

Identifying Cancer Disease Using Softmax-Feed Forward Recurrent Neural Classification

P. Saranya* and P. Asha

Department of Computer Science and Engineering, Sathyabama Institute of Science and Technology, Chennai, India

*Corresponding Author: P. Saranya. Email: saranyapcse0001@outlook.com

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Abstract: In today's growing modern world environment, as human food activities are changing, it is affecting human health, thus leading to diseases like cancer. Cancer is a complex disease with many subtypes that affect human health without premature treatment and cause death. So the analysis of early diagnosis and prognosis of cancer studies can improve clinical management by analyzing various features of observation, which has become necessary to classify the type in cancer research. The research needs importance to organize the risk of the cancer patients based on data analysis to predict the result of premature treatment. This paper introduces a Maximal Region-Based Candidate Feature Selection (MRCFS) for early risk diagnosing using Soft-Max Feed Forward Neural Classification (SMF2NC) to solve the above problem. The predictive model is based on a different relational feature learning model, which is possessed to candidate selection to reduce the dimensionality. The redundant features are processed marginal weight rates for observing similar features' variants and the absolute value. Softmax neural hidden layers are trained using the Sigmoid Activation Function (SAF) to create the logical condition for feed-forward layers. Further, the maximal features are introduced to invite a deep neural network constructed on the Feed Forward Recurrent Neural Network (FFRNN). The classifier produces higher classification accuracy than the previous methods and observes the cancer detection, which is recommended for early diagnosis.

Keywords: Cancer detection; extensive data analysis; candidate feature selection; deep neural classification; clustering; disease influence rate

1 Introduction

Identifying the early stage of cancer is essential for diagnosing and treating cancer to reduce disease growth from the risk to the patient health. Due to the different gene expressions of cancer, the type may be varied. So the risk identification is varied due to features of the cancer category. The cancer classification using Personal Health Record (PHR) data can be used as a valuable feature source by observing more data from the patient. However, using the health care profile, the physical features are directly observed from patients, and accurate cancer classification remains challenging with the original high-dimensional features and small data model size. So we need feature reduction to reduce the dimensionality from non-related parts.



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Feature selection and classification are essential in knowledge learning analyses to make decisions in real-world datasets. It is critical in identifying the disease and predicting results to categorize the dataset for Early Risk Prediction (ERP). Mainly the implementations are carried out to supportive for biomedical datasets. Feature selection (FS) and classification are well supported for biomedical data processing in the high imperative high dimensional dataset. Due to various research and implementation is not well sufficient to predict classification accuracy. We need a dedicative approach using the neural network based on the classification model to solve the classification problem. The feature mining result takes Systematic Decisions (SD) or a human thinkable approach based on the data statistics or input resources observed from the cancer patients. Due to the accurate word entitles, the data processes are challenging to process because the raw data contain high dimensionality datasets.

Fig. 1 shows the essential operation of dataset classification using the feature selection approach. Data mining in medical fields is most useful for the knowledge process for medical diagnosis to classify the results. Based on NLP (Natural language processing), the preprocessing is initialized to do datasets, or PHR information is ready to organize for optimization results. The feature selection holds the information or sets rules for selecting a type definition of data. Classification revives the type of definition to produce the optimized result.

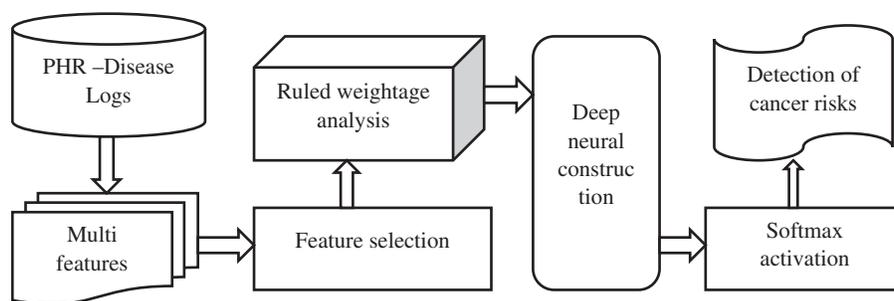


Figure 1: Process of disease prediction based on feature selection and classification

The Candidate Feature Selection Model (CFSM) frequently selects the attribute to specify the filter case. Finding the proper subset of prescient features is critical in its own particular right. For instance, the doctor may settle on a choice in light of the chosen elements, whether a risky medical procedure is essential for treatment or not. Candidate selection in directed learning has been very much considered to select the data based on disease relation. The principal objective is to discover a feature subset that produces to support higher classification exactness.

