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Incorporating Artificial Fish Swarm in Ensemble Classification Framework for Recurrence Prediction of Cervical Cancer

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ABSTRACT IoT has facilitated predominant advancements in cancer research by incorporating Artificial intelligence (AI) that enables human decision-makers to achieve a better decision. Recently, Least Absolute Shrinkage and Selection Operator (LASSO) classifier has launched in predicting recurrence cancer genes in the cervix. At the initial phase, the recurrence gene expression of lncRNA is collected from Geo Datasets. Secondly, data imputation, accomplished with Mode and Mean Missing method (MMM-DI). Thirdly, feature selection is compassed using Hilbert-Schmidt independence criterion with Diversity based Artificial Fish Swarm (HSDAFS). In the HSDA.FS algorithm, the diversity parameter is added based on the gene value, and their risk score of the lncRNAs is computed using the Artificial intelligence (AI) technique. Finally, recurrence prediction, an ENsemble Classification Framework (ENSCF), is proposed based on recurrent neural networks. The prognostic factor is computed with a risk score of nine lncRNA signatures for 300 samples taken from GSE44001. The Chi-Square method has been used to obtain statistical results. The survival of the patient with recurrence cervical cancer is shown using the proposed model.

INDEX TERMS Artificial intelligence, cervical cancer, feature selection, the Internet of Things (IoT), recurrence prediction, risk score.

I. INTRODUCTION

Today IoT ensures many benefits that streamline and enhance smart health [1] in predicting severe health issues like Cervical Cancer [2]. Cervical cancer is a significant cause of mortalities among women across the world. With the convergence of AI and IoT techniques, proactive predictions can be carried out to predict, diagnose, treat, and monitor the patients in and out of the hospital environment [3]. The consistent rise of the Internet of Things (IoT) approach has

made it feasible to incorporate various AI-based methodologies and communicating interfaces. With the IoT concept's help, physical entities can get connected anytime, and any place using an internet facility can detect themselves to other commodities [3]. The smart entity is a critical function that enables the IoT concept. This Cervical cancer in women is considered to be the most severe gynecological problem worldwide. Around 11,270 new cases and 4070 deaths were the estimated populations identified in the United States in 2009. In Japan, between 6000 and 7000, new cervical cancer cases are reported annually. Clinical prognosis was good at the earliest stage of cervical carcinoma under surgery or other

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clinical therapies instead of the patients' invasive stage. Generally, the recurrence percentage rate of cervical cancer varies for different stages furnished as per the International Federation of Gynecology and Obstetrics (FIGO). It falls between 10% and 20% for stages IB to IIA and stages IIB –IVA it falls between 50% to 70%, which is in the nearly advanced stage. The survival rate lies between 15% and 20% for recurrence cervical patients whose prognosis is one year. Thus, the accuracy for prognosis bio factors seems to be a high risk for cervical cancer. A lack of studies that proved genetic elements are the biomarkers for cervical cancer prognostication [2].

Tokunaga *et al.* [4] proposed the chemotherapy treatment for patients who have recurrent uterine cervical cancer (RUCC) by applying Concurrent Chemo Radiotherapy (CCRT). They uncovered no significant difference in the cancer patients' survival rate after these treatments as before, even after a post-CCRT interval or chemotherapy regimen. The studies relevant to cancer gene expression have determined the gene signature used to analyze the recurrence prediction of cervical carcinoma.

The leading cause of ineffective treatment in cancer lies in RNA as it transcripts long nucleotide extended up to 200; they lose the capability to generate new protein [4]. However, there is still a possibility where protein can contribute to tumor modulation progression in biological relevant processes such as remodeling chromatin and pre and post transcription [5], [6]. Some new studies have also provided details regarding lncRNAs and survivals of human cancers, including cancers like breast and other relevant cancers [8].

In this era, lncRNAs possess many functions that brought predominant factors in the field of molecular biology. But still, there is a lack of understanding in analyzing the role of lncRNAs' function. There are limited lncRNAs, and the new reports have uncovered features and novel functionalities of the gene molecules. Some distinct functions of lncRNAs involve nuclear structure integrity, gene expression regulation, remodeling chromatin, processing pre, and post-transcription [9], [10]. Deep learning plays a vital role in feature selection to analyze these characteristics of gene expression. Generally, deep learning algorithms extract high-level abstraction in the learning process. It provides good algorithms in feature selection in hierarchical levels. This method provides a layered learning process in selecting hidden features and handling a huge quantity of data [11]. Identifying target genes for lncRNAs is an important aspect of predicting the recurrence of cervical cancer. An AI-based neural network carries out this process.

Gene Expression Omnibus (GEO) database [12] is considered a worldwide common and accessible repository that includes a database and freely propagates and shares the public's need for gene expression and other functional geo accession datasets. Thus, long coding R.N.A. can be downloaded from the GEO dataset, and it is possible to perform lncRNA profiling on patients with cervical cancer. Hilbert-Schmidt

independence criterion with Diversity-based Artificial Fish Swarm (HSDAFS) is introduced for gene selection in the recurrence prediction. From the GEO database, long coding nucleotide was constructed for the few training datasets, and then predictive accuracy is analyzed with the remaining data during testing.

The paper is organized as follows: Section 2 described the related work on Cervical cancer classification, feature selection with AI, and deep learning with IoT concepts. Section 3 provides brief details of the proposed methodology. Section 4 provides results and discussion, followed by the conclusion and future works in Section 5.

II. LITERATURE REVIEW

Various research groups worldwide have been focusing on smart health [13], [14], health and patient monitoring [15], [32], [42], and other areas where AI and IoT technologies have significant potential. Especially for cervical cancer, AI tools and technologies are being developed [16]. For cancer treatment, AI-assisted or deep learning-oriented diagnostic technologies have a huge impact [17].

Ghoneim *et al.* [18] proposed a Cervical cancer cell detection using Convolution neural networks (CNNs). Cell images are fed to an AI-based CNNs model to extract the deep-learned cervical cancer features. With the help of an extreme learning machine (ELM) classifier, input images are classified. CNN's technique is deployed through transfer learning and fine-tuning. Multilayer perceptron, another AI model-based autoencoder classifier are also implemented for the classification of cancer cells.

