Statistical models to increase disease resilience and uniformity in animal production

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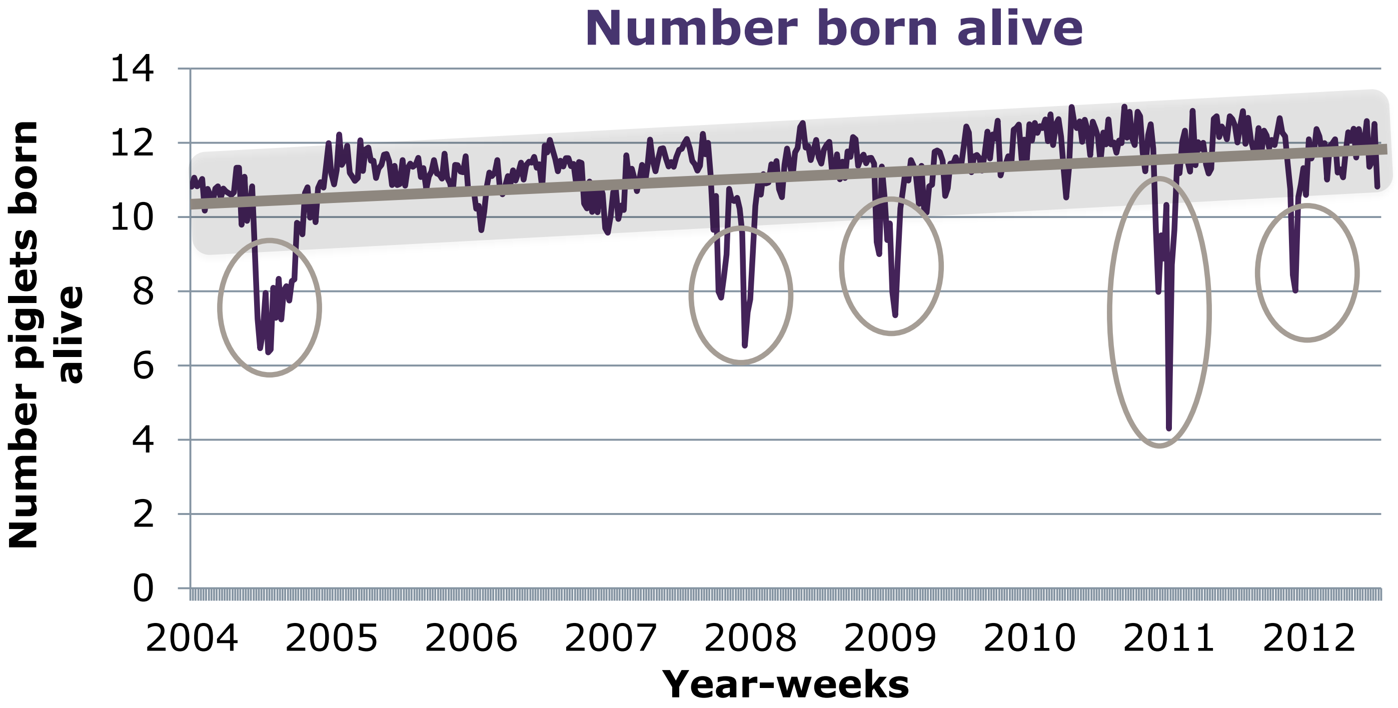
Increasing disease resilience is challenging

- Genetic component on resistance
    - Ability of the animal to combat diseases
- Genetic component on tolerance
    - Ability of animal to minimize negative effects of disease and keep reduction in production minimal
- Both require data on amount of pathogen
    - Disease data is scarce
    - Data on pathogen burden even more scarce

Can we use fluctuations in production? We can detect outbreaks.



