



Universidad
Zaragoza



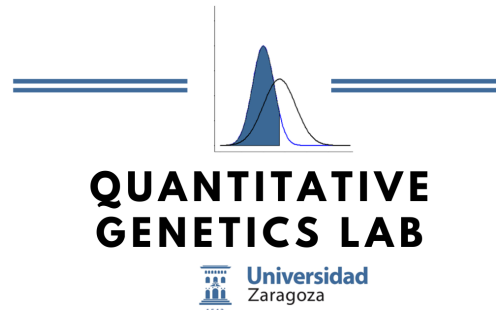
Facultad de Veterinaria
Universidad Zaragoza



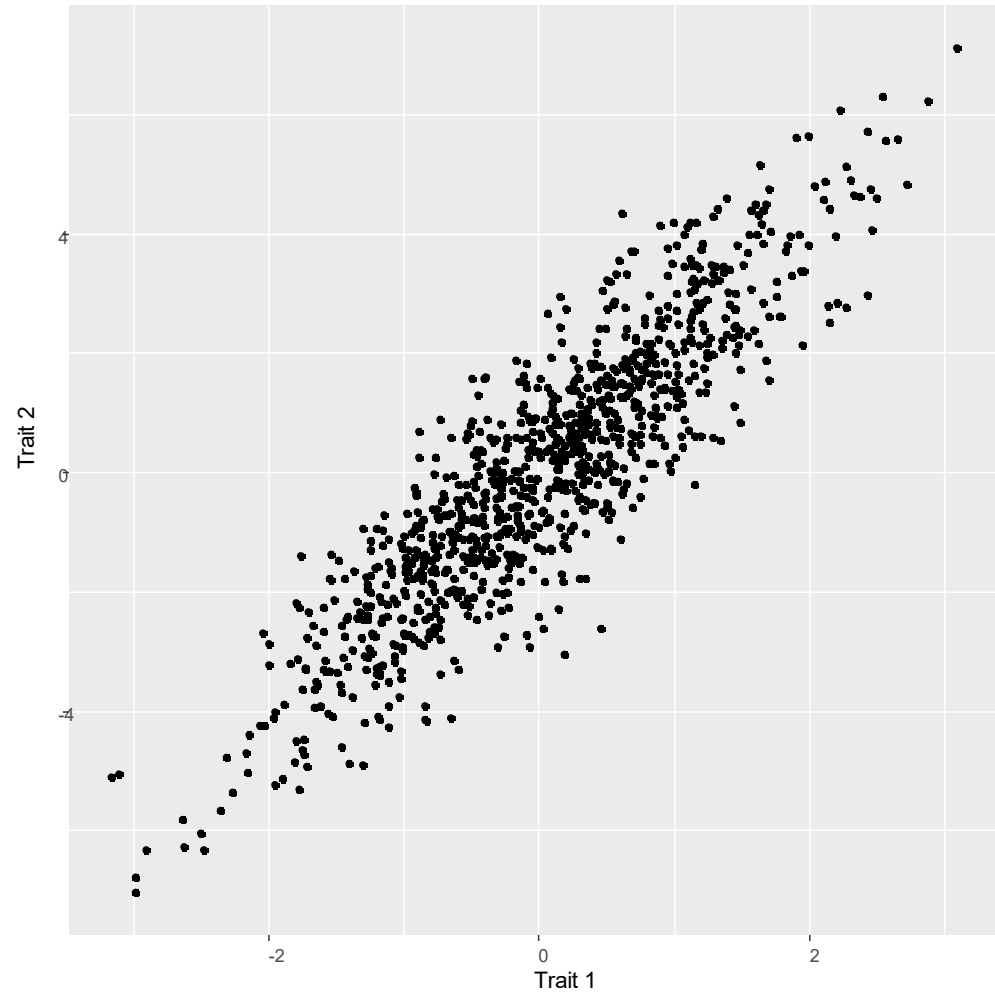
Departamento de
Anatomía, Embriología
y Genética Animal
Universidad Zaragoza

A non-linear recursive model for predicting calving difficulty and birth weight in cattle

