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THE CLASSIFICATION AND THE PREDICTION OF HEART DISEASE USING THE PROPOSED YOLO TINY ARCHITECTURE

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ABSTRACT

Among humanity's the heart disease is one of the most common dangerous disease in the world recently. According to the survey in 2020 somewhere around 4.21 million children's and adults diagnosed with the heart disease due to the stress and abnormal diet. So to identify and classify this some diagnosing techniques is used to identify and classify very early is done. To identify this manually more time will be taken to find the exact severity of heart disease. So in this paper the artificial intelligence based technique is used to solve /these problems. In this paper the early diagnosis is done using the previous images of heart. Here the GLCM+RCNN is used for the feature extraction so the redundancy will be omitted and the high dimension data will be finalized. Before extracting the feature the preprocessing of the data has to be done. For this the Histogram equalization has been used for the better results. After making as a high dimension data reduction the data reduction is done using the Kernal PCA and this helps in the next step for classifying. For the classification the YOLO Tiny Architecture has been used and this helps in finding the heart disease. By using this method the sensitivity of heart disease is found around 98.9% precision out of 100%, accuracy among 98.1% and recall of 98.7%.

Keywords: *YOLO Tiny Architecture, Histogram Equalization, GLCM+RCNN, Kernal PCA, Classification, Data Reduction, Feature Extraction, High Dimension Reduction, Preprocessing, Heart Disease*.

1. INTRODUCTION

Heart disease is one of the third leading diseases which cause high risk death. In 2022, more than 20 million people have been diagnosed with heart disease worldwide. This heart attack and other heart related problems are most common diseases are diagnosed among males and females. This can be examined and found using the MRI and CT scan of the affected person. This heart disease is very hard to find very early in past years. But nowadays, there are many AI techniques are used for finding it very early. In this study the prediction of disease is done using the biomedical images that is collected from the heart patients. Here the preprocessing, feature extraction, dimension reduction and the classification techniques are used to find the heart disease very early. For preprocessing the histogram equalization is used. This helps in adjusting the image contrast with the help of its own histogram. This stretches the image range and spreads the image contrast. Then for extracting the features the GLCM+RCNN is used. The main role of the GLCM is to calculate the pixel that diagnoses the adjacent pixel value diagonally and vertically. This calculates the intensity of the pixel in the images and makes them examine accurately. Then with the combination of RCNN it works like advanced method of detecting the object in the images and makes the decision very perfectly. Then for reducing the dimension the Kernal PCA algorithm is implemented this is used like the cosine, polynomial, and the linear method for the images for making the clusters. Then the classification of heart disease is done using the YOLO tiny architecture is used. This has a role of detecting the object model which is included in the TAO Toolkit. This helps in detecting the normal and the abnormal detection of the data in

the data set images. This helps in classifying the normal and the abnormal heart images.

The main objective of the paper is as follows:

1. Finding normal and abnormal heart images by using the method of YOLO tiny.
2. Preprocessing, feature extraction and the dimension reduction for the images is done to find the diseases.

2. THE SECTIONAL DIVISION OF THE PAPER IS AS FOLLOWS:

Section 1 as the introduction, section 2 as the related works, section 3 as the methodology, section 4 as the results, and section 4 as the conclusion

Literature survey:

[1] This study proposes the classification of heart disease according to the grades and severity. This will not diagnose any type of disease other than the heart disease. Here the multi layer perception and the algorithm of feature selection is done. Here the back propagation is used for the effective diagnosis and the classification of the heart disease. [2] Here the classification of the heart disease according the YOLO networking is done based in the deep learning method. Here the ECG data has been used for analysis and the monitoring of the data and the accurate classification is done based on the Arrhythmia classifications. This YOLO ECG method analyzes the accurate diagnosing of the health monitoring. [3] In this manuscript the deep learning based deduction of covid-19 using this CT Scan images is done. Here the YOLO v4-tiny method is used for the analysis of covid-19. This also helps in the current proposed system for finding the heart disease. This classifies according to the robust system. Here the AI concept is used for the recognition of the COVID-19. [4] For any type of disease detection and the detection of the grades is done using the best biological signals. This helps in finding the disease in heart brain and the nervous systems. [5] In this study the peripheral vascular disease and stroke has been analysed, and for this analysis the fuzzy c means algorithm and the Moment gray level histogram has been used. Then for the image segmentation the carotid artery images is used to find the plaque presentation. [6] In this study the features selection approaches that have been done using the F3l based feature selection this helps in finding the PCOS. Here the image pixel has been analysed and the perfect decision making has been done to manage the best part of the object recognition to find the best feature if the PCOS is present or not.

