

Transfer Learning Techniques for Biomedical Image Analysis and Automated Disease Detection Systems

Vivek Sharma
System Analyst
MITS Deemed University
viveks@mitsgwalior.in

Corresponding Author: *Vivek Sharma (viveks@mitsgwalior.in)

Received: 10 July 2026 | Revised: 10 August, 2026 | Accepted: 11 September 2026

Abstract—Medical imaging is a valuable tool for disease detection, and advancements in diagnostic imaging technologies have enabled the early identification of various medical conditions. However, conventional manual image analysis approaches are time-consuming and often affected by intra- and inter-observer variability. These constraints can be circumvented through the use of automated medical image processing algorithms, which offer diagnostic solutions that are accurate, efficient, and consistent. This study presents a hybrid GRU+BiLSTM-based framework for biomedical image classification and automated disease detection using the NIH ChestX-ray14 dataset. The proposed approach incorporates image preprocessing techniques, including denoising, enhancement, augmentation, normalization, and data balancing, to improve image quality and model robustness. The suggested Hybrid GRU+BiLSTM model attained a 97.3% accuracy (ACC), 96.9% precision (PRE), 97.5% recall (REC), and 97.8% F1-score (F1), as shown in the experimental data. Results from comparisons with other methods demonstrate that the suggested model is superior than VGG16, ResNet50, DenseNet-121, and EfficientNet-B4. The results show that the suggested framework is useful for automated and dependable biomedical image-based disease identification.

Keywords—Image Classification, Machine Learning, Transfer Learning, Clinical Practice, Oral Disease, Medical Imaging, Reliability, Artificial Intelligence.

I. INTRODUCTION

Healthcare systems increasingly rely on accurate and timely diagnosis to improve patient outcomes. Medical imaging supports non-invasive disease detection, clinical decision-making, treatment planning, and continuous patient monitoring [1]. Medical imaging is an important component of modern healthcare systems, enabling non-invasive visualization of anatomical structures and supporting disease diagnosis, treatment planning, and patient monitoring [2][3]. Various imaging techniques, including X-ray, computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography (PET), are widely used for detecting diseases such as pneumonia, lung cancer, emphysema, and cardiovascular abnormalities [4]. Chest X-ray images provide valuable information about pulmonary

conditions, where abnormalities such as pneumonia and pulmonary nodules appear as visible patterns that require accurate interpretation for effective clinical decisions [5].

The increasing volume and complexity of medical images have created significant challenges for traditional manual analysis methods. Although expert interpretation plays a critical role in diagnosis, manual assessment is time-consuming and affected by intra- and inter-observer variability [6][7]. Automatic medical image analysis systems are necessary since human visual analysis has its limitations; these systems must be able to reliably and efficiently aid in diagnostics [8][9][10].

The possibility for biomedical image classification and illness identification to enhance healthcare outcomes has attracted substantial research interest. However, developing reliable automated systems remains challenging because medical image datasets are often limited in size, require expert annotations, and involve high data acquisition costs [11][12]. The use of transfer learning approaches, which apply the information from pretrained models to medical imaging applications with little labelled data, has emerged as an effective approach to address these restrictions [13].

Recent advancements in ML and DL have significantly enhanced biomedical image analysis and automated disease detection systems [14][15]. In several areas of healthcare, DL models can detect patterns of illness and automatically extract complicated picture attributes [16]. Transfer learning-based approaches further improve model performance by enhancing feature representation and reducing dependency on large annotated datasets, making them effective solutions for accurate and intelligent medical image analysis [17][18].

A. Motivation and Contribution

There is an urgent need for intelligent, automated technologies to aid medical personnel in making correct disease diagnoses due to the exponential expansion of medical imaging data. This time-consuming manual interpretation process is prone to inter-observer variability and can affect diagnostic reliability. Transfer learning and DL techniques have proven effective: they help extract complex image

features and boost classification performance using small medical datasets. Therefore, this study is motivated to develop an efficient transfer learning-based biomedical image analysis framework for automated disease detection and improved healthcare decision support. This research offers several key contributions as listed below:

- Developed an automated biomedical image analysis framework for accurate disease detection using advanced DL techniques.
- Used the NIH ChestX-ray14 dataset to test how well the new illness categorization method worked.
- Applied image preprocessing techniques, including denoising, enhancement, augmentation, normalization, and data balancing, to improve model robustness.
- suggested a hybrid GRU+BiLSTM model for precise biomedical image classification and efficient feature learning.
- Compared the proposed model performance with existing DL models to demonstrate its effectiveness.
- used common performance measurements, such as ACC, PRE, REC, F1, and confusion matrix analysis, to assess the suggested framework.

