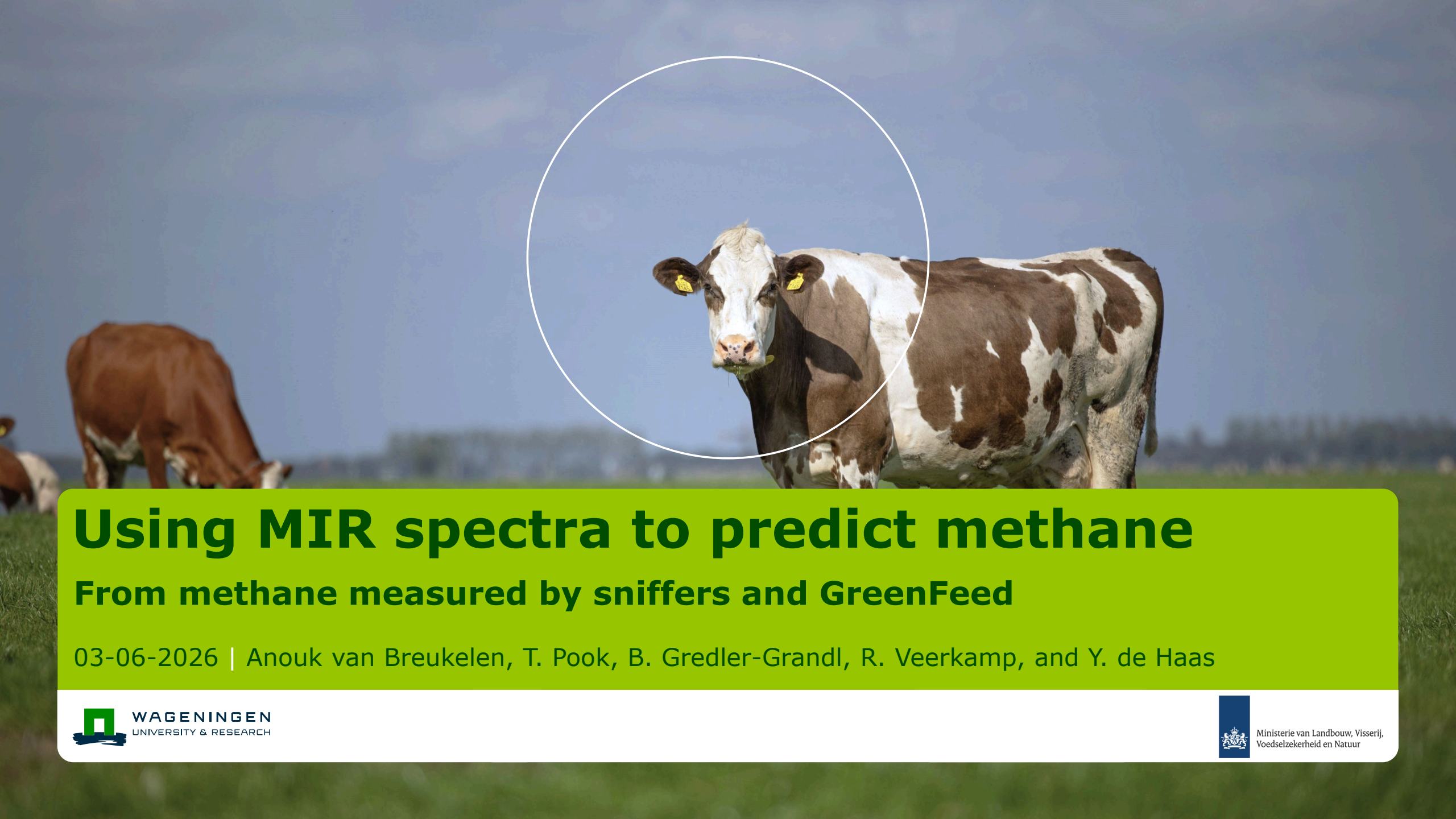


Using MIR spectra to predict methane

From methane measured by sniffers and GreenFeed

03-06-2026 | Anouk van Breukelen, T. Pook, B. Gredler-Grandl, R. Veerkamp, and Y. de Haas

