Measuring enteric methane in dairy cows in the Netherlands

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Introduction

- Anouk van Breukelen
  - PhD candidate at Animal Breeding and Genomics group, Wageningen Universiteit & Research (2020-2024)

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Projects

Ministerie van Landbouw, Natuur en Voedselkwaliteit

- **Climate envelope (start 2018)**
  - Methane measurements (Sniffer and Greenfeeds)
  - Genetic parameters, microbiability, N and P efficiency

- **Climate Smart Cattle Breeding (start 2020)**
  - Goal to develop breeding values for methane
  - Recording in milking robots on 100 farms
  - Parameter estimation and developing a selection index

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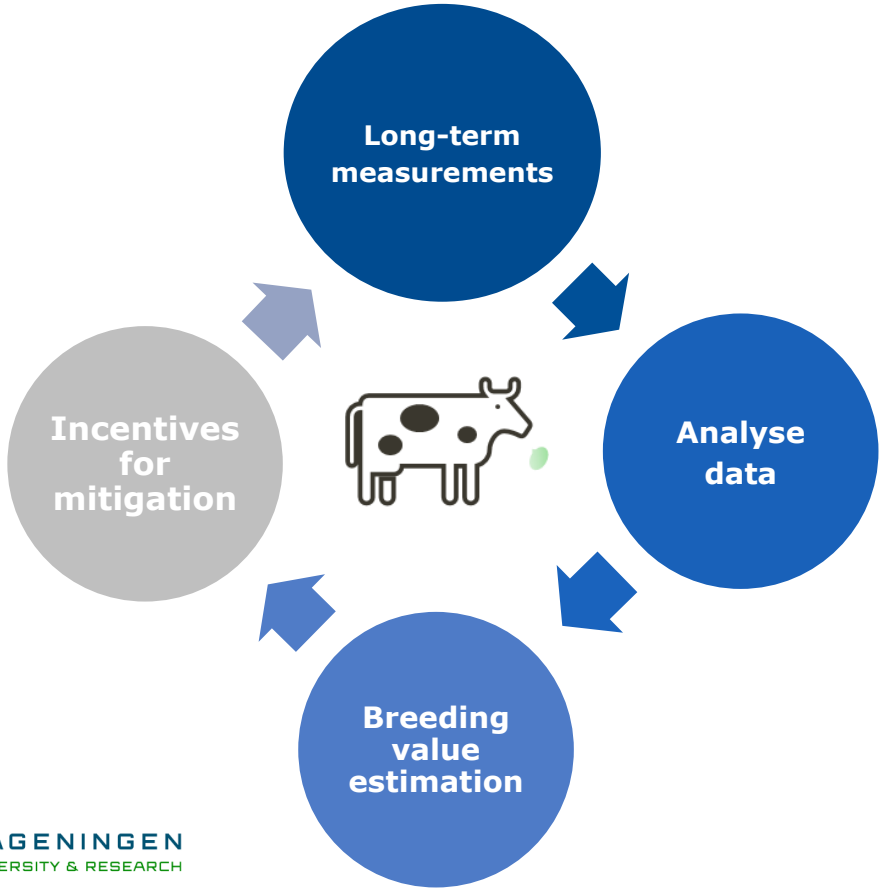
Climate smart cattle breeding



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Methods of measuring methane

Sniffer

- Installed nearby milking robot
- Measures concentration (ppm)
- High throughput
- Cost effective

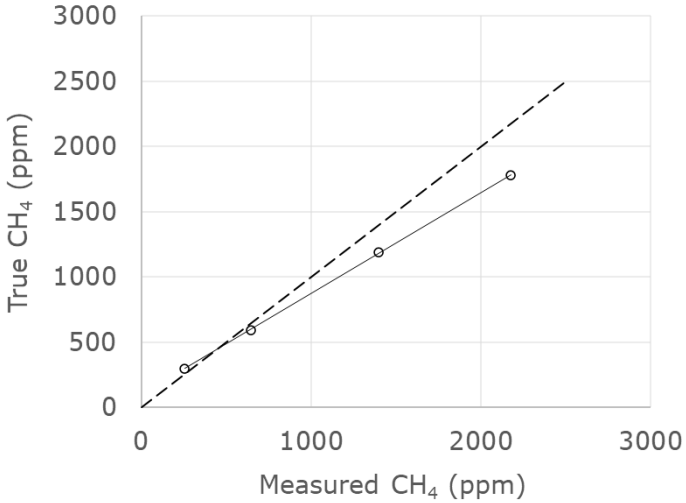
GreenFeed

(C-lock Inc. Rapid City, SD, US)