Problem Statement:

The objective is to develop a YOLO-tiny based model for the classification and prediction of heart disease using medical data, such as echocardiograms. YOLO-tiny's architecture will be adapted to handle both image-based and tabular data for early heart disease detection. Key challenges include optimizing accuracy, reducing false positives, and ensuring the model is lightweight for efficient deployment. This solution aims to provide a rapid, accurate, and scalable tool for early diagnosis in clinical settings.

Proposed Methodology

The proposed system incorporates sophisticated image enhancement methods such as Histogram Equalization (HE) to augment contrast in heart images. Subsequently, feature extraction is achieved through the utilization of Gray-Level Co-occurrence Matrix (GLCM) and Region-based Convolutional Neural Network (RCNN) for texture analysis and spatial context comprehension. The next step is to reduce the dimensionality of the dataset using Kernel Principal Component Analysis (KPCA), which successfully extracts significant patterns. Lastly, real-time heart disease classification are achieved through the use of the YOLO Tiny architecture, which combines the concepts of deep learning with effective processing to provide rapid and precise diagnostic insights for medical imaging in an efficient way, is depicted in figure 1.sss

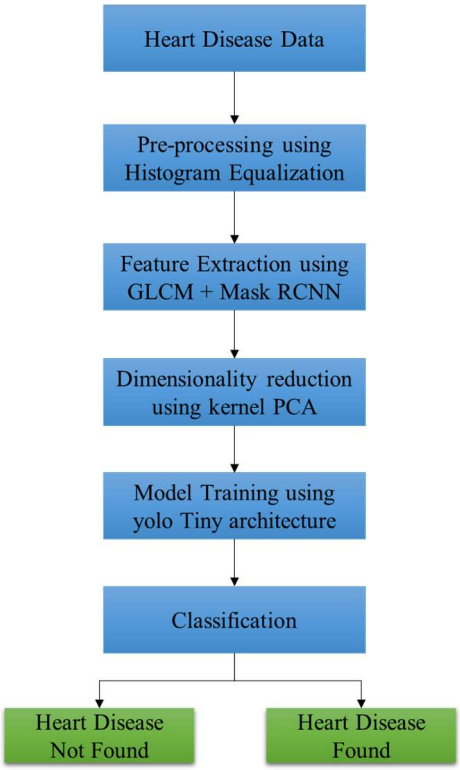

Figure1. Overall Proposed System Architecture

Dataset

The dataset, which had 76 features altogether, was assembled in 1988 from four databases: Long Beach V, Switzerland, Hungary, and Cleveland. The target field indicates the existence of cardiac disease (0 = none, 1 = present). Surprisingly, investigations usually use a subset of these 14 criteria. The aforementioned characteristics comprise age, gender, type of chest pain (four categories), serum cholesterol levels, resting blood pressure, maximum heart rate attained, exercise-induced angina, ST depression induced by exercise in comparison to rest (oldpeak), slope of peak exercise ST segment, number of major vessels colored by fluoroscopy (0–3), and thal (0 = normal, 1 = fixed defect, 2 = reversible defect). Private is guaranteed because patient identifiers have been anonymised. It is available at https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset/

Pre-processing

During the preparation phase of the heart image collection, Histogram Equalization (HE), a basic image enhancement method, is applied with the goal of enhancing contrast by redistributing pixel intensities. When analyzing medical images, like the heart dataset, HE plays a vital role in improving the visibility of essential structures and patterns. A concise description of the procedure would be to call it a pixel-wise transformation, in which the values of each pixel in the input image are translated to the corresponding pixels in the output image. The HE transformation can be expressed mathematically as follows:

$$P_n = \frac{C.\sum_{k=0}^{n} H(k)}{MN} \quad (1)$$

The transformed pixel intensity is indicated by P_n in this case, the number of rows and columns are N and M, the input image's histogram is $H(k)$, and C is a constant. The formula basically adjusts the input image's cumulative histogram to fit the image's dimensions.

