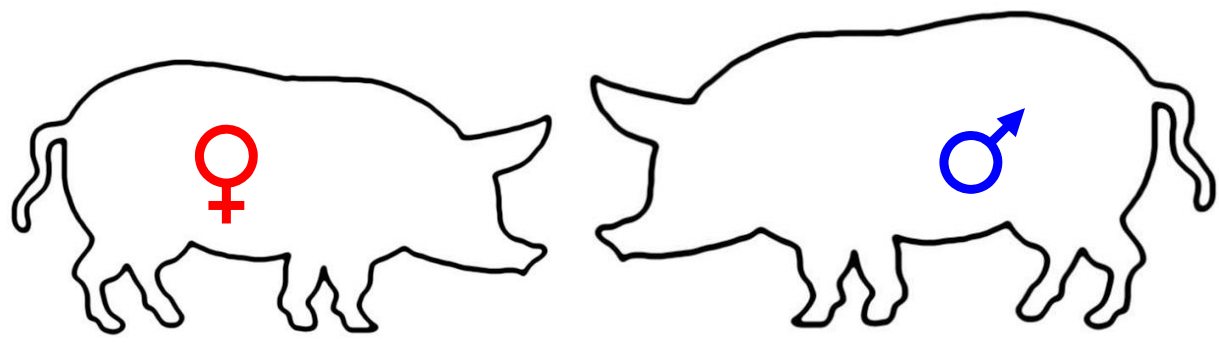


Statistical tools to detect genetic variation for a sex dimorphism in piglet birth weight

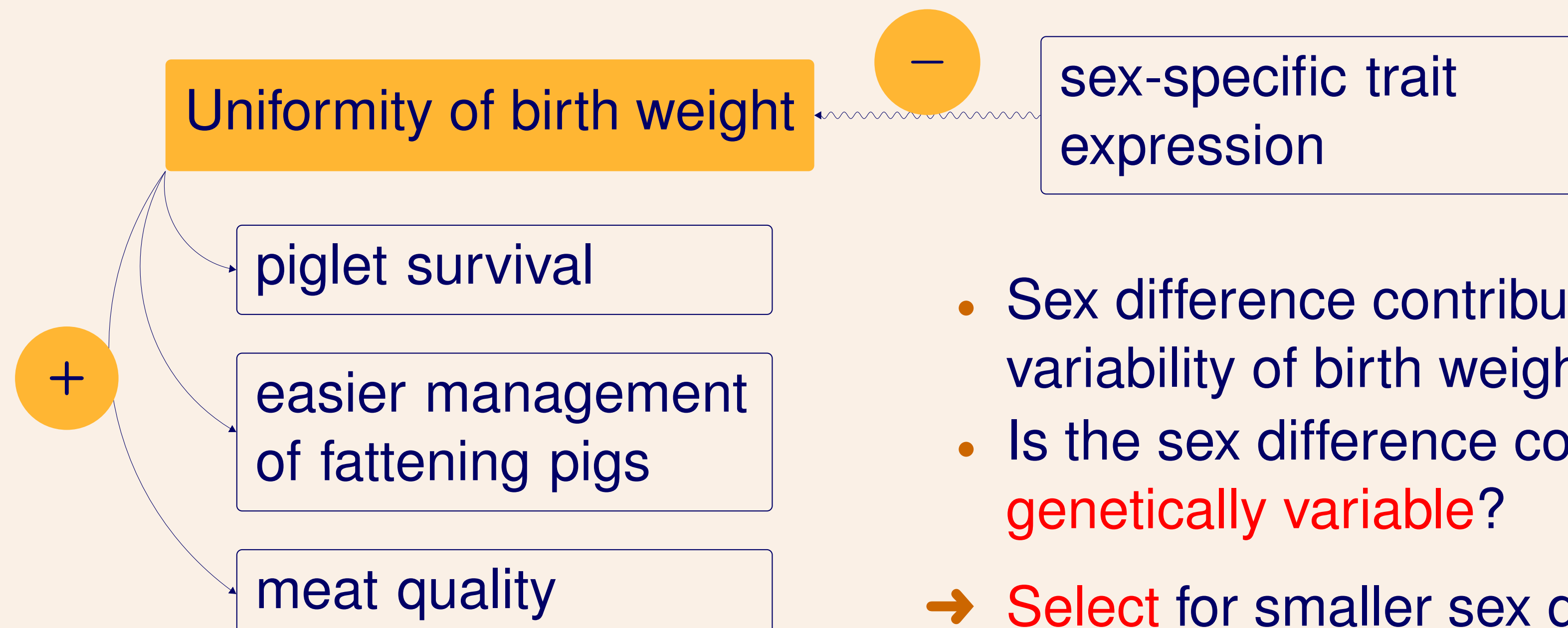
Dörte Wittenburg, Friedrich Teuscher, Norbert Reinsch

Motivation and Problem

The old story...



