IEEE Access
Multidisciplinary ⋮ Rapid Review ⋮ Open Access Journal

Received April 2, 2022, accepted April 14, 2022, date of publication May 9, 2022, date of current version May 18, 2022.

Digital Object Identifier 10.1109/ACCESS.2022.3173736

Detection of Infectious Respiratory Disease Through Sweat From Axillary Using an E-Nose With Stacked Deep Neural Network

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This work was supported in part by the Directorate of Research and Community Service; in part by the Directorate General of Higher Education, Research, and Technology; in part by the Indonesian Ministry of Education, Culture, Research and Technology through the Penelitian Terapan Unggulan Perguruan Tinggi (PTUPT) Program; in part by the Institut Teknologi Sepuluh Nopember (ITS) through the Project Scheme of the Publication Writing and IPR Incentive Program (PPHKI); and in part by the Indonesian Ministry of Education, Culture, Research and Technology through the Matching Fund (MF) Kedaireka Program.

This work involved human subjects or animals in its research. Approval of all ethical and experimental procedures and protocols was granted by Rumah Sakit Islam Jemursari Surabaya under Application No. 001.EC.KEP.RSIAY.03.21 and Rumah Sakit Umum Daerah Dr. Soetomo under Application No. 0173/KEPK/IV/2021.

ABSTRACT Several methods have been used to detect infectious respiratory diseases, for example, by taking samples from blood, saliva, and phlegm. Although these methods generated high accuracy, they raised more problems that increased the risk of spreading and required more time to detect. Therefore, an accurate, quick, and low-cost device is required to help detect infectious respiratory diseases. This study proposes a new approach for detecting infectious respiratory diseases using an electronic nose (E-nose) through sweat samples from the human axilla. E-nose became safer by taking samples through the axillary because infectious respiratory diseases are not transmitted through sweat. This study proposes two new feature extraction techniques called stable value and highest slope. This study also proposes a stacked Deep Neural Network (DNN) for effective infectious respiratory disease detection. In the proposed stacked DNN, five fine-tuned DNN models obtained from hyperparameter tuning are stacked then the output of each DNN model became the input of the meta-model in the form of a fully connected layer. The proposed feature extraction method outperformed the existing feature extraction and was able to separate data between classes better. Furthermore, the proposed stacked DNN model generated an accuracy of 0.934 in the testing data, outperforming DNN single models and other state-of-the-art machine learning algorithms.

INDEX TERMS Axillary, deep learning, electronic nose, feature extraction, infectious respiratory disease, stacked.

I. INTRODUCTION

Sweat is the result of the metabolism of the body that comes out through the skin. The sweat that comes out of the body contains substances humans no longer need. The result of body metabolism in sweat contains several substances, such as ammonia, hydrocarbons, alcohol, acids, ketones, and others [1]. Various substances in sweat produce Volatile Organic Compounds (VOCs) [2]. Besides being produced by sweat, VOCs are also produced from several other sources;

The associate editor coordinating the review of this manuscript and approving it for publication was Mehul S. Raval.

breath, blood, urine, feces, and more. VOCs released through the body are not only influenced by human metabolism but can also indicate the health status of a person [3], [4].

Several methods have been used to detect diseases by taking samples from blood, saliva, phlegm, feces, and others [5], [6]. For some people, sampling using this method is painful, uncomfortable, and can take several hours to obtain the results. Although these methods generated high accuracy, they raised more problems, increasing the risk of spreading infectious respiratory diseases. For infectious respiratory disease, sampling from saliva, feces, and phlegm can increase the risk of spreading the disease [7].

An electronic nose (E-nose) is a device that resembles the functions of the human nose. E-nose is designed from several sensors that are sensitive to certain gases. E-nose applications in the biomedical field and the medical industry have increased in recent decades due to the need for technology that can produce rapid, painless, accurate, and inexpensive diagnoses [6]. E-nose as a method for detecting disease requires specific knowledge of the metabolic products generated by the disease. Knowledge of certain gas mixtures of VOCs produced by humans in response to several types of disease provides essential information about target compounds (biomarkers) needed to develop the most effective approach for disease detection via E-nose.

Several E-nose applications for disease diagnosis used samples from breath, urine, feces, and others [6], [8], [9]. However, there have not been any studies and applications that utilize samples from sweat in the human axilla to detect infectious respiratory diseases. Therefore, this study proposes a new approach for the rapid detection of infectious respiratory diseases by axillary odor using E-nose. The respiratory disease in this study is SARS (Severe Acute Respiratory Syndrome). E-nose is designed from several metal-oxide semiconductor gas sensors that are highly sensitive to certain gases. Then it takes a sample from sweat in the human axilla and stores the VOCs contained in the sweat. This device became safer by taking samples through the axilla [10].

Several feature extraction techniques have been used in E-nose, such as using statistical parameters, namely mean, standard deviation, minimum value, maximum value, skewness, or kurtosis. Mean, standard deviation, minimum value, and maximum value were used in E-nose to differentiate types of civet coffee [11], [12]. Other studies use E-nose to detect adulteration in beef [13], [14] with statistical features, namely, extraction, mean, standard deviation, skewness, and kurtosis. These previous studies used a beaker glass to accommodate samples in the form of coffee and meat connected by a tube and E-nose so that the sampling process is stable. Meanwhile, taking samples directly from the sweat of the axilla using an E-nose can make the collected data unstable due to the movement of the axilla.

In addition to using E-nose collection samples from the axillary to avoid disease transmission, accurate detection of infectious respiratory disease also plays a crucial role in preventing the disease from spreading further. Artificial intelligence (AI) and machine learning on E-nose can improve its ability to identify and detect diseases. Several AI has been used to help E-nose diagnose diseases, including Canonical Discriminant Analysis to detect airway colonization by Aspergillus fumigatus with an accuracy of 89% [15]. Principal Component Analysis (PCA), and Linear Discriminant Analysis (LDA) to differentiate between inflammatory joint diseases with an accuracy of 71% [16]. LDA to differentiate between cystic fibrosis (CF) and primary ciliary dyskinesia (PCD) with maximum specificity of 95% [17]. PCA and Support Vector Machine (SVM) to detect chronic kidney disease (CKD), diabetes mellitus (DM), and healthy subjects with an accuracy of 100% [18], and LDA to detect pneumoconiosis with sensitivity, specificity, accuracy, and area under the receiver operating characteristic curve (AUROC) in the test set of 66.7%, 71.4%, 70.0%, and 0.86, respectively [19]. Deep learning or Deep Neural Network (DNN) also has been used to detect diabetes with an accuracy of 96.29%. The use of DNN proved that the accuracy of disease diagnosis has increased [9]. However, none of the previous studies mentioned above-used sweat from axilla as samples.

