1 Introduction

Animals are commonly observed for more than one trait because many traits affect overall profitability of an animal. There are a few general categories of traits that apply to nearly all species. These are Production, Reproduction, Health, Behaviour, and Conformation. In dairy cattle, for example, production traits include milk, fat, and protein yields, and somatic cell scores, while in beef cattle, production includes growth and carcass composition. Reproduction is the ability to reproduce viable offspring without problems or delays in re-breeding, pregnancy, or parturition. Failure to become pregnant, difficulty with giving birth, or small litter size (in swine) are traits that cost producers money. Health traits relate to the ability of the animal to produce under stressful conditions. General immunity to fight off disease causing organisms is a useful trait for selection, but these traits often have low heritability. Behavioural traits, such as temperament, aggressiveness towards progeny, desire to eat, and general ease of handling are traits that are not studied very much in livestock, but which contribute towards overall profitability. Conformation traits are important in some traits, such as horses or dairy cattle. Animals must have the correct body shapes to be able to jump hurdles, run fast, give more milk with fewer problems, and to win show competitions.

Multiple trait (MT) analyses make use of genetic and environmental correlations among traits in order to achieve greater reliabilities on EBVs. MT analyses are advantageous in the following situations.

- **Low Heritability Traits** When the difference between genetic and residual correlations is large (e.g. greater than .5 difference) or when one trait has a much higher heritability than the other trait, then the trait with the lower heritability tends to gain more in accuracy than the high heritability trait, although both traits benefit to some degree from the simultaneous analysis.

- **Culling** Traits that occur at different times in the life of the animal, such that animals may be culled on the basis of earlier traits and not be observed for traits that occur later in life can cause bias in EBVs of the later life traits. An MT analysis that includes all observations on an animal upon which culling decisions have been based, has been shown to partially account for the selection that has taken place, and therefore gives unbiased estimates of breeding values for all traits. Severe selection will tend to cause bias in most situations.

There are a couple of disadvantages to MT analyses.

- **Estimates of Correlations** An MT analysis relies on accurate genetic and residual
correlations. If the parameter estimates are greatly different from the unknown true values, then an MT analysis could do as much harm as it might do good.

- **Computing Cost** MT analyses require more computing time and increased computer memory in order to analyze the data. Software programs are more complicated, more memory and disk storage are usually needed, and verification of results might be more complicated.

If culling bias is the main concern, then an MT model must be used regardless of the costs or no analysis should be done at all, except for the traits not affected by culling bias. More and more MT analyses are being conducted in animal breeding.

### 2 Models

MT situations may be simple or very complicated. A simple situation will be described. Consider two traits with a single observation per trait per animal. Table 1 contains data on body condition scores (1 to 10) and percentage fat in the tail of fat-tailed sheep at 120 days of age in Tunisia. Body condition is the degree of fatness in the body frame. A score of 1 is a very thin animal with bones sticking out and general unhealthy appearance. A score of 10 is a very fat animal, but perhaps prone to foot problems or back problems. A score of 5 is average and generally well-conditioned and healthy looking.

<table>
<thead>
<tr>
<th>Animal</th>
<th>Sire</th>
<th>Dam</th>
<th>Group</th>
<th>Trait 1</th>
<th>Trait 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2.0</td>
<td>39</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2.5</td>
<td>38</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>9.5</td>
<td>53</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4.5</td>
<td>45</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>5.5</td>
<td>63</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>2.5</td>
<td>64</td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>4</td>
<td>2</td>
<td>8.5</td>
<td>35</td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>5</td>
<td>3</td>
<td>8.0</td>
<td>41</td>
</tr>
<tr>
<td>9</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td>9.0</td>
<td>27</td>
</tr>
<tr>
<td>10</td>
<td>2</td>
<td>4</td>
<td>1</td>
<td>7.5</td>
<td>32</td>
</tr>
<tr>
<td>11</td>
<td>2</td>
<td>5</td>
<td>2</td>
<td>3.0</td>
<td>46</td>
</tr>
<tr>
<td>12</td>
<td>6</td>
<td>10</td>
<td>3</td>
<td>7.0</td>
<td>67</td>
</tr>
</tbody>
</table>

A model should be specified separately for each trait. Usually, the same model is assumed for each trait, and this can greatly simplify the computational aspects, but such an assumption may be unrealistic in many situations. The same model will be assumed for both traits.
Let the model equation for trait $t$ be

$$y_{tij} = G_{ti} + a_{tj} + e_{tij},$$

where $G_{ti}$ is a group effect with 3 levels, $a_{tj}$ is a random, animal additive genetic effect for trait $t$, and $e_{tij}$ is a random residual environmental effect for trait $t$.