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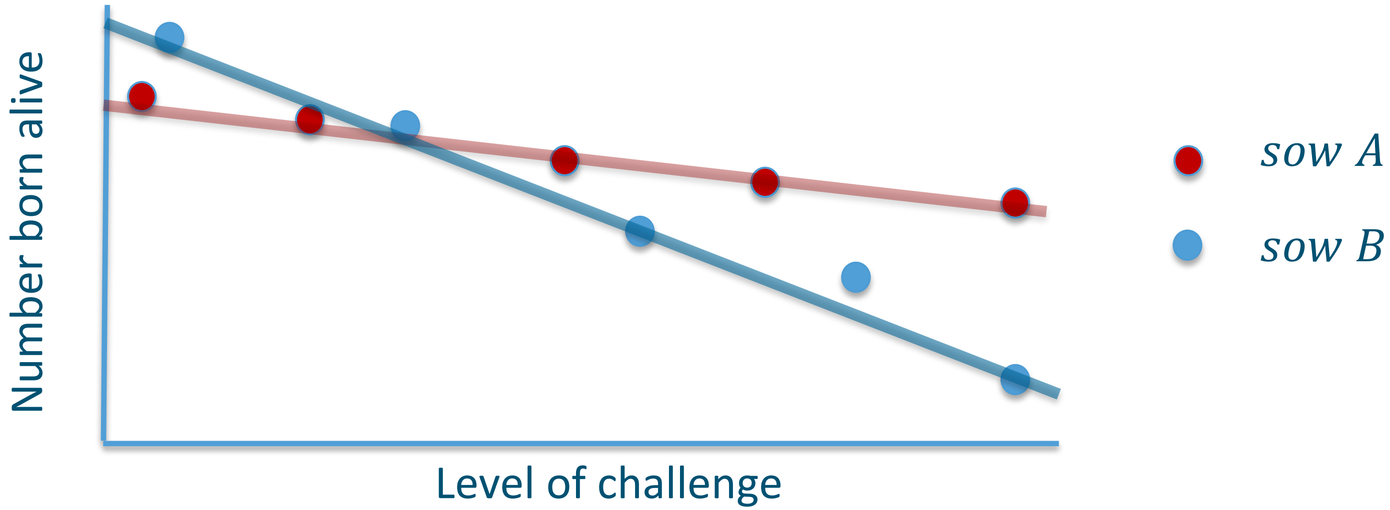
Rashidi et al. 2014

