

Modelling of grouped recorded data for different population structures in pig breeding

Mahmoud Shirali¹, Bjarne Nielsen², Tage Ostersen², Ole Christensen¹, Per Madsen¹, Guosheng Su¹, Just Jensen¹

¹*Center for Quantitative Genetics & Genomics, Aarhus University, Denmark*

²*SEGES, Pig Research Centre, Denmark*



Objective: To investigate the effect of population structure in the data on grouped analysis:

- *Model group records with varying group sizes*
 - *Considering multiple random effects*
 - *Asses genetic parameter and breeding values*
- 1) *Develop methodology based on analysing simulated data*
 - 2) *Applying the method to real data*

Modelling pooled data with varying group size and different random effects

- **Individual record:**

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_c\mathbf{c} + \mathbf{Z}_a\mathbf{a} + \mathbf{e}$$

- **Group record:**

$$\mathbf{T}\mathbf{y} = \mathbf{T}(\mathbf{X}\mathbf{b} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_c\mathbf{c} + \mathbf{Z}_a\mathbf{a} + \mathbf{e})$$

$$\sigma_{a^*}^2 = \mathbf{z}_a^* \mathbf{A} \mathbf{z}_a^{*'} \sigma_a^2 = \sum_{j=1}^{n_g} \mathbf{A}_{jj} \sigma_a^2 + n_g (n_g - 1) \mathbf{A}_{jj'} \sigma_a^2$$

$$\sigma_{l^*}^2 = \mathbf{z}_l^* \mathbf{z}_l^{*'} \sigma_l^2 = \sum_{k=1}^{N_L} n_{lk}^2 \sigma_l^2$$

$$\sigma_{c^*}^2 = \mathbf{z}_c^* \mathbf{z}_c^{*'} \sigma_c^2 = n_g^2 \sigma_c^2$$

$$\sigma_{e^*}^2 = n_g \sigma_e^2$$

Real data

- **Low within pen relationship (Case 1)**
 - 23824 animals for analysis in 709 sections in 15 years
 - Majority 1 littermate per pen.
 - 47868 animals in pedigree
 - Group size : **8 to 14** pigs per pen

- **Large within pen relationship (Case 2)**
 - 100285 pigs with phenotype
 - 112959 pigs with pedigree
 - Group size : **6 to 15** pigs per pen

Simulation of data

- Pedigree & data structure from low and large within pen relationship data are used
- Breeding values
$$\mathbf{a}_i = \frac{1}{2} \mathbf{a}_s + \frac{1}{2} \mathbf{a}_d + m_i$$
- Mendelian sampling term has expected value of 0 and variance of
$$\text{var}(m) = \frac{1}{2} \left[1 - \frac{(F_s + F_d)}{2} \right] \sigma_A^2$$
- No selection
- Taking into account inbreeding
- 10 replicates

	σ_a^2	σ_c^2	σ_l^2	σ_e^2	h^2
simulated	300	70	40	490	0.33

Simulation: genetic parameter estimation

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{c} + \mathbf{S}\mathbf{l} + \mathbf{e}$$

$$\mathbf{y}^* = \mathbf{X}^*\mathbf{b} + \mathbf{Z}^*\mathbf{a} + \mathbf{W}^*\mathbf{c} + \mathbf{S}^*\mathbf{l} + \mathbf{e}^*$$

Scenario	Analysis	σ_a^2	σ_c^2	σ_l^2	σ_e^2
	Simulated	300	70	40	490
Case 1	Individual	298 (18)	71 (5)	44 (11)	490 (13)
	Pooled	241 (60)	70 (26)	76 (91)	495 (254)
Case 2	Individual	298 (15)	71 (2)	40 (3)	492 (6)
	Pooled	302 (43)	72 (7)	31 (16)	491 (75)

Simulation: accuracy of breeding value estimation

Scenario	Individual	Pooled
Case 1	0.67 (0.02)	0.34 (0.03)
Case 2	0.70 (0.01)	0.48 (0.02)