- Placed in the barn/ pasture
- Flux method (g/day)
- Medium throughput
- Costly
- Records head position

Developing a sniffer and lessons learned

- 17 first generation sniffers
  - WD-WUR, Carltech BV, NL
  - Prone to calibration drift
  - Accuracy limitations
  - Susceptible to environment
  - Difficult to carry and mount
  - Data transfer was constrained



Developing a sniffer and lessons learned

- 90 second generation sniffers
  - Improved housing
    - IP65 for barn conditions
  - Communication integration
    - SQL database uploaded to Microsoft Azure
  - Higher accuracy (potentially)
    - For future clients Carltech will implement a more stable but more expensive methane sensor
  - Still a developing technology

Installation of sniffers

- 60 sniffers currently installed on farm
- Aim to record on 100 farms
- Sniffers will be installed for 2 years
- Recording methane on over 15,000 cows

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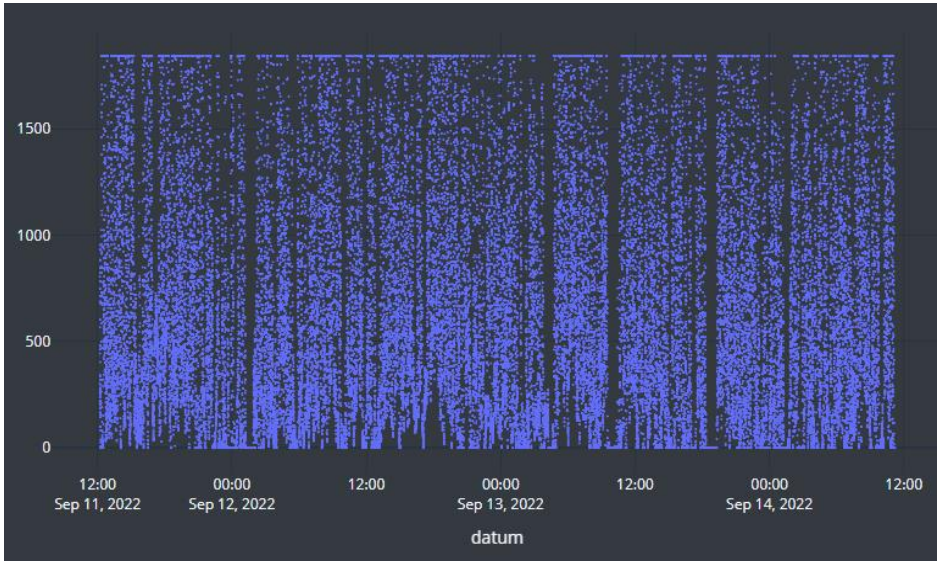
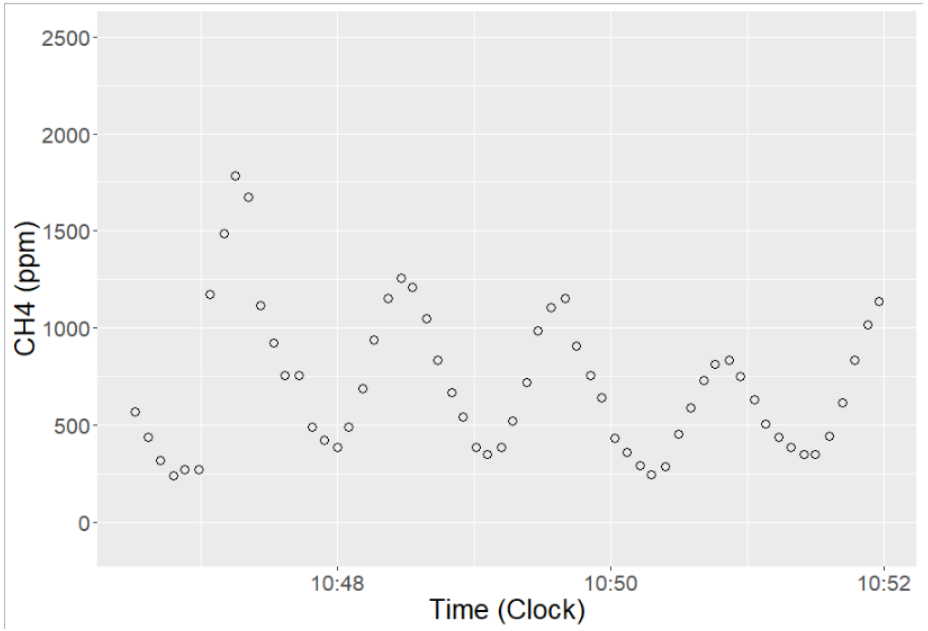
What we measure





