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Hybrid Feature Selection Model for Computer Aided Diagnosis System in Lung Segmentation

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Abstract: The difficult lung disorder classification module in computer-aided diagnosis (CAD) is called feature selection. This is mostly caused by the growing quantity of features that must be accurately and thoroughly examined. When the input dataset or feature sets are large, classification becomes a very time-consuming operation. In order to improve the efficiency of the classification subsystem, feature selection often involves choosing the most appropriate, practical features and minimizing redundancy. Therefore, choosing the best features can effectively boost any CAD system's accuracy, decrease its time complexity, and enhance its performance. This study presents and evaluates a hybrid feature selection technique that combines Tabu Search with the multi-objective Particle Swarm Optimization algorithm(PSOA). Only a single bag of the ideal solution was offered by the single-objective feature selection algorithms. By generating a series of optimal solutions that trade many objectives against one another, this method overcame the drawback of the conventional single-objective algorithm. The use of multiple objectives made sure that the fewest features with the greatest impact on classification were chosen, and it enhanced accuracy while reducing error rates for the input dataset under consideration. Using a multi-objective feature with a local Tabu search allowed for the selection of fewer features while also reducing the amount of errors that occurred. After that, it was validated by being compared to well-known feature optimization methods such as PSO and Bee Colony to confirm that it was accurate. As a result, the proposed algorithm for feature selection resulted in improvements in terms of accuracy, specificity, sensitivity, recall, and error rate, as demonstrated by the numerical results.

Keywords: *CAD, Single objective feature selection algorithm, PSOA.*

1. Introduction

Based on the data contained in the medical images produced by the aforementioned imaging modalities, doctors examine the images to assess the problems and suggest appropriate treatment measures. The development of CAD systems has significantly reduced the amount of human work required for the diagnosis of problems in light of recent advancements in disciplines like artificial intelligence, machine learning, pattern recognition, medical imaging, radiography, computer hardware, and computer vision [1]. The CAD system examines medical photos as input, searches for any worrisome patterns, and alerts the doctors to the existence of ROI. Radiologists may notice a malignancy, a concussion, or a nerve blockage as the suspicious pattern or ROI. Furthermore, analyses such ROI and offers the doctors a second view based on precedent-setting circumstances [2].

A quantitative attribute utilized in the analysis and interpretation of images is called an image feature. A feature is a piece of information taken from the photos that describe a pattern or Region in terms of numerical values. Feature extraction is a sort of dimensionality reduction used in image processing that efficiently depicts interesting areas of an image as a feature vector from an initial collection of measured data [3]. Spatial features, transformation features, shape features, and texture features are several types of features that can be found in medical images. The issue of texture classification in image processing is resolved by combining feature detection, feature extraction, and feature selection. Gray level, amplitude, and spatial distribution are typically used to describe spatial features. Amplitude, which is used to distinguish bones

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from tissues in medical pictures, represents the body masses' absorption properties [4].

Feature extraction is used in medical imaging to distinguish between problematic and non-pathological lung areas. High-level and low-level features can both be found in an image. Dots, lines, and edges are used to represent low-level features, whereas shape and texture can be used to represent high-level features. The selection and extraction of features are crucial to the categorization system. Based on the geometric characteristic of ROI, shape features are extracted. Area, bounding box, convex area, eccentricity, equiv-diameter, extension, filled area, main axis length, minor axis length, orientation, perimeter, and solidity are some often retrieved form properties [5]. The pattern of an image is represented by the texture. Similar to shape-based features, texture-based features are frequently employed to classify the ROI in lung pictures. The related features of the Gray Level Co-occurrence Matrix (GLCM) indicate the texture of an image that may be retrieved from various image orientations. Energy, entropy, contrast, homogeneity, correlation, cluster prominence, cluster shadow, similarity, and dissimilarity are a few often utilized GCLM textures [6].

The difficult lung disorder classification module in computer-aided diagnosis (CAD) is called feature selection. This is mostly caused by the larger amount of features that must be accurately assessed. When the input dataset or feature sets are large, classification becomes a very time-consuming operation. Choosing the most relevant, useful characteristics while reducing redundancy is the basic goal of feature selection when it comes to enhancing the performance of the classification subsystem. Hence, choosing the best features can help any CAD system work better and boost accuracy while reducing time complexity [7].The labeled slice in the input dataset is stored against the retrieved features. If all of the retrieved features are provided to the classifier as input, classifying input slices can become a time-consuming and computationally intensive task. Only the most effective characteristics that have a significant impact on classification are chosen during the feature selection phase to boost classification accuracy by removing redundant and undesired features. Filter, Wrapper, and Hybrid techniques are used to classify features [8].

