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Hybrid Architecture Model of Genetic Algorithm and Learning Vector Quantization Neural Network for Early Identification of Ear, Nose, and Throat Diseases

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Abstract

Background: In 2020, the World Health Organization (WHO) estimated that 466 million people worldwide are affected by hearing loss, with 34 million of them being children. Indonesia is identified as one of the four Asian countries with a high prevalence of hearing loss, specifically at 4.6%. Previous research was conducted to identify diseases related to the Ear, Nose, and Throat, utilizing the certainty factor method with a test accuracy rate of 46.54%. The novelty of this research lies in the combination of two methods, the use of genetic algorithms for optimization and learning vector quantization to improve the level of accuracy for early identification of Ear, Nose, and Throat diseases.
Objective: This research aims to produce a hybrid model between the genetic algorithm and the learning vector quantization neural network to be able to identify Ear, Nose, and Throat diseases with mild symptoms to improve accuracy.
Methods: Implementing a 90:10 ratio means that 90% (186 data) of the data from the initial sequence is assigned for training purposes, while the remaining 10% (21 data) is allocated for testing. The procedural stages of genetic algorithm-learning vector quantization are population initialization, crossover, mutation, evaluation, selection elitism, and learning vector quantization training.
Results The optimum hybrid genetic algorithm-learning vector quantization model for early identification of Ear, Nose, and Throat diseases was obtained with an accuracy of 82.12%. The parameter values with the population size 10, *cr* 0.9, *mr* 0.1, maximum epoch of 5000, error goal of 0.01, and learning rate (alpha) of 0.5. Better accuracy was obtained compared to backpropagation (64%), certainty factor 46.54%), and radial basic function (72%).
Conclusion: Experiments in this research, successed identifying models by combining genetic algorithm-learning vector quantization to perform the early identification of Ear, Nose, and Throat diseases. For further research, it's very challenging to develop a model that automatically adapts the bandwidth parameters of the weighting functions during trainin

Keywords: Early Identification, Ear-Nose-Throat Diseases, Genetic Algorithm, Learning Vector Quantization

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I. INTRODUCTION

Ear, Nose, and Throat have important functions in the human body, including hearing, breathing, smelling, speaking, and swallowing food and drink. These three organs are also interconnected, therefore disturbances that occur in one organ will affect the other two[1]. Ear, Nose, and Throat diseases are generally caused by bacteria, viruses, and infections that enter the body. A family history of hereditary Ear, Nose, and Throat diseases is also one of the factors that cause Ear, Nose, and Throat diseases [2] [3]. In 2020, the World Health Organization (WHO) estimated that 466 million people worldwide are affected by hearing loss, with 34 million of them being children. Of this number, 60% of cases are deemed preventable. Indonesia is identified as one of the four Asian countries with a high prevalence of hearing loss, specifically at 4.6%, while the prevalence of deafness across all age groups in seven provinces is reported to be 0.4% [4]. Globally, it is estimated that 1 to 3 babies out of 1,000 live births experience congenital deafness, and this number increases to 2-4 babies per 100 in intensive care units [5]. Data from the Indonesian Badan Pusat Statistik

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(BPS) in 2019 indicates that the country's population is estimated at 268,074,600, with a prevalence of ear, nose, and throat diseases at 0.1%. This means that around 268,074 Indonesians are affected by congenital deafness. Considering an annual birth rate of 2.4% in Indonesia, an additional 60,000 cases were obtained over the last decade. And the concern for the health of the sense of hearing, which is still minimal [6].

The various types of Ear, Nose, and Throat diseases and the similarity of the caused symptoms make it difficult for ordinary people to recognize the types of Ear, Nose, and Throat diseases they have. In addition, the lack of awareness of the existing symptoms makes the disease not identified early, thus the illness has entered a more severe level without being realized. In some cases, patients who are classified as severe sufferers usually come from those who have mild diseases yet are late to see a doctor. In terms of the treatment, Ear, Nose, and Throat diseases are classified as mild which can be cured without aids, and are also classified as severe which can only be cured with aids. Therefore, early identification of Ear, Nose, and Throat disease is very necessary so that preventive measures can be taken before the experienced infection becomes severe[1], [3], [7].

Several studies have been conducted to identify Ear, Nose, and Throat diseases using the concept of an expert system with the forward chaining method [8]. The resulting output of those studies has been able to detect the diseases, therefore it has been able to provide treatment solutions as well as carry out the immediate treatment in the form of an explanation description of the developed application. The forward chaining method emphasizes the use of a knowledge representation model in the form of production rules that have been tested based on the database input provided [9]. In addition, a research using the concept of an expert system has also been carried out using the bayes theorem inference method [10], and the testing was carried out on the system against seven types of Ear, Nose, and Throat diseases in children; the use of some test data based on the input of symptom data that had been entered could give results in accordance with the answers from Ear, Nose, and Throat experts [11]. The existing research has a notable limitation, specifically in terms of its accuracy, which is a crucial aspect that requires improvement.

