

Data processing pipeline for peak alignment and background correction for methane measurements from sniffers installed in automatic milking systems

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HIGHLIGHTS

- Adjusted pipeline for processing of methane data from sniffers.
- Pipeline adjusts milking time allocation and background concentration correction.
- Background correction improves the average methane concentration level.
- New pipeline yields more accurate methane concentration phenotypes.
- New pipeline improves the reliability of the methane emission phenotype.

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ABSTRACT

Accurate measurement of methane concentration from dairy cows is essential for genetic evaluation and effective mitigation strategies. While sniffers installed in automated milking systems (AMS) provide a non-invasive method for capturing enteric methane emissions during milking, attributing these measurements to specific animals remains challenging. Simple timestamp synchronization between AMS and sniffer data is insufficient due to clock drift, cow behavior variability, and background methane interference. In this study, we present a data processing pipeline that enhances the alignment of methane measurements with individual milking events. The proposed pipeline consists of two key components: (1) a peak-detection algorithm that refines the start and end times of methane measurements to improve their attribution to specific milkings, and (2) an estimation of local background methane concentrations using plateau regions within each time series. This two-step approach enhances the accuracy of individual-level methane data and accounts for behavioral variability across cows. By improving the accuracy and reducing variance while maintaining the heritability and repeatability levels of sniffer-derived methane phenotypes, the proposed pipeline provides a practical foundation for large-scale phenotyping and supports the integration of methane traits into genetic evaluation and breeding programs aimed at reducing emissions.

1. Introduction

Methane (CH₄) is a greenhouse gas with a global warming potential greater than that of carbon dioxide (CO₂), despite its lower atmospheric concentration (Jeong et al., 2022). Due to its strong radiative forcing, methane plays a crucial role in climate change, making its mitigation a key target in global climate strategies (Intergovernmental Panel on

Climate Change (IPCC), 2023). In 2021, the Global Methane Pledge was launched under the leadership of the European Union and the United States, and by 2023, nearly 160 countries had joined, committing to reduce anthropogenic methane emissions by at least 30 % by 2030 (IEA, 2023). Ruminants, especially dairy cows, contribute to anthropogenic methane emissions through enteric fermentation. This need holds regardless of the mitigation pathway pursued, as both nutritional

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interventions (including feed additives) and genetic selection are recognized as viable approaches to reduce enteric methane in ruminants (Roques et al., 2024), with most methane being released via eructation during digestion (Hristov et al., 2013; Knapp et al., 2014; Haque, 2018).

A key aspect of reducing methane emissions through selective breeding is the ability to measure emissions from many individual cows, regardless of which methane-phenotype definition is employed (Manzanilla-Pech et al., 2025). Recent technological advances have focused on capturing high-volume methane emission data from dairy cows, particularly measured during milking in automated milking systems (AMS) (Zhao et al., 2020). These methods enable the collection of measurements in a production environment without interfering with an animal's natural behavior. Measuring methane in AMS most often involves using sensors that detect gas concentration in the air exhaled by cows, known as sniffers (Garnsworthy et al., 2012). Sniffer devices draw air samples from the feeder area via a sampling tube near the cow's nostrils. This technique provides a non-invasive and continuous method for monitoring emissions at the individual animal level, facilitating a better understanding of intra- and inter-animal variability in methane output (Garnsworthy et al., 2012).

High-throughput phenotyping, enabled by sensor technologies and automated systems, demands robust data processing and cleaning pipelines to generate reliable individual-cow observations for genetic evaluation (Klingström et al., 2025; Schodl et al., 2024). Next to the quantity of data required for breeding value estimation, a key parameter that impacts the reliability of the evaluation is the accuracy of emissions measurements. Here, the sniffers present several technical challenges despite guidelines for measuring methane emissions using sniffers (Jonker and Waghorn, 2020). Ensuring the accuracy of the collected data is difficult. Although sniffers are typically installed at the feeder station within the AMS, they are not an integral part of the AMS system. Aligning methane measurements collected with the sniffer to the identification number of the milked cow can be a significant challenge. Since sniffers and AMS units operate with separate clocks, timestamp misalignment can result in incorrect attribution of measurements to specific milkings (Jonker and Waghorn, 2020). Misalignment of the data, such as assigning data from one individual to another, assigning only part of the data from milking to an individual, or using an inappropriate background level to correct the measurements from a particular milking, may lead to less accurate genetic evaluations (Laner et al., 2011). Simply timestamp synchronization between the methane sniffer and the AMS is insufficient to ensure reliable attribution of measurements to individual cows, as it does not guarantee that recorded methane concentrations correspond to the animal being milked.

The assumption that milking time equals measurement time is often misleading. Methane measurements are valid only when the cow's head is near the sensor, and the animal is actively exhaling toward it. This behavior cannot be consistently predicted or controlled in most available sniffer devices. Moreover, determining the exact moment a meaningful reading begins, relative to the cow's entry into the milking stall, can be challenging. There may be delays in sniffers picking up the signal, which can complicate attribution. As a result, synchronizing based on timestamps alone does not ensure that the recorded measurement corresponds to the cow currently being milked.

Additionally, background methane concentrations and residual emissions from previous cows can interfere with subsequent cows' readings, further reducing the accuracy of individual-level data. Together, these factors highlight the need for a more robust, reproducible method for associating sniffer-based methane measurements with individual cows, beyond simple time-based synchronization. (Milkevych et al., 2022). Therefore, post-processing of the data is essential to filter out invalid measurements, accurately associate readings with individual animals, and ensure data quality.