One of the main methods used by Computer-Aided Diagnosis (CAD) systems is medical picture classification. The CAD system uses classification to divide up the input image into various classes. Any CAD system's primary goal is to increase classification accuracy. Early classification techniques rely on geometrical traits, texture features, or a combination of the two. Disease-specific classification of medical images is done, and classification precision is determined by the classifier being utilized [9]. Every ROI in the classification system is evaluated against a threshold level. After the ROI reaches the threshold, it is divided into various classes based on the classifiers and training system employed. The classification techniques used for medical images can be divided into four categories: statistical techniques, rule-based techniques, neural network classifiers, and support vector machine (SVM) classifiers [10]. The statistical techniques include supervised techniques like Bayesian classifiers and supervised techniques like k-means and fuzzy clustering. A series of if-then rules are used by rule-based classifiers to determine classification. High-dimensional data can be classified accurately using a support vector machine [11].

What follows is the outline for the rest of the paper. The related work is briefly described in part 2, and the methodology and the theoretical foundations of the methods used are described in section 3. The simulation results and analysis are presented in section 4. For the chapter's final section, "key findings" we summarize the most important results.

2. Existing Work Done:

According to studies, it is very important to differentiate between the two forms of lung cancer, small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC), in order to improve the survival rate of patients. A few researchers have developed a diagnostic method for lung cancers. In addition, using feature extraction, feature selection, and prediction models, a diagnostic approach based on the structural and physicochemical characteristics of proteins implicated in either type of tumors that were deduced from the sequence was developed [12]. A total of 1497 protein properties were calculated, and 12 attribute weighting models identified their key components. In addition, machine learning models included an attribute weighting model that was applied to the original database as well as seven SVM models, three ANN models, and two NB models that were both freshly built. Using 10-fold cross and wrapper validation, the model's accuracy was determined. Eventually, it was discovered that applying the model to datasets produced by attribute weighting models rather than the original dataset improved the model's performance on lung cancer tumor type prediction [13].

The tumor region was segmented and the abnormalities in the MR brain image were identified using a unique segmentation and classification model, which was proposed by a few more researchers. To smooth the images and remove the noise components, the distribution-based adaptive median filtering technique was used during pre-processing. Also, the skull region was eliminated utilizing the clever method of adaptive threshold-based edge detection [14]. In the proposed work, the region of interest was predicted via segmentation using a novel multiangle cellular automata model. Novel texture extraction and better classification performance It was discovered from the study of the data that this model's performance had significantly improved. Dynamic angle projection patterns and priority particle cuckoo search optimization are the best feature selection techniques [15]. To categorize the anomalies of the segmented image, the Pointer Kernel Classifier (PKC) was employed using these optimized features as input to the Support Vector Machine (SVM). The sensitivity, specificity, accuracy, FPR, TPR, and ROC parameters of this work were compared to those of previous techniques. It was concluded that the PKC's performance was preferable to that of other methods [16].

Another team of researchers carried out a study that mainly concentrated on noise removal methods, the extraction of features from the grey-level co-occurrence matrix (GLCM), and the use of region-growing segmentation to separate the brain tumor from the input slices. After segmentation, morphological filtering was applied to improve the edges. The performance accuracy was trained and evaluated using the probabilistic neural network classifier [17]. The detailed coefficients from the LL and HL sub-bands were chosen from a dataset made up of MRI pictures that had been divided into five levels. These sub-bands were derived from input photos that had been wavelet decomposed. Using the grey-level co-occurrence matrix (GLCM) function, statistical textural parameters like energy, correlation, entropy, and homogeneity were retrieved. When training and evaluating the effectiveness of the PNN classifier, the textural features derived from various degrees of wavelet decomposition were taken into account [18]. The datasets that were used in this research were created by seasoned radiologists. They have taken into account 650 samples from the DICOM collection, of which 18 are normal brain tissues and the rest are infected tumor brain tissues. Their approach has outperformed other methods in the identification and classification of pictures into normal and malignant tumors from brain MR images [19].