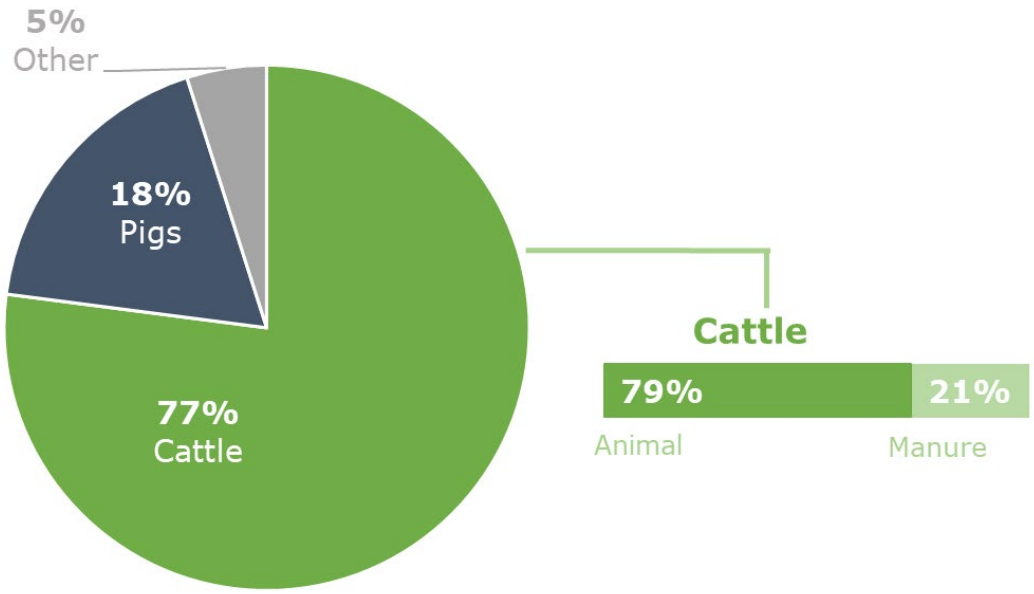
WAGENINGEN
UNIVERSITY & RESEARCH

Ministerie van Landbouw, Visserij, Voedselzekerheid en Natuur

Introduction

Methane emissions in the Netherlands

- 55% emission mitigation by 2030, and climate neutral in 2050
- 2/3rd of methane from farming