Because the AMS and the gas analyzer operate as separate units and the latter continuously samples exhaled air, the data obtained during milking sessions undergo multiple processing stages. First, milking

events are identified based on patterns in methane concentration. Next, local baseline regions, representing background methane levels within the barn, are determined. This differentiation separates cow-related emissions from background levels caused by environmental factors such as barn ventilation, manure storage, or general air movement (Chadwick et al., 2011; Kuipers et al., 2025). Accurate background estimation is crucial for precisely quantifying individual animal emissions per milking event.

In our previous analyses using this dataset, we aligned milking sessions with methane measurements based on the AMS start and end timestamps. Frequent synchronization of the AMS and the sniffer clocks with the same time server was performed to prevent the time drift effect, and milking times were additionally adjusted to account for the experimentally determined time lag of the sniffer device (Pszczola et al., 2017). These analyses yielded results comparable to those of other experiments conducted at the time. Nonetheless, more advanced data post-processing could lead to more reliable results.

To address these limitations, a post-processing approach is required that refines both the temporal attribution of methane measurements to individual milking events and the estimation of local background methane concentrations. The main objective of this study was to develop and validate a data-processing pipeline to improve the accuracy and repeatability of methane phenotypes derived from sniffer data collected in automated milking systems, thereby enhancing their applicability for genetic evaluation and methane mitigation strategies in dairy cattle.

2. Materials and methods

2.1. Methane measurements

The Local Ethical Committee approved all animal treatments for Experiments on Animals in Poznań, Poland (decision number 64/2012).

2.2. Measuring set-up

The CH₄ measurements were collected on Polish Holstein-Friesian cows at two commercial farms in western Poland. Methane emission on Farm 1 was measured during 2 periods: one from December 2, 2014, to February 3, 2016, and the other from June 1, 2016, to September 17, 2016. On Farm 2, the measurements were taken from February 5, 2016, to March 14, 2016. The measurements were recorded during milking in an AMS (Lely Astronaut A4; Lely Holding, Maassluis, the Netherlands). Methane concentration was measured using an FTIR analyzer (GASMET 4030; Gasmet Technologies Oy, Helsinki, Finland). Air was sampled at the feeding bin of the AMS unit using a heated sampling line. Measurements were taken continuously and stored in the dataset every 5 s as 5-second averages. Every 24 h, gaseous nitrogen was used to automatically adjust the analyzer's zero point. The sniffer system clock was synchronized with an external time server every 24 h, and each gas measurement was timestamped. Farm 1 was equipped with 3 AMS units, and Farm 2 had 2 AMS units. At each farm, the methane concentration in the AMS units was measured over a 24-hour period. The change between AMS units was performed automatically (Pszczola et al., 2017). Timestamps indicating the start and end of milking events were obtained from the AMS systems. The system time on the computer where the AMS system was installed, used to timestamp milking event data, was synchronized every 24 h with the same external time server as the sniffer system. The methodology used for previous methane measurements calculations, including data description, is provided in (Pszczola et al., 2017).

2.3. Data processing

The data processing and background correction pipeline presented in this paper (Fig. 1) integrates methane concentration measurements obtained from the sniffer system with milking event information from