The candidate features are labelled into classes that carry the type definition using Subset Feature Classification (SFC), type data identifiers, and a wrapping class container. Finally, the feature selection has the relational disease weight information rules to define the category. The classification categorizes the class labels for the information type under the neural network. Generally, non-redundant features dropping the quantity of redundant/repetitive elements can drastically diminish the learning calculations' running time and yields a broader classifier for accuracy. This guides in enhancing comprehension of the concealed thought of a genuine classification issue. The Artificial Neural Network (ANN) contains three processing parts, starting from input processing called the input layer, which includes multi-process to take input based on the feature selection. The centralized layer is called the hidden layer, and this may be the single or multi-perspective model set with the number of neurons trained by deep neural through a soft-max activation function. The final layer produces the output with neurons projected classification form of class. Artificial intelligence frameworks have discovered far-reaching use in disease classification, expanding feature classification.

2 Related Works

Cancer is a serious worldwide health problem usually associated with genetic abnormalities that cause severe disease. In [1], these cancer cells form particular molecules called biomarkers, which indicate the presence of anomalies and release them into the cardiovascular system. In [2] author discusses. However, there is still a lack of tools or models to automate the analysis of human cells to determine the presence of cancer. In [3], the Author defined C-reactive protein (CRP), the serum marker of inflammation, as associated with a decrease in Heart Rate Variability (HRV), a standard medical tool for assessing autonomic function.

In [4], the Author discussed Acute Lymphoblastic Leukemia (ALL), a type of cancer in which the bone marrow produces more lymphocytes. On the other hand, Multiple Myeloma (MM) is another type of cancer in which cancer cells accumulate in the bone marrow rather than being released into the bloodstream. Therefore, they are congested and interfere with producing healthy blood cells. Traditionally, this process is done manually by skilled professionals for a considerable period. In [5], the Author describes the classifier selection and decision tree by choosing the right features to categorize cancer risk. Also, this uses the clustering ensemble approach in the minor factor considering non-important features to classify the results. In [6], the parts are classified based on the nearest neighbour classification to produce the category to categorize the data. This provides an attribute weighting factor to choose the features compared with K-Nearest Neighbor (KNN) and decision tree algorithms.

In [7], the Support Vector Machine (SVM) intends to define cancer recognition based on bagged ensembles. Still, the support values don't produce effective feature selection because non-dimensionality leads to none related feature selection to reduce the classification accuracy. In [8], the Author described lung cancer prediction based on hidden knowledge-based techniques like naïve Bayes, Artificial neural Networks to discover the secret principle of the feature. It makes it a difficult time to predict the data. In [9], the Author describes the type-2 fuzzy logic system Fuzzy C-Means (FCM) based on the wavelet feature selection depending on the hybrid learning process. In [10], the Author describes the image processing principle-based lung cancer detection using the feature segmentation approach; the segmented value is a feature consideration to classify the weights in a feed-forward backpropagation network. The features increase the deviation principle for redundant dataset decisions, leading to inaccuracy in classification.

The automated decision and classification were based on the oral lesion using a deep learning model to detect cancer [11]. The variety makes decision forums under different Weightage to predict the result, but complex patterns were derived for tackling this difficult task.

The Self-training subspace clustering algorithm was used to find the features, and the accurate identification of data considers the low-rank features for finding the match case parts. The non-relevant features lead to inaccurate classification [12].