B. Justification and Novelty

The proposed study addresses the challenges of accurate biomedical image classification and automated disease detection by developing an efficient DL-based framework. The novelty is the use of an effective preprocessing approach combined with the hybrid of GRU+BiLSTM, to improve feature learning and classification ACC. This proposed approach would enhance diagnostic ACC, addressing challenges such as complex image patterns and sparse medical data. The framework provides an effective and high-tech method for automated illness diagnosis and smart healthcare systems.

C. Organization of the Paper

The paper is organized as follows: Section II reviews existing biomedical image analysis and automated disease detection studies. Section III presents the dataset, preprocessing, and model development. Section IV discusses experimental results and comparisons, while Section V concludes the paper and outlines future research directions.

II. LITERATURE REVIEW

A detailed review of existing research studies in Biomedical Image Analysis and Automated Disease Detection was carried out to identify recent advancements, existing challenges, and effective approaches for developing the proposed study.

S et al. (2026) handles the complexity and diversity of medical images, which are challenges for traditional ML algorithms. Using pretrained Mobile Net and VGG19 models, it suggests a Hybrid DL Framework that combines CNNs with transfer learning. Applied to real-world chest X-ray images, the framework achieved 92.98% ACC, improving deep feature extraction, adaptability, and classification performance [19].

Maheswari and Gomathi (2025) the development of DL algorithms for the diagnosis of ovarian cancer using ultrasound pictures. After CNNs extracted features, RF was utilized to categorization of benign and malignant ovarian tumors. Outperforming XGBoost's 89% performance, the CNN + RF model earned the greatest ACC of 94.07% [20].

Arivukarasi and Nithisha (2025) explains in broad strokes how to build datasets and collect data for lung disease detection systems that use DL. They perform efficient preprocessing and labeling operations, conduct a systematic analysis of various institutional and publicly available data, and handle important concerns such class imbalance, inter-site variance, and ethical considerations. performance evaluation reveals that developed data framework, which filters data, has high classification parameters with 0.985 AUC and 96.4% ACC when it classifies into various classes of lung diseases [21].

Saba et al. (2025) offers a DL system that can identify and categories VHD and other heart problems from ECG shots. In order to facilitate automated diagnosis, a bespoke CNN was programed using image and signal processing principles. Trained on 413 images and tested on 104 samples, the model achieved 94.23% ACC, 0.96 PRE, 0.91 REC, and 0.93 F1 [22].

Kalita and Borgohain (2024) Advanced feature engineering and ML support glaucoma diagnosis by identifying effective biomarkers. The study combines handcrafted structural and nonstructural features, including statistical, spectral, and geometric characteristics, to develop a reduced feature set. Evaluated on the SMDG-19 dataset, the Extra Tree Classifier achieved 85.42% ACC using tenfold cross-validation [23].

Mulla, Patel and Gupta (2023) presented a system for automatically detecting glaucoma in order to overcome the difficulties of both manual screening and early diagnosis. Fundus images are processed using CNN-based optic cup and disc segmentation, followed by ellipse fitting and major-axis ratio analysis. A SeResNet152 model is also trained to classify glaucoma and non-glaucoma fundus images, achieving Dice scores of 0.79 and 0.91 and an AUC of 0.936 [24].

Alslatie et al. (2022) introduced two types of abnormalities are diagnosed based on AI techniques. The two classes are atelectasis and cardiomegaly. The acquired images are segmented to localize the chest region and then enhanced using gray-level transformation methods. The enhanced images are passed to two pretrained CNNs: shuffle and mobile net. The transfer learning approach is utilized in this stage. The automated features are extracted from the last fully connected layer. Each CNN deserves to have the two most representative features for the two classes. These four features are passed to support the vector machine classifier. the test ACC was 96.7% [25].

Table I summarizes recent research studies in Biomedical Image Analysis and Automated Disease Detection, highlighting the proposed methodologies, datasets used, results achieved, and key limitations of existing approaches.