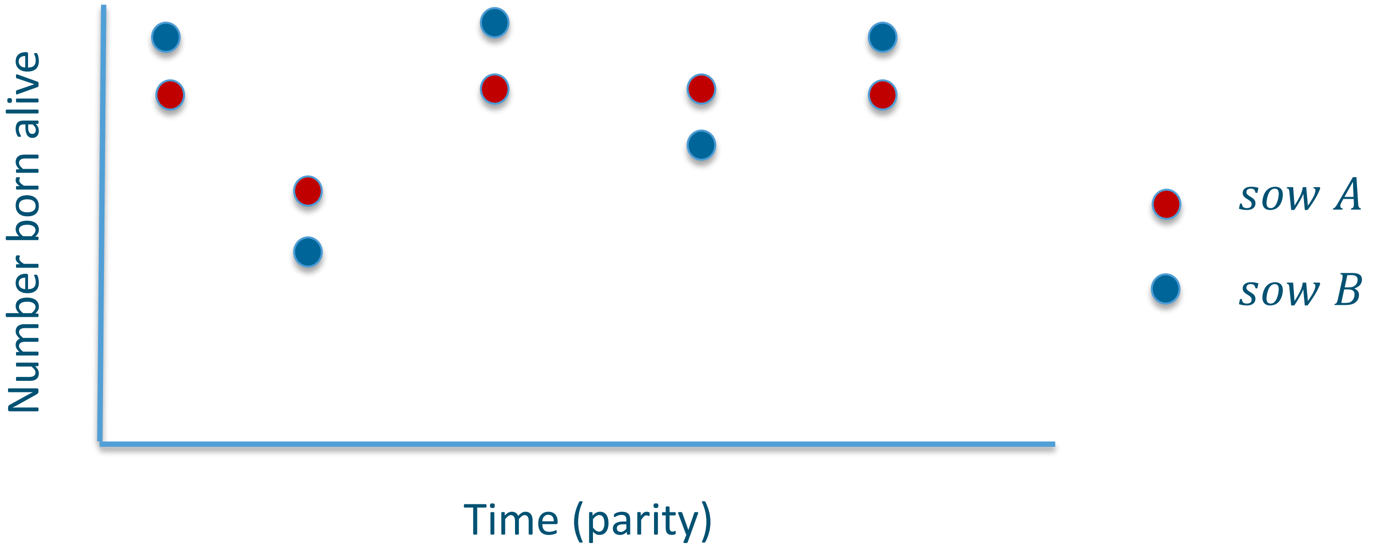
Variation related to level of challenge



- Reaction norm model

$$y = fixed\ effects + a_{intercept} + a_{slope}CL + e$$

Variation over time



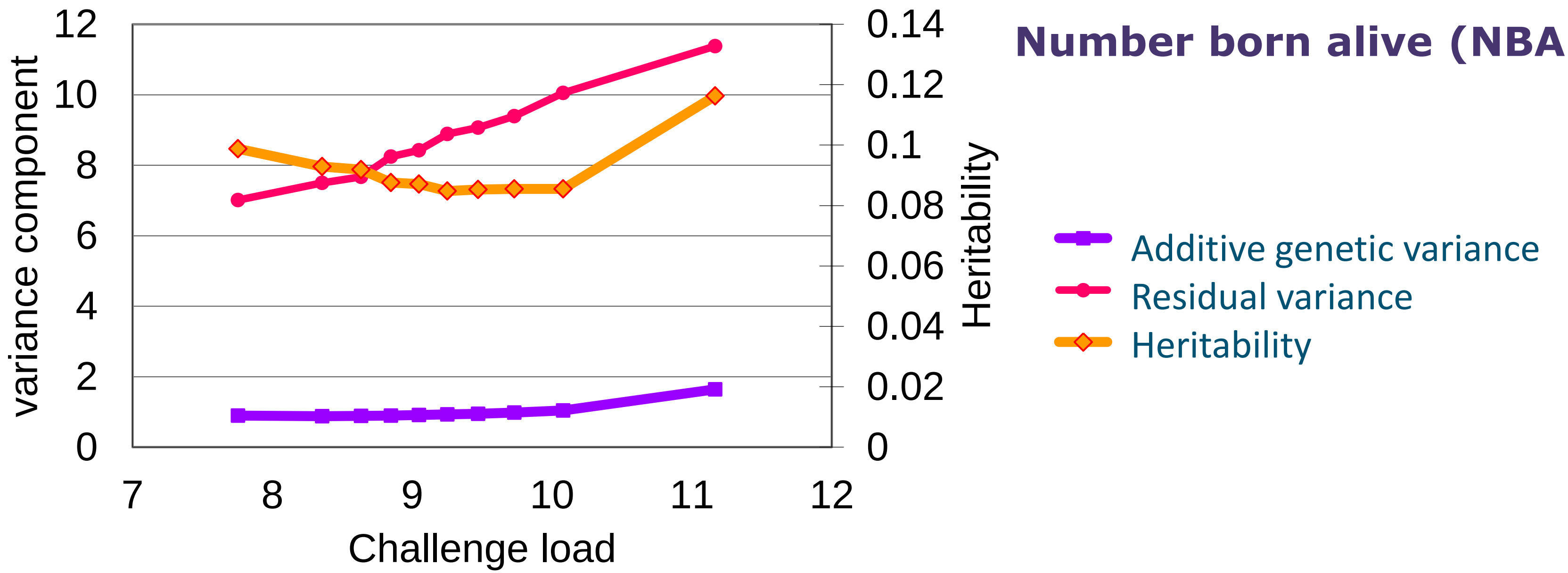
- Uniformity model (DHGLM)

$$y = fixed\ effects + a_{mean} + e \longleftarrow Ve = \exp(fixed + a_{variance})$$