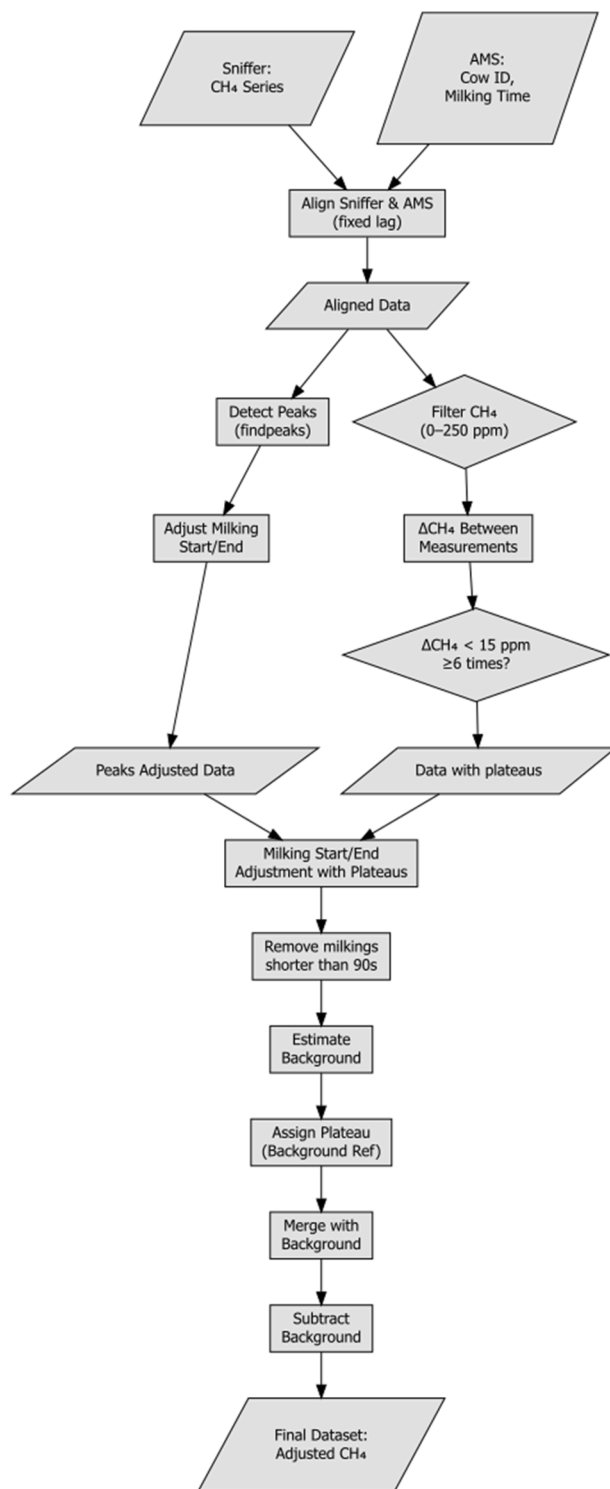


Fig. 1. Flowchart of the data processing pipeline.

the AMS. A total of 479 unique cow IDs were recorded. On average, 100 milking events per cow were registered, resulting in 47651 milking events in total. The 26662 daily methane phenotypes were calculated, yielding an average of 56 per cow. For methane measurements to be suitable for genetic analyses, they must be accurately linked to the specific animal contributing the emission signal. Because the RFID system used in the AMS does not allow unique animal identification for proprietary reasons, direct matching was not possible. Therefore, CH₄ measurements were aligned with AMS milking records through

timestamp synchronization. The initial temporal alignment used a manual fixed time shift to account for the sniffer device's response delay. This delay was experimentally estimated from a subset of randomly selected milking events and assumed to remain constant throughout the measurement period.

2.4. Peaks identification

After timestamp synchronization between the two systems, the methane time series underwent automated peak detection to identify local maxima associated with the start and end of milking events. Peak detection was performed using the *findpeaks* function from the *pracma* package version 2.4.4 (Borchers H.W., 2023) in R 4.5.0 (R Core Team, 2025) with default parameters (*nups* = 1, *ndowns* = *nups*, *zero* = "0", *peakpat* = NULL, *minpeakheight* = -Inf, *minpeakdistance* = 1, *threshold* = 0, *npeaks* = 0, *sortstr* = FALSE). Peaks were used to define preliminary milking boundaries: the onset of a milking event corresponded to the first peak initiating an increase in methane concentration, whereas the termination corresponded to the end of the final peak within that segment. These boundaries were refined through inspection of plateau regions located immediately before or after the milking. If a plateau flanked a milking event, the start or end time was adjusted accordingly. Milkings containing internal plateau segments - indicating periods without a cow present - were removed from further processing.

2.5. Background correction

Once the corrected milking intervals are established, the methane data undergo initial preprocessing. For plateau identification, only methane measurements within the 0–250 ppm range were considered to eliminate extreme or implausible values. Differences between consecutive methane measurements (ΔCH_4) are then calculated, forming the basis for identifying plateaus. Plateau regions are defined as sequences of at least six successive measurements with ΔCH_4 values below 15 ppm, representing periods of stable methane concentrations unrelated to cow presence.

After identifying plateau regions, they were used to estimate the background of methane concentration associated with each milking event. For every plateau, the mean CH₄ value, the first quartile, and the duration of the plateau were calculated. Only plateaus with first-quartile CH₄ concentrations between 7 and 50 ppm and durations shorter than 2500 s were retained for further analysis to avoid extreme or unrepresentative values. Each milking was assigned to the nearest qualifying plateau, and the first quartile of that plateau was used as the background concentration. This background value was then subtracted from all CH₄ measurements within the milking. Negative corrected values resulting from this subtraction were removed as they were considered erroneous. Plateau duration distributions were summarized using histograms, and scatter plots evaluated the relationship between plateau duration and background CH₄ concentration.

To evaluate the influence of background correction on methane concentration levels, the mean CH₄ values per milking event were computed for the dataset before and after background correction.

To ensure reliable phenotyping, milking events shorter than 90 s were removed as they were considered unlikely to capture representative methane emission patterns. The remaining dataset constituted the final, corrected, and time-aligned methane concentration profiles per milking.

2.6. Performance evaluation

To validate the accuracy of the proposed pipeline, a manual verification procedure was performed. A random sample of 100 milking events was selected, and for each case, methane emission time series plots were generated with algorithm-predicted milking events overlaid. These plots enabled precise visual annotation of the actual start and end

points for each milking period. This manually labeled dataset served as the ground truth for quantitative evaluation. The algorithm's performance is compared to the existing method (Pszczola et al., 2017) using boundary-based and classification-based metrics. The mean absolute error (MAE) is computed for start and end point predictions:

$$MAE = \frac{\sum_{i=1}^n |y_i - x_i|}{n}$$

Where: n - number of observations, y - predicted time, x - visually identified time.

Classification quality was evaluated using the F1-score by:

$$F1 = \frac{2 \cdot TP}{2 \cdot TP + FP + FN}$$

Where: TP - True Positive, occurs when the algorithm identifies a particular timepoint as part of a milking event, and the visual identification confirms that milking was indeed taking place at that time. FP - False Positive, refers to a time point the algorithm classifies within a milking event, while visual identification does not confirm that. FN - False Negative, is a time point that the algorithm classifies outside a milking event, although the visual inspection indicates that this point occurs within a milking event. TN - True Negative, occurs when both the algorithm and the visual inspection agree that a particular timepoint is not part of a milking event.

