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Article

A Hybrid Deep Learning Framework for Multi-Disease Detection in Biomedical Images

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Abstract: Biomedical image analysis has become an important tool in the diagnosis and treatment planning for a number of diseases in the early stages. Manual image interpretation of biomedical images, however, is time-consuming, requires expertise, and introduce human errors, particularly if there are multiple different diseases and the visual patterns are similar. Traditional machine learning approaches rely on features handcrafted by experts and are not successful in learning intricate structures in medical images relevant to disease. While deep learning models like Convolutional Neural Networks have recently helped with biomedical image detection and classification, the majority of current methods are primarily applicable for detecting single disease and lack capability of modeling inter-dependencies between the abnormalities in image regions. For this reason, this work introduces a hybrid model using a combination of CNN, GNN and RL based networks for the multi-disease detection task in biomedical images. It is designed as a cascading network where CNN networks are used to extract the deep spatial features from the input medical images, the Graph Neural Network learns the relationship among the disease-relevant regions and the Reinforcement Learning determines the informative features and optimizes the classification decision. Experimental evaluation is carried out using the MedMNIST+ benchmark dataset, where multiple biomedical image categories are embraced, encompassing chest X-ray, dermatoscopic images, retinal OCT, retinal fundus and breast ultrasound images. The accuracy and F1 score achieved by the proposed CNN-GNN-RL framework were found to be 96.3% and 95.4% respectively, which improved significantly compared to the precision of the CNN, ResNet50, DenseNet121, CNN-RL and CNN-GNN models. The results show that the proposed method that integrates spatial feature extraction, graph-based relational learning and reinforcement learning based optimization can achieve a higher classification accuracy, lower misclassification rate and stronger robustness of the model compared with the other three methods. Thus, the suggested framework might be helpful to improve the intelligence computer-aided diagnosis system for the accurate and automated detection and diagnosis of multiple diseases in biomedical images.

Keywords: Biomedical Images, Multi-Disease Detection, Convolutional Neural Network, Graph Neural Network, Reinforcement Learning.

1. Introduction

Biomedical image analysis has become a vital part of contemporary health-care services, as accessing medical images like X-rays, computed tomography (CT) scans, magnetic resonance imaging (MRI) scans, ultrasound images, retinal images, and histopathology images are essential for disease diagnosis, treatment planning, and patient monitoring (Ahmed et al., 2022). These images, if analyzed correctly, can help healthcare workers catch any abnormalities early and treat them accordingly. But, in biomedical Imaging field manual analysis is tedious, complicated and experience-based process of doctors, radiologists and pathologists. Some diseases may have similar visual patterns in many cases, making diagnosis more challenging and potential for human error greater. Thus, increasingly there is a need for intelligent computer-aided diagnosis (CAD) systems that can assist medical professionals in rapid, reliable, and precise diagnosis of diseases (Asnaoui et al., 2021). Biomedical image analysis had been popularly performed using traditional image processing and machine learning methods in the past few years. Generally speaking, these methods were of three types, pre-processing the image, segmentation, extracting handcrafted features, selecting features, and classification (Ashhar et al., 2021). They used facet detection, thresholding, location growing, texture analysis, histogram-based techniques etc. as ordinary methods, Gray Level Co-occurrence Matrix, Local Binary Patterns, Principal Component Analysis, Support Vector Machine, K-Nearest

Neighbor, Decision Tree, Random Forest and Artificial Neural Networks. Although these methods provided useful results in some medical imaging applications, their performance mainly depended on manually designed features and expert knowledge (Archana et al., 2025). Complex disease patterns, large variations in images, noisy images, and high dimensional biomedical data were among the issues that were challenging for traditional methods. Consequently, their performance in multi-disease detection tasks lacked in level of accuracy, lack of generalization, and lacked level of robustness. Deep learning is one of the biggest techniques to be applied to medical image analysis in recent years. However, Deep learning models are particularly useful as they can automatically learn important features from Biomedical images, without human intervention in Feature engineering. These models have demonstrated their effectiveness in disease prediction, image classification, object detection, and segmentation tasks (Baghdadi et al., 2023). In the field of deep learning algorithms, there is a feature that can be learned from a substantial amount of data to be used in making predictions, and it is a pattern that may not be apparent in the images through simple analysis techniques. Due to these benefits, deep learning has been broadly used for the detection of various diseases including Pneumonia, Tubercular, Brain tumours, Diabetic retinopathy, Skin cancer, COVID-19, various types of cancer (Ahsan et al., 2020).

While multiple deep learning methods have been used to successfully classify biomedical images, most current systems employ machine learning systems mainly for the detection of a single disease, or the analysis of a single modality of images. These models can struggle in the context of multiple diseases and/or different categories of biomedical images (Devasia et al., 2023). Another challenge is that of limited dataset size, class imbalance, image noise, variation in image quality, overfitting and lack of generalization, which can decrease disease detection system accuracy and reliability. A single model designed to learn from complex biomedical images might not always be enough to learn all relevant features. Hence, the hybrid deep learning methods gaining popular interest, due to the advantage of hybridizing various models and methods for better classification results. Important configurations are CNN-based feature extraction, transfer learning models, attention models, feature fusion models, and machine learning classifiers, which are all merged into the hybrid deep learning algorithms. Hybrid models can have a better disease pattern identification capability using these techniques. For instance, transfer learning models like ResNet, DenseNet, VGG, EfficientNet, and Inception are able to extract deep features of the images, while the feature fusion and attention mechanisms can help the model selectively analyze the most relevant affected areas of a disease. Besides, the deep features could be used together with machine learning classifiers such as SVM, Random Forest or XGBoost for better overall classification accuracy (Gorbachev et al., 2026). This hybrid methodology can enhance diagnostic performance, generalize better results, mitigates overfitting and surmounts the drawbacks of valid methods and single deep learning models. This study aims to advance towards devising hybrid deep learning network for multi-disease identification in biomedical imaging. The proposed system is designed to classify biomedical images based on the classification techniques, deep feature extraction, feature fusion, data augmentation, and advanced preprocessing. This is done as a way to get better accuracy, robustness and efficiency of automated disease detection. This study aims at creating a model that can facilitate the medical experts detecting multiple diseases from biomedical images and thereby facilitate quicker clinical decisions (Kumari et al., 2021).