Objectives

- To quantify genetic variation for litter size:
    - in response to (disease) challenges in pigs
    - in uniformity
- To investigate response to selection in disease resistance and tolerance using:
    - reaction norm model
    - uniformity model

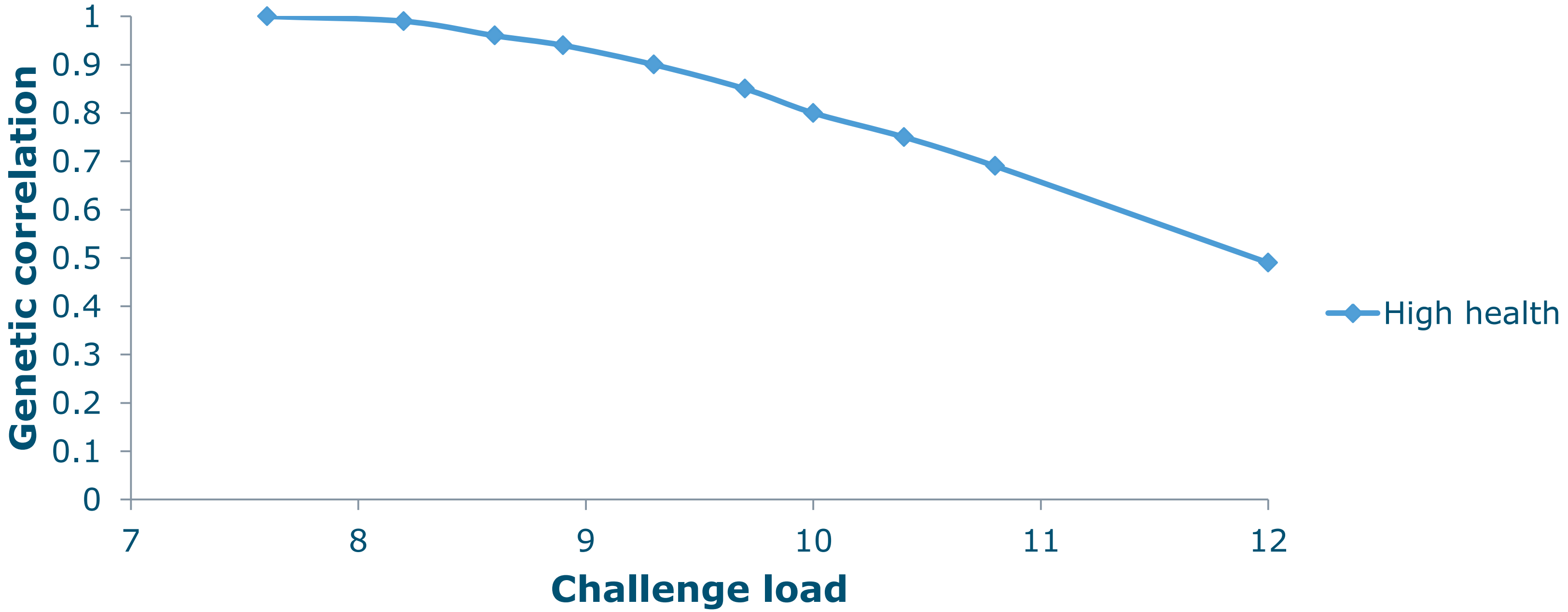
Reaction norm model: Variance components with increasing challenge load



Number born alive (NBA)