F1-score ranges from 0 to 1, where a score of 1 means perfect classification. To statistically evaluate whether the new algorithm provided a significantly better fit to the ground truth compared to the data before correction, a paired Wilcoxon signed-rank test was applied to the F1-score across all validated milking events.

The MAE assesses how precisely the algorithm localizes event boundaries, while the F1-score measures how well it identifies the full duration of milking events. Using both metrics provides a more comprehensive evaluation of the algorithm, capturing both boundary detection accuracy and overall classification performance.

2.7. Repeatability and heritability

To evaluate the impact of the proposed pipeline on genetic evaluation, we estimated repeatability and heritability for phenotypes obtained with the old and new pipelines. The analyzed phenotype was the average methane concentration during milking. Before averaging, the appropriate background concentration was subtracted from each measurement to ensure accurate results. The milking averages were then corrected for the effect of the AMS used to take the measurements and diurnal variation of methane concentration using the following linear regression model:

$$CH_{4ijkl} = AMS_j + DiurnalPattern_k + e_{ijkl},$$

where CH_{4ijkl} is the average methane concentration during a milking session l , measured in automatic milking system (AMS) j at time-of-day k . The correction was performed for each herd separately. The $DiurnalPattern_k$ was modelled using a 5th order Fourier series as suggested by Løvendahl and Bjerring (2006).

$$DiurnalPattern_k = \sum_{n=1}^5 (\beta_{1,n} \sin(n\phi_k) + \beta_{2,n} \cos(n\phi_k)),$$

where ϕ_k is the time of day scaled to radians as $2\pi s/86400$, where s is the second of the day. The model was fitted using the lm function in R (R Core Team, 2025).

After accounting for the diurnal pattern and for the AMS, the daily averages were calculated for each cow and used in subsequent analyses. The variance components were estimated using ASReml 4.2 (Gilmour et al., 2015) using the following model:

$$CH_{4ijklm} = \mu + HYW_k + LAC_l \times \sum_{n=0}^4 \beta_{ln} \phi_n(DIM_m) + a_i + pe_i + e_{ijklm},$$

where CH_{4ijklm} is the average daily methane concentration measured on animal i in herd-year-week (HYW) k in lactation (LAC) l , and the m th day in milk (DIM), and μ is the overall intercept. Cows in a second or higher lactation were grouped together. The general lactation curve was modelled within each lactation using a fourth-order Legendre polynomial. Random effects were the animal effect (a), permanent environment (pe), and residual error (e). The additive genetic effects are modelled as $a \sim N(0, A\sigma_a^2)$, where A is the numerator relationship matrix based on the pedigree. The permanent environmental effect was distributed as $pe \sim N(0, I\sigma_{pe}^2)$, where I is the identity matrix.

The repeatability was calculated as:

$$r = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2},$$

and heritability was calculated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}.$$

3. Results

Applying the new adjusted procedure altered the average methane levels, as illustrated by the frequency distribution of differences between mean CH_4 concentrations per milking from uncorrected and corrected data (Fig. 2), indicating that the differences were slightly shifted toward the positive side of the distribution. In most cases, the change, however, was relatively small. Most differences lie between -100 and 100 ppm. The distribution of methane concentrations appears approximately normal. However, in some cases, the differences between corrected and uncorrected means were more pronounced. Both big negative and substantial positive differences were observed.

The background level of methane was determined as the first quartile of methane concentrations in the nearest plateau region. A total of 51,662 plateau regions were identified in the entire dataset. For background correction, only plateau regions with a first-quartile methane value between 7 and 50 ppm were included in the analysis. After this filtering step, only 2929 plateau regions were considered stable enough for further study. The majority of plateau regions were shorter than 250 s. Longer plateau regions were less frequent (Fig. 3A). Short plateaus (less than 500 s) occur across the CH_4 range (0–50 ppm) and are the most common and densely clustered. Plateaus at higher CH_4 levels (above 35 ppm) tend to be short, rarely lasting longer than 1000 s. Their number decreases with increasing plateau duration (Fig. 3B). The first quartile of methane levels was used for the plateau region.

Differences between the mean methane level before background correction and the mean methane level after correction are shown as a scatter plot in Fig. 4. Each point represents a measurement, and the red line indicates where the points would be if the values remained constant. Most of the points are just below the line, indicating that the CH_4 levels dropped slightly after the correction, as expected, since the background noise was removed. The fact that the points stay close to the line means that the correction was applied consistently across the data. There are also no points above the line, so the correction did not increase any values above their previous levels.

