introduction
○○○

RR models

Group models
○○

Data
○

Results
○○○○○○

Group recordings accounted for drop out animals

B. Nielsen[1], T. Ostersen[1], H. Gao[2], G. Su[2], J. Jensen[2], P. Madsen[2], O.F.Christensen[2], M. Shirali[2]

[1]SEGES, Pig Research Centre, DK-1609 Copenhagen, Denmark

[2]Center for Quantitative Genetics and Genomics, Aarhus University, 8830 Tjele, Denmark

August 29, 2018

AARHUS UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

gudp

PIG RESEARCH CENTRE

Introduction

- Breeding for reduced feed intake is important to
  1. reduce cost
  2. reduce CO2 emission
- Individual feed records are costly

Haw can we get more phenotypes?

- Solution: Group records of feed intake
- Problem: How to handle drop out animals

PIG RESEARCH
CENTRE

Introduction

- Breeding for reduced feed intake is important to
  1. reduce cost
  2. reduce CO2 emission
- Individual feed records are costly

Haw can we get more phenotypes?

- Solution: Group records of feed intake
- Problem: How to handle drop out animals

PIG RESEARCH
CENTRE

Feed intake of groups

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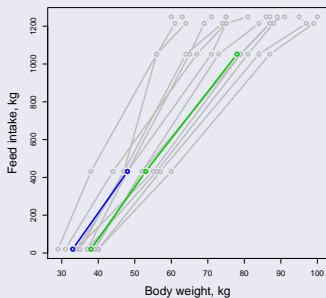individual body weights

Literature

Olson et al. (2006) *J Anim Sci 84:88-92*

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

$$y_{jk} \quad = \sum_{i=1}^{n_{jk}} \boldsymbol{x}_{ijk}^T \boldsymbol{\alpha} + \sum_{m=1}^{d} \beta_m \sum_{i=1}^{n_{jk}} w_{ijk}^m + \sum_{m=0}^{q} \gamma_{jkm} \sum_{i=1}^{n_{jk}} w_{ijk}^m$$

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

$$\begin{pmatrix} \gamma_{j0} \\ \vdots \\ \gamma_{jq} \end{pmatrix} \sim N(\boldsymbol{0}, \boldsymbol{\Gamma} \otimes D), \quad \begin{pmatrix} a_{ij0} \\ \vdots \\ a_{ijs} \end{pmatrix} \sim N(\boldsymbol{0}, \boldsymbol{G} \otimes A),$$

$$\begin{pmatrix} p_{ij0} \\ \vdots \\ p_{ijr} \end{pmatrix} \sim N(\boldsymbol{0}, \boldsymbol{P} \otimes \boldsymbol{I}), \qquad e_{jk} \sim N(0, n_{jk} \sigma_e^2)$$

PIG RESEARCH
CENTRE

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

$$\Delta w'_{s12} G \Delta w_{s12} \quad where \quad \Delta w_{s12} = \left(\begin{array}{c} w_2^0 - w_1^0 \\ \vdots \\ w_2^s - w_1^s \end{array} \right)$$

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

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

PIG RESEARCH
CENTRE

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

$$\Delta \boldsymbol{w}'_{s12} \boldsymbol{G} \Delta \boldsymbol{w}_{s12} \quad where \quad \boldsymbol{\Delta w}_{s12} = \begin{pmatrix} w_2^0 - w_1^0 \\ \vdots \\ w_2^s - w_1^s \end{pmatrix}$$

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

$$BV_{ij} = \frac{\boldsymbol{a}_{ij} \Delta \boldsymbol{w}_{s12}}{w_2 - w_1}$$

PIG RESEARCH
CENTRE

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

$$\Delta \boldsymbol{w}'_{s12} \boldsymbol{G} \Delta \boldsymbol{w}_{s12} \quad where \quad \boldsymbol{\Delta w}_{s12} = \begin{pmatrix} w_2^0 - w_1^0 \\ \vdots \\ w_2^s - w_1^s \end{pmatrix}$$

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

$$BV_{ij} = \frac{\boldsymbol{a}_{ij} \Delta \boldsymbol{w}_{s12}}{w_2 - w_1}$$

PIG RESEARCH CENTRE

Data

	Number
Animals	12567
Groups	1018
Group size	[7;14]
Records	3704
Drop out animals	356

Variance estimates of different models

obs	animals	a11	a12	a22	p11	p12	p22	e
*3704	12567	237	1.25	0.050	699	1.73	0.034	88.1
46732	12599	20	0.11	0.003	66	0.74	0.011	14.5

* *The group record is the sum for the group, and therefore the scale is different*
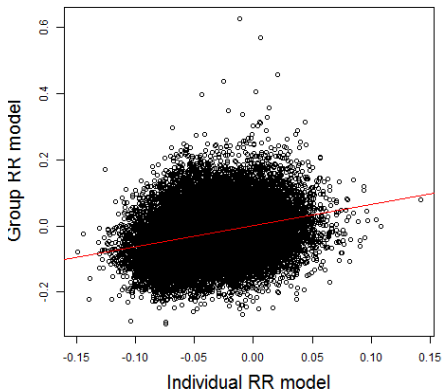
Small groups (<7 animals) were removed

REML estimats by DMU (P. Madsen,2013)

PIG RESEARCH
CENTRE

introduction
○○○

RR models

Group models
○○

Data
○

Results
○●○○○○○

Residual plot, within groups
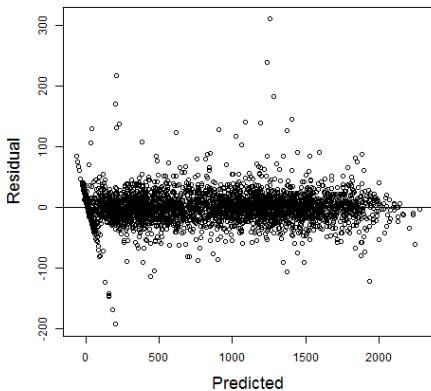
Breeding values of group and individual RR models

Corr=0.29

Discussion

- 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

PIG RESEARCH
CENTRE

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

PIG RESEARCH
CENTRE

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

PIG RESEARCH
CENTRE

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

Thank You !