Because the two traits will be analyzed simultaneously, the variances and covariances need to be specified for the traits together. For example, the additive genetic variance-covariance (VCV) matrix could be written as

$$\mathbf{G} = \begin{pmatrix} g_{11} & g_{12} \\ g_{12} & g_{22} \end{pmatrix} = \begin{pmatrix} 1 & 2 \\ 2 & 15 \end{pmatrix},$$

$$\mathbf{G}^{-1} = \begin{pmatrix} g_{11}^{11} & g_{12}^{12} \\ g_{21}^{12} & g_{22}^{12} \end{pmatrix} = \frac{1}{11} \begin{pmatrix} 15 & -2 \\ -2 & 1 \end{pmatrix},$$

and the residual environmental VCV matrix as

$$\mathbf{R} = \begin{pmatrix} e_{11} & e_{12} \\ e_{12} & e_{22} \end{pmatrix} = \begin{pmatrix} 10 & 5 \\ 5 & 100 \end{pmatrix},$$

$$\mathbf{R}^{-1} = \begin{pmatrix} e_{11}^{11} & e_{12}^{12} \\ e_{21}^{12} & e_{22}^{12} \end{pmatrix} = \frac{1}{975} \begin{pmatrix} 100 & -5 \\ -5 & 10 \end{pmatrix}.$$

The genetic and residual correlations are, respectively,

$$\rho_g = \frac{2}{(15)^{.5}} = .516,$$

$$\rho_r = \frac{5}{(1000)^{.5}} = .158$$

with

$$h_1^2 = \frac{1}{11} = .0909,$$

and

$$h_2^2 = \frac{15}{115} = .1304.$$

For all data, then

$$\text{Var} \begin{pmatrix} a_1 \\ a_2 \end{pmatrix} = \begin{pmatrix} A g_{11} & A g_{12} \\ A g_{12} & A g_{22} \end{pmatrix}.$$

The structure of the residual VCV matrix over all observations can be written several ways depending on whether allowance is made for missing observations on either trait for some animals. If all animals were observed for both traits, then

$$\text{Var} \begin{pmatrix} e_1 \\ e_2 \end{pmatrix} = \begin{pmatrix} I e_{11} & I e_{12} \\ I e_{12} & I e_{22} \end{pmatrix}.$$
3 MME

Let the model for one trait, in matrix notation be

\[ y = Xb + Za + e, \]

then the MME for one trait could be written as

\[ \begin{bmatrix} (X'X X'Z) + \begin{pmatrix} 0 & 0 \\ 0 & A^{-1}k \end{pmatrix} \end{bmatrix} \begin{pmatrix} \hat{b} \\ \hat{a} \end{pmatrix} = \begin{pmatrix} X'y \\ Z'y \end{pmatrix}, \]

or more simply as

\[ (B + H^{-1})\hat{s} = r. \]

MT MME for two traits with animals observed for both traits, would be

\[ \begin{bmatrix} \begin{pmatrix} B_{e_{11}} & B_{e_{12}} \\ B_{e_{21}} & B_{e_{22}} \end{pmatrix} + \begin{pmatrix} H^{-1}g^{11} & H^{-1}g^{12} \\ H^{-1}g^{21} & H^{-1}g^{22} \end{pmatrix} \end{bmatrix} \begin{pmatrix} r_{1e_{11}} + r_{2e_{12}} \\ r_{1e_{21}} + r_{2e_{22}} \end{pmatrix}, \]

Often observations for all traits are available on each animal. With two traits one of the two trait observations might be missing. This complicates the construction of MME, but they are still theoretically well-defined. Thus, an EBV could be calculated for an animal that has not been observed for a trait, through the genetic and residual correlations to other traits and through the relationship matrix. The models for each trait could also be different and this provides another layer of complexity to MT analyses.

4 Results

Both single trait and multiple trait analyses were conducted for this example with the results shown in Table 2.
Animal EBVs for both traits are highly correlated to each other between single and multiple trait analyses. There would be very little, if any, re-ranking of animals. Variances of prediction error from single trait analyses were slightly larger than those from the multiple trait analyses. In this example, there would be little advantage to multiple trait analyses. However, if observations were missing or if the difference between residual and genetic correlations was greater, then a multiple trait analysis would be more beneficial.