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Evaluation of artificial neural network and adaptive-network-based fuzzy inference system for ovarian and lung cancer prediction

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ABSTRACT

Aims: Every year, a significant number of individuals lose their lives due to cancer or undergo challenging treatments. Indeed, the development of an effective cancer prediction method holds great importance in the field of healthcare.

Methods: Machine learning methods have played a significant role in advancing cancer prediction models. In this context, this study focuses on exploring the potential of two machine learning methods: Artificial neural network (ANN) and adaptive-network-based fuzzy inference system (ANFIS) for cancer prediction. In this study, two different types of cancer, ovarian cancer and lung cancer, are taken into consideration. For the prediction of ovarian cancer, three specific biomarkers, namely human epididymis protein 4 (HE4), carbohydrate antigen 125 (CA-125), and carcinoembryonic antigen (CEA), are used to develop a prediction model. For the prediction of lung cancer, six different variables are utilized in the development of both the ANN and ANFIS methods.

Results: The findings demonstrated that the proposed methods had an accuracy rate of at least 93.9% in predicting ovarian cancer. With an accuracy rate of at least 89%, the proposed methods predicted lung cancer. Also, the proposed ANN method outperforms the ANFIS method in terms of predictive accuracy for both ovarian cancer and lung cancer.

Conclusion: This study suggests that the ANN method provides more reliable and accurate predictions for these specific cancer types based on the chosen variables or biomarkers. This study highlights the potential of machine learning methods, particularly ANN, in improving cancer prediction models and aiding in the early detection and effective management of ovarian and lung cancers.

Keywords: ANN, ANFIS, cancer prediction

INTRODUCTION

Cancer is a group of diseases in which abnormal cells multiply uncontrollably anywhere in the body. There are numerous forms of cancer that can affect different organs and tissues in the body.[1] Lung cancer remains the leading cause of cancer-related deaths globally. It affects both men and women and is responsible for a significant number of deaths each year. It is often diagnosed at advanced stages, making it more challenging to treat effectively.[2] Additionally, ovarian cancer (OC) is the sixth most common gynecological malignancy, with an increasing incidence rate with age and postmenopausal status.[3] Although it is not as common as some other cancers, ovarian cancer has a high mortality rate due to the challenges associated with early detection. Carbohydrate Antigen 125 (CA-125) is a primary biomarker used in the diagnosis of ovarian cancer and assessing treatment effectiveness. One of the primary biomarkers for diagnosing OC recurrence and evaluating treatment efficacy is the CA-125 test, which is now regarded as an important component in assessing patients with adnexal masses.[3,4] Therefore, CA-125 has been approved for use as a tool for detecting residual ovarian cancer in patients who have completed first-line therapy and are undergoing diagnostic second-look procedures.[5]

In addition to CA-125, Human Epididymis Protein 4 (HE4) is most widely used as a diagnostic and prognostic biomarker for ovarian malignancies.[2] HE4 is a protein that is overexpressed in ovarian cancer cells and is particularly useful in distinguishing between benign and malignant ovarian tumors. Drapkin et al.[6] characterized the HE4 gene product in benign and malignant tissues in order to identify features that will aid in further clinical follow-

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up as an ovarian cancer biomarker. It can be measured through blood tests and has shown promising results in improving the accuracy of ovarian cancer diagnosis, assessing prognosis, and monitoring treatment response.

Sørensen and Mosgaard[7] investigated whether the Cancer Antigen 125 (CA-125) together with the Tumor Marker Carcinoembryonic Antigen (CEA) could distinguish between malignant ovarian and malignant non-ovarian disease. The findings of the study supported the idea that, in addition to the Risk of Malignancy Index (RMI), the CA-125/CEA test should be used as a criterion for further evaluation in patients referred to the hospital with an undetected pelvic tumor. The study conducted by Li et al.[5] investigated the diagnostic accuracy and performance of the Risk of Ovarian Malignancy Algorithm (ROMA) as compared to the individual tumor markers HE4 and CA-125 in the prediction of epithelial ovarian cancer. The findings of the study revealed that for epithelial ovarian cancer and OC prediction, CA-125 has a higher diagnostic accuracy than HE4.

