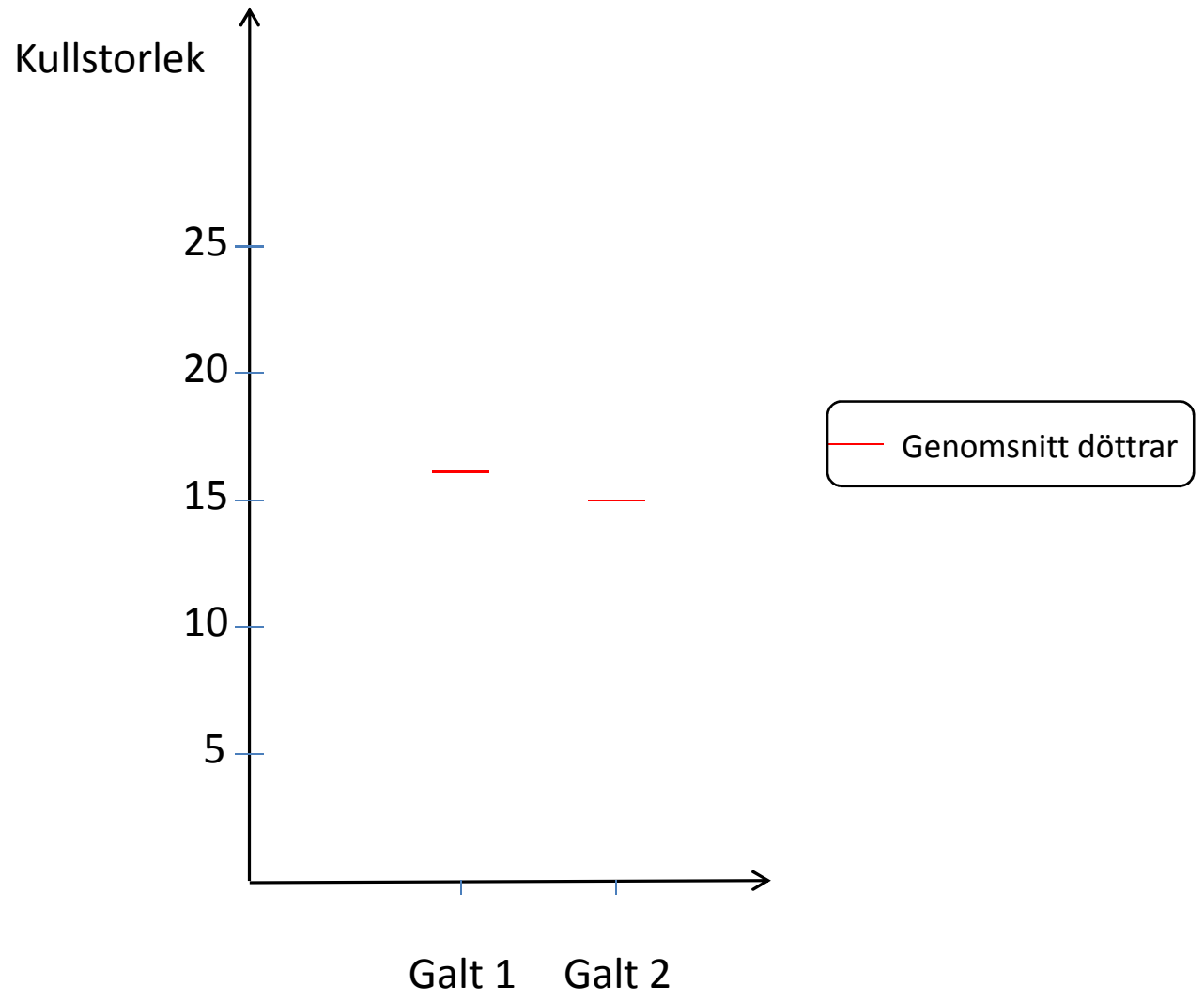