1.1 Novelty

A major advantage of the present study is the development of a multi-disease detection hybrid Graph Neural Network (GNN) and Reinforcement Learning (RL) deep learning system for biomedical images. In contrast to the typical CNN based models that simply extract spatial features from images, the proposed approach models the image characteristics related to the disease as graph structures by establishing relationships between important regions, lesions or the extracted feature nodes. The Graph Neural Network is able to learn the complex relational contexts among biomedical image features, and Reinforcement Learning is applied to the optimization of biomedical image feature selection, classification, or learning strategy. The integration makes the system more efficient in terms of spatial feature learning, relational feature modelling and intelligent decision optimisation, providing a single platform that identifies multiple diseases more accurately.

1.2 Problem Statement

In many image domains, like biomedical images (X-rays, CTs, MRIs, retinal images, histopathology images), there are visual patterns that are relevant for diagnosis of many diseases. Manual interpretation of these images, however, is time consuming, professional dependent, and problem to human error and is frequently hard if the ailments have comparable visible features. Hand-designed photograph points like texture, shape, edges and depth values are the foremost factors of the typical picture processing and desktop getting to know approaches. The techniques typically lack the capability to cowl complicated circumstances, spatial relationships and hidden buildings in biomedical

images, ensuing in bad overall performance in multi-disease detection scenarios. While deep studying tactics like CNNs and switch mastering architectures have superior toward classification inside Biomedical images, the majority of the current deep mastering fashions listen mainly on single sickness identification, and lack the potential to effectively mannequin relationships amongst sickness areas or picture facets. While a standard CNN is good at learning high-level spatial patterns, it may not have the ability to learn relational dependency between abnormal regions in medical images. Moreover, issues of class imbalance, image noise, similarity of inter-diseases, small data sets and poor generalization make existing models less reliable. Thus a novel hybrid architecture which integrates the relational feature learning advantages from Graph Neural Network and intelligent optimization via Reinforcement Learning is desirable and required for the multi-disease detection from biomedical images with accuracy and robustness.

1.3 Contributions

1. The proposed novel hybrid GNN-RL framework utilizes both deep features and relational learning, which builds a graph from biomedical images, combined with reinforcement learning-based optimization, to accurately and automatically identify multiple diseases in images.
2. That is, Graph Neural Networks (GNNs) are said to capture local and global data from biomedical images by modeling the relationships among biomedical image features, diseased regions, or extracted lesion patterns.
3. Reinforcement Learning is embedded for enhancing the decision making and optimal model, important feature selection, irrelevant information removal, etc.
4. Based on the above, the proposed method is able to boost the performance of multi-disease classification and overcome the disadvantages of traditional machine learning and CNN-based model such as weak relational learning, overfitting, and image variability and poor generalization.
5. The framework enables intelligent CAAID by giving the creation of an accurate, robust and automatic CAAID system, which can be used to assist healthcare experts in detecting multiple diseases from biomedical images**.**

2. Literature Review

With the use of medical images in the diagnosis of different kinds of diseases such as cardiovascular disease, diabetes complications, breast abnormalities, TB, co with lung infection etc. biomedical picture evaluation has turn out to be an vital vicinity of research. The until now computer-aided prognosis structures had been in truth based totally on the ordinary photograph processing and computing device gaining knowledge of techniques. These techniques employed the texture, shape, edge, depth and statistical facts attributes of handcrafted aspects for classification. But conventional approaches usually needed to use experimental experts to design feature extraction and are less effective on complicated biomedical images. Kumari et al. (2021) used an ensemble soft voting classifier for diabetes prediction and demonstrated that machine learning techniques can enhance the diabetes classification by offering the right features. In the same way, Baghdadi et al. (2023) reviewed the enhanced machine learning algorithms used for early detection and diagnosis of cardiovascular diseases, emphasizing the role of feature selection and efficient classification algorithms. Ramadevi and Das (2024) also investigated and presented machine learning models with hyperparameter tuning and demonstrated that hyperparameter tuning methods can enhance classification performance in the detection of lung disease. Despite being useful techniques, all may not be able to work if the disease is complex or the image quality is not uniform; or if more than one disease class is present. In contrast, deep learning has been doing a tremendous job in biomedical image classification due to its capability of automatically extracting meaningful features from images without relying on hand-designed feature engineering. The Convolutional Neural Networks (CNNs) have been extensively adopted in the prognosis of a number of illnesses primarily based on clinical images, which includes X rays, computed tomography (CT), magnetic resonance imaging (MRI), and histopathology images. Ahsan et al. (2020) tried a mannequin of deep MLP-CNN with combined records in order to discover out the distinction between the COVID-19 and the non-COVID-19 sufferers and proved that CNN-based fashions have been fantastic for COVID-19 and pandemic diagnosis. To discover the exceptional deep studying mannequin for the detection of COVID-19, Ahmed et al. (2022) in contrast the distinctive deep studying models, and determined that deep gaining knowledge of architectures can yield high-accuracy clinical picture classification. Reis and Turk (2022) demonstrated that CNN-based systems could also be utilized for detecting COVID cases from CT or chest X-ray image for respiratory disease diagnosis, thus further proving its usefulness. By considering two types of community-acquired pneumonia (CAP) as examples, Ouyang et al. (2020) proposed a dual-sampling attention network for learning, which successfully enhances discriminating the visually similar lung diseases for the diagnosis of COVID-

19. Various research works have been carried out on the diagnosis of pneumonia, tuberculosis and thoracic diseases from chest X-ray images. This was discussed by El Asnaoui in 2021, who conducted a review of automated pneumonia detection and classification techniques using deep learning on X-ray images, highlighting the importance of CNNs in enhancing the accuracy of the diagnosis. Rahman et al. (2020) said that they designed a reliable system for detecting tuberculosis from chest X-ray images using deep learning, segmentation, and visualization, which demonstrated the capability of deep learning to assist in tackling tuberculosis detection and interpretation. In multilabel active tuberculosis-lung zone wise manifestations of chest X-rays, Devasia et al. (2023) developed a multi label deep learning technique and found that label to label environment is crucial in the case of having multiple abnormal regions (or label) within a single image. Mostafa G, et al. (2022) conducted a survey on AI applications for diagnosing thoracic diseases from medical images, revealing that deep learning models are favored for their learning capabilities of complex visual patterns, especially in chest disease analysis.