Kim *et al.* [19] proposed a nomogram to predict Disease-Free Survival (DFS) that long lasts for five years. This technique was appropriate only for patients treated with a radical hysterectomy at the early stage. The nomogram devised was validated with bootstrapping internally, and performance assessment was made using the concordance index and curve with calibration. And from Asan Medical Center, external validation was performed using a patient's separate data set. Some analysis was made, such as the disease stage, count of positive lymph nodes, involvement of the parameter, and invasive depth were determined as factors of independent risk for recurrence of a cervical disease whose p-value is less than 0.05.

Yoshida *et al.* [20] proposed an estimated study of cervical cancer where possessed Post-Recurrence Survival (PRS) of patients along with Relapsed Uterine Cervical Cancer (RUCC) was analyzed. P.R.S also influenced clinic pathological indicators. With the Kaplan Meier method and Cox regression model's help, some single and multivariate analyses were performed. The cervical cancer patients undergoing surgery possess longer median survival than patients not undertaken surgery.

Mabuchi *et al.* [21] presented a new analysis that identified the prognostic factors by establishing a new method for predicting the extension of life in recurrence cancer patients who had already undergone radiotherapy. The study listed

some prognosis factors such as relapse site, the status of symptoms, initial chemoradiotherapy, and treatment modality. These four clinical factors made physicians predicting cervical cancer more precisely.

Huang *et al.* [22] proposed a new idea where the investigation initialized with cervical cancer profile of the gene expression used to predict the patient's prognosis. After the classification process [7], it was proven that 19 genes expressed differently among the normal and abnormal genes. The work also proposed analysis with multivariate sequences that proved the 7-gene signature and different stages, as stated in FIGO. It reveals various prognostic factors relevant to recurrence-free survival (RFS) of cervical cancer patients.

Lee *et al.* [23] discovered a new gene set model to analyze disease-free survival by implementing cDNA-mediated Annealing, Selection, extension, and Ligation (DASL) assay dataset where the cervical carcinoma patients underwent radical treatment with optional adjuvant therapy. A medical analysis method was developed with the same dataset, which led to predicting cervical cancer gene recurrence, compared with other models.

Geeitha *et al.* [24] proposed significant features for selecting relevant genes deploying Bacterial Foraging Optimization (BFO) with HSIC. This algorithm produces global optimum in selecting relevant features using E-Coli bacteria using the Chemotaxis process.

Roy *et al.* [25] proposed a task-aware feature selection using deep neural networks. The first hidden layer selected appropriately relevant genes that reduced the original dimensional features and proved that feature selection with a deep neural network was superior to principal component analysis (PCA) and improved classification performance.

Elgin Christo *et al.* [26] designed a framework with bio-relevant algorithms and gradient descendant backpropagation neural network for feature selection and classification. Data imputation was effectuated by the hot-deck method. Differential evolution with optimization methods was implemented for feature selection. Adaboost SVM was established with a fitness function. The optimal features were selected using the correlation method, and the features are then trained using the deep learning method. The author explored Wisconsin Diagnostic Breast Cancer (W.D.B.C.) dataset.

Lora *et al.* [27] validated the model using prognostic factors by predicting the patients by time factors in Locally Advanced Cervical Cancer (LACC). Those patients were treated with concurrent chemoradiotherapy in a separate cohort. The external validity of the model with prognostic factors was accounted for in relevant to discrimination, calibration, performance measures of various metrics, and the decision curve analysis.

Paik *et al.* [28] determined to devise and compute prognostic models individually among the cervical cancer patients who had undergone a radical hysterectomy. Prognostic models are developed for all cancer patients at the early

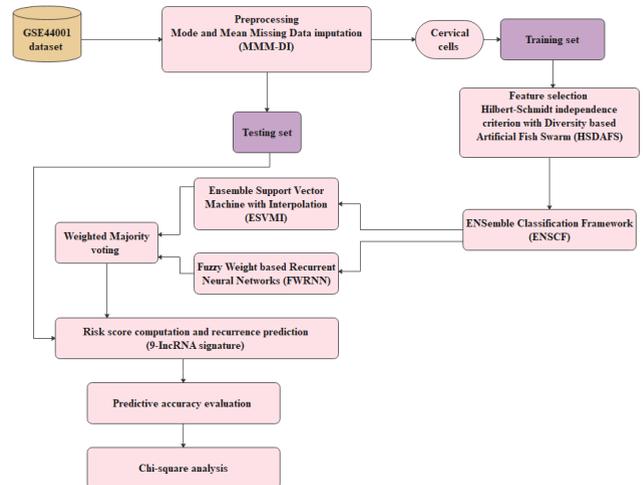


FIGURE 1. The architecture of the proposed system.

stage, including Overall Survival (OS), Disease-Free Survival (DFS), recurrence in lymphatic and hematogenous. The proposed model presented the difference in survival prediction in every risk group by Kaplan-Meier plot.

Mao *et al.* [29] gathered cervical cancer patients' lncRNA expression data segregated into three types of tests: training, validation, and testing. Nine-lncRNA signature was framed from the training set by proposing the LASSO Cox regression algorithm associated with 10-fold cross-validation. Finally, the prognostic value was validated, along with the risk score is associated with all three types of tests. Kaplan-Meier analysis and other parametric measures comprise C-index, two types of curving: time-dependent Receiver Operating Characteristic (ROC) curves and dynamic Area under the ROC Curve.

III. PROPOSED METHODOLOGY

In this proposed work, classification is undergone with two target classes: recurrence and non-recurrence genes. The state-of-the-art of the proposed work lies in the prognostic factor by computing the risk score in classifying recurrence genes. An initial step preprocessing is carried out using Data imputation with Mode and Mean Missing (MMM-DI) for missing data imputation. Filtered Cervical cancer cells are collected from the sensor. The trained data is then taken for the feature selection process. The gene selection is performed by the Hilbert-Schmidt independence criterion with Diversity based Artificial Fish Swarm (HSDAFS) algorithm. Then recurrence prediction is performed by ENSCF. ENSCF combines two classifiers' results. The Ensemble Support Vector Machine with Interpolation (ESVMI) and the Deep learning technique Fuzzy Weight based Recurrent Neural Networks (FWRNN). Finally, the risk score was validated in gene samples using Chi-square analysis. The proposed work consists of four major stages: preprocessing, gene selection, risk score computation, and recurrence prediction, represented as an architecture diagram shown below in figure 1.