According to the research that a group of academics provided, it is important to evaluate the relationships between radionics-based features found in CT scans and the histology of tumors, the existence of lymph nodes, and distant metastasis. The purpose of this effort was to evaluate the effectiveness of the ML classifiers. Using various feature categories, these classifiers were refined to detect metastatic and histopathological patterns [20]. They generated and employed a total of 51 histogram features, 53 first-order intensity features, and a total of 22 characteristics from COM2D and COM3D matrices. The ReliefF approach was used in conjunction with a ranking search algorithm to find relevant features. Measures of sensitivity and specificity, as well as the area under the receiver operating characteristic curve (ROC), were used to evaluate the categorization [21].The K-fold cross-validation approach was initially used to assess the classification. This model was believed to be able to supplement whole-body scans without them being necessary for the decision support systems based on metastatic prediction [22].

A hybrid strategy was put up by a group of researchers for the classification of brain tumors. This model combines the Discrete Wavelet Transform (DWT), which was used to extract features, the Principal Component Analysis (PCA), which was used to reduce the number of features, and the Support Vector Machine (SVM), which was used to classify MRI images [23]. The image underwent DWT processing in order to extract the characteristics. However, due to the availability of a large number of features, the Principal Component Analysis (PCA) technique had to be used to reduce the number of features [24]. For the purpose of categorizing the input photos as normal or abnormal, the Kernel SVM classifier was created. For the investigation, a dataset of MRI brain scans from 25 cases was acquired. Eventually, the analysis of the result revealed that the model had a linear accuracy of 90% [25].

3. Purpose of the Work

1) To create a feature selection algorithm that chooses the fewest features that have the most influence on the classification of the dataset.

4. The Proposed Work:

In this study, we present and evaluate a hybrid feature selection algorithm that combines the Particle Swarm Optimization technique with Tabu Search to achieve many goals simultaneously. The ideal solution was contained in a single box when using the feature selection methods that only considered one aim. By generating many optimal solutions that allow for the negotiation of competing goals, this method overcomes the shortcomings of the standard single-objective algorithm. For the input dataset taken into account, the multi objective approach ensured better accuracy with a reduced error rate by selecting the minimal features with strong impact on classification.