The study conducted by Ferraro et al.[3] aimed to evaluate the diagnostic value of HE4 and CA-125 levels for the diagnosis of OC. The levels of HE4 and CA-125 in the blood samples of patients with suspicious pelvic masses were assessed. They compared the diagnostic performance of HE4 and CA-125 individually and in combination. Zhen et al.[4] conducted a meta-analysis of the available information on the diagnostic accuracy of HE4 and CA-125. The results of the study showed that HE4 and CA-125 could be helpful biomarkers for OC diagnosis, with HE4 having a higher diagnostic accuracy than CA-125 in separating OC from other benign gynecological diseases. Zhu et al.[8] investigated how the HE4 protein affects malignant biological behaviors and how its gene expression profile alters in response to HE4 in ovarian cancer cells. Bolstad et al.[9] determined that HE4 levels are related to their age and smoking status in healthy individuals. Ribeiro et al.[10] found that recombinant HE4 increases matriptase activity in a dose-dependent manner, demonstrating for the first time that HE4 can stimulate the activity of at least one serine protease. Kumbasar et al.[2] suggested that HE4 could be used as a biomarker in the diagnosis of non-small cell lung cancer. Bashizadeh-Fakhar et al.[11] presented the efficacy of ROMA, CA-125, and CEA as predictors of peritoneal spread in the early diagnosis of low-grade serous ovarian cancer. Dochez et al.[12] explored the predictive abilities of CA-125, HE4, the RMI, and ROMA algorithms for ovarian cancer in women. Additionally, in women with a presumed benign ovarian tumor, a combination of increased CA-125 and HE4 appeared to be a good diagnostic tool for confirming ovarian cancer, and it can be utilized in conjunction with individual markers. Dai, Hu, and Ding[13] assessed the overall diagnostic significance of HE4 in combination with CA-125 in OC patients.

In this paper, OC prediction was evaluated considering HE4, CA-125, and CEA using ANFIS and ANN methods. Furthermore, ANFIS and ANN methods were developed considering six different variables: smoking, anxiety, peer pressure, alcohol, coughing, and chest pain for lung cancer prediction. Accurate cancer predictions are of paramount importance for improving patient outcomes in numerous cancer types characterized by high aggressiveness and low median survival rates. Over the years, advancements in statistics and computer engineering have motivated scientists to harness computational methods for disease prognosis. Such research has demonstrated significantly higher accuracy compared to empirical predictions. Notably, the integration of artificial intelligence (AI) into clinical cancer research in recent years has further elevated the accuracy of cancer prediction.[14] Lu et al.[15] employed decision trees, ROMA, and logistic regression to classify ovarian cancer and benign ovarian tumors. Kappen and Neijt[16] highlighted the potential of ANNs to predict patient survival at least as effectively as Cox's technique while enabling the discovery of prognostic factors. Furthermore, it was demonstrated that, utilizing the ANN, prognostic factors may be easily discovered. Floyd et al.[17] developed an ANN using radiologic findings as inputs to predict biopsy results, outperforming radiologists in diagnostic accuracy for cases assigned to biopsy.

When comparing the network output to the radiologists' categorical judgment for cases assigned to biopsy, the ANN shows much superior diagnostic performance than the radiologists. Burke et al.[18] conducted a comparative study between the Tumour, Node, and Metastasis (TNM) staging system and the ANNs, revealing improved accuracy when incorporating commonly obtained demographic and anatomic information into the TNM variables. Kim and Cho[19] utilized evolutionary ANNs to classify tumor classification based on microarray gene expression data, incorporating dimension reduction and information gain methods. Saritas[20] employed ANNs to predict the severity of a mammographic breast tissue masses. Ecke et al.[21] adopted systematic sextant patterns for prostate biopsies, with prostate volume being a crucial variable in their ANN model, demonstrating its potential for routine biopsy decision-making. Enshaei et al.[22] analyzed multiple parameters for ovarian cancer using three algorithms: decision tree, ANNs, and Bayesian network.