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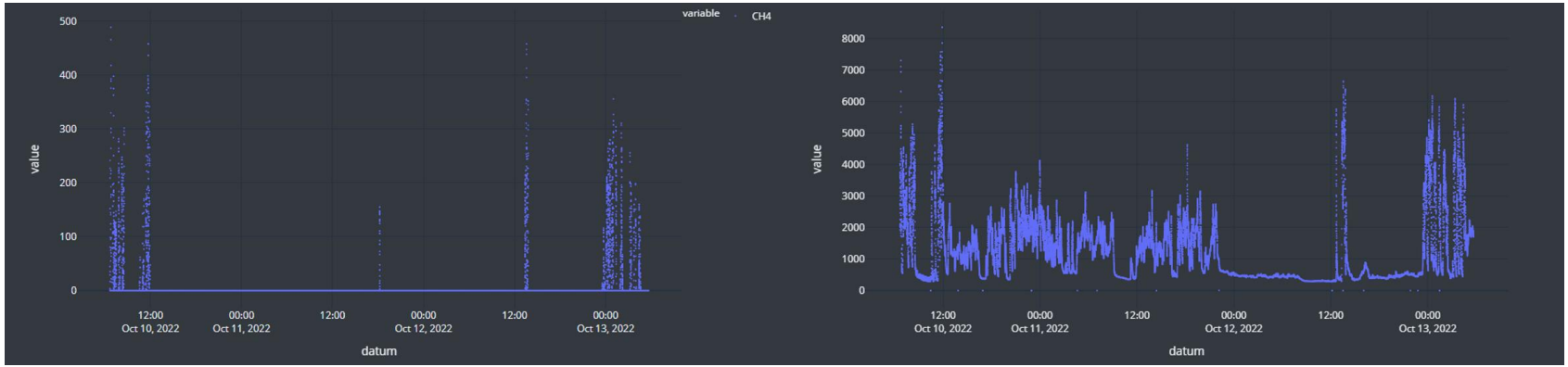
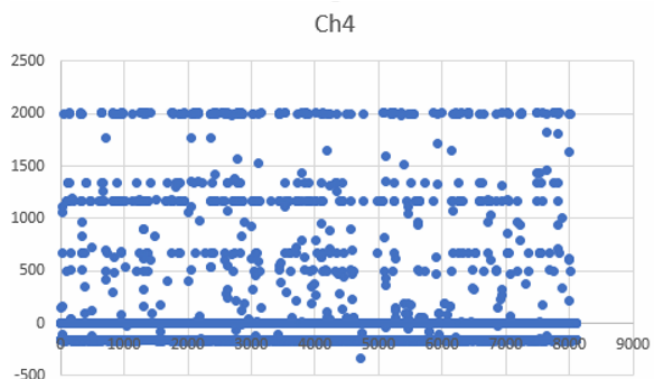
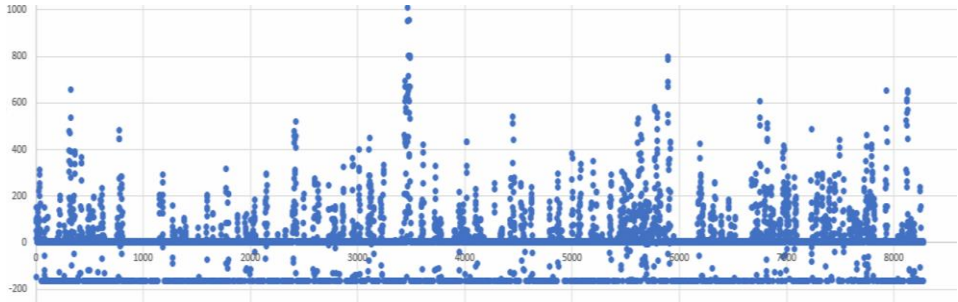
Filtering is essential