TABLE I. COMPARATIVE REVIEW OF EXISTING STUDIES ON BIOMEDICAL IMAGE CLASSIFICATION AND AUTOMATED DISEASE DIAGNOSIS

Author	Proposed Work	Dataset	Findings	Limitations & Future Work
S et al. (2026)	Hybrid CNN with transfer learning using MobileNet and VGG19 for chest X-ray classification.	Chest X-ray images	92.98% accuracy	Limited to chest X-rays; broader disease and modality validation is required.
Maheswari and Gomathi (2025)	CNN feature extraction with Random Forest for ovarian cancer detection.	Ovarian ultrasound images	94.07% accuracy	Limited transfer-learning integration; larger and diverse datasets are needed.
Arivukarasi and Nithisha (2025)	Preprocessing and dataset framework for deep-learning-based lung disease detection.	Institutional and public lung datasets	96.4% accuracy, 0.985 AUC	Dataset variability and class imbalance remain challenging; stronger generalization is needed.
Saba et al. (2025)	Custom CNN with image and signal processing for cardiac abnormality detection.	517 ECG images	94.23% accuracy, 0.93 F1-score	Relatively limited dataset; pretrained and transfer-learning models could improve robustness.
Kalita and Borgohain (2024)	Combined structural and nonstructural features for glaucoma diagnosis.	SMDG-19 glaucoma dataset	85.42% accuracy	Relies on handcrafted features; deep transfer-learning approaches remain unexplored.
Mulla, Patel and Gupta (2023)	CNN-based segmentation and SeResNet152 for glaucoma classification.	183 retinal fundus images	0.936 AUC; Dice scores of 0.79 and 0.91	Limited validation data; broader datasets and multimodal evaluation are required.
Alslatie et al. (2022)	Transfer learning with pretrained ShuffleNet and MobileNet combined with SVM.	Chest X-ray images	96.7% accuracy	Limited to two abnormalities; extension to multiple diseases and imaging modalities is needed.

Research gaps: Previous research has shown that DL and ML are efficient tools for analyzing biomedical images and detecting diseases; nevertheless, there are still many open questions in this area. Most current methods rely on large annotated data sets, demand substantial computing resources and have limited capacity to transfer knowledge learned across a variety of medical imaging scenarios. The conventional models tend to have problems dealing with complex image patterns, class imbalance, and the scarcity of labeled clinical image databases. A strong and effective framework that makes use of cutting-edge learning techniques like hybrid DL models and transfer learning is thus necessary to enhance the performance of automated biomedical image classification and disease detection systems.

III. RESEARCH METHODOLOGY

The suggested approach employs the NIH ChestX-ray14 dataset for automated disease detection and biomedical image analysis. To achieve this, it employs a series of image preprocessing techniques, including normalization, enhancement, augmentation, denoising, and enhancement, to improve the image quality and strengthen the model. For efficient feature learning and disease classification, the prepared dataset is utilized to construct the hybrid GRU+BiLSTM model, which is then split into training, validation, and testing subsets. Fig. 1 shows the whole workflow of the proposed biomedical image analysis and illness detection system, and the performance of the framework is assessed using ACC, PRE, REC, F1, and confusion matrix analysis.

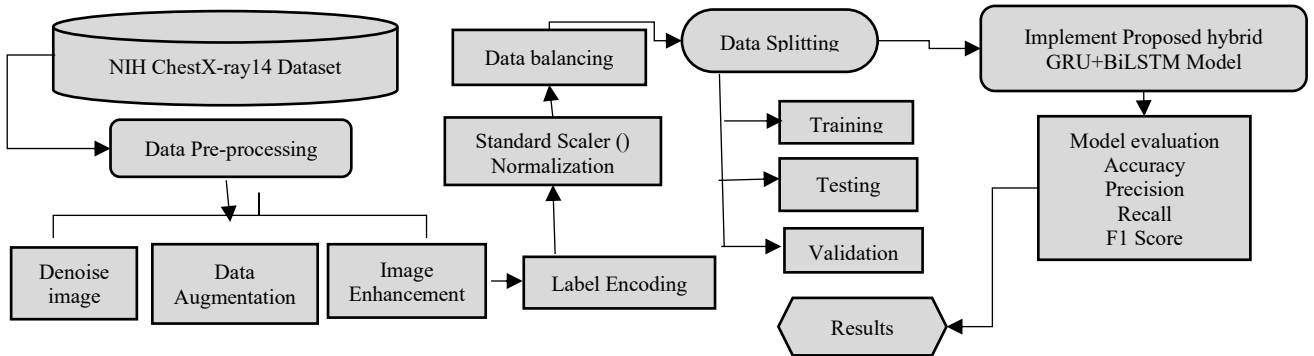


Fig. 1. Systematic Workflow of the Proposed Hybrid GRU+BiLstm Model for Biomedical Image Analysis and Disease Detection