The ensemble learning methods have been used in E-nose to detect diabetes using majority voting with support vector machine as the base-model [20] and to detect a mixture of beef and pork using majority voting with K-nearest neighbor as the base-model [13]. The AdaBoost ensemble learning method has also been used to identify ginseng [21]. The results show that using ensemble learning can improve model performance. Meanwhile, in other areas, Alotaibi *et al.* proposed a stacked deep learning method using ResNet as a base-model to detect cyber attacks [22]. The results show that the stacked deep learning method can increase the accuracy of cyberattacks detection. Hence, the motivation for this study can be formulated as follows:

1. Several types of research have used an E-nose to detect diseases. However, no research used sweat from axillary as the sample even though it can be a sign of a disease. Moreover, viruses that cause infectious respiratory diseases are not found in sweat
2. Several feature extraction methods have been used on the E-nose, but no feature extraction method generates a stable value from E-nose. The stable value is significant for sweat sampling from axillary because sampling using this method is greatly influenced by the movement of the axilla.
3. A reliable detection model is needed so that E-nose can accurately detect infectious respiratory diseases. Based on previous research, DNN and ensemble learning stacking can improve detection accuracy.

According to these motivations, the main contributions of this study are:

1. Development of new extraction feature techniques for E-nose data.

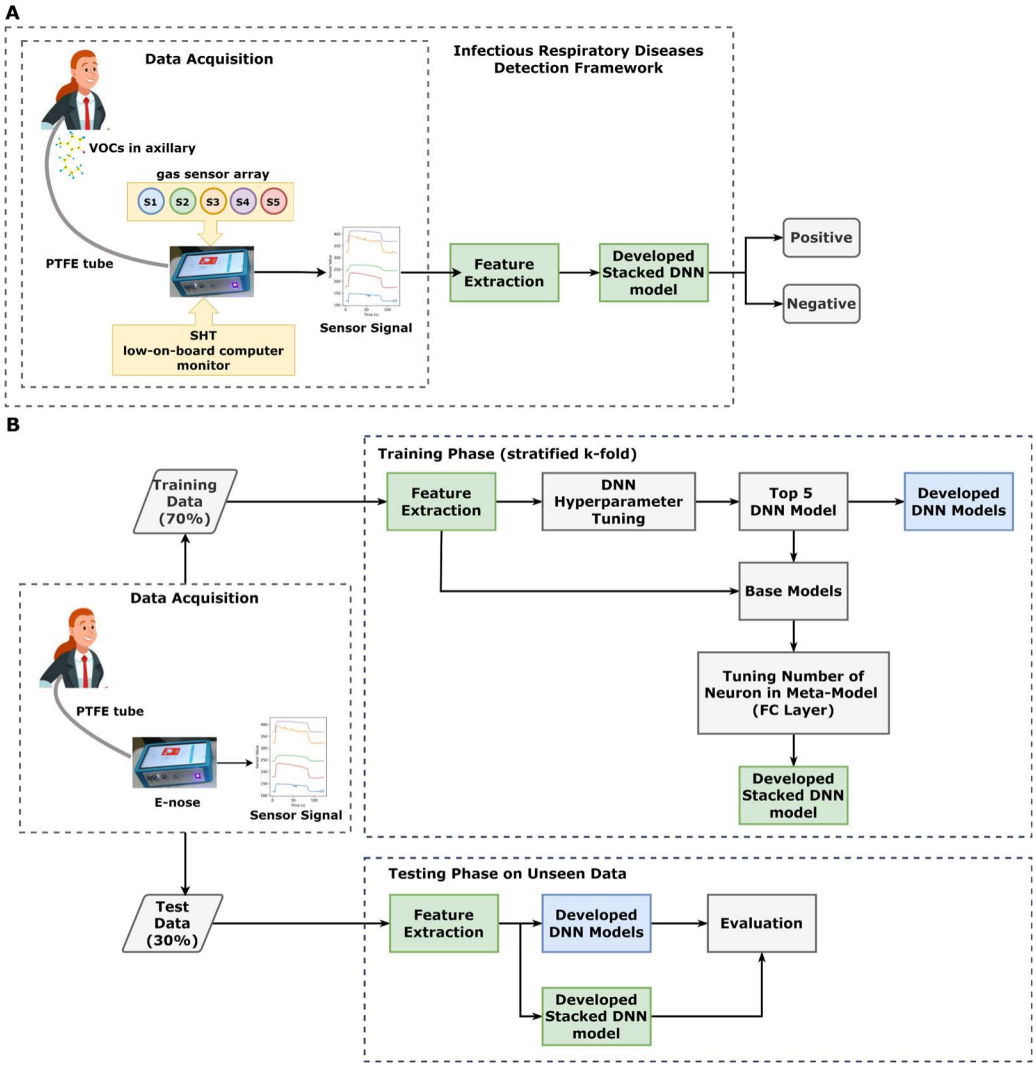

FIGURE 1. Proposed infectious respiratory diseases detection scheme.

2. Detection of infectious respiratory diseases using E-nose by taking samples from the axillary using stacked DNN.

The rest of the study is arranged in the following order: Section 1 describes the background of the research. Section 2 explains the proposed method. Section 3 presents the results of experiments and discussions. Finally, Section 4 contains conclusions from the experiment.

II. MATERIALS AND METHOD

This study aimed to detect infectious respiratory diseases through the axillary using E-nose. The proposed infectious respiratory diseases detection scheme is illustrated in Fig. 1, in which panel A shows the brief detail of how E-nose detected infectious respiratory diseases, while panel B illustrates the detailed overview of the proposed infectious respiratory diseases detection scheme. In both Panel A and B, The first stage was the data acquisition. A Polytetrafluoroethylene (PTFE) tube was clamped towards the middle of the axillary. E-nose consisting of five metal-oxide semiconductor gas sensors inhaled VOCs from the axillary's sweat and VOCs were converted into an electronic signal. In Panel A, after completing the data acquisition stage and obtaining the sample, the sample was further processed through feature extraction. The features obtained were used as input from the developed stacked DNN model that predicted whether the subject had an infectious respiratory disease (positive) or not (negative). The feature extraction and construction of a stacked DNN model are described in detail in Panel B.

