Classification of Human Gender from Sweat Odor using Electronic Nose with Machine Learning Methods

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2021 IEEE Asia Pacific Conference on Wireless and Mobile (APWiMob) | 978-1-7281-9475-2/21/$31.00 ©2021 IEEE | DOI: 10.1109/APWIMOB51111.2021.9435205

Abstract— **Both human biological genders have the same hormone but at different levels. The difference in hormone levels makes the two genders distinguishable from several aspects. One of the things that are influenced by hormones is sweat. The odor of sweat is related to the apocrine glands found in human armpits. This experiment studied the classification of both genders based on daytime sweat in adult human armpits. The sampling method used an electronic nose (E-nose) system to collect the armpit sweat odor. The E-nose system sensor array consisted of seven sensors: TGS 822, TGS 2612, TGS 2620, TGS 826, TGS 2603, TGS 2600, and TGS 813. These sensors generate resistance ratio (Rs/Ro) values which are learned by the machine learning methods for classification and disease potential based on the volatile organic compound (VOC) in sweat. The study shows the male samples have higher amine gas than female samples, one of which is Trimethylamine (TMA). TMA is a compound that will be broken down into trimethylamine-N-oxide (TMAO), a factor to various cardiovascular diseases. The result achieved 94.12% accuracy in classifying human biological gender using principal component analysis (PCA) as the pre-processing method and support vector machine (SVM) as the machine learning method.**

Keywords—Classification, Electronic nose, Human gender, Machine learning, Sensor

I. INTRODUCTION

Male and female are the two biological genders commonly found in living beings. Males and females have several characteristics that can be distinguished from one another. These differences can be in the form of physical appearance, hormonal, and behavior. These differences also apply to humans, which differentiate them based on their biological sex into male and female. Women (adult female human) and men (adult male human) also have observable differences. Physically, the differences between women and men can easily be seen in the adulthood phase. The adult age considered by the World Health Organization (WHO) is over 19 years old [1]. An example of physical differences between the two sexes in humans are that men tend to be more muscular, and women tend to have a curvier body. Other example includes men having more hair in some parts while women only in certain parts. The presence of hormones in both sexes influences physical differences between them. The hormone androstenedione and estrogen (sometimes refer to as oestrogen) mostly influence the physical indexes of women [2], [3]. On the other hand, the hormone testosterone mostly influences the physical indexes of men. Testosterone affects the growth of male characteristics such as physical strength, more resonant voice, as well as the growth of more body hair, such as beard. Androgens affect the production of testosterone in the body and are influenced by the hormone androstenedione [3], [4]. Thus, this hormone affects the physical indexes of women. Apart from physical effects, hormones also affect other things such as sweat.

One of the hormones that affect sweat is estrogen [5]. Estrogen in the human body regulates body temperature through blood flow. This body temperature affects sweat excretion. The hormone estrogen, which mostly affects the female reproductive system, allows a difference between women's and men's sweat. A study has shown that women have a lower average sweat secretion rate (SSR) than men [6]. This difference was observed in both pre-pubertal and adult ages. Another study studied the differences in sweat between the genders with a sample of eccrine sweat [7]. Eccrine is a sweat gland whose primary function of sweat is to regulate body temperature. The study showed no significant difference between metabolite composition and concentrations between the sexes based on eccrine sweat. Previous studies have shown that there may be differences in sweat between the two genders, depending on the sweat sample studied. Unlike eccrine, the apocrine gland is responsible for body odor. Although apocrine does not directly produce odors, the protein content in sweat supports bacterial growth [8]. This bacterial growth affects body odor. The level difference in sweat compounds causes male odor smells like cheese while female odor smells like onion or grapefruit.

Generally, we distinguish the two genders based on vision. In common sense, we would classify someone who is masculine, has short hair, or has excess body hair as male. Meanwhile, we classify someone who appears feminine with long hair as female. We commonly use this method because of the prevailing social norms. However, visual gender classification is not always precise. A woman can experience hirsutism, which results in the growth of excess hair in several parts of the body. Polycystic ovary syndrome (PCOS) is the cause of this anomaly. Besides, it is not uncommon to find "handsome" ladies and "pretty" boys nowadays due to current social development. Suppose we only rely on the classification using vision. In that case, misclassification might happen to some women with hirsutism, "handsome" ladies, and "pretty" boys. This study offers a biological gender classification of humans using the odor of sweat. Like hormones, although both genders have the same composition in sweat, they both have different composition levels. This difference is what causes the difference in the smell of sweat between the two genders.