Real data analysis: low within pen

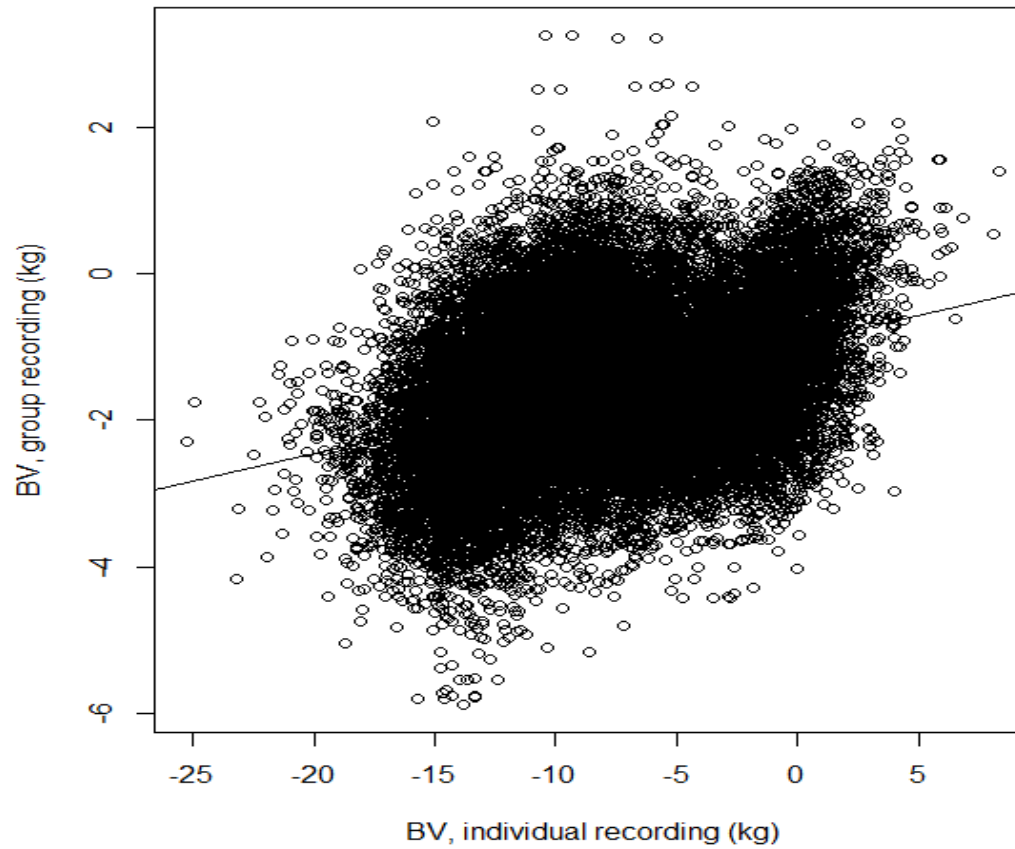
Modelling feed efficiency

$$y_{ij} = YHM_i + b_1 SBW_j + b_2 ADG_j + a_j + c_j + e_{ij}$$

$$y_{ij}^* = YHM_i^* + b_1^* n_j^* + b_2^* SBW_j^* + b_3^* ADG_j^* + a_k^* + e_{ijk}^*$$

Trait	σ_c^2	σ_a^2	σ_e^2	Total	h^2
Individual RFI	6.6	16.7	73.2	96.5	0.17
Sum group RFI	-	18.8	93.0	111.8	0.17

Accuracy: low within relationship



$$\text{Cor}(BV_{\text{individual}}, BV_{\text{group}}) = \mathbf{0.36}$$

Real data analysis: large within pen relationship

Modelling growth

$$y_{ijk} = YHM_i + SEX_j + a_k + c_k + l_k + e_{ijk}$$

$$y_{ijkl}^* = YHM_i^* + SEX_j^* + b_1^* n_k^* + a_l^* + c_l^* + l_l^* + e_{ijkl}^*$$

Trait	Analysis	σ_a^2	σ_c^2	σ_l^2	σ_e^2
ADG	Individual	2691 (113)	694 (18)	424 (19)	4219 (51)
	Pooled	2909 (370)	434 (88)	484 (74)	5661 (864)

*The accuracy of breeding value estimation = **0.65***

Conclusions

- *Developed model for pooled data considers:*
 - *multiple fixed and random effects*
 - *varying group sizes*
- *Developed model can be used for genetic parameter estimation*
 - *With larger standard error*
- *A close genetic relationship within a pen is favourable for breeding value estimation*
- *Genetic parameter estimation with group records on feed intake and growth is feasible*