



➤ Genetic correlation: a heritable parameter

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Introduction

 Genetic correlation is a relevant parameter in breeding programs

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-  Can be used to improve inferences about less routinely measured traits,
-  Part of the information to define weights of the traits in the selection index,
-  Very important parameter when dealing with antagonistic traits.

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 -  Can be used to improve inferences about less routinely measured traits,
 -  **Part of the information to define weights of the traits in the selection index,**
 -  **Very important parameter when dealing with antagonistic traits.**
-  Typically genetic correlation is treated as a parameter common for all individuals.

INTERBULL BULLETIN NO. 60. 20-21 May 2024, Bled, Slovenia

Genetic correlations: a parameter or a latent phenotype in genetic evaluations?

B.C.D. Cuyabano¹, P Croiseau¹, F Shokor^{1,2}, MR Motta³, S Aguerre^{1,4}, and S Mattalia^{1,4}

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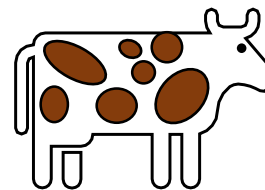
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French Montbéliarde dairy cattle



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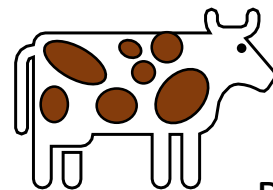
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Production x Fertility

~800k cows with records for both traits

~ 4 million animals in pedigree

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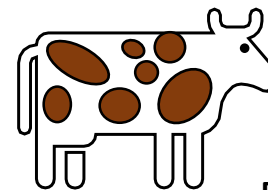
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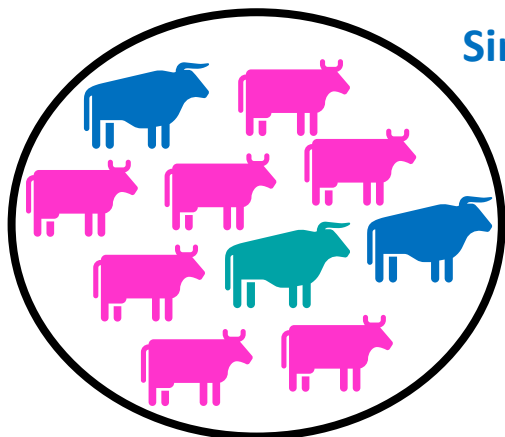


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Sires with 500+ daughters



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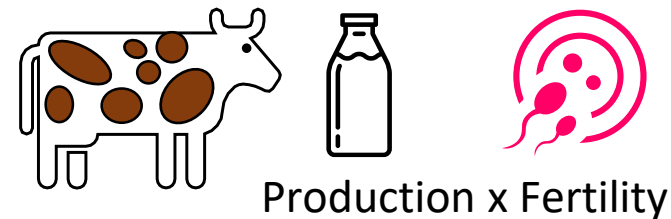
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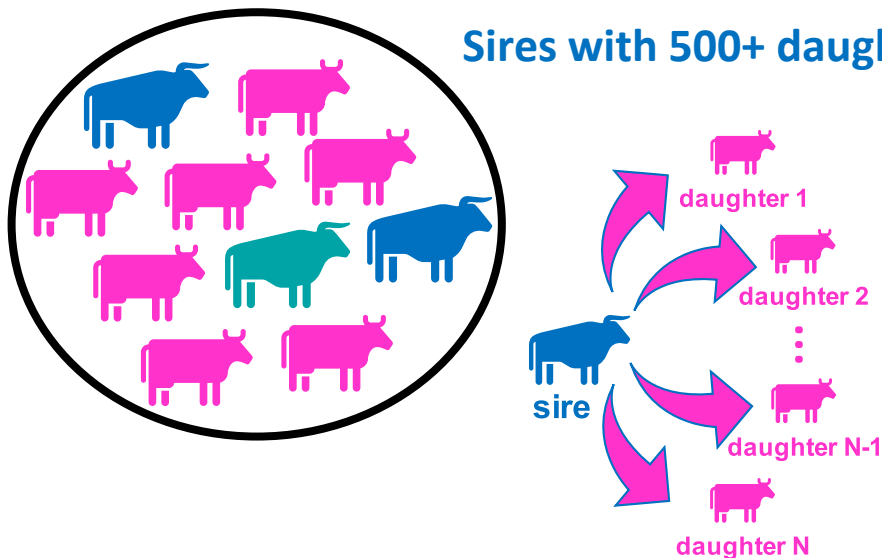
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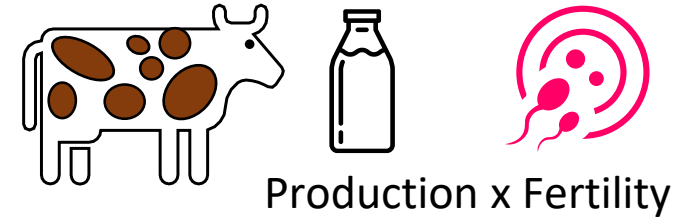
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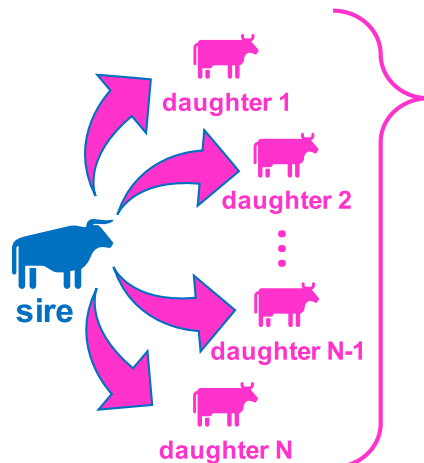
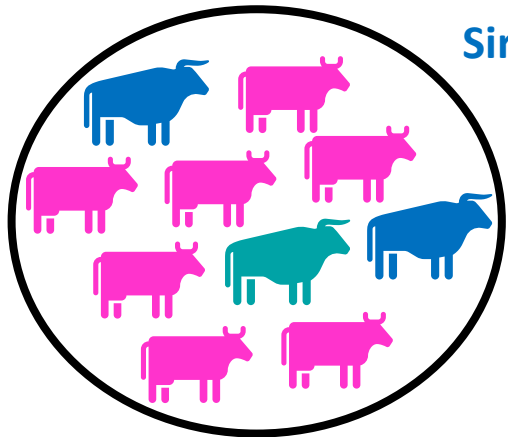
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Obtained the correlation between the EBVs of PROD and FERT from the daughters to have a genetic correlation per sire