A. MODE AND MEAN MISSING DATA IMPUTATION (MMM-DI)

Data imputation with Mode and Mean Missing (MMM-DI) method is propounded to replace the unfilled data in the gene data samples. The data with missing values were refilled with the proposed imputation technique for the remaining genes that possess the characteristics of a similar type. The mode represents the high-frequency value of the given samples. Mean focuses on the given data's central value, also called the given dataset's average value. Equation (1) represents the data imputation formula

$$\bar{x} = \frac{\sum_{i=1}^N x_i}{N} = \frac{x_1 + x_2 + \dots + x_N}{N} \quad (1)$$

Here, N in the recurrence data samples represents total gene observations, and x denotes individual instances. The equation shows the mean of a dataset. The average value represents the mean value of all samples of recurrence genes. The missed value in the dataset is substituted with Mode and Mean Missing method.

$$MM_{DI} = \frac{mode + mean}{2} \quad (2)$$

B. HILBERT-SCHMIDT INDEPENDENCE CRITERION WITH DIVERSITY-BASED ARTIFICIAL FISH SWARM (HSDAFS)

The selection of a subset of informative features and genes becomes a challenging task. To solve this problem, proposed a new model, namely the Hilbert-Schmidt Independence Criterion with Diversity-based Artificial Fish Swarm (HSDAFS). HSDAFS is performed based on biological activities [30], [31] for optimal selection of genes. Here, the algorithm perceives its outward interpretation in its sight for gene selection cervical cancer. In the cervical cancer genes, GX_i is the current position of an AF, and its visual locality is considered GX_v at a certain moment to select genes. If the new position is better than the current position in its visual, it moves further a point in the same direction and then reaches the next position, GX_{next}, or else, it explores its vision in the tour. Global optimum selection of the gene sample is chosen by permitting definite local optimum along with some indecision. Let GX = (x₁, x₂, ..., x_n) (genes) and GX_v = (x₁^v, x₂^v, ..., x_n^v) then the following equation is represented as follows:

$$Gx_{ij}^v = Gx_{ij} + \alpha Visual.rand(), i \in (0, n), j \in (0, m) \quad (3)$$

$$GX_{next} = GX + \alpha \frac{GX_v - GX}{||GX_v - GX||}.GStep.rand() \quad (4)$$

Here rand() generates random numbers that fall from zero to one, GStep is taken as step length, and x_i is the variable that optimizes the features, n taken as the number of gene variables. The AF algorithm possesses variables and functions as two parts. Variables comprise G.X. as the current position of AF, GStep is step length in motion, and Visual indicates visual distance. The next part, namely functions, comprises AF behaviours represented by AF_P, AF_S, AF_F,

AF_M and AF_E for the functions such as prey, swarm, move and evaluate, respectively. The remaining behaviours, namely evaluating behaviour and swallowing behaviour, are implemented based on the AF's environment concerning the evaluation by helping the A.F. select proper genes. Then the swallowing behaviour can be executed depending upon the increase of fitness value generally for nominal optimization that crosses the specified threshold in updating the AF_S process. Global best AF information is appended to the functions of AF to enhance the accuracy of HSDAFS. The understanding of attitudes in HSDAFS is described below as minimum consideration:

1) BEHAVIOUR IN PRAYING (AF_P)

Say GX_j is the gene samples' current position for recurrence prediction and selects a state GX_j in a random method covering visual distance. The optimal selection of genes in A.F. is represented by Y = f(G.X.). Thus,

$$GX_j = GX_i + \alpha AF_V.rand() \quad (5)$$

If Y_i < Y_j is considered as a minimum error, it moves further one step forward, taking the same direction as gene vector considering the sum of GX_j and the X_{bestAF}, X_{bestAF}, is denoted as best AF state in all AFs till now

$$GX_i^{t+1} = GX_i^t + \alpha * \left(\frac{X_j - X_j^t}{||X_j - X_j^t||} + \frac{X_{bestAF} - X_i^t}{||X_{bestAF} - X_i^t||} \right) * AF_S * rand() \quad (6)$$

Otherwise, select a state X_j for gene vector chosen randomly for the second time and decide if it takes the forward direction of gene selection or no need for a recurrence dataset. Suppose a forward direction is not satisfied to some extent even after undergoing maximum iterations. In that case, AF needs to move randomly, thus helping A.F. retreat from the field's local end.

$$GX_i^{t+1} = GX_i^t + \alpha * AF_V.rand() \quad (7)$$

2) BEHAVIOUR IN SWARMING (AF_S)

Let the terms X_i, X_c, n_f be considered a current state, centre position, and the number of its companions within the AF's visual range. If f_c < f_i and f_c < AF_{delta}* f_i / n_f, which means the associate center's purpose has higher accuracy of gene samples, and environment that surrounds is less crowded. Later AF moves further one step taking the direction of the sum of the vector of both X_c and X_{bestAF}

$$GX_i^{t+1} = GX_i^t + \alpha * \left(\frac{X_c - X_i^t}{||X_c - X_i^t||} + \frac{X_{bestAF} - X_i^t}{||X_{bestAF} - X_i^t||} \right) * AF_S * rand() \quad (8)$$

Or else, the first step is executed.