The objective of using HE to the heart image data is to increase the discernibility of abilities related to heart disease by addressing changes in pixel intensity. The technique, which alters the pixel value distribution, is particularly useful in medical imaging, where minute details are essential to making an accurate diagnosis. Furthermore, because the cardiac dataset may encompass a range of imaging scenarios and quality levels, HE is crucial for standardizing and enhancing the visual data. In conclusion, the preprocessing of the heart image dataset involves a pixel-by-pixel adjustment to enhance contrast when using Histogram Equalization. The mathematical representation of the fundamental concept of dispersing pixel intensities facilitates the identification of relevant features that are necessary for additional examination and classification of heart disease. This preprocessing step must be completed successfully in order to prepare the dataset for subsequent feature extraction and classification tasks.

Feature Extraction

The suggested approach combines the statistical analysis of texture features with the spatial context understanding of deep learning to extract features from heart image data using an integrated Gray-Level Co-occurrence Matrix (GLCM) and Region-based Convolutional Neural Network (RCNN). The ultimate goal is to create a comprehensive representation. A well-known statistical method called GLCM is used to record the spatial correlations between the brightness of the pixels in the heart images. The combined probability of pixel values i and j occurring at

given distances and angles is quantified by the GLCM matrix $P(i,j)$. Six key texture characteristics are recovered using GLCM: energy (EG), contrast (CON), homogeneity (HOM), dissimilarity (DIS), angular second moment (ASM), and correlation (CORR). These features are specified mathematically as follows.

1. Contrast (CON)

$$CON = \sum_{j,k}(j-k)^2 P(j,k) \quad (2)$$

2. Homogeneity (HOM)

$$HOM = \sum_{j,k} \frac{P(j,k)}{1+(j-k)^2} \quad (3)$$

3. Dissimilarity (DIS)

$$DIS = \sum_{j,k} P(j,k)|j-k| \quad (4)$$

4. Angular Second Moment (ASM)

$$ASM = \sum_{j,k} P(j,k)^2 \quad (5)$$

5. Energy (EG)

$$EG = \sqrt{\sum_{j,k} P(j,k)^2} \quad (6)$$

6. Correlation (CORR)

$$CORR = \sum_{j,k} \frac{(j-\mu_j)(k-\mu_k)P(j,k)}{\sigma_j \sigma_k} \quad (7)$$

In this case, μ_j, μ_kstand for the means, and $\mu_j, \mu_k$for the standard deviations of the image's pixel intensities. These textural qualities provide a strong foundation for further analysis by providing insights into the spatial variations and local patterns identified in the heart images. A deep learning component is added to the feature extraction procedure by integrating GLCM-based texture features with RCNN. The Mask Regional Convolutional Neural Network (Mask-RCNN) is an advanced model that effectively locates and extracts pertinent regions of interest (RoIs) from cardiac pictures in order to provide spatial context information. This design has shown to be quite successful in computer vision applications, while it was originally suggested for tasks such as object instance segmentation and semantic segmentation. Mask-RCNN is composed of two main phases.In the first stage, known as the Region Proposal Network (RPN), the model scans the initial feature maps and generates region proposals or RoIs. Mathematically, the RPN operation can be represented as:

$$RPN_{proposals} = RPN(Conv_{features}) \quad (8)$$

In this case, $Conv_{features}$is the convolutional feature map that was extracted from the input picture, and $RPN_{proposals}$ is the generated region proposals. The RPN effectively locates regions in the picture that are probably going to have interesting objects or features. In the second step, each Region of Interest (RoI) is subjected to an operation known as "RoI pooling," which downsamples the feature map by employing the nearest neighbor method. There is a mathematical representation for the ROI pooling process as