In panel B, the data acquisition process was carried out in two hospitals in Surabaya, namely Rumah Sakit Umum Daerah Dr. Soetomo (RSUD Dr. Soetomo) and Rumah Sakit Islam Jemursari (RSI Jemursari) Surabaya. The process was the same as the data acquisition in Panel A. The data obtained were divided into 2, namely training data and test data, with a proportion of 70% and 30%, respectively. The next stage was the training phase, which used training data. In this phase, the

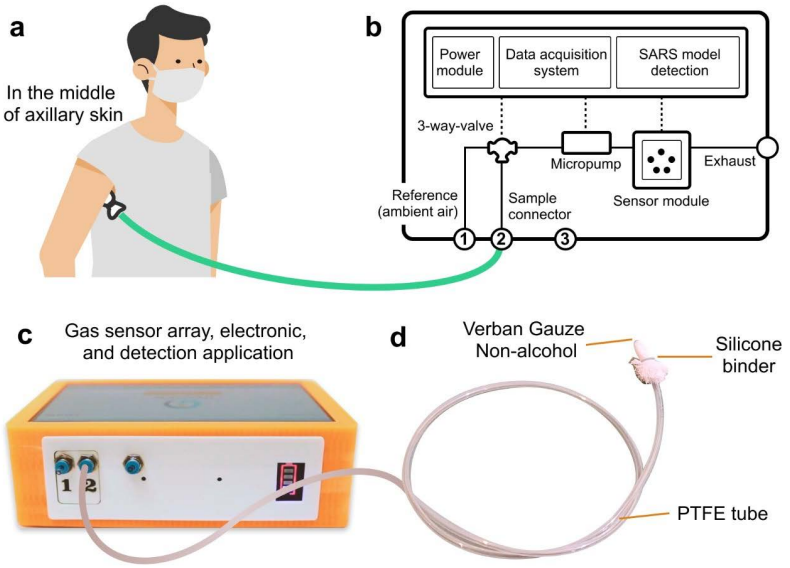

FIGURE 2. The design of E-nose device.

proposed feature extraction techniques were compared with previous feature extraction techniques. Feature extraction was conducted to obtain the features which would be the input of DNN hyperparameter tuning. DNN hyperparameter tuning was carried out using a random search method and stratified k-fold cross-validation to obtain the top 5 DNN models that were well-generalized. The tuned hyperparameters were the number of neurons in each layer. The next step was to build a stacked DNN, an ensemble learning using stacking type, in which the stacking consists of two models, namely base-model and meta-model. This type of ensemble stacked several base-models of which output from respective base-model became the input of the meta-model. The meta-model generated output or final prediction from ensemble learning. In this study, The top 5 DNN models were used as the base-model from stacked DNN. This study used a fully-connected layer (FC Layer) as the meta-model. This study tuned the number of neurons in the meta-model to obtain the correct number of neurons. The number of neurons that produced the highest average cross-validation score was selected as the number of neurons for the meta-model. After completion, the result obtained was called the developed stacked DNN model. Developed Stacked DNN model and Developed DNN models (Top 5 DNN models) obtained from the training phase were tested using new data, namely test data, to compare the performance. This stage was called the testing phase.

A. E-NOSE AND DATA ACQUISITION SCHEME

Details of the E-nose are illustrated in Fig. 1 and 2. In Fig. 1 (Panel A, data acquisition stage), based on the previous study, methane and ethanol [23], [24] were volatile organic compounds (VOCs) found in axillary and could be used as a biomarker. This study used the reference to determine the gas sensors. E-nose was built using five gas sensors, namely S1, S2, S3, S4, and S5. These five gas sensors were assembled into an Arduino microcontroller. Each sensor had a sensitivity to certain VOCs (propane, benzene, methane, ammonia, alcohol, etc.), resulting in a signal pattern that described the VOCs present in sweat in the axillary for both positive and negative subjects. VOCs from sweat in the axillary entered the E-nose device (sensor module) through a PTFE tube. In addition, the E-nose was also composed of an SHT sensor to monitor changes in temperature and humidity in the sensing chamber. Furthermore, it was also equipped with a low-on-board computer and monitor to observe the sampling process and determine the sampling results.

The designed E-nose device consisted of 2 main parts, namely sensing and sampling unit, as illustrated in Fig. 2 (a) and (b). In Fig. 2 (a), a PTFE tube placed in the center part of the axillary skin was connected to the E-nose device through a sample connector. The end of the PTFE tube connected to the axillary skin was covered in a non-alcohol gauze bandage and a silicone binder, as shown in Fig. 2 (d). In Fig. 2 (b) and (c), the E-nose device consisted of numerous electronic components, mechanic components, and software models, namely a monitor, low-on-board computer, power module, data acquisition system, three-way-valve, micropump, sensor module inside the sealed gas chamber, exhaust, and SARS model detection. These components were housed in a three-dimensional (3D)-printed housing. The sensors were developed with Tin Dioxide (SnO_2) material. They were also composed of an Al_3O_3 micro-ceramic tube, heater, and electrode. The type of sensor used was metal-oxide semiconductor with details of each sensor as follows: S1, S2, S3, S4, and S5 were suitable for detecting propane, benzene, methane, ammonia, and alcohol (ethanol) respectively. As aforementioned, there were five gas sensors used; therefore, the sensor module comprised five sensing

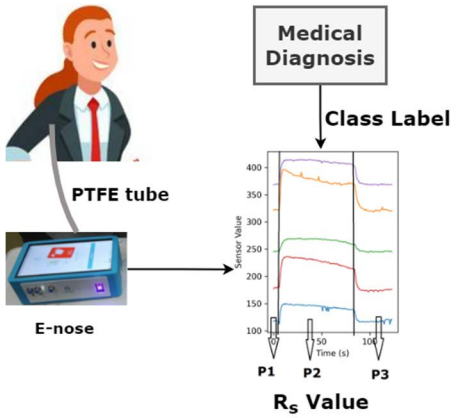

FIGURE 3. Data acquisition scheme.

devices arranged as an array. The model developed in this study (Developed Stacked DNN model) was stored in the SARS model detection part.

The data acquisition stage was one of the most important activities in this study, as shown in Fig. 3. The hospital staff inserted a PTFE tube into the right axillary of the subject. The tube was connected to E-nose. E-nose inhaled VOCs from the axillary's sweat and the VOCs were converted into an electronic signal (analog to digital or ADC) and saved the electronic signal in the E-nose device. The E-nose device was equipped with a low-on-board computer and a monitor screen to observe the data acquisition process. There were 3 processes carried out by E-nose every time a sample was taken [25]. The first process took in the air around the E-nose, called P1. The second process was the sampling process, called P2; E-nose took sweat data from the right axillary. The last process, called P3, was cleaning the E-nose from any odor left. The time needed to retrieve each data was 190 seconds, where P1 took 10 seconds, P2 took 120 seconds, and P3 took 60 seconds. The sample taken in the form of signal was then stored in the E-nose in the form of the Comma Separated Value (CSV) format. The gas sensor resistance value (R_s) is calculated as a response based on the ADC value presented in Equation 1, in which to calculate R_s, Equation 2 needs to be calculated first.

$$R_s = \frac{V_C - V_{RL}}{V_{RL}} \times RL \tag{1}$$

$$V_{RL} = \frac{V_C - ADC}{1023} \tag{2}$$

In which V_C is the standard voltage of the microcontroller (5 V), V_{RL} is the current sensor voltage, RL is sensor load resistance, and ADC is the Analog to Digital Converter value. This study used the R_s value in the experiment.

The data collected using E-nose were confirmed with a diagnosis from a doctor to determine whether or not the subject belongs to the healthy class (negative) or infectious respiratory class (positive). Before using the data obtained from the hospitals, the data had been processed so that personal information, such as name, address, telephone number, and others were not stored in the dataset. Therefore

TABLE 1. Demographic of samples data.