3) BEHAVIOUR IN FOLLOWING (AF_F)

Assume GX_i is taken as AF's current state for gene selection in cervical cancer samples and let AF explore through its neighborhood area to identify ' GX_j ' that possess larger fitness f_j . If $f_j < f_i$ and $f_j < AF_{delta} * f_i / n_f$ that declares GX_j has a higher fitness value and the same behaviour occurs for the surrounding environment that is less crowded, GX_i moves further one step taking the direction of the sum of the vector of the GX_j and $X_{best_{AF}}$.

$$GX_i^{t+1} = GX_i^t + \alpha * \left(\frac{X_j - X_j^t}{\|X_j - X_j^t\|} + \frac{X_{best_{AF}} - X_i^t}{\|X_{best_{AF}} - X_i^t\|} \right) * AF_S * rand() \quad (9)$$

4) BEHAVIOUR IN MOVING (AF_V)

A random state is chosen by AF that covers the visual range, and then it steps forward in this state which is the usual behaviour of AF

$$GX_i^{t+1} = GX_i^t + \alpha * AF_V * rand() \quad (10)$$

In the above equations, for upgrading the classifier's accuracy for gene selection with recurrence samples, a new diversity parameter ' α ' is added to the original equations. This diversity parameter is added based on the gene value and their risk score of the nine lncRNAs. Three signatures, such as ATXN8OS, C5orf60, and INE1, possess positive coefficients that notify higher expression levels. It is associated with shorter disease-free survival and the remaining six lncRNAs signatures, such as DIO3OS, EMX2OS, KCNQ1DN, KCNQ1OT1, LOH12CR2, and RFPL1S, possess negative coefficients whose expression level was negative concerning cervical cancer recurrence. If the risk score is higher than the diversity factor, the factor is reduced simultaneously. Based on the sorted value of the risk score for selected, then Diversity is updated. In this proposed research work number of genes is taken as an input and accuracy as a function.

In the gene selection algorithm, Hilbert-Schmidt Independence Criterion (HSIC) [33], [34] comes with two variables, x and y , chosen randomly. It is considered independently provided for any contiguous bounded function of x and y variables selected randomly, which is not correlated. Assume the other two multivariate variables x and y randomly selected along joint probability distribution p_{xy} . Let \mathcal{X} and \mathcal{Y} considered as support the x and y random variables, respectively [35]. Assume \mathcal{F} as a separate function Reproducing Kernel Hilbert Space (R.K.H.S.) belongs to the real-valued functions between X and \mathbb{R} in universal kernel $k(., .)$. Simultaneously, assume \mathcal{G} to be a separate R.K.H.S. belonging to real-valued functions between Y and \mathbb{R} in universal kernel $b(., .)$... Every coefficient is interrelated with cross-covariance that lies within \mathcal{F} and \mathcal{G}

$$cov(f(x), g(y)) = \mathbb{E}_{x,y}[f(x)g(y)] - \mathbb{E}_x[f(x)]\mathbb{E}_y[g(y)] \quad (11)$$

where $f \in \mathcal{F}$, $g \in \mathcal{G}$, and expectation function is taken as \mathbb{E}

Algorithm 1 HSDAFS Based Gene Selection Algorithm

Input: Initialize the gene population: visual, maximum number of iterations, crowd factor, diversity parameter ' α '. Initialization of X_i for each artificial fish AF_i ($i = 1, 2, \dots, n$)

Output: Selected gene features with recurrence prediction

1. Evaluating every AF_i (genes), $F(X_i)$ ($i = 1, 2, \dots, n$) (accuracy)
2. while ($t < \max$ iteration)
3. for each AF_i (gene) do
 - 3.1 Execute Behavior in Follow step on GX_i (t); Calculate $X_{i,f}$ with diversity factor by equation (7)
 - 3.2 Execute Behavior in Swarm on $GX_i(t)$; Calculate $X_{i,sw}$ with diversity factor by equation (6)
4. if $F(GX_{i,F}) < F(GX_{i,sw})$
 $GX_i(t+1) = GX_{i,F}$
5. else
 $GX_i(t+1) = GX_{i,sw}$
6. end if
7. end for
8. if $GF(X_{best_{AF}}) < GF(\text{bulletin})$
 $\text{bulletin} = X_{best_{AF}}$ from Equation (7)
9. end if

end while

C. ENSEMBLE CLASSIFICATION FRAMEWORK (ENSCF)

An Ensemble Classification model works with a combination of the Ensemble SVM interpolation method and fuzzy weight-based recurrent neural network. Generally, Ensemble classification is a classifier algorithm that falls under supervised learning as it is trained multiple times and then used for predictions [36], [37]. Thus produces a hypothesis in a single term. This hypothesis is not enough to prove the model creates an ensemble framework. Every single classifier is trained using multiple classifiers in the ensemble model. As a result, new data streams emerge by predicting the cervical cancer stages, and thus, the ensemble model is updated. At first, training samples are split into two types, positive and negative samples of cervical cancer denoted as 'P' and 'N'. An ENSCF model overview is shown in figure 2.

1) ENSEMBLE SUPPORT VECTOR MACHINE WITH INTERPOLATION (ESVMI)

The ESVMI is one of the multi-class classifications. This model segregates the defined set of $\{+1, -1\}$ marked in the training cervical cancer dataset through a hyperplane which is undoubtedly maximally distant between positive and negative cervical cancer data samples. This model segregates the hyperplane optimally in the cervical cancer feature that corresponds to the input cervical cancer, which lies on a non-linear decision boundary. Additional information about the ensemble SVM is described in [38]. By taking a set of N different cervical cancer instances (f_i, y_i) with $f_i \in \mathbb{R}^D$, $y_i \in \mathbb{R}^d$. Then ESVMI is modeled in such a way

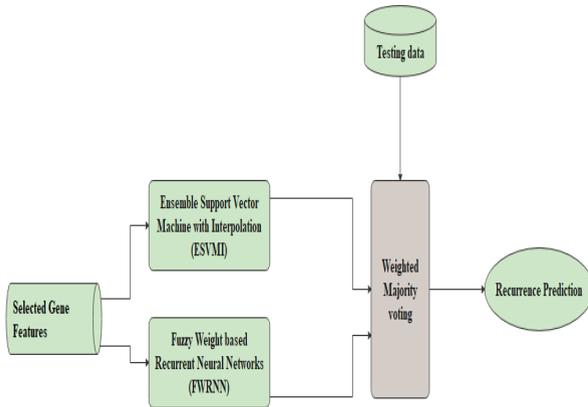


FIGURE 2. Ensemble classification framework (ENSCF) model.