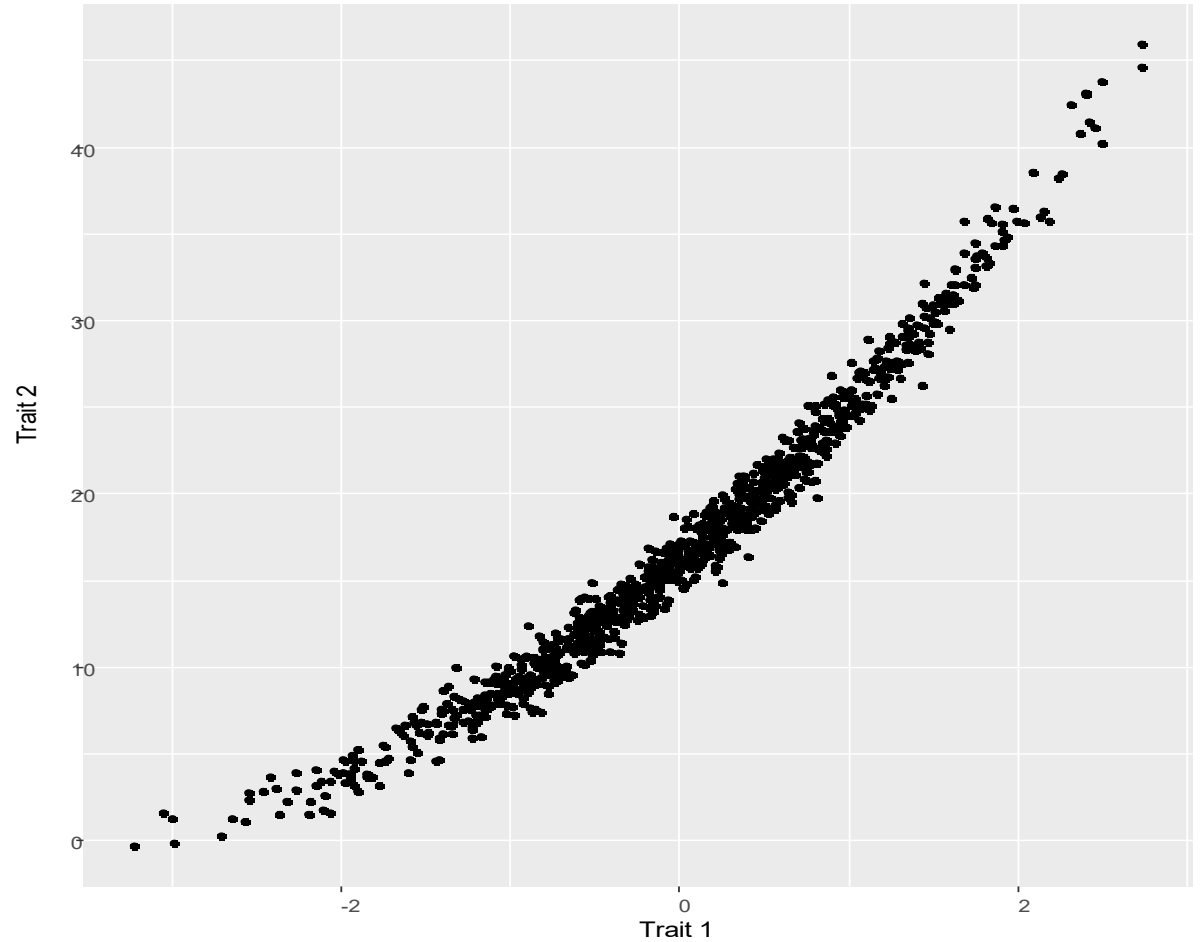
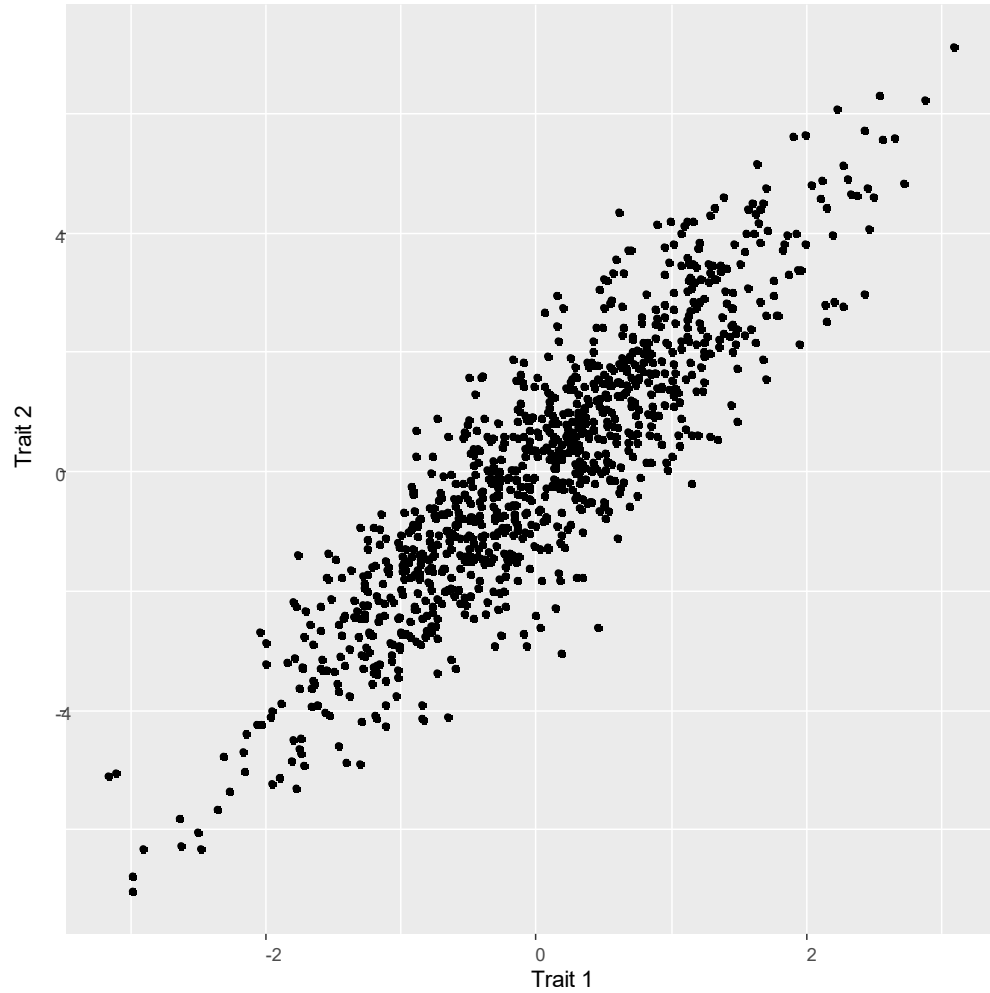
L. Varona, D. López-Carbonell, C. Hervás-Rivero, M. Sánchez-Díaz, J. Altarriba.