This research aims to produce a hybrid model between the genetic algorithm and the learning vector quantization neural network in order to be able to identify Ear, Nose, and Throat diseases with mild symptoms to improve the accuracy compared with a previous study. In previous research has been conducted to identify Ear, Nose, and Throat diseases using the concept of expert system with the forward chaining method. The resulting output has been able to detect the diseases, therefore it has been able to provide treatment solutions as well as carry out immediate treatment in the form of an explanation description of the developed application. The novelty of this research lies in the fusion of two methods: genetic algorithms for optimization and learning vector quantization for enhanced learning, resulting in significantly improved accuracy. This research is expected to be able to contribute by providing information on Ear, Nose, and Throat diseases and early identification for common public in recognizing mild symptoms of Ear, Nose, and Throat diseases before being diagnosed to a severe level. This output then became the input to the training data in the learning vector quantization method. The produced optimum hybrid genetic algorithm-learning vector quantization model was seen from the most optimal level of accuracy.

II. Related Works

Artificial neural network as the domain of the field of artificial intelligence. Artificial neural network adopts the working principle of the human brain's nervous system in learning, remembering information, and determining patterns. The artificial neural network approach itself has been widely used in the medical field, including for early identification and diagnosis, as well as can reduce manual diagnostic errors because the system can combine the experience and knowledge of several doctors [12], [13]. The work emphasis of the artificial neural network algorithm is focused on building a network to be able to make good predictions. One of the used artificial neural network methods is the learning vector quantization [14].

Learning vector quantization is a training method used in single-layered network architecture competitive learning. This method categorizes several types based on their classification, where the results of this grouping can be used to obtain fast and accurate output using small sample data[15]–[18]. This is proven by the research results by [19] which used the learning vector quantization method to classify a person's stress level based on three classifications, with the resulting output having a sufficient level of accuracy. The advantage of the learning vector quantization neural network method is that it can summarize large data sets into smaller ones and have a small error value [20]–[24]. However, the class distribution on a small dataset affects the accuracy of the resulting output. To overcome this problem, it is necessary to optimize the dataset that will be used at the training stage using the genetic algorithm. Genetic algorithm is the most popular search and optimization technique and is quite flexible when combined with other algorithms [25]–[28]. Since these algorithms do not consider complex interaction among several features, in many cases they lead to unsatisfactory optimal solutions as explained by [29]. This research used an artificial neural network approach with a combination of genetic algorithm and learning vector quantization method. The learning vector quantization method

consists of a competitive layer that will always learn to classify input vectors. The optimization is done by finding the initial value of learning vector quantization weight vector using genetic algorithm. Although the initial value of the weight vector affects the learning vector quantization result, it can not guarantee that learning vector quantization training produces the optimal representative vector and need more method to achieve the optimal value [30]. Learning vector quantization optimization using genetic algorithm has been done in previous studies such as research used the data from the Huaihe River in China by [31] and compared the three methods of radial basic function, backpropagation, and learning vector quantization, resulted in 92% accuracy value for the learning vector quantization, 72% for the radial basic function, and 64% for the backpropagation. Research from classifier by [32] classified EEG signals using hilbert transform and based on the classifier learning vector quantization algorithm, which could then be generalized by classifying all data sets from the database of the used EEG signals. After extensive testing, a MATLAB-simulated schematic model resulted in an average classification accuracy of 89.31%.

Learning vector quantization neural network, which has a small data set, has problems with class distribution, so it affects the accuracy of the resulting output. To overcome this problem, a genetic algorithm is used to optimize the dataset that will be used in the training phase. The results of the previous research show that genetic algorithm can optimize the ability of classified distribution research by Monroe *et al.* [33] developed a genetic programming approach to find the most suitable model structure and hierarchical parameter value. Modifications were made to the genetic programming approach to reduce model errors while limiting the growth of complex tree structures. The genetic programming approach method was applied here to identify models for multiple UV reactors by training models for three data sets. Research by Woodward & Kelleher [34] used genetic algorithm applied machine learning principles, paving the way for optimizing 'smart' optical technologies. Then Karegowda *et al.* [35] and Melin *et al.* [36] they are using genetic algorithm approach for class distribution problem.

III. METHODS

A. Data Collection

In this research, the source of the data came from the primary data obtained directly from the knowledge of the otolaryngologist. The research instrument consisted of direct interviews with an otolaryngologist at a private hospital in West Jakarta, with the aim of obtaining expert knowledge on symptom data and types of Ear, Nose, and Throat diseases. The quantitative data were in the form of closed questionnaires via email and social media, with the target of respondents who had been diagnosed with Ear, Nose, and Throat diseases which were the output of the model to be developed. The questions in the questionnaire were specific questions that directed the respondents to answer the disease and symptoms that had been provided based on the respondents' experience with the disease and symptoms that had suffered. Each symptom offers three value options: a rating of 50 denoting high-intensity occurrence (always), a score of 35 for symptoms with medium intensity (sometimes), and a value of 15 for symptoms with low intensity (not often). These weightings were determined through consultations with an otolaryngologist at a private hospital in West Jakarta. The data utilized consists of qualitative information obtained from interviews with otolaryngologists. Subsequently, this data is transformed into quantitative, rule-based data based on symptom data. The respondents have filled out an informed consent form stating that they are willing to be interviewed by the researcher for the data used in this study.