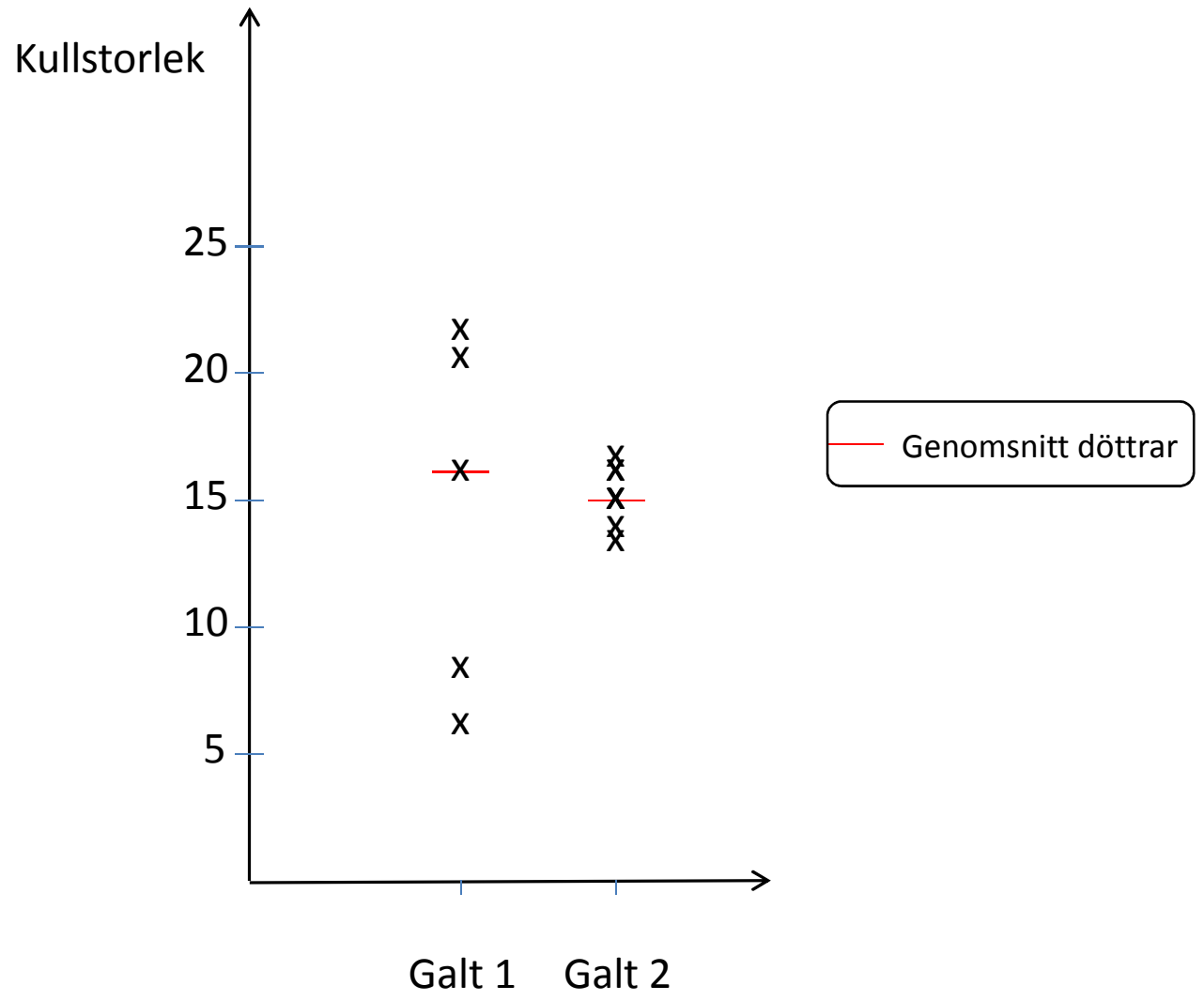