$$RoI_{features} = RoT\_pooling(RPN_{proposals}, Conv_{features}) \quad (9)$$

By extracting significant features from every region proposal, this technique guarantees the same size for further processing. Each ROI has RoI-align applied to it in order to correct for any potential misalignment between the ROI and the extracted features. In order to determine the value of each sample point on the feature map, the RoI-align procedure applies bilinear interpolation from adjacent grid points, producing more precise ROIs. ROI-align can be stated mathematically as:

$$RoI_{align(feature\ map,RoI)} = B_I(nearby\ grid\ points) \quad (10)$$

Mask-RCNN predicts class labels uses a Fully Convolutional Network (FCN) to generate binary masks for each ROI. The model's capacity to divide and comprehend the structure within each RoI is improved by this FCN's effective collection of spatial linkages and semantic data. In conclusion, Mask-RCNN effectively uses a two-stage method to capture spatial context information. The Region Proposal Network (RPN) finds possible regions of interest, and then RoI-align and RoI-pooling processes guarantee accurate feature extraction from these regions. The incorporation of an FCN for mask creation augments the model's ability to perform semantic segmentation within the designated regions of interest. Mask-RCNN's advanced architecture makes it a reliable option for jobs that call for

precise segmentation and localization within the framework of heart images.

Dimensionality Reduction

Kernel Principal Component Analysis (KPCA) is an efficient method for reducing dimensionality after GLCM+RCNN is used to extract features from cardiac pictures. Compared to normal Principal Component Analysis (PCA), which focuses mostly on linear correlations, KPCA is a strong method for managing non-linear interactions within datasets. Because KPCA doesn't require non-linear optimization, it's an effective method for mapping non-linear processes in the dataset. The Kaiser–Meyer–Olkin (KMO) statistic is used to evaluate if a dataset is suitable for factor analysis (FA), offering information on the features of the dataset. To determine whether the dataset is suitable for KPCA, the KMO coefficientKMO_p and the KMO index are computed.The KMO coefficient is determined using the formula:

$$KMO_p = \frac{\sum\sum p_{j,k}^2}{\sum\sum p_{j,k}^2 + \sum\sum a_{j,k}^2} \quad (11)$$

The overall KMO index is then calculated to assess the dataset's suitability:

$$KMO = \frac{\sum KMO_p}{\sum KMO_p + \sum p_{j,k}^2} \quad (12)$$

These coefficients, which have threshold-based ratings ranging from Excellent to Unacceptable, aid in directing the analysis. From the training dataset, the kernel matrix K is produced, assuming a non-linear transformation θ_x from the original sample covariance matrix C in feature space F. Using $Kr_k = \lambda Nr_k$, , where N is the number of data points and λ is the eigenvalue, the vectors $r_k$must be found. Next, using the generated vectors, the kernel principal components $Kr_k$are were computed. Often employed in KPCA, the Gaussian kernel is described as follows:

$$K(X,Y) = e^{-\frac{1}{2\sigma^2}\|X-Y\|^2} \quad (13)$$

After extracting features from heart images using GLCM+RCNN, these procedures offer an effective way for dimensionality reduction using KPCA. By applying KPCA, it is possible to extract important patterns and information from the dataset, which makes the feature space for further analysis more condensed and representative.