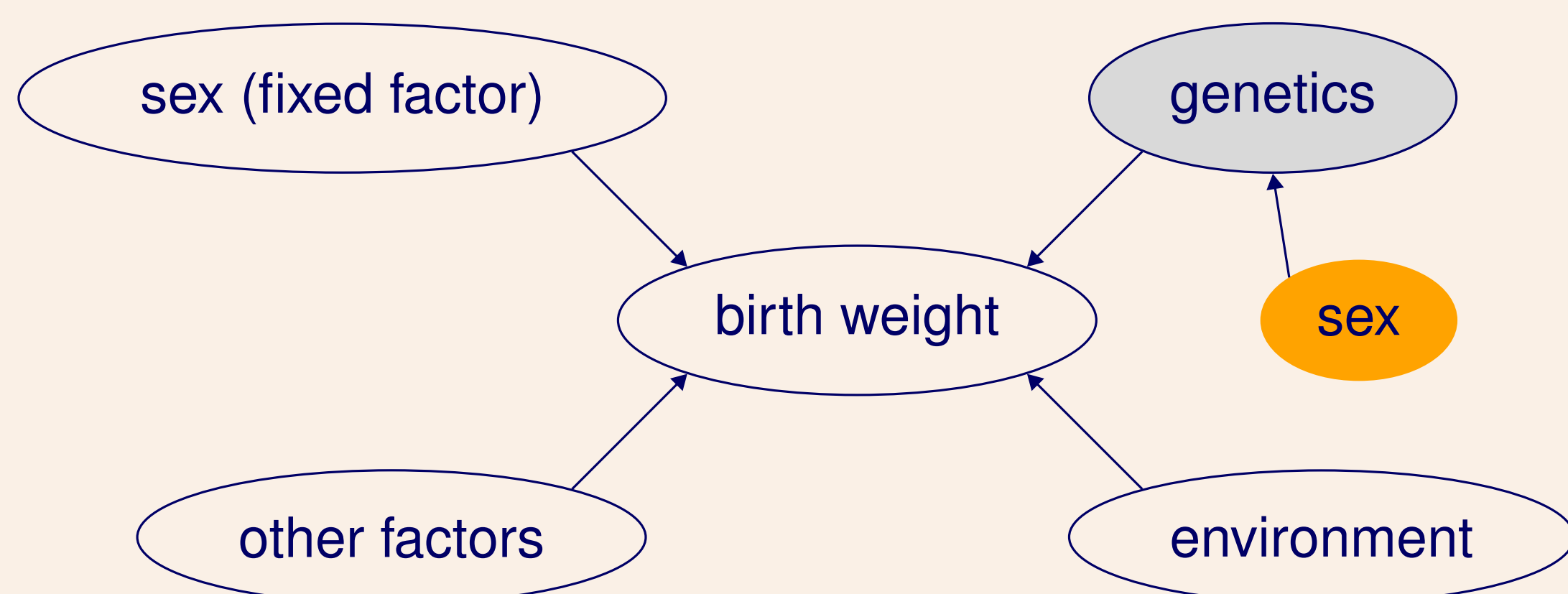
... male piglets are heavier and more variable at birth than females.