Herrero-Medrano et al., 2015

Selection in a different environment



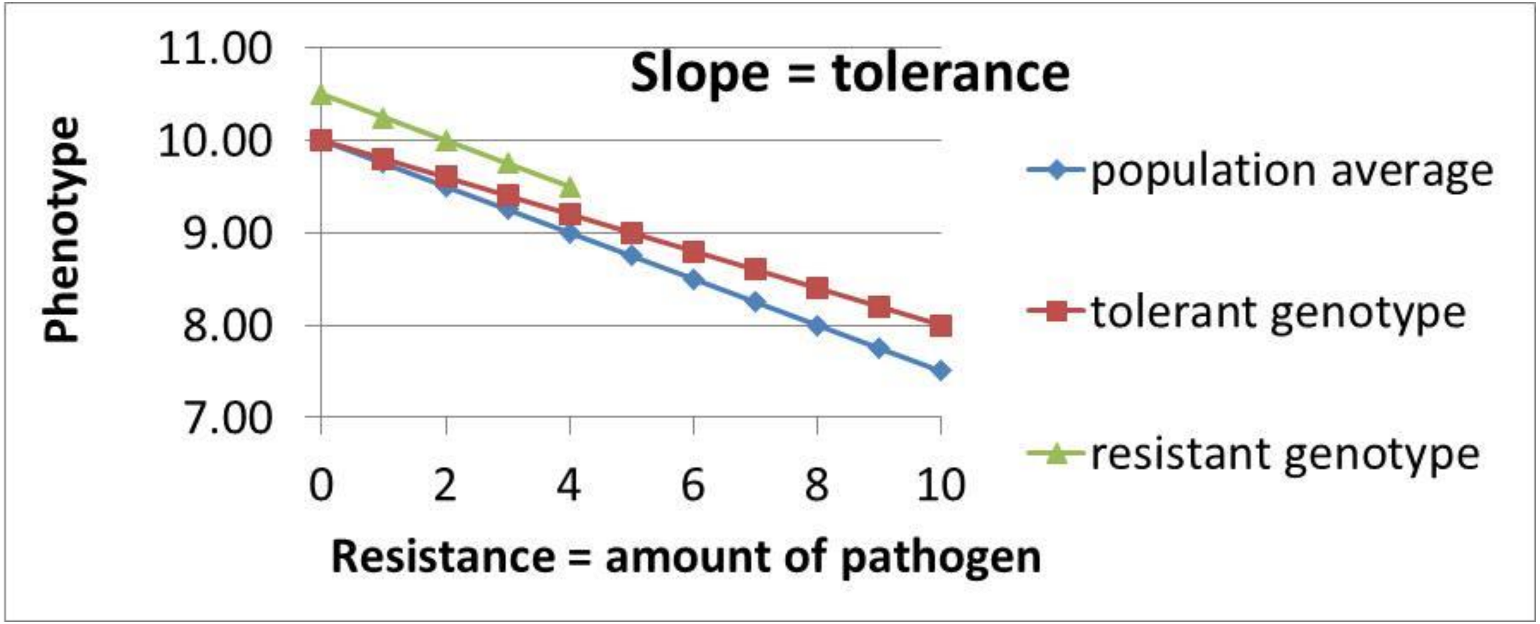
Herrero-Medrano et al., 2015

Genetic variance in uniformity

	Genetic variance Ve exponential model	Genetic coefficient of variation Ve
Number born alive	0.16	0.40
Total number born	0.03	0.17

Genetic variance in uniformity especially for number born alive

Simulation



- Breeding values for level (A_{level}), resistance (A_{res}) and tolerance (A_{tol})

Simulation

- Disease outbreaks: 10% of the time periods
- Endemic diseases: 10% incidence
- 100 sires, 100 half-sib offspring
- 10 observations/animal
- Average reduction in phenotype due to disease: 1 phenotypic standard deviation