Genetisk variation i heterogen varians

Lars Rönnegård

SLU, Uppsala



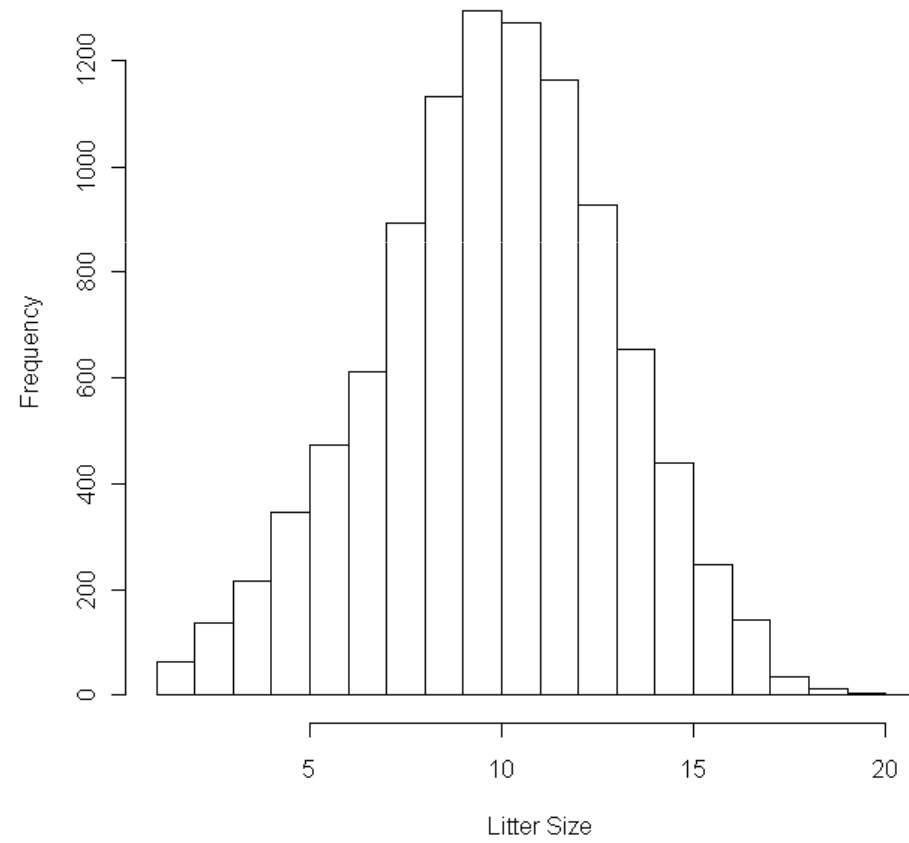


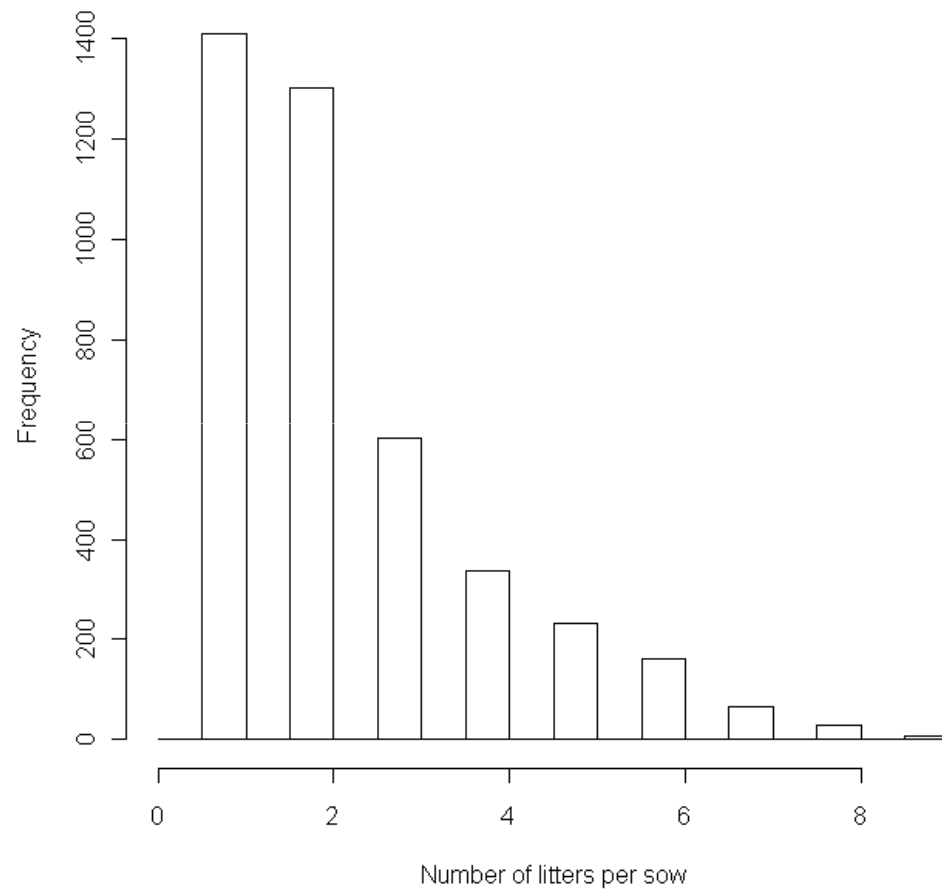
Data: kullstorlek hos gris

Data from Danish Pig Production.

- Pig litter size from 4,149 sows
 - mean litter size 10.3
- The data includes 10,060 records from these 4,149 sows in 82 herds.
- Fixed effects: herd, season, type of insemination, parity

Histogram of studied trait





Modell

$$y = \mathbf{X}\beta + \mathbf{Z}a + \mathbf{W}u + e$$

$$a \sim N(0, \mathbf{A}\sigma_a^2) \quad \text{Breeding values}$$

$$u \sim N(0, \mathbf{I}\sigma_u^2) \quad \text{Permanent environmental effect}$$

Modell

$$y = \mathbf{X}\beta + \mathbf{Z}a + \mathbf{W}u + e$$

$$a \sim N(0, \mathbf{A}\sigma_a^2) \quad \text{Breeding values}$$

$$u \sim N(0, \mathbf{I}\sigma_u^2) \quad \text{Permanent environmental effect}$$

$$V(e) = \exp(\mathbf{X}_d\beta_d + \mathbf{Z}a_d + \mathbf{W}u_d)$$

$$a_d \sim N(0, \mathbf{A}\sigma_{a_d}^2) \quad \text{Breeding values controlling the residual variance}$$

$$u_d \sim N(0, \mathbf{I}\sigma_{u_d}^2)$$

Resultat

Table 1 - Comparison between DHGLM estimates and the estimates obtained by Sorensen & Waagepetersen (2003 Genetics)

	Mean model		Model for residual variance					
	σ_a^2	σ_p^2	Fixed effects			Variances		ρ
			b_0	b_{ins}	b_{par}	$\sigma_{a_d}^2$	$\sigma_{p_d}^2$	
DHGLM	1.36	0.44	1.72	-0.17	0.32	0.09	0.06	(-0.52)
S&W 2003	1.62	0.60	1.77	-0.17	0.35	0.09	0.06	-0.62

Resultat

Table 1 - Comparison between DHGLM estimates and the estimates obtained by Sorensen & Waagepetersen (2003 Genetics)