3.1. Adjustment of the milking period allocation

To evaluate the quality of the new algorithm for identifying the start and end of milking, a comparative analysis was conducted with the previously used method (dataset before correction). One hundred

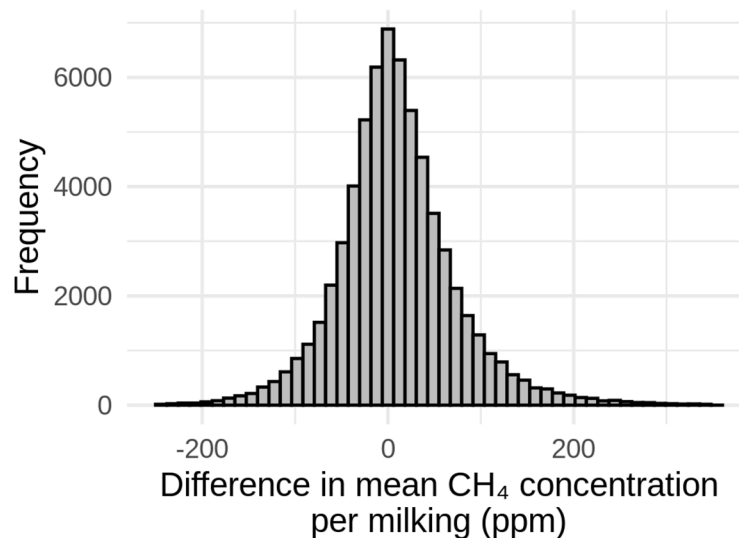


Fig. 2. Differences in mean CH₄ concentration per milking between unadjusted and adjusted data.

randomly sampled and manually verified cases were used as a reference set (ground truth). The mean absolute error was calculated for the start and end of milking of each dataset separately. The MAE in identifying the milking start time was reduced from 41.1 s to 12.4 s, and the error in determining the end time decreased from 98.2 s to 31.9 s (Table 1).

For each time point within the evaluated periods, a classification was made as either milking or non-milking, and its correctness was assessed against the ground truth. A difference in classification between the data before and after adjustment can be seen in Fig. 5. Based on this comparison, the F1-score was calculated (Table 1). Before adjustment, the median F1-score for the dataset was 0.84. After correction, the dataset's metric increased to 0.99. The Wilcoxon signed-rank test showed that the difference in this metric between datasets is statistically significant ($P < 0.001$).

3.2. Repeatability and heritability

The adjusted pipeline was shown to reduce overall phenotypic variance by 15 %, permanent environment variance by 11 %, genetic variance by 17 %, and residual variance by 16 %. The heritability was slightly lower (by 2 %) after correction than before, while repeatability increased by 2 %. Given the standard error of the estimates, no significant differences were obtained. The ratio (see Table 2).

4. Discussion

Effective methane mitigation strategies in dairy production require a comprehensive approach integrating accurate measurement technologies, advanced data processing, and predictive modeling (Ross et al., 2024). In addition, improvements in farm management practices, such as optimizing milking schedules and enhancing barn ventilation, can further contribute to reducing methane emissions (Ghassemi Nejad et al., 2024). This study presents a robust processing pipeline to improve the accuracy of methane emission measurements from dairy cows collected using a sniffer in automated milking systems.

Various methods exist for measuring methane emissions from cows under production conditions (Storm et al., 2012), with the sniffer being advantageous for its non-invasive nature and its ability to gather a high volume of data. Observations are collected during milking sessions, during which cows are provided with concentrated feed in the feed bin, ensuring their muzzle remain close to the measurement tube. The measurements become unreliable once the feed bin is emptied due to increased head movement. Limiting readings of low concentrations or

specific recording durations is suggested as a solution.

As Boutes et al. (2024) indicated, the distance between the cow's head and the sniffer inlet is a critical factor influencing measurement accuracy. The authors observed that cows are free to move their heads during milking since the AMS operates in a semi-open environment. Such behavior appears to occur randomly and is difficult to predict, making it challenging to account for the development of automated data processing algorithms.

It should, however, be assumed that the optimal measurement period – when the cow's nostrils are close to the sniffer inlet – might be shorter than the milking time itself. This could result in the measurement period ending before the AMS milking event is completed, leaving the measurements to align imperfectly with the AMS milking event, necessitating further definition and optimization.

Moreover, the variability in the length of the measurement event is influenced by the time required for the sampled gases to reach the analyser, which can depend on factors such as the distance from the inlet to the analyser and the inlet's airflow efficiency. As noted by Jonker and Waghorn (2020), "Differences in sampling flow rate, sampling tube volume, and cuvette size lead to varying response times across analysers, making precise alignment unlikely." Therefore, in this study, we assumed that the start and end of each measurement during a single milking event should be determined individually.

In Løvendahl et al. (2024), the authors proposed a pipeline for processing CH₄ emissions data, which was developed and validated to provide useful phenotypes for genetic analysis and breeding value estimation based on CH₄ measurements collected using the sniffer method. The pipeline included modules for: 1) raw data acquisition, 2) data monitoring, 3) time synchronization with AMS cow-ID data, 4) estimation of background atmospheric concentrations, 5) calculation of cow-related changes in gas concentrations, and 6) acquisition of condensed measures after milking events or test days. Points 3) and 4) were subject to optimization in our study.

Milkevych et al. (2022) proposed a matched filter theory approach to handle the synchronization problem, which showed improved data attribution in a Danish setup. Implementing the proposed method in practice requires consideration of timing skew variation, and the data must undergo additional advanced transformations. In this paper, we propose an algorithm that fine-tunes the start and end times of the milking event using previously synchronized data.