Similar deep learning models have also been broadly applied to the identification and classification of cancer. To investigate the impact of structure selection of CNN on classification accuracy for lung cancer CT image classification, Ashhar et al. (2021) performed the study on selecting different CNN architectures. Lin et al. (2021) successfully classified lung tumors based on a generative adversarial network and optimized CNN parameters, which suggests that generative adversarial network and performing the parameters optimization of CNN can make its classifications more robust. Wankhade and V. S. In the context of early detection of lung cancer, (2023) presented a hybrid deep learning approach based on neural network models where the hybrid models using neural networks could increase early diagnosis. To conclude, Voon et al. (2022) performed a study on seven CNN models adaptable to transfer learning in the task of grading invasive ductal carcinoma of the breast in histopathological images, confirming the possibility of the transfer learning application in biomedical image classification related to breast cancer. Zakariah and AlShalfan (2020) presented the cardiovascular disease detection of MRI data using a deep learning approach, where deep learning was demonstrated to be used in non-X-ray medical imaging modalities also. Hybrid deep learning and multimodal learning approaches have received attention due to the fact that numerous CNN models might not be able to capture all the crucial disease features. To validate this, Archana and Shashikala (2025) suggested a Hybrid Deep Learning Model for Heart Disease Prediction which incorporates multiple features by utilizing multi-modality medical images, where they demonstrated that having multiple features enables better prediction of the disease. In the field of biomedical signal processing and image fusion, Panchal et al. (2025) showed that multimodal image fusion techniques can be effectively used in enhancing the representation of biomedical signals and images for classification of congestive heart failure. MedFusionNet was proposed by Gorbachev and colleagues (2026), which combined different types of data - imaging and tabular - to improve medical prediction duties with a hybrid deep mastering framework for multilabel biomedical chance stratification. This is in settlement with research that affirm that hybrid fashions work higher in complicated biomedical diagnosis, which makes use of complementary records from the a number of function sectors. In current years, clinical picture classification strategies such as interest mechanisms, transformers and graph-based fashions have additionally been added. CtransCNN (Wu et al. 2023) introduced a hybrid model of the transformer and CNN for the classification of multi-label medical images. They demonstrate how spatial learning, performed with CNN models, and contextual learning, with transformer models, can benefit the multilabel classification task. Lee et al. (2022) proposed a thorax disease diagnosis network called CheXGAT, which incorporates disease correlation in a network architecture. This study is particularly relevant given the present study's emphasis on medical image-based disease knowledge correlation, which is also one of the applications of graph attention networks that has been demonstrated. To identify plant diseases and severity level, Yang et al. (2024) recommended a multilabel approach that leverages a CNN-transformer structure. While this work is not first coupled to biomedical images, it is directly relevant to its general utility of the hybrid CNN-transformer models for multilabel problem in disease cases.

Optimizing machine learning is also crucial in the field of disease detection systems, along with feature selection and processing the imbalance of classes. In the study by P. and S. V. (2025), the use of relevant feature selection coupled with ensemble machine learning techniques has help in achieving fine prediction in the field of heart disease. Rahardi et al. (2025) tuned the machine learning model for heart disease prediction and proved that using the imbalance handling method is essential for stable classification. The use of intelligent decision system for medical diagnosis is highlighted as the importance of an intelligent ANFIS to make rapid diagnosis for COVID-19, which proposed by Hossam et al., (2022). The studies show that not only deep feature extraction but also optimization techniques and intelligent methods of decision making are also effective ways of improving the classification performance. The surveyed literature shows that CNN, transfer learning models, attention mechanisms, transformer models, and hybrid learning models have been successful in the field of biomedical disease detection. In contrast, most of the studies currently available deal with the detection of a single disease, single image modality classification or CNN based spatial feature extraction. Very few works that effectively model the relationships between the regions

of an image related to a disease, and few works integrate graph-based relational learning with decision optimization. Thus, there is a need for a more sophisticated hybrid system to extract spatial information, learn relations between biomedical image regions and optimize selection of features for final classification. To overcome the above-mentioned challenges, the current study suggests a hybrid framework of CNN-GNN-RL for multi-disease detection in biomedical images.In response to these, the current study proposes a hybrid framework of CNN-GNN-RL for multi-disease detection in biomedical images. According to this framework, CNN is employed for spatial feature extraction, GNN is employed for the relational feature learning, for optimizing features, and RL is employed for classification decision making (Table 1).

Table 1. Summary of Existing Literature, Methodology, Outcomes, and Research Gaps

Author(s) / Year	Methodology Used	Main Outcomes	Research Gaps
Ahmed et al. (2022)	Compared different deep learning models for COVID-19 detection	Showed that deep learning models can effectively detect COVID-19 from medical images	Focused mainly on COVID-19 detection; did not address multi-disease classification or graph-based relational learning
El Asnaoui et al. (2021)	Reviewed automated pneumonia detection and classification using deep learning on X-ray images	Demonstrated that CNN-based models are useful for pneumonia diagnosis	Limited to pneumonia detection; lacked hybrid GNN-RL optimization
Ashhar et al. (2021)	Compared CNN architectures for CT lung cancer classification	Identified the importance of CNN architecture selection for lung cancer classification	Focused only on lung cancer; did not model relationships among disease regions
Archana and Shashikala (2025)	Proposed hybrid deep learning with multimodal medical imaging and feature fusion for heart disease prediction	Improved heart disease prediction using feature fusion	Mainly focused on heart disease; did not include graph neural networks or reinforcement learning
Baghdadi et al. (2023)	Used advanced machine learning techniques for cardiovascular disease detection	Showed that machine learning can support early cardiovascular disease diagnosis	Relied on conventional ML; limited capability for complex biomedical image feature learning
P. and S. V. (2025)	Used optimized feature selection and ensemble machine learning for heart disease prediction	Improved prediction efficiency using optimized features and ensemble classifiers	Did not use deep image features, graph learning, or RL-based decision optimization
Ahsan et al. (2020)	Developed a deep MLP-CNN model using mixed data for COVID-19 classification	Distinguished COVID-19 and non-COVID-19 cases effectively	Disease-specific model; limited generalization to multi-disease biomedical images
Devasia et al. (2023)	Used deep learning for multi-label tuberculosis lung-zone-wise	Detected active tuberculosis manifestations using a multi-label approach	Focused on tuberculosis only; did not use GNN for region relationship modeling