shown as [39]

$$\sum_i a_i K(fe, fe_i) we_i + b, \quad i \in [1, N] \quad (12)$$

$K(fe, fe_i)$ is considered kernel function, a is taken as parameter α , and b is taken as the threshold of the SVM, respectively. The distance-based weighting method is one of the standard interpolation methods [40]. The similarity of the points is the factor used in the distance-based weighting method. It gives way for predicting the presumption of cervical cancer positions that are not known by weighting the nearer positions of cc data points. The distance weighing model computes the distance between the unrevealed cervical cancer position and the known position. And by using the semi variance value, the weight value is solved. Ensemble system mainly depends upon the Diversity of any classifier for its success. Here, in the proposed model, we use the majority voting method. The different classifiers' results are aggregated in this voting method and then selected by voting to take an optimal decision. The purpose depends on dividing the cancer samples equally into equal size subsets like the minority class. The process is repeated until an equal size of samples is met. But still, the records remain unique, except the different subsets may contain duplicated records.

2) FUZZY WEIGHT-BASED RECURRENT NEURAL NETWORKS (FWRNN)

Recurrent Neural Network (RNN) can attach hidden layers and previous ones circularly [41]–[49]. These RNN's hidden layers are also termed recurrent units; they store their historical cervical cancer samples among the gene sequence. In **Figure 3**, one of the RNN hidden-layers sequential structures is shown. The hidden layers linked may be extended to several networks, containing an input sequence in a pointed posture. An RNN comprises an enormous depth model; the quantity of the hidden layers is identical concerning the input sequence's length. The weight value is generated via the fuzzy membership function to improve the classifier's classifier accuracy.

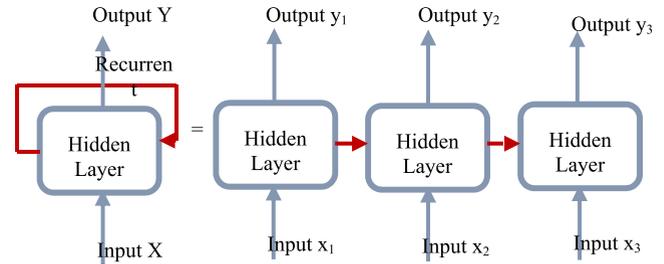


FIGURE 3. Work procedure of recurrent neural network (RNN).

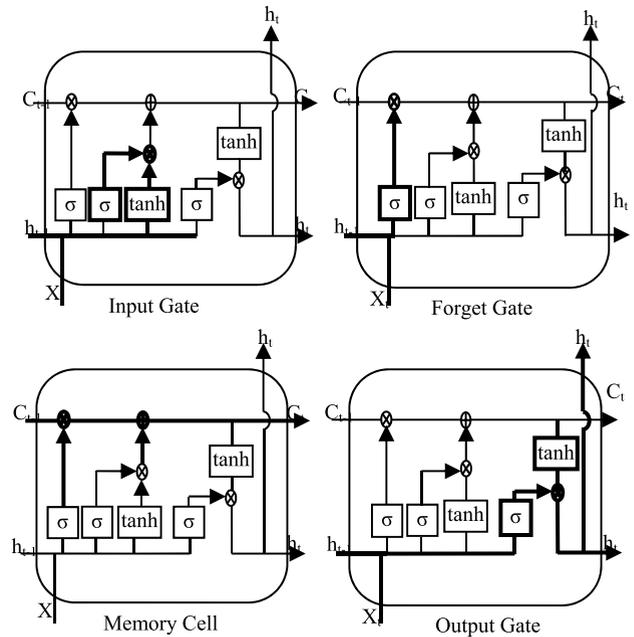


FIGURE 4. Model of long short-term memory (L.S.T.M.) block.

The architecture of an L.S.T.M. block is shown in **Figure 4**, which comprises four components: input gate, forget gate, memory cell, and output gate.

In the above model of L.S.T.M., there flow two parallel lines that deal with the hidden layer information and memory, considered as significant variance in RNN. The function of Hidden layer 'h' is to calculate the output value dependent upon the gene samples of cervical cancer with recurrence prediction and previously stored uncovered details of cervical cancer, and its estimated result is forwarded to the next layer and memory through c . The memory cell holds that recurrence prediction outcome and forgets previously stored duplicated ones, thus fabricating an updated outcome to influence hidden layer cell.

3) INPUT GATE

It accepts cervical cancer samples from the hidden layer stored priorly and the current data from cervical cancer samples. Then it computes to obtain recurrence prediction results with the following equation:

$$i_t = \sigma(fw_{x_t}x_t + fw_{h_t}h_t + b_i) \quad (13)$$

where the result of the input gate is i_t ; current input and previously-stored hidden layer output is x_t and h_{t-1} , respectively; The weights of the inputs are represented as fw_{x_i} and fw_{h_i} ; input gate bias is b_i . And 's' is declared in two terms, such as activation function and a soft sign function that is produced as follows:

$$\sigma_{softmargin}(x) = \frac{x}{1 + |x|} \quad (14)$$

where x is represented as an independent variable. A short-term memory is produced through the input gate:

$$\tilde{c}_t = \tanh l (fw_{xc}x_t + fw_{hc}h_{t-1} + b_c) \quad (15)$$

where fw_{xc}, fw_{hc} are declared as weights for x_t, h_{t-1} respectively and b_c as bias for \tilde{c}_t .

4) FORGET GATE

This gate resembles the input gate with the same computational formula but differs in weights such as (fw_{xf}, fw_{hf}) and bias is given as (b_f) :

$$f_t = \sigma (fw_{xf}x_t + fw_{hf}h_{t-1} + b_f) \quad (16)$$

5) MEMORY CELL

This computation for this current memory (c_t) is given by the below equation

$$c_t = f_t.c_{t-1} + i_t.\tilde{c}_t \quad (17)$$

where, c_{t-1} is the memory cell output stored previously.