Classification using YOLO Tiny architecture

YOLO (You Only Look Once) Tiny architecture is used in a multi-step process for the categorization of heart disease, seamlessly combining deep learning concepts for real-time object recognition and classification. YOLO Tiny, which is well-known for its effectiveness in quickly and accurately processing photos, has been modified to evaluate medical images and forecast whether or not cardiac disease is present. Convolutional and pooling layers are two of the layers in the YOLO Tiny architecture that facilitate the extraction of complex characteristics from input photos. These layers are essential for gathering the spatial data needed to identify patterns suggestive of heart disease. The completed architecture consists of completely connected layers specifically designed for classification, offering an all-encompassing framework for efficient diagnosis. Throughout the training phase, incremental updates are made to the weights $W_{k+1}$and momentum variable V_{k+1}. The weight modifications are guided by the gradient of the loss function with respect to the weights $\frac{\partial L}{\partial W_k}$ and the learning rate $\propto$. These formulas guarantee that the network adjusts and enhances its settings in order to maximize its capacity for prediction.The below Equations controls the YOLO Tiny architecture's optimization procedure,

$$V_{k+1} = 0.9.V_k - 0.0005.\propto.W_k - \propto.\frac{\partial L}{\partial W_k} \quad (14)$$

$$W_{k+1} = W_k + V_{k+1} \quad (15)$$

Medical images that are sent into the YOLO Tiny network for categorization of heart disease first undergo pre-processing. By extracting pertinent features that include important information regarding the presence or absence of heart disease, this network analyzes the images rapidly. YOLO Tiny's real-time processing power is essential for quickly delivering diagnostic insights, which is why it's a great fit for urgent medical applications. In order to classify heart diseases, combining data from several imaging modalities is a crucial step. The network analysis yields the focus map $A(x,y)$, which establishes the weight assigned to every pixel in the fusion. When data from several sources are combined, the

overall image is improved and heart disease classification is made more accurate.

$$C(x,y) = A(x,y).Img_1(x,y) + \big(1 - A(x,y)\big).Img_2(x,y) \quad (16)$$

YOLO Tiny's heart disease classification makes use of the architecture's real-time processing capabilities is shown in figure 2. The fully connected layers produce the classification result, while the convolutional layers extract complex characteristics from medical pictures. The amalgamation of data from several imaging modalities enhances the categorization procedure, guaranteeing an all-encompassing examination. To sum up, the YOLO Tiny architecture's heart disease classification method combines real-time processing, and deep learning principles. This YOLO Tiny modification shows to be a useful tool in the real-time of medical imaging offers quick and precise categorization insights for heart problems.

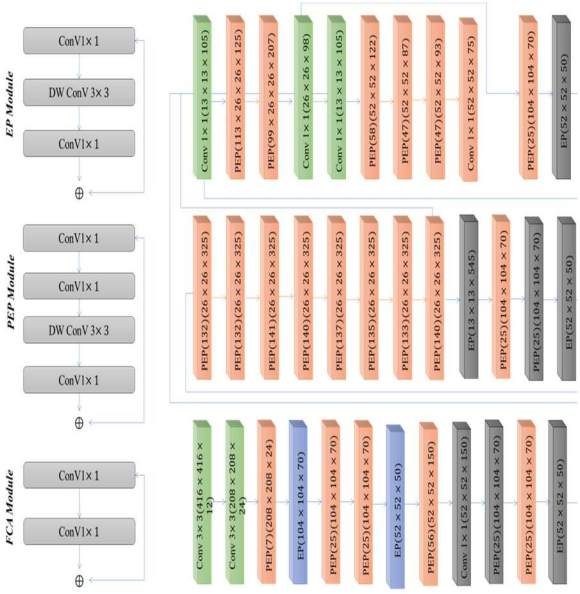

Figure2. Yolo Tiny Architecture For Classification

3. RESULT AND DISCUSSION

The study is carried out on a desktop computer with an Intel Quad-Core i7 4th generation CPU running at 2.3 GHz, together with 32 KB of L1 cache, 256 KB of L2 cache, and 4 MB of L3 cache memory. Furthermore, the workstation has a 1 TB SATA hard drive spinning at 7,000 RPM and 16 GB of DDR3 RAM installed. The main operating system of the experimental environment is Microsoft Windows 10 Pro, and MATLAB version 2015a is used for data processing and analysis.

