Double hierarchical generalized linear models for micro-sensitivity in daily feed intake

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Introduction

- Analysis daily feed intake has focused on
    - estimating genetic variation in feed intake curves
    - possibilities to change feed intake curve by selection
    - early feed intake is strongly correlated to lean tissue growth

- Modeling: Two-stage or random regression

- Previous studies:
    - genetic variation do exist along the trajectory
    - opportunity for changing feed intake curve (Huisman et al., 2005; Bermejo et al., 2003)

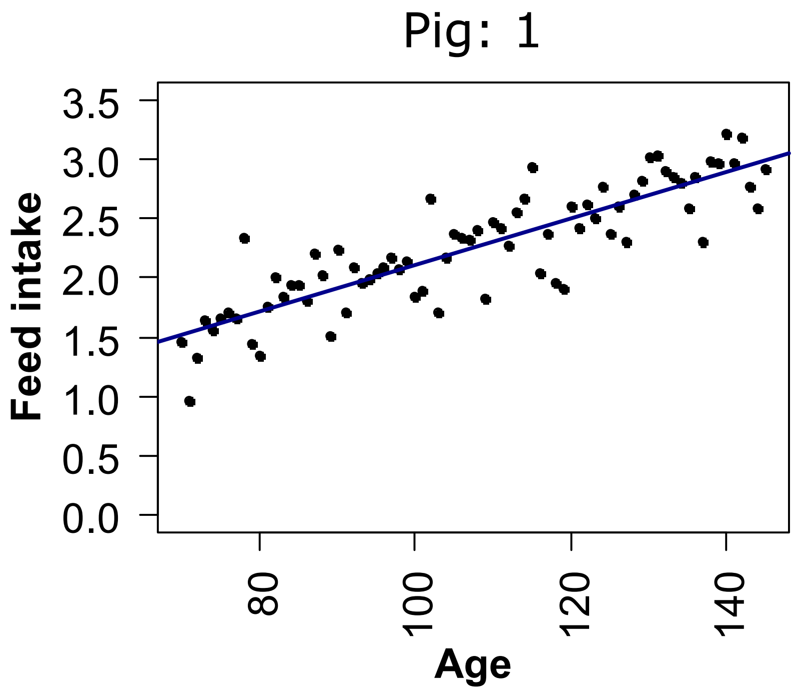
Introduction

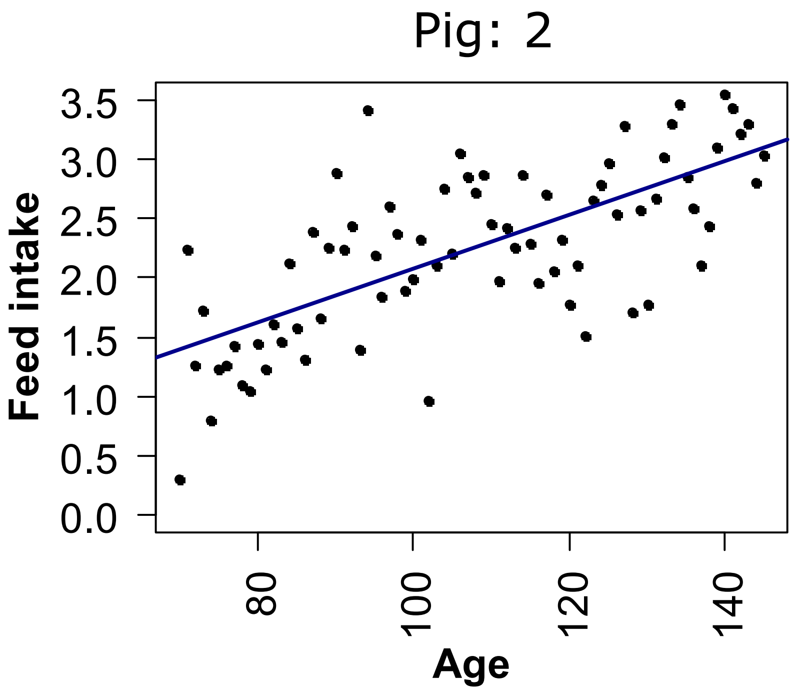
- Pigs and environmental sensitivity
  - Macro-environment
    - Identifiable (e.g., temperature, housing, diets)
    - Linear-reaction norms models (Knap and Su, 2008; Hermesch et al., 2006)
  - Micro-environment
    - Undefined

- Genetic variance of micro-environmental sensitivity can be studied through genetic variance in residual variance (Hill and Mulder, 2010)

- h^2 for residual standard deviation of 0.46 (Eissen, 1999)

Introduction


Pig: 1


Pig: 2

- Residual variability in daily feed intake reflects (Hermesch et al., 2010)
  - maintenance of metabolic homeostasis
  - response to micro-environmental challenges, e.g. air flow
  - Sub-clinical disease (Henryon et al., 2001)