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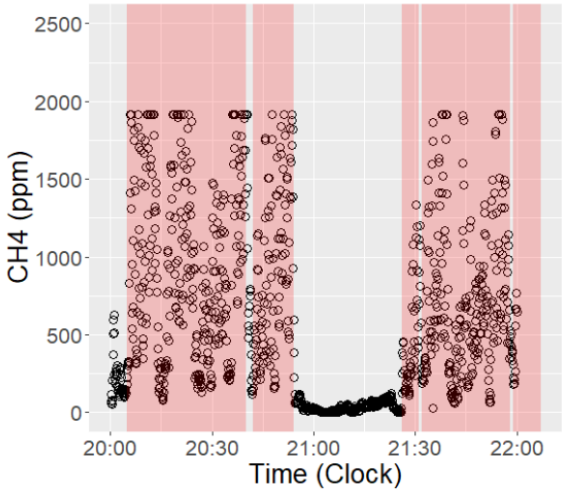
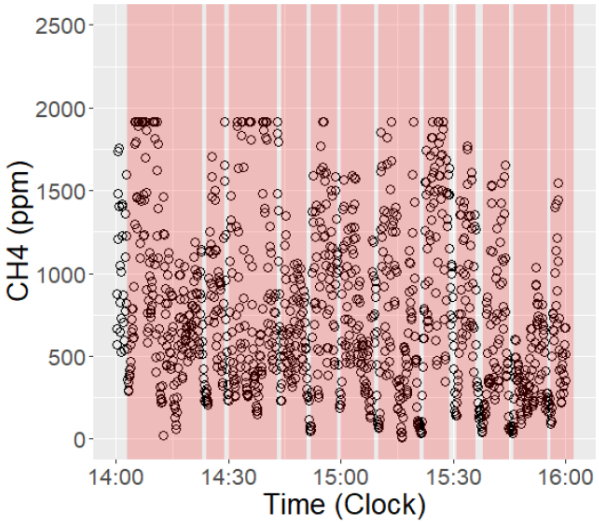
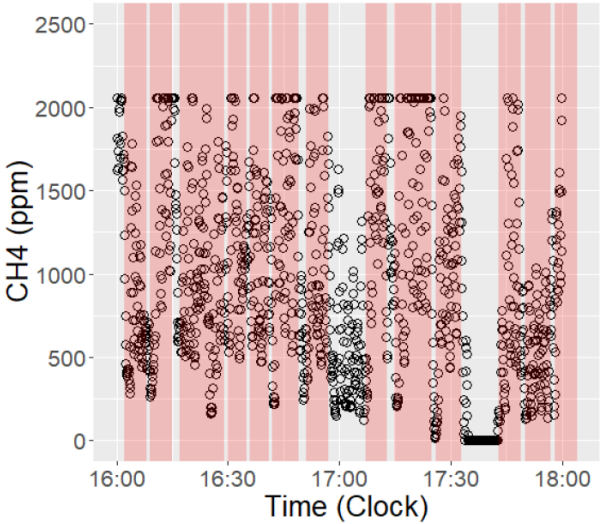
Matching methane with cow ID

- Using the IDs recorded by the milking robot
  - Based on timestamp, and an algorithm to check if the alignment is correct or delayed







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Sniffer data March 2023

	N farms	N cows	N records	Min records/cow	Max records/cow	Mean records/cow
Visit mean	54	6,516	604,565	1	271	56
Weekly mean	52	4,664	36,370	1	37	8

