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Development of an Ear Tag System for Diagnosing Swine Respiratory Diseases Using Long Short-Term Memory Networks

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ABSTRACT

In the Japanese livestock industry, while the number of pig farms is decreasing, the number of pigs raised per farm is increasing, leading to larger-scale operations. This scaling-up raises the risk of widespread damage from rapid infectious disease outbreaks. Furthermore, respiratory diseases such as pneumonia inhibit growth, delay shipments, and reduce cost-effectiveness for farmers. Consequently, there is a demand for systems that can detect illnesses early. Previous research constructed a disease diagnosis model using the cepstrum and Δ-cepstrum of body-conducted sounds from pigs as inputs, employing LSTM. However, variations among individual pigs were found to decrease the accuracy of the disease diagnosis model. Therefore, this study investigates the construction of machine learning models for individual subjects, aiming to eliminate the effects of individual differences by detecting abnormalities on a case-by-case basis.

Keywords: *Body conducted sound, Ear tag sensor, Disease detection, LSTM, Autoencoder*

1. INTRODUCTION

Porcine respiratory diseases cause significant economic damage in the livestock industry, with annual losses due to Porcine Reproductive and Respiratory Syndrome (PRRS) estimated at $664 million annually in the U.S. [1]. Hence, to prevent severe complications and widespread infections among individuals, the early detection of porkets afflicted with respiratory diseases is crucial. Furthermore, the recent trend towards large-scale porket farming has exacerbated labor shortages, highlighting the need for using technology for efficiently monitor the health status of pigs [2]. Mito et al. [3] proposed a system that utilizes a microphone array and cameras installed in pigpens to detect and locate the source of coughing and sneezing sounds, which are indicators of porcine respiratory diseases. However, environmental noise within pigpens hinders the accurate localization of these sounds. M. Guarino et al. [4] investigates the use of an intelligent alarm system for early disease detection in pigs through online monitoring of cough sounds. Initially developed in laboratory settings, the system was tested on 44 pigs in field conditions using close-range microphones. The classification accuracy was 85.5% for coughs and 86.6% for other sounds. However, the reliance on close-proximity microphones presents practical challenges for real-world application, as environmental noise impacts performance. Lagua et al. [5] discusses a commercially available AI system designed for monitoring respiratory health in swine, integrating temperature and humidity sensors with audio technologies. The system captures body-conducted sounds from individual pigs to detect respiratory diseases, employing machine learning algorithms for effective disease surveillance and management in livestock farming. However, the current system still faces limitations, particularly regarding accuracy and practical applicability in real-world settings. They suggest that further advancements in AI and sensor technology are necessary to create smarter, more reliable solutions for comprehensive health monitoring in livestock. To address this need, we are developing a system that

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uses ear tag sensors to detect the body-conducted sounds of pigs, analyzes the biometric data in the cloud, and notifies farmers. Previously, models used cepstrum and Δcepstrum as inputs and employed Long Short-Term Memory (LSTM) networks for disease diagnosis [6]. However, individual differences among pigs caused a decrease in model accuracy. Therefore, this study has explored constructing individual machine learning models for each pig to mitigate the impact of these variations by detecting anomalies individually.

2. COLLECTION OF BODY-CONDUCTED SOUNDS

The animal experiment was approved by the Agricultural Research Organization's Expert Committee on Experiments. Pigs are often fitted with ear-tags for identification. In this context, our research group developed ear-tag sensors [7] that incorporated electronic circuits and miniature sensors to record body-conducted sounds. To collect data from pigs with respiratory diseases, we conducted animal experiments by intentionally infecting the animals with bacteria. Ear-tag sensors were attached to pigs at 5 w of age and data were collected during both healthy periods (2–3 d) and periods of illness (2 w).