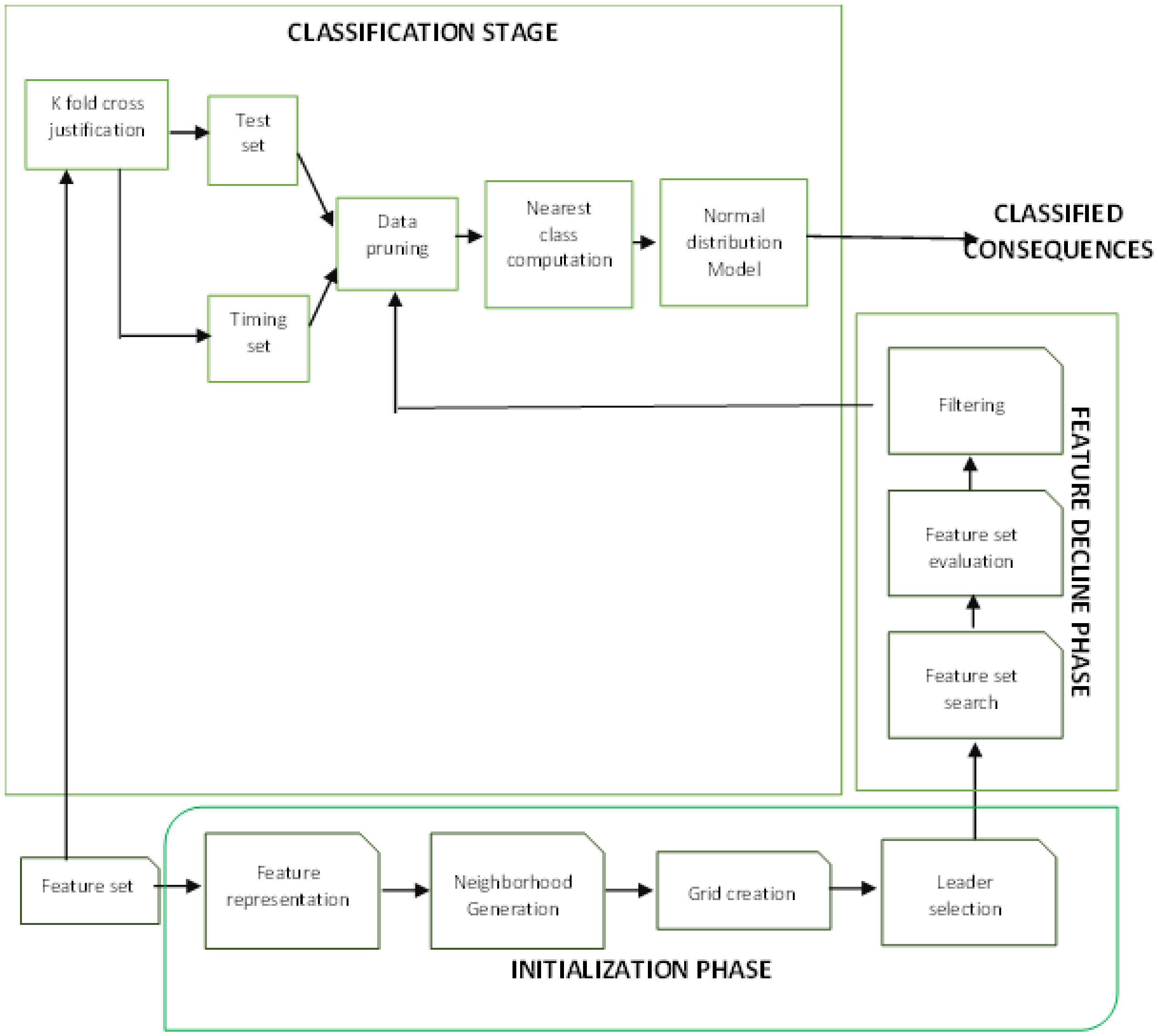

Fig 1: Outline of the existing MOPSO-TS feature selection.

In Figure 1, we can see the steps that make up the system structure of the multi-objective feature selection algorithm: initialization, feature reduction, and classification. The input to the initialization phase was features taken from the lung slices. During this first stage, features were represented, neighbourhoods were generated, grids were created, and a leader was chosen. Throughout the feature reduction process, irrelevant and unnecessary features were eliminated. An extensive amount of input data was classified in order to sort it into several categories. Cross-validation, data-pruning, nearest-class calculation, and a normal distribution model were all part of the classification step. Using a cross-validation method, the input data was separated into a training set and a testing set. In order to determine the class probability, data was pruned. The collection of learned features was compared to the real input features using nearest class calculation. In the end, a normal distribution model was utilized to sort the data.

Multi Objective Particle Swarm Optimization (MOPSO) was combined with Tabu Search to create the hybrid model utilized in the current MOPSO-TS feature selection (TS). Features were represented as a decimal value between 0 and 1 and are used as input to the algorithm after being extracted from CT slices. The multi-objective strategy ensured that the fewest possible features were chosen with the lowest possible error rate. In MOPSO, the swarm was given a random starting point, and its neighbours were calculated by adding and removing features at random. Once the swarm's speed of movement was calculated, they were all relocated to the new locations. The leader's neighbours were formed, and the resulting swarm was used as the basis for the following iteration.

The test data's classification was the goal of the classification process. The test data was categorized according to the normal distribution. The feature set's distribution around the mean was calculated using a normal distribution. To determine the class with the highest probability and classification of the test dataset, we calculated the mean value and deviation for each feature and performed a normal distribution. The following steps detail the categorization procedure, which took the nearest neighbour label as input.

1. The values of the training samples that are associated with each class were determined.
2. For each class of training samples, the mean of each feature was calculated, yielding a row vector of feature means.
3. We calculated the sample-wide standard deviation for each variable.
4. We will apply the conventional normal distribution to the test values to determine their distribution.
5. We used the class probabilities as a multiplier to the function's output values. A probability value for each category will be included in the test data.
6. The most probable category was selected as the one to use for the validation set.

5. Result and Discussion:

The feature selection algorithm's efficacy was measured with the help of the DICOM standard dataset. A multi-class classification was done, and each ailment was given a name. Out of a possible 40 features, an average of 8 were chosen. Particle swarm optimization and bee colony optimization were used as benchmarks for this study's comparisons. Accuracy, Sensitivity, Specificity, Precision, Error Rate, and F-Score are some of the often-utilized performance measures that were put to use in assessing the suggested task.