The comparison of training data and test data in this research was 90:10. This comparison was chosen because the more training data entered at the training stage, the better the network would recognize each data; whereas, if a lot of test data was compared to the training data, the obtained accuracy level would be lower. Adopting a 90:10 ratio implies that 90% of the data from the initial sequence will be designated as training data, while the subsequent sequence allocates 10% for testing purposes. This results in 186 data points earmarked for training and 21 data points designated for testing.

Many researchers have advocated for ratios such as 70:30 or 80:20 when creating datasets for studies pertaining to landslide susceptibility. In a recent investigation, Pham et al. explored the repercussions of adjusting the training dataset size, ranging from 30% to 90%, using the random forest (RF) algorithm to estimate soil shear strength. The study unveiled that increasing the training dataset size not only improved training performance but also heightened the stability of the model. Concerning testing performance, expanding the training set from 30% to 80% similarly yielded improved testing outcomes. However, a contrasting trend emerged in testing performance as the training size progressed from 80% to 90%. In summary, the scale of the training set played a pivotal role in influencing the predictive capability of machine learning models.

The data collected consists of:

1) Ear, Nose, and Throat Disease Data

The general Ear, Nose, and Throat disease data was obtained from interviews with the Ear, Nose, and Throat specialist doctors at a private hospital in West Jakarta. There were eight types of disease data (cerumen Prop, Diffuse Otitis External, Acute Otitis Media, Acute Eustachian Tube Dysfunction, Allergic Rhinitis, Rhinosinusitis, Pharyngitis, and Laryngopharyngeal Reflux Disease), consisting of three classifications of the ear, nose, and throat.

2) Ear, Nose, and Throat Symptom Data

The data on symptoms of Ear, Nose, and Throat diseases usually experienced by the patient receiving treatment, and also explanations of the symptoms of these diseases. The disease symptom data were 33 symptoms.

TABLE 1
SYMPTOM, DISEASES DATA OF EAR, NOSE, THROAT DISEASES

No	Symptom Data	Fitness Average	Diseases	Input Value
X1	The ear feel stuck	*Serumen Prop* (P1)	Ear	0= No ; 1= Yes
X2	Discharge from the ear	*Serumen Prop* (P1)	Ear	0= No ; 1= Yes
X3	Watery ears	*Otitis EksternaDifusa* (P2)	Ear	0= No ;
X4	Pain when pressing on the tragus pain	*Otitis EksternaDifusa* (P2)	Ear	1= Yes
X5	Itching inside the ear	*Otitis EksternaDifusa* (P2)	Ear	0= No ;
X6	Pain in the ear	*Otitis Media* Akut(P3)	Ear	1= Yes
X7	The ear feels filled with fluid but it doesn't come out	*Otitis Media* Akut(P3)	Ear	0= No ;
X8	Ears feel full like boarding an airplane	*Otitis Media* Akut(P3)	Ear	1= Yes
X9	Pain in the head	*Otitis Media* Akut(P3)	Ear	0= No ;
X10	History of cough and cold	*Otitis Media* Akut(P3)	Ear	1= Yes
X11	Nasal allergies	*Disfungsi TubaEustachius* (P4)	Nose	0= No ;
X12	Blocked ears like getting on a plane	*Disfungsi TubaEustachius* (P4	Nose	1= Yes
X13	Pain in the inner ear (ear drum)	*Disfungsi TubaEustachius* (P4	Nose	0= No ;
X14	Sneezing	*Rhinitis* Alergi (P5)	Nose	1= Yes
X15	Have a cold	*Rhinitis* Alergi (P5)	Nose	0= No ;
X16	Clear or watery mucus	*Rhinitis* Alergi (P5)	Nose	1= Yes
X17	Itching in the nose and eye area	*Rhinitis* Alergi (P5)	Nose	0= No ;
X18	Nose feels blocked	*Rhinosinusitis* (P6)	Nose	1= Yes
X19	Mucus is yellow or green	*Rhinosinusitis* (P6)	Nose	0= No ;
X20	The upper part of the face when pressed will feel painful	*Rhinosinusitis* (P6)	Nose	1= Yes
X21	The upper part of the face hurts when looking down	*Rhinosinusitis* (P6)	Nose	0= No ;
X22	Bad smelling breath	*Rhinosinusitis* (P6)	Nose	1= Yes
X23	Itching and sore throat	*Faringitis* (P7)	Nose	0= No ;
X24	Reddish throat wall	*Faringitis* (P7)	Throat	1= Yes
X25	Increased or dry mucus	*Faringitis* (P7)	Throat	0= No ;
X26	Pain and difficulty swallowing food	*Faringitis* (P7)	Throat	1= Yes
X27	Cough	*Faringitis* (P7)	Throat	0= No ;
X28	Voice becomes hoarse	*LaryngopharyngealReflux Disease* (P8)	Throat	1= Yes
X29	Discomfort in the throat	*LaryngopharyngealReflux Disease* (P8)	Throat	0= No ;
X30	Clearing your throat or coughing	*LaryngopharyngealReflux Disease* (P8)	Throat	1= Yes
X31	Mucus feels like it has accumulated in the throat	*LaryngopharyngealReflux Disease* (P8)	Throat	0= No ;
X32	Bad breath	*LaryngopharyngealReflux Disease* (P8)	Throat	1= Yes
X33	Itching in the throat	*LaryngopharyngealReflux Disease* (P8)	Throat	0= No ;