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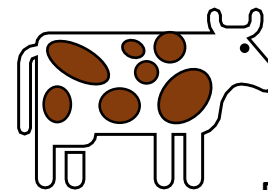
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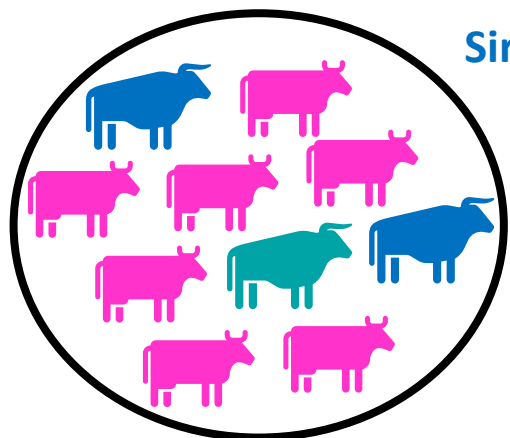
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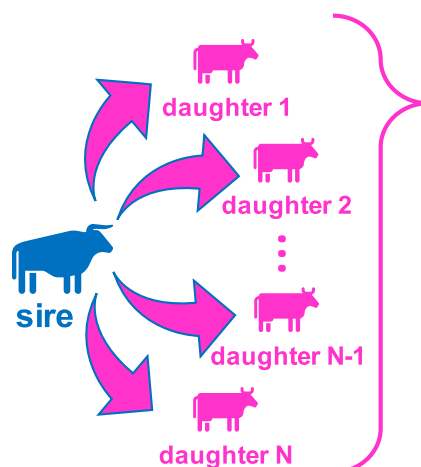
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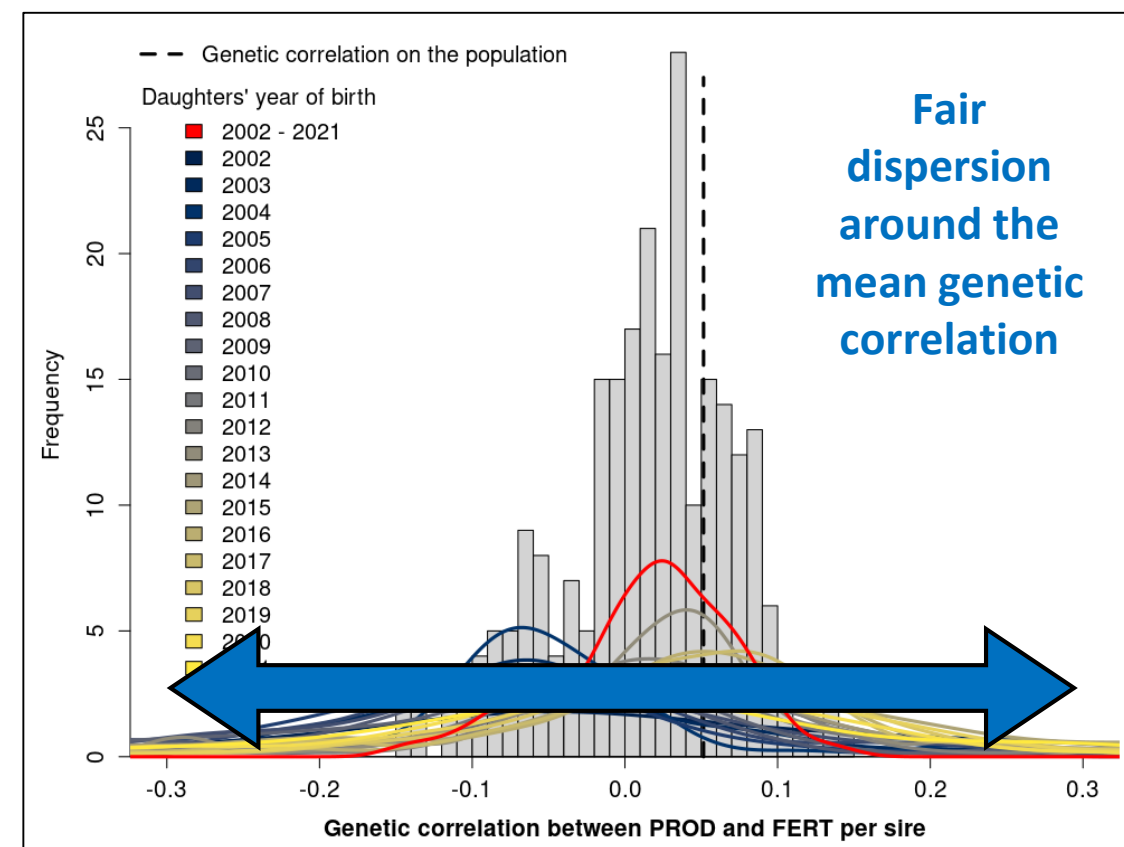
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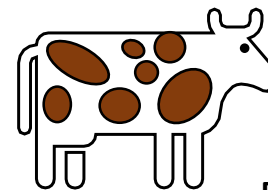
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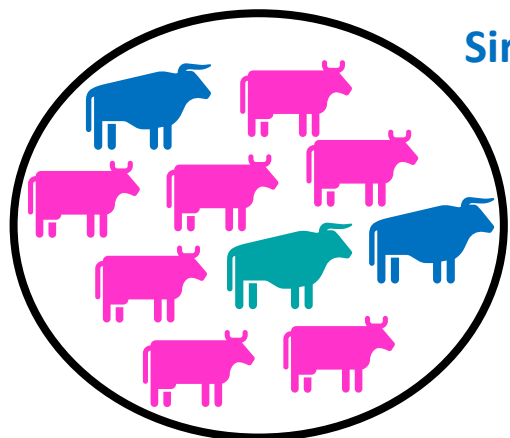
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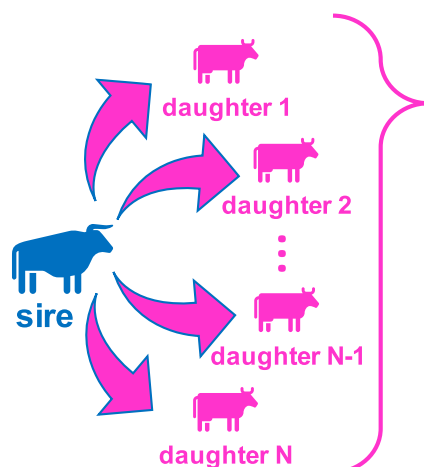
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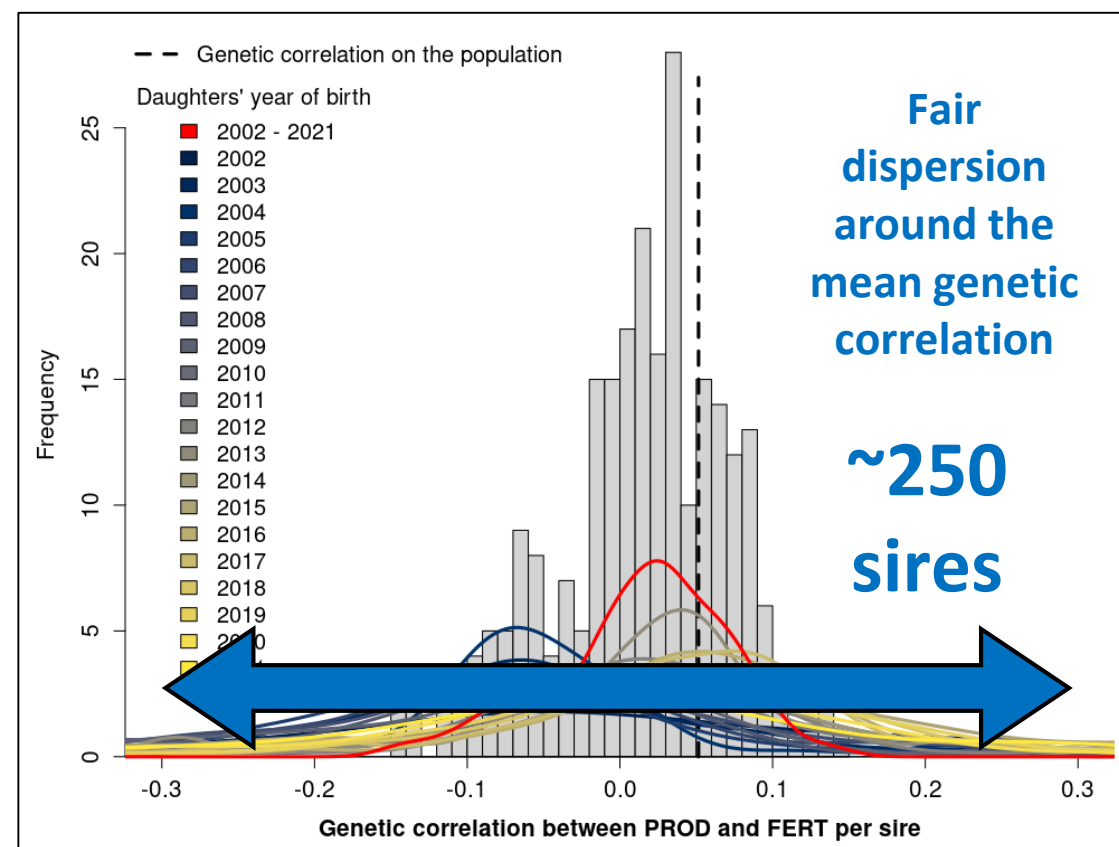
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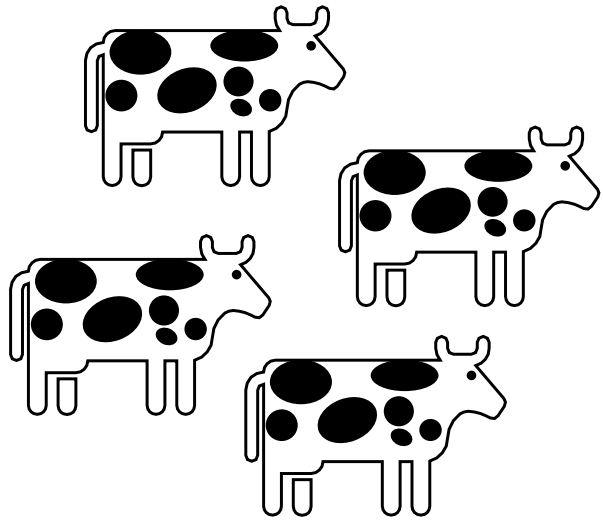


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Up-scaling the study

Study on French Holstein dairy cattle



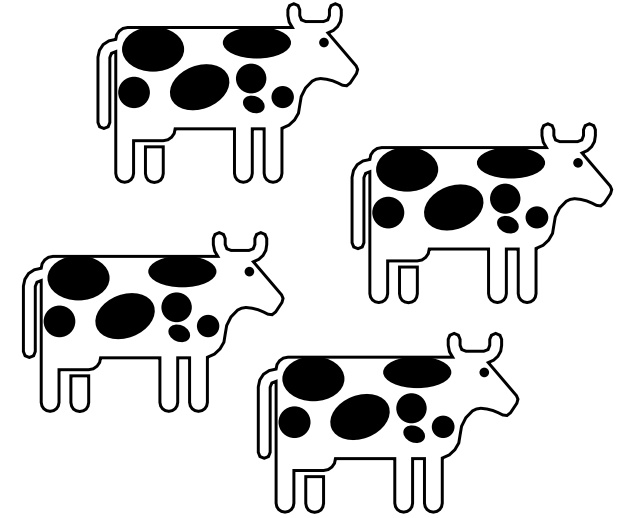
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 Phenotypes in the form of yield deviations:

 Milk (MY) and protein yield (PY)



 Cow conception rate (CR)



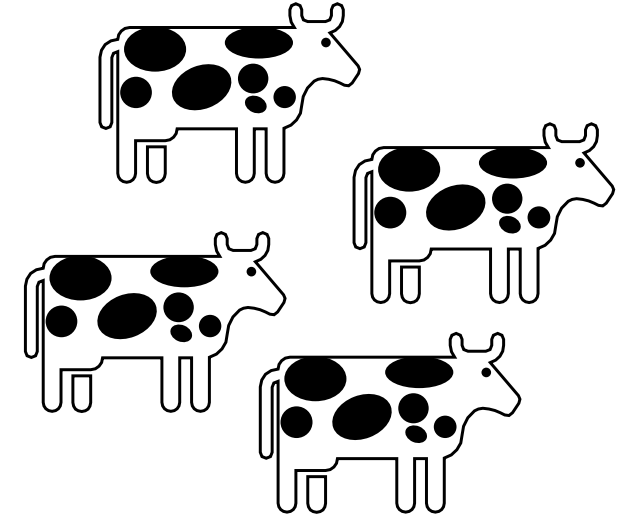
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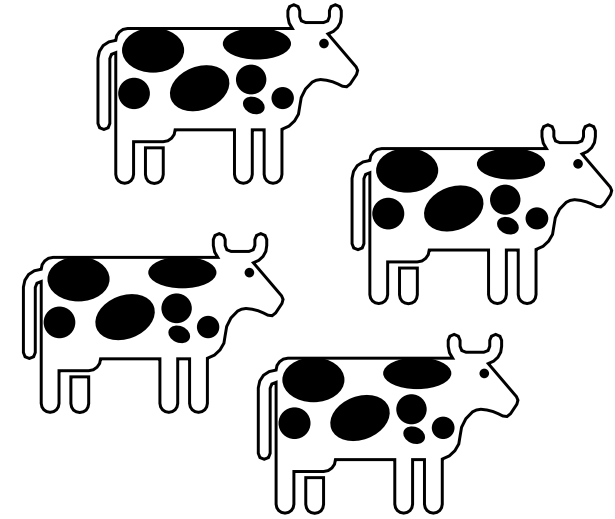
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 ~4.5 million cows born between 1991-2020 with complete records,

 ~8.5 million animals in pedigree.

(~3,400 bulls 1991-2015)

Genetic parameters

	MY	PY	CR
MY	0.223 (0.001)	0.78 (0.05)	-0.15 (0.03)
PY		0.378 (0.001)	-0.20 (0.04)
CR			0.006 (0.002)

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Genetic correlations at the individual level

Individual-Specific Genetic Correlation

CSH Cold Spring Harbor Laboratory

bioRxiv

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(currently under review in a peer-reviewed journal)

New Results

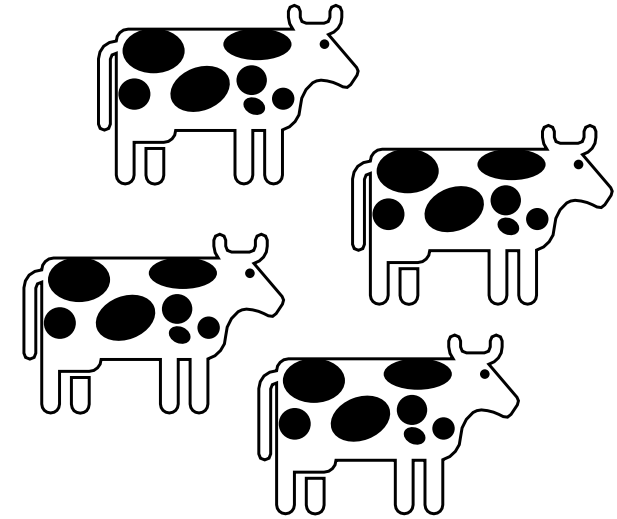
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doi: <https://doi.org/10.1101/2025.03.13.643026>

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Individual-Specific Genetic Correlation

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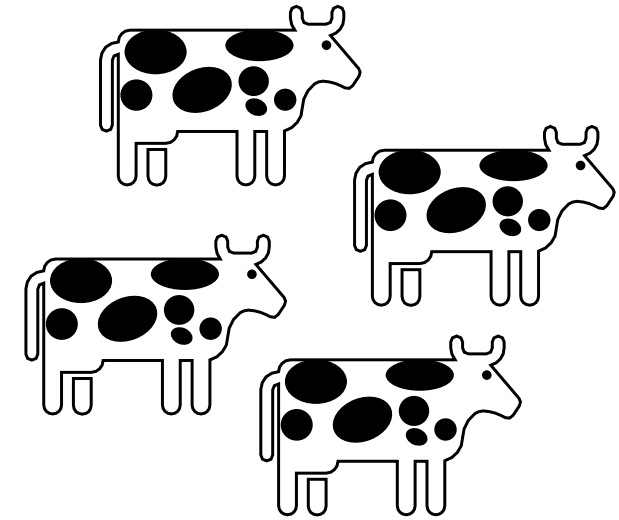
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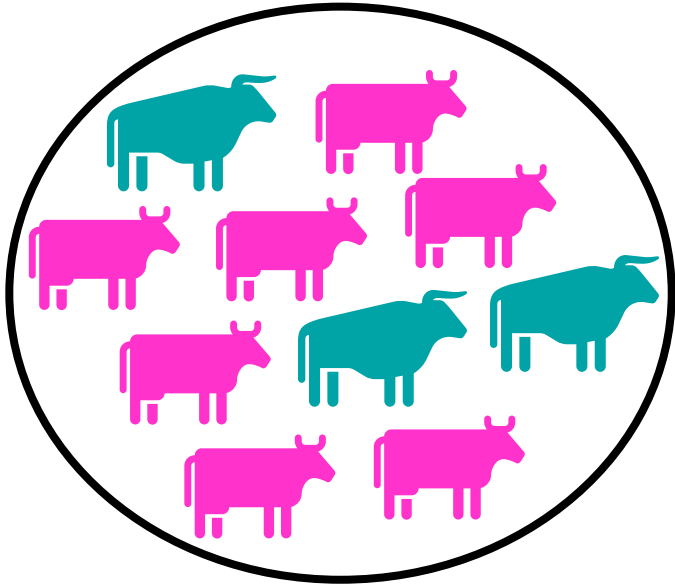
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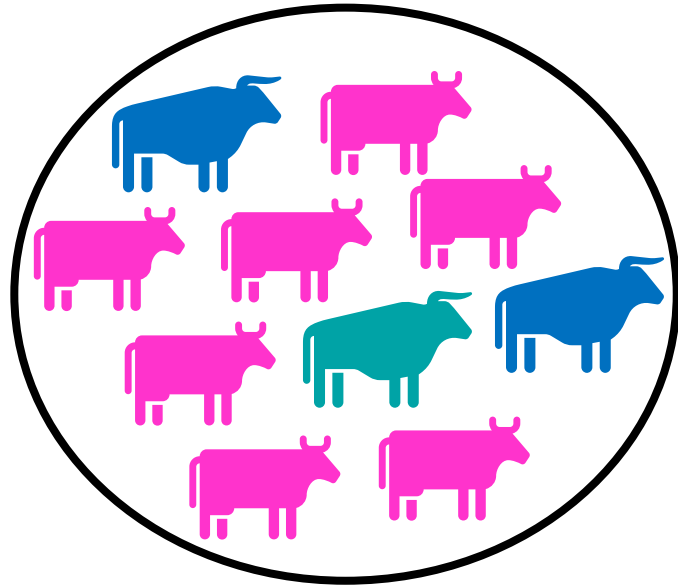