Objective

Estimate breeding values for micro-environmental sensitivity (EBV_d) in daily feed intake, and variance components

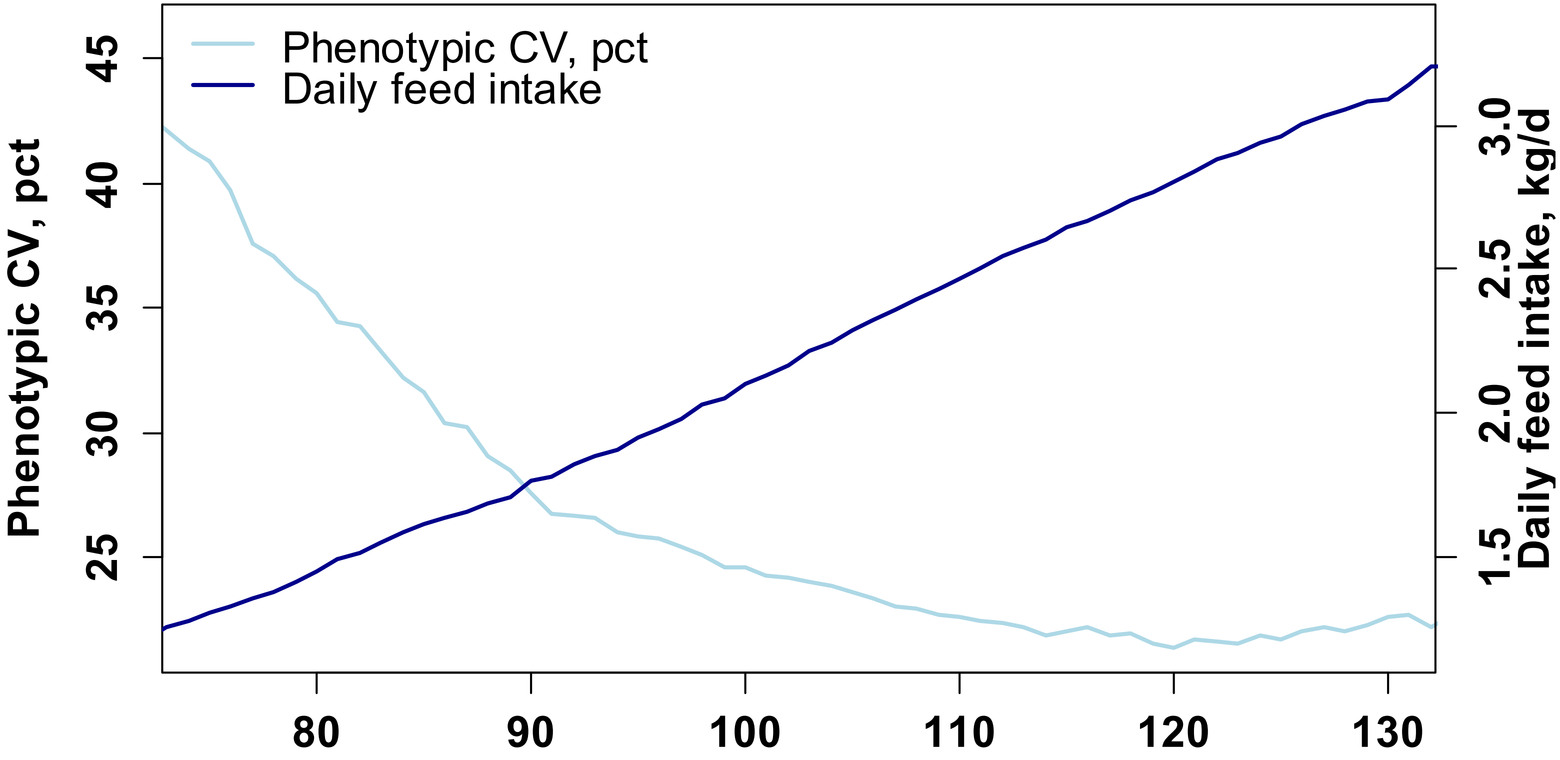
- Double hierarchical generalized linear model (**DHGLM**; Felleki et al., 2012)

Data

- National test-station
  - 2008 - 2012
  - 8,804 Duroc boars
  - 65 records per pig, ranging from 40 to 77
  - 570,901 daily feed intake records after editing

- Pedigree traced back to 1st of Jan 1992
  - 21,128 animals

Data


Phenotypic CV, pct
Daily feed intake
Phenotypic CV, pct
25
30
35
40
45
80
90
100
110
120
130
Daily feed intake, kg/d
1.5
2.0
2.5
3.0

Model

- Mean model

$$Y = X\beta + Z_1pe + Z_2p + Z_3a + e$$

Fixed effects:

- Initial BW
- 2nd order legendre polynomials with barn*year*season (168 levels) specific coefficients

Model

- Mean model

$$\mathbf{Y} = \mathbf{X\beta} + \mathbf{Z_1 pe} + \mathbf{Z_2 p} + \mathbf{Z_3 a} + \mathbf{e}$$

Random effects:

- Legendre polynomials up to 2nd order
  - Pen (571 levels)
  - Non-genetic animal (8804 levels)
  - Additive genetic (21128 levels)
- Residuals

Model

- Mean model

  $$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{pe} + \mathbf{Z}_2\mathbf{p} + \mathbf{Z}_3\mathbf{a} + \mathbf{e}$$

- Residual dispersion model

  $$V(\mathbf{e}) = \exp(\mathbf{X}\boldsymbol{\beta}_d + \mathbf{W}_1\mathbf{p}_d + \mathbf{W}_2\mathbf{a}_d)$$

  Fixed effects:

  - Age classes (77 levels)

Model

- Mean model

  $\mathbf{Y} = \mathbf{X\beta} + \mathbf{Z_1 pe} + \mathbf{Z_2 p} + \mathbf{Z_3 a} + \mathbf{e}$

$$\begin{bmatrix} \mathbf{a} \\ \mathbf{a_d} \end{bmatrix} \sim N\left(\mathbf{0}, \mathbf{G} \otimes \mathbf{A}\right)$$

- Residual dispersion model

  $V(\mathbf{e}) = \exp(\mathbf{X\beta_d} + \mathbf{W_1 p_d} + \mathbf{W_2 a_d})$

  <u>Random effects:</u>

  - Non-genetic animal
  - Additive genetic

Estimation scheme

- IRWLS algorithm (modified from Felleki et al., 2012)
  1) Initialize residual variance weights

     $\mathbf{y} \sim N(\mathbf{X\beta} + \mathbf{Z_1pe} + \mathbf{Z_2p} + \mathbf{Z_3a}, \mathbf{I}\sigma^2/\mathbf{w})$
  2) Compute $\mathbf{y}_d = \mathbf{e}^2/(1-\mathbf{h})$ and $\mathbf{w}_d = (1-\mathbf{h})/2$
  3) Fit a Gamma GLMM with link log and weights $(1-\mathbf{h})/2$ to $\mathbf{y}_d$
  4) Compute $\mathbf{w} = \text{diag}(E(\mathbf{y}_d)^{-1})$
  5) Run a bivariate normal-gamma model for $\mathbf{y}$ and $\mathbf{y}_d$ estimating
  6) Update $\mathbf{y}_d$ and residual variance weights ($\mathbf{w}$ and $\mathbf{w}_d$) in each iteration
  7) Repeat steps 5 and 6 until convergence

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Model selection

- 10 fold cross validation
  - Exclude randomly 10 observations per pig
  - Repeated 10 times

- Measures of fit
  - Mean square prediction error

$$MSPE = \frac{1}{n}\sum_{i=1}^{n}\left(y_i - \hat{y}_i\right)^2$$

  - Cor(observed, predicted)

