

# Current evaluation and methane index

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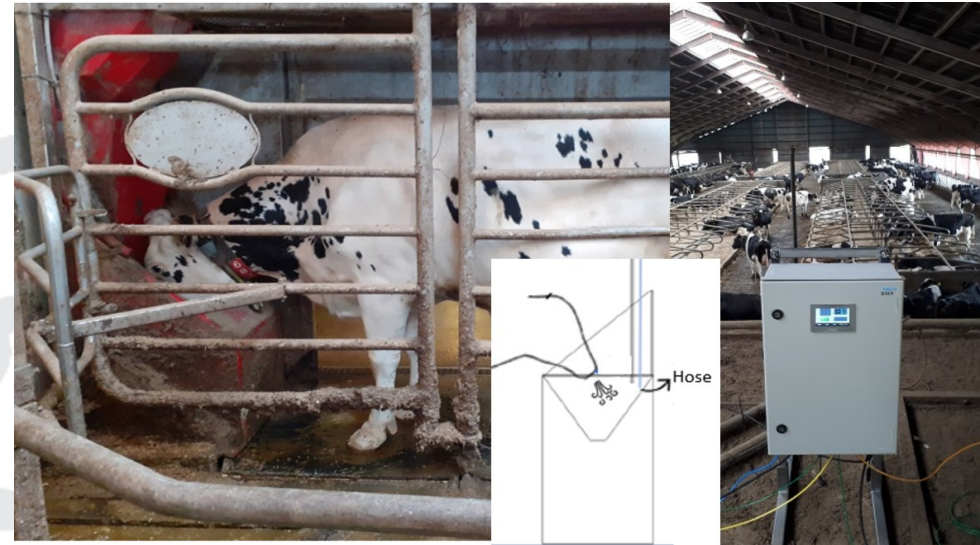


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# Data

- Methane index is based on sniffer data



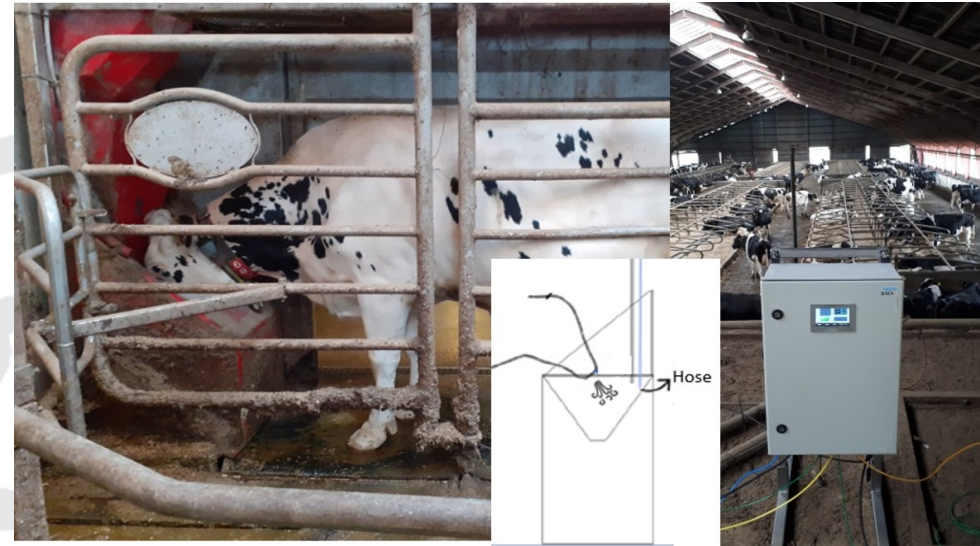
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# Data