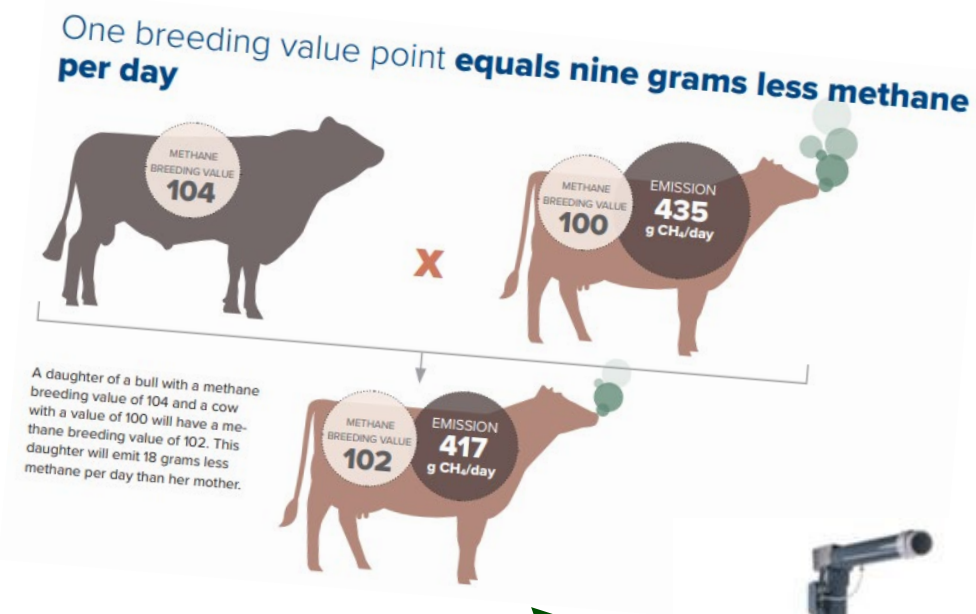


Bruggen et al, 2020

Introduction

Breeding for low methane

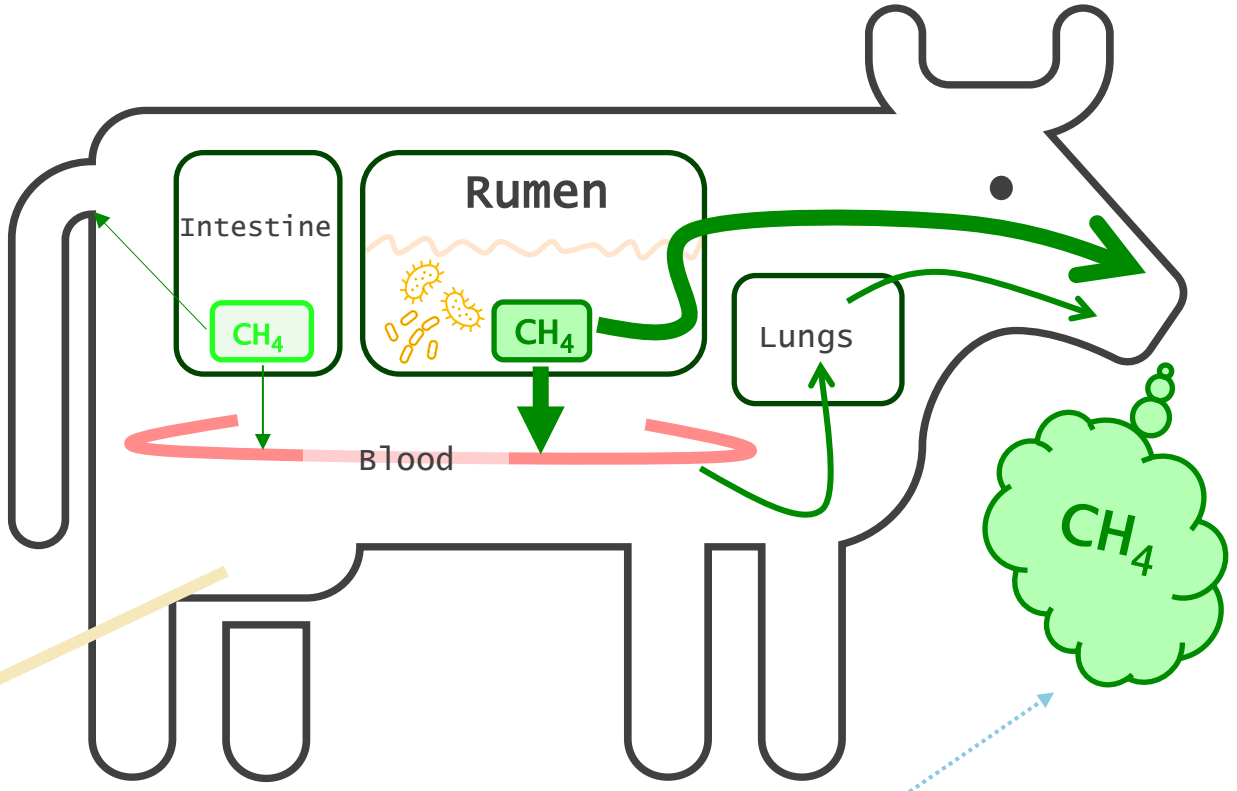
- Methane EBV based on sniffer and GreenFeed records
- Phenotyping is costly and labor-intensive
- Interest in other data sources to improve the reliability of methane EBVs