Multi-modality medical imaging techniques are increasingly used in clinical practice and research. Related multimedia image analysis and group learning programs are overgrowing, adding unique value to clinical applications. They were inspired by the recent success of using in-deep learning techniques in medical image processing [13]. Then select the principle of redundant features, but this doesn't ensemble the classifier to predict relation data produce inaccuracy.

Reference [14], describes the image processing based on a multi-model deep learning process with the ensemble learning process. It selects the features based on a cross-fusion feature selection model trained with a Convolutional Neural Network. (CNN) [15].

Reference [16] introduces a 3D-classification system using neural networks and feature selection to classify heart disease based on imaging. By reducing the number of features, the number of diagnostic tests minimizes the patient's need for a physician, but the collective feature needs the data for classification. In [17], Intensity-based statistical feature selection methods are used to predict the results

used in this study of heart disease databases, showing that accuracy is superior to older classification techniques.

Health research minimizes the importance of various data processing technologies based on taxonomic features [18]. In Machine-to-Machine (M2M) correspondence from cell configurations, systems that participate in creating distances far from vehicle configurations and sensor configurations [19]. The reviews and methods compare the inaccuracy of the feature selection model under the redundant forms discussed and issues of health data mining technology [20]. In this study, Non-cellular Small lung cancer (NSCLC) is high-risk cancer usually scanned for diagnosis, diagnosis and treatment by PET-CT. However, PET-CT scans should produce at least 640 images per patient in the existing hospital setting. In [21], An optical biosensor design with high-resolution detection based on vibration holes is proposed for a Two-Domain Photonic Crystal (2DPhC) with a free spectral range near $FSR = 630$ nm. This sensor analyses the internal components of blood.

3 Maximal Region-Based Feature Selection and Feed-Forward Neural Classification

The contribution is to implement an early cancer prediction through a deep learning approach for indenting cancer disease from PHR data. These intent methods reduce the problematic consideration to resolve the feature selection and classification mitigations. Because the high dimensional dataset in medical diagnoses using an artificial neural network makes an easy prediction and classification system. This proposed implementation intends a new method of Identifying Cancer Disease Based on Maximal Region-Based Candidate Feature Selection Using Soft-max Feed Forward Neural Classification (SMF²NC) for Early Risk Diagnosing.

To improve the feature selection, make an efficient approach in preprocessing to point the data to reduce dimensionality, category as the classes' label. The Multi-Attribute Case Prediction Model (MACPM) is used for categorization using the artificial neural network in profound moral to improve the classification accuracy. To deploy a Deep Neural Classifier (DNC) for classification using the relational cluster based on the optimal feature selection model. The optimal feature defines the Radial Basis Function (RBF) to identify the marginal closest weight. The proposed scheme is easy to implement by redundant features that carry the performance of the present approach and is significantly superior to the competing research work for classification accuracy.

Fig. 2 shows initially, and the PHR dataset contains the multiple records collected from hospitals for cancer data analytics. It is observed in preprocessing to reduce dimensionality using Stable Auction Mapping (SAT) to prepare a noiseless null record dataset for feature selection. This selects the relevance identified portion to predict the features on varying weights to make a single cluster. At first, a couple of relational features are obtained by finding the comparability of attributes between every single member value in the dataset. Selection connectives are used in light of Maximal Stable External Region (MSER) to identify the relation to featured clustering. An additional feature selection rule is used to reduce the high-dimensional dataset.

Further, the selected features are connected to an optimized Deep Artificial Neural Network classifier based on a feed-forward neural network. The means for each component are predicted, and a mean grid trained with multiple iterated neural in hidden layers, utilizing the average of the classification structures, is built. The features are segmented into the classification network based on the average mean value.

3.1 Marginal Feature Clustering

Initially, to process the relational feature based on marginal values, which consider the multi attributes have the same similarity. Select the identical unique features, as similar on another feature nature weights are obtained by correlated weight margins. Then create a fuzzy membership function-based rule and estimate the total mean rate between lower and upper bound limits to check the condition belongs to the feature limits and defined selected features. It creates a decision tree traversal by shifting max weights closest to the individual class.

