Analysis of methane measured in young dairy sires after accounting for variation in dry matter intake

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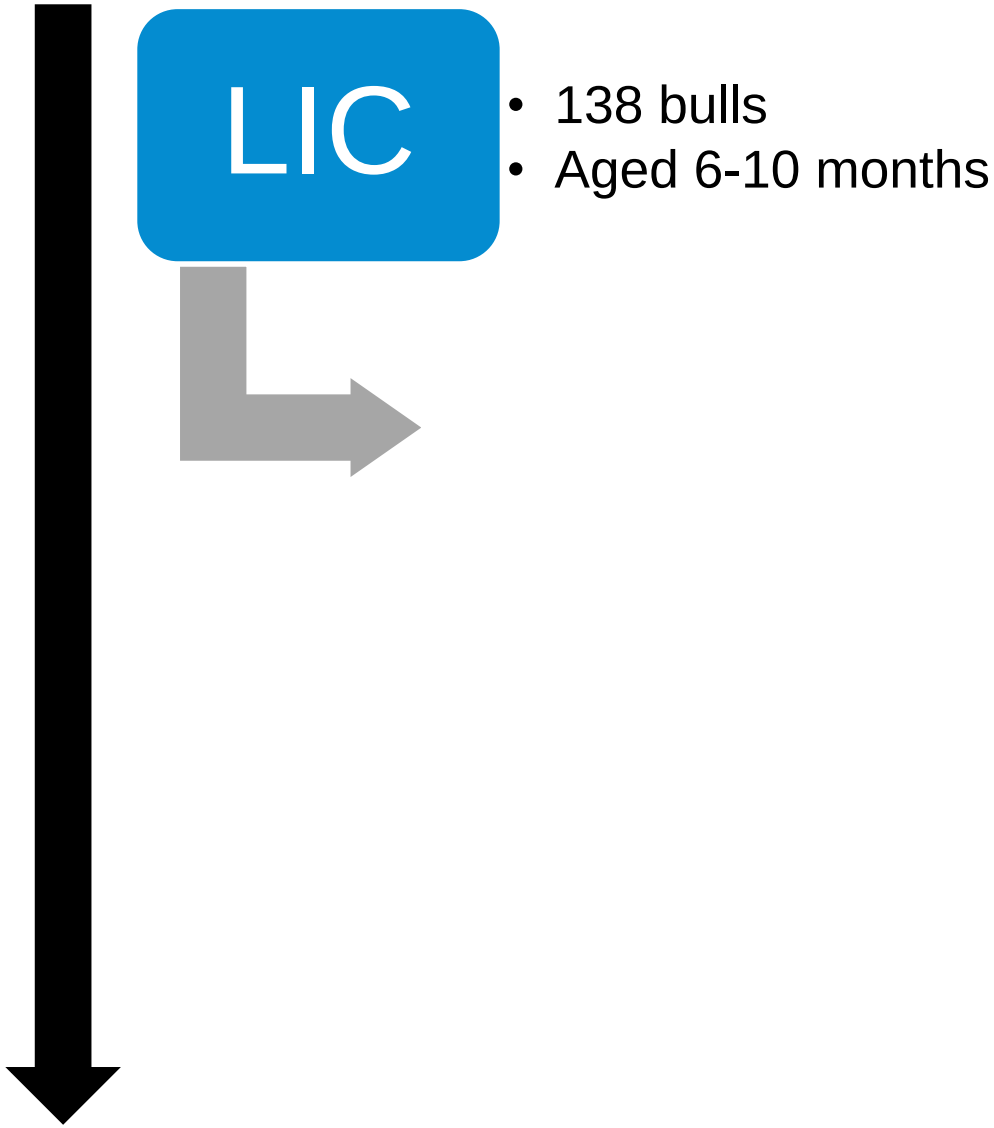
Data Collection Timeline