Description	Detail
Number of data	659
Number of subject	214
Female	133
Male	195
Locality	East Java Province, Indonesia
Multiple clinical conditions	No

third parties cannot identify the personal information in the dataset. The consent from the hospitals where the data were collected and the consent of the subject participating in this study was also obtained. For patient consent, respective hospital staff asked the subject to fill out a consent form and submit a copy of the identification card. Data samples used in this study are explained in detail in Table 1.

B. PROPOSED FEATURE EXTRACTION METHODS

At the feature extraction stage, sweat data in the form of digital signal data was extracted using 6 types of statistical parameters that had been used in the previous E-nose applications, namely mean, standard deviation, minimum value, maximum value, skewness, and kurtosis [11]–[14]. Besides these six statistical parameters, this study proposed two new feature extraction techniques, called stable value and maximum slope value. Therefore, each signal data from MOS produced eight features.

The pseudocode of the proposed feature extraction can be seen in Algorithm 1. Several variables had to be initialized to obtain a stable and maximum slope value, namely REGION, MIN_SLOPE, MAX_SLOPE, and DELTA_SLOPE. The signal was divided into six REGION (area). MIN_SLOPE was the minimum slope of each signal that can be accepted. MAX_SLOPE was the maximum slope of each signal that can be accepted. DELTA_SLOPE was the difference between two slopes, where the specified DELTA_SLOPE is 0.1, the closer the DELTA_SLOPE value to 0, the more stable or constant the signal was. Another input for Algorithm 1 was the data signal obtained in the second process.

The first step in Algorithm 1 was to smooth the data signal using Fast Fourier Transform (FFT) and Inverse Discrete Fourier Transform (IFFT). First, the signal used FFT to convert the signal into a frequency form using Equation 3, where X_k was the signal in the frequency domain, x_n was the signal in the time domain, N was the number of samples taken, and $e^{-\frac{i2\pi}{N}kn}$ was the constant value of a signal (a twiddle factor which was any of the trigonometric constant coefficients that are multiplied by the data in the course of the algorithm in FFT).

$$X_k = \sum_{n=0}^{N-1} x_n . e^{-\frac{i2\pi}{N}kn} \tag{3}$$

Afterward, the signal in the form of frequency was smoothened by using Equation 3 and returned in the time

Algorithm 1 Proposed Feature Extraction Techniques

Input: REGION ← 6
MIN_SLOPE ← -1
MAX_SLOPE ← 1
DELTA_SLOPE ← 0.1
Data Signal in the second process (D)

Output: List of the stable value of Data Signal (allStableValues)
List of the highest slope of Data Signal (allHighestSlope)

Method:

```
allStableValues, allHighestSlopes = [], []
for each sensor in D do
    Step 1: smoothing each sensor from D with FFT
    dataPerSensor ← calculate FFT of D(sensor) using Equation 3
    dataPerSensor ← calculate IFFT of dataPerSensor using Equation 4
    Step 2: Calculate slope
    Slopes = []
    for each adjacent signal point in do
        Slope ← Calculate slope using Equation 5
        Slope Slopes ← Slope
    end for
    Step 3: Calculate the highest slope of Slopes
    HighestSlope ← calculate the highest slope of Slopes using Equation 6
    allHighestSlopes ← HighestSlope
    Step 4: calculate stableValue
    stableValue = []
    Divide Slopes and dataPerSensor into REGION
    for each Slopes and dataPerSensor in REGION do
        MaxSlope ← Maximum Slopes(REGION)
        MinSlope ← Minimum Slopes(REGION)
        if MinSlope >= MIN_SLOPE and MaxSlope <= MAX_SLOPE
            if abs(Slopes(REGION)) < DELTA_SLOPE
            stableValue ← DataPerSensor(REGION)
            end if
        end if
    end for
    avgStableValue ← Calculate average of stableValue using Equation 7
    allStableValues ←avgStableValue
end for
return allStableValues, allHighestSlopes
```

domain using IFFT using Equation 4.

$$x_n = \frac{1}{N}\sum_{k=0}^{N-1} X_k e^{\frac{i2\pi}{N}kn} \tag{4}$$

The next step was to calculate the slope value. The slope of a straight line shows how steep the straight line is, where the line is a set of points of which members consist of more than one point. Equation 5 was used to calculate the slope of the line or two adjacent points. Furthermore, the maximum slope value for each sensor was calculated using Equation 6.

$$slope = \frac{(y2 - y1)}{(x2 - x1)} \tag{5}$$

$$HighestSlope = maximum(slope) \tag{6}$$

Finally, the last step was to determine the stable value for each sensor. The smoothened signal and slopes were divided into six regions; in each region, the minimum and maximum slope values were calculated. If the minimum slope value was more than or equal to MIN_SLOPE and the maximum slope value was less than or equal to MAX_SLOPE, it was assumed that there was a stable value in that region. Furthermore, if the value was less than DELTA_SLOPE, the signal was stable or constant because the slope value was close to 0; then, the stable value was stored. Once all the stable values in the sensor were obtained, the average of the stable value on the sensor was calculated using Equation 7, where T was the number of stable signals on the sensor.

$$Average = \frac{1}{T}\sum_{t=1}^{T} stableValue \tag{7}$$

C. PROPOSED STACKED DEEP NEURAL NETWORK

The data obtained in the data acquisition stage was divided into training and test data with a percentage of 70% and 30% respectively. In this stage, training data was used to find DNN models with hyperparameter tuning. The five best DNN models were used as the base-model for stacked DNN. The test data contained unseen data used for independent testing of stacked DNN and DNN base-models for final evaluation. Cross-validation used during training is stratified k-fold, a sampling technique in which the sample in each class is selected in the same proportion as it appears in the population. This study attempted several folds, and the number of folds that produced the best result is 5-fold, which the data is divided into five equal folds; in each fold, the class distribution became balanced according to the class distribution of the entire population. This stratified k-fold is carried out to ensure that the DNN base-models obtained from hyperparameter tuning and stacked DNN model had a good performance using different validation and training data. This cross-validated hyperparameter tuning aimed to ensure that the best hyperparameter provided stable accuracy on each fold.