6) OUTPUT GATE

This gate is calculated using the current input, memory, and hidden layer result stored previously. This computation is done using the below formulas:

$$o_t = \sigma (fw_{x0}x_t + fw_{h0}h_{t-1} + b_0) \quad (18)$$

$$h_t = o_t.\tanh(c_t) \quad (19)$$

Here, results of the output gate and current hidden layer are denoted by o_t and h_t , respectively. The weights for x_t and h_{t-1} is represented by w_{x0} and w_{h0} and b_0 for bias o_t , correspondingly. The number of base classifiers comprises nearly $k = 2$ for the final devised model decided by cervical cancer classification measure and recurrence prediction. In case numbers of training cervical cancer subsets (gene samples) are more significant than base classifier value $k = 2$, the FWRNN model may update a newly trained base classifier ESVM and FWRNN with the minimum error in the new ensemble method. Thus error caused due to this base classifier L_i can be represented in the following equation

$$Error = \sum_{i=1}^n (100 - acc_i) \quad (20)$$

The weight of a classifier is initialized to 1. But it is not suitable for all the classifiers. So it has to be changed based on the risk score of the feature or gene samples based on the selected cervical cancer samples. The weight of the classifier is generated newly via the use of the fuzzy trapezoidal

function. In the fuzzy, three intervals are chosen based on the importance of the features. If the recurrence prediction risk is low, then the level belongs to a; if the feature's importance is medium, then the level belongs to b; if the recurrence risk is high, it belongs to c.

$$\mu_A(fw) = \begin{cases} \left(\frac{fw - a}{b - c}\right), & a \leq fw \leq b \\ \left(\frac{c - x}{c - a}\right), & b \leq fw \leq c \\ 0 & else \end{cases} \quad (21)$$

Our ensemble model takes the class that possesses a high accumulation of weight. The result of the local trainer is also weighted by assigning the weight. The results from each classifier are combined concerning their weight, and then those weights are normalized to avoid any additional classifiers outweighing the old ones. Predict the recurrence class label 'y' via majority (plurality) voting of each classifier C_j :

$$y = \arg \max_i \sum_{j=1}^m fw_j X_A(C_j(x) = i) \quad (22)$$

Compute a weighted majority vote by associating a weight fw_j with a classifier where X_A is the characteristic function [$C_j(x) = i \in A$], and A is the set of unique class labels. With the weighted coefficients devised by the LASSO regression model, a Nine-lncRNA signature with positive and negative risk score was determined with the gene expression. The risk score of every instance of gene expression is computed in correspondence with the RNA expression and LASSO coefficient denoted by Exp_i and L_i .

$$Risk\ Score = \sum_{i=1}^n Exp_i * L_i \quad (23)$$

By computing these risk scores, different high and low-risk categories and their respective median scores were validated.

IV. RESULTS AND DISCUSSION

Gene expression data set was downloaded from GEO datasets containing normalized data with lncRNA profiles for each victim. 300 samples were extracted from the GSE44001 accession taken, split into 150 training cohorts and 150 testing or validating cohorts. Recurrence CC genes are filtered using IoT driven system. The CC samples are then analyzed under a microscope for feature selection. The recurrence samples are diagnosed for cytology tests using the RNN algorithm. In this process, the high-risk and low-risk lncRNA signatures are differentiated and taken for colposcopy testing shown in Figure 5. For high-risk recurrence CC genes, intensive screening was prescribed every six months, and for low-risk factors colposcopy, testing can be carried out directly for further treatment.

At the initial stage, the LASSO Cox regression model associated with 10-fold cross-validation was trained with 150 instances to study the cervical cancer gene expression. **Figure 6** shows 20 samples of gene expression value. These results were appended with lncRNA coefficients in the risk

TABLE 1. Risk assessment and survival status of CC recurrence.

lncRNA Signature	Risk Value	Risk Assessment	Risk Level of CC Recurrence	Survival Status
ATXN8OS (A)	3.3156 2585	A*3.315625 85=HE	High Risk	Short er-DFS
C5orf60(C)	0.1398 7057	C*0.139870 57=HE	High Risk	Short er-DFS
DIO3OS(D)	- 0.4321 6636	D*- 0.43216636= LE	Low Risk	Long er-DFS
EMX2OS(E)	- 0.9224 7218	E*- 0.92247218= LE	Low Risk	Long er-DFS
INE1(I)	1.1330 9789	I*1.1330978 9=HE	High Risk	Short er-DFS
KCNQ1D N(K1)	- 4.4805 5889	K1*- 4.48055889= LE	Low Risk	Long er-DFS
KCNQ1OT 1(K2)	- 0.0806 7727	K2*- 0.08067727= LE	Low Risk	Long er-DFS
LOH12CR 2(L)	- 0.0973 7496	L*- 0.09737496= LE	Low Risk	Long er-DFS
RFPL1S(R)	- 0.6662 2831	R*- 0.66622831= LE	Low Risk	Long er-DFS

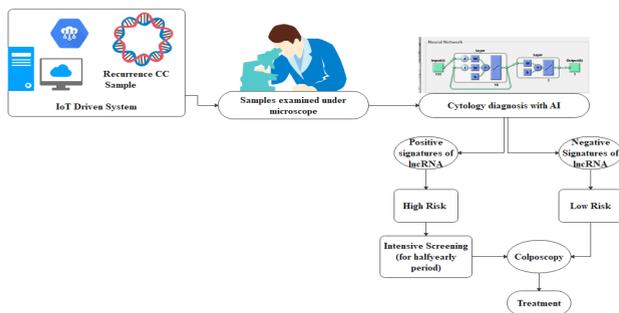


FIGURE 5. AI-Based IoT Model in Predicting Recurrence CC genes.

score shown in **Table 1** to analyze the positive and negative coefficients based on the cervical cancer gene expression.

From the risk score computation, it is already found that signatures with ATXN8OS, C5orf60, and INE1 possess positive values. That results in a higher level of gene expression with a minimum duration of survival time, with six signatures with DIO3OS, EMX2OS, KCNQ1DN, KCNQ1OT1,

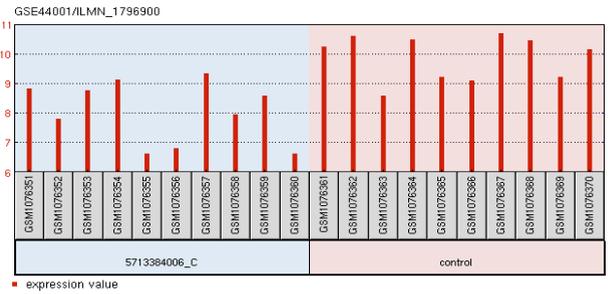


FIGURE 6. Samples of Recurrence Cervical gene expression value (Gene id: ILMN_179690).