Individualized Sire
Genetic Correlation

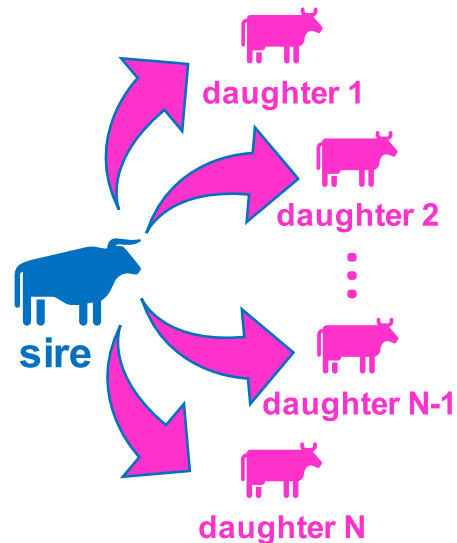
iSGC



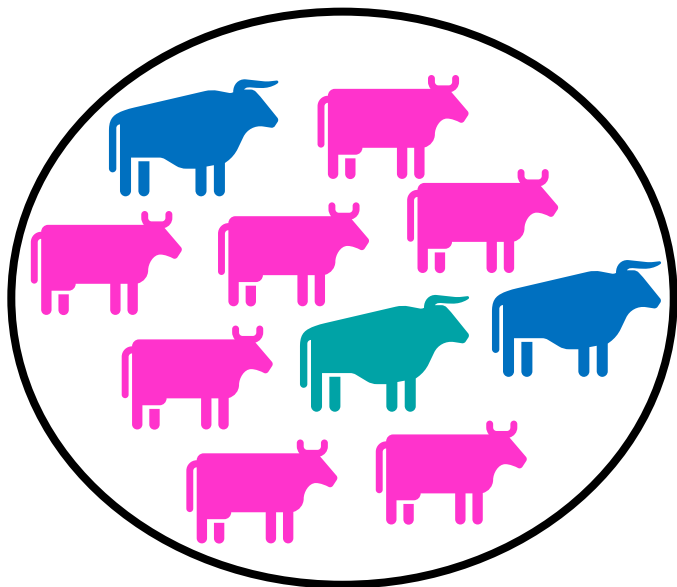
Individual-Specific Genetic Correlation



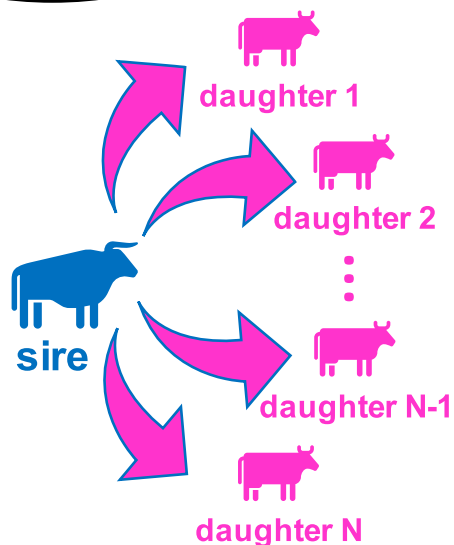
Sires with
500+
daughters



Individual-Specific Genetic Correlation



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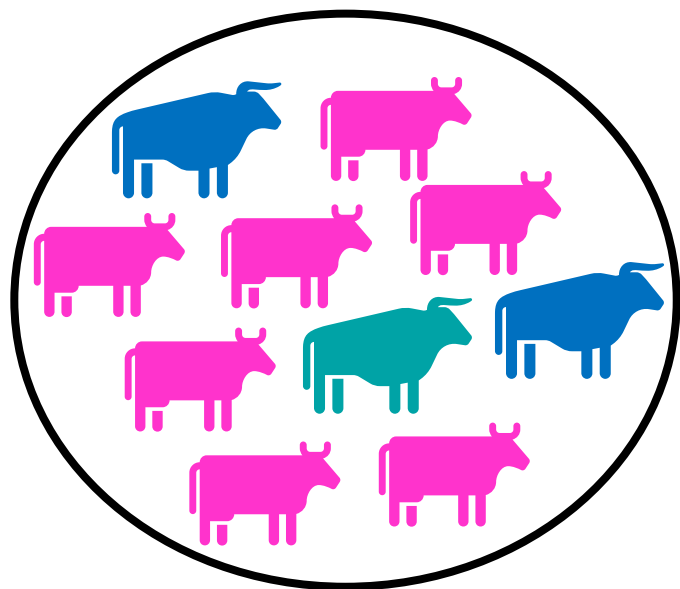


The expected daughter's breeding value is the parent-average

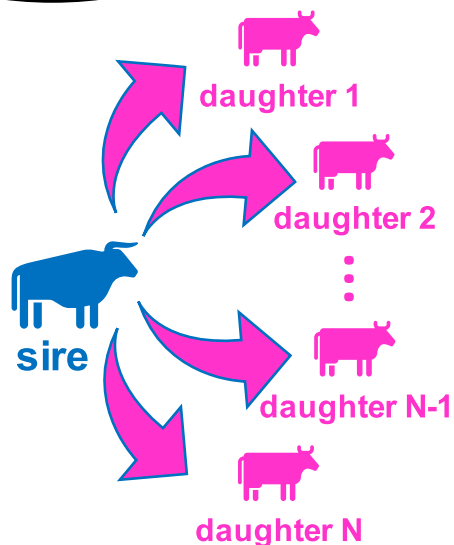
$$1. \quad g_{\text{trait 1}} = \frac{1}{2} g_{\text{dam, trait 1}} + \frac{1}{2} g_{\text{sire, trait 1}}$$

$$2. \quad g_{\text{trait 2}} = \frac{1}{2} g_{\text{dam, trait 2}} + \frac{1}{2} g_{\text{sire, trait 2}}$$

Individual-Specific Genetic Correlation



Sires with
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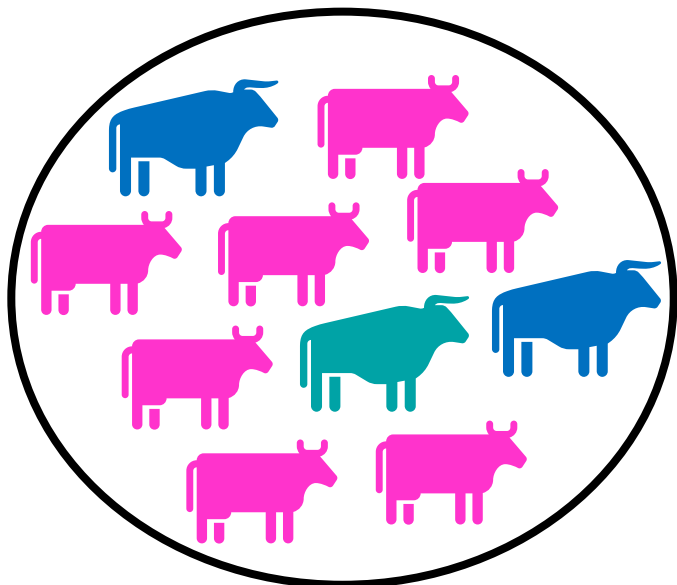
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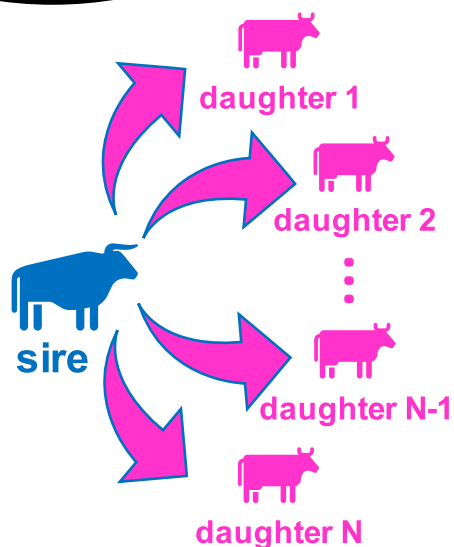
$$2. \quad g_{\text{trait 2}} - \frac{1}{2} g_{\text{dam, trait 2}} = \frac{1}{2} g_{\text{sire, trait 2}}$$

Remove
maternal
information
from the
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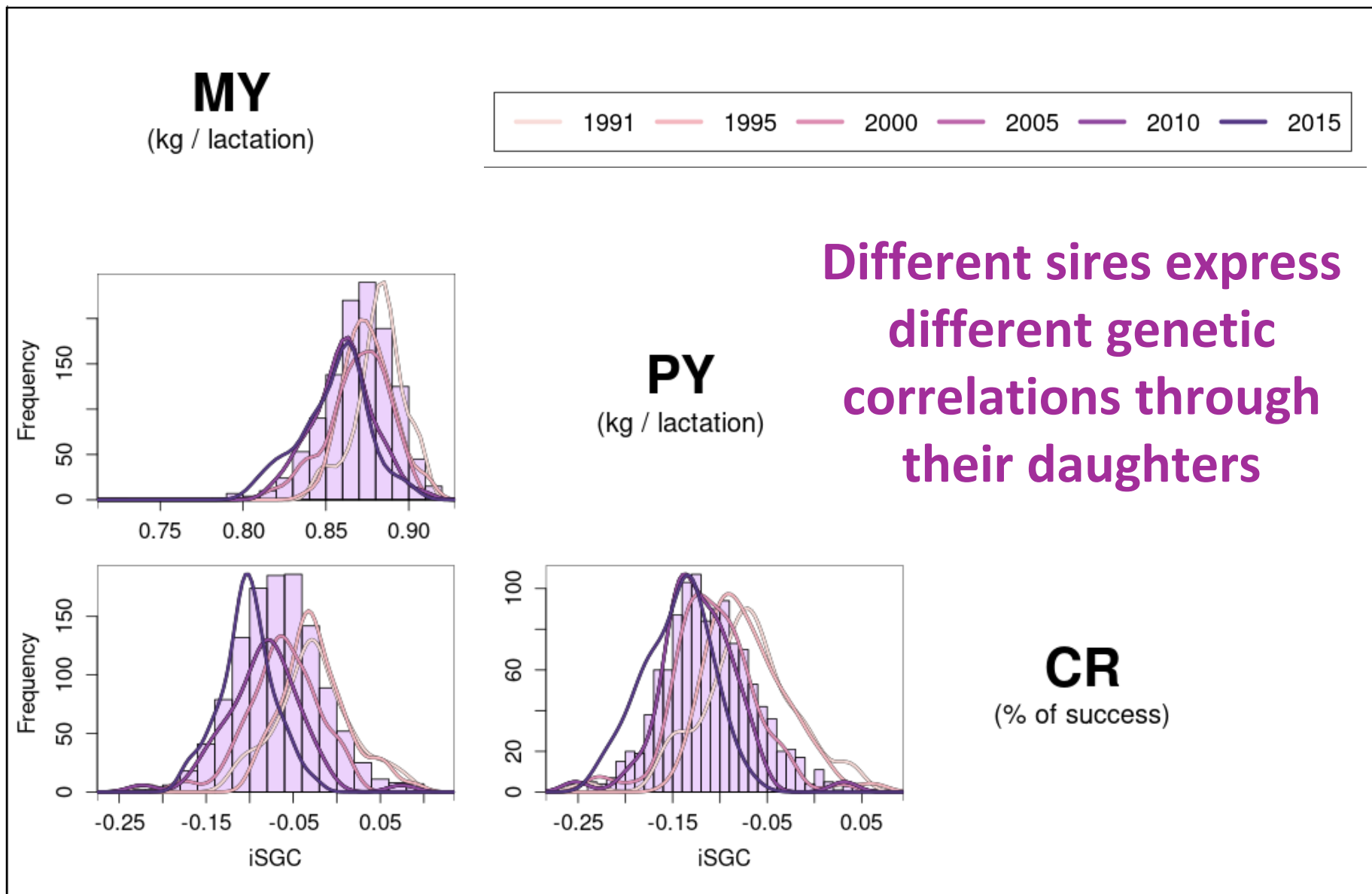
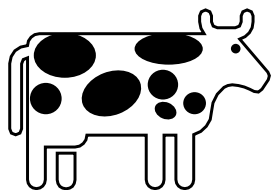
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$$\text{iSGC} = \text{cor} \left(\underbrace{g_{\text{trait 1}} - \frac{1}{2} g_{\text{dam, trait 1}}}_{\text{Daughters' BV corrected for their dams}}, \underbrace{g_{\text{trait 2}} - \frac{1}{2} g_{\text{dam, trait 2}}}_{\text{expresses only the sire information}} \right)$$