DNN is a part of deep learning used in thousands of applications (Sabilla *et al.*, 2020) and consists of more than one hidden layer. The main advantage of DNN is that it is a ''structure agnostic'' which means that no special assumptions need to be made about the format of the input (for example, the input must be an image, video, sound, or something else). The number of MOS in the E-nose was five, then the number of features generated from the feature extraction process by all MOS was 40 features, hence the number of neurons in the input layer was 40 neurons. DNN consisted of a fully connected layer or a set of layers in which all neurons are connected to neurons in the previous or next layer. Each neuron connected to other neurons has a weight. In mathematical form, a fully connected network can be represented as follows, $x \in \mathbb{R}$ is the input to the fully connected layer, $y_i \in \mathbb{R}$ is the *i-th* output from the fully connected layer, so $y_i \in \mathbb{R}$ can be calculated using Equation 8, where σ is a nonlinear function or activation function and w_i is a parameter that can be learned in the network or called weights.

$$y_i = \sigma(w_1 x_1 + \ldots + w_m x_m) \tag{8}$$

So Equation 9 can be used to calculate the entire output of y.

$$y = \begin{pmatrix} \sigma(w_{1,1}x_1 + \ldots + w_{1,m}x_m) \\ \cdot \\ \cdot \\ \cdot \\ \sigma(w_{n,1}x_1 + \ldots + w_{n,m}x_m) \end{pmatrix} \tag{9}$$

Each layer has a neuron and an activation function from the hidden layer to the output layer, in which this activation function determines whether the neuron is active or not. Several activation functions that are widely used include Sigmoid, Tanh, ReLU, and Softmax. ReLU is an activation function that generates better results in several experiments [26]; therefore, this study used ReLU as an activation function in the hidden layer. ReLU has a threshold from 0 to infinity, as can be seen in Equation 10, in which ReLU makes a delimiter on the number zero, meaning that if x is less than 0 then x is 0, and if x is greater than 0 then x is the number itself. This study used the sigmoid activation function in the output layer because it converts the input value of x to a non-linear of which the value is between 0 and 1, so it is suitable to solve binary problems. Sigmoid can be calculated using Equation 11.

$$f(x) = \begin{bmatrix} x & x > 0 \\ 0 & x \leq 0 \end{bmatrix} \tag{10}$$

$$f(x) = \frac{1}{1 + e^{-x}} \tag{11}$$

In DNN, there is a parameter called the loss function, which shows the missing or inappropriate value of each possibility generated by the DNN model so that this loss function estimates the quality of weights, biases, and parameters. This function is executed when the learning value results in a significant loss value. The loss function in the deep learning binary classification is Binary Cross-Entropy (BCE) or Log Loss. BCE is calculated using Equation 12, in which y is the actual class and p is the predicted class. If the results are far from the actual value, it means that the performance of the model is not optimal.

$$BCE(y, p) = -y.log(p) - (1 - y).log(1 - p) \tag{12}$$

Each error represents a loss function, so the weights and biases must be readjusted. This process is called the backpropagation algorithm. In DNN, there is also a parameter called optimizer, which changes the weight value and minimizes the loss function. The optimizer used Equation 13 to change the weight with the learning rate value, where the new weight is denoted by $*W$, the old weight is denoted by W_x, the learning rate is denoted by a, and $(\frac{\partial_{error}}{\partial W_x})$ is the notation of derivative of error related to weight. Adam was used as an optimizer to train and test the model in this study because it has advantages such as involving small memory, working well with enormous amounts of data, and efficient computing capabilities [27]. This study used 0.0001 as the value of the learning rate because it produced the best performance based on experiments.

$$*W_x = W_x - a(\frac{\partial_{error}}{\partial W_x}) \tag{13}$$

The hyperparameters sought to obtain in the DNN base-models are the number of neurons in the hidden layers. This study used three hidden layers because the previous trial using fewer or more hidden layers did not generate better results. The list range of hyperparameters can be seen in Table 2.

Several methods can perform hyperparameter tuning, namely grid search, and random search. In grid search, the best hyperparameter search is done by using all combinations of existing parameters and evaluating each model. Therefore,

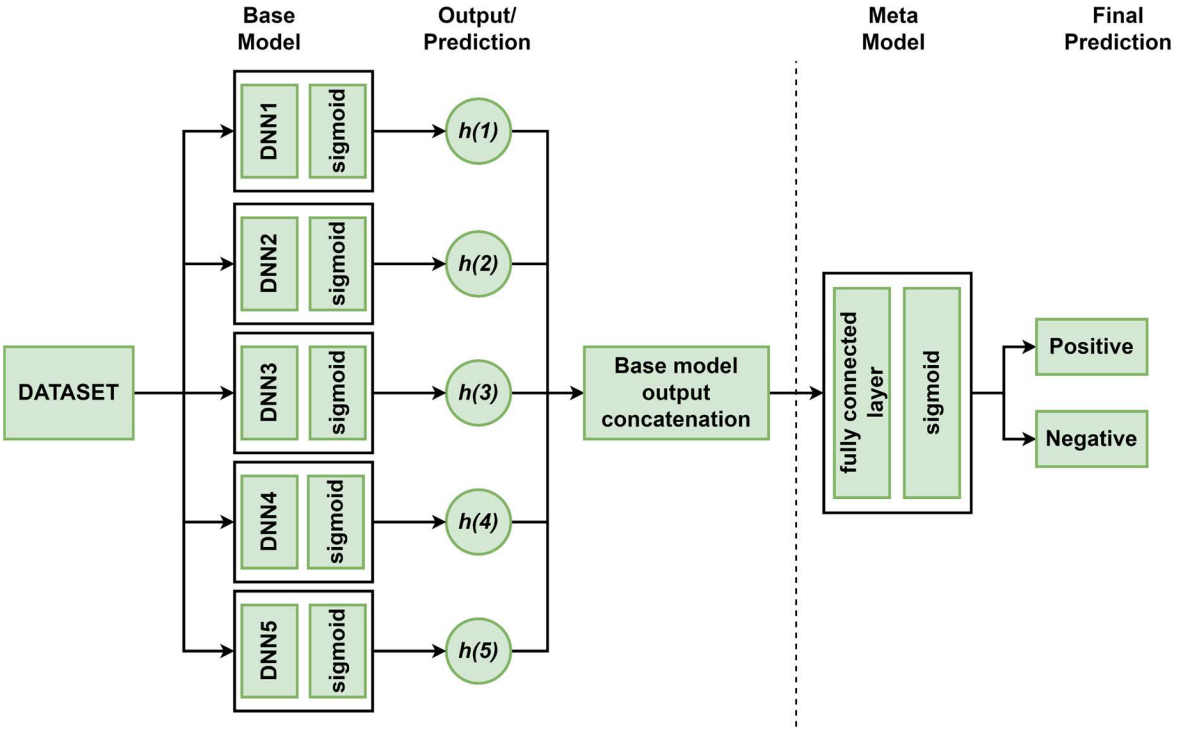

FIGURE 4. Proposed stacked DNN.

TABLE 2. Hyperparameter ranges of DNN used for the experiment.

Hyperparameter	Choice
Number of neurons in the 1st hidden layer	range(64,256)
Number of neurons in the 2nd the hidden layer	range(64,256)
Number of neurons in the 3rd the hidden layer	range(256,1024)

grid search takes a lot of time and resources. In contrast, random search is a technique where random combinations of hyperparameters are used to determine the best solution for the model. It is similar to grid search but has been proven to generate results efficiently. Comparatively, random search has an advantage over grid search, such as the time required to perform a search can be determined based on the distribution of the search space [28]. Hence this study used a random search algorithm to perform hyperparameter tuning. The iteration used in this study is 40 iterations.