The odor is identic with the sense of smell. In the human body system, odor recognition is carried out using the olfactory system. For example, when we want to recognize kitchen ingredients without seeing their physical form, we will try to sniff out the ingredients to recognize them based on their smell. An artificial nose has been developed so far, which is called the electronic nose (E-nose). The structure of the E-nose follows the human olfactory system where the sensor array acts as the receptor [9]. In E-nose, the sensor array is usually built from several gas sensors that have the sensitivity to different gases [9]–[11]. The Taguchi Gas Sensor (TGS) sensor is a gas sensor used on the E-nose. This sensor has demonstrated its ability in a paper studying odor differences between humans [12]. Sampling in the study was taken from two adult men. Sweat is taken five days at two times, the morning after waking up and eight hours after. The difference in the sweat of the two samples can be observed using principal component analysis (PCA), which is visualized in a scatterplot. The study also found that TGS 822 and TGS 2602 showed a high response to human body odor. In addition to recognizing human odors, this sensor is also proven to distinguish the aroma of Indonesian black tea, which is classified into three quality classes [13]. The study used 12 sensors, 11 of which are TGS sensors. Based on these studies, it is hoped that the TGS sensor can also be used to classify human biological gender based on their body odor.

This study proposes a biological gender classification using an E-nose. The sensors used are of the TGS 822, TGS 2612, TGS 2620, TGS 826, TGS 2603, TGS 2600, and TGS 813 types. The samples of people consist of both genders taken at the afternoon time. The location of sweat taken was under the armpits. The sample taking location is because the armpit is a part of the body that forms a fold. Thus, this area has a high sweat production. Besides, there are also exist apocrine glands in the armpits, which affect the body odor. Several mechanisms are performed on each sample of this research. Each person clamps the hose that will absorb the smell of sweat in the armpits. The smell of sweat is then directed to the sensor tube, and each sensor will detect the respective gas compounds. The value generated by the sensor will be classified using several machine learning methods and evaluated based on its accuracy. The rest of the paper is organized as follows. Section two discusses the materials and methodology in this study, covering data sampling to modeling and evaluation. The results of section two will be discussed in section three. Finally, section four will discuss the conclusions drawn based on the results obtained from section three.

II. MATERIALS AND METHOD

A. Materials

Experiments were carried out with certain limitations. The experimental environment includes training hardware using a virtual machine provided by Google Colab with the following specifications:

- 2vCPU @ 2.2 GHz
- 13GB RAM

In this experiment, the E-nose system uses the Arduino Mega with seven sensors. The list of sensors and their specifications are as in TABLE I. The sensor will react to the gas contained in the sample and respond with its resistance ratio (Rs/Ro). The Rs/Ro values generated by the sensor will be passed by Arduino Mega and received by the software installed in the sampling hardware.

The human armpit is the axilla region. The axilla region produces odorless sweat. However, the composition contained in the sweat when it meets aerobic bacteria can produce odors. This metabolic process produces ethanol (alcohol) gas, which is the target of all sensors used. Also, axilla bacteria produce methanethiol (methyl mercaptan) and ammonia in the axilla region. [14], [15]. Trimethylamine is also present in human sweat, which causes odor [16]. These three gases are also the targets of the TGS 2603 and TGS 826 sensors. Therefore, the selected sensors are as seen in TABLE I.