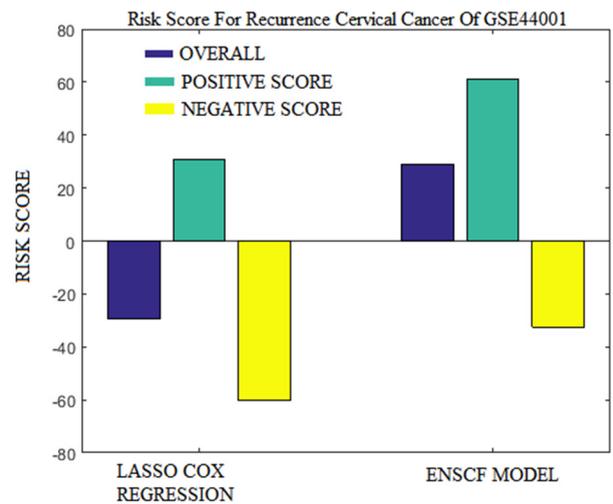


FIGURE 7. Positive and Negative Risk Score for 300 samples.

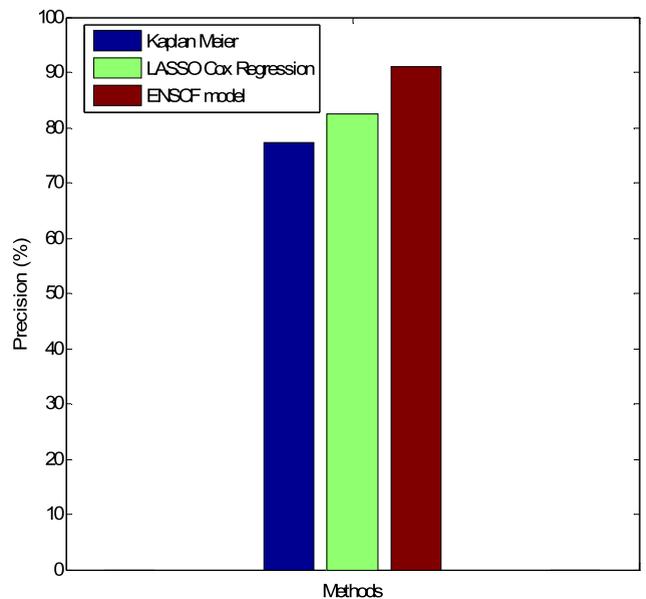


FIGURE 8. Precision results evaluation of recurrence prediction methods.

LOH12CR2, and RFPL1S possess negative coefficients whose gene expression is negative when compared to the positive signatures and holds less probability of cancer

TABLE 2. Risk score for recurrence and non-recurrence cervical cancer.

RISK SCORE	OVERALL SCORE	POSITIVE SCORE (RECCUR ENCE)	NEGATIVE SCORE (NON- RECURRENCE)
LASSO COX REGRES SION	-29.2861	30.7428	-60.0289
ENSCF MODEL	28.77	61.272	-32.502

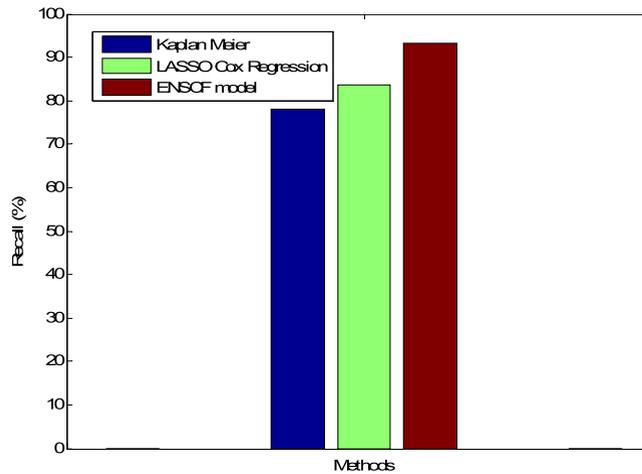


FIGURE 9. Recall results evaluation of recurrence prediction methods.

recurrence. The finally higher recurrence rate for positively expressed signature coefficients is proved by Chi-square analysis. The outcome of the E.N.S.C.F. model in our work is compared to other existing methods like Kaplan Meier and LASSO Cox regression shown in Table 2. The corresponding graph is depicted in **Figure 7**. Consequently, precision, recall, f-measure, and accuracy are applied to recurrence prediction shown in **Table 3**.

$$\text{Precision} = \text{TP}/(\text{TP} + \text{FP}) \tag{24}$$

$$\text{Recall} = \text{TP}/(\text{TP} + \text{FN}) \tag{25}$$

F-measure can be computed by finding the precision weighted harmonic mean and recall.

$$F = 2 \frac{P + R}{P.R} \tag{26}$$

$$\text{Accuracy} = (\text{TP} + \text{TN})/(\text{TP} + \text{TN} + \text{FP} + \text{FN}) \tag{27}$$

Figure 8 shows the precision outcome of the recurrence prediction methods of Kaplan Meier, LASSO Cox regression and proposed ENSCF model. The proposed E.N.S.C.F. model

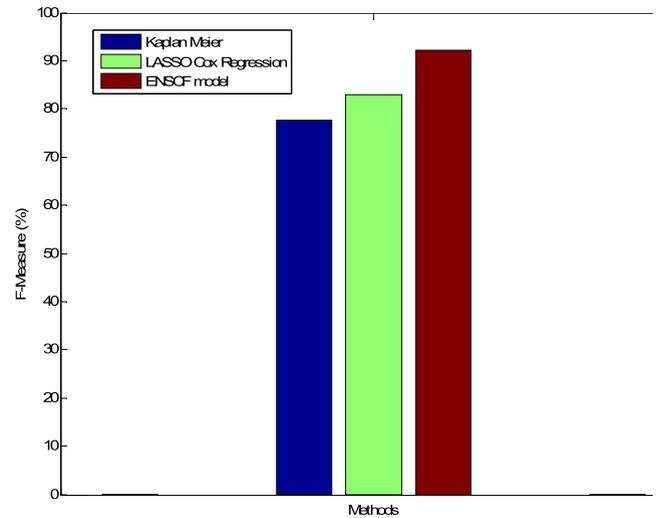


FIGURE 10. F-measure results evaluation of recurrence prediction methods.