Results

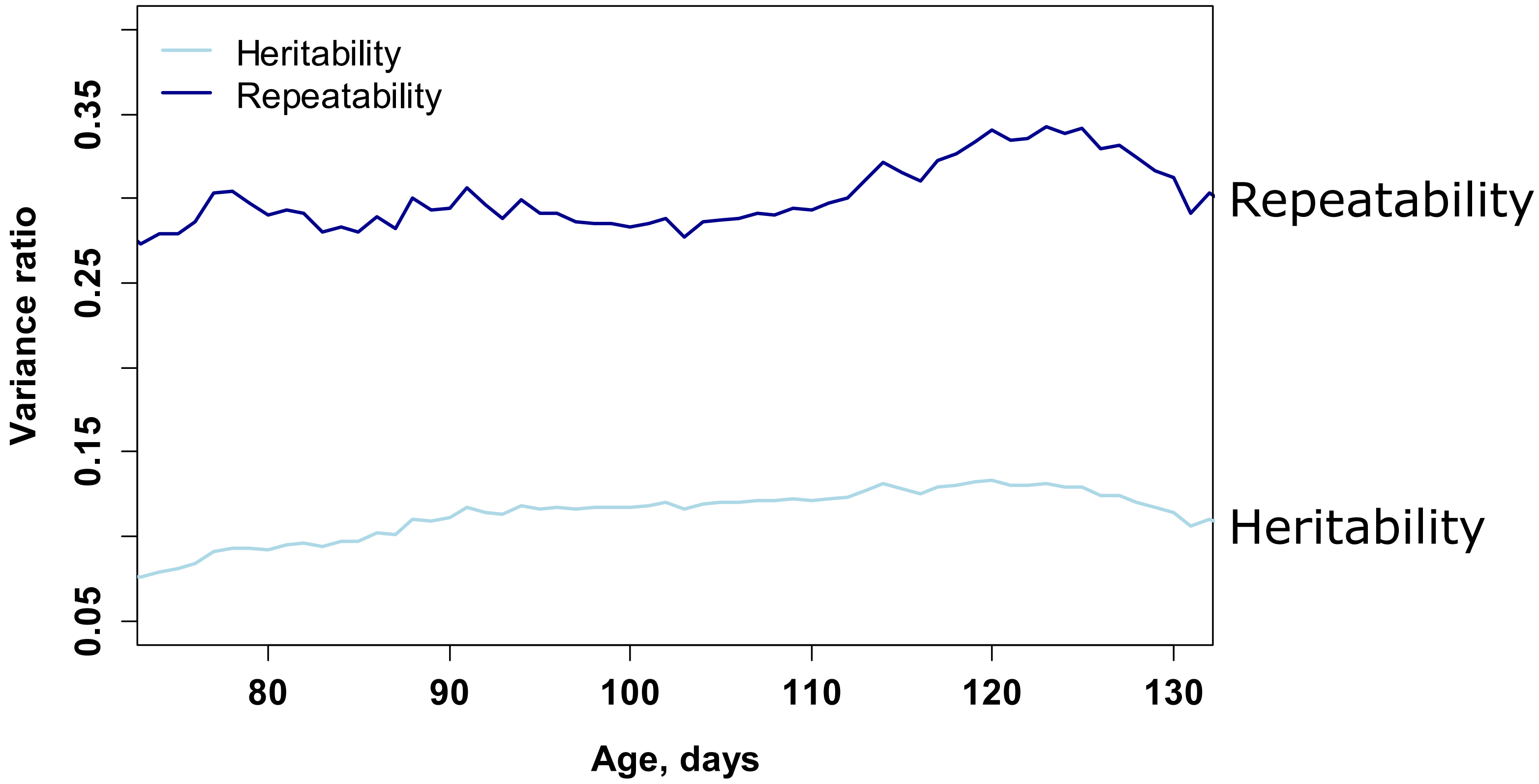
Model	MSPE	Correlation
Leg(1, 1)	0.2808 (0.002)	0.7858 (0.001)
Leg(2, 2)	0.2703 (0.002)	0.7975 (0.001)
Leg(1, 1, 1)	0.2797 (0.002)	0.7898 (0.001)
Leg(2, 2, 2)	0.2684 (0.002)	0.8008 (0.001)
Genetically structured		
Leg(1, 1)	0.2758 (0.002)	0.7977 (0.001)
Leg(Ø, 2, 2)	0.2683 (0.002)	0.8036 (0.001)
Leg(1, 1, 1)	0.2757 (0.002)	0.7978 (0.001)
Leg(2, 2, 2)	0.2633 (0.002)	0.8080 (0.001)

Results

Model		**EBV_I**	**EBV_L**	**EBV_d**
DHGLM	EBV_I	**0.038 (0.003)**		
	EBV_L	0.47 (0.04)	**0.033 (0.002)**	
	EBV_d	0.51 (0.03)	0.92 (0.01)	**0.023 (0.001)**
DHGLM sqrt-trans	EBV_I	**0.0049 (0.0004)**		
	EBV_L	-0.38 (0.04)	**0.0032 (0.0002)**	
	EBV_d	-0.43 (0.03)	0.92 (0.01)	**0.024 (0.0008)**

- Genetic coefficient of variation ~ 15%

Heritability of feed intake



Genetic correlations

	70	80	90	100	110	120	130	140
70	**0.08**							
80	0.97	**0.08**						
90	0.89	0.97	**0.10**					
100	0.78	0.90	0.98	**0.10**				
110	0.65	0.81	0.92	0.98	**0.11**			
120	0.53	0.71	0.86	0.95	0.99	**0.12**		
130	0.43	0.62	0.79	0.90	0.97	0.99	**0.10**	
140	0.34	0.55	0.73	0.86	0.94	0.98	0.99	**0.08**

Results

- Pearson moment-correlations

EBVs for traits	EBV_d
Daily gain (30 to 100)	0.34
Meat percentage	-0.12
Feed conversion ratio	0.18

- Genetically correlated with fast, but relatively fat growing pigs
- Implications for feed efficiency?

Conclusion

- DHGLM RR-model was developed
- Heritability of FI: 0.08 - 0.12 (mean)
- Genetic variance in micro-environmental sensitivity was estimable
    - Genetic coefficient of variation of 15%
    - EBV_d was positive strongly correlated to the mean trend
    - EBV_d was correlated to production traits

- How does micro-environmental sensitivity correlate to macro-environmental sensitivity?