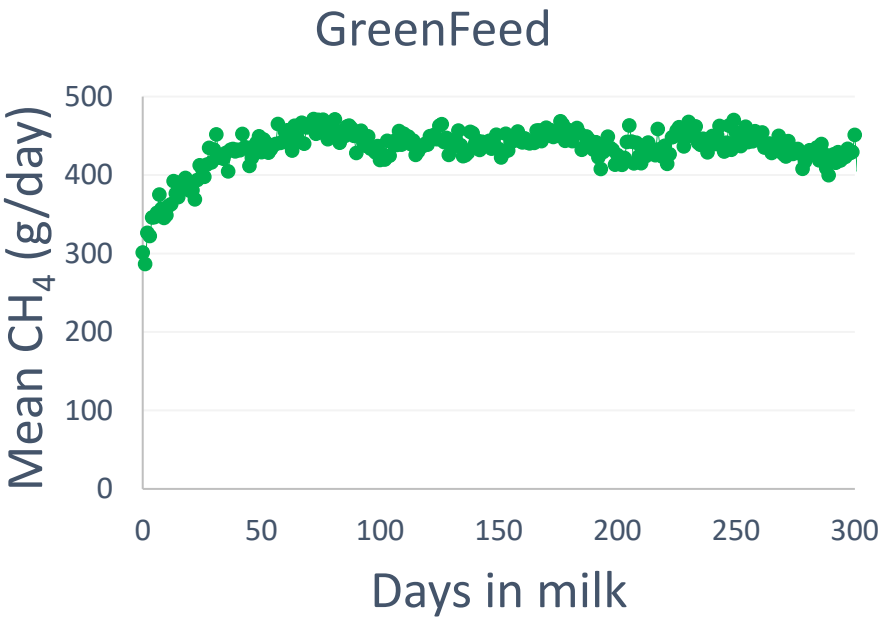
Research objectives (CSCB)

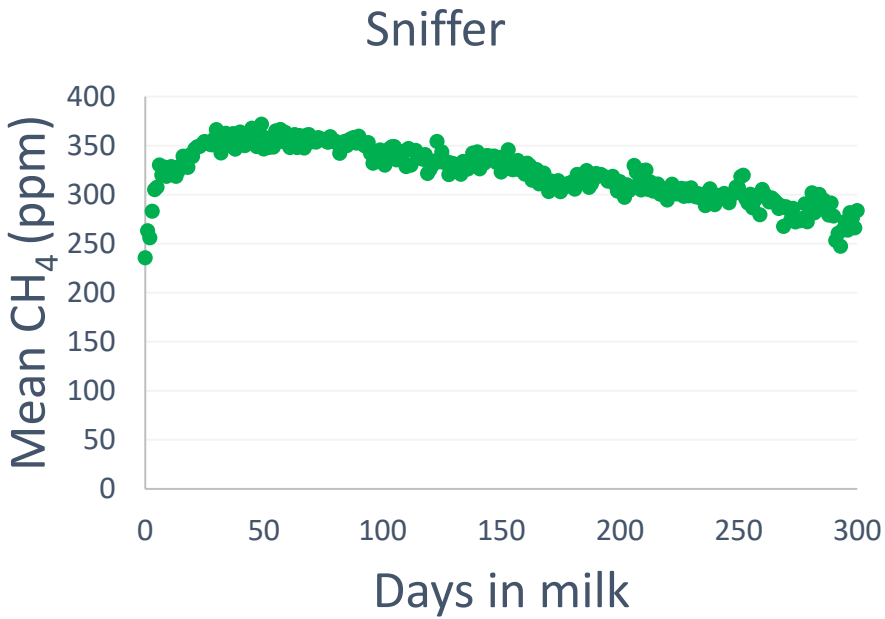
- Estimate genetic parameters
- Estimate phenotypic and genetic correlations with cows measured with sniffers and GreenFeed
- Estimate genetic correlations with other breeding goal traits

Material and methods

Number of	GF	Sniffer	Both total	Both recording overlaps
Farms	16	15	6	4
Cows	822	1,800	184	75
Daily records	24,284	170,826		1,786
Weekly records	4,358	30,982		334