5.1. Accuracy:

It is a typical metric for classifying test results numerically. Increased precision indicates a more efficient system. In Figure II, we see a comparison of the current feature selection model's accuracy to that of certain popular feature selection algorithms. The proposed method improved classification accuracy despite having fewer features than MOPSO alone by virtue of the incorporation of local Tabu search.

$$\text{Accuracy} = \frac{TN+TP}{Total\ data\ Sample}\ X100 \quad (1)$$

5.2. Specificity:

Specificity was defined as the absence of incorrect data classification. True Negative Rate is another name for it (TNR). Figure II displays the specificity of the current method in comparison to commonly utilized methods.

$$\text{Specificity} = \frac{TN}{TN+FP}\ X100 \quad (2)$$

5.3. Precision:

The present work is believed to have the precision to provide useful outcomes. The value of precision indicates what fraction of valid affirmative identifications were made. Figure II displays the results of a comparison between the current model and the commonly used PSO and BCO techniques in terms of accuracy. The present system's accuracy was determined by

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

5.4. Sensitivity:

The accuracy with which the model places the test data into one of its classes constitutes the present method's sensitivity. How many true positives were successfully detected was the question it addressed. True Positive Rate is another name for it (TPR). Figure II displays the results of a comparison between the present strategy and the commonly adopted PSO and BCO approaches with regards to Recall.

$$Senstivity = \frac{TP}{TP+FN}\ X100 \quad (4)$$

5.5. Error rate: It represents how many instances the classifier algorithm got wrong. The comparison with existing approach is shown in Figure III.

$$\text{Error rate} = 1 - \text{Accuracy} \quad (5)$$

5.6. F Score:

The mean harmonic weight of the test's accuracy and reliability. It gives a more accurate assessment of the test's effectiveness. Figure IV displays the results of the F-score and error Rate calculations.

$$\text{F} - \text{Score} = \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}\ X\ 2 \quad (6)$$

Table I: The Evaluation matrices comparison of the proposed method with existing approach.

Algorithms	Accuracy	Specificity	Precision	Sensitivity
Bee Colony	73.14	87.51	64.48	82.49
PSO	78.86	75.38	67.12	87.49
Proposed work (MOPSO+Tabu Search)	91.68	93.47	77.59	88.42

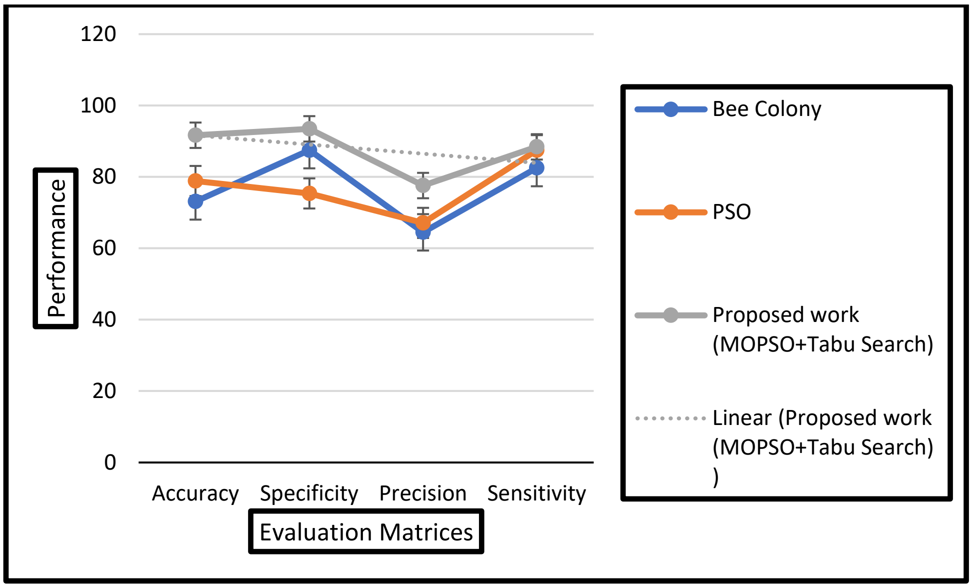

Fig II: The Evaluation matrices comparison of the proposed method with existing approach.

The current feature selection model's performance was compared to that of the Bee Colony and PSO algorithms. Using only 8 features, the current model outperformed all of those other algorithms in terms of performance metrics. The current technique performed well on the considered dataset since a smaller subset of features was chosen for sequential processing. The k-nearest neighbor approach was used to perform the classification, using class probabilities drawn from a normal distribution.

Table II: The Error Rate and F-Score comparison of the proposed method with existing approach.