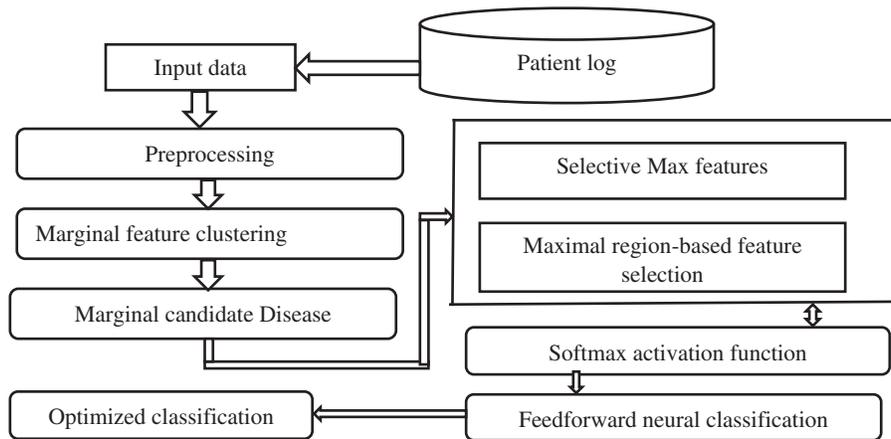


Figure 2: Architectural process SMF²NC

The attribute feature selection is proposed for the interior focuses.

Algorithm:

Input: Preprocessed Feature set Frs

Output: classified optimal class

Step 1: Unitize the computed features as Fr1, Fr2....Frn. from Frs

Compute Max ruled Weightage constant

Examine the closest feature from feature cluster set Frs.

Selective For each dataset D_i from Frs.

Feature Term T = Extracted decision node from Di.

Subset Ss = $(\sum_{n=1}^{\text{size}(Ds)} \text{node value} \in Di) + Frs$

End for

Repeat

Step 2: Compute the relative feature Ri from Frs ←Ss

Initialed the ruled upper bound up. From the closest mean term

Ri←Fs(Selective term)

Append the cluster set Cs = $\sum Cs (Di) + Frs$

Step 3: Estimate the marginal multiple unique features of the Decision tree;

For each fuzzy ruled feature as a cluster group

Estimate the centroid cluster mean depth value From Ri.

Absolute mean $m = \frac{\sum Frs(Ws(Ri))}{\text{average} = Frs}$

End

Find closest relative feature weight from Max weight.

Obtain class (Di)

Step 4: mean weight split by class weight feature Cri

(Continued)

Algorithm: (continued)

- Step 5: Compute R_i as a relative cluster group
 Step 6: $R_i \rightarrow Frs(m) + Cri$
 Step 7: return R_i as an Absolute feature cluster group
-

The above algorithm has been constructed to analyse the result's significance and dependency. Furthermore, lower and upper approximations in fuzzy preference investigation can be interpreted as the positive and negative decision class

3.2 Marginal Candidate Disease Influence Rate

In this stage, the marginal influence rate is estimated using R_i absolute features weight. This method uses the event similarity to find the presence of features occurrence or event support measures measured according to candidate support value. The most affected influence rate is calculated by the mean rate observed from most infection rates in a cardiac feature. Also, the mean rate is referred to as features present in each event class. According to the value of Event Support, a specific event has been selected and produced as a result.

Pseudo Code of Event Prediction:

Input: Term set R_i as T_s , Event Taxonomy ET as $Frs(m)$

Output: Event E

Start

 Read T_s and taxonomy ET .

 For each event class Ec

$$\text{Compute Event Support } Es = \sum_{i=1}^{size(T_s)} Ts(i) \in ET(Ec) / size(ET(Ec)) - (17)$$

 End

 Event Es = Choose the event class with maximum event support.

Stop

The process of occurrence event prediction is presented above the pseudocode, and the method computes the event support for various event classes. Finally, a single event has been selected as a possible event to produce a result.

