7's first record in year 1 was made with two other contemporaries, calculate

$$d_7 = 1 - \frac{1 * 1}{3} = \frac{2}{3}.$$

Animal 7's second and third records were made with three contemporaries each, so accumulate the following:

$$d_7 = d_7 + (1 - \frac{1}{4}) + (1 - \frac{1}{4})$$

or

$$d_7 = \frac{2}{3} + \frac{3}{4} + \frac{3}{4} = 2.1666667.$$

Now adjust for the fact that we must also estimate PE effects for this animal. The adjustment is

$$\begin{aligned} d_7 &= d_7 - \frac{d_7 * d_7}{d_7 + k_p} \\ &= 2.16667 - \frac{4.694444}{5.1666667} \\ &= 1.25806452. \end{aligned}$$

Finally, add $a^{ii}k_a$, diagonal element from $\mathbf{A}^{-1}k_a$, to give

$$d_7 = 1.25806 + 2(1.33333) = 3.92473.$$

This is done for all animals with records. Animals without records have $d_i = k_a$. For animals 1 through 12 the results are

$$\begin{aligned} d_1 &= 1.33333 \\ d_2 &= 1.33333 \\ d_3 &= 1.33333 \\ d_4 &= 1.33333 \\ d_5 &= 1.33333 \\ d_6 &= 1.33333 \\ d_7 &= 3.92473 \\ d_8 &= 3.62893 \\ d_9 &= 3.62893 \\ d_{10} &= 3.66667 \\ d_{11} &= 3.26667 \\ d_{12} &= 3.26667 \end{aligned}$$

Step 2 Convert the above numbers into a number that would represent an equivalent number of progeny, n_i , by

$$n_i = (d_i - k_a) / .5k_a.$$

This gives

$$\begin{aligned} n_1 &= 0.00000 \\ n_2 &= 0.00000 \\ n_3 &= 0.00000 \end{aligned}$$

$$\begin{aligned}
n_4 &= 0.00000 \\
n_5 &= 0.00000 \\
n_6 &= 0.00000 \\
n_7 &= 3.88710 \\
n_8 &= 3.44339 \\
n_9 &= 3.44339 \\
n_{10} &= 3.50000 \\
n_{11} &= 2.90000 \\
n_{12} &= 2.90000
\end{aligned}$$

Step 3 Add contributions to parents. Animals must be processed from youngest to oldest. Let $\alpha = (4 - h^2)/h^2 = 10.11111$. The contribution to a parent is

$$q_i = .25\alpha t_i / (1 - .25t_i),$$

where

$$t_i = n_i / (n_i + \alpha),$$

or

$$q_i = .25\alpha * n_i / (.75n_i + \alpha).$$

The value q_i is added to the n_s of the sire of i and to the n_d of the dam of i . The q_i values of animals 7 through 12 are given below.

Animal	ne_i	t_i	q_i
7	3.88710	.277686	.754293
8	3.44339	.254040	.685706
9	3.44339	.254040	.685706
10	3.50000	.257143	.694657
11	2.90000	.222886	.596653
12	2.90000	.222886	.596653

For animal 7, for example, $q_i = .754293$ is added to n_1 and n_2 because the parents of 7 are animals 1 and 2. Animal 1 receives contributions from animals 7, 10, and 12, or

$$ne_1 = 0.0 + .754293 + .694657 + .596653 = 2.045603$$

Similarly for all parents,

$$\begin{aligned}
ne_2 &= 0.0 + .754293 + .596653 = 1.350946 \\
ne_3 &= 0.0 + .685706 + .596653 = 1.282359 \\
ne_4 &= 0.0 + .685706 + .694657 = 1.380363 \\
ne_5 &= 0.0 + .685706 = .685706 \\
ne_6 &= 0.0 + .685706 + .596653 = 1.282359
\end{aligned}$$

In real datasets, animals could very likely have both records and progeny.

Step 4 Set up selection index equations with progeny on the animal, on its sire, and on its dam. Assume the sire and dam are unrelated. Use n_i as the number of progeny for animal i . Take animal 7 as an example with sire equal to animal 1 and dam equal to animal 2, and calculate

$$\begin{aligned}
 m_1 &= (n_1 - q_7)/(n_1 - q_7 + \alpha) \\
 &= (2.045603 - .754293)/(1.291310 + 10.111111) \\
 &= 1.291310/11.402421 \\
 &= .113249 \\
 m_2 &= (n_2 - q_7)/(n_2 - q_7 + \alpha) \\
 &= (1.350946 - .754293)/(.596653 + 10.111111) \\
 &= .055722 \\
 t_{1,2} &= (m_1 + m_2)/4 \\
 &= (.113249 + .055722)/4 \\
 &= .042243 \\
 q_{1,2} &= \alpha t_{1,2}/(1 - t_{1,2}) \\
 &= .445958
 \end{aligned}$$

Now $q_{1,2}$ is the contribution (in progeny equivalents) to the number of effective progeny for animal 7. Thus,

$$\begin{aligned}
 R &= (n_7 + q_{1,2})/(n_7 + q_{1,2} + \alpha) \\
 &= (3.88710 + .445958)/(4.333058 + 10.111111) \\
 &= .299987.
 \end{aligned}$$

This approximation is much less than the value of .3680 derived from the diagonal of \mathbf{C}_{aa} . The small number of records in this example could be a cause for the disagreement.