3. CONSTRUCTION OF THE ANOMALY DETECTION MODEL

The autoencoder is a representative method for anomaly detection that compresses and reconstructs input data using an encoder and a decoder, respectively. Anomalies are detected by measuring the difference (reconstruction error) between the input and output. An LSTM model using a spectrogram of body-conducted sounds as input can accurately distinguish between pre- and post-illness states [8]. Building on these findings, the current study aimed to achieve high-precision anomaly detection using an LSTM autoencoder that used a spectrogram of body-conducted sounds as input.

3.1 LSTM Autoencoder

The LSTM autoencoder learns a vector representation of the time-series data in the encoder and reconstructs the time series in the decoder using the current hidden state and values predicted at the previous time step. The time-series data were denoted as $X = \{x^{(1)}, x^{(2)}, \ldots, x^{(L)}\}$, and the hidden state of the encoder at each time point $h_E^{(i)}$. Here, $i \in \{1, 2, \ldots, L\}$ and $h_E^{(i)} \in R^C$, where c represents the number of LSTM units in the encoder's hidden layer. In the LSTM autoencoder, the encoder compresses the data in chronological order, whereas the decoder reconstructs the data in reverse chronological order. Thus, the final state of the encoder, $h_E^{(L)}$, is used as the initial state for the decoder, $h_D^{(L)}$, and the time-series data are output in the order of $\{x^{(L)}, x^{(L-1)}, \ldots, x^{(1)}\}$[8].

3.2 Calculation of Reconstruction Error

Initially, the LSTM autoencoder model generated a 5-s output from a 5-s input. When calculating the reconstruction error, overlapping 5-s frames were used within data segments longer than 14 s. The mean and distribution differences of the reconstruction errors obtained in this manner were utilized as indicators to classify the states before and after disease onset.

3.3 Kullback-Leibler Divergence

In this study, the Kullback–Leibler (KL) divergence was used to measure the differences between probability distributions and served as a classification metric. KL divergence is a measure of how one probability distribution diverges from the second-expected probability distribution. When Q and P are discrete probability distributions, KL divergence is defined by Equation (1) [9]:

$$D(P \parallel Q) = \sum_{i=1}^{N} P(x_i) \log \frac{P(x_i)}{Q(x_i)} \quad (1)$$

For instance, if Q and P represent the probability distributions of the reconstruction errors for healthy data, the KL divergence value would be small due to the minimal difference between the distributions. However, if Q represents the reconstruction error distribution of data from healthy pigs and P represents data from diseased pigs, substantial differences in the distributions would lead to a larger KL divergence value. Therefore, by substituting reconstruction error with KL divergence, an improvement in accuracy was achieved.

3.4 Identification Results for Five Pigs

The process of training the model and detecting anomalies is described. Initially, approximately 50% of the data from a single healthy pig were used as training data and approximately 20% were used as validation data to build the model. Subsequently, the remaining data from healthy and diseased pigs were input into the built model as test data. The output results were used to calculate the

reconstruction error or KL divergence, and the anomalies in the pigs were detected based on predefined thresholds. In this study, the thresholds were set to the maximum values of the reconstruction error or KL divergence from the validation data.

To effectively implement an anomaly detection system on a real farm, it is imperative to classify all pigs with high accuracy, regardless of the presence of symptoms. Therefore, pigs A to E, showing a range of lung lesions from severe to mild, were used to validate the effectiveness of the LSTM autoencoder and KL divergence. Each pig had a machine learning model built specifically for it. The identification results for pigs A–E are shown in Figures 1–5. Except for pig D, the LSTM Autoencoder models using spectrograms as input could accurately distinguish between the pre-illness and illness states. Moreover, the use of KL divergence improved the accuracy of disease identification in pigs B –E. However, pig D showed a low identification accuracy of 0–20%. This was attributed to the presence of significant outliers in the reconstruction error or KL divergence of the 's validation data of pig D, which were set as thresholds. Consequently, the data that were actually diseased were incorrectly classified as healthy, leading to a decrease in accuracy.