Feb 2021



- 138 bulls
- Aged 6-10 months

Dec 2022

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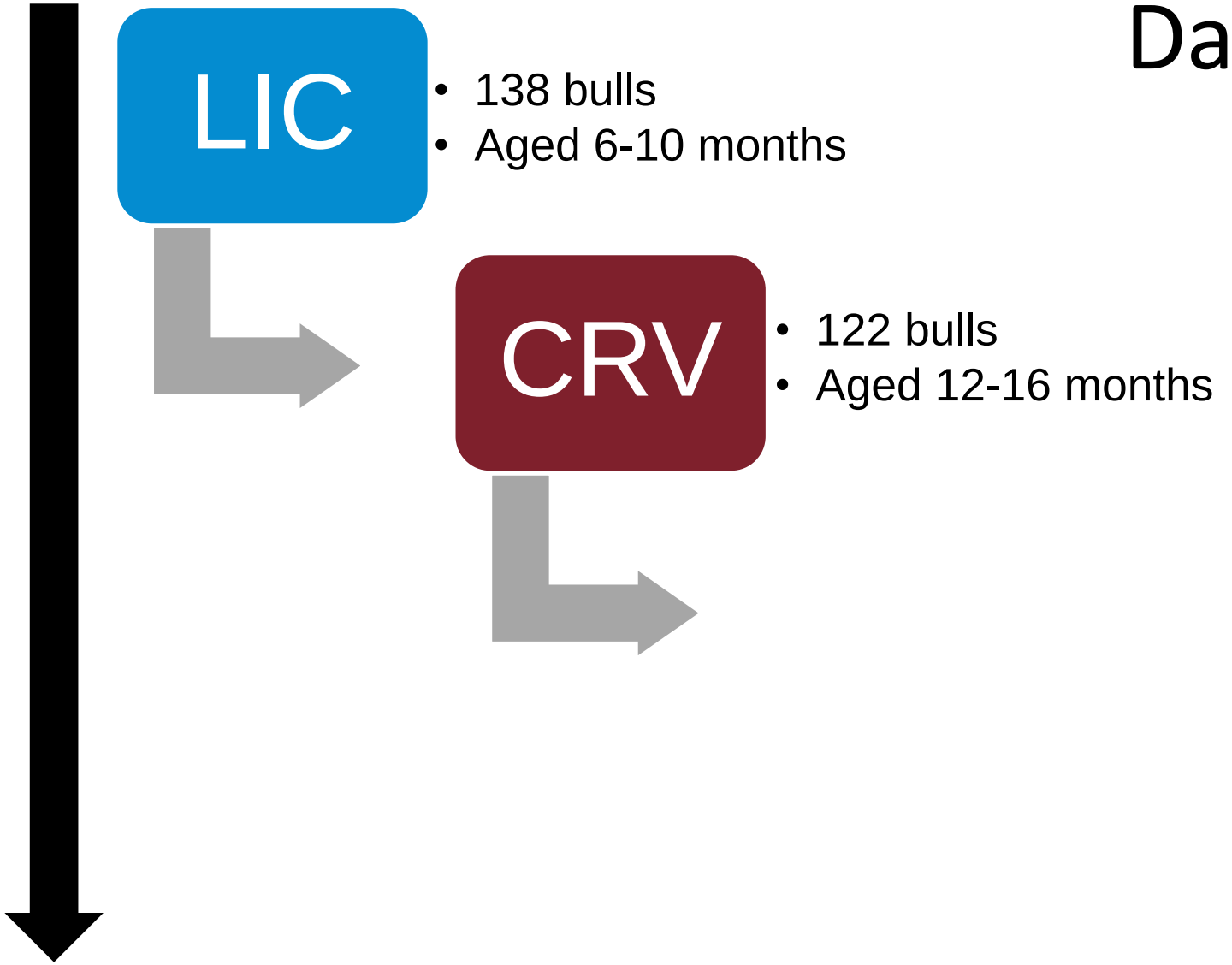
Data Collection Timeline