Results: Phenotypic variation





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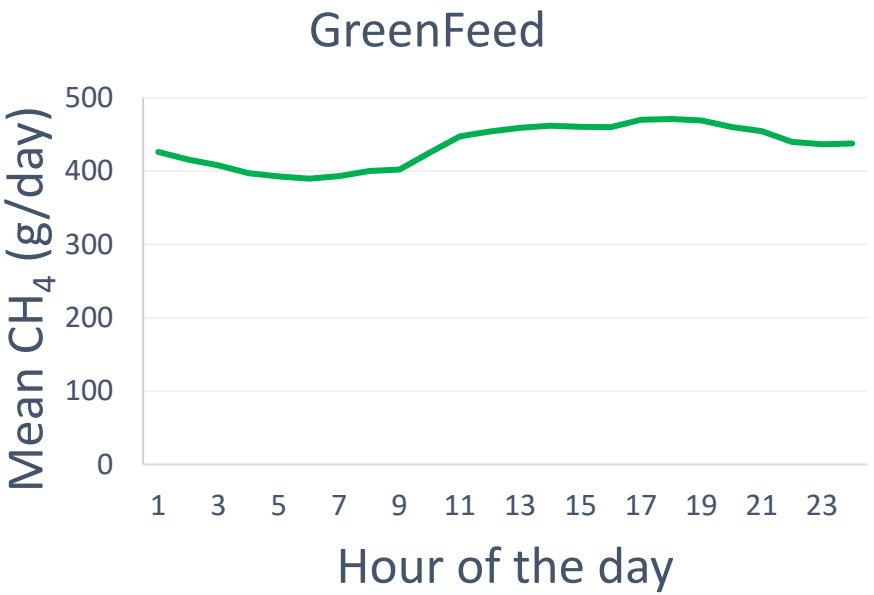
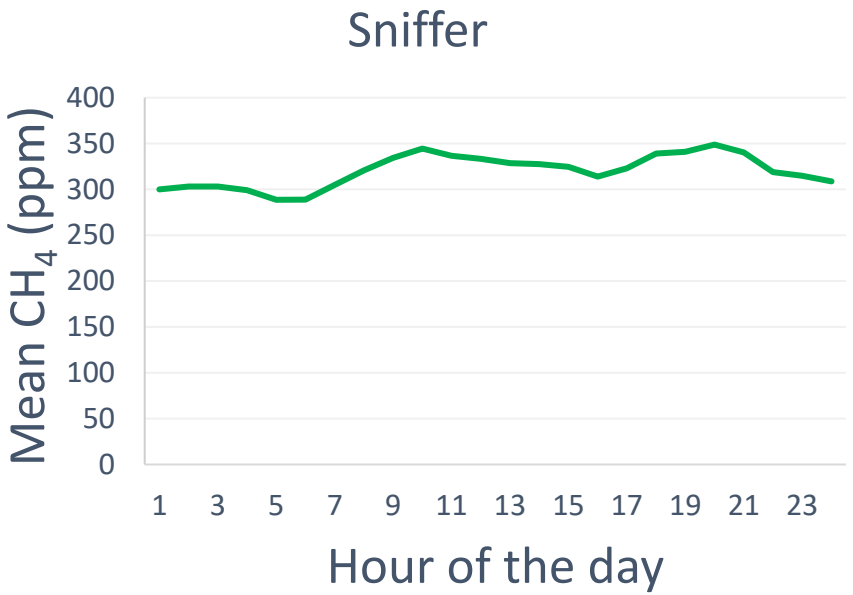
Results: Phenotypic variation





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Genetic analyses: Methods

- Visits corrected for hour of the day, before averaging per day/ week

$$y_i = \mu + Farm_i . \sum_{j=1}^{1} (\sin j\theta 2\pi + \cos j\theta 2\pi)$$

- Bivariate repeatability animal models in ASReml 4.2

Fixed effects:
- Herd x Year x Week
- Breed fraction x Breed
- Days in milk
- Parity