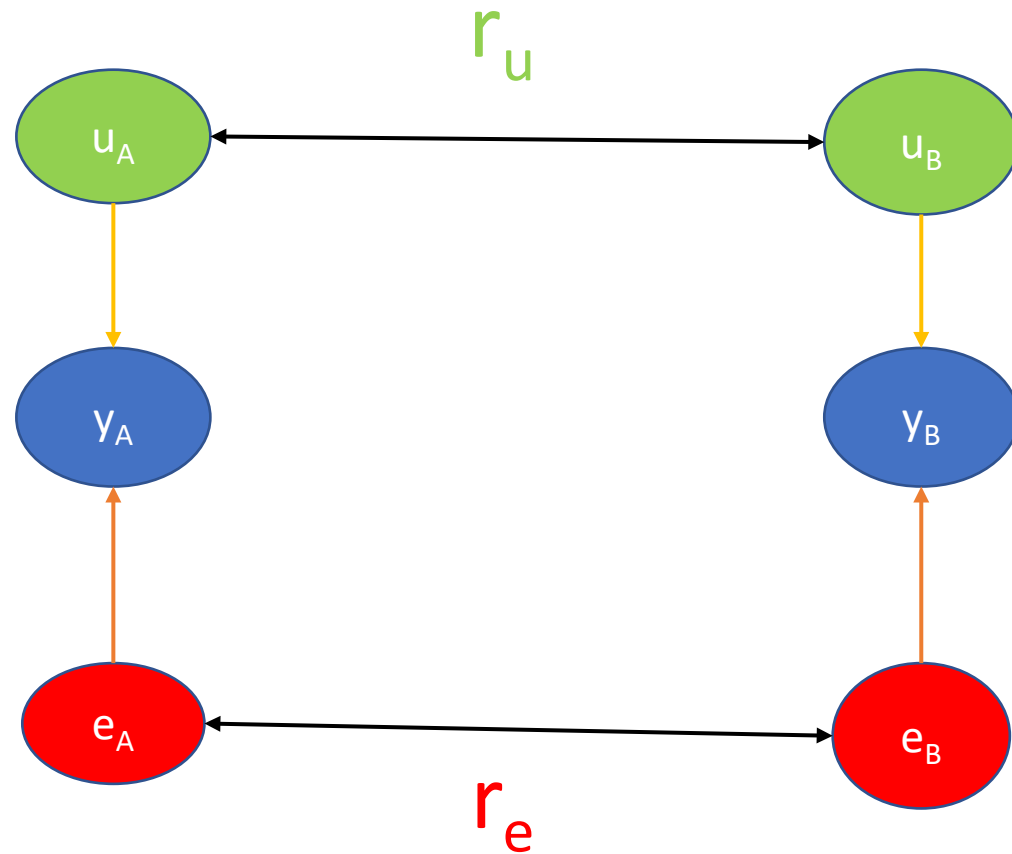
Multiple Traits



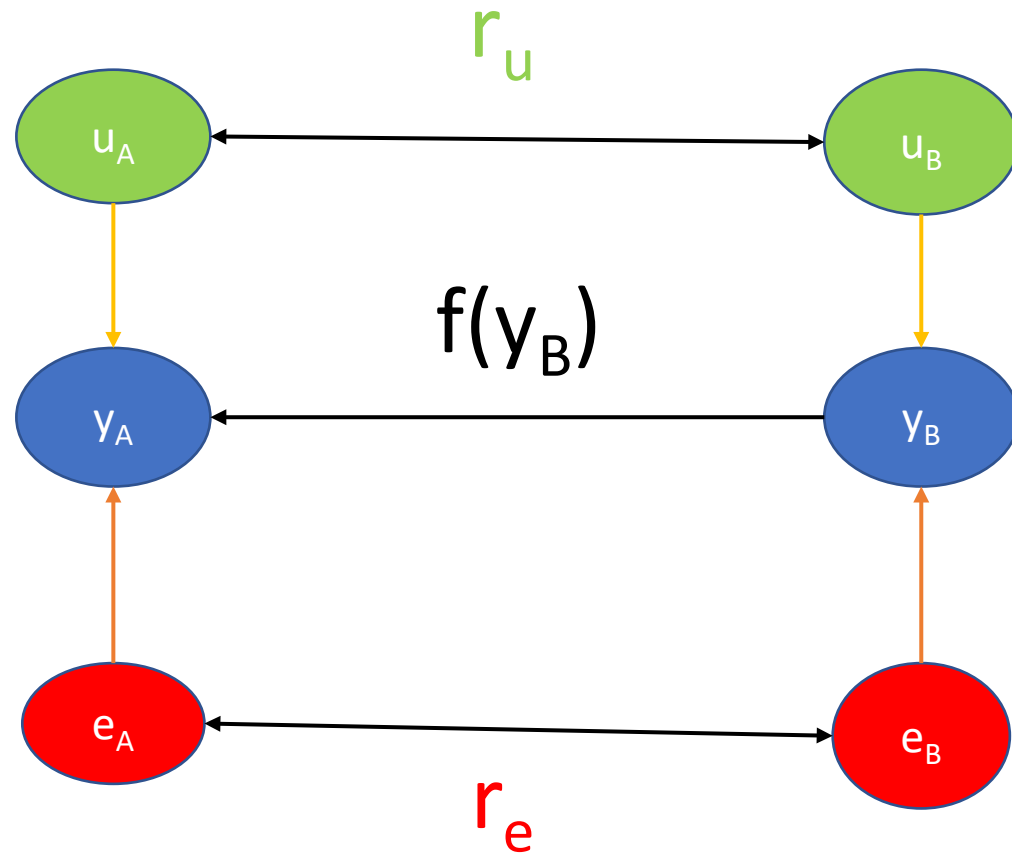
Multiple Traits



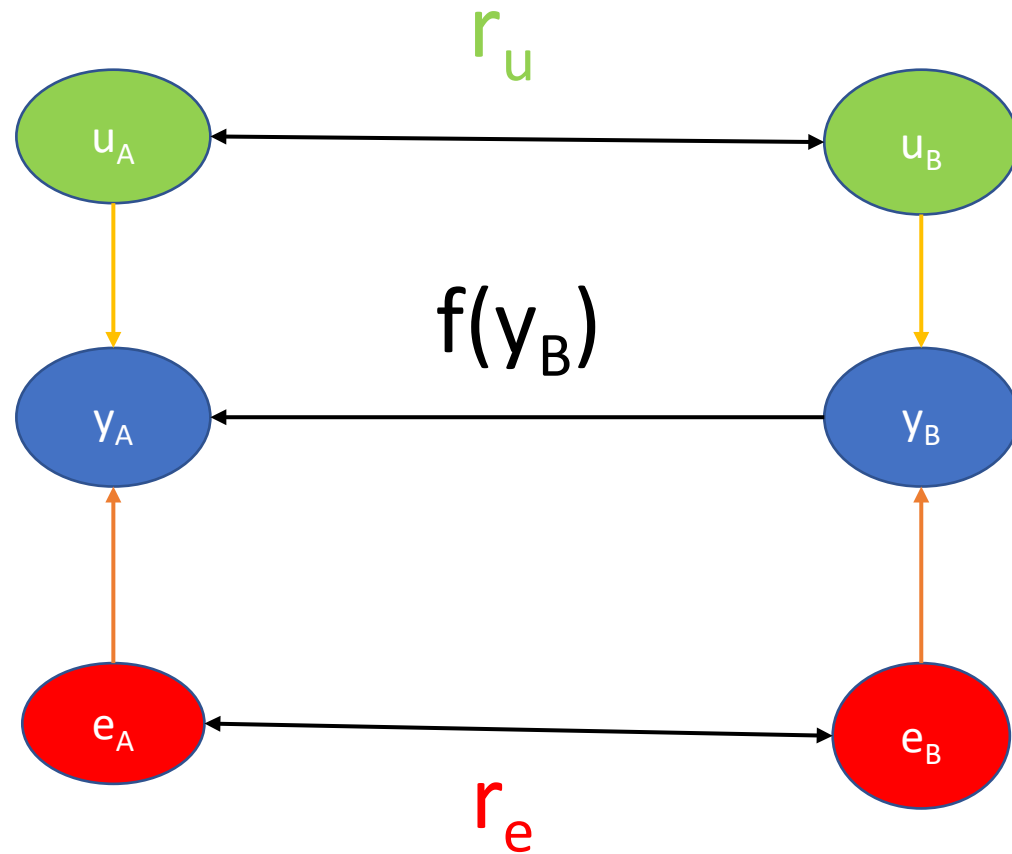
Multiple Trait Models



Recursive Models

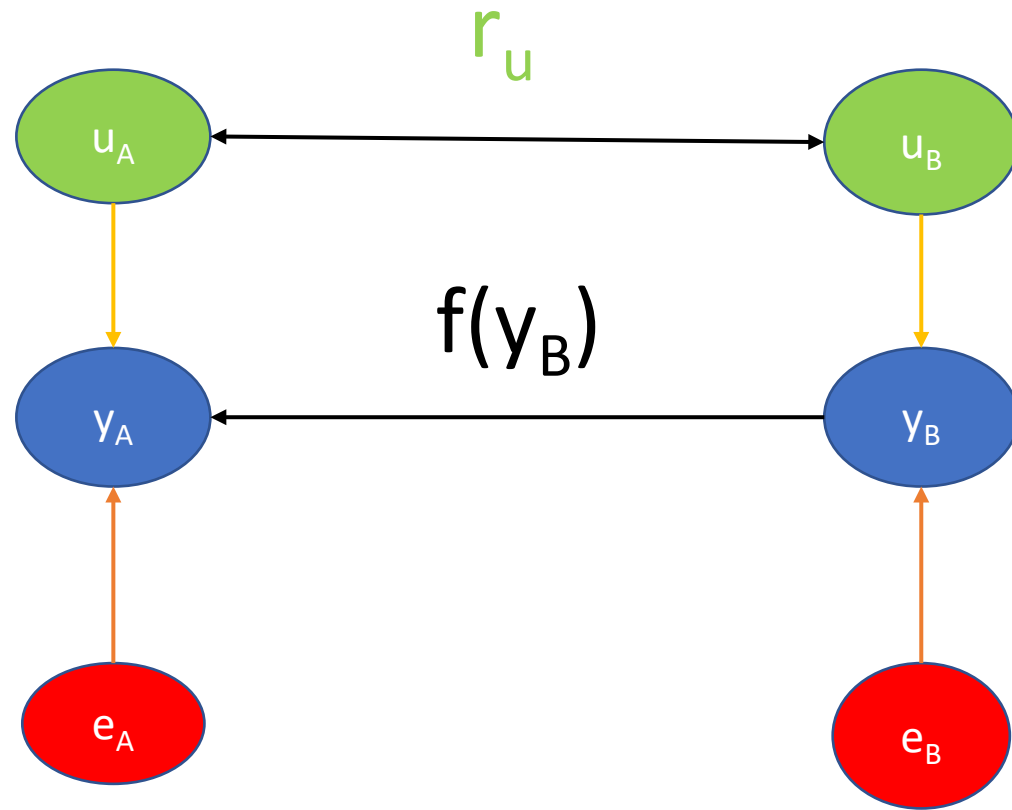


Recursive Models



Non identifiable

Recursive Models



Data (Rubia Gallega)

	No Help	Help
Males	73743 (41.54 Kg. $\pm$ 6.01)	41506 (45.04 Kg. $\pm$ 8.14)
Females	91130 (39.96 Kg. $\pm$ 5.53)	34902 (42.05 Kg. $\pm$ 6.95)
Total	164873 (40.67 Kg. $\pm$ 5.80)	76408 (43.67 Kg. $\pm$ 7.77)



<https://www.tasteatlas.com/best-rated-beef-in-western-europe>

Data (Rubia Gallega)

	No Help	Help
Machos	73743 (41.54 ± 6.01)	41506 (45.04 ± 8.14)