B. Data Sampling

The sample consists of 17 female and seven male adults aging over 19 years. Each person needs to tightly clamps the hose in their armpit when taking the sample. The data sampling consists of several phases: 60 seconds of delay phase, 120 seconds of sampling phase, and 100 seconds of purging. Data were collected in the early to mid-afternoon time (12 pm to 4 pm). Before sampling, the E-nose needs to be heated for a few minutes to calibrate the sensor. It is

TABLE I. E-NOSE SENSORS VOLATILE COMPOUND TARGET

Sensor	Volatile Compound Target
TGS 822	Air, Methane, Carbon-monoxide, n-Hexane Benzene Ethanol, Acetone
TGS 2612	Air, Methane, Ethanol, Iso-Butane, Propane
TGS 2620	Air, Methane, CO, Iso-butane, Hydrogen, Ethanol
TGS 826	Air, Iso-butane, Hydrogen, Ammonia, Ethanol
TGS 2603	Air, H2S, Hydrogen, Methyl mercaptan, Trimethyl amine, Ethanol
TGS 2600	Air, Methane, CO, Ethanol, Hydrogen
TGS 813	Air, Carbon-monoxide, Methane, Ethanol, Propane, Iso-butane, Hydrogen

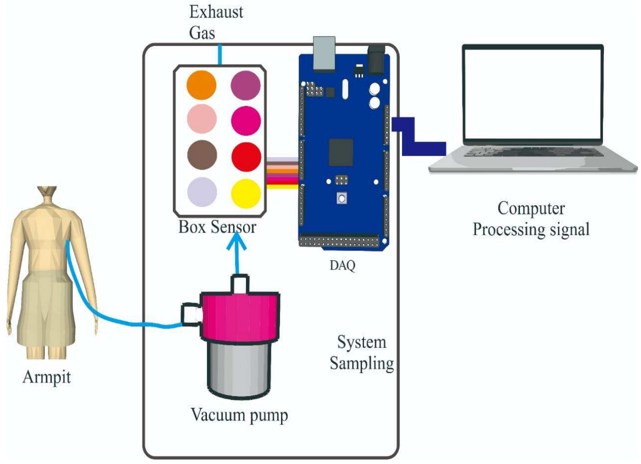

Fig. 1. Data Sampling Illustration for Armpit Sweat

necessary to ensure that the tube is pointed directly to the armpit skin to avoid incorrect data collection. The sensors' responses from the samples collected were stored in comma-separated values (CSV) file with the biological gender sample as the file name for easy data processing. The data acquisition is illustrated in Figure 1 and explained in the next paragraph.

Fig. 1 illustrates the data sampling process. The hose is placed on the inner armpit. The hose used to take samples from different people will also be changed to avoid data collection errors. Hose length about 40-50 cm depending on needs. The aroma of the sweat armpits is inhaled by the pump to be dissipated in the sensor room. The sensor room contains a TGS sensor and detects the gas according to the sensor type. Sampling was carried out for 280 seconds in total, as previously mentioned. The odor that the gas sensor has detected will then be removed through the exhaust hole to prevent accumulation in the sensor chamber. The sensor sends analog signal data to the microcomputer. The microcomputer converts analog signals to digital signals and sends them to the computer for classification using machine learning [17].

C. *Classification*

Fig. 2 shows the methodology flow of this study. In this methodology, each TGS sensor produces data sent by the microcontroller to the computer. The data in the form of a CSV file is preprocessed to improve accuracy by reducing some features. The preprocessed data is divided to undergo a training and testing mechanism then enter the classification stage using machine learning. The classification results are evaluated using accuracy values. More detail about each step will be discussed in this section.

The loaded data contains several samples taken from the 60th to 180th-second (sampling phase) of the overall record. To normalize the data, the values on each sensor are subtracted by its mean. The data is then aggregated to retrieve the mean, minimum, and maximum value features of each sensor based on its file name. Clustering model training uses the aggregated data to divide them into two clusters. The results are displayed on a scatter plot to analyze the distribution of data from each class.