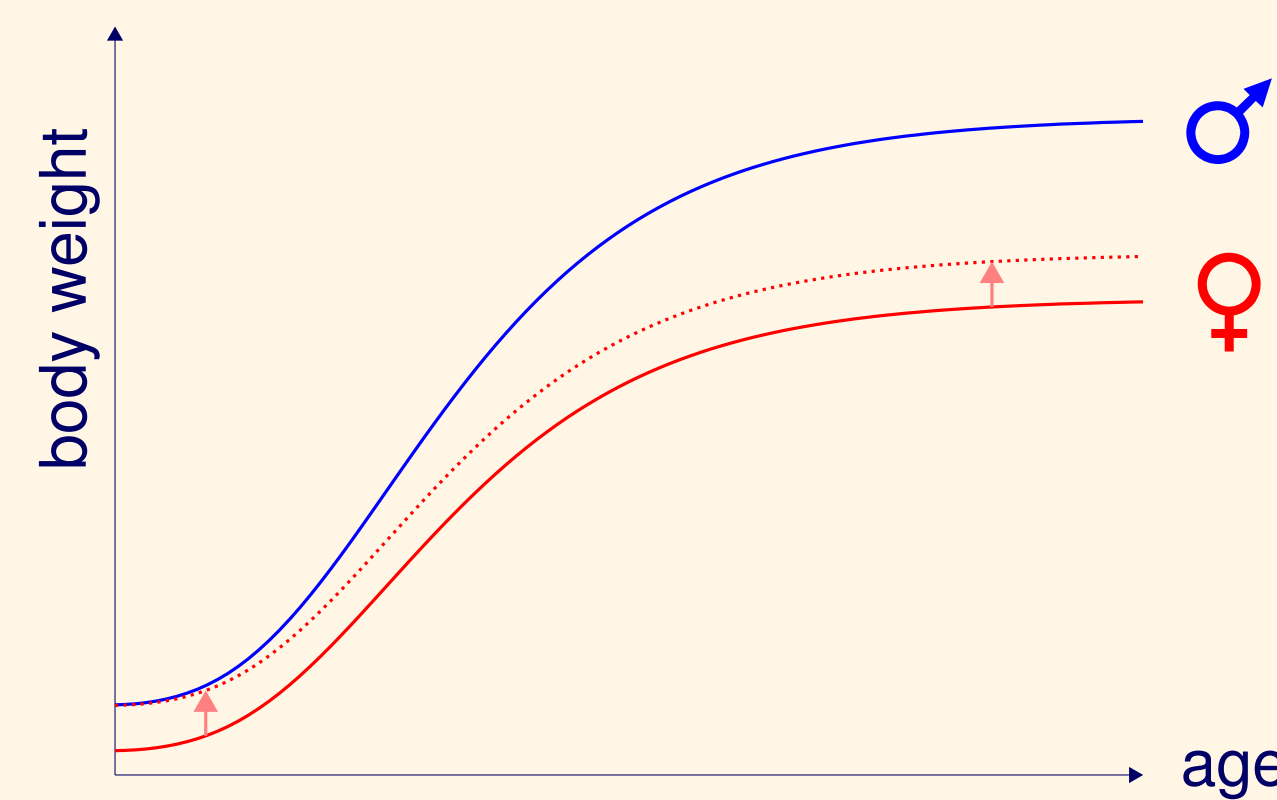
- Sex difference contributes to within-litter variability of birth weight.
- Is the sex difference constant or **genetically variable**?
- **Select** for smaller sex difference (i.e. smaller within-litter variance).

Approach

Distinct breeding values for male and female birth weight. Are they different?



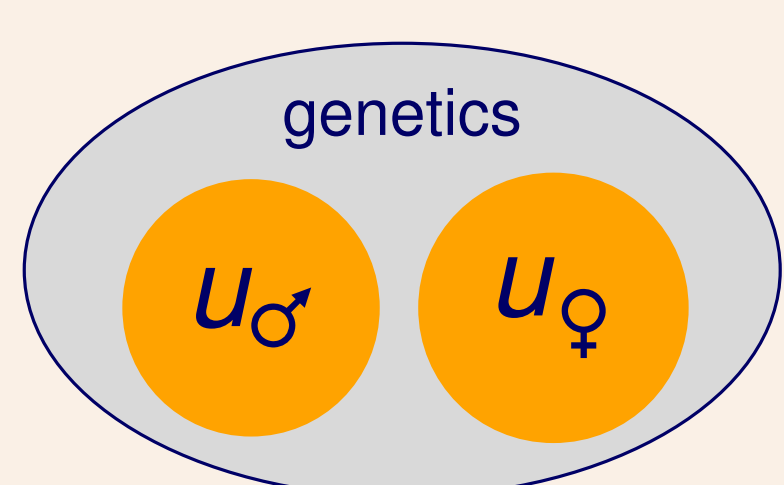
Conclusions



- Sex difference in birth weight is genetically variable.
- Y-chromosome is involved.
- Heritability is small (3–4 %).
- Breeding to increase uniformity at birth may reduce sex difference in later ages.