Hembras	91130 (39.96 ± 5.53)	34902 (42.05 ± 6.95)
Total	164873 (40.67 ± 5.80)	76408 (43.67 ± 7.77)

Birth Weight	No Help	Help
<35	16879 (73.7%)	6034 (26.3%)
35-44	113000 (74.3%)	39134 (25.7%)
45-54	30887 (56.1%)	24179 (43.92%)
>55	4107 (36.8%)	7051 (63.2%)

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Pedigree: 522,885 entries

Genotypes: 4,578 individuals (39,532 SNPs)

Model (ssGBLUP)

$$\mathbf{y}_{BW} = \mathbf{X}_{BW}\mathbf{b}_{BW} + \mathbf{W}_{BW}\mathbf{sh}_{BW} + \mathbf{M}_{BW}\mathbf{p}_{BW} + \mathbf{M}_{BW}\mathbf{m}_{BW} + \mathbf{Z}_{BW}\mathbf{u}_{BW} + \mathbf{e}_{BW}$$

$$\mathbf{y}_{CD} = f(\mathbf{y}_{BW}) + \mathbf{X}_{CD}\mathbf{b}_{CD} + \mathbf{W}_{CD}\mathbf{sh}_{CD} + \mathbf{M}_{CD}\mathbf{p}_{CD} + \mathbf{M}_{CD}\mathbf{m}_{CD} + \mathbf{Z}_{CD}\mathbf{u}_{CD} + \mathbf{e}_{CD}$$

Model (ssGBLUP)

$$y_{BW} = X_{BW}b_{BW} + W_{BW}sh_{BW} + M_{BW}p_{BW} + M_{BW}m_{BW} + Z_{BW}u_{BW} + e_{BW}$$

$$y_{CD} = f(y_{BW}) + X_{CD}b_{CD} + W_{CD}sh_{CD} + M_{CD}p_{CD} + M_{CD}m_{CD} + Z_{CD}u_{CD} + e_{CD}$$

$$f(y_{BW}) \left\{ \begin{array}{l} 1. f(y_{BW}) = \lambda_1(y_{BW} - \overline{y_{BW}}) \\ 2. f(y_{BW}) = \lambda_1(y_{BW} - \overline{y_{BW}}) + \lambda_2(y_{BW} - \overline{y_{BW}})^2 \end{array} \right.$$

Results

MODEL	DIC
I (LINEAL)	1181763.26
II (NON LINEAL)	1181418.71

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I (LINEAL)	1181763.26
II (NON LINEAL)	1181418.71