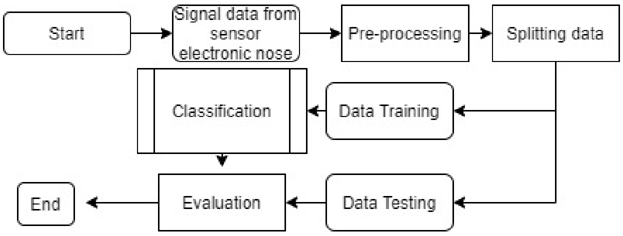

Fig. 2. Research Methodology Flow

After that, feature selection was carried out based on the analysis of variance (ANOVA) to determine which features were influential and would be used based on the null hypothesis (H_0). H_0 states that the mean of the dependent variable is the same for all groups. H_0 rejection means that each group's mean is not the same. Therefore, it can be concluded that the corresponding feature affects the dependent variable. The method used is the one-way ANOVA that looks for the F-value (F statistics). The F-value is taken from the ratio between the mean squared between-group and within-group (Equation 1). The mean is obtained from calculating the variance. In other words, F-value finds the similarity between variance of the groups' means (Mean Squared between) and mean of the groups' variances (Mean Squared within), as shown in Equation 2 and Equation 3, respectively. The obtained F statistic is then used to find the p-value based on the sample's numerator and denominator (degree of freedom). P-value is the probability of a statistical measure. The rejection of H_0 happens if the p-value is smaller than the determined significant-value, usually 0.05.

$$F = \frac{MS_{between}}{MS_{within}} \tag{1}$$

$$MS_{between} = \frac{SS_{between}}{df_{between}} \tag{2}$$

$$MS_{within} = \frac{SS_{within}}{df_{within}} \tag{3}$$

$$SS_{between} = \sum \frac{(\sum x)^2}{n} - \frac{(\sum\sum x)^2}{n_T} \tag{4}$$

$$SS_{within} = \sum\sum(x^2) - \sum \frac{(\sum x)^2}{n} \tag{5}$$

$$df_{between} = k - 1 \tag{6}$$

$$df_{within} = n_T - k \tag{7}$$

In Equations 4 and 5, x denotes the data from the sample, n and n_T denotes the amount of data from the sample in a corresponding class, and the total data count from the sample. In finding the degree of freedom (*df*) shown in Equation 6 and 7, k represents the number of classes in the sample. In this case, k equals two, namely male and female.

$$\text{Accuracy} = \frac{(TP + TN)}{TP+TN+FN+FP} \tag{8}$$

TP = True Positive

TN = True Negative

FP = False Positive

FN = False Negative

The sample collected has an uneven distribution of classes, which has more data on the female class. This uneven distribution can cause the classification model to bias towards the class with the most records. Therefore, it is necessary to perform oversampling on the data to adjust the number of the two classes.

After the data goes through the pre-processing stage, the data is ready to be used as training data in the classification model. In conducting the training, several models are used and evaluated based on their accuracy. The calculation of accuracy is defined in Equation 1. The classification algorithms used will be discussed in the subsubsection after this. Besides being compared based on the algorithm, the model is also compared based on each algorithm's hyperparameter tuning. The search for the optimal parameter of each algorithm is carried out using the grid search method. The grid search method takes a set of values for each hyperparameter of the model we want to tune. This method then iterates over each possible parameter combination and fetches the best one based on the specified metrics. In this experiment, the metrics used for comparison on the search grid is the accuracy metrics. In this training, the data will go through Principal Component Analysis (PCA) before entering the training stage.

a. Support Vector Machine (SVM)

SVM is a linear classifier that divides data based on the hyperplane formed. Sometimes, data is better divided on a dimension than another. SVM will change the dimensions of the data using the kernel. The kernel is one of the hyperparameters in SVM. Other than the kernel, the hyperparameters tuned were C and gamma. C is the regularization parameter, and gamma is the coefficient for several kernel types. SVM has proven to be successful in many cases, including classification. In a study, the result found that the parameter C greatly influenced this model [18].

b. Decision Tree

This model builds rules represented in the form of a tree based on training data. Each node in the tree is a decision made based on the value of a particular data feature. The leaf of this tree is the final prediction from the data. The maximum depth of the tree can be set as a hyperparameter in this model. Although the decision tree is not as complicated as the SVM, this model has proven to perform well in E-nose classification problem [19]. In forming a tree, this model calculates Gini impurity (Equation 9) or entropy index (Equation 10) to split the data. From the Equation 2 – 3, *c*, *i*, and p_i denote the number of classes, the *i*-th class, and the probability of *i*-th class on the corresponding feature, respectively. These calculations are hyperparameter to be fixed when modelling a decision tree.

$$Gini = 1 - \sum_{i=1}^{c} (p_i)^2 \tag{9}$$

$$Entropy = 1 - \sum_{i=1}^{c} -p_i log_2(p_i)^2 \tag{10}$$

c. K-Nearest Neighbor (K-NN)