Hambali and Gbolagade[23] utilized the Synthetic Minority Oversampling Technique (SMOTE) to address imbalanced datasets, developing a hybrid SMOTE and ANN technique for diagnosing ovarian cancer. Hart et

al.[24] leveraged personal health information to construct a multi-parameterized ANN for predicting lung cancer risk. Charati et al.[25] employed ANNs to estimate survival rates for gastric cancer patients and identify influential factors. Nejatzadeh et al.[26] collected relevant data to create an ANN based prediction model for laryngeal cancer, identifying 24 significant factors for more accurate predictions. Nasser and Abu-Naser[27] developed an ANN model for lung cancer identification after preprocessing and transforming data to enhance predictive analysis, with age emerging as a crucial factor.

Daoud and Mayo[28] presented the data preprocessing tools and architectures in recent ANN based cancer prediction models, showcasing ANNs' versatility as filters, predictors, and clustering methods. Takeuchi et al.[29] compared ANN and logistic regression analysis for prostate cancer diagnosis, emphasizing ANN' ability to prevent unnecessary biopsies and missed cancer cases. Muhammad et al.[30] created an ANN capable of calculating pancreatic cancer risk in the general population, utilizing readily available personal health data to identify high-risk individuals cost-effectively. Nayak et al.[1] integrated the Analysis of Variance (ANOVA) and Kruskal-Walis methods to evaluate relevant features, incorporating elephant herding optimization into ANN analysis across various cancer datasets such as breast, lung, and cervical cancer. Appaji et al.[31] employed diagonal correlation matrices to assess input attributes and described breast cancer diagnosis using deep learning approaches with Recurrent Neural Networks. Ma et al.[32] combined factorization machine and deep neural network structures to predict drug combination synergies, enhancing drug discovery. Prisciandaro et al.[33] presented that both fundamental research and clinical decision-making can greatly benefit from the use of ANN.

Madhu and Kumar[34] employed edge detection to preprocess graphical data, reducing data processing time and storage requirements for convolutional neural networks. Chuang et al.[35] developed a convolutional neural network model capable of categorizing normal and tumor samples from various cancer types. Lee et al.[36] identified predictive risk factors for lung cancer-related diseases using big data analytics and created a lung cancer prediction model based on the Deep Neural Network method. Tan et al.[37] utilized a fuzzy adaptive learning control network in conjunction with adaptive resonance theory to evaluate ovarian cancer and investigate proteome patterns using varying feature sets. Hamdan and Garibaldi[38] presented a hybrid methodology that combined the strengths of ANNs with fuzzy inference for survival modeling. Mahmoudi, Lahijan, and Kanan[39] employed Genetic Algorithms (GAs) and Particle Swarm Optimization (PSO) for gene selection in the ANFIS classifier, evaluating its robustness against noisy data. Hidayah et al.[40] used the ANFIS to classify colon cancer. Ziasabounchi and Askerzade[41] developed a hybrid learning algorithm to identify parameters in their ANFIS model, demonstrating its adaptability as a predictive mechanism for heart disease. Kalaiselvi and Nasira[42] introduced an approach for diabetes and cancer detection using the ANFIS and adaptive group-based k nearest neighbor. Wang et al.[43] utilized survival data to enhance the predictive performance of the ANFIS method, efficiently assessing functional relationships between covariates and time in complex prognostic scenarios. Rahouma et al.[44] employed K-means clustering for tumor segmentation, followed by feature extraction using a growing neural gas network. They used hybrid learning, combining descent and least square methods with ANFIS, to determine classification parameters.

Uyar et al.[45] used the GA based trained recurrent fuzzy neural network (RFNN) and ANFIS to predict breast cancer. The results of the study demonstrated that the RFNN with nine variables was the most accurate overall. Mishra and Bhoi[46] used the ensemble Kalman filter during the preprocessing phase. For classification, ANFIS was used. Furthermore, the newly evolved manta ray foraging optimization was hybridized with ANFIS during classification.