- Methane index is based on sniffer data
- Data delivery



Aarhus University  
→ Data collection and processing to daily observations

Methane data

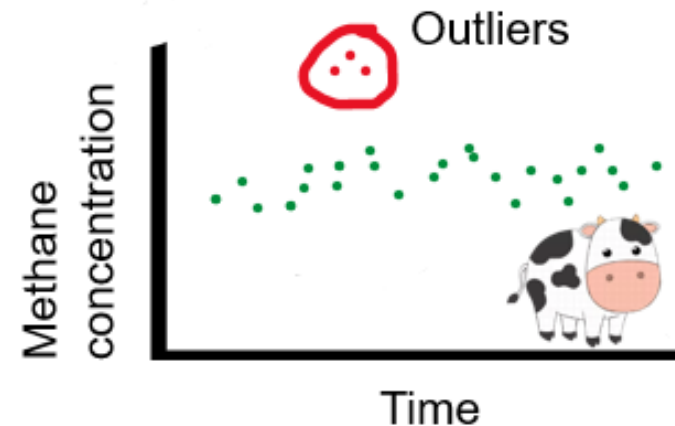
SEGES  
→ Data cleaning and genetic evaluation

- Four times a year: for the evaluations in february, **NAV** may, august, and november



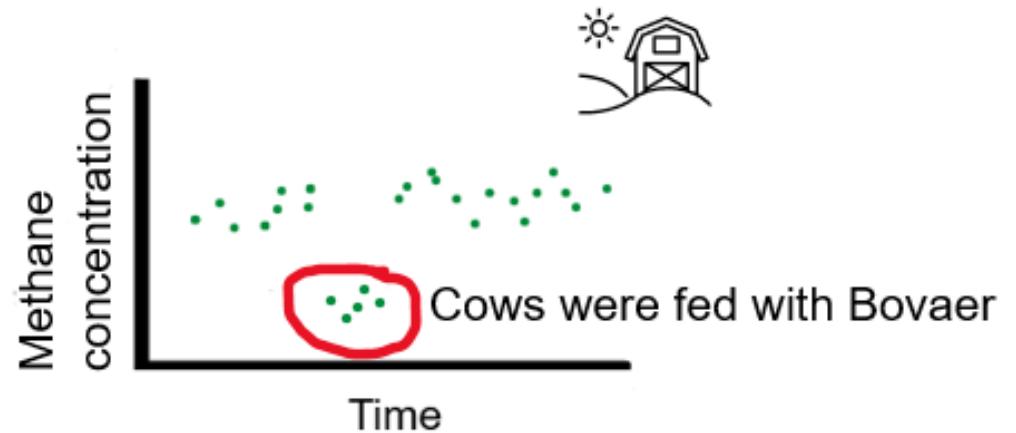
# Data editing

- Check for unreliable methane concentrations
  - Outside the calibration range of sniffers (10,000 ppm)
- Check for outliers
  - On cow & farm/day level
  - Are there some days / values that are off the range?



# Data editing

- 3-NOP (Bovaer) – data not included in current evaluation
- ☹️ No central registration of periods when Bovaer is fed
  - Current practice: contact farmers directly (very time consuming)
  - Solution: editing step to check the mean concentrations and report days when the methane concentration drops with 25 %



# Data editing

## Further filtering

- Observations between 1 and 365 days in milk
- Observations between parity 1 and 5
- Minimum 5 observations per lactation

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# Genetic evaluation

- Model developed at Aarhus University
- First parity and higher parities separately evaluated
  - More weight on higher parities (1:2)

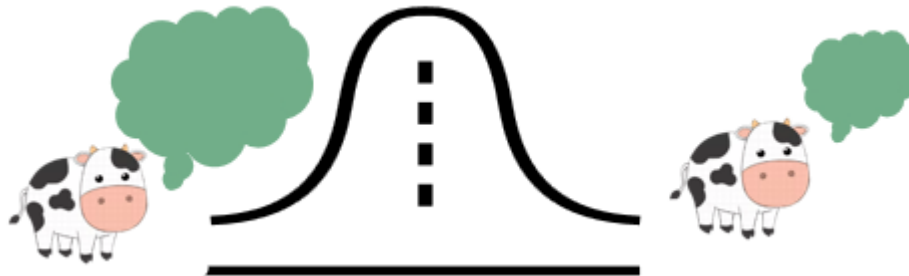
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# Genetic evaluation

- Single step model
  - ALL available information used at the same time (genotypes, pedigree, phenotypes)
- Breeding values multiplied with -1
  - Higher breeding values = less methane