This model is a lazy learner based on the nature of grouped objects having similar features. K-NN classifies new data based on the n-nearest neighbor from the training data, which takes the majority voting based on those neighbors [20]. The number of nearest neighbors that are set as the hyperparameter of this model. The acquisition of the nearest neighbor utilizes the distance calculation of each data points to the queried data.

$$\sqrt{\sum_{n=1}^{m} (x_n - y_n)^2} \tag{11}$$

$$\sum_{n=1}^{m} |x_n - y_n| \tag{12}$$

$$\max(|x_n - y_n|) \tag{13}$$

The calculation is performed between the data points from the training data (x_n) and the queried data (y_n). The distance calculation metric is hyperparameter in this model. Some of the most popular distance metrics are Euclidean (Equation 11), Manhattan (Equation 12), and Chebyshev (Equation 13). From Equation 2 – 4, *m* denotes the total number of features with *n* being the *n*-th feature.

III. EXPERIMENTAL RESULT

This section will discuss the result from the method proposed at the previous section. Data aggregation for feature extraction results in three times the number of sensors used, resulting in 24 feature columns. A large number of columns can cause model training to be slow. It is not guaranteed that all the extracted feature columns affect model learning. Therefore, it is necessary to select features using ANOVA. This method analyzes all features with the target. If the alternative hypothesis (H_1) is accepted, it can be concluded that a feature influences the target. Rejection of H_0 and acceptance of H_1 occurs when the score of the analysis is greater than the probability value of H_0 (p-value). In ANOVA, the analysis score is obtained from the F-test using the F-distribution. The obtained F-value is then converted into a p-value based on the degree of freedom. In this experiment, the significant value was 0.05. If the p-value is smaller than this significant value, then H_0 will be rejected. TABLE II lists the ten smallest p-values of all features.

With the specified significant value, the H0 is rejected on the mean feature of the TGS 2603 sensor. This rejection means that the mean of the TGS 2603 sensor in the two classes is

TABLE II. TOP 10 SMALLEST P-VALUE BASED ON ANOVA F-VALUE TEST

Feature	F-value	P-value
TGS 2603, mean	5.432	0.029
TGS 2612, mean	3.347	0.081
TGS 2620, max	2.328	0.141
TGS 826, max	1.357	0.256
TGS 826, mean	1.256	0.257
TGS 2620, mean	1.078	0.310
TGS 822, max	0.618	0.440
TGS 2600, mean	0.566	0.460
TGS 813, max	0.359	0.555
TGS 2600, min	0.316	0.580

TABLE III. HYPERPARAMETER TUNING OF SVM, DECISION TREE, AND K-NN

Model	Hyperparameter	Values	Best
SVM	C	100, 10, 1, 0.1	100
	gamma	0.1, 1, 0.01, 0.5	0.5
Decision Tree	Criterion	Gini, Entropy	Entropy
	Maximum depth	None, 3, 5, 7	3
K-NN	Weights	Uniform, Distance	Distance
	Metrics	Euclidean, Minkowski, Manhattan	Manhattan
	N neighbor	2, 3, 4, 5, 6, 7	2

TABLE IV. ACCURACY OF EACH MODEL WITH BEST HYPERPARAMETERS

Model	Accuracy
SVM	94.12%
Decision Tree	82.35%
K-NN	88.23%

different. From this analysis, it can be concluded that the TGS 2603 sensor affects both classes. This sensor has a high sensitivity to odorous gases, including Trimethylamine (TMA), methyl mercaptan, H2S, and ethanol. Figure 3 portrays the mean plot of the TGS 2603 sensor in the two classes. It appears that the average male sample is higher than that of women, which means that the concentration of the target gases in the male class is higher than the female class.

