

# Abstract Submission Form

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**Preferred presentation**

Poster

**Preferred session**

Session 8: Global challenges in measuring methane in ruminants

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**Title of your paper**

Data Collection and Preparation for Genetic analysis of Methane Emissions in Danish Dairy Cattle

## Insert ABSTRACT text

In Denmark proposals ranging from 17 to 100 euros per ton CO<sub>2</sub>e have been suggested as a carbon emission tax for the agricultural sector to meet the legally binding 2030 greenhouse gas reduction target. Enteric methane (CH<sub>4</sub>) from cows' digestion is a significant contributor prompting interest in genetic selection for low CH<sub>4</sub> emitting dairy cows as one of the mitigation strategies.

To facilitate the development of a genetic model and conduct genetic evaluations for methane emission in dairy cattle it is necessary to establish a comprehensive database with individual CH<sub>4</sub> measures from numerous cows. This requires equipment that is affordable, can be installed on private farms, and has a high capacity to measure CH<sub>4</sub>. For this, we use sniffers based on the Guardian NG CH<sub>4</sub> sensor and an additional CO<sub>2</sub> sensor both measuring gas concentrations in robotic milking systems (AMS). These sniffers equipped with a two-channel multiplex setup are capable of measuring gas concentrations every second in AMS feed bins.

Currently, we are collecting CH<sub>4</sub> data from approximately 2,800 cows across 10 dairy farms daily. Our database holds gas records from about 12.300 cows across 33 herds comprising approximately 6,300

Holstein, 3,600 Jersey, 1,500 Red Danish Cattle, and 800 cross-bred cattle. Most sniffers are relocated between farms twice a year. Installation, daily data transfer monitoring, and equipment maintenance require ongoing technical assistance.

Given the high volume of data generated by each sniffer daily, there is a need for an automated pipeline to clean the data and ensure the creation of a high-quality dataset with reliable gas concentrations that can be converted into methane phenotypes to be used for developing genetic models. The initial step involves detecting equipment errors based on daily data reports. Equipment errors can be caused by various factors such as rodent damage, clogged filters, or broken parts.

Assigning gas measurements to individual cows relies on identification from the AMS system. We use a matching filter approach based on CO<sub>2</sub> concentration to test for time drift in the sniffer. If necessary, the time in the sniffer is synchronized with the AMS. Additionally, this method is used for quality control of sniffer data, with unclear signals during milking resulting in data discard.

To filter out environmental noise, reliable data is split into baseline readings when the AMS is not occupied, and cow data when the AMS is occupied. Idle periods are pruned to prevent carry-over effects from preceding or subsequent cows. Measured gas concentrations are affected by time, date, sniffer, and AMS unit. Linear mixed models are used to obtain estimates of the effects. Diurnal effects are modeled using a Fourier approach. Cow visits are likewise pruned in the ends. Moreover, for each visit, gas concentrations not significantly exceeding baseline are omitted to minimize records where the cow's head is away from the inlet. The remaining data is adjusted for baseline concentrations.

Phenotypes such as CH<sub>4</sub> concentration and CH<sub>4</sub>/CO<sub>2</sub> ratio for visit or week are calculated based on reliable data. Computation of other expressions of methane traits like methane production or intensity requires additional information such as milk yield. These phenotypes can be used for the development of genetic models.

## **Enter keywords**

enteric methane, dairy cattle, sniffer data, genetic selection, data preparation pipeline