Random effects:
- Additive genetic
- Parity x permanent environmental
- Residual

Results: Parameter estimates weekly

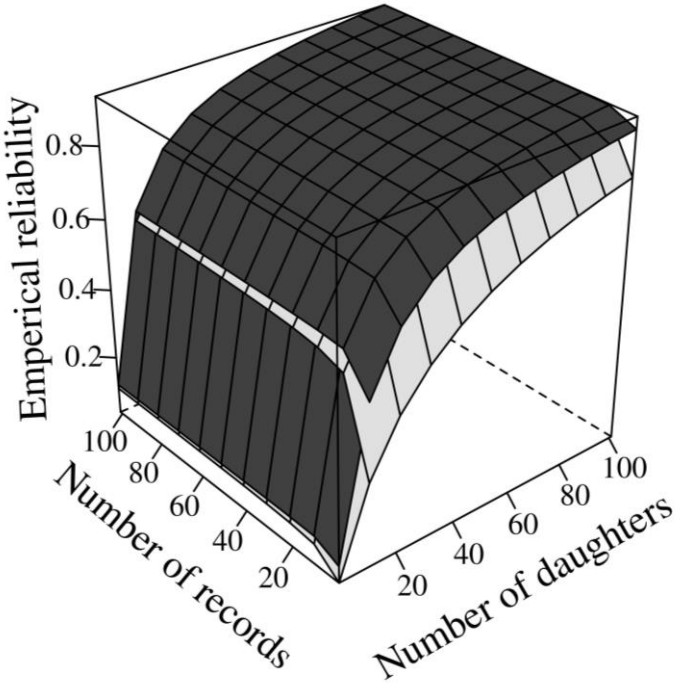
	GF CH_4	GF CO_2	Sniffer CH_4	Sniffer CO_2
GF CH_4	**0.33 ± 0.04**	0.75 ± 0.01	0.37 ± 0.05	0.19 ± 0.06
GF CO_2	0.65 ± 0.05	**0.34 ± 0.05**	0.31 ± 0.05	0.24 ± 0.06
Sniffer CH_4	0.76 ± 0.15	0.72 ± 0.16	**0.32 ± 0.02**	0.84 ± <0.01
Sniffer CO_2	0.41 ± 0.18	0.60 ± 0.17	0.93 ± 0.01	**0.32 ± 0.02**

Heritabilities are reported on the diagonal, phenotypic correlations above and genetic correlations below the diagonal

Number of records to estimate breeding values

$$r^2_{cow} = \frac{n_{rec} * h^2}{1 + (n_{rec} - 1) * rep}$$

$$r^2_{sire} = \frac{\frac{1}{4} n_{daugh} r^2_{cow}}{1 + \frac{1}{4}(ndaugh - 1) r^2_{cow}}$$



- For a reliability of 50% for a bull EBV we need 5 records on weekly mean CH_4, measured on 10 different daughters