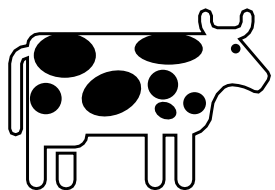
Individual-Specific Genetic Correlation

1161 sires
with 500+
daughters

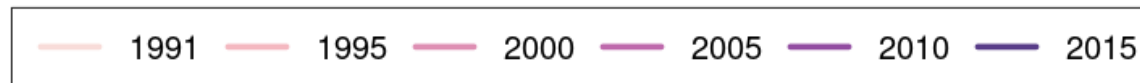
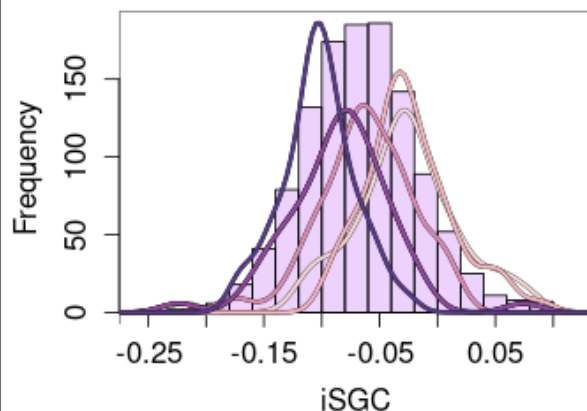
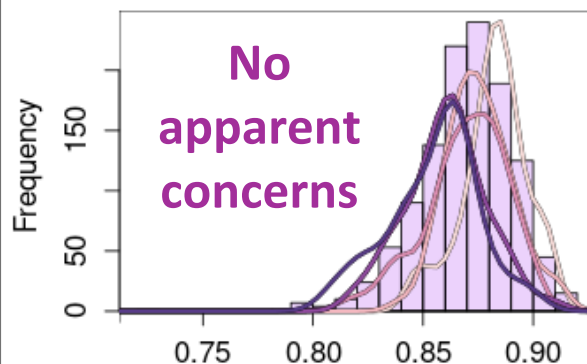


Individual-Specific Genetic Correlation

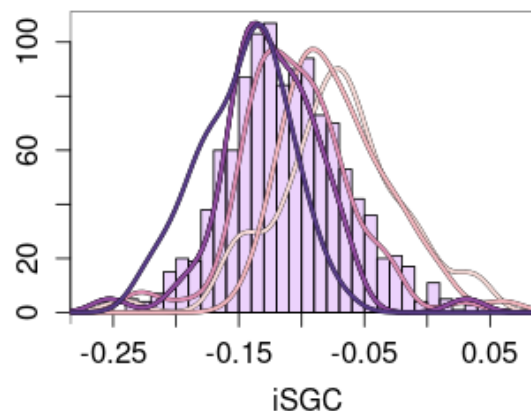
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MY
(kg / lactation)



PY
(kg / lactation)

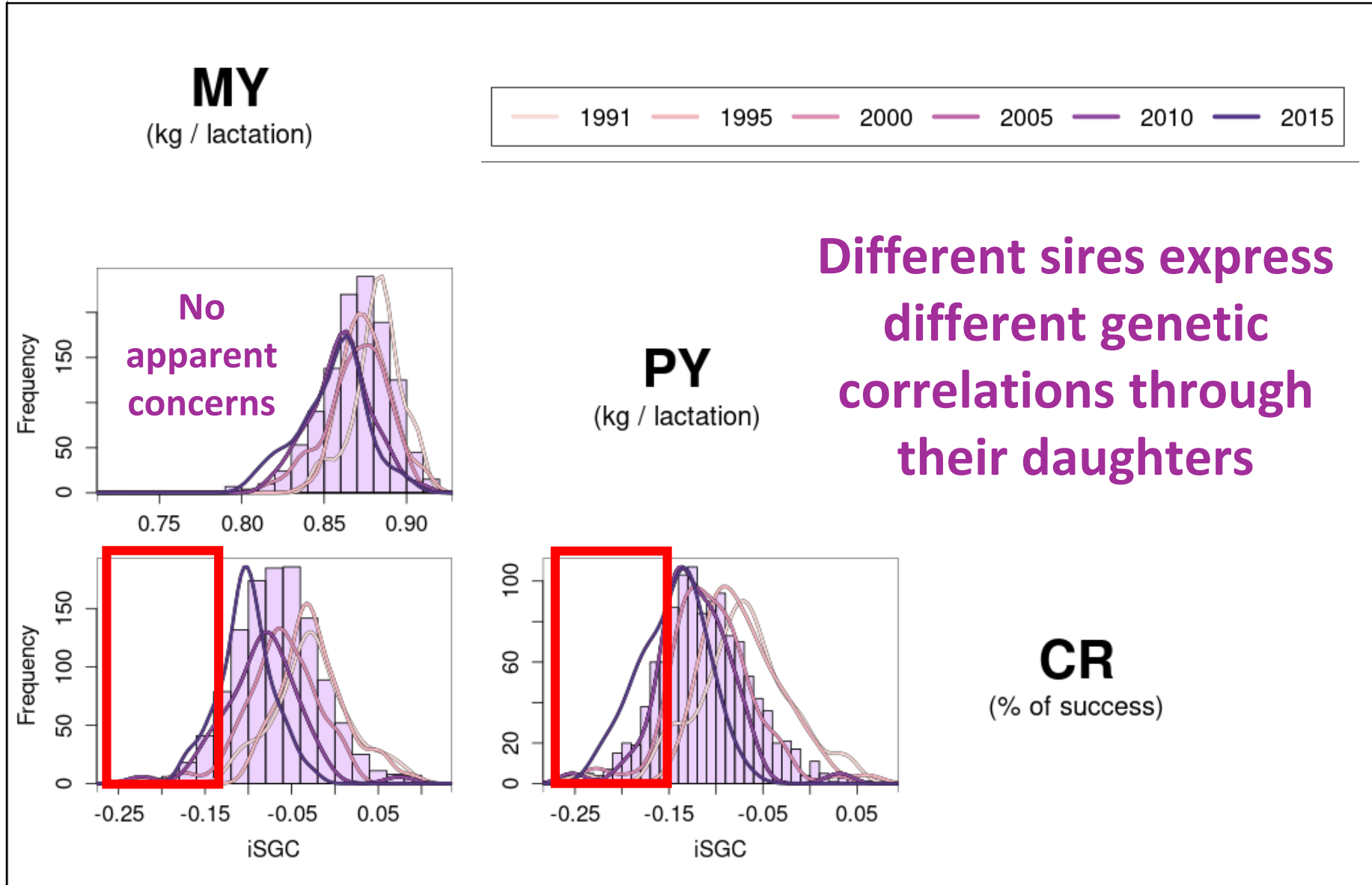
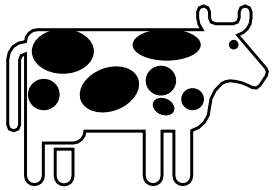