MODEL II	BW	CD
σ_u^2	3.47 (0.32)	0.022 (0.002)
σ_m^2	2.47 (0.27)	0.014 (0.001)
$cov(u, m)$	-0.53 (0.19)	-0.004 (0.001)
σ_p^2	0.25 (0.05)	0.001 (0.000)
σ_{sh}^2	7.55 (0.12)	0.040 (0.007)
σ_e^2	18.26 (0.20)	0.120 (0.001)
λ_1	0.010771 (0.000629)	
λ_2	0.000357 (0.000011)	

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Recursive vs Non-recursive scale

$$h_d^2 = \frac{\sigma_{uCD}^2}{\sigma_{uCD}^2 + \sigma_{mCD}^2 - \sigma_{umCD} + \sigma_{pCD}^2 + \sigma_{sCD}^2 + \sigma_{eCD}^2} = \frac{\sigma_{uCD}^2}{\sigma_{TCD}^2}$$

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$$h_d^{2*} = \frac{\sigma_{uCD}^2 + \delta\sigma_{uBW-CD} + \delta^2\sigma_{uBW}^2}{\sigma_{TCD}^2 + \delta\sigma_{TBW-CD} + \delta^2\sigma_{TBW}^2}$$

$$\delta = \frac{\partial f(y_{BW})}{y_{BW}}$$

MODEL	δ
I	λ_1
II	$\lambda_1 + 2 \times \lambda_2 \times (y_{BW} - \overline{y_{BW}})$

Recursive vs Non-recursive scale

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$$r_{dBW-CD} = \frac{\sigma_{uBW-CD}}{\sqrt{\sigma_{uBW}^2 \times \sigma_{uCD}^2}}$$

$$\delta = \frac{\partial f(y_{BW})}{y_{BW}}$$

MODEL	δ
I	λ_1
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Recursive vs Non-recursive scale

$$h_d^2 = \frac{\sigma_{uCD}^2}{\sigma_{uCD}^2 + \sigma_{mCD}^2 - \sigma_{umCD} + \sigma_{pCD}^2 + \sigma_{sCD}^2 + \sigma_{eCD}^2} = \frac{\sigma_{uCD}^2}{\sigma_{TCD}^2}$$

$$h_d^{2*} = \frac{\sigma_{uCD}^2 + \delta\sigma_{uBW-CD} + \delta^2\sigma_{uBW}^2}{\sigma_{TCD}^2 + \delta\sigma_{TBW-CD} + \delta^2\sigma_{TBW}^2}$$

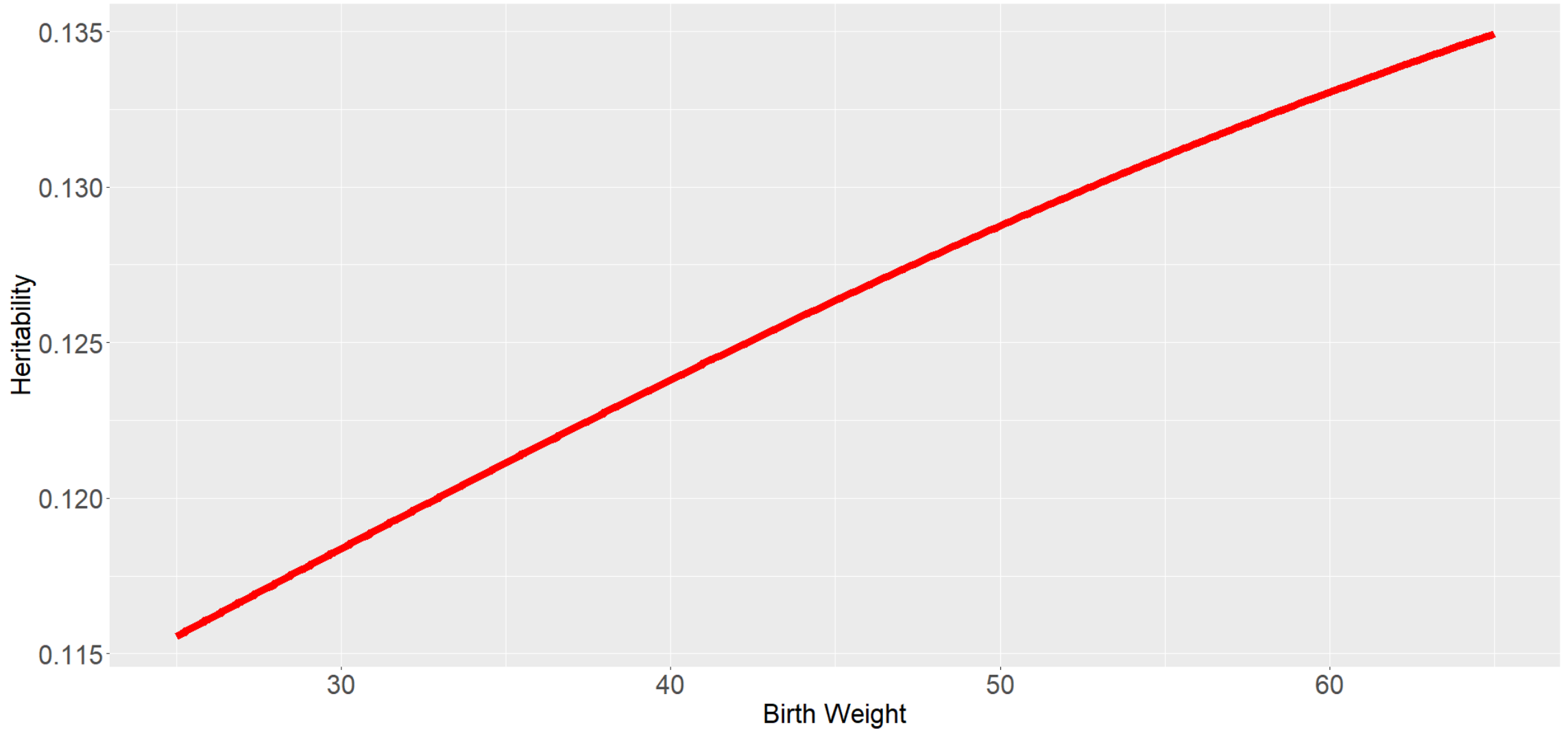
$$r_{dBW-CD} = \frac{\sigma_{uBW-CD}}{\sqrt{\sigma_{uBW}^2 \times \sigma_{uCD}^2}}$$