Compared with more advanced synchronization approaches based on matched filtering or complex signal transformations, our method prioritizes interpretability, ease of implementation, and robustness to

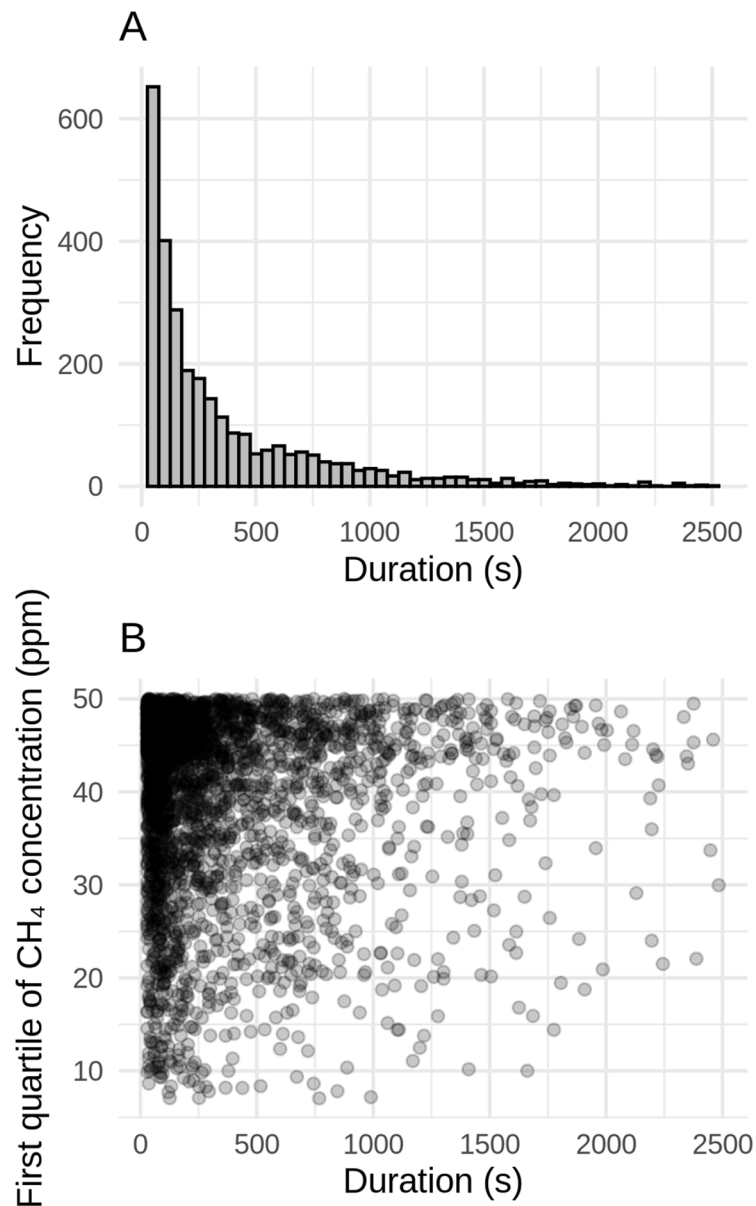


Fig. 3. Characteristics of methane plateau regions identified in sniffer-based CH₄ concentration time series.

heterogeneous farm conditions. These properties are particularly important in breeding programs, where pipelines must be stable over time, and applicable to large-scale, multi-farm data sets.

The precision of individual measurements for cows depends on the accuracy of the data recorded by the analyser and the precision of the analysis of collected records. During milking, CH₄ concentrations vary widely, following regular patterns of breath and eructation. According to the literature, individual methane emissions at the herd level exhibit a variability of 32 % (Boutes et al., 2024), ranging from 22 % to 67 %, as observed by Bell et al. (2014), depending on the farm.

The procedure developed in this paper demonstrated better alignment of methane concentration measurements with the start and end of milking events. The adjustments mainly consisted of incorporating peaks misclassified outside the milking, removing peaks misclassified within milking start or end regions, and eliminating milkings containing detected plateau regions (Fig. 5). This indicates that, despite synchronizing the sniffer with AMS, subsequent data processing steps are necessary to achieve values as close as possible to the most realistic ones.

Correcting the methane concentration measurements for the background helps quantify the amount of gas cows produce more accurately.

Without the background correction (Fig. 4), the mean methane concentration seems to be overestimated. Several options for correcting background methane concentrations have been proposed in the literature. Some used the mean or median of the CH₄ concentration when no milking was recorded. These statistics can be accurately adjusted for background, given that the time without cows in the AMS is sufficiently long. In the previous data processing pipeline, the background was set to the median gas concentration during the period when the AMS system was cleaned (Pszczola et al., 2017). Cleaning is performed only several times a day, not after each milking, so the background gas concentration may vary over time. Therefore, a better approach is to adjust the background value more frequently. The plateau periods between milkings are often short, and the mean or median would be prone to being influenced by sudden peaks that the cows did not produce during milking (e.g., cows passing through AMS but rejected from milking). In this study, we used the closest plateau detected by the proposed pipeline and the closest plateau prior to milking to adjust the gas concentration. A first-quartile statistic was proposed to eliminate the impact of sudden increases in CH₄ concentration within the plateau, ensuring the capture of the background CH₄ concentration in the barn. Capturing the closest