3.3 Maximal Region-Based Feature Selection

This stage considers the maximal region similarity measurement by covering the boundary limit of scaling values estimated from the Event class. This creates rough groups to set the fuzzy rules for the non-deterministic as lower features. All over the relational features are maximum weight, which is closest to cardiac principle features weights are clustered. The multi attributes have the same similarity, identical to nature considered unique features similar group weightage features, identical to another feature nature. The relational features are disease-relevant margins as essential features like ESR and CRP gone with immunity weights.

Input marginal features weight as Es

Obtain relative cluster group Vs.

Start

The initialized feature set FS

Perform Data Preparation.

Compute maximum region layer From Fs as feature vector Fv

Source set Ss = Fuzzy rule dataset.

For each source s

For each class l

For each feature n

size(N)

If $Fv(Pl) \in s$ then

i = 1

Count = count + 1.

Compute cardiac principle C as A_{min} and maximum A_{max}

$$CI = \frac{Fv(CDIR)}{Fv(\text{marginal weight})} \times Fv(NI)$$

Compute Infection rate in previous layer IrPl.

$$IrPl = \frac{Fv(1 - 1)(\text{Immunity} + \text{CRP})}{Fv(1 - 1)(\text{marginal weight})} \times Fv(1 - 1)(NI)$$

Compute Cancer infection rate $IR = CI / IrPl$

End

End

Compute Infection Transmission Support ITS.

$$ITS = \left(\frac{Fv(\text{Immunity} + \text{CRP})}{Fv(\text{marginal weight})} \times Fv(NI) \right) \times \text{Std}(IR)$$

If $ITS > Th$, then

Add to vulnerable set $VS = \sum(\text{Sources} \in Vs) \cup s$

End

Stop

Every segment vector is then utilized as an input vector, while the normal of every attribute at maximal features. Calculate the minimum A_{min} and maximum A_{max} values of each column (or attribute) in the dataset. Calculate the A_{min} value and A_{max} value is similar to corresponding features be selected to extract as redundant features. In the training phase, the network is trained by providing input and output based on selected features by constructing a neural network.

3.4 Soft-Max Feed Forward Neural Network

At this stage, the classifier finalizes the result for medical recommendation by the risk of patients and its categorized class based on the sigmoid activation function. The slight weight control initialized all the feature

weights fed into the hidden layer through the softmax activation function. The activation function trains the neurons to tune the resultant clusters into mean depth values to create a logical rule for the neurons.

The feed-forward network is optimized with an adaptive forager search algorithm rule obtained as a training rule into a recurrent neural network, tuning neurons to the closest weight prediction. During this phase, the neural network can adjust the connection weights to match its output with the actual production in an iterative process until a desirable result is reached. Based on the sinusoidal weight, the importance of the Maximum feature is attained to the neural decision gradually increased; if the redundant weight is found, they spread the value into the nearest class without backpropagation to avoid link broken during training—this reduced search optimization of relevance feature fed forward into the next layer.

The activation function trains remains the $f(x) = \begin{cases} y = 1 & \text{if } \sum_{i=1}^n w_i x_i \geq b \\ y = 0 & \text{otherwise} \end{cases}$ where $f(x)$ remains the logistic activation of neuron trained with Intra-class logistic transformation, $w_{(t+1)} = w_t - \mathbb{N}\Delta w_t$ and $b_{(t+1)} = b_t - \mathbb{N}\Delta b_t$. The training function be Iterate till the end the neuron get the closer mean value.

We begin to function W approximately b . We track all the information using each corrugation function to find and repeat the corresponding prediction result and find and calculate the square error loss.

A fully integrated feed-forward of the neuron is illustrated in the construction of the network

$$net_{i(t)} = \sum_{j=1}^j w_{ij} y_{j(t)} + x_{i(t)}, \quad i = 1 \dots j \text{ And}$$

$$Ti \frac{dy(t)}{dt} = -yi(t) + \varphi(net_i) + x_{i(t)}, \quad i = 1 \dots j$$

The frequent neurons of Weightage are optimized in constant τ_i based on the current unit i as a valid training weightage based on the Intra-class logistic activation function. The input $X(i)$ and $Y(i)$ bet activated based on the weightage $w(i)$.

Algorithm:

Input: Its features as Current Sample scan, Adapted feature $rule\ net_{i(t)} \rightarrow Apt$.