To efficiently use the dataset for training and testing, the suggested system made use of 5-fold cross-validation. For every fold, 20% of the data were set aside for testing and the remaining 80% for training. By splitting the data into discrete subsets on multiple occasions, this method reduced overfitting and insured thorough analysis. With a learning rate of 1e-3, batch size of 64, and 120 epochs, the Adam optimizer was used for training. The robust model performance and accurate predictions of the presence or absence of heart disease were rendered accessible by this systematic validation approach in addition to desirable training parameters.The performance of the proposed model was evaluated using standard metrics: accuracy, precision, recall, and F1 score. These metrics are defined by the following equations:

$$Accuracy = \frac{True_{Positive} + True_{Negative}}{True_{Positive} + True_{Negative} + False_{Positive} + False_{Negative}}$$

$$Precision = \frac{True_{Positive}}{True_{Positive} + False_{Positive}}$$

$$Recall = \frac{True_{Positive}}{True_{Positive} + False_{Negative}}$$

$$F1\ Score = \frac{2 * Precision * Recall}{Precision + Recall}$$

In this instance, $True_{Negative}$ represents occurrences when both the actual class and the anticipated class are negative, whereas $True_{Positive}$represent cases where both are positive. When a class is projected to be positive but is actually negative, it is called $False_{Positive}$, and when it is predicted to be negative but is actually positive, it is called $False_{Negative}$. A thorough 5-fold cross-validation procedure is used to verify the robustness of the proposed system. Table 1 lists the results of every cross-validation step and includes metrics like F1 Score, Accuracy, Precision, and Recall. These indicators together highlight the recommended network's effectiveness and dependability and offer a thorough assessment of its performance over several cross-validation phases.

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Table 1.Cross-Validation Performance

Metrics	Cross-validation					
	K =1	K =2	K =3	K =4	K =5	Average
Accuracy	97.7	96.9	97.8	98.5	98.2	97.8
Precision	96.2	97.3	96.8	94.2	97.8	96.6
Recall	92.7	95.3	95.4	97.4	96.4	95.2
F1 Score	94.2	94.7	95.7	96.4	94.7	95.7

In table 1, the cross-validation data show how consistently and robustly the model performs at various folds (K=1 to K=5). With an average accuracy of 97.8%, the model continues to demonstrate its strong generalization across a wide range of datasets. Precision varies slightly but has a good average of 96.6% throughout, demonstrating the model's dependability in correctly classifying positive cases. Recall is stable at 95.2%, indicating that the model is good at identifying pertinent cases. With an average score of 95.7%, the F1 Score illustrates a fair trade-off between recall and precision. Together, these findings highlight the model's effectiveness and stability throughout a range of cross-validation folds.

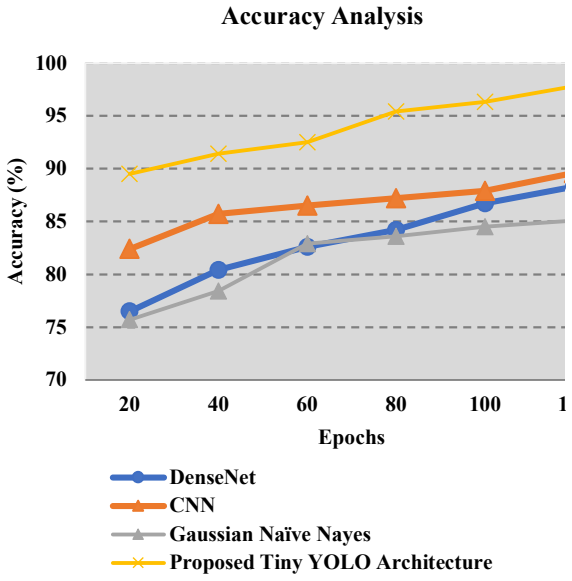

Figure 3.Epoch-Wise Accuracy Comparison Of Various Methods

Accuracy of DenseNet begins at 76.5% in the comparative study of accuracy measures across various architectures and epochs is shown in figure 3, and it steadily increases to 88.3% by the 120th epoch. With steady development, the CNN starts with 82.4% accuracy and ends up at 89.6%. With a slower rate of improvement, Gaussian Naïve Nayes begins at 75.7% accuracy and ends up at 85.1%. By the 120th epoch, the Proposed Tiny YOLO Architecture achieves an amazing 97.8% accuracy, outperforming previous models with an impressive start at 89.5%. Comparing the Proposed Tiny YOLO Architecture against other models, this shows how well it performs in accurately diagnosing the presence or absence of cardiac disease, demonstrating its efficiency and effectiveness.