The purpose of stacked DNN was to improve the ability to detect infectious diseases using E-nose. There were two types of components models in stacked DNN, namely the first-level model or commonly referred to as the base-model and the meta-model. Each base-model at the training stage used the same dataset and produced predictions for each base-model. The meta-model used the prediction results from the base-model to produce a final prediction which was the final prediction of stacking. The final prediction result from stacking used Equation 14, where $H(x)$ was the final prediction of stacking, N was the number of base-models, h' was the meta-model, and $h_N\,(x)$ was the prediction of the base-model.

$$H\,(x) = h'(h_1\,(x)\,, \ldots, h_N\,(x)) \tag{14}$$

After obtaining the five best DNN models, these models became the base-models for the stacked DNN. The meta-model on the stacked DNN was a fully connected layer composed of several neurons. This study tested several numbers of neurons as components of the meta-model, namely 64, 128, and 256 neurons. The number of neurons that composed the meta-model was selected based on the number of neurons providing the best mean cross-validation score using the training data. Furthermore, the stacked DNN was tested using test data and the result was compared with each DNN base-model to determine whether using stacked DNN increased the accuracy compared to the accuracy of the base-model. Fig. 4 is the proposed stacked DNN architecture, in which the base-model consisted of the five best DNN models resulting from hyperparameter tuning. Prediction or output from each DNN base-model was combined or concatenated and became the input for the meta-model. Moreover, the meta-model generated the final prediction of the stacked DNN. The five best DNN models and stacked DNN were trained with 100 epochs and a batch size of 32.

D. EVALUATION METRICS

The values often used in evaluation metrics in classification problems are True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). Data correctly classified as positive and negative is called TP and TN,

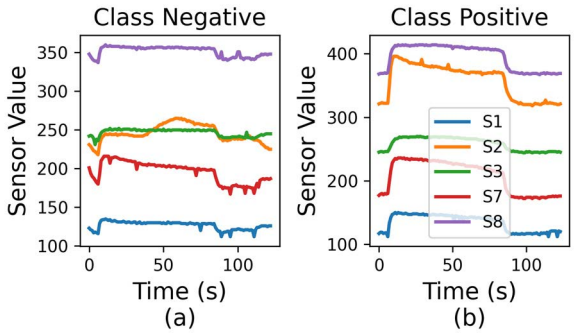

FIGURE 5. Example result of data signal (a) Negative class (b) Positive class.

while data that are wrongly classified as positive and negative is called FP and FN. This study used several metrics to evaluate the model. Accuracy is used to show how accurate the model performs the classification. Recall or sensitivity is the number of true positive predictions compared to all true positive data. Precision is the number of positive results compared to all positive predicted data. F-Score is the average precision and recall compared to weighting. Specificity is the number of true negative predictions compared to all negative data. Equations 15 to 19 are used to calculate these metrics. In addition to these metrics, the measurement of model performance evaluation also uses Receiver Operating Characteristics (ROC) and Area Under Curve (AUC). ROC is a probability curve and AUC is an area that shows the level of accuracy of the model empirically. The classification results show poor performance if the ROC Curve is close to the baseline and show good performance if the ROC Curve is closer to the 1.0 point.

$$Accuracy = \frac{(TP + TN)}{TP + TN + FP + FN} \tag{15}$$

$$Recall(Sensitivity) = \frac{TP}{TP + FN} \tag{16}$$

$$Precision(P) = \frac{TP}{TP + FP} \tag{17}$$

$$F - Score = \frac{2 \times (R \times P)}{(R + P)} \tag{18}$$

$$Specificity = \frac{TN}{TN + FP} \tag{19}$$

III. RESULTS AND DISCUSSION

A. RESULTS OF DATA ACQUISITION

There were 659 samples obtained, 353 samples classified as negative, and 306 classified as positive. The example results of the data acquisition can be seen in Fig. 5, in which (a) was the signal from the negative class and (b) was the signal from the positive class, in which the x-axis shows the time, and the y-axis shows the sensor value. From Fig. 5, it was difficult to distinguish data between positive and negative classes because each data produced a different signal. As shown in the example of negative class data, the signal generated looked unstable although there were still some stable signals. This incident was due to the movement of the axilla.

TABLE 3. Distribution of training and test data from both classes.

Class	Training data (70%)	Test data (30%)	Total (100%)
Positive	214	92	306
Negative	247	106	353

TABLE 4. The structure of dataset.

No.	Initial feature	Description	Type
1	sampling_id	Identification number for each subject, distinct value	Numeric
2	PROCESS	processes carried out by E-nose every time a sample was taken	Character
3	DATE	Date and time of sampling	Date and Time
4	S1	Output value from Sensor 1	Numeric
5	S2	Output value from Sensor 2	Numeric
6	S3	Output value from Sensor 3	Numeric
7	S4	Output value from Sensor 4	Numeric
8	S5	Output value from Sensor 5	Numeric
9	temp	Temperature in E-nose device	Numeric
10	humidity	Humidity in E-nose device	Numeric
11.	Class	Class of each data (0 = Negative Class, 1 = Positive Class)	Numeric

Based on the sampling result on 659 data, the dataset used in this study is arranged as shown in detail in Table 3. In the dataset, there are 11 initial features, since not all initial features are used to create the model. They had to go through the feature extraction process first to obtain the features used to create the model detection. Initial features used for further processing in the proposed feature extraction method were S1, S2, S3, S7, and S8. There were two classes in this study, namely 0 which indicated negative class, and 1 which indicated positive class). The distribution of training and test data can be seen in Table 4.

B. RESULTS OF PROPOSED FEATURE EXTRACTION METHODS

The proposed feature extraction was compared with two other feature extraction previously used in E-nose data. The proposed feature extraction technique was expected to be able to separate data between classes well. This study used PCA to compare the old feature extraction with the proposed feature extraction qualitatively. Fig. 6 is the comparison of data visualization using PCA. PCA is a technique used to reduce data dimensions but still retain data information. PCA is also