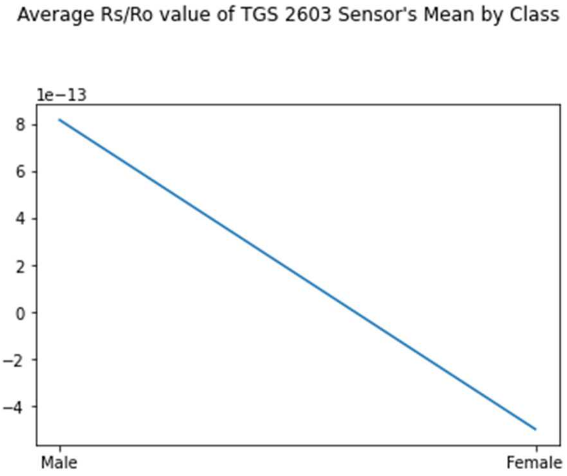

Fig. 4 Average Rs/Ro Value of TGS 2603 Mean by Class

One of the targets of the TGS 2603 sensor is the TMA gas. Excess TMA composition leads to a fishy odor in sweat. This disorder is called trimethylaminuria (TMAU), which occurs when flavin-containing-monooxygenase 3 (FMO3) fails to break down TMA into odorless trimethylamine-N-oxide (TMAO). TMAU does not cause physical side effects, but sufferers might experience social problems because of the smell produced. Some studies also report the TMAO to be a factor in cardiovascular diseases, including stroke or even death. [21], [22]. Apart from TMA, this sensor is also sensitive to methyl mercaptan gas. This gas can cause coma, anemia, and even death if exposed in high amounts.

Data that has gone through the feature selection is used in clustering modeling. Before clustering, the data dimensions are reduced to two dimensions using PCA with two components. The results of the clustering are plotted along with the centroids, as shown in Fig. 4. Blue dots represent the first cluster, and green stars represent the second cluster. A large red dot represents the centroid of each cluster. Each data is labeled with its original class to analyze its distribution in the plotting data.

After clustering, the data is then oversampled to balance it using synthetic minority oversampling technique (SMOTE). SMOTE is a K-NN-based oversampling method to increase the number of minority data. The decision of using oversampling was because of the limited number of samples. Oversampling results in equal amount of data with 17 data on each class and 34 in total.

Model training uses balanced data. SVM, decision tree, and K-NN were used and evaluated with tuned hyperparameters. The tested parameter and its best values can be seen in TABLE III with additional parameter for number of components in PCA ranging from zero to nine. Each combination of these parameters is tested and selected based on the highest accuracy. The Values column shows the parameters tested, and the Best column shows the best parameters of the model. The best parameter of each model is then evaluated based on its accuracy. The results of the accuracy of each model with the best parameters can be seen in TABLE IV. In addition, the best number of PCA components for SVM is eight, decision tree is seven, and K-NN is five. The result shows that SVM achieved the highest

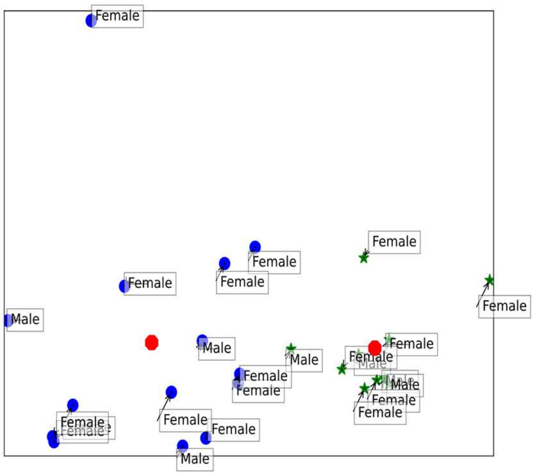

Fig. 3 Scatter Plot of Data Samples Clustering

accuracy followed by K-NN and decision tree using the best parameter of each model.

The visualization of predictions in classification often uses a confusion matrix. This matrix stores true positive, true negative, false positive, and false negative information from a model's predictions. This matrix can help calculate the accuracy and analyze the result of a model. Fig. 4 shows the confusion matrix of the best model. From the figure, the SVM model can correctly predicted all the Female class while it mistakenly predicted two of the Male class data.

IV. CONCLUSIONS

This section will cover the conclusion from feature selection to the model evaluation according to the previous section. From the results of the feature selection, there are seven out of eight sensors in this experiment that affect the biological gender classification based on body odor. The seven sensors are TGS 822, TGS 2612, 2620, TGS 832, TGS 826, TGS 2603, and TGS 2600. The aggregation feature that affects the target mostly is the mean of the sensor, followed by its maximum value.