Numerous comparative studies indicate that the proposed ANN and ANFIS based methods consistently outperform alternative approaches in terms of prediction accuracy. The purpose of this study is to develop both the ANFIS and ANN methods for cancer prediction. There has not been a comparative study of ANN and ANFIS methods for predicting ovarian and lung cancer. Specifically, proposed methods employ HE4, CA-125, and CEA markers for ovarian cancer prediction and incorporate six variables for the development of methods for lung cancer prediction. The accuracy, sensitivity, and specificity of the proposed methods were computed, and the overall prediction ability of ANN and ANFIS was compared. The limitation of this study is that ovarian and lung cancer were taken into account. In addition, hybrid methods can be used to improve prediction performance in the future.

METHODS

This study does not require an ethics committee. All procedures were carried out in accordance with the ethical rules and the principles.

In this study, two different cancer datasets were utilized to develop prediction methods. The main objective of this paper is to create a prediction method for lung and ovarian cancer by accurately computing, analyzing, and applying the most useful artificial intelligence tools, ANN

and ANFIS. The first dataset was obtained from Lu et al.[15] and contains various variables related to ovarian cancer. However, for the purpose of this paper, the focus was specifically on the biomarkers HE4, CA-125, and CEA, which are important indicators of ovarian cancer. Rows that contained missing values were removed from the dataset. The descriptive statistics of the ovarian cancer dataset are summarized in Table 1. These biomarkers were used as inputs for the prediction model developed in this study. The second dataset was obtained from[47] and specifically focused on lung cancer. Six different input variables were considered for this dataset, including smoking, anxiety, peer pressure, alcohol consumption, coughing, and chest pain. These variables were selected as potential predictors for lung cancer (Table 2). ANN and ANFIS were used to develop the prediction models.

Table 1. Descriptive statistics of ovarian cancer dataset

	Count	Minimum	Mean	Maximum
HE4	320	16.71	182.66	3537.6
CA-125	320	3.75	339.389	>5000
CEA	320	0.2	3.358	138.8

Human epididymis protein 4 (HE4), Carbohydrate antigen 125 (CA-125), Carcinoembryonic antigen (CEA)

Table 2. Descriptive statistics of lung cancer dataset

	Count	Min.	25%	50%	75%	Max.
Smoking*	309	1	1	2	2	2
Anxiety*	309	1	1	1	2	2
Peer pressure*	309	1	1	2	2	2
Alcohol consumption*	309	1	1	2	2	2
Coughing*	309	1	1	2	2	2
Chest pain*	309	1	1	2	2	2

* Yes=2, No=1

ANN

ANNs are computer algorithms. These algorithms are commonly used to sort a collection of patterns into one of several categories. The classification rules are learned by the network from examples rather than being written into the algorithm.[17] ANNs offer several benefits in various applications. The benefits mentioned are as follows: (i) Adaptive learning, (ii) Self-organization, (iii) Real-time operation, (iv) Fault-tolerance.[48]

The general application steps of ANN can be summarized as follows.[49] In the first step, a suitable ANN model is selected to begin the neural network design. In this paper, a feed forward back propagation neural network model was selected. In the second step, the number of hidden layers, hidden neurons, input parameters, and other parameters of ANN are determined. Once the network design process is completed, the proposed model is then initialized. The dataset is loaded, and the proposed ANN has learned from a training data set. The output of the proposed ANN is analyzed. The testing phase of the proposed ANN model is then initiated. Finally, the performance of the ANN is evaluated. The pseudocode of ANN is given in Figure 1.[50]

```
Input : ProblemSize, InputPatterns, iterations_max, learn_rate
Output : Network
Network ← ConstructNetworkLayer ();
Network_weight ← InitializeWeights(Network,ProblemSize);
for i = 1 to iterations_max do
        Pattern_i ← SelectInputPattern(InputPatterns);
        Output_i ← ForwardPropagate(Pattern,Network);
        BackwardPropagateError (Pattern,Output,Network);
        UpdateWeight (Pattern, Output, Network, learn_rate);
end
return network;
```