Output: optimized class pattern

Start: compute the Disease influence rate and occurrence of feature Max weight term

 Read Apt . Data values and Scs . Data values.

 For each fed layer class P_c

 Compute the hidden layer neurons weight to c as set = $\int_{i=1}^{size(Apt)} \sum Apt(i).class = c$

 Closest pattern $Pps =$ Closest pattern (Cset).

 For each closest pattern on the relative link from Influence rate, each pattern p

 Each similarity feature is categorised based on Max cancer's risk-affected rate.

 Disease Proficient feature selection $DPfs = \frac{\int_{i=1}^{size(p)} \sum P(i) == Scs(i)}{size(p)}$

 End

 Compute cumulative rate $DPFS = \frac{\sum_{i=1}^{size(pps)} Pfs}{size(pps)}$

 End

 Optimized cancer personal recommendation (CPR) = PFs return set maximum values

Stop

The input features are trained with the classification structures. They are then labelled with neural weights, represent the classes, and the input factors aid in separating the area learning about relational features from the hidden neurons. The activation function tunes each neuron to optimize the classification accuracy by class by reference.

The Recurrent neural algorithm consists of artificial neurons activating functions that involve a hidden layer due to binary classification problems. For each neuron, the perceptron uses the activation function. Therefore, repetitive nerve cells spread relative weights along the cluster group nature to find the optimal class based on the nerve structure. The activation function reduces the number of layers in the two layers by changing the weight assigned to the perceptron that determines each neuron's weighted input. Cognitive classes are bias weights for classifying cancer disease classes based on feature substation weights.

4 Result and Discussion

The proposed Maximal Region-Based Candidate Feature Selection Using Soft max-Feed Forward Neural Classification-based cancer prediction algorithms have been implemented and tested for their efficiency Python deep learning framework. The resultant parameters are tested with the confusion matrix to produce the result performance. The implementation provides higher efficiency than the previous test case results in the method Fuzzy C-Means (FCM), Convolution Neural Network (CNN). [Tab. 1.](#) shows the details of the bio-medical dataset that are processed to test the performance of the proposed systems.

Table 1: Proposed simulation parameters

Parameters used	Values processed
Dataset used	NSCLC, Lung cancer patient UCI corpus
Simulation environment	Python anaconda
Number of attributes	<20
Number of class	3 (High, low, moderate)

The details used for evaluating performance produced by different methods are presented in [Tab. 1.](#) Accordingly, the procedures are measured for their execution in various parameters. The results obtained have been presented in detail in this section.

The confusion matrix calculate based on True Positive (TP), False Negative (FP), True Negative (TN), and False Negative (FN).

$$Precision = \frac{TP}{Tp + FP} \quad (4.1)$$

$$Recall = \frac{TP}{Tp + FN} \quad (4.2)$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}. \quad (4.3)$$

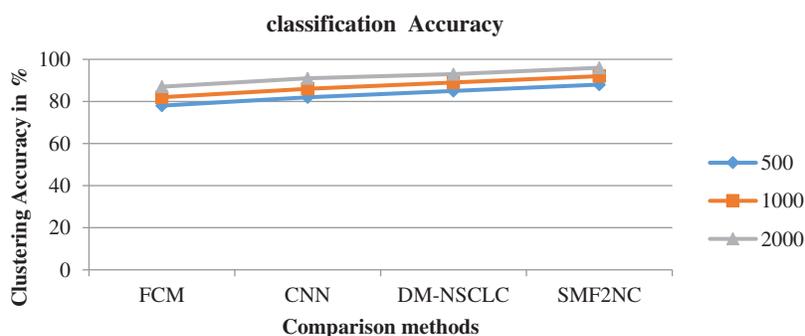
$$F1 \text{ score} = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (4.4)$$

The accuracy in classification from the big data toward disease prediction is presented in [Tab. 2,](#) where the proposed SMF2NC approach has produced higher clustering accuracy than other methods.