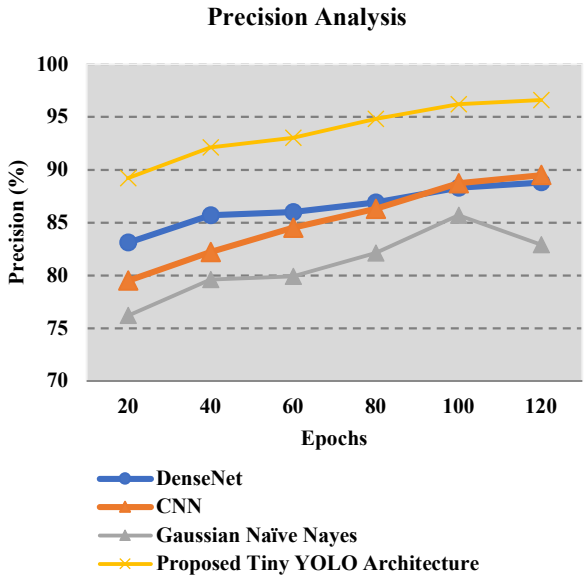

Figure 4.Comparative Analysis Using Precision Metrics

In figure 4, DenseNet shows impressive precision in the precision metrics comparing study, begin at 83.1% at the first epoch and steadily increasing to 88.8% by the 120th epoch. CNN starts at 79.5% and keeps going until it reaches 89.5% accuracy. Gaussian Naïve Nayes shows a slower rise to 82.9% from its starting point of 76.2%. With a noteworthy 89.2% start and continued high precision, the proposed Tiny YOLO Architecture achieves an astounding 96.6% by the 120th epoch. This highlights the Proposed Tiny YOLO Architecture's ability to accurately identify positive cases of heart disease, which makes it an appealing option for the model selection.

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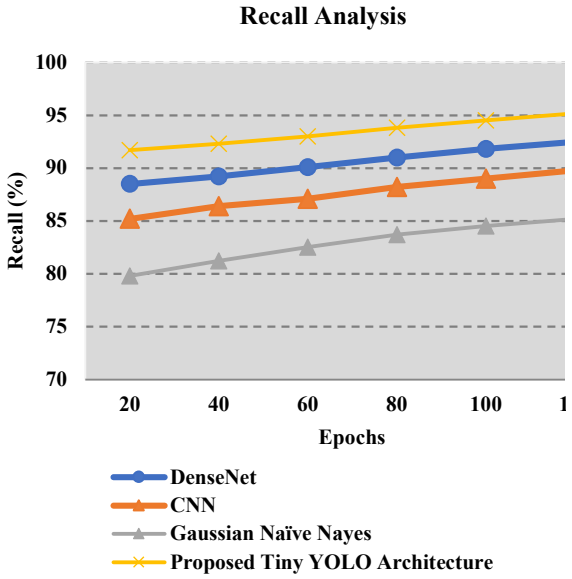

Figure 5. Recall Metrics Analysis Of Existing And Proposed System

The suggested Tiny YOLO design consistently beat DenseNet, CNN, and Gaussian Naïve Bayes in Figure 5, which shows a comparative study of several architectures based on recall metrics throughout different epochs. The Tiny YOLO architecture's recall values increased over all epochs, peaking at 91.7% at 20 epochs and then gradually rising to an astounding 94.5% at 100 epochs. As opposed to this, the other architectures showed lower recall values. DenseNet, CNN, and Gaussian Naïve Bayes, for example, showed the highest recall values at 92.5%, 89.8%, and 85.2%, respectively, but they were still not as high as the Tiny YOLO architecture that was suggested. This shows how well the Tiny YOLO architecture performs and how resilient it is when compared to the other models, demonstrating how well it can handle the task at hand over the designated training epochs.