Figure 1. Pseudocode of ANN[50]

In this paper, ANN is used to predict ovarian cancer and lung cancer. The proposed ANN methods involve the use of a hidden layer consisting of 10 neurons. Hyperbolic tangent sigmoid transfer function is used as transfer function. Levenberg–Marquardt algorithm is employed to train the ANN methods. For ovarian cancer, two ANN methods are created using different input numbers. In first ANN method (ANN _2), two input including HE4 and CA-125 are utilized to create a prediction method for ovarian cancer (Figure 2). In the second ANN method (ANN _3), three input including HE4, CA-125, and CEA, are used for ovarian cancer (Figure 3). For lung cancer, six inputs including smoking, anxiety, peer pressure, alcohol, coughing, and chest pain, are used to create the ANN method (Figure 4).

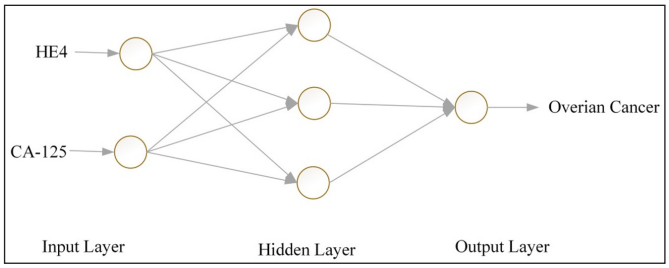

Figure 2. The proposed ANN_2 method for ovarian cancer

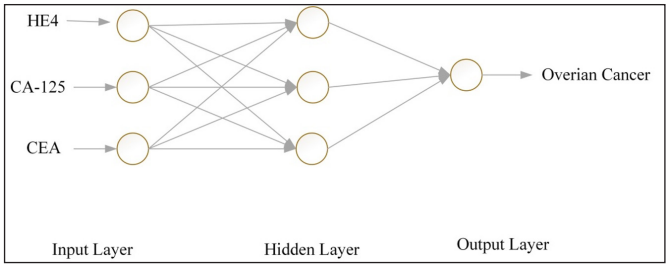

Figure 3. The proposed ANN_3 method for ovarian cancer

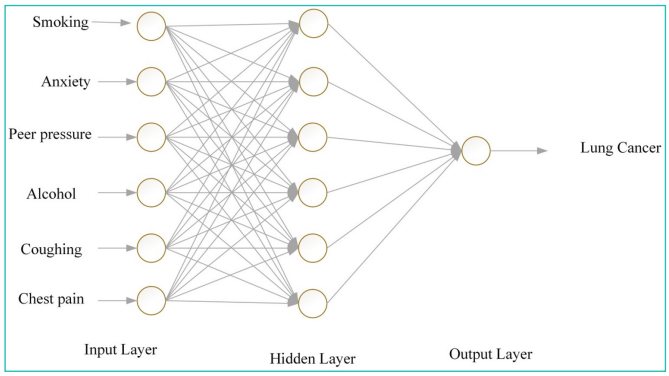

Figure 4. The proposed ANN method for lung cancer

ANFIS

The ANFIS is a powerful computational network that harnesses both the learning capabilities of ANNs and the decision-making proficiency of Fuzzy-Logic systems.[41] ANFIS is uniquely positioned to perform input-output mapping by amalgamating human knowledge with specified input-output data pairs through a hybrid learning approach. This integration combines rule-based systems with neural network learning capabilities to construct a fuzzy inference system (FIS) based on a set of input–output data. What sets ANFIS apart is its capacity to use explicit linguistic terminology for variables, simplifying the interpretation of modeling findings.[43] The ANFIS architecture is illustrated in Figure 5[51] and explained as follows.