For animal 1, the parents are unknown and so

$$\begin{aligned}
 R &= n_1/(n_1 + \alpha) \\
 &= 2.045603/(2.045603 + 10.111111) \\
 &= .168269,
 \end{aligned}$$

which is greater than the value of .1371 from \mathbf{C}_{aa} and shows that approximations do not work in all cases. For animal 12, with sire equal to animal 1 and dam equal to animal 2, and calculate

$$\begin{aligned}
 m_1 &= (n_1 - q_{12})/(n_1 - q_{12} + \alpha) \\
 &= (2.045603 - .596653)/(1.448950 + 10.111111) \\
 &= 1.448950/11.560061 \\
 &= .125341 \\
 m_2 &= (n_2 - q_{12})/(n_2 - q_{12} + \alpha) \\
 &= (1.350946 - .596653)/(1.754293 + 10.111111)
 \end{aligned}$$

$$\begin{aligned}
&= .117862 \\
t_{1,2} &= (m_1 + m_2)/4 \\
&= (.125341 + .117862)/4 \\
&= .060801 \\
q_{1,2} &= \alpha t_{1,2}/(1 - t_{1,2}) \\
&= .654562
\end{aligned}$$

Now $q_{1,2}$ is the contribution (in progeny equivalents) to the number of effective progeny for animal 12. Thus,

$$\begin{aligned}
R &= (n_{12} + q_{1,2})/(n_{12} + q_{1,2} + \alpha) \\
&= (2.9 + .654562)/(3.554562 + 10.111111) \\
&= .2601,
\end{aligned}$$

which is only slightly higher than .2544 given by C_{aa} .

Reliabilities are required to determine the 'official' status of an animal's EBV. The approximations that are used should be on the conservative side for safety reasons.

There may also be a method of determining approximate reliabilities by using Gibbs sampling, but not allowing the variances to change in each round. The starting values would be the solutions to the MME and the known variances. Then about 200 rounds of sampling should give a good estimate of the prediction error variance of the EBVs for each animal, which can then be used to arrive at reliability. Two hundred samples would be calculated for each animal, and the standard deviation of those samples would estimate the square root of the prediction error variances. This would be similar to computing 200 more iterations in the solution phase of the program.

6 Selection of Animals to Have Later Records

Often records on animals are taken over time, as the animal ages. Consequently the observed value of the first record determines if that animal makes a second record, and so on. Thus, selection could affect the mean and variance of later repeated records. This type of selection is handled adequately by HMME **provided** that all first records of animals and pedigrees are known for all animals. If these provisions are not met, then EBVs and estimates of fixed effects from a repeated records analysis could be biased by culling, with the magnitude determined by the severity of the culling.

7 Permanent Effects?

Permanent environmental effects may not really be permanent. Environmental effects are encountered all through the life of any living animal. There are certain effects that become part of that animal's performance ability for the entirety of its life. However, there could be many effects that become incorporated into the animal's performance ability as the animal gains experience and encounters new events. For example, a tennis player may develop a wicked backhand shot due to a coach that forced the player to practice it endlessly. A few years later, a different coach may work more on the player's serve. Thus, environmental effects accumulate over time. Both coaches now affect that player's performance ability for the rest of his(her) life. Eventually age, injury, stress, success become other environmental effects.

A model with one permanent environmental effect per animal represents an average of all such environmental effects over the performance lifetime of the animal. There is not an easy way to model accumulated environmental effects with time. Putting a time effect into the model is not sufficient, because the time effects may be different for each animal.

The accumulated effects are averaged into the PE effect, and the deviations around that (animal by time interaction effects) become part of the residual effect. Either a random regression model or a multiple trait model are recommended for repeated record situations because of the above problems.

8 EXERCISES

Below are scores (out of 200) of dogs in three different agility competitions. Assume a repeated records animal model where the score has a heritability of 0.25, and a repeatability of 0.45. Each trial was held in a different city with a different judge and course setter.

Scores (out of 200) for three agility competitions for dogs.

Dog	Sire	Dam	Age	Trial 1	Trial 2	Trial 3
1	-	-	7	135		150
2	-	-	6	110		
3	1	2	4	127	134	130
4	1	2	4	108	140	
5	1	-	4	95		104
6	1	-	5	138	161	
7	3	-	2	154		166
8	3	4	2		155	140
9	5	-	1		128	
10	5	6	1			117

1. Write a complete repeated records model for these data.
2. Construct HMME and solve. Which dogs are tops?
3. Provide prediction error variances for the EBV.
4. Show how to estimate the variances for one round of EM-REML, or one round of Gibbs sampling.
5. Predict a record of animal 9 in Trial 3, if it had been entered. Also give a prediction error variance for that record.