Different sires express
different genetic
correlations through
their daughters

CR
(% of success)

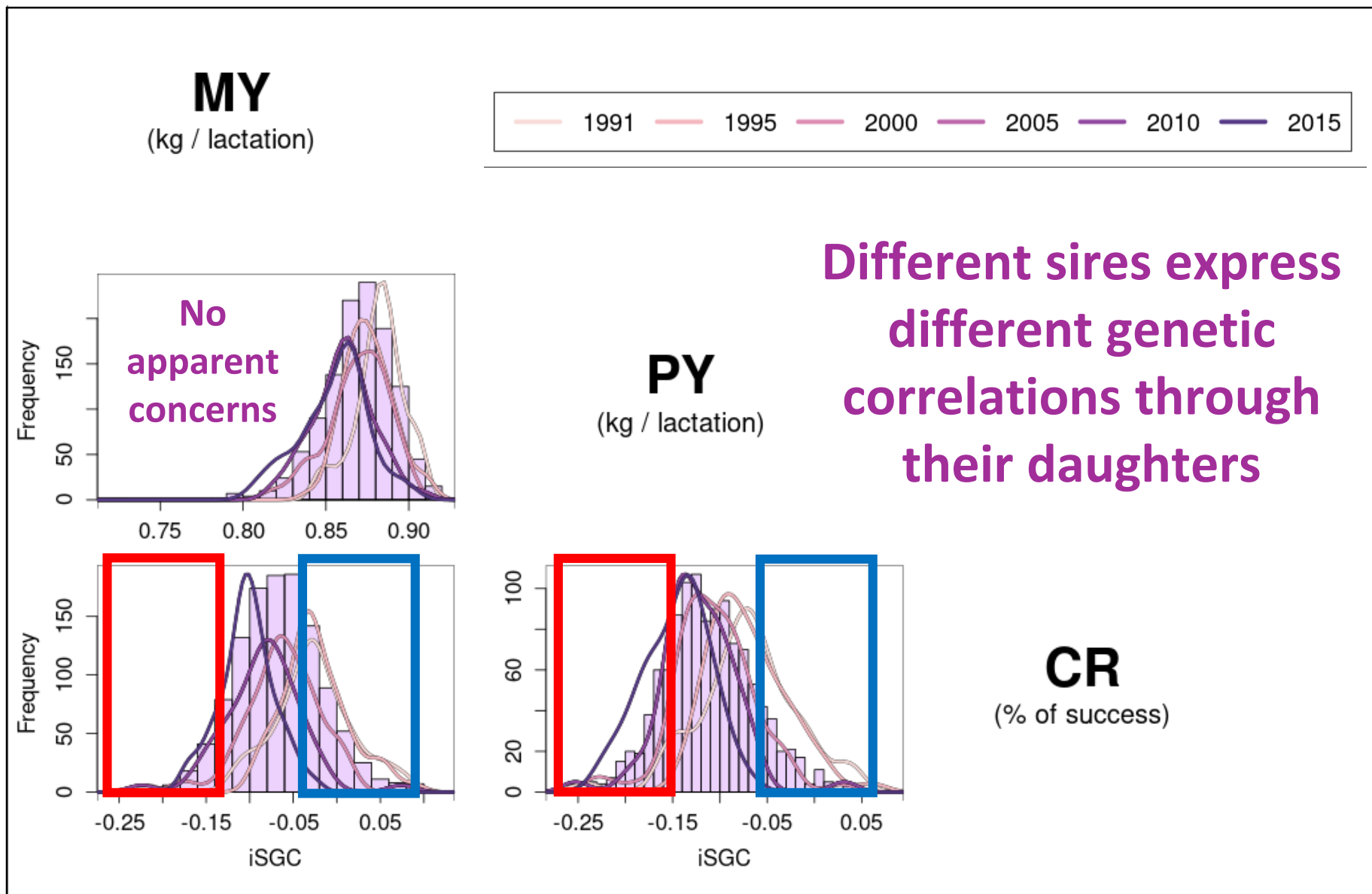
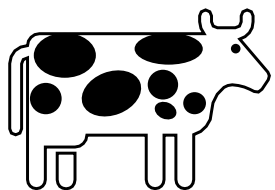
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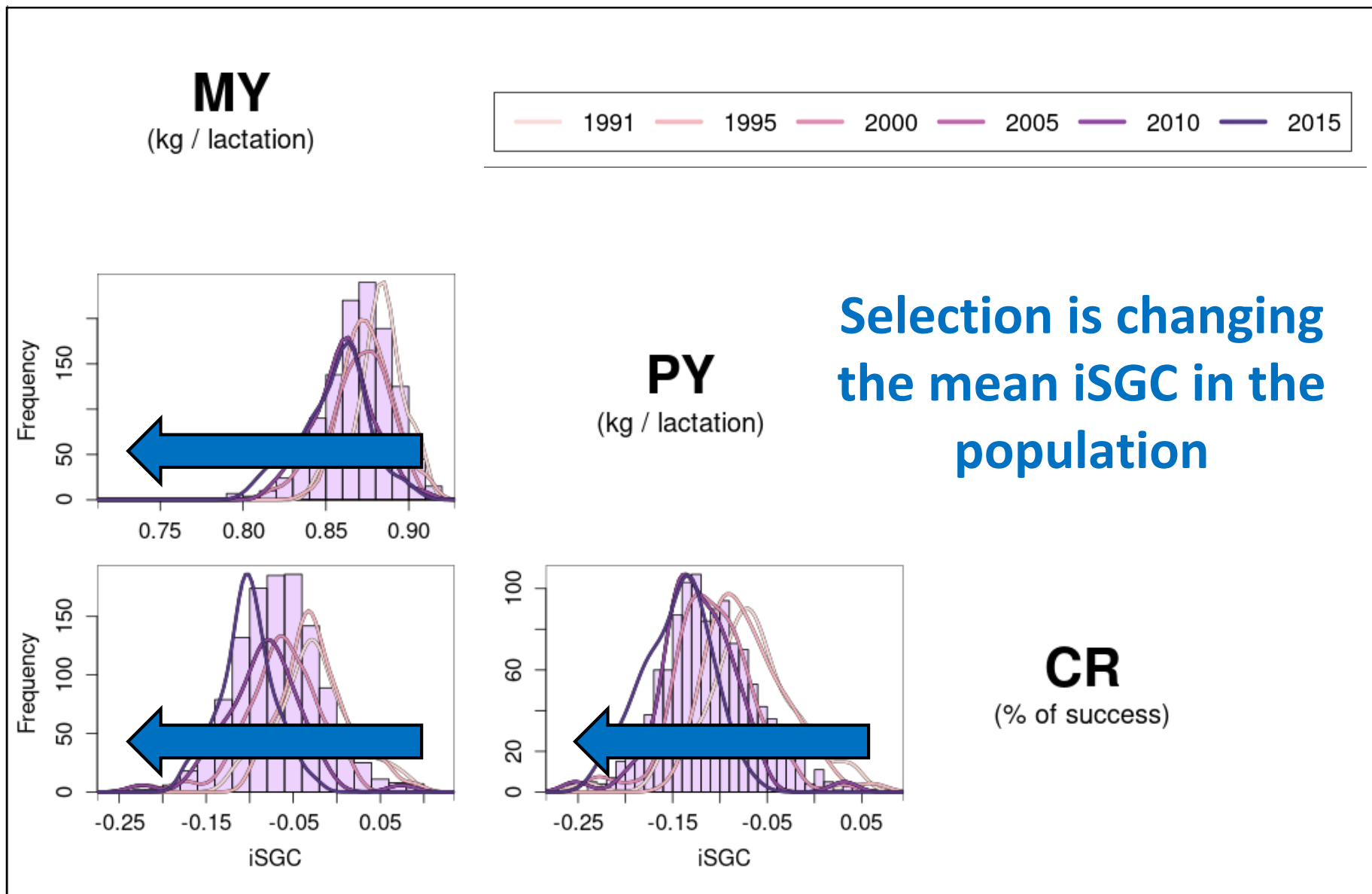
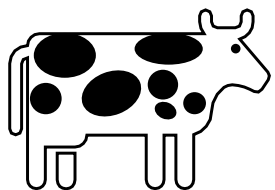
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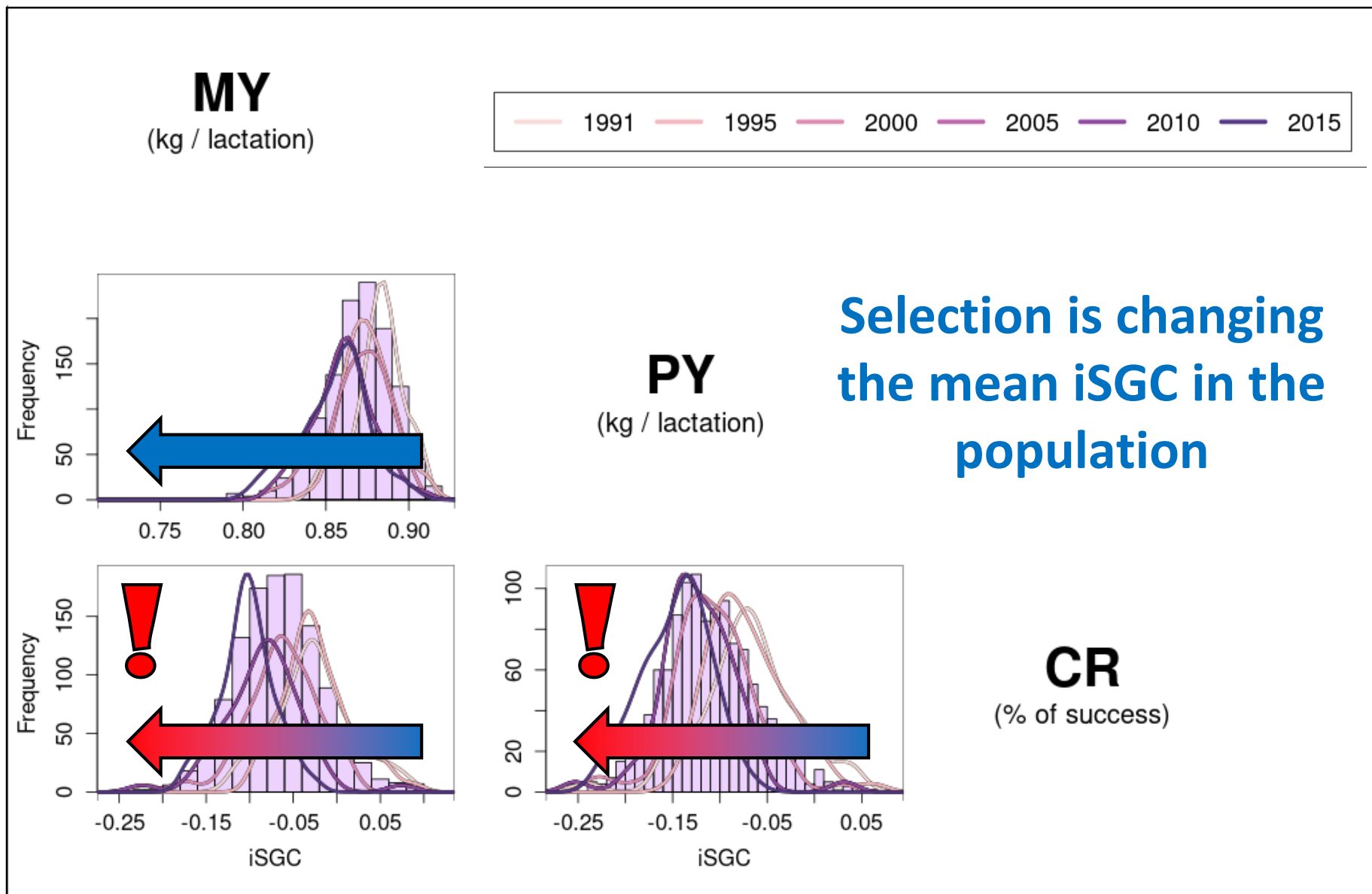
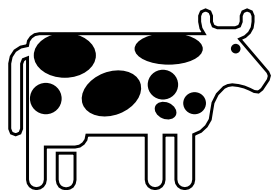
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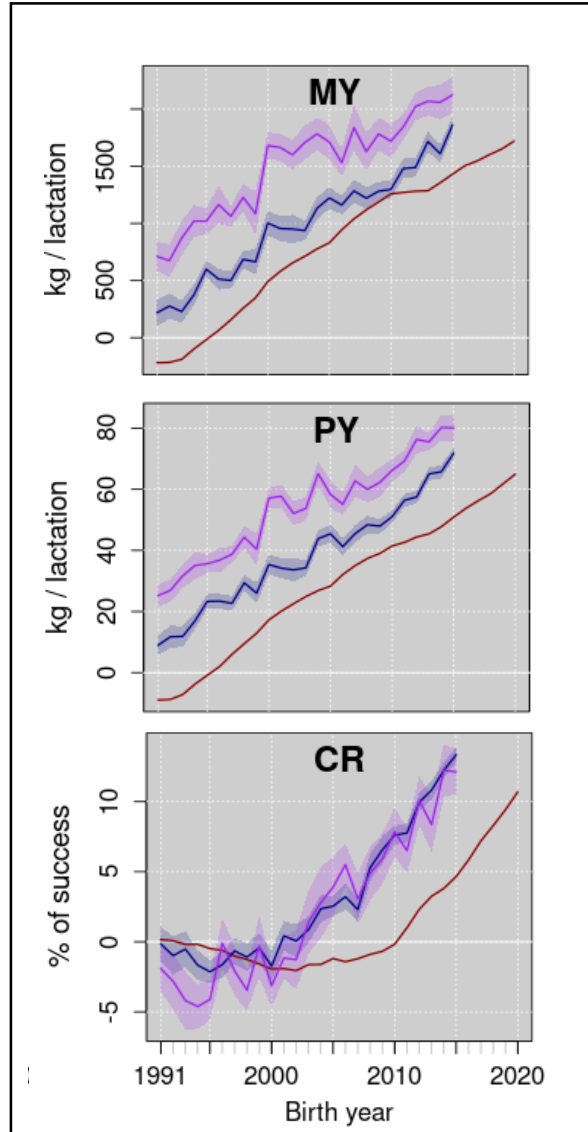