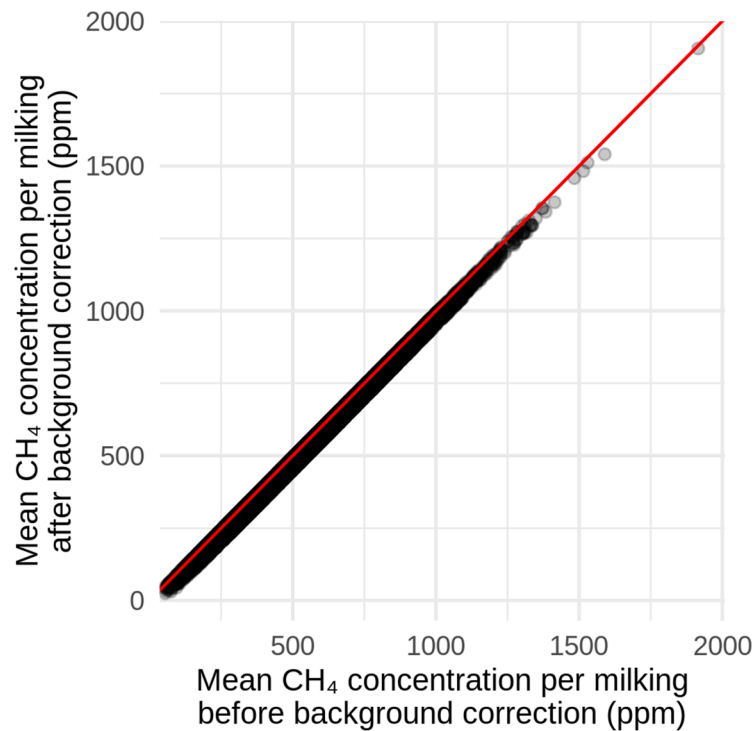


Fig. 4. Effect of background correction on mean CH₄ concentration per milking.

Table 1
Performance metrics for datasets before and after pipeline adjustment.

Metric	Before adjustment	After adjustment
MAE of milking starts (sec)	41.1	12.4
MAE of milking end (sec)	98.2	31.9
Median of F1-score	0.84	0.99

plateau appears to be a more robust technique in large-scale measurement schemes where the farm management practices related to AMS cleaning may be unknown.

The application of the new pipeline resulted in a substantial reduction in overall phenotypic variance (approximately 15 %), primarily driven by a decrease in the residual component. This pattern is consistent with effective removal of measurement noise from the methane emission data rather than with changes in the underlying genetic architecture of the trait. This reduction indicates that the proposed pipeline can better assign start and end points for milking events, effectively removing measurements that contain ambient air or result from incomplete milkings. Despite the significant reduction in phenotypic variance, both repeatability and heritability estimates remained stable across the two pipelines. The minor fluctuations observed were well within the range of standard errors. This suggests that the new algorithm, while successfully improving the assignment of milking events, did not distort the underlying genetic structure of the daily methane concentration data, making the resulting estimates more reliable.

The strengths of the proposed pipeline extend beyond its computational simplicity. First, the method relies exclusively on signal-derived features within individual methane time series, avoiding assumptions about fixed temporal offsets or stable barn conditions. Second, the pipeline is fully transparent and reproducible, with each processing step directly interpretable in terms of animal behavior and sensor response. Third, the approach is computationally lightweight and therefore scalable to millions of observations, which is critical for routine genetic evaluation. Finally, the method was quantitatively validated against manually annotated reference data, demonstrating substantial

improvements in boundary detection accuracy and phenotype repeatability. At the same time, these advantages should be interpreted in light of the methodological assumptions underlying the approach's signal-based nature.

Despite these strengths, several limitations of the proposed pipeline should be acknowledged. Because the method relies on signal-derived features such as local peaks and plateau regions, its performance may be affected by excessive noise or artefacts in the raw methane time series, for example, due to sensor malfunction, unstable sampling conditions, or atypical animal behavior. In addition, practical issues related to sniffer operation under commercial conditions, such as partial obstruction of the sampling tube by feed particles or dust during pellet feeding, have been reported to affect signal quality (van Breukelen et al., 2025) and may introduce additional variability if not adequately monitored. Although standard quality control procedures were applied in this study, large-scale or long-term deployments may benefit from additional upstream data screening or adaptive filtering to ensure consistent signal quality before the pipeline is applied. Future work should therefore explore integrating automated data quality assessment steps, particularly when extending the approach to heterogeneous datasets or different sniffer technologies. Moreover, as previous large-scale studies have reported substantial differences in the mean level and variability of methane records obtained with different sniffer versions (van Breukelen et al., 2025), combining data across sensor generations may require additional harmonization steps, such as accounting for device or version effects in statistical models or applying within-version standardization.

Improved attribution and background correction of sniffer-based methane measurements may have important implications for downstream production and breeding applications. More accurate temporal alignment of methane records with individual milking events is expected to reduce non-biological noise arising from animal behavior in the milking robot, which has been shown to influence sniffer-derived methane phenotypes and their relationships with feeding behavior and production traits (Garnsworthy et al. 2012; Boutes et al. 2024; Jonker and Waghorn 2020; van Breukelen et al. 2025). By improving the signal-to-noise ratio of methane phenotypes, the proposed pipeline may facilitate more reliable investigation of associations between methane