The scatter plot from the clustering results shows that the two classes overlap in the second dimension. From this plot, it can be hypothesized that the SVM results will be better than the K-NN. This hypothesis is based on how the model works. SVM transforms the dimension of data to separate them adequately. Hence, the data may be separable in another dimension. The SVM accuracy of 94.12% proves this hypothesis, which is better than the K-NN accuracy of 88.23%. The lowest accuracy being the decision tree with 82.35% of accuracy. The confusion matrix shows that the SVM model has a slight bias towards the Female class. This is because the model incorrectly predicted the Male class as a Female class.

This study proves that E-nose can predict a human's biological gender using the smell of armpit sweat. This prediction has a reasonably good accuracy of 94.12% with the combination of PCA as pre-processing for dimensionality reduction and SVM as the machine learning method. In addition, based on the average of the TGS 2603 sensor selected through ANOVA, it is seen that men's sweat has a higher amine gas composition than women. Underarm odor analysis using the E-nose is possible to help detect the composition of human sweat. This detection can help health workers diagnose diseases or disorders caused by the composition present in sweat, such as TMAU.

ACKNOWLEDGMENT

This research was funded by Special Program for Research Against COVID-19 (SPRAC) managed by AUN/SEED-Net and the Indonesian Ministry of Research and Technology or National Agency for Research and Innovation and the Indonesian Ministry of Education and Culture under Penelitian Terapan Unggulan Perguruan Tinggi (PTUPT) Program, and under PMDSU Program managed by Institut Teknologi Sepuluh Nopember (ITS).

REFERENCES

[1] L. F. Canêo and R. Neirotti, “The importance of the proper definition of adulthood: What is and what is not included in a scientific publication,” *Brazilian Journal of Cardiovascular Surgery*, vol. 32, no. 1. Sociedade Brasileira de Cirurgia Cardiovascular, pp. 60–61, Jan. 01, 2017, doi: 10.21470/1678-9741-2016-0049.

[2] C. M. Buchanan, J. S. Eccles, and J. B. Becker, “Are adolescents the victims of raging hormones? Evidence for activational effects of hormones on moods and behavior at adolescence.,” *Psychol. Bull.*, vol. 111, no. 1, pp. 62–107, 1992, doi: 10.1037/0033-2909.111.1.62.

[3] V. Tangpricha and M. den Heijer, “Oestrogen and anti-androgen therapy for transgender women,” *The Lancet Diabetes and Endocrinology*, vol. 5, no. 4. Lancet Publishing Group, pp. 291–300, Apr. 01, 2017, doi: 10.1016/S2213-8587(16)30319-9.

[4] E. Cashdan, “Hormones and competitive aggression in women,” *Aggress. Behav.*, vol. 29, no. 2, pp. 107–115, Mar. 2003, doi: 10.1002/ab.10041.

[5] N. Charkoudian and N. Stachenfeld, “Sex hormone effects on autonomic mechanisms of thermoregulation in humans,” *Autonomic Neuroscience: Basic and Clinical*, vol. 196. Elsevier B.V., pp. 75–80, Apr. 01, 2016, doi: 10.1016/j.autneu.2015.11.004.

[6] K. Main, K. O. Nilsson, and N. E. Skakkebæk, “Influence of sex and growth hormone deficiency on sweating,” *Scand. J. Clin. Lab. Invest.*, vol. 51, no. 5, pp. 475–480, 1991, doi: 10.3109/00365519109091642.

[7] M. Harker, H. Coulson, I. Fairweather, D. Taylor, and C. A. Daykin, “Study of metabolite composition of eccrine sweat from healthy male and female human subjects by 1H NMR spectroscopy,” *Metabolomics*, vol. 2, no. 3, pp. 105–112, Sep. 2006, doi: 10.1007/s11306-006-0024-4.

[8] A. M. KLIGMAN and J. S. STRAUSS, “The bacteria responsible for apocrine odor.,” *J. Invest. Dermatol.*, vol. 27, no. 2, pp. 67–71, Aug. 1956, doi: 10.1038/jid.1956.79.

[9] W. Ping, T. Yi, X. Haibao, and S. Farong, “A novel method for diabetes diagnosis based on electronic nose,” *Biosens. Bioelectron.*, vol. 12, no. 9–10, pp. 1031–1036, Nov. 1997, doi: 10.1016/S0956-5663(97)00059-6.