$$r_{dBW-CD}^* = \frac{\sigma_{uBW-CD} + \delta\sigma_{uBW}^2}{\sqrt{\sigma_{uBW}^2 \times (\sigma_{uCD}^2 + \delta\sigma_{uBW-CD} + \delta^2\sigma_{uBW}^2)}}$$

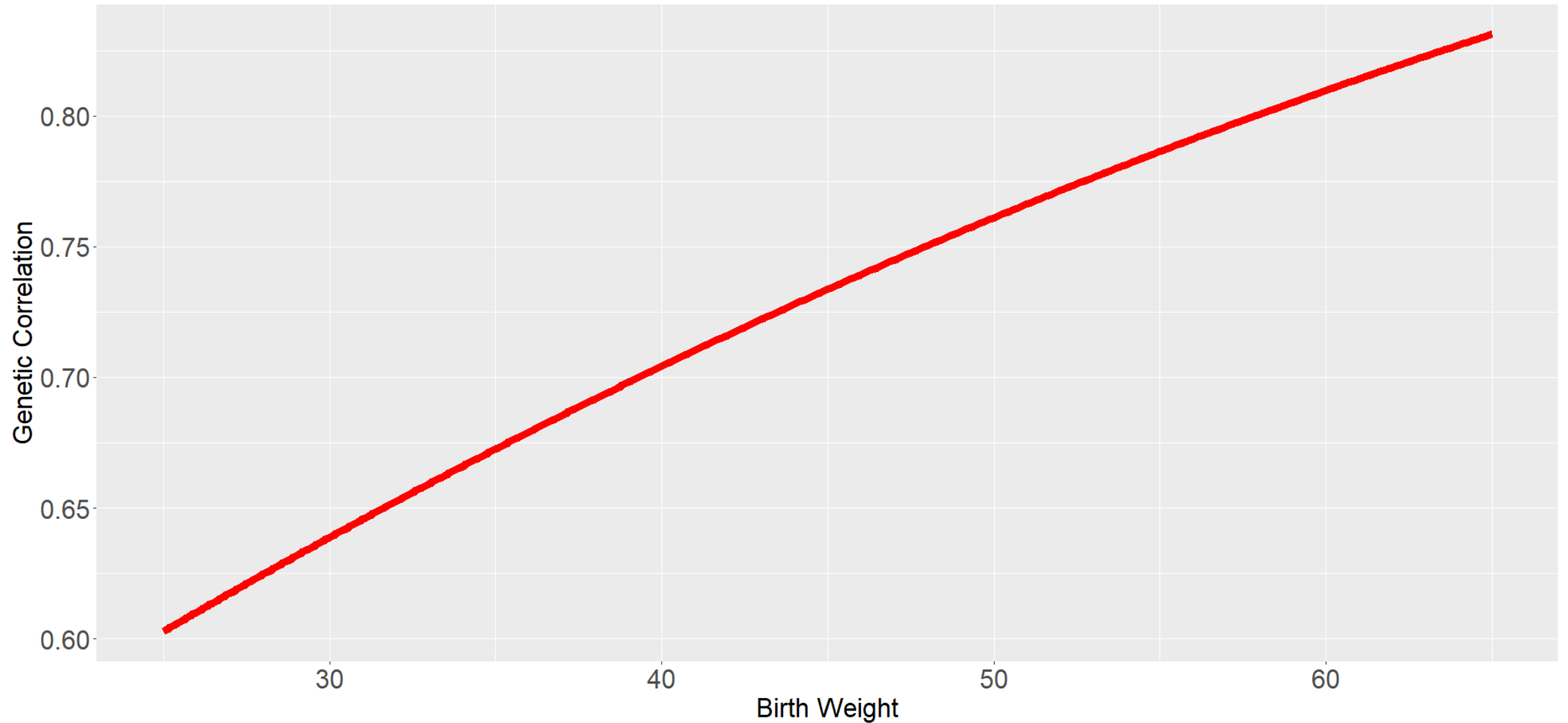
$$\delta = \frac{\partial f(y_{BW})}{y_{BW}}$$