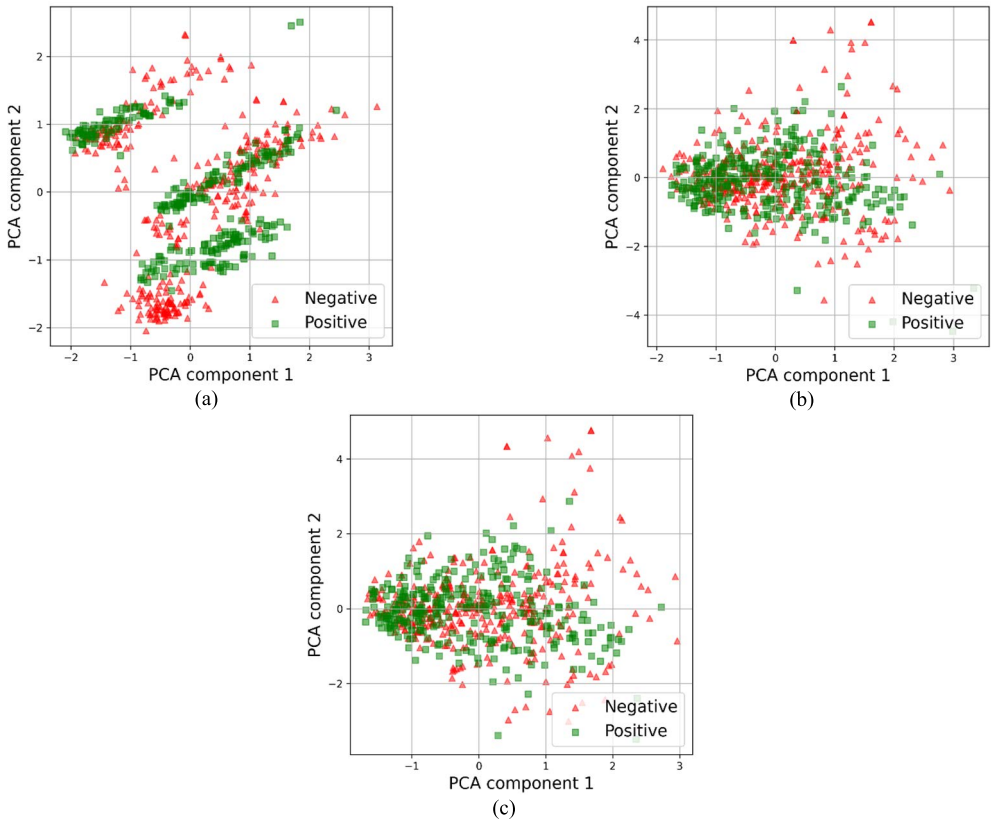

FIGURE 6. Data visualization using PCA (a) proposed feature extraction (b) Feature extraction 1 (c) Feature extraction 2.

TABLE 5. Feature extraction methods performance comparison with DNN.

Feature Extraction Methods	Evaluation	Score
Feature extraction 1	Mean cross-validation	0.844
	Standard deviation of the cross-validation	0.037
Feature extraction 2	Mean cross-validation	0.839
	Standard deviation of the cross-validation	0.028
Proposed feature extraction	Mean cross-validation	**0.905**
	The standard deviation of the cross-validation	**0.013**

commonly used for data visualization. By using PCA for data visualization, the data became analyzable. Fig. 6 (a) was data visualization with proposed feature extraction, Fig. 6 (b) was data visualization using feature extraction 1 (mean, standard deviation, minimum value, and maximum value) [11], [12], and Fig. 6 (c) was data visualization using feature extraction 2 (mean, standard deviation, skewness, and kurtosis) [13], [14]. The features extracted using the proposed technique resulted in a more clustered form and were distinguishable between positive and negative classes, while features extracted using the old techniques looked mixed and overlapped between classes.

The proposed feature extraction and the result of hyper-parameter tuning of DNN in Table 5 showed that the mean cross-validation score had increased compared to using feature extraction 1 and feature extraction 2. This result proved that the proposed feature extraction could distinguish positive and negative classes better than the previous technique.

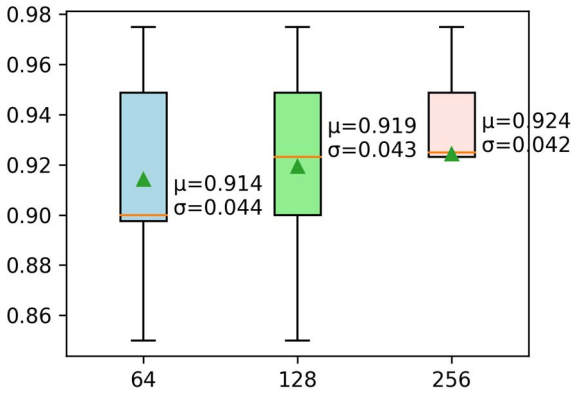

FIGURE 7. Comparison of mean cross-validation scores for the number of neurons in the meta-model of stacked DNN.

C. RESULTS OF PROPOSED STACKED DEEP NEURAL NETWORK

The experiment result using hyperparameter tuning with stratified k-fold to obtain the five best DNN models can be seen in Table 4. DNN models are named according to the ranking order of the hyperparameter tuning. Table 6 shows the architecture for the five best DNN models and the comparison

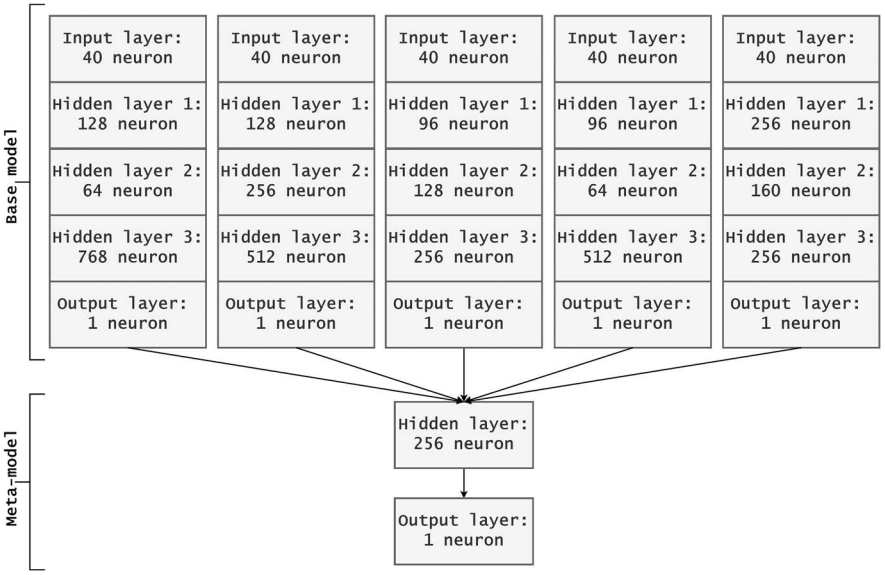

FIGURE 8. Architecture of the developed stacked DNN.

TABLE 6. Top 5 DNN model obtained from hyperparameter tuning.

