Group recordings accounted for drop out animals

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Introduction

Breeding for reduced feed intake is important to
1. reduce cost
2. reduce CO2 emission

Individual feed records are costly

How can we get more phenotypes?
- Solution: Group records of feed intake
- Problem: How to handle drop out animals
Introduction

Breeding for reduced feed intake is important to:
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Solution: Group records of feed intake

Problem: How to handle drop out animals
Feed intake of groups

E.g from 0kg feed to 1200kg feed and individual body weights

Literature

Su et al. (2018) *Genet Sel Evol* 50:42
Shirali, et al. Session 42 (17:45)
Group feed intake and individual body weight gain
Group feed regressed on individual weight

\[ y_{jk} = \sum_{i=1}^{n_{jk}} x_{ijk}^T \alpha + \sum_{m=1}^{d} \beta_m \sum_{i=1}^{n_{jk}} w_{ijk}^m + \sum_{m=0}^{q} \gamma_{jm} \sum_{i=1}^{n_{jk}} w_{ijk}^m \]

\[ + \sum_{i=1}^{n_{jk}} \left( \sum_{m=0}^{s} a_{ijm} w_{ijk}^m + \sum_{m=0}^{r} p_{ijm} w_{ijk}^m \right) + e_{jk} \]

\[
\begin{pmatrix}
\gamma_{j0} \\
\vdots \\
\gamma_{jq}
\end{pmatrix}
\sim N(0, \Gamma \otimes D),
\]

\[
\begin{pmatrix}
a_{ij0} \\
\vdots \\
a_{ijr}
\end{pmatrix}
\sim N(0, G \otimes A),
\]

\[
\begin{pmatrix}
p_{ij0} \\
\vdots \\
p_{ijr}
\end{pmatrix}
\sim N(0, P \otimes I),
\]

\[ e_{jk} \sim N(0, n_{jk} \sigma_e^2) \]
Feed conversion in sub-period

Growth interval from $w_1$ to $w_2$:

$$f.c._{ij}(\Delta w_{12}) = \frac{y_{ij2} - y_{ij1}}{w_2 - w_1}$$

Genetic variances

$$\Delta w'_{s12} G \Delta w_{s12} \text{ where } \Delta w_{s12} = \begin{pmatrix} w_2^0 - w_1^0 \\ \vdots \\ w_s^2 - w_s^1 \end{pmatrix}$$

Breeding values for $f.c._{ij}$

$$BV_{ij} = \frac{a_{ij} \Delta w_{s12}}{w_2 - w_1}$$
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### Data

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<thead>
<tr>
<th>Number</th>
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<tbody>
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<td>Animals</td>
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<tr>
<td>Groups</td>
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<td>Records</td>
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<td>Drop out animals</td>
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Variance estimates of different models

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</table>

* The group record is the sum for the group, and therefore the scale is different

Small groups (<7 animals) were removed

REML estimates by DMU (P. Madsen, 2013)
Residual plot, within groups
Breeding values of group and individual RR models

Corr=0.29
Discussion

- $\text{Corr} = 0.29$
- Relation between animals within groups
  - Mean littermates per litter: 1.13
  - More littermates in the same pen led to a higher accuracy of BV (Su et al., 2018)
- More data and higher order might increases accuracy of BV
- Genomic relationship might increase accuracy of BV
Conclusion

- RR-model on longitudinal group records can be used to predict individual BV’s of feed conversion ratio
- RR-model can account for drop out animals
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Thank You!