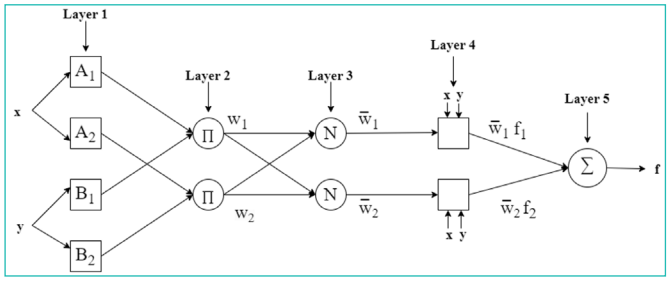

Figure 5. ANFIS architecture[51]

In Layer 1, each node i is an adaptable node whose node output is specified by

$$O_{1,i} = \mu_{A_i}(x) \quad \text{for} \quad i = 1,2 \quad \text{or} \qquad (1)$$

$$O_{1,i} = \mu_{B_{i-2}}(y) \quad \text{for} \quad i = 3,4 \qquad (2)$$

The node's input is represented by x (or y), while its associated fuzzy set is represented by A_i (or B_{i-2}). In Layer 2, every node is a fixed node labeled $\prod$. For instance,

$$O_{2,i} = w_i = \mu_{A_i}(x) \times \mu_{B_i}(y), \; i = 1,2 \qquad (3)$$

Every node's output indicates a rule's firing strength. In Layer 3, each node is a fixed node with the label N. Following equation is used in this layer:

$$O_{3,i} = \bar{w}_i = \frac{w_i}{w_1+w_2}, \; i = 1,2 \qquad (4)$$

In Layer 4, every node i is an adaptive node with a node function:

$$O_{4,i} = \bar{w}_i f_i = \bar{w}_i (p_i x + q_i y + r_i) \qquad (5)$$

The parameter set is $\{p_i, q_i, r_i\}$, and the output of Layer 3 is $\bar{w}_i$. In Layer 5, the fixed node with the labeled Σ is the single node. Following equation is used in this layer:

$$O_{5,1} = overall\ output = \sum_i \bar{w}_i f_i = \frac{\sum_i w_i f_i}{\sum_i w_i} \qquad (6)$$

Details about the architecture of ANFIS can be found in Jang and Sun[51] and Karaboga and Kaya.[52]

In this study, ANFIS plays a pivotal role in predicting both ovarian cancer and lung cancer. For ovarian cancer detection, we deploy two distinct ANFIS methods, each employing different sets of input variables. In the first ANFIS method (ANFIS_2), we utilize two inputs: HE4 and CA-125, to develop a prediction model. In the second ANFIS method (ANFIS_3), we expand the input two to three variables, incorporating HE4, CA-125, and CEA. The FIS structure for both ANFIS_2 and ANFIS_3 for ovarian cancer prediction is generated using the Trimf membership function. The fuzzy system is created using the grid partitioning method. For FIS training, we opt for the hybrid method and set the number of epochs at 1000. Additionally, we establish that each input should be associated with four membership functions.

Concerning lung cancer prediction, we rely on six input variables: smoking, anxiety, peer pressure, alcohol, coughing, and chest pain, to construct an ANFIS method. We configure the number of epochs for training at 10, and each input is associated with three membership functions. Similar to ovarian cancer prediction, we employ the hybrid method for FIS training and the grid partitioning method for constructing the fuzzy system. The Trimf membership function guides the development of the ANFIS method for lung cancer prediction.

RESULTS

Cancer is one of the leading causes of death worldwide. The impact of cancer is not limited to the patients alone but also extends to their families, friends, and communities. Cancer prediction plays a crucial role in the field of oncology. Accurate and early prediction of cancer can significantly impact the selection of appropriate treatment strategies for cancer patients. By identifying individuals who are at high risk or are likely to develop cancer, healthcare professionals can intervene at an early stage, potentially leading to improved outcomes and survival rates. A comparative analysis of methods in healthcare is given in Table 3. It is clearly seen that no exact method is available for use in healthcare. Each

method has a variety of advantages. In this paper, a comparative analysis of ANN and ANFIS is presented, considering two different cancer types.