Feb 2021



Dec 2022

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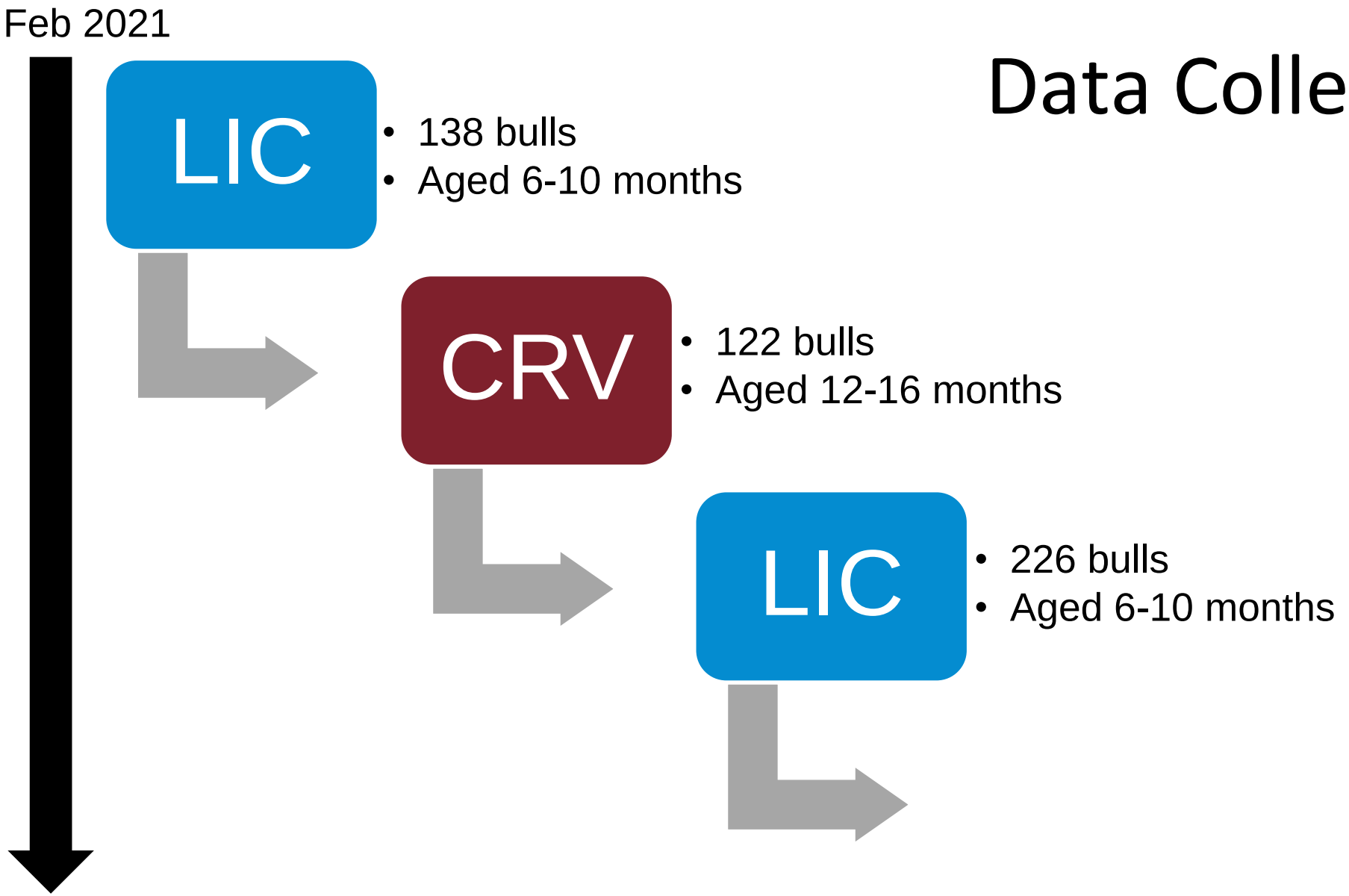
Data Collection Timeline



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Data Collection Timeline

Feb 2021

LIC
- 138 bulls
- Aged 6-10 months

CRV
- 122 bulls
- Aged 12-16 months

LIC
- 226 bulls
- Aged 6-10 months

CRV
- 45 bulls
- Aged 12-16 months

Dec 2022

531 bulls

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Data

- Daily methane (CH4; g/day)
  - Measured via Greenfeed visits
  - Visits vary in number and duration
  - Total time per day 120 to 4,222s (2-70 min)
  - Mean time was 893s (~15min)
- Daily dry matter intake of pen-fed animals
- Genotypes
  - A mix of panels of varying densities
  - Approximately 6,300 SNPs in common

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Model

- JWAS in Julia
- MCMC chains of 200,000 plus 25,000 chain burn-in keeping every 10th sample

- Y = CG + Year + pJ + het + BullPermEnv + BullBV + e

  - CG – day-group-pen assignment
  - Year – location-year combination
  - pJ – proportion of Jersey breed
  - het – heterosis coefficient between Holstein-Friesian and Jersey
  - BullPermEnv – random permanent environmental effect of bull
  - BullBV – random genetic effect of bull