The proposed methodology is described in depth in the next section:

A. Dataset Description and Analysis

The data used in this study comes from the NIH ChestX-ray14 dataset, which includes information on 30,805 distinct patients across 14 illness categories and a normalcy class. Emphysema, inflammation, mass, pneumothorax, atelectasis, oedema, effusion, hernia, cardiomegaly, pulmonary fibrosis, nodule, and consolidation are the categories of this disease. Here are some data visualizations:

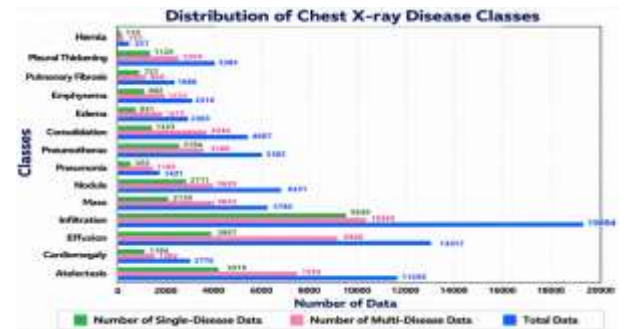


Fig. 2. Distribution of Chest X-Ray Disease Classes

The Fig. 2 displays the distribution of chest X-ray images according to illness classes, along with the total number of images in each class (single-disease, multi-disease, and total) for each class of disease. It illustrates the dataset's class imbalance and gives a rundown of the data available for training and testing the suggested classification model.



Fig. 3. Chest X-Ray Disease Samples

In this Fig. 3 chest X-ray images have been presented as representative examples of various thoracic conditions such as consolidation, cardiomegaly, pneumothorax, effusion, atelectasis, emphysema, infiltration, pleural thickening, nodules, and masses. These labeled samples illustrate the variety of disease patterns in the dataset and show the great variety of abnormalities to support medical image classification and training of disease models.

B. Data Pre-Processing

The NIH ChestX-ray14 dataset was utilized for data preparation, involving data integration, cleaning, and preprocessing operations. The preprocessing pipeline included image denoising, image enhancement, data augmentation, label encoding, data labeling, and normalization to improve image quality and model performance. The major preprocessing steps are summarized as follows:

- **Denoise image:** Denoising images is a preprocessing method that keeps texture and structure information intact while removing noise and artefacts. Because of this, following image analysis and DL models are more accurate and dependable, and the quality of the images is improved.

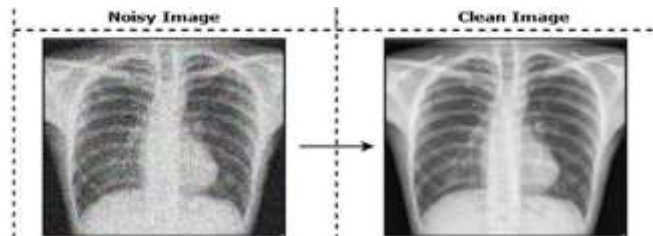


Fig. 4. Image Denoising Process for Chest X-Ray Images

The Fig. 4 illustrates the transformation of a noisy chest X-ray image into a clean image through denoising techniques, improving image quality and enhancing important features for accurate biomedical image analysis.

- **Image Enhancement:** Image enhancement improves the visual quality of an image by adjusting contrast, brightness, sharpness, and texture to highlight important details. It enhances feature visibility, making images more suitable for accurate analysis, segmentation, and DL-based classification tasks.
- **Data Augmentation:** The training dataset was enhanced via data augmentation to make it more diverse and balanced by creating altered versions of the original photos through random cropping, mirroring, horizontal flipping, zooming, and rotating. Improved classification ACC, increased model robustness, and decreased overfitting risk were all results of these augmentation strategies, which exposed the network to more image variants.
- **Label Encoding:** Label encoding converts categorical class labels into unique numerical values, enabling ML and DL models to process them efficiently.