TABLE 3. Metrics evaluation vs recurrence prediction methods.

METRICS	METHODS		
	KAPLA N MEIER	LASSO COX REGRESSI ON	ENSCF MODEL
PRECISION (%)	77.37	82.34	91.14
RECALL (%)	78.08	83.56	93.15
F-MEASURE (%)	77.72	82.94	92.13
ACCURACY (%)	79.90	84.47	92.69
ERROR (%)	20.09	15.52	7.30

gives higher precision results of the 91.14%, other methods such as Kaplan Meier and LASSO Cox regression give the lesser precision value of 82.34% and 77.37%, respectively.

Recurrence prediction results of recall metric concerning three methods such as Kaplan Meier, LASSO Cox regression and proposed ENSCF model is shown in **Figure 9**. The proposed ENSCF model produces recall results of 93.15%, higher than Kaplan Meier and LASSO Cox regression methods producing lesser recall values of 83.56% and 78.08%, respectively.

F-Measure results regarding three recurrence prediction methods, such as Kaplan Meier, LASSO Cox regression, and the proposed ENSCF model, are depicted in **Figure 10**. The proposed ENSCF model bestows f-measure results of 92.13%, higher than Kaplan Meier and LASSO Cox regression confers lesser f-measure value of 82.94% and 77.72%, respectively.

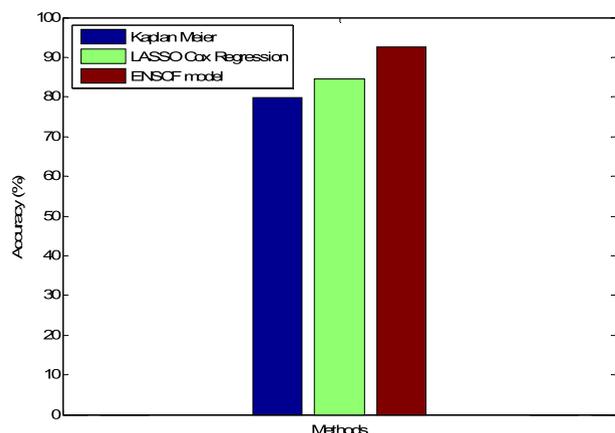


FIGURE 11. Accuracy results evaluation of recurrence prediction methods.

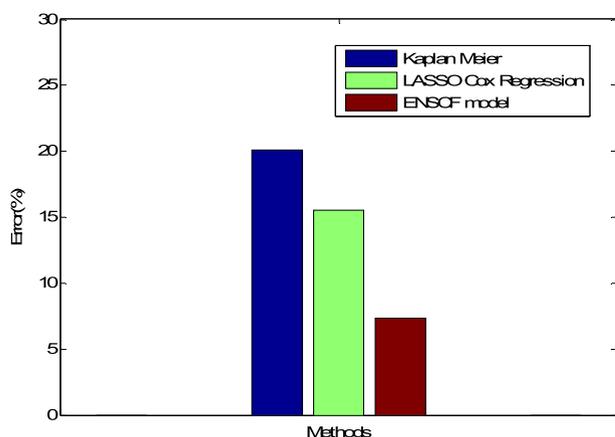


FIGURE 12. Error results evaluation of recurrence prediction methods.

Overall results comparing three different recurrence prediction methods, such as Kaplan Meier, LASSO Cox regression, and the proposed ENSCF model, are exhibited in **Figure 11**. The suggested ENSCF model trots out the improved outcome of the 92.69% accuracy. Kaplan Meier and LASSO Cox regression method give lesser accuracy value of 84.47% and 79.90%, respectively.

Error value of three prediction methods such as Kaplan Meier, LASSO Cox regression, and proposed ENSCF model is depicted in **Figure 12**. The proposed ENSCF model gives lesser error results of the 7.30%, Kaplan Meier and LASSO Cox regression method give higher error value of 15.52% and 20.09%, respectively.

V. CONCLUSION AND FUTURE WORK

IoT-based health care's potential has increased the accessibility of the health services and transition with AI techniques to be more proactive and integrated systems. Recurrence Prediction in Cervical Cancer becomes a challenging task. This has been solved with AI based neural network technique. In this paper, initially, data imputation with Mode and Mean Missing(MMM-DI) is launched to replace the missing data. Secondly, gene selection is performed by the Hilbert-Schmidt independence criterion with Diversity based Artificial Fish

Swarm (HSDAFS) algorithm. If the risk score is higher than the diversity factor, the factor is reduced simultaneously. Based on the sorted value of the risk score for selected, then Diversity is updated.

Then recurrence predicting in cervical cancer disease is performed by ENSEmble Classification Framework (ENSCF). In ENSCF combines the results of two classifiers such as Ensemble Support Vector Machine with Interpolation (ESVMI) and Fuzzy Weight based Recurrent Neural Networks (FWRNN). Nine-lncRNA signature is implemented for identifying disease-free survival duration of cervical cancer. Finally, the risk score was validated in gene samples using Chi-square analysis. As a consequence, precision, recall, f-measure, and accuracy are used for recurrence prediction. It was proved by Chi-square analysis that the risk score was higher for positive gene signatures and low for negative gene signatures with a low-risk group. The recurrence gene data set is downloaded from the GSE44001 dataset. The proposed study determines the high and low-risk scores. It predicts the disease-free survival duration with the nine signatures, which provides a valid computational indication for cervical cancer clinical treatment. Further signatures of differentially expressed genes for recurrence cancer need to be found with more samples and taken for future work.

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