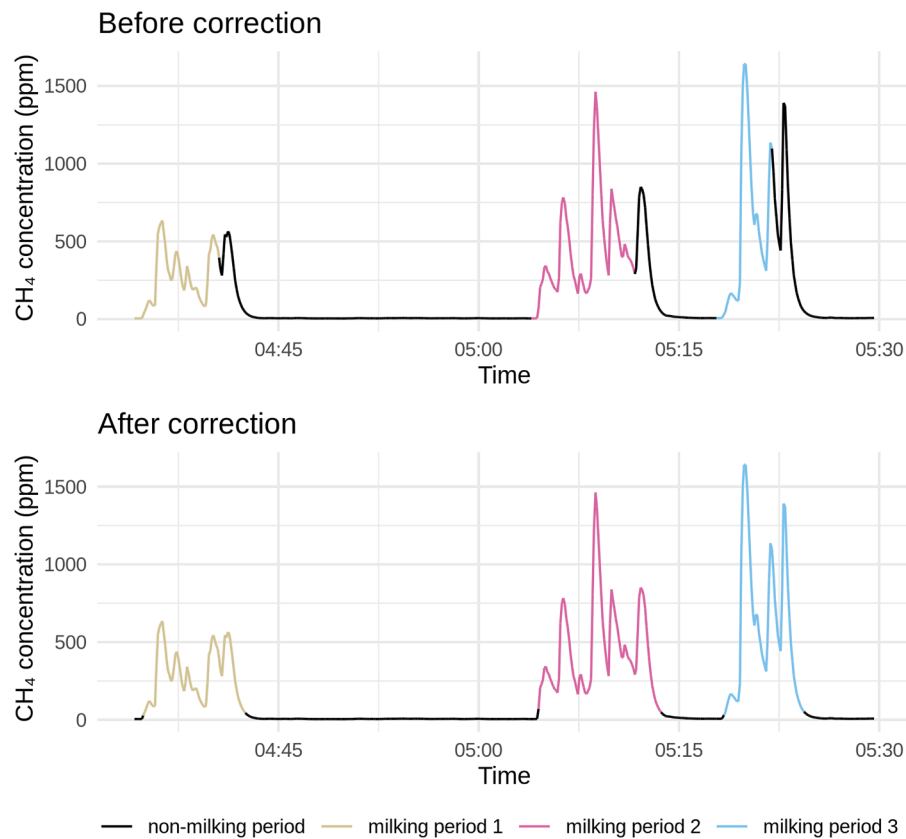


Fig. 5. Visual representation of temporal alignment between sniffer-derived CH₄ concentration and AMS milking records before and after adjustment.

Table 2

Variance components, heritability, and repeatability before and after pipeline adjustment.

Parameter	Before adjustment	After adjustment
Genetic variance	4671	3899
Permanent environment variance	6660	5953
Residual variance	21,075	17,710
Phenotypic variance	32,405	27,561
Repeatability	0.350 (S.E. 0.017)	0.357 (S.E. 0.017)
Heritability	0.144 (S.E. 0.042)	0.141 (S.E. 0.042)

emissions, milk yield, and feeding-related traits, even when methane production is partially derived from milk yield information, as in commonly used sniffer-based prediction models. In this context, reduced measurement error is expected to attenuate spurious variability and may increase the power to detect biologically meaningful relationships, without implying stronger causal links.

Similarly, improved phenotyping may support more consistent estimation of methane intensity traits, such as methane emissions per unit of milk, which have shown variable and sometimes weak genetic correlations with production traits across measurement technologies and studies (Fresco et al., 2024; Manzanilla-Pech et al., 2025; van Breukelen et al., 2025). These differences likely reflect both biological heterogeneity and methodological differences between direct and indirect methane proxies, underscoring the importance of robust, transparent phenotyping pipelines. From a breeding perspective, improved repeatability and reduced residual variance of methane phenotypes directly contribute to more reliable genetic evaluation and breeding value estimation, thereby supporting the integration of methane-related traits into selection objectives aimed at reducing emissions while maintaining productive performance.

Observed differences in the relationships between methane

phenotypes and production-related traits across studies likely reflect methodological contrasts in both measurement systems and phenotype definitions. In particular, methane production estimated from sniffer measurements is, by construction, partially dependent on milk yield, whereas methane traits derived from milk mid-infrared spectra are less directly linked to production level, which may contribute to heterogeneous correlation patterns reported in the literature. In addition, although GreenFeed units, like sniffers, measure methane concentration in exhaled air, flux-based methane production estimates obtained with GreenFeed do not rely on milk yield information for their calculation and therefore tend to show stronger biological associations with dry matter intake. In this context, improving the accuracy and repeatability of sniffer-derived methane phenotypes primarily serves to reduce measurement noise, thereby facilitating more robust inference within a given phenotype definition rather than reconciling differences across fundamentally distinct methane traits.

5. Conclusions

In this study, we developed a dedicated data-processing pipeline for methane concentration measurements collected with a sniffer system. The pipeline includes adjusting milking start and end times through peak detection and identifying plateau regions in the time series. This pipeline increases the method's robustness against individual variation in cow behavior during milking. Additionally, the detected plateau regions are used to estimate local background methane concentrations, which are essential for generating corrected values that more accurately represent the actual emissions associated with each animal. A nearly threefold decrease in the MAE of milking start and end is observed with the proposed method. The algorithm is readily transferable across farms and devices, contributing to more reliable methane phenotyping for selective breeding and emission monitoring in commercial dairy operations. By improving the accuracy and reducing residual error variance

while maintaining the heritability and repeatability levels of sniffer-derived methane phenotypes, the proposed pipeline provides a practical foundation for large-scale phenotyping and supports the integration of methane traits into routine genetic evaluation and breeding programs aimed at emission mitigation.

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CRediT authorship contribution statement

M. Ryczek: Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **T. Strabel:** Writing – review & editing, Resources, Project administration, Funding acquisition. **M. Pszczola:** Writing – review & editing, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no conflict of interest.

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