C. StandardScaler() Normalization

Given the different scales of each descriptor, the dataset was standardized using the StandardScaler () method to transform the data so that the mean of the resulting distribution is zero and the standard deviation is one. This transformation is achieved by subtracting the mean value of each observation and dividing by the standard deviation, as shown in Equation (1):

$$z = \frac{x - \mu}{\sigma} \quad (1)$$

where z is the transformed value of the feature, x is the original value of each descriptor, μ is the mean, and σ is the standard deviation of the feature in the dataset.

D. Data Balancing

Data balancing is performed to address class imbalance by ensuring that all classes are adequately represented during model training. Techniques such as oversampling, under sampling, or synthetic sample generation improve the model's ability to learn minority class patterns. This process enhances classification ACC, reduces prediction bias, and improves the overall robustness of the trained model.

E. Data Splitting

Three subsets of the dataset are created: 20% for testing, 20% for validation, and 60% for training. This split ensures effective model learning, hyperparameter tuning, and unbiased performance evaluation.

F. Proposed Hybrid Gated Recurrent Unit (GRU) and Bidirectional Long Short-Term Memory (Bilstm) (Hybrid GRU+Bilstm) Model

In this work, a DL-based hybrid GRU and BiLSTM model is proposed for effective biomedical image analysis and automated disease detection. The proposed hybrid model combines the strengths of GRU and BiLSTM networks to effectively capture both short-term and long-term dependencies in sequential data. BiLSTM improves context awareness and prediction ACC by bidirectional processing of the sequence, while GRUs are computationally economical and aid in reducing the vanishing gradient problem. This hybrid approach is particularly suitable for time-series forecasting and sequence modeling tasks where capturing temporal patterns is critical. The GRU updates are defined as Equation (2) to (5):

$$z_t = \sigma(W_z x_t + U_z h_{t-1} + b_z) \quad (2)$$

$$r_t = \sigma(W_r x_t + U_r h_{t-1} + b_r) \quad (3)$$

$$\bar{h}_t = \tanh(W_h x_t + U_h (r_t \odot h_{t-1}) + b_h) \quad (4)$$

$$h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \bar{h}_t \quad (5)$$

The hybrid GRU+BiLSTM model effectively balances computational efficiency and predictive power, making it a robust choice for sequential data tasks. The GRU component accelerates learning while maintaining essential memory, and the BiLSTM component captures bidirectional dependencies, resulting in improved forecasting ACC. Experimental results demonstrate that this architecture outperforms individual GRU or LSTM models in terms of error reduction and convergence speed. The proposed Hybrid GRU+BiLSTM model was implemented with optimized hyperparameters, including a learning rate of 0.001, batch size of 32, optimizer as Adam, dropout rate of 0.5, binary cross-entropy loss function, and 300 training epochs. The model was trained using these configurations to achieve effective feature learning, improved convergence, and robust biomedical image classification performance. The selected hyperparameter settings enhanced the model's ability to capture complex image patterns and improve automated disease detection ACC.

G. Evaluation Metrics

Different assessment criteria were used to test the performance of the proposed model. A confusion matrix was generated to analyze the classification outcomes by representing correct and incorrect predictions for each class. The matrix provided the values of True Positives (TP), False Positives (FP), True Negatives (TN), and False Negatives (FN), which were used to compute key evaluation metrics such as ACC, PRE, REC, and F1 as described below:

Accuracy: The ratio of the number of input samples to the total number of instances that the trained model properly identified is called the ACC metric. It is calculated as shown in Equation (6)

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \quad (6)$$

Precision: A model's ACC is defined as the percentage of positive occurrences that it properly predicts relative to the total number of positive occurrences. This metric, which can be represented as Equation (7), measures how well the classifier can detect positive classifications

$$Precision = \frac{TP}{TP+FP} \quad (7)$$

Recall: A percentage of true positives anticipated to exist in the dataset as a whole is shown by this statistic. Evaluating the model's ACC in detecting positive cases can be done mathematically using Equation (8)