	Mean model		Model for residual variance					
			Fixed effects			Variances		
	σ_a^2	σ_p^2	b_0	b_{ins}	b_{par}	$\sigma_{a_d}^2$	$\sigma_{p_d}^2$	ρ
DHGLM	1.36	0.44	1.72	-0.17	0.32	0.09	0.06	(-0.52)
S&W 2003	1.62	0.60	1.77	-0.17	0.35	0.09	0.06	-0.62

$$\sigma_{a_d} = 0.30$$

Öka avelsvärden a_d med 1 SD
 => Ökar residualvariansen med 30%

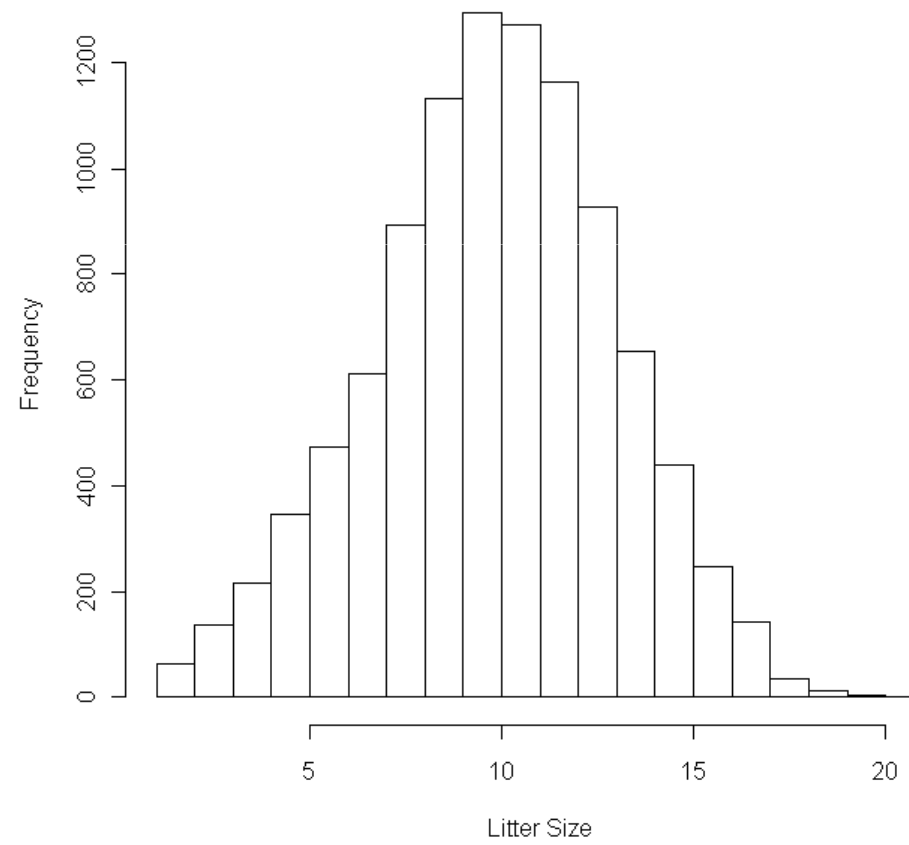
Resultat

Table 1 - Comparison between DHGLM estimates and the estimates obtained by Sorensen & Waagepetersen (2003 Genetics)

	Model for residual variance							
	Mean model		Fixed effects			Variances		
	σ_a^2	σ_p^2	b_0	b_{ins}	b_{par}	$\sigma_{a_d}^2$	$\sigma_{p_d}^2$	ρ
DHGLM	1.36	0.44	1.72	-0.17	0.32	0.09	0.06	(-0.52)
S&W 2003	1.62	0.60	1.77	-0.17	0.35	0.09	0.06	-0.62

Om vi bara selekterar på vanligt avelsvärde så minskar residualvariansen.