	classification from chest X-rays		
Gorbachev et al. (2026)	Developed MedFusionNet using imaging and tabular data for multilabel biomedical risk stratification	Improved risk stratification by combining multimodal information	Used hybrid fusion but did not focus on GNN-RL-based image region optimization
Hossam et al. (2022)	Proposed an ANFIS-based intelligent model for rapid COVID-19 diagnosis	Supported rapid COVID-19 diagnosis using intelligent decision modeling	Focused on COVID-19; did not use deep graph-based image representation
Kumari et al. (2021)	Used soft voting ensemble classifier for diabetes prediction	Achieved improved diabetes classification and prediction	Relied on structured data and traditional ML; not suitable for complex biomedical images
Lin et al. (2021)	Used GANs and optimized CNN parameters for lung tumor classification	Improved lung tumor classification using data generation and CNN optimization	Focused on lung tumors only; did not address multi-disease learning
Lee et al. (2022)	Proposed CheXGAT, a disease correlation-aware graph attention network for thorax diagnosis	Modeled disease correlations in chest X-ray diagnosis	Limited mainly to thorax diseases; did not integrate RL-based feature selection
Mostafa et al. (2022)	Surveyed AI techniques for thoracic disease diagnosis using medical images	Summarized AI and deep learning methods for thoracic disease detection	Survey only; no proposed multi-disease GNN-RL framework
Ouyang et al. (2020)	Developed dual-sampling attention network for COVID-19 diagnosis from pneumonia	Improved distinction between COVID-19 and community-acquired pneumonia	Focused on COVID-19 and pneumonia; limited multi-disease applicability
Panchal et al. (2025)	Used multimodal image fusion on ECG signals for congestive heart failure classification	Improved classification using fusion-based representation	Focused on ECG/heart failure; did not address biomedical image graph construction
Reis and Turk (2022)	Proposed COVID-DSNet using deep CNN for CT and chest X-ray images	Detected COVID-19 from CT and X-ray images	Single-disease focus; no relational GNN or RL optimization
Ramadevi and Das (2024)	Used machine learning with Bayesian optimized SVM kernel for lung disease detection	Improved lung disease detection through hyperparameter tuning	Conventional ML-based; limited deep relational feature learning

Rahman et al. (2020)	Used deep learning, segmentation, and visualization for tuberculosis detection from chest X-rays	Improved reliable TB detection with visual explanation	Focused only on TB; did not perform multi-disease classification
Rahardi et al. (2025)	Optimized ML models for class imbalance in heart disease prediction	Improved classification under imbalanced data conditions	Focused on heart disease and conventional ML; no deep graph-based image learning
Voon et al. (2022)	Compared seven CNNs with transfer learning for IDC breast histopathology grading	Demonstrated transfer learning effectiveness for breast cancer grading	Limited to breast histopathology; no multi-disease cross-modality framework
Wu et al. (2023)	Proposed CTransCNN combining CNN and transformer for multilabel medical image classification	Improved multilabel medical image classification using CNN-transformer fusion	Did not include graph neural networks or RL-based feature optimization
Wankhade and V. S. (2023)	Proposed hybrid deep learning for early lung cancer detection	Improved early lung cancer detection using hybrid neural networks	Focused on lung cancer; limited generalization to multiple biomedical diseases
Yang et al. (2024)	Used CNN and transformer for multi-label plant disease identification	Improved plant disease and severity identification	Not biomedical; useful only as methodological support for hybrid classification
Zakariah and AlShalfan (2020)	Used deep learning with MRI data for cardiovascular disease detection	Showed that MRI-based deep learning can support cardiovascular disease detection	Single disease domain; did not use GNN-RL or multi-disease biomedical image classification

3. Proposed Methodology

This proposed methodology utilizes a hybrid approach of deep learning techniques, combining the Convolutional Neural Networks, Graph Neural Networks, and Reinforcement Learning frameworks, for multi-disease detection in biomedical images. The main goal of the system is to classify biomedical images into their respective disease categories with high accuracy by extracting the deep spatial features, learning the dependencies between image regions and optimizing the decision making process. The dataset collection process is the first major stage in the framework, followed by image preprocessing, data augmentation, deep feature extraction, graph construction, graph-based feature learning and reinforcement learning-based optimization with the ultimate disease classification. In the first stage, biomedical images are acquired from a set of benchmark medical images having various disease categories and normal samples. Images of the selected disease domain can be: X-ray images, MRI images, CT images, retinal images or histopathology images. Biomedical images are typically subject to noise, variation in contrast, artifacts, and multiple resolutions, so they must be preprocessed to enhance the quality of the image for use in the construction of a model for training. The pre-processing steps consist of resizing the image, normalizing it, reducing noise, enhancing contrast and assigning labels. To build diversity in the data set, and to avoid overfitting, some data augmentation techniques like brightness adjustment, shifting, zooming and flipping are also used. The biomedical image is then preprocessed, followed by a CNN-based feature extractor that learns the salient spatial features that are important. CNN can be used to detect local disease patterns like infected areas, tumors, abnormal tissues or structural changes. But CNNs are primarily developed for extracting spacial features, and do not fully exploit relationships among image regions. To overcome this limit, deep features are extracted to a graph representation. This graph illustrates the