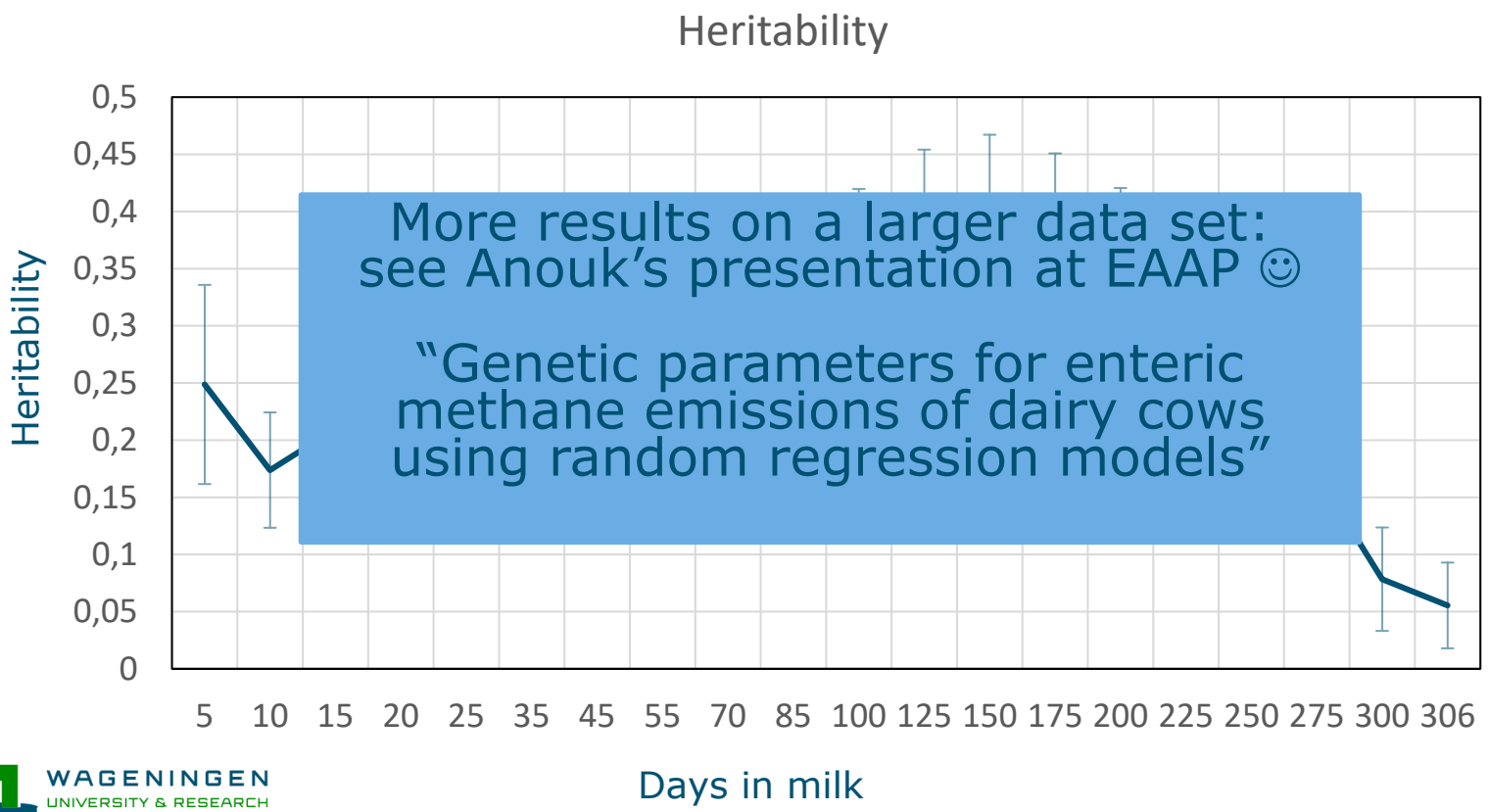
Current work: random regression model (first results)

- Model to estimate the genetic parameters:

$$y_{ijlk} = \mu + HJW_i + Par_j + \sum_{k=0}^{2} \emptyset(t)_{lk}\beta_k + \sum_{k=0}^{2} \emptyset(t)_{lk}a_{lk} + \sum_{k=0}^{2} \emptyset(t)_{lk}pepar_{lk} + e_{ijl}$$

- HYW: Fixed interaction between herd, year, and week of the measurement
- Par: fixed effect for parity
- Beta: Fixed regression on days in milk
- Random regressions on the additive genetic (a) and permanent environmental effect within parity (pepar)

Current work: random regression model (first results)



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Conclusions

- Methane measured by either device is heritable
- The moderate genetic correlation suggests, the two devices rank cows similarly from low to high emitting and that selection for lower CH_4 with either method will have the same directional effect
- Breeding values can be estimated with a moderate to high reliability

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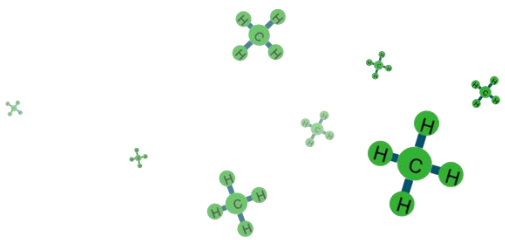

Publications

https://www.sciencedirect.com/science/article/pii/S0022030222001722

https://www.sciencedirect.com/science/article/pii/S0022030223001807

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