Table 2: Accuracy in classification

Classification accuracy (%)			
Methods/Number of records	500	1000	20000
FCM	78	82	85
CNN	82	84	86
DM-NSCLC	84	85	87
SMF2NC	85	87	88

The classification accuracy performance is produced by mean rate precision and recall rate compared with different methods, as presented in Fig. 3. The proposed SMF2NC approach has made higher clustering accuracy under various diseases considered.

**Figure 3:** Accuracy in classification

The performance in disease prediction and its accuracy have been measured by considering the different disease classes. The results obtained are presented in Tab. 3. The proposed SMF2NC approach has produced higher disease prediction accuracy than other methods.

Table 3: Analysis of Disease Prediction

Disease prediction accuracy (%)			
Methods/Number of records	500	1000	2000
FCM	65	72	77
CNN	67	76	81
DM-NSCLC	71	79	83
SMF2NC	78	82	85

The accuracy of disease prediction produced by different methods is measured and presented in Fig. 4. The proposed SMF2NC approach has made higher disease predictions than other approaches.

The ratio of false classification introduced by different methods is measured and presented in Tab. 4, where the proposed SMF2NC approach has produced fewer incorrect ratios than other methods.

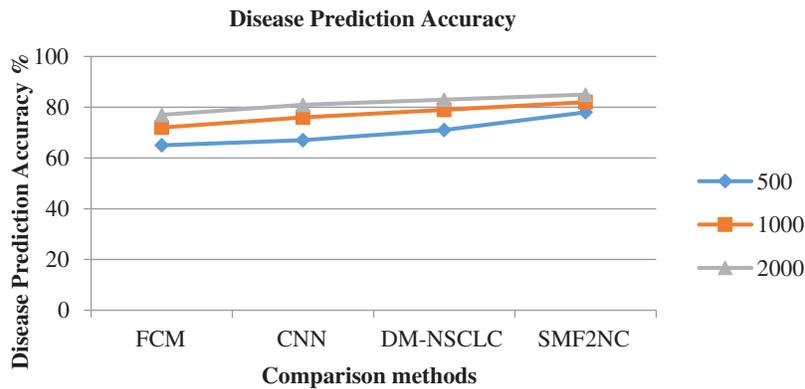


Figure 4: Analysis of disease prediction accuracy

Table 4: Analysis of false ratio

False classification ratio (%)			
Methods/Number of records	500	1000	2000
FCM	35	28	23
CNN	33	24	19
DM-NSCLC	29	21	17
SMF2NC	14	9	11

The accuracy of disease prediction produced by different methods is measured and presented in Fig. 5. The proposed SMF2NC approach has made higher disease predictions than other approaches in each class.

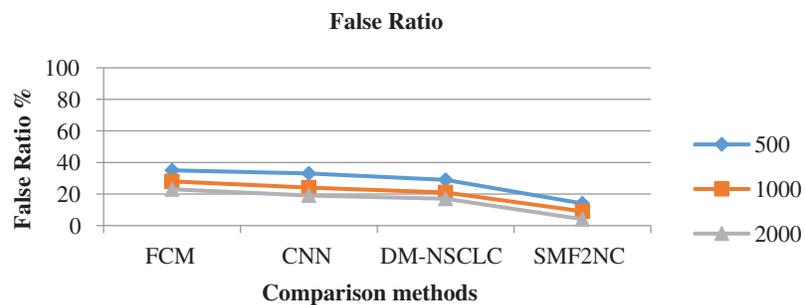


Figure 5: Analysis of false classification ratio

5 Conclusion

To conclude, cancer prediction reduces the dimensionality of the data analysis nature. It also provides its users with predictive results that give them the status that produces a premature influence rate for early diagnosis treatment. The Identifying Cancer Disease Based on Maximal Region-Based Candidate Feature Selection Using Soft max-Feed Forward Neural Classification for Early Risk Diagnosing algorithm provides higher performance based on the input provided by the feature-based classification approach. Suppose the system increases the disease prediction accuracy up to 94% well than other dissimilar methods. In that case, the percentage of people who have a portion who die from cancer will eventually decrease, even if their current state of mind is provided with their awareness.

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