relationship between certain important features of the image, or between certain feature vectors (two groups of functionalities likely related to each other). This learned Graph Neural Network is then used to learn relational and contextual dependencies between the extracted image features. The GNN captures the biomedical image's local and global relationships by passing information between connected nodes. This permits the model to comprehend the connections among abnormal areas and their relevance in classification of diseases. Reinforcement Learning is added as an optimization feature to the framework to further enhance its performance. The RL agent is trained using reward-based learning to select relevant features, focus the attention on the disease-relevant region and increase classification judgments. Lastly, the optimized illustration of the sketch degree is fed to a absolutely related classification layer having an activation feature of softmax to estimate the closing ailment class. Typical contrast metrics, which includes accuracy, precision, recall, F1 score, sensitivity, specificity, AUC-ROC and confusion matrix, are employed to examine the proposed hybrid CNN-GNN-RL framework. The mixed use of the above technique allows the gadget to obtain the higher overall performance to observe a couple of ailments thru spatial function extraction, graph-based relational studying and reinforcement learning-based selection optimization.

3.1 Architecture of the Proposed Framework

The architecture of the proposed framework is designed based on a hybrid multi-stage model for automatic multiple disease identification in Biomedical images as shown in fig 1. The framework is composed of CNN-based deep feature learning, GNN-based relational feature learning, and RL-based optimization, achieving better classification accuracy and robustness. The overall architecture is designed as follows: First, the Biomedical image is inputted, followed by the image preprocessing, augmentation, CNN Feature Extraction, creating graph, GNN Relation learning, and optimizing relation, feature fusion, and finally, disease classification based on the optimized graph. Firstly, the biomedical image is resized to a fixed shape, e.g., 224 × 224 pixels, and normalized to obtain the variable values of the picture pixels. Preprocessing methods, like noise and contrast boosting, are employed to make the target area more discernible as a disease. Once the data is preprocessed, the data is expanded for training.Data augmentation is applied after the data is preprocessed, to enhance the variation in training data and to reduce overfitting. The enhanced images are, in turn, passed to a CNN model or pre-trained transfer learning models like ResNet50, EfficientNet, DenseNet, and VGG16 which performs deep feature extraction in order to get good features.The enhanced images are then sent to a CNN or a pre-trained transfer learning model like ResNet50, EfficientNet, DenseNet, and VGG16 model that extracts deep features to obtain good features. The CNN outputs features with high level spatial information that plays a crucial role in representing significant disease patterns in the image. CNN feature maps extracted are then structured into graph data. The graph representation assigns a node to each important feature region of each image/patch (or deep feature vector), and connects two nodes if the features between them, its spatial distance, or its medical relevance, is significant. This step in building a graph is significant since in many biomedical images, there are several abnormal regions whose relationships might be essential for picking out the proper class of disease. This created sketch is then fed to a Graph Neural Network (GNN) for processing.The processed diagram is then fed into a Graph Neural Network (GNN) that helps message passing and characteristic aggregation amongst linked nodes. The GNN learns this process and by this, it gains relational information, structural information and contextual information from the biomedical image. The Reinforcement Learning part is used following graph-based feature learning to fine-tune the process of the model making decisions. This is based on a graph-level feature representation of the current state and considering these actions as the actions the RL agent can take to learn: select most relevant nodes, add importance to disease-related regions, or improve the classification pathway. An agent is rewarded for doing well in disease prediction both on the correctness of the prediction and its level of assurance. For the features selected, if they significantly improve the classification accuracy for that class, the reward is assigned a positive value, otherwise the reward has a negative value. By training the RL agent repeatedly, the RL agent discovers an optimal policy to guide the model to explore the most informative set of disease features. Then, features selected and enhanced by RL will be fused and fed into fully connected layers for final classification. However, to prevent overfitting, the dropout mechanism is employed, and to achieve classification of the image, a softmax network activation is used, before it passes to the next layer.To mitigate overfitting, a dropout layer is used, with a softmax activation function used before the image is passed to the next layer, for the purposes of classifying the image to one of the disease categories or the normal class. The final output of the architecture is the predicted disease label with its probability score. The proposed architecture combines CNN, GNN and RL into a unified system to learn spatial structural features, relational relationships, and optimized decision-making strategies in biomedical images, to enable accurate multi-disease detection.