Individual-Specific Genetic Correlation

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Genetic progress

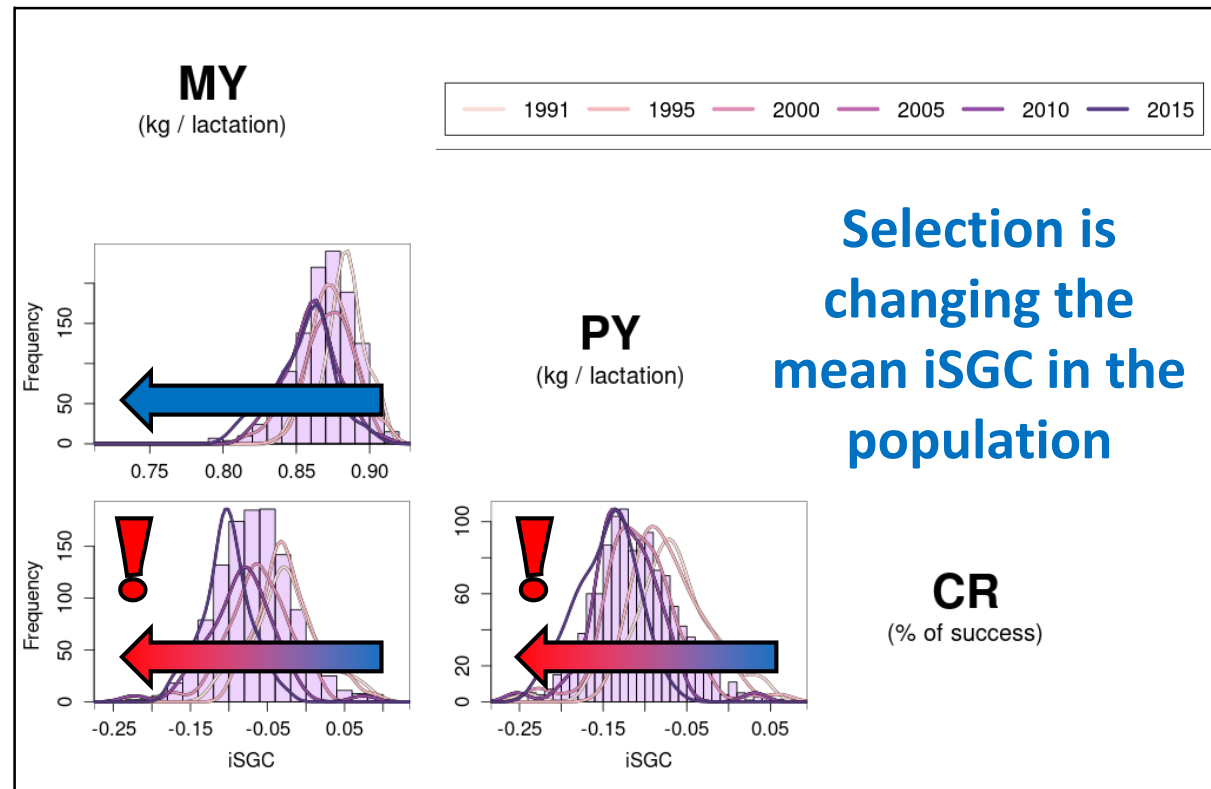
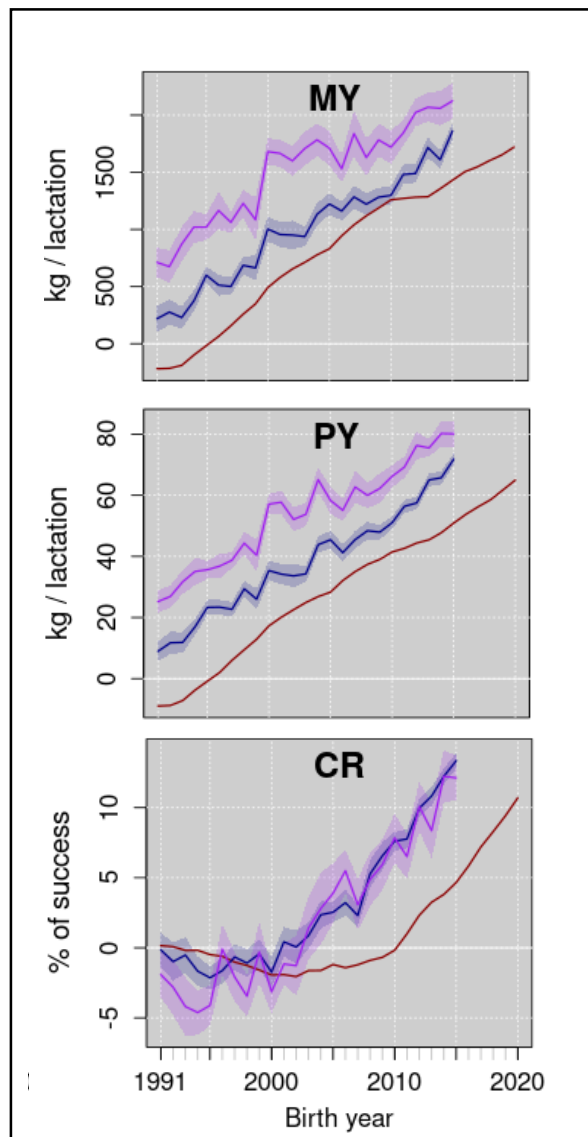