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	CH4 (g/day)	DMI (kg/day)
Heritability	**0.10**	**0.10**
	(0.06, 0.16)	(0.05, 0.17)
Repeatability		
Genetic Variance		
Perm Env Variance		
Residual Variance		
Phenotypic Variance		

95% lower and upper credibility intervals in parentheses

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Heritability	**0.10**	**0.10**
	(0.06, 0.16)	(0.05, 0.17)
Repeatability	**0.30**	**0.37**
	(0.27, 0.34)	(0.34, 0.41)
Genetic Variance		
Perm Env Variance		
Residual Variance		
Phenotypic Variance		

95% lower and upper credibility intervals in parentheses

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Repeatability	**0.30**	**0.37**
	(0.27, 0.34)	(0.34, 0.41)
Genetic Variance	202	0.43
	(113, 325)	(0.22, 0.76)
Perm Env Variance	395	1.13
	(295, 498)	(0.85, 1.41)
Residual Variance	1,365	2.63
	(1,331, 1,398)	(2.57, 2.70)
Phenotypic Variance	1,961	4.19
	(1,869, 2,077)	(3.97,4.47)

95% lower and upper credibility intervals in parentheses

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Methane and Dry Matter Intake

	Correlations
Genetic	**0.48** (0.12, 0.73)
Phenotypic	**0.28** (0.24, 0.32)

95% lower and upper credibility intervals in parentheses

- Genetic correlations higher than phenotypic correlations
- 95% CI wider for genetic correlations than phenotypic correlations
- All have significant density above zero
- Selection for lower methane would be associated with lower intakes

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Residual Methane

Genetic and Statistical Properties of Residual Feed Intake

Kennedy B, Van Der Werf J, Meuwissen T

Journal of Animal Science, (1993), 3239-3250, 71

- Residual methane EBVs from a selection index using methane and DMI EBVs

- Residual methane that is independent of ***phenotypic*** DMI
  - Selection for genetic residual methane where correlated changes in DMI do not compromise the overall selection efforts

- Residual methane that is independent of ***genetic*** DMI
  - Selection for residual methane while holding DMI EBV constant

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Phenotypic regression

P =	CH4	DMI
CH4	1961	25.4
DMI	25.4	4.19

G =	CH4	DMI
CH4	202	4.6
DMI	4.6	0.43

$$\begin{bmatrix} \mathrm{var}(y_f) & \mathbf{c}'_s \\ \mathbf{c}_s & \mathbf{P}_s \end{bmatrix}$$

$$\begin{bmatrix} \mathrm{var}(g_f) & \mathbf{g}'_s \\ \mathbf{g}_s & \mathbf{G}_s \end{bmatrix}$$

$$\mathbf{b}'_s = \mathbf{c}'_s \mathbf{P}_s^{-1}$$

$$\mathbf{b}' = (1 - \mathbf{b}'_s)$$

b’ = [1 -6.06]

CH4_phen_EBV = CH4_EBV + -6.06*DMI_EBV

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Genetic regression

P =	CH4	DMI
CH4	1961	25.4
DMI	25.4	4.19

G =	CH4	DMI
CH4	202	4.6
DMI	4.6	0.43

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$$\begin{bmatrix} \mathrm{var}(g_f) & \mathbf{g}'_s \\ \mathbf{g}_s & \mathbf{G}_s \end{bmatrix}$$

$$\mathbf{b}'_s = g'_s G_s^{-1}$$

$$\mathbf{b}' = (1 - \mathbf{b}'_s)$$

b’ = [1 -10.7]

CH4_gen_EBV = CH4_EBV + -10.7*DMI_EBV

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EBV correlations

	CH4	CH4_phen	CH4_gen	DMI
CH4	1.00			
CH4_phen	0.97	1.00		
CH4_gen	0.90	0.98	1.00	
DMI	0.46	0.23	0.02	1.00

- CH4_phen_EBV = Methane_EBV + -6.06*DMI_EBV
- CH4_gen_EBV = Methane_EBV + -10.7*DMI_EBV

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Summary to date:

- Heritability and repeatability of daily methane yield in bulls were low to moderate
- Repeatability is not high so more measurements will improve prediction accuracy
  - but this comes at a cost (fewer bulls or larger facility)
- Genetic and phenotypic correlations between methane and DMI were positive
- After accounting for genetic variation in DMI, there was genetic variation in methane remaining

Scope exists to reduce daily methane yields while maintaining DMI

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