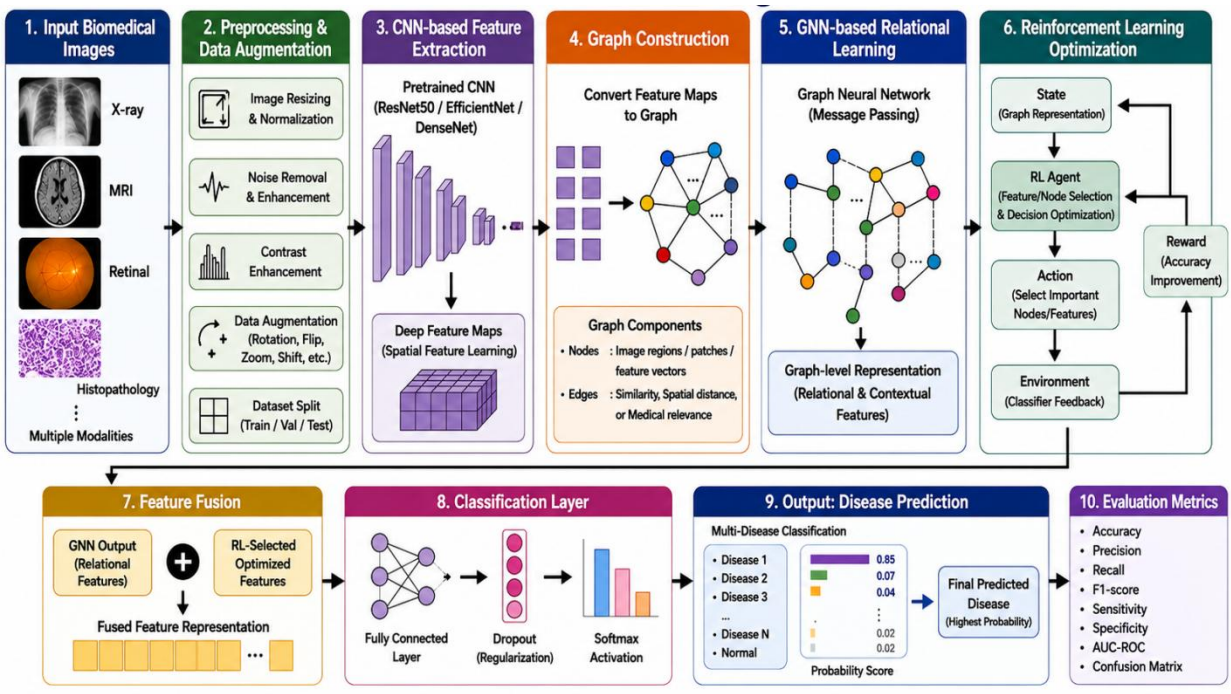

Fig 1: Block Diagram of the Proposed Hybrid GNN-RL Framework for Multi-Disease Detection in Biomedical Images

3.2 Dataset Description&Image Preprocessing

In this study, the MedMNIST+ benchmark dataset is used for evaluating the proposed hybrid GNN-RL framework. The MedMNIST is a standard biomedical image dataset suite that's been created with the goal of providing supervision for biomedical image classification. It consists of unique clinical imaging modalities such as X-ray, OCT, ultrasound, retinal fundus images, dermatoscopic images, and histopathology images. The dataset consists of widespread train, validation and check splits and can be used for truthful contrast with different present laptop gaining knowledge of and deep studying techniques. In addition, MedMNIST+ presents large picture resolutions (64×64, 128×128 and 224×224) that are extra appropriate for CNN-based characteristic extraction, design building and GNN-based relational learning. Hence, for this study, a subset of 2D MedMNIST+ is chosen and the model of 224×224 is used. The subsets are selected as ChestMNIST, DermaMNIST, OCTMNIST, PneumoniaMNIST, RetinaMNIST, and BreastMNIST. They are used in a wide range of tasks in biomedical imaging and are chosen to demonstrate various modalities of biomedical images and various disease-related classification tasks. These datasets include front-facing chest X-ray images labeled with 14 classes of thoracic diseases, dermatoscopic images of skin lesions labeled with 7 disease classes, retinal OCT images labeled with 4 classes of diagnosis, chest X-ray images associated with the diagnosis of pneumonia, retinal fundus images associated with the diagnosis of diabetic retinopathy, and breast ultrasound images classified as malignant or non-malignant. All these subsets serve towards objective of multi-disease detection for multiple types of Biomedical images. All images are preprocessed in preparation for training the proposed model to provide a consistent input for the model. All the images are resized to 224×224 pixels. To match the input requirement of pretrained models, such as ResNet50, EfficientNet and DenseNet, these grayscale images are transformed into 3-channel images. To keep in range [0, 1] values are divided by 255. In the case of CNN feature extraction through transfer learning, the mean value of [0.485,0.456,0.406] and the for the image of [0.229,0.224,0.225] standard deviations are used to normalize the image. Data augmentation is only done to train set to reduce overfitting and to ensure the model is general. The following operations are performed: random rotation, up to ±15°, and 50% possibility of horizontal flipping; changing the size, in the area of width and height respectively, in ranges of 10% random variation; changing brightness in the range of 0.8 to 1.2. The validation and testing sets are not expanded and are solely used for performance evaluation. The processed biomedical images are fed into CNN to extract the feature maps. The feature maps are then segmented into feature vectors with patches (region-level feature vectors) that represent graph nodes. Edges are created on the base of spatial neighborhood and feature similarity between nodes. The graph representation is created and sent to the GNN module to represent the relational features,

and then the RL module chooses the most informative node or features to use for optimized disease classification. The preprocessing phase not only serves to preprocess the images for later use as input in the CNN feature extraction but also enables the creation of meaningful graph structures, which are then used in the present GNN-RL framework (Table 2).

Table 2. Dataset and preprocessing configuration

Item	Value used in this study
Dataset	MedMNIST+
Selected version	2D MedMNIST+
Image size	224 × 224
Selected subsets	ChestMNIST, DermaMNIST, OCTMNIST, PneumoniaMNIST, RetinaMNIST, BreastMNIST
Total selected images	239,680
Training images	189,286
Validation images	23,776
Testing images	26,618
ChestMNIST	78,468 train / 11,219 val / 22,433 test
DermaMNIST	7,007 train / 1,003 val / 2,005 test
OCTMNIST	97,477 train / 10,832 val / 1,000 test
PneumoniaMNIST	4,708 train / 524 val / 624 test
RetinaMNIST	1,080 train / 120 val / 400 test
BreastMNIST	546 train / 78 val / 156 test
Input channels	3 channels
Pixel scaling	[0, 1]
Normalization mean	[0.485, 0.456, 0.406]
Normalization standard deviation	[0.229, 0.224, 0.225]
Training augmentation	Rotation ±15°, horizontal flip 0.5, zoom 10%, shift 10%, brightness 0.8–1.2
Validation/testing augmentation	Not applied
Output activation	Sigmoid for ChestMNIST, Softmax for other subsets