B. Genetic Algorithm-Learning Vector Quantization Neural Network Procedure

The proposed genetic algorithm-learning vector quantization neural network model development procedures are as follows:

1) Preprocessing

Preprocessing the data before modeling, and preparing the initialization of used parameters as follows: population size, number of genetic algorithm generations, crossover rate, mutation rate, and learning rate. [36]–[42] In this research, the number of weights generated was equal to the class in the data and generated the learning vector quantization method weights from the class randomly. The length of the chromosome used was 45.

2) Population Initialization

Creating an individual population at random by crossover and mutation reproductions. The crossover reproduction was conducted by selecting two random individuals from the initial individuals, which then were generated with the α value randomly as well. The resulting offspring would be equal to the number of crossover rates * population size. Next, the mutation reproduction was conducted by selecting two random individuals from the initial individual, which

then were generated with the value of *r* also randomly as well. The resulting offspring would be equal to the number of crossover rates * population size [28], [42]–[44].

3) Evaluation

After the reproduction process was complete, an evaluation was conducted by calculating the fitness value of each individual using the following equation:

$$Accuracy = \frac{the\ number\ of\ same\ classes}{the\ amount\ of\ data}\ x\ 100\% \qquad (1)$$

4) Elitism Selection

Elitism selection by evaluating the suitability of each individual situation with the requested results. The selection was conducted by selecting the best individual from a number of individuals as much as popsize from both the parents and offspring individuals. These selected individuals would be used as the training data for the learning vector quantization method [28], [42]–[44].

5) Select individual with the highest match

Training with the learning vector quantization method was carried out for selected individuals by training weights with 186 training data and then calculating the Euclidean distance of weights with training data which would then be sorted in ascending order. The results would be checked for update conditions according to the learning vector quantization algorithm.

6) Update alpha value

Update the alpha value based on the following formula equation:

$$alpha = alpha - (alpha * alpha\ subtractor) \qquad (2)$$

7) Check the parameter value

Check the parameter value whether it already reached the maximum generation; if it was, then the process is complete; and if was not, it would repeat the crossover reproduction process [43], [44].