[10] R. Sarno, K. Triyana, S. I. Sabilla, D. R. Wijaya, D. Sunaryono, and C. Fatichah, “Detecting Pork Adulteration in Beef for Halal Authentication Using

an Optimized Electronic Nose System," *IEEE Access*, vol. 8, pp. 221700–221711, 2020, doi: 10.1109/ACCESS.2020.3043394.

[11] R. Sarno, S. I. Sabilla, D. R. Wijaya, D. Sunaryono, and C. Fatichah, "Electronic nose dataset for pork adulteration in beef," *Data Br.*, vol. 32, p. 106139, Oct. 2020, doi: 10.1016/j.dib.2020.106139.

[12] C. Wongchoosuk, M. Lutz, and T. Kerdcharoen, "Detection and Classification of Human Body Odor Using an Electronic Nose," *Sensors*, vol. 9, no. 9, pp. 7234–7249, Sep. 2009, doi: 10.3390/s90907234.

[13] D. Lelono, K. Triyana, S. Hartati, and J. E. Istiyanto, "Classification of Indonesia black teas based on quality by using electronic nose and principal component analysis," in *AIP Conference Proceedings*, Jul. 2016, vol. 1755, no. 1, p. 020003, doi: 10.1063/1.4958468.

[14] S. W. Brusilow and E. H. Gordes, "Ammonia secretion in sweat.," *Am. J. Physiol.*, vol. 214, no. 3, pp. 513–517, 1968, doi: 10.1152/ajplegacy.1968.214.3.513.

[15] C. J. Denawaka, I. A. Fowlis, and J. R. Dean, "Source, impact and removal of malodour from soiled clothing," *J. Chromatogr. A*, vol. 1438, pp. 216–225, Mar. 2016, doi: 10.1016/j.chroma.2016.02.037.

[16] S. Tjoa and P. Fennessey, "The identification of trimethylamine excess in man: Quantitative analysis and biochemical origins," *Anal. Biochem.*, vol. 197, no. 1, pp. 77–82, Aug. 1991, doi: 10.1016/0003-2697(91)90358-Z.

[17] D. Sunaryono, S. Rochimah, R. Sarno, S. I. Sabilla, I. Ahmad Sabilla, and D. Sekarini, "Geotagging for mapping distribution of meatballs containing borax based on electronic nose detection," in *Proceedings - 2020 International Seminar on Application for Technology of Information and Communication: IT Challenges for Sustainability, Scalability, and Security in the Age of Digital Disruption, iSemantic 2020*, Sep. 2020, pp. 353–358, doi: 10.1109/iSemantic50169.2020.9234279.

[18] M. Pardo and G. Sberveglieri, "Classification of electronic nose data with support vector machines," *Sensors Actuators, B Chem.*, vol. 107, no. 2, pp. 730–737, Jun. 2005, doi: 10.1016/j.snb.2004.12.005.

[19] S. Wakhid, R. Sarno, S. I. Sabilla, and D. B. Maghfira, "Detection and Classification of Indonesian Civet and Non-Civet Coffee Based on Statistical Analysis Comparison Using E-Nose," *Int. J. Intell. Eng. Syst.*, vol. 13, no. 4, 2020, doi: 10.22266/ijies2020.0831.06.

[20] D. Sunaryono, J. Siswantoro, and R. Anggoro, "An android based course attendance system using face recognition," *J. King Saud Univ. - Comput. Inf. Sci.*, Jan. 2019, doi: 10.1016/j.jksuci.2019.01.006.

[21] S. H. Zeisel and M. Warrier, "Trimethylamine N-Oxide, the Microbiome, and Heart and Kidney Disease," *Annual Review of Nutrition*, vol. 37. Annual Reviews Inc., pp. 157–181, Aug. 21, 2017, doi: 10.1146/annurev-nutr-071816-064732.

[22] H. S. Nam, "Gut microbiota and ischemic stroke: The role of trimethylamine N-oxide," *Journal of Stroke*, vol. 21, no. 2. Korean Stroke Society, pp. 151–159, May 01, 2019, doi: 10.5853/jos.2019.00472.