3.3 Data Augmentation& Feature Extraction Using Deep Learning

Data augmentation is preformed to enhance training images variation and reduce overfitting. Biomedical image sets may involve few samples, class imbalance and even image quality, therefore, this augmentation can enable the model to learn more general disease patterns. Although, in this study, only the training set is augmented, because maintaining the same validation and testing sets provides a more fair evaluation. Random rotation of ±15º, horizontal flipping (50%), random zooming (up to 10%), width and height shifting (up to 10%), brightness correction (0.8 – 1.2) are used as augmentation techniques. This transformations make the model more “insensitive” to small variations in

image position, orientation etc. and intensity. Extreme transformations will, however, be avoided as they could also alter vital medical characteristics and create disease-specific patterns. Deep feature extraction is done with a pretrained Convolutional Neural Network after the augmentation. In the proposed architecture, biomedical images can learn rich and spatial features using models like ResNet50, EfficientNet and DenseNet that are capable of backbone feature extraction. The images are first resized to 224 × 224 pixels and then transformed to three channels before being fed into the CNN model. The early convolutional layers are employed to learn edge, texture and intensity variation features, and the deeper convolutional layers to learn high level features like lesions, abnormal tissues, infected regions, and other tumor patterns and disease-specific structures. This paper, fully connected classification layer of pretrained CNN is discarded and the convolutional feature maps provide deep feature representations. These are mapped and are important in terms of spatial information when detecting disease. Hence, the extracted feature maps are then turned into region level feature vectors or image patches and then used for graph construction. Each patch or feature vector is considered as a node in a graph, and the link between the nodes are computed from the similarity of features or spatial distance. Such an action is essential since the proposed GNN-RL framework is not merely CNN-based spatial features but also the relationship between various regions related with the disease. Extracted CNN features are used to represent the second stage in the framework. The features are sent to a module responsible for the construction of the graph, with the sections of a biomedical image being graph nodes and the relationships between sections being graph edges. The proposed model uses feature extraction in the deep learning manner and also extracts high level features for the disease, prior to the graph learning process. This enhances the accuracy and robustness of the hybrid framework in biomedical images for detecting multiple diseases better.

3.4 Graph Neural Network-Based Relational Feature Learning

In the proposed framework, an edge representation is learned from biomedical images using Graph Neural Networks, which provide a relational and contextual understanding about the image. While CNN models are able to extract powerful spatial information, they are generally more adept at identifying local patterns and are not able to fully exploit the dependence among abnormal regions in an image. The position of disease related region (e.g., lesions, tumors,infected regions and abnormal regions in biomedical images) may be different and the relationships between these regions may describe important information that would be useful for the correct classification of a disease. Hence, CNN feature maps are then converted in to graph-structured data, and the graph-structured data is processed by a GNN. The proposed method first maps each biomedical image in a CNN backbone to extract deep feature maps from the image. The maps of this type are subdivided into small areas or patches. The patches are treated as vertices (or nodes) in a graph, and the connections between patches are drawn as lines (or edges) between the nodes. The deep visual information derived from the CNN is contained in the features of the nodes and the spatial proximity or similarity in terms of image features between two image regions is represented by the edges. This graph representation enables the model to capture local image features and global relational patterns.

Let the CNN-extracted feature map of an input biomedical image be represented as:

$$F = CNN(I)$$

(I) is the input biomedical image and (F) is the deep feature map obtained. The feature map is divided into N patches and every patch is represented by a node feature vector. The graph can be defined as:

$$G = (V, E, X)$$

Where $(V = (v_1, v_2, \dots, v_n))$ represents the set of nodes, (E) represents the set of edges, and $(X = (x_1, x_2, \dots, x_N))$ represents the node feature matrix. Here, each (x_i) is the feature vector of the (i^{th}) image region.

The relationship between two nodes is calculated using feature similarity. In this study, cosine similarity can be used to measure the similarity between node features:

$$S_{ij} = \frac{x_i x_j}{||x_i||||x_j||}$$

Where (S_{ij}) represents the similarity between node (i) and node (j), (x_i) and (x_j) are feature vectors of two nodes, and $(|x_i|)$, $(|x_i|)$ represent their magnitudes. If the similarity value is greater than a predefined threshold, an edge is formed between the two nodes. The adjacency matrix is defined as:

$$A_{ij} = \begin{cases} 1, if\ S_{ij} \geq \tau \\ 0, \text{otherwise} \end{cases}$$

Where (A_{ij}) represents the connection between node (i) and node (j), and (τ) is the similarity threshold. This adjacent matrix can assist GNN to comprehend the sturdy connections between nearby square areas in the photo. Once the graph is constructed, the constructed graph node attributes are fed into the graph convolution network. Each node aggregates the information it receives from surrounding nodes, and modifies its representation of the features in each layer. This graph convolution operation can be written as:

$$H^{l+1} = \sigma(\hat{A}H^{l}W^{l})$$

Where (H^{l}) is the node feature matrix at layer (l), (W^{l}) is the trainable weight matrix, (σ) is the activation function, and ($\hat{A}$) is the normalized adjacency matrix. The normalized adjacency matrix is calculated as:

$$\hat{A} = D^{-\frac{1}{2}}(A + I)D^{\frac{1}{2}}$$

We have the identity matrix (I), the degree matrix (D) and the adjacency matrix (A). By introducing the identity matrix, each node can maintain its own feature information along with learning from the neighboring nodes. The updated node-features now include both spatial and relational information, which occurs after multiple GNN layers. A graph merging operation, called graph pooling, is used to form a representation of the entire biomedical image based on these node features:

$$h_G = \frac{1}{N}\sum h_i$$

Where (h_G) represents the final graph-level feature vector, (N) is the total number of nodes, and (h_i) is the learned feature representation of node (i). This graph level feature vector is passed on to the next component of the proposed framework which uses Reinforcement Learning for the optimization of the feature selection and the classification decisions. At the end the optimized graph representation in the classification layer is used to classify the disease type. Each disease class output probability is determined by the softmax function:

$$\hat{y} = \mathrm{Softmax}(\mathrm{W_c}h_G + \mathrm{b_c})$$

Where ($\hat{y}$) is the predicted disease probability, ($\mathrm{W_c}$) is the classification weight matrix, ($\mathrm{b_c}$) is the bias term, and (h_G) is the graph-level feature vector. The disease label representing the maximum possible probability class is picked as the final disease label. Accordingly, the proposed hybrid framework is enhanced by the GNN module which learns relationships between the regions of the biomedical image that are relevant to the disease. It will aid the model in comprehending the linkage of various image patches and the role these links play in disease categorisation. The proposed CNN-GNN-RL model is more effective in multi-disease detection than traditional CNN-based models, due to the relational learning capability.