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

F1 score: The F1 is the harmonic mean of PRE and REC, providing a balanced evaluation of both metrics. It ranges between 0 and 1, where a higher value indicates better classification performance, and it is mathematically expressed as Equation (9)

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (9)$$

IV. RESULTS AND DISCUSSION

In this section, the experimental framework and the performance evaluation of the proposed hybrid GRU+BiLSTM model for biomedical image classification and automated disease detection are described. These tests were conducted on the Intel i9-13900K processor, 64 GB of DDR5 memory, and NVIDIA RTX 4090 graphics card with 24 GB of VRAM, running on Windows 11 Pro operating system. The model was built with the libraries: Pandas, NumPy, Matplotlib, Seaborn, and Scikit-learn, for data processing, visualization, and performance analysis, respectively, in Python. Training and testing of the proposed model were conducted using the NIH ChestX-ray14 dataset, which had undergone suitable preprocessing procedures. The model's efficacy was assessed with essential classification measures, such as F1, REC, ACC, and PRE. Reliable classification performance was indicated by the suggested model's 97.3% ACC, as shown in Table II. Furthermore, the PRE of 96.9%, REC of 97.5%, and F1 of 97.8% demonstrate the model's effectiveness in accurately identifying disease patterns from biomedical images.

TABLE II. PERFORMANCE ASSESSMENT OF THE PROPOSED MODEL FOR BIOMEDICAL IMAGE CLASSIFICATION AND AUTOMATED DISEASE DETECTION

Matrix	Proposed hybrid GRU+BiLSTM model
Accuracy	97.3
Precision	96.9
Recall	97.5
F1-score	97.8

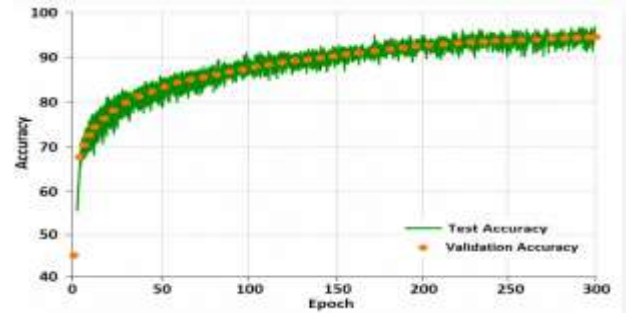


Fig. 5. Training and Validation Accuracy Curve of the Proposed Model

The ACC curves for the training and validation sets, spanning 300 epochs, are displayed in Fig. 5 for the proposed model. Both curves exhibit a consistent upward trend throughout the training process, indicating continuous learning and gradual performance improvement with each epoch. The training and validation curves being so closely aligned shows that the model is convergent, learning well, and has strong generalizability with no overfitting.

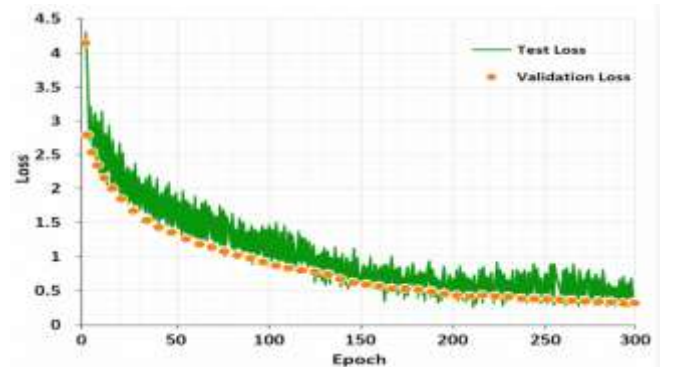


Fig. 6. Training and Validation Loss Curve of the Proposed Model

The suggested model's loss curves for training and validation across 300 epochs are shown in Fig. 6. A steady decline in both loss curves with increasing epoch count indicates efficient learning and ongoing optimization throughout training. A stable model with strong generalizability and low overfitting is demonstrated by the training and validation loss curves closely converging.