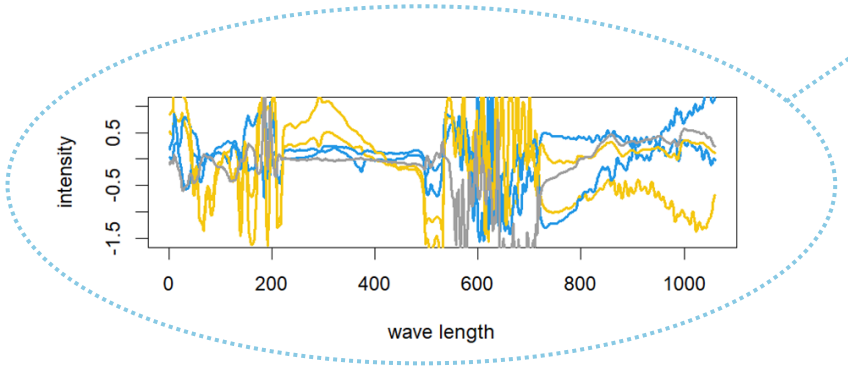


Introduction

Estimating enteric CH_4 from MIR spectra

- Accuracies in the literature range from 0.01-0.87





Predictive model

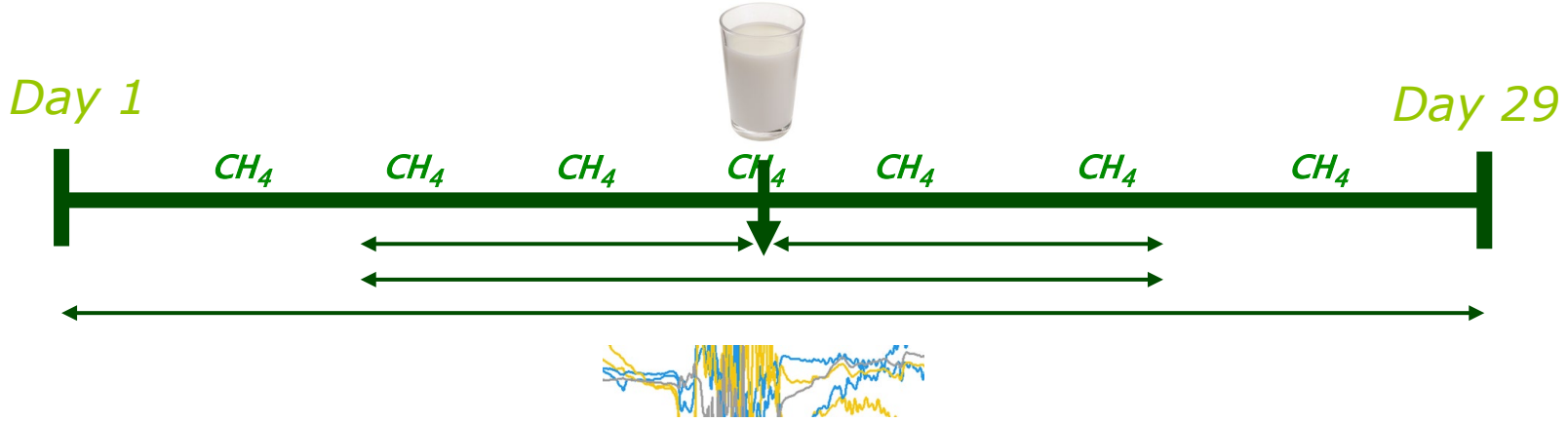
Objectives

- To predict enteric CH_4 of Dutch Holstein dairy cows from MIR spectra using large datasets with reference data collected with:
  1. The GreenFeed system
  2. Sniffers

Materials

GreenFeed or sniffer reference data

	Records	Cows	Farms	Mean CH_4
Sniffer	8,940	3,548	46	520
GreenFeed	1,541	789	12	446



- Average **CH_4 of 6 days before, after or 13/ 29 days around** the day of the MIR sample (including at least 14 visits)
- Up to 405 days in milk

Materials

MIR spectra

- 508 informative wavelengths used for prediction
- Pre-processing:
  - First-derivative Savitzky-Golay filter
  - Standardized by mean-centering and scaling
  - Smoothing
  - Outlier removal using Mahalanobis distances
- MY, DIM (using the first three Legendre polynomials), and parity as additional predictors