MODEL	δ
I	λ_1
II	$\lambda_1 + 2 \times \lambda_2 \times (y_{BW} - \overline{y_{BW}})$

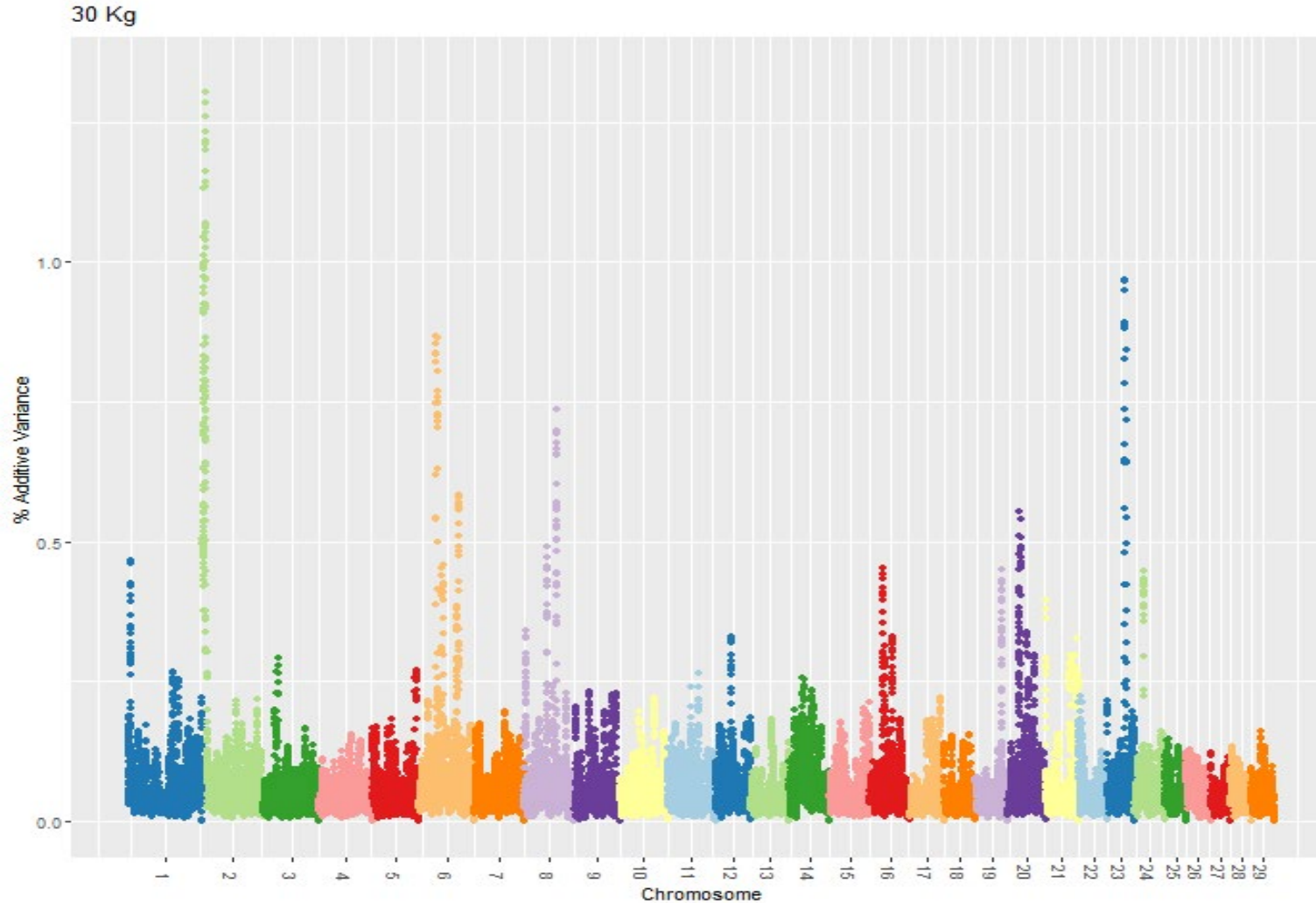
Heritability



Genetic Correlation



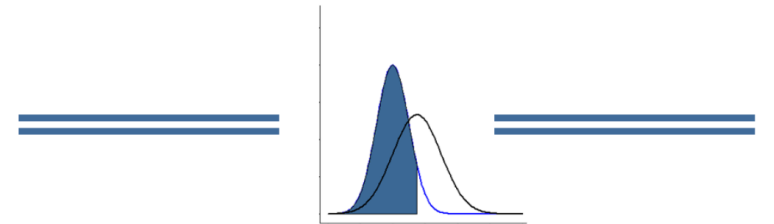
GWAS (Calving Difficulty)



Conclusions

- Phenotypic relationships between traits can be non-linear
- The Multiple Trait Model involves linear relationships between traits
- Recursive models can be defined with non-linear relationships
- The genes involved in genetic variation may vary across the parametric space of the causal variable

Thank you



**QUANTITATIVE
GENETICS LAB**



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