Histogram of studied trait

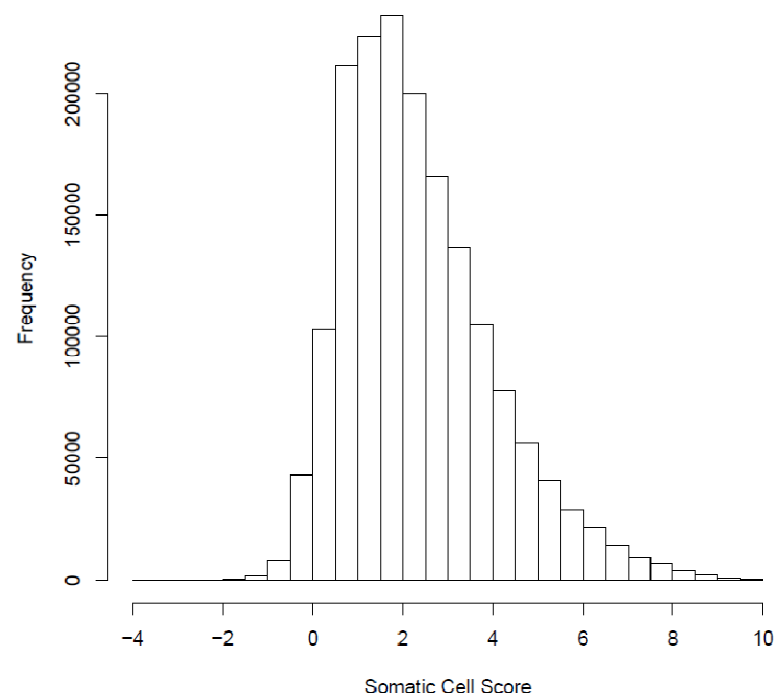


Dairy Data

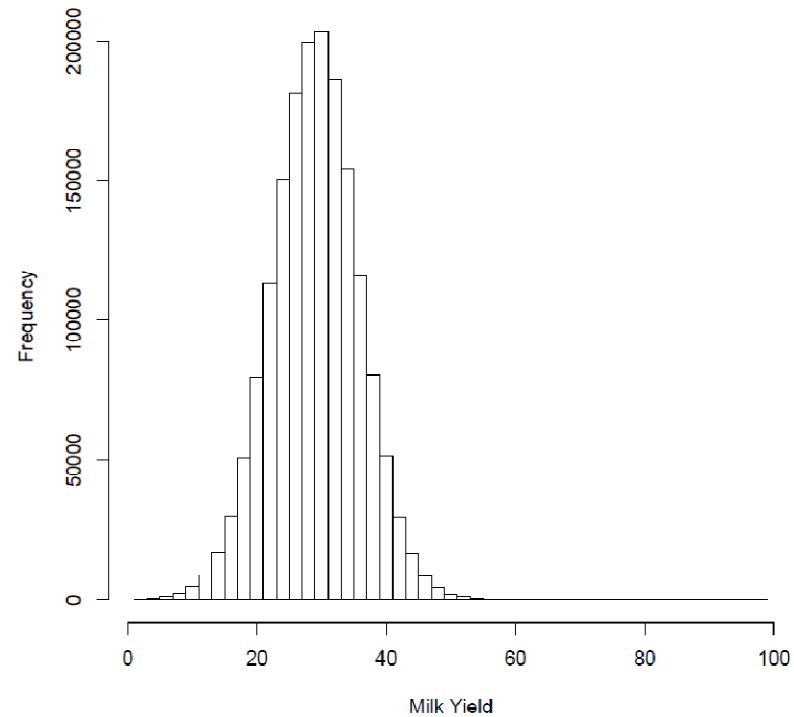
- Swedish Holstein
- Records: 1,693,154
- Animals: 177,411
- Years: 2002-2009

Histograms of studied traits

Histogram of Somatic Cell Score



Histogram of Milk Yield



Diskussion

- Ska man se till att data är normalfördelat?
Eller ska man helt enkelt analysera den egenskap man selekterar på?
- Svårt att få bra skattningar om man har få upprepade mätningar per individ.
- Hur viktar man de två olika avelsvärdena i ett avelsprogram?

Tack!

www.larsronnegard.se