Cancer prediction involves analyzing various factors, including patient demographics, medical history, genetic markers, biomarkers, and imaging data, among others. Machine learning techniques, such as ANNs, have been widely employed in cancer prediction models due to their ability to learn complex patterns and relationships from large datasets. In this study, ANN and ANFIS based methods are created to predict ovarian cancer and lung cancer.

In this study, a binary classification problem with two classes was created, and the results were classified as either positive or negative. Four results were possible.[53]

- True Positive (TP) refers to a situation where both the actual value and the prediction's results are positive.
- False Positive (FP) refers to a situation where a prediction provides positive results even though the actual value is negative.
- True Negative (TN) refers to a situation where both the actual value and the predictions' results are negative.
- False Negative (FN) refers to a situation where a prediction provides negative results while the actual value is positive.

The values of TP, FP, TN, and FN were given in Table 4 and Table 5. Accuracy, sensitivity, and specificity were calculated using the following equations, respectively[54]

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (7)$$

$$Sensitivity = \frac{TP}{TP+FN} \quad (8)$$

$$Specificity = \frac{TN}{FP+TN} \quad (9)$$

Table 4. The performance metrics for prediction methods for ovarian cancer

Dataset	Methods	True benign	True cancer	Total	Accuracy rate
Ovarian cancer					
	ANFIS_2				0.939
	Predicted benign	84	4	88	
	Predicted cancer	3	23	26	
	Total	87	27	114	
	ANN_2				0.965
	Predicted benign	85	3	88	
	Predicted cancer	1	25	26	
	Total	86	28	114	
	ANFIS_3				0.939
	Predicted benign	84	4	88	
	Predicted cancer	3	23	26	
	Total	87	27	114	
	ANN_3				0.965
	Predicted benign	85	3	88	
	Predicted cancer	1	25	26	
	Total	86	28	114	

Artificial neural network (ANN), Adaptive-network-based fuzzy inference system (ANFIS)

Table 3. Comparative analysis of methods in healthcare

Author(s)	DT	ROMA	LR	ANN	TNM	ENN	BN	SMOTE	GA	CNN	DNN	XGBoost	ANFIS	RFNN	MaFO
Lu et al.[15]	✓	✓	✓												
Kappen and Neijt[16]				✓											
Floyd et al.[17]				✓											
Burke et al.[18]				✓	✓										
Kim and Cho[19]						✓									
Saritas[20]				✓											
Ecke et al.[21]				✓											
Enshaei et al.[22]	✓			✓			✓								
Hambali and Gbolagade[23]				✓				✓							
Hart et al.[24]				✓											
Charati et al.[25]				✓											
Nejatzadeh et al.[26]				✓					✓						
Nasser and Abu-Naser[27]				✓											
Madhu and Kumar[34]										✓					
Lee et al.[36]											✓	✓			
Ziasabounchi and Askerzade[41]													✓		
Kalaiselvi and Nasira[42]													✓		
Wang et al.[43]													✓		
Uyar et al.[45]									✓				✓	✓	
Mishra and Bhoi[46]													✓		✓
This study				✓									✓		

*Decision Trees (DT), Risk of Ovarian Malignancy Algorithm (ROMA), Logistic Regression (LR), ANN, Evolutionary Neural Network (ENN), Bayesian Network (BN), Synthetic Minority Oversampling Technique (SMOTE), Genetic Algorithm (GA), Convolutional Neural Networks (CNN), Deep Neural Network (DNN), Extreme Gradient Boosting (XGBoost), ANFIS, Recurrent Fuzzy Neural Network (RFNN), Manta Ray Foraging Optimization (MaFO)

In Table 4, the performance metrics for prediction methods for ovarian cancer are given. The results showed that the proposed methods predicted ovarian cancer with at least a 93.9% accuracy rate. In Table 5, the performance metrics of prediction methods for lung cancer are presented. In Table 5, the proposed methods predicted lung cancer with at least an 89% accuracy rate. The results of sensitivity and specificity are given in Table 6. The findings of the study indicate that the ANN method used in this study showed better results when applied to two specific cancer datasets. This suggests that the ANN approach has the potential to improve the accuracy and effectiveness of cancer prediction or classification compared to the ANFIS based method.