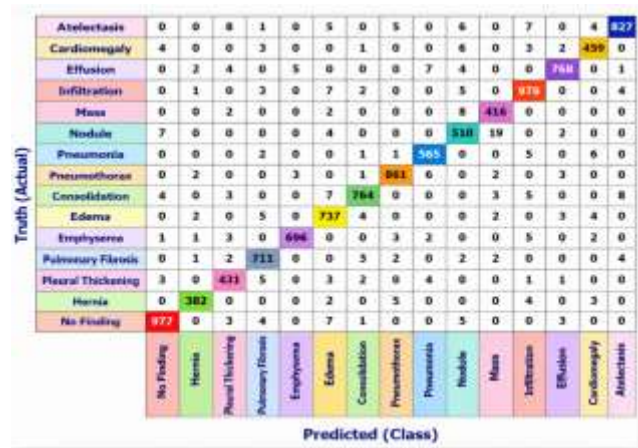


Fig. 7. Confusion Matrix for the Proposed Model

The confusion matrix shown in Fig. 7 compares the predicted classes with the actual classes for the proposed chest X-ray disease classification model for all the classes. The highlighted diagonal values indicate correct classifications, while the off-diagonal entries represent misclassified samples, providing a comprehensive evaluation of the model's classification performance.

A. Comparative Analysis

The effectiveness of the proposed model is assessed by comparing its performance with current models, which is provided in Table III. The suggested hybrid GRU+BiLSTM model demonstrated its strong classification capabilities with a 97.3% ACC, 96.9% PRE, 97.5% REC, and 97.8% F1. Compared with existing models, including VGG16, ResNet50, DenseNet-121, and EfficientNet-B4, the proposed model showed improved performance and a better balance between PRE and REC. These findings validate the effectiveness, reliability, and robustness of the proposed hybrid GRU+BiLSTM model for biomedical image classification and automated disease detection.

TABLE III. PERFORMANCE COMPARISON OF EXISTING MACHINE LEARNING AND DEEP LEARNING MODELS FOR BIOMEDICAL IMAGE CLASSIFICATION AND DISEASE DETECTION

Model	Accuracy	Precision	Recall	F1-score
VGG16 [26]	72	74.32	75.41	73.14
ResNet50 [27]	75.2	57.91	67.83	62.47
DenseNet-121[28]	80.48	83	78	80
EfficientNet-B4 [29]	96.72	92.30	87.14	89.67
Proposed Hybrid GRU+BiLSTM Model	97.3	96.9	97.5	97.8

The proposed hybrid GRU+BiLSTM model achieved an ACC of 97.3%, demonstrating its high effectiveness in biomedical image classification and automated disease detection. This superior ACC indicates that the model can efficiently learn complex image patterns and provide more reliable predictions compared with conventional approaches. The improved ACC highlights the capability of the proposed model to enhance diagnostic performance and support accurate disease identification from biomedical images.

V. CONCLUSION AND FUTURE STUDY

Biomedical image analysis has become an important research area in healthcare, enabling early disease detection, accurate diagnosis, and improved patient care. This paper presents a system for automated biomedical image classification and disease detection that combines GRU with BiLSTM. The approach makes use of DL techniques and good image preprocessing to extract useful features from medical pictures. An evaluation and comparison with existing DL techniques were conducted to assess the performance of the proposed model. The findings show that the suggested Hybrid GRU+BiLSTM model outperformed VGG16 (72%), ResNet50 (75.2%), DenseNet-121 (80.48%), and EfficientNet-B4 (96.72%). Its ACC reached 97.3%. The improved classification capability of the proposed model highlights its effectiveness in learning complex biomedical image patterns and enhancing diagnostic performance. Overall, the proposed framework provides a reliable, accurate, and efficient approach for automated disease detection and can support future intelligent healthcare applications.

The availability of annotated medical picture datasets and the processing requirements of DL-based models are two limitations of the proposed study. Future works will address the extension of the framework with the use of larger multi-modal datasets, efficiency of the model, and generalization for clinical settings in practice.

- **Funding:** This research received no external funding.
- **Institutional Review Board Statement:** Not applicable.
- **Informed Consent Statement:** Not applicable.
- **Data Availability Statement:** The data supporting the findings of this study are available from the corresponding author upon reasonable request.
- **Conflicts of Interest:** The author declares no conflict of interest.

How to cite this article:

V. Sharma, "Transfer Learning Techniques for Biomedical Image Analysis and Automated Disease Detection Systems," *Journal of Global Research in Multidisciplinary Studies*, vol. 1, no. 3, pp. 09–15, Jul.–Sep. 2026., Doi XXX

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