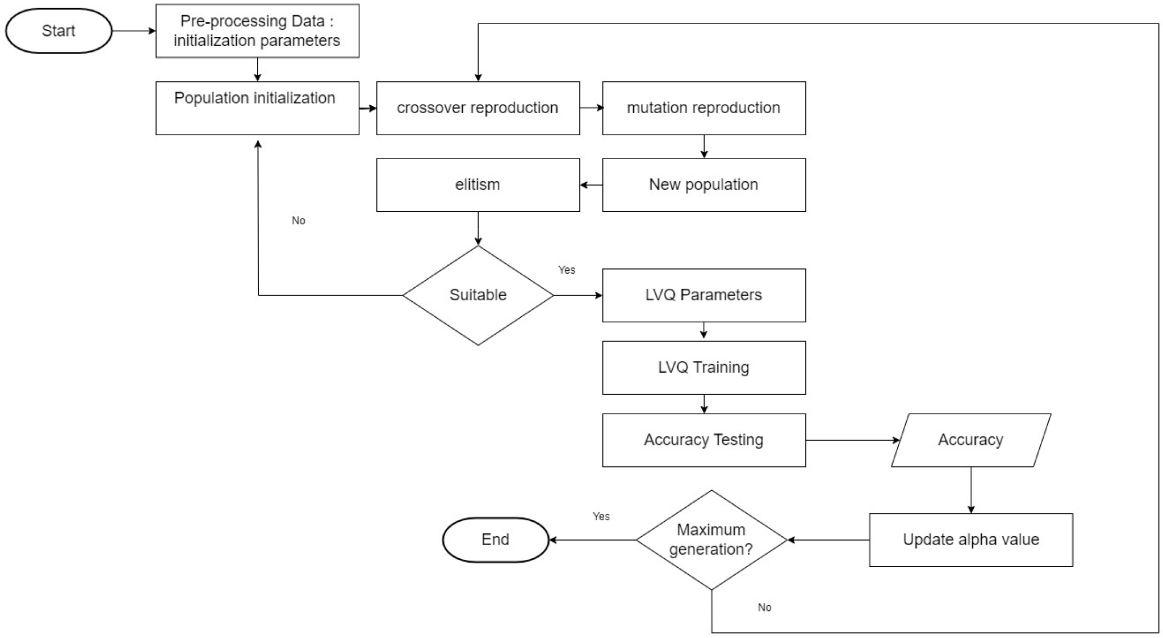

Fig. 1 Genetic Algorithm-Learning Vector Quantization Neural Network Procedure

C. The Proposed Genetic Algorithm- Learning Vector Quantization Neural Network Diagnosis Model

Learning vector quantization is a method used along with the artificial neural network which includes supervised learning. The competitive layer will always learn to classify input vectors. The class in this layer is very dependent on the distance between the input vectors. Whenever two input vectors approach the same output, the competitive layer will put the input vectors into the same class.

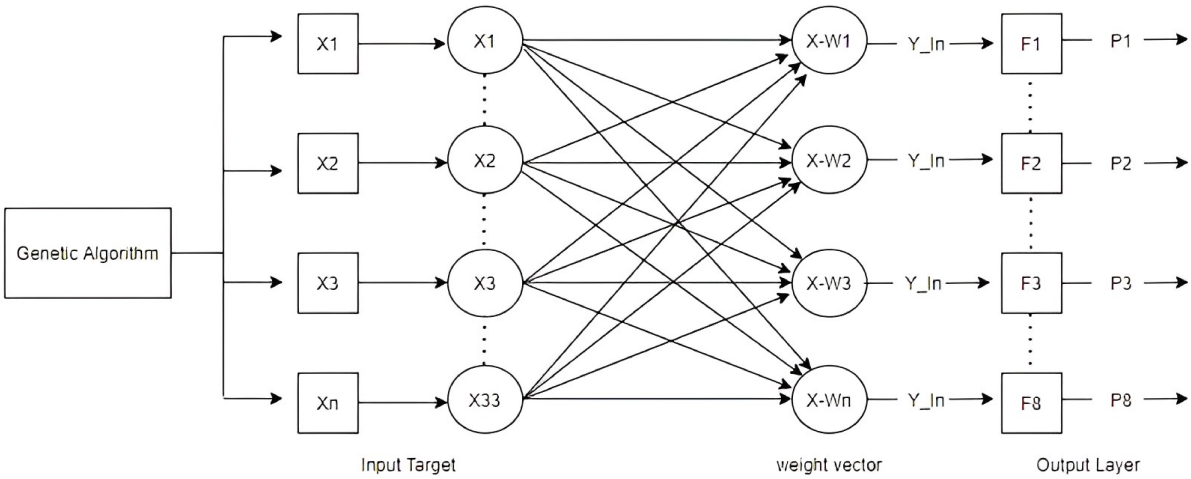

Fig. 2 Model of Genetic Algorithm-Learning Vector Quantization for earlier identification of Ear, Nose, and Throat diseases

IV. RESULTS

In this research, using a 90:10 ratio means that 90% of the data from the initial sequence is designated as training data, with the remaining 10% allocated for testing purposes. This allocation results in 186 data points for training and 21 data points for testing. Many researchers have advocated for ratios such as 70/30 or 80/20. In a recent investigation revealed that increasing the size of the training dataset not only enhanced training performance but also bolstered the model's stability. Regarding testing performance, expanding the training set from 30% to 80% similarly led to improved testing results. However, a divergent pattern in testing performance emerged as the training size progressed from 80% to 90% [45]. In summary, the size of the training set played a pivotal role in influencing the predictive capability of machine learning models.

The genetic algorithm method began by mapping the existing problem into the form of string chromosomes. This algorithm duplicated the natural evolutionary process where the main focus was that the most superior individuals would survive, while the weaker individuals would become extinct. The advantages of these individuals were tested through a function known as the fitness function. This fitness in genetic algorithm represented the quality of the individual whether it was the optimal solution seen from the results of the resulting fitness value, and then became a reference for the next genetic algorithm process.

In the process of designing the application for the early identification of Ear, Nose, and Throat diseases, there are 33 Ear, Nose, and Throat disease symptom data serving as input variables denoted by the letter X. Specifically, X1 represents the first variable corresponding to the initial symptom, X2 denotes the second symptom variable, and so forth. Subsequently, the value of each input variable is established based on the symptoms reported by the user. These values are represented numerically, taking the form of one or zero. The numerical value of zero signifies the absence of the respective symptom, whereas a value of one indicates the presence of the symptom. The forthcoming list comprises the 33 symptoms data, which will function as input variables along with their corresponding values for the artificial neural network application under development as shown in Table 1. The target that is the output of the application is represented in numerical form from 1 to 8, if the user gets an output with the numeric 1 then the user experiences cerumen prop disease, etc.