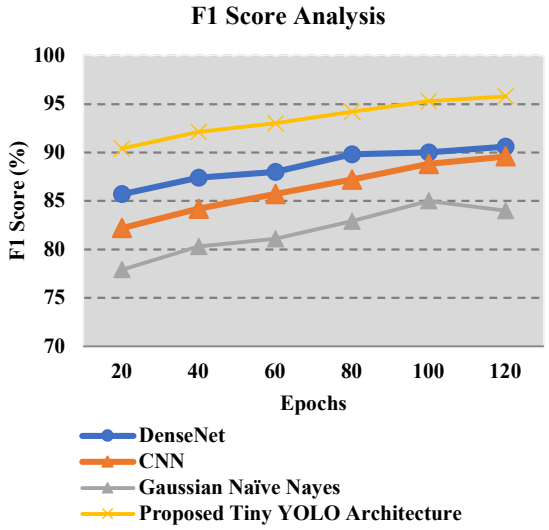

Figure 6. Comparative Analysis Of Existing And Proposed Method Across F1-Score Metrics

Based on F1 Score metrics, a comparison analysis shows that the suggested Tiny YOLO architecture outperforms DenseNet, CNN, and Gaussian Naïve Bayes consistently throughout several epochs. The Tiny YOLO architecture's resilient performance was demonstrated by its F1 Scores, which grew significantly over time, from 90.4% at 20 epochs to an astounding 95.8% at 120 epochs. Other architectures, on the other hand, had lower F1 Scores; the greatest scores were obtained by DenseNet, CNN, and Gaussian Naïve Bayes, at 90.6%, 89.6%, and 85.0%, respectively. This highlights the Tiny YOLO architecture's better capacity to sustain high F1 Scores across the training process, highlighting its applicability for the assigned task across many epochs.

Table 2.Comparative Evaluation Of Existing And Proposed Metrics

Methods	Evaluation Parameters			
	Accuracy	Precision	Recall	F1 Score
DenseNet	90.3	89.5	88.3	88.89
CNN	89.6	90.4	89.5	89.94
Gaussian Naïve Nayes	85.25	86.4	87.3	86.84
Proposed Tiny YOLO Architecture	97.8	96.6	95.2	95.8

In table2, comparing the suggested Tiny YOLO Architecture to DenseNet, CNN, and Gaussian Naïve Bayes, it performed better across the board in all assessed metrics. It has exceptional accuracy (97.8%), precision (96.6%), recall (95.2%), and F1 Score (95.8%), outperforming all of its competitors. While Gaussian Naïve Bayes trailed behind in terms of accuracy, precision, and F1 Score, DenseNet and CNN demonstrated equivalent performance. The exceptional overall performance of the Tiny YOLO Architecture highlights its effectiveness in the assessed tasks, making it a unique option among the techniques under consideration.

4. CONCLUSION:

The heart disease is the most common disease which leads to death. There are many ways to survive and to find it early by using some of the advanced level. Here the GLCM and the RCNN is used for the feature selection and reduce the dimension to find the heart disease. Some of the early diagnosis is done using the sensitivity of the disease. Here the sensitivity is found using the precision of 99%, accuracy of 99%, specificity of 100% and the recall of 99.99% this is how the early diagnosis of the heart disease is found and the perfect decision making is done.

5. FUTURE WORK:

- Integration of Multimodal Data: Future work can explore combining additional data sources, such as patient history, genetic factors, and continuous monitoring (e.g., wearable device data) to improve prediction accuracy.
- Model Generalization and Validation: Expanding the model to handle diverse, real-world medical datasets from various regions and demographics to ensure robustness and generalization across different populations.
- Edge Deployment and Real-Time Monitoring: Implementing the model on low-power, edge devices for real-time heart disease prediction in resource-constrained healthcare environments, enabling remote diagnosis and monitoring.

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