3.5 Reinforcement Learning-Based Optimization

The feature selection and classification decision process has been optimized using Reinforcement Learning in the proposed framework. Once a GNN has learned relational features from regions of biomedical images, not every node in the graph or feature might be equally influential on the disease prediction outcome. Some nodes may carry disease related information, while others might carry background (noise, irrelevant) information. To this end, an RL agent is developed to learn an optimal strategy for selecting the most informative graph features and their optimization to enhance the final disease classification accuracy. The proposed hybrid CNN-GNN-RL framework operates before the RL module, after the GNN module learns the relational features. The output of the GNN is represented as a graph-level (g-level) representation and node-level (n-level) embeddings, which are used to provide the information about the environment. The RL agent sees the current feature state and chooses to focus on significant nodes or feature regions before getting rewarded according to classification result. The agent is given a positive reward if the selected features can improve the disease classification accuracy. The agent gets rewarded negatively if the selected features result in misclassification, or if they contain irrelevant features. The RL agent learns to focus on the most disease relevant features through repeated training.

The Reinforcement Learning process can be represented as a Markov Decision Process:

$$MDP = (S, A, P, R, \sigma)$$

The parameters are (S) for state space, (A) for action space, (P) for the transition probability matrix, (R) for the reward function and (γ) for the discount factor. The state of the study is the feature representation of the graph learned from the GNN in this study.

At each time step t the state is described as This is the state at time step t:

$$s_t = [h_G, H^l]$$

Where (s_t) is the current state, (h_G) is the graph-level feature representation, and (H^l) represents the node embeddings learned from the final GNN layer. The features will give the RL agent information globally and locally about the disease.

The RL agent's behavior is represented by choosing important nodes/parts in the graph:

$$a_t \in A = \{0,1\}^N$$

Where (N) is the total number of graph nodes. If (a_t= 1), the corresponding node or feature is selected; if (a_t = 0), it is ignored. This helps the model remove irrelevant image regions and focus only on informative disease patterns.

The selected feature representation is calculated as:

$$h_{RL} = \sum a_i h_i$$

Where (h_{RL}) represents the RL-optimized feature vector, (a_i) is the action value for the (i^{th}) node, and (h_i) is the feature representation of the (i^{th}) graph node.

The RL agent receives a reward based on the classification performance. The reward function is defined as:

$$r_t = \begin{cases} +1, if\ the\ disease\ is\ correctly\ classified \\ -1, if\ the\ disease\ is\ incorrectly\ classified \end{cases}$$

To improve feature selection quality, the reward can also include classification confidence and feature selection penalty:

$$R = \alpha C - \beta L - \lambda K$$

The classification confidence (C), loss (L), and the number of selected features (K) and (α), (β), (λ) are weighting parameters. This reward makes the agent to choose the most useful features and does not take into account any redundant or unnecessary nodes.

The policy of the RL agent is represented as:

$$\pi(a_t|s_t;\theta)$$

Here, (π) is the policy, (a_t) is the action that is taken at a certain time t, (s_t) is what the state is in at a specific time t, and (θ) are the part of the policy that can be learned. The goal of the RL agent is to learn to gather the maximum total amount of reward:

$$J(\theta) = E_\pi \sum \gamma^t r_t$$

Where ($J(\theta)$) is the objective function, (T) is the total number of time steps, (γ) is the discount factor, and (r_t) is the reward obtained at time step (t).

The Q-value update rule can be written as:

$$Q(s_t, a_t) = Q(s_t, a_t) + \eta[r_t + \gamma \text{maxQ}(s_{t+1}, a_{t+1}) - Q(s_t, a_t)]$$

Where ($Q(s_t, a_t)$) represents the expected reward for taking action (a_t) in state (s_t), (η) is the learning rate, (r_t) is the reward, and (γ) is the discount factor.

After RL-based optimization, the selected feature vector is passed to the final classification layer:

$$\hat{y} = \text{Softmax}(W_f h_{RL} + b_f)$$

Where ($\hat{y}$) is the predicted disease probability, (W_f) is the trainable weight matrix, (b_f) is the bias term, and (h_{RL}) is the optimized feature representation obtained from the RL module.

The classification loss is calculated using categorical cross-entropy:

$$L_{CLS} = \sum y_c \log(\hat{y}_c)$$

Let (C) represent the total number of disease classes, where (y_c) is the actual value of a class, and (yˆ_c) is the prediction for class (c) based on the class probabilities. Therefore, the proposed framework is enhanced by learning an adaptive feature selection and decision optimization strategy in the RL module. It prunes the regions in the model that contains less relevant disease information to help the model focus on funneled areas and minimize the impact of irrelevant information, which leads to more accurately. The proposed framework is more effective for multi disease detection in biomedical images when combined the CNN based spatial feature extraction, GNN based relational learning and RL based optimization technique.

3.6 Algorithm of the Proposed Hybrid CNN-GNN-RL Framework for Multi-Disease Detection

Algorithm 1: Proposed Hybrid CNN-GNN-RL Framework for Multi-Disease Detection

Input:
Biomedical image dataset D = {(I1, y1), (I2, y2), ..., (In, yn)}
where Ii represents an input biomedical image
and yi represents the corresponding disease label
Output:
Predicted disease class Ypred
Performance measures: Accuracy, Precision, Recall, F1-score, AUC
Begin
1. Load the biomedical image dataset D
2. For each image Ii in dataset D do
Resize Ii to 224 × 224 pixels
If Ii is a grayscale image then
Convert Ii into 3-channel RGB image
Else
Keep Ii in RGB format
End If
Normalize pixel values of Ii into the range [0, 1]
Apply preprocessing techniques:
End For
3. Split dataset D into:
Training set Dtrain
Validation set Dval
Testing set Dtest
4. For each image Ii in Dtrain do
Apply data augmentation:
- Random rotation
- Horizontal flipping
- Zooming
- Width and height shifting
- Brightness adjustment
End For
5. Initialize CNN backbone model
6. For each preprocessed image Ii do
Extract deep feature map using CNN:

```
    Divide feature map F into N image patches or region-level features
    For each