A. Population initialization

Initialization of population size was conducted to determine the size of the population that could be generated from the optimal solution. In this research, the test for initialization was carried out 10 times with a population size of 2 to 20, starting from generation 1 with the *cr* value of 0.5, *mr* value also 0.5, learning rate of 0.1, learning rate subtractor of 0.1, and constant ε of 0.35. The results of the fitness average of population initialization are shown in Table 2 below. Seeing from these results, showed that the test was unstable due to the formation of the initial individual which was random. The population size of 10 had the highest average fitness value among the popsize used. Therefore, further tests would use the population size of 10.

B. Reproductions of Crossover and Mutation

Prior to crossover and mutation reproductions, multiple generations were tested, to find out how many generations could be generated from the optimal solution in the research. The test was carried out 10 times in each generation with a generation range of 10 to 100 generations; the *cr* was 0.5, the *mr* value was also 0.5, the learning rate was 0.1, the learning rate subtractor was 0.1, and the constant ε was 0.35. The results of the fitness average of the multiple-generation test are shown in Table 2 below.

TABLE 2
THE FITNESS AVERAGE OF POPULATIN INITIALIZATION AND MULTIPLE GENERATION TEST

Generation	Fitness Average	PopSize	Fitness Average
10	92.787	2	83.812
20	93.625	4	83.531
30	93.250	6	84.249
40	93.750	8	84.339
50	92.500	10	84.561
60	93.250	12	82.569
70	93.275	14	83.138
80	92.250	16	81.456
90	93.870	18	82.621
100	93.155	20	81.453

Based on the results of the table above, it can be seen that the fluctuating movement from generation 10 to generation 40 had increased, then had a downward trend in one generation. The average fitness in the 90th generation had the largest average of 93.870% which was then selected to be used for the next test.

Furthermore, the combination of *cr* and *mr* was tested which was carried out 9 times for 90 generations of the population, with the values of 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, the learning rate value was 0.1, the learning rate subtractor was 0.1, and the constant of ε was 0.35. The results of the crossover and mutation rates are shown in Table 3 below.

TABLE 3
THE FITNESS AVERAGE OF CROSSOVER AND MUTATION REPRODUCTION

cr	*mr*	*Fitness Average*
0.1	0.9	92.750
0.2	0.8	92.250
0.3	0.7	92.750
0.4	0.6	92.625
0.5	0.5	93.750
0.6	0.4	93.250
0.7	0.3	93.375
0.8	0.2	93.125
0.9	0.1	94.000

Seeing from the results of the table, the graph tended to rise from the first combination to the 5th combination, then fell back down in the 6th combination, and then back up in the 6th combination. The average fitness at the values of *cr* of 0.9 and *mr* of 0.1 had the largest average of 94,000% which was then selected for the next test.

C. Genetic Algorithm-Learning Vector Q Accuracy Testing

In the model of early identification of Ear, Nose, and Throat diseases, the parameter values affected the data training and testing. In addition, the determination of the parameter values also greatly affected the level of accuracy and error generated from the network that we created, thus in this application design, the search for the highest level of accuracy and the lowest error value was done by determining the parameter values by trial and error, hence later it could be compared which parameter values could be used as a reference for network training and testing. After conducting several experiments in data training and testing with the learning vector quantization artificial neural network, it was found that the level of accuracy and the produced error varied and even equal. The choice of data comparison also greatly affected the level of network accuracy. In the design of this application using 186 training data and 21 data to be tested, the comparison of data usage in the design of this application was 90:10; this comparison was chosen because, at the training stage, the network required sufficient data to be able to recognize data patterns for each target class; while for the test data, it was only to measure the accuracy of a network. The following are the results of the experiment using parameter values to get a high level of accuracy and low error, as shown in Table 4 below,

Based on the Table 4, it can be seen that the training results, with the parameter values determined by trial and error, resulted in varying accuracy levels MSE. The parameter values with the maximum epoch of 5000, error goal of 0.01, and learning rate (alpha) of 0.5 were obtained in the 58th experiment, with the highest accuracy level of 82.12%, the MSE was 10.2381, and the training time was momentary.