DNN Models	Architecture	Mean cross-validation score	Standard deviation of the cross-validation score
DNN1	Number of neurons in the 1st hidden layer: 128 Number of neurons in the 2nd hidden layer: 64 Number of neurons in the 3rd hidden layer: 768	0.905	0.013
DNN2	Number of neurons in the 1st hidden layer: 128 Number of neurons in the 2nd hidden layer: 256 Number of neurons in the 3rd hidden layer: 512	0.902	0.021
DNN3	Number of neurons in the 1st hidden layer: 96 Number of neurons in the 2nd hidden layer: 128 Number of neurons in the 3rd hidden layer: 256	0.900	0.016
DNN4	Number of neurons in the 1st hidden layer: 96 Number of neurons in the 2nd hidden layer: 64 Number of neurons in the 3rd hidden layer: 512	0.900	0.023
DNN5	Number of neurons in the 1st hidden layer: 256 Number of neurons in the 2nd hidden layer: 160 Number of neurons in the 3rd hidden layer: 256	0.900	0.025

TABLE 7. Evaluation perfomance obtained from DNN base models and proposed stacked DNN with test data.

Developed Models	Accuracy	Precision	F-score	Recall (Sensitivity)	Specificity	AUC	Number of Parameters
DNN1	0.904	0.861	0.902	0.946	0.868	0.968	64,193
DNN2	0.919	0.904	0.914	0.924	0.915	0.979	170,369
DNN3	0.879	0.854	0.872	0.891	0.867	0.96	49,633
DNN4	0.874	0.860	0.865	0.870	0.877	0.961	43,937
DNN5	0.919	0.904	0.914	0.924	0.915	0.974	93,089
Stacked DNN	**0.934**	**0.916**	**0.930**	**0.946**	**0.925**	**0.981**	**423,014**

of the mean cross-validation score and standard deviation of the cross-validation score. These five best DNN models then become the base-model of stacked DNN.

The next experiment used three number of neurons as a meta-model, namely 64, 128, and 256. It was tested using stratified k-fold cross-validation to measure the performance of the stacked DNN. The experiment result can be seen in Fig. 7 in the form of a boxplot diagram. By using a boxplot diagram, the distribution of cross-validation scores for each fold can be seen. It is noticed that the meta-model with 256 neurons produces the highest mean cross-validation score of 0.924 and the lowest standard deviation of cross-validation score (0.042) compared to 64 neurons and 128 neurons. These results showed that stacked DNN with a meta-model consisting of 256 neurons had better generalization on different training and validation data. Therefore the number

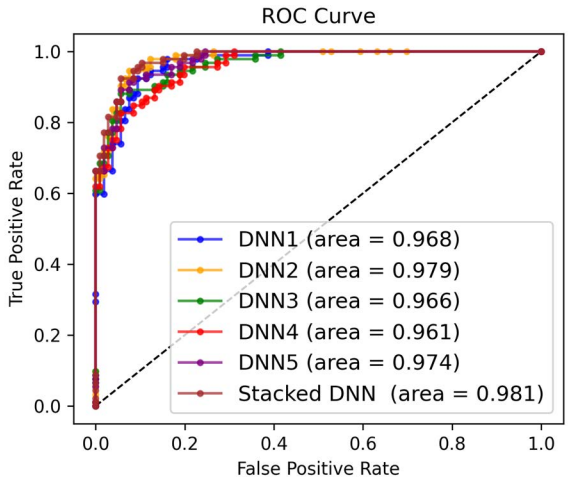

FIGURE 9. ROC Curve for DNN base models and proposed stacked DNN with test data.

TABLE 8. Confusion matrix of DNN base models and proposed stacked DNN with test data.

Models	TP	FP	TN	FN
DNN1	87	14	92	5
DNN2	85	9	97	7
DNN3	82	14	92	10
DNN4	80	13	93	12
DNN5	85	9	97	7
Stacked DNN	87	8	98	5

TABLE 9. Comparison of the proposed method with other machine learning algorithms.

Methods	Accuracy
LDA [19]	0.758
SVM [18]	0.803
DNN [9]	0.808
Proposed feature extraction methods and stacked DNN	**0.934**

of neurons selected for the meta-model on the stacked DNN was 256 neurons. The entire architecture of the developed stacked DNN is illustrated in Fig. 8.

The next experiment evaluated the developed stacked DNN and 5 developed DNN base-models using test data. The proposed stacked DNN consistently showed the best performance compared to the 5 DNN base-models in terms of accuracy, precision, recall or sensitivity, f-score, specificity, and AUC, as shown in Table 7. The proposed stacked DNN produced accuracy, specificity, and sensitivity of 0.934, 0.925, and 0.946. Therefore the advantage of combining the predicted results from the fine-tuned DNN base-models on the stacked DNN has been proven. The high specificity and sensitivity values produced by stacked DNN (0.925 and 0.946, respectively) obtained from the evaluation using test data indicated the advantages of stacked DNN to avoid false alarms; hence, it could reduce the risk of transmission of infectious respiratory diseases. Furthermore, the high precision value of the stacked DNN (0.916) indicated that positive cases of infectious respiratory disease were classified with a strong relationship. The number of parameters of stacked DNN also did not exceed 500,000. Therefore the stacked DNN model could be run on the E-nose, which consists of a low-on-board computer to help detect infectious respiratory diseases.

This study used a confusion matrix and ROC curve to take a deeper look at the effectiveness of stacked DNN. By using the ROC curve, we could see the ability of the model to separate true positive and true negative cases. In ROC, True Positive Rate (TPR) was compared to False Positive Rate (FPR). The proposed stacked DNN model had the best performance compared to the DNN base-models and produced an AUC score of 0.981. Tested DNN models produced lower AUC than the proposed stacked DNN as shown in Fig. 9.

Based on the confusion matrix in Table 8, tested DNN models had a higher number of FN than stacked DNN. Having a small number of FN was significant because incorrectly identifying the positive class (sick) to negative class (healthy) can cause the patient not to obtain the proper treatment and increase the risk of contracting infectious respiratory diseases in healthy people. This study concluded that the proposed stacked DNN provided the best performance compared to tested DNN models based on the overall evaluation results.

This study also compared the proposed stacked DNN with machine learning algorithms previously used for disease detection, as shown in Table 9. It can be concluded that the stacked DNN method and the proposed feature extraction outperformed other methods previously used for disease detection using E-nose.

IV. CONCLUSION

In this study, we proposed two new feature extraction methods and combined them with the old feature extraction methods to help detect infectious respiratory disease through sweat from axillary with an E-nose. Based on data visualization using PCA, the proposed feature extraction method made the data more clustered and distinguished between positive and negative classes in the classification of infectious respiratory diseases with E-nose compared to previously used feature extraction methods. This study also proposed a stacked deep learning method called stacked DNN, which consists of 5 DNN base-models stacked together using a meta-model to produce final predictions of respiratory infectious diseases through sweat from axilla using E-nose. The proposed Stacked DNN produced an accuracy of 0.934, also high sensitivity and specificity values. The proposed Stacked DNN was proven to improve the performance of tested DNN models. With these results, the detection of infectious respiratory diseases was proven to be able to use samples from axilla sweat and could be used to help detect infectious respiratory diseases. For future studies, it is suggested to carry out the detection of infectious respiratory diseases with more than two classes to diagnose potential cases of infectious respiratory diseases.

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