Theory

- Animal model with genetic effect differing between sexes



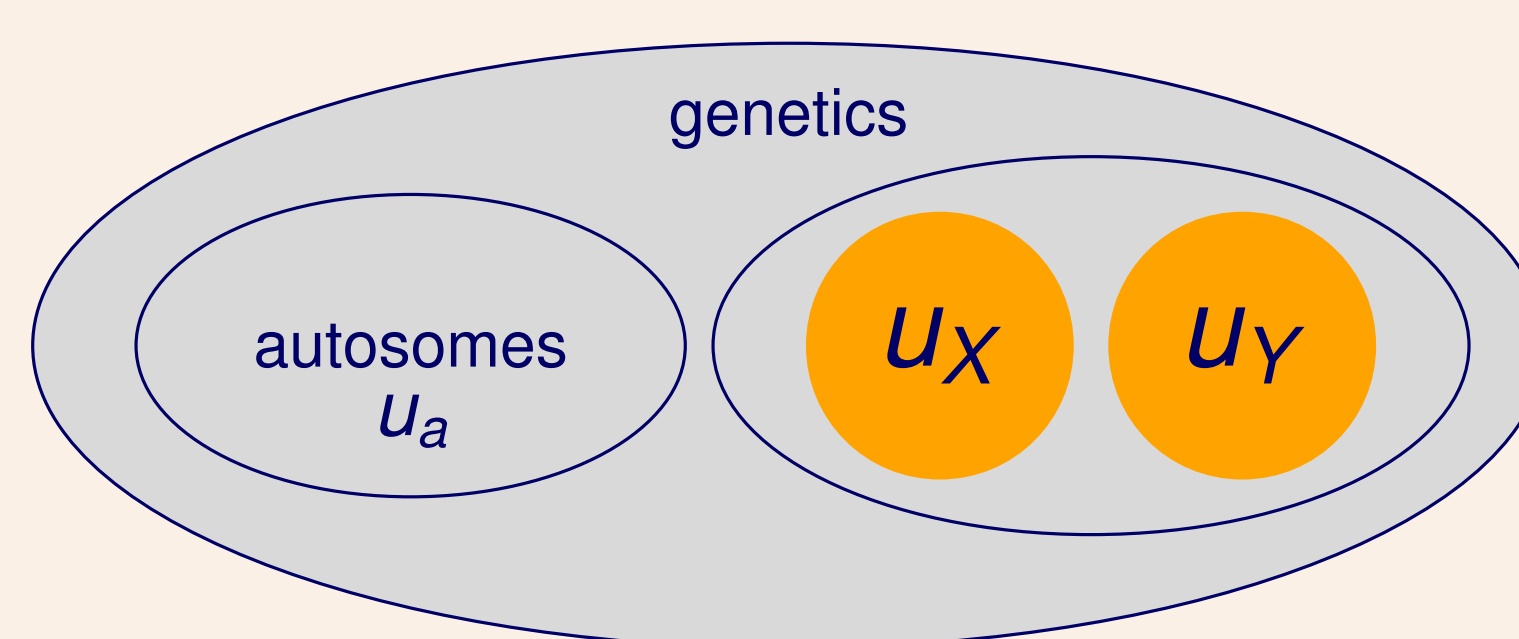
$$\text{Cov}(\mathbf{u}_\sigma, \mathbf{u}_\varphi) = \mathbf{A}\sigma_{\sigma,\varphi}$$

$$\sigma_{\sigma,\varphi} = \rho \sigma_\sigma \sigma_\varphi$$

$$H_0: \rho = 1 \text{ and } \sigma_\sigma^2 = \sigma_\varphi^2$$

$\mathbf{A}$: numerator relationship matrix
 $\mathbf{S}$: relationship for X-chromosomal loci

- Pedigree approach with effect of sex-linked genes



$$u_\sigma = u_a + u_X + u_Y$$

$$u_\varphi = u_a + u_X$$

$$\text{Var}(\mathbf{u}_X) = \mathbf{S}\sigma_X^2, \text{Var}(\mathbf{u}_Y) = \mathbf{I}\sigma_Y^2$$

$$H_0^{(1)}: \sigma_Y^2 = 0 \text{ or } H_0^{(2)}: \sigma_X^2 = 0$$

Measure of heritability

- Difference in genetic effect $u_\sigma - u_\varphi$
- Difference in phenotype $T_\sigma - T_\varphi$

→ Heritability

$$h^2 = \frac{\text{Var}(u_\sigma - u_\varphi)}{\text{Var}(T_\sigma - T_\varphi)}$$

Data

- Landrace (LR): 57 647 piglets
- Large White (LW): 45 619 piglets
- Pedigree with ≤ 11 generations

Null distribution of the test statistic was approximated as a mixture of χ^2 -distributions.

Results

- Genetic correlation ρ was close to one.
- Breeding values significantly differed in line LR ($p = 0.004$) but not in LW ($p = 0.099$).
- Y-chromosomal effect was significantly present in line LR ($p < 0.001$) and also in combination of model ① & ② ($p = 0.022$).