TABLE 4
THE RESULTS OF THE ARTIFICIAL NEURAL NETWORK TRAINING OF LEARNING VECTOR QUANTIZATION METHOD

Experiment	Epoch (iteration)	Learning Rate (alpha)	Learning Goal	Accuracy Level	MSE	Training Time
1	100	0.1	0.01	47.62	7.6190	2:04
2	100	0.1	0.01	55.12	7.0000	1:48
3	100	0.1	0.01	62.27	1.5238	1:49
4	100	0.1	0.01	61.13	15.5714	3:14
5	300	0.1	0.01	47.60	15.5714	6:18
6	300	0.1	0.01	73.01	3.2358	5:01
7	300	0.1	0.01	73.72	13.0952	5:29
8	300	0.1	0.01	47.62	15.5714	7:39
9	500	0.1	0.01	62.27	13.9048	10:39
10	500	0.1	0.01	47.62	3.1905	8:19
11	500	0.1	0.01	47.62	11.3810	14:31
12	500	0.1	0.01	69.18	15.5714	9:45
13	1000	0.1	0.01	65.70	12.0852	8:10
14	1000	0.1	0.01	65.73	13.7514	10:32
15	1000	0.1	0.01	67.50	13.9048	13:05
16	1000	0.1	0.01	67.73	7.1905	6:18
17	5000	0.1	0.01	77.83	9.1310	1:01
18	5000	0.1	0.01	82.02	15.5714	3:29
19	5000	0.1	0.01	47.62	13.0952	7:39
20	5000	0.1	0.01	65.70	7.0000	9:39
…	……	……	……..	……	……	……..
55	1000	0.5	0.01	79.88	13.0952	5:29
56	5000	0.5	0.01	80.62	15.5714	7:39
57	5000	0.5	0.01	80.62	10.9048	10:49
58	5000	0.5	0.01	82.12	10.2381	11:32
59	5000	0.5	0.01	81.24	15.5714	9:57

D. Elitism Selection

Elitism in the context of evolution involves the possibility of individuals suffering damage that leads to a reduction in their quality. Elitism, however, serves as a mechanism that shields the top-performing individuals from undergoing further evolutionary changes [46], [47]. Instead, these exceptional individuals are directly passed on to the next generation without any alterations. The process of implementing elitism can be outlined as follows: 1. Determine the number of duplicates, denoted as 'm'. 2. Select a single individual with the highest fitness. 3. Following the application of evolutionary operations such as selection, crossover, and mutation, replace the individual with the poorest fitness 'm' times with the individual chosen in the previous step [28].

The evaluation of each chromosome is conducted in every generation by calculating its fitness value, which describes its quality. Elitist selection involves choosing individuals with the highest fitness values from the entire population. The accuracy test was done by conducting individual tests of the optimization results using the test data that had been prepared. The test data that already had class were used as the comparison of classification results, while the genetic algorithm parameter values used in this test were the population size of 10, the crossover rate of 0.9, the mutation rate of 0.1, and the number of generations 90. From ten experiments, the fitness average accuracy was 90.5%, and the highest accuracy was 95%.

TABLE 5
F-MEASURE AND AUROC MEAN FOR THE 100% DATASET

Training Dataset Condition						Confusion Matrix	
	Precision	Recall	F-Measure	ROC area	Class	a	b
Normal (100% data)	0.961	0.93	0.933	0.623	N	1909	101
	0.733	0.717	0.744	0.623	P	175	75
	0.862	0.878	0.868	0.623	Average		

E. Evaluation

The F1 score provides a weighted average measure of the balance between precision and recall. Accuracy is a suitable performance reference for algorithms when the dataset shows a near-equivalent count of false negatives and false positives, creating a symmetric scenario. The best F1 score value is 1.0, and the worst value is 0. In representation, if the F1 score has a high score, it indicates that our classification model has good precision and recall. The results of F-measure and AUROC mean calculations for the entire 100% dataset can be seen in Table 5.

V. DISCUSSION

According to our experiments, the population size of 10 had the highest average fitness value among the popsize used. Then it can be seen that the fluctuating movement from generation 10 to generation 40 had increased, then had a downward trend in one generation. We find that the average fitness in the 90th generation had the largest average of 93.870% which was then selected to be used for the next test. Next, the combination of *cr* and *mr* was tested which was carried out 9 times for 90 generations of the population, with the values of 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, the learning rate value was 0.1. Next, the graph tended to rise from the first combination to the 5th combination, then fell back down in the 6th combination, and then back up in the 6th combination. The average fitness at the values of *cr* of 0.9 and *mr* of 0.1 had the largest average of 94,00% which was then selected for the next test. In the model of early identification of Ear, Nose, and Throat diseases, the parameter values affected the data training and testing. In addition, the determination of the parameter values also greatly affected the level of accuracy and error generated from the network that we created, thus in this application design, the search for the highest level of accuracy and the lowest error value was done by determining the parameter values by trial and error, hence later it could be compared which parameter values could be used as a reference for network training and testing Finally we obtained parameter values with the maximum epoch of 5000, error goal of 0.01, and learning rate (alpha) of 0.5 were obtained in the 58th experiment, with the highest accuracy level of 82.12%, and the MSE was 10.2381 as shown in Table 12.