Genetic progress

— Bulls

— Cows

Sires with
500+
daughters



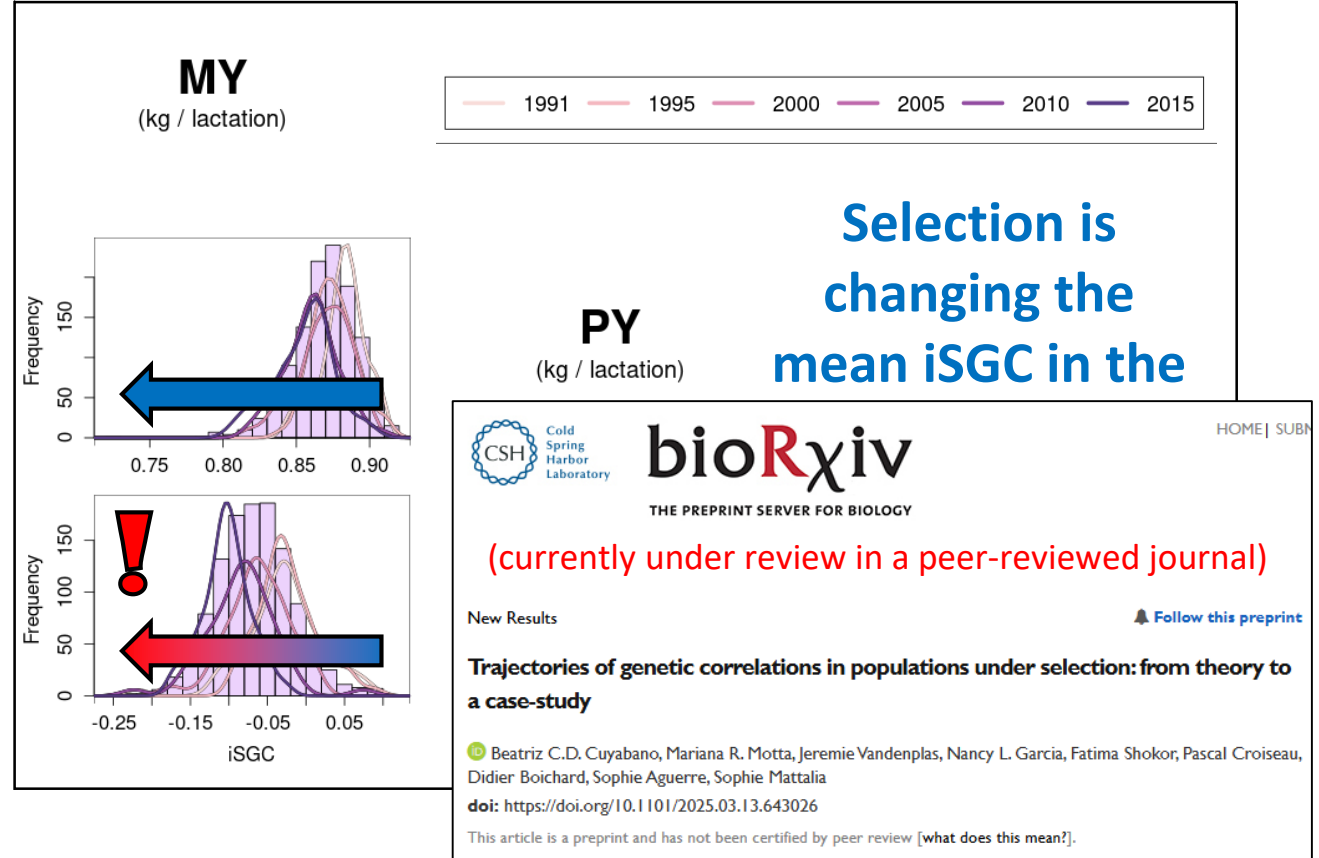
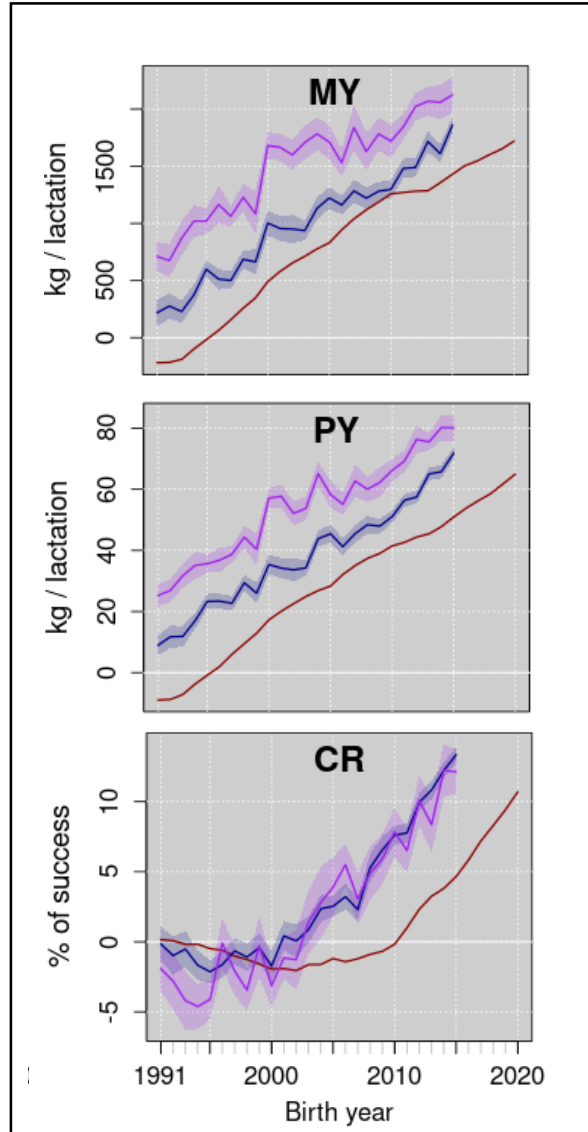
Positive genetic progress does not imply that we are breaking the genetic correlation between traits

Genetic progress

— Bulls

— Cows

Sires with
— 500+
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Genetic correlations in populations under selection:

+ ↘ always

- ↘ ↗ → depending on the weights in the selection index

**Could we select for less negative
genetic correlations?**

A heritable parameter

 To enable selection for genetic correlations, we need to know whether iSGCs are heritable,

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-  Variance component estimation on the iSGCs:

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-  To enable selection for genetic correlations, we need to know whether iSGCs are heritable,
-  Variance component estimation on the iSGCs:
 -  iSGC treated as the trait of interest,
 -  1161 sires with 500+ daughters, to whom iSGC were calculated,
 -  Pedigree tracing back four generations for each one of the sires: 5,811 animals.

A heritable parameter

	MY	PY	CR
MY	0.223 (0.001)	0.78 (0.05)	-0.15 (0.03)
PY		0.378 (0.001)	-0.20 (0.04)
CR			0.006 (0.002)

} Genetic parameters

A heritable parameter

	MY	PY	CR	Genetic parameters
MY	0.223 (0.001)	0.78 (0.05)	-0.15 (0.03)	
PY	0.45	0.378 (0.001)	-0.20 (0.04)	
CR	0.46	0.38	0.006 (0.002)	

h^2_{iSGC}

A heritable parameter

	MY	PY	CR
MY	0.223 (0.001)	0.78 (0.05)	-0.15 (0.03)
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Genetic parameters

h^2_{iSGC}

**iSGCs
are
heritable!**

Take-home messages

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 Defines the relationship between traits.

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Thank you for your attention!



INRAE



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