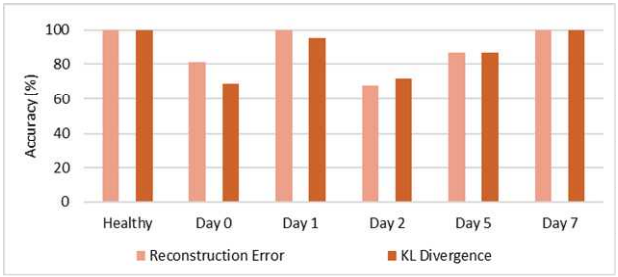

Figure 1. Results for Pig A (severe infection). The input was a spectrogram, with thresholds set for each method. 'Day' indicates the number of days post-infection.

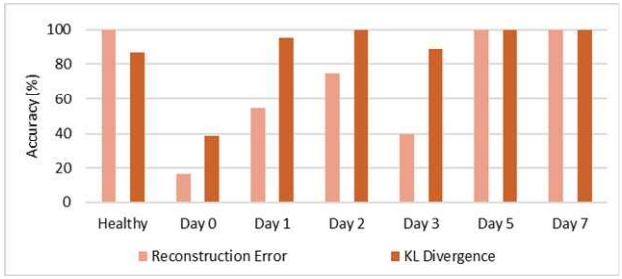

Figure 2. Results for Pig B (moderate severity infection). The input was a spectrogram with a threshold set for each method. 'Day' indicates the number of days post-infection.

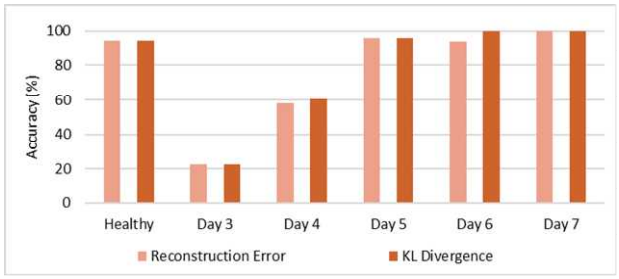

Figure 3. Results for Pig C (moderate severity infection). The input was a spectrogram with a threshold set for each method. 'Day' indicates the number of days post-infection.

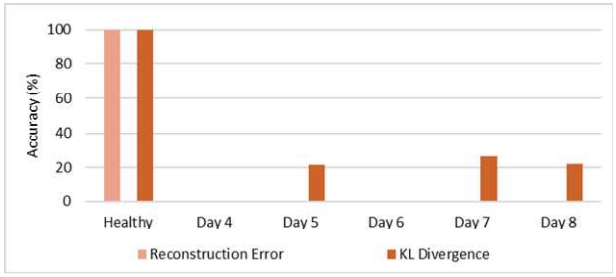

Figure 4. Results of Pig D (mild severity infection). The input was a spectrogram with a threshold set for each method. 'Day' indicates the number of days post-infection.

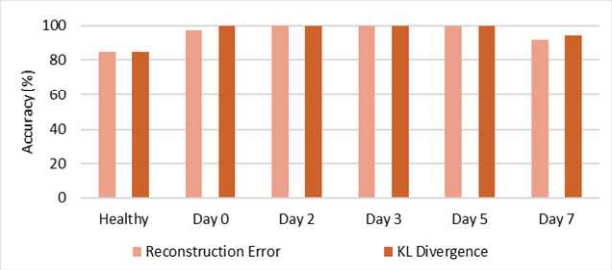

Figure 5. Results of Pig E (mild severity infection). The input was a spectrogram with a threshold set for each method. 'Day' indicates the number of days post-infection.

4. CONCLUSION

In this study, we addressed the issue of reduced identification accuracy due to individual differences by building a separate machine-learning model for each pig and detecting anomalies. Using an LSTM autoencoder with spectrogram inputs enabled highly accurate differentiation between healthy and diseased conditions, and incorporating the Kullback–Leibler divergence further improved the disease detection rates. However, for certain pigs, the classification accuracy declined substantially. Therefore, in future work, we plan to improve accuracy by using a different metric from the KL divergence and tuning the model hyperparameters through cross-validation.

5. ACKNOWLEDGMENTS

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