Table 5. The performance metrics for prediction methods for lung cancer

Dataset	Methods	True non-cancer	True cancer	Total	Accuracy rate
Lung cancer					
	ANFIS				0.89
	Predicted non-cancer	5	8	13	
	Predicted cancer	3	84	87	
	Total	8	92	100	
	ANN				0.92
	Predicted non-cancer	9	4	13	
	Predicted cancer	4	83	87	
	Total	13	87	100	

Artificial neural network (ANN), Adaptive-network-based fuzzy inference system (ANFIS)

Table 6. Comparison of proposed methods

Method	Sensitivity	Specificity
Ovarian cancer		
ANFIS_2	0.965	0.851
ANN_2	0.988	0.893
ANFIS_3	0.965	0.852
ANN_3	0.988	0.893
Lung cancer		
ANFIS	0.625	0.913
ANN	0.692	0.954

Artificial neural network (ANN), Adaptive-network-based fuzzy inference system (ANFIS)

DISCUSSION

Prediction accuracy varies according to the cancer types. For example, Faisal et al.[55] presented that a gradient-boosted tree was shown to achieve 90% accuracy, outperforming all other individual and ensemble classifiers for lung cancer. Lu et al.[15] determined that accuracy for ROMA, Decision Tree, and Logistic Regression were determined as 0.956, 0.921, and 0.974, respectively, for ovarian cancer prediction. Hassan et al.[56] achieved a maximum accuracy of 90.68% for breast cancer detection and prediction. In the light of previous studies, it can be said that it is possible to obtain a value above 90% accuracy in cancer prediction. Additionally, new prediction methods are needed to obtain better results in the prediction of all cancer types. In this study, the accuracy rate of cancer prediction by ANN was determined to be 96.5.

To properly evaluate the data, AI and machine learning techniques are needed. ANNs are used in most machine learning today. With the recent increase in processing power, ANNs have become incredibly common and can now be used almost anywhere.[57] ANFIS is a hybrid analytical method. In order to generate an output, ANFIS essentially learns the characteristics of the supplied data and adjusts the system parameters to meet the required error criterion of the system.[58] In this paper, ANN and ANFIS have been implemented for modeling and predicting lung and ovarian cancer. Millions of individuals suffer from the terrible effects of cancer every year, whether it be from cancer-related deaths or the challenges posed by the disease itself.[59] Therefore, even a little advancement in modeling and forecasting can make significant improvements.

CONCLUSION

The importance of accurate cancer prediction has attracted the interest of researchers, as it plays a crucial role in selecting appropriate treatment strategies and improving patient outcomes. While various methods for cancer prediction exist, no single method can effectively predict every type of cancer. In this study, two specific methods, namely the ANN and the ANFIS, were employed for cancer prediction. In literature, comparative research between the ANN and ANFIS methods for ovarian and lung cancer prediction has not yet been conducted.

The research findings indicate that both the ANN and ANFIS methods showed promising results in predicting cancer. These methods demonstrated their potential as effective tools for cancer prediction, although it is important to note that their performance may vary depending on the specific cancer type and dataset used. The accuracy rate of ANN based cancer prediction in this study was found to be 96.5. To improve results in the prediction of all cancer types, new prediction techniques can be created. To further enhance the prediction accuracy and effectiveness of these methods, future studies could explore the use of different parameters for constructing the ANN and ANFIS models. By optimizing the model parameters, researchers can potentially improve the prediction capabilities and overall performance of these methods.

In conclusion, the study's findings highlight the potential of ANN and ANFIS methods for cancer prediction.

Further research exploring different parameters, feature selection methods, and diverse cancer types will contribute to the development of more advanced and reliable prediction models in the future.

ETHICAL DECLARATIONS

Ethics Committee Approval

This study does not require an ethics committee.

Informed Consent

This study does not require an informed consent.

Referee Evaluation Process

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The authors have no conflicts of interest to declare.

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Author Contributions

All the authors declare that they have all participated in the design, execution, and analysis of the paper, and that they have approved the final version.

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