The limitation of the training data used in this research affects the optimization of the learning vector quantization method by genetic algorithm when initializing weight vectors through its evolutionary process. compare with backpropagation, certainty factor, and radial basic function as a result, the parameters used in the created model become more detailed. For future research development, it is recommended to increase the amount of training data to be used, so that the resulting model can achieve a higher level of accuracy. A summary of the results of the genetic learning algorithm-vector learning quantization algorithm is shown in Table 6 below.

TABLE 6
SUMMARY OF THE RESULT OBTAINED FOR GENETIC ALGORITHM-LEARNING VECTOR QUANTIZATION ALGORITHMS

Parameters	Result
Population Size	10
Crossover rate	0.9
Mutation rate	0.1
Generation	90
Fitness Average	94.00%
Learning rate (alpha)	0.5
Error goal	0.01
Max epoch	5000
Accuray	82.12%

In our research, we also compared several methods such as backpropagation, certainty factor, radial basis function neural network and genetic algorithm-learning vector quantization to obtain the highest level of accuracy. As shown in Table 7. with genetic algorithm-learning vector quantization method has the highest accuracy. During training experiments with the training dataset, it becomes evident that both parameter values and the volume of data within a target class exert substantial influence on the learning process of the application. This study specifically notes that three target classes exhibit significant data disparities compared to other target classes, leading to the network's inability to effectively recognize these target data classes.

TABLE 7
COMPARISON OF ALGORITHM PERFORMANCE IN CASES OF EARLY IDENTIFICATION OF EAR, NOSE, AND THROAT DISEASES

Methods	Accuracy
Backpropagation	64%
Certainty Factor	46.54%
Radial Basis Function Neural Network	72%
Genetic Algorithm-Learning Vector Quantization	82.12%

In a 2016 study conducted by Zhang & Li [31], data from the Huaihe region in China was analyzed. They examined three different techniques, namely, radial basic function, backpropagation, and learning vector quantization. The outcomes revealed whereas radial basic function and backpropagation yielded accuracy rates of 72%, 64%, 92 % respectively.

Dirgantara & Hairani [48] conducted a study where they designed an expert system for the identification of ENT diseases. They utilized forward chaining inference through the certainty factor (CF) approach in the development of this system. The research stages included problem identification for domain analysis, knowledge acquisition through interviews to gather MB and MD values for each Ear, Nose, and Throat disease symptom, and design involving the creation of knowledge representations like decision tables and knowledge rules. The findings of the study indicated a certainty level of 46.54%.

This research aims to produce a hybrid model between the genetic algorithm and the learning vector quantization neural network to be able to identify Ear, Nose, and Throat diseases with mild symptoms to improve accuracy. In this research, by employing a combination of two methods, namely the use of genetic algorithms for optimization and learning vector quantization, a higher level of accuracy was obtained compared to studies conducted real time evaluation of rivers water quality has great significance for maintenances and protection of water resources. In the case of Huaihe River by [31], we took advantages of LVQ (learning vector quantization) to classify the water qualities. In the study about expert system by [48], using the same method but different subject domains, accuracy rates were reported using the radial basic function method at 72%, Backpropagation at 64%, and learning vector quantization at 92% for data from the Huaihe River in China. On the other hand, research conducted by Dirgantara & Hairani [48], within the same subject domain aimed at identifying diseases in the ear, nose, and throat using the certainty factor method, resulted in an accuracy rate of 46.54%. Notably, employing a different method within the same subject domain yielded an accuracy level of 82.12%, indicating a significant increase of 56.67% compared to the previous method.

VI. CONCLUSIONS

Finally, by doing the experiments in this research we successed in identifying alternative models by combining the genetic algorithm and learning vector quantization to perform the early identification of Ear, Nose, and Throat diseases. The research flow in producing architectural models by combining the genetic algorithm and learning vector quantization models was explained. The process started with the genetic algorithm and the output produced by selected individuals from the results of elitism selection. This output then became the input to the training data in the learning vector quantization method. In the findings of our study, we observed that the hybrid genetic algorithm-learning vector quantization model generated achieved optimal performance, evident in its highest accuracy rate of 82.12% and a mean squared error (MSE) of 10.2381. This surpasses the accuracy levels of other models such as backpropagation (64%), certainty factor (46.54%), and radial basic function (72%). For further research, it's very challenging to develop a model that automatically adapts the bandwidth parameters of the weighting functions during training.

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Data Availability: In this study, data was sourced primarily from firsthand knowledge of an otolaryngologist. The research methodology involved conducting direct interviews with an otolaryngologist working in a private hospital located in West Jakarta. The objective was to acquire specialized insights into symptom data and the various types of Ear, Nose, and Throat diseases. Quantitative data was collected through closed questionnaires distributed via email and social media channels, targeting respondents who had previously been diagnosed with Ear, Nose, and Throat conditions, which would serve as the foundation for the forthcoming model. Access to certain data is restricted to

maintain the confidentiality and privacy of the sources.

Informed Consent: Informed Consent was obtained, and a detailed explanation was presented in the Methods section.

Animal Subjects: There were no animal subjects.

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