Algorithms	Error Rate	F-Score
Bee Colony	0.31	73.09
PSO	0.26	75.48
Proposed work (MOPSO+Tabu Search)	0.08	93.14

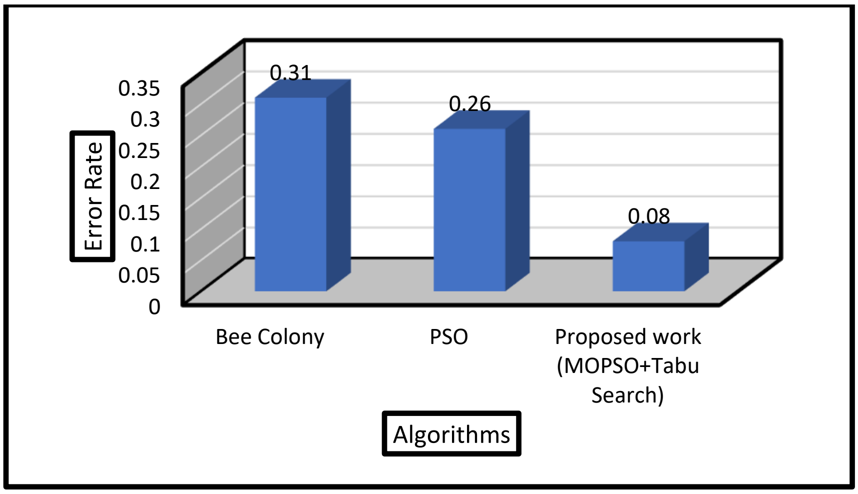

Fig III: Error Rate comparison of the proposed method with existing approach.

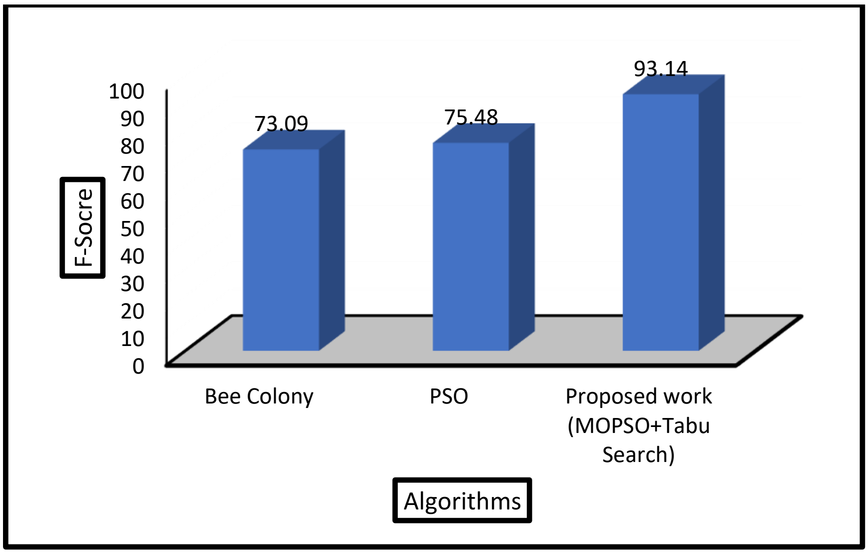

Fig IV: F-Score comparison of the proposed method with existing approach.

The Bee Colony Optimization (BCO) algorithm utilized a randomization mechanism for the beginning of the process. The algorithm consisted of a number of parameters, each of which needed to be adjusted to achieve the desired results. The method utilized a probabilistic strategy while conducting local search. With only 8 features, the current model outperformed all of the aforementioned algorithms in terms of performance metrics, demonstrating superior performance. The current technique was successful in its application to the dataset that was under consideration due to the sequential processing of data, which involved the selection of a smaller number of features.

6. Conclusion and Future Scope:

The lungs are one of the most important parts of the human body. Lung disorders account for the vast majority of global health problems. By drawing attention to any irregularities in a patient's anatomy, CAD systems help radiologists examine and interpret medical images.

To address the issue of CAD systems' inaccuracy, this study suggested a hybrid feature selection methodology. To get beyond the limitations of a single-objective feature-selection algorithm, this method use a multi-objective PSO algorithm in conjunction with Tabu search to produce many optimal solutions. In this job, we were provided a feature set that included both shape and texture characteristics. There were three main parts to the system's structure: initialization, feature reduction, and classification. To ensure that fewer features were chosen with a lower error rate, the multi-objective feature was combined with a local Tabu search. Then, it was compared to well-established feature optimization methods as PSO and Bee Colony to ensure its accuracy. Hence, the suggested feature selection algorithm enhanced accuracy, specificity, sensitivity, recall, and error rate, as shown by the numerical results.

Improvements to the sample line approach for extracting lung coordinates from different orientations are suggested to increase segmentation accuracy, as shown by the current work. It also hints that merging clinal test findings and state-of-the-art machine learning models will increase the CAD systems' accuracy even further.

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