Estimation of breeding values and response to selection

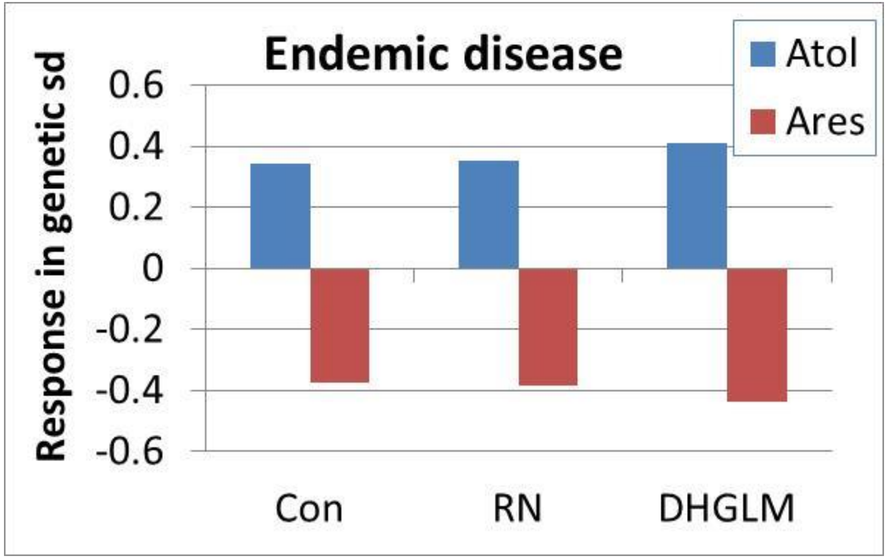
- Conventional model (Con)
- Reaction norm model using herd-period average as covariate (RN)
- Uniformity model (DHGLM)
- EBV for level, slope and variance
- Correlations among EBV and with true breeding values
- Selection index to predict response to selection
    - $H = A_{level} + A_{tol} - A_{res}$

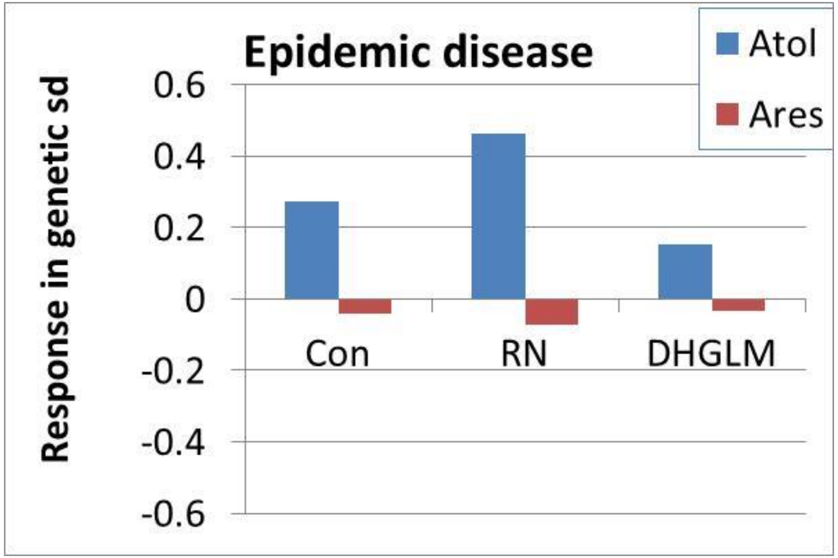
Correlations EBV TBV sires

	Endemic disease		Epidemic disease	
	A_{tol}	A_{res}	A_{tol}	A_{res}
EBV mean conventional	0.32	-0.35	0.26	-0.04
EBV slope RN	-0.40	0.40	-0.93	0.15
EBV variance DHGLM	-0.62	0.60	-0.05	0.12

EBV variance better suitable for endemic diseases and EBV slope better suitable for epidemic diseases

Response to selection





- Response in resistance or tolerance depends on type of disease
- RN model very suitable for epidemic diseases
- Uniformity model (=DHGLM) suitable for endemic diseases

Conclusion

- We found substantial genetic variance:
  - in resilience to disease outbreaks, e.g. due to PRRS
  - in uniformity of litter size, especially for number born alive

- Reaction norm model is suitable for epidemic diseases
- Uniformity model is more suitable for endemic diseases

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Topigs Norsvin
PROGRESS IN PIGS

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Course GxE, uniformity and stability

- 19-23 October 2015
- Wageningen, The Netherlands
- Teachers
  - Piter Bijma
  - Philip Gienapp
  - Marcos Malosetti
  - Han Mulder

- http://www.wageningenur.nl/nl/activiteit/Indepth-Course-Genotype-by-environment-interaction-uniformity-and-stability.htm

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