<100 Breeding value >100

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# Genetic evaluation

- Single step model
- ALL available information used at the same time (genotypes, pedigree, phenotypes)

- **First publication May 2025 (only HOL bulls)**
- **Since May 2026: Breeding values calculated for all breeds and all animals**
- **BUT not included in NTM!**

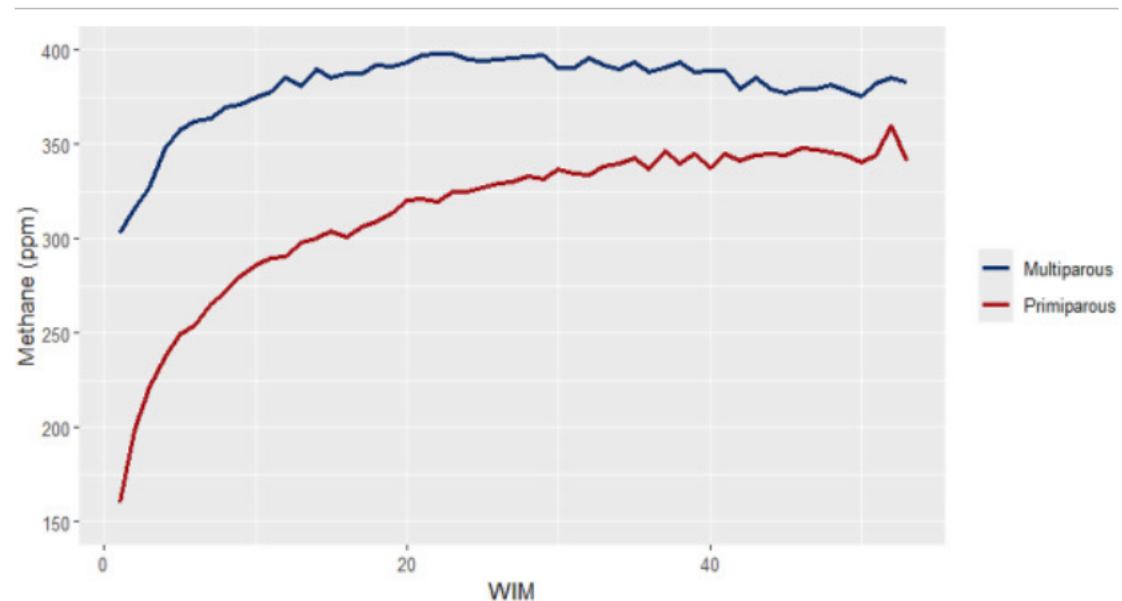
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# Genetic evaluation

Includes correction for

- Parity
- Lactation stage (week in milk)
- Herd-year-season x AMS x sniffer



Effect of week in milk

# Genetic parameters

- Heritability 0.13 for first parity, 0.19 for higher parities
- 13% / 19% of the variation is due to genetics!
- Other traits: milk yield 0.44, calving ease & mastitis 0.04

# Genetic parameters

- Heritability 0.13 for first parity, 0.19 for higher parities
- 13% / 19% of the variation is due to genetics!

## Why is that important?

- Higher heritability: Less data needed for high accuracy of breeding values and more genetic progress
- Methane is medium heritable  
→ Continuous data recording necessary!

# 10% best and 10% worst cows

- Cows ranged based on their breeding values

		First parity			Higher parities		
		Cows	Mean EBV	Mean CH4 (in ppm)	Cows	Mean EBV	Mean CH4 (in ppm)
HOL	10% best	181	116.68	296.75	358	118.34	295.56
	10% worst	181	81.99	562.56	358	83.08	666.65
JER	10% best	141	115.24	430.73	226	117.77	401.66
	10% worst	141	76.81	551.40	226	77.90	520.81
RDC	10% best	63	115.85	398.53	119	116.32	350.58
	10% worst	63	84.13	613.71	119	82.68	696.07

- Substantial difference in phenotypic measurements (e.g. 300 ppm for HOL)

# Conclusion

- Work in progress!
- International collaboration important to avoid duplication of work, maximize benefits by sharing data and improve efficiency and accelerate progress
- Current international and Nordic collaborations are already making a difference

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# Questions?

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