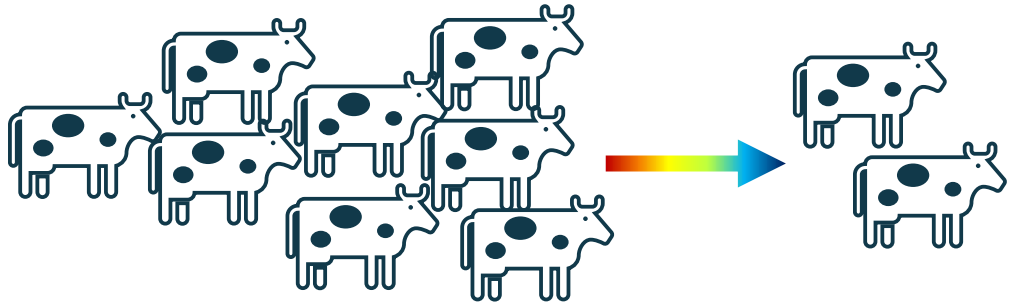
Methods

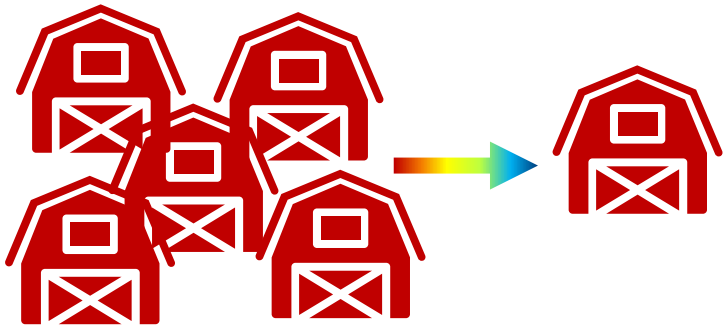
Partial Least Squares Regression (PLSR)

- The sniffer and GreenFeed reference data were modelled separately

- Validation scenarios:
  - Animal independent cross-validation
    - 80/20 train-test with 10-fold CV
  - Herd independent cross-validation
    - Leave-one-farm-out with 10-fold CV

  - Process repeated 15 times to report mean RMSE and r





Results

Trait definition and animal independent CV

- Models trained on GreenFeed data outperformed those trained on sniffer data
- Stringent data filtering may result in losing animals/ farms from the training set

	Sample	N anim	N rec	RPE	Accuracy	RMSE
Sniffer	6d before	951	1,500	34%	**0.42**	**237 ppm**
	6d after	884	1,342	34%	**0.31**	**244 ppm**
	13d	2,105	4,074	36%	**0.42**	**231 ppm**
	29d	3,548	8,940	37%	**0.40**	**225 ppm**
GF	6d before	522	835	19%	**0.60**	**86 g/day**
	6d after	471	727	17%	**0.57**	**76 g/day**
	13d	666	1,126	17%	**0.62**	**77 g/day**
	29d	789	1,541	17%	**0.62**	**79 g/day**

Results

Additional predictors

- Including spectra results in higher accuracies than the other traits
- Including MY and parity as predictors on top of spectra results in a minor improvement

		No spectra		With spectra	
		Accuracy	RMSE	Accuracy	RMSE
Sniffer	Spectra			**0.4**	**233**
	Parity	0.17	249	**0.42**	**231**
	MY	0.1	252	0.4	232
	DIM	0.04	253	0.4	233
	Parity + Breed + MY + ECM + DIM	0.18	249	**0.42**	**231**
GF	Spectra			**0.58**	**79**
	Parity	0.23	94	0.59	78
	MY	0.24	94	**0.62**	**76**
	DIM	0.13	96	0.58	79
	Parity + Breed + MY + ECM + DIM	0.34	91	**0.62**	**77**

Results

Leave-one-farm-out CV

- Predictions for **unseen farms** have lower accuracy

		RPE	Accuracy	RMSE
Sniffer	**Mean ± SD**	**47% ± 0.06%**	**0.13 ± 0.15**	**236 ± 69 ppm**
	Farm with lowest r	41%	-0.30	173 ppm
	Farm with highest r	107%	0.39	313 ppm
GF	**Mean ± SD**	**24% ± 6%**	**0.31 ± 0.20**	**102 ± 32 g/day**
	Farm with lowest r	32%	-0.16	135 g/day
	Farm with highest r	16%	0.59	70 g/day

Conclusions

- Phenotypes recorded by GreenFeed units outperform phenotypes recorded by sniffers
- Unable to accurately predict CH_4 for unseen farms
- Genetic analyses are needed to determine if the MIR predictions are heritable and genetically correlated to CH_4
  - Including across farms not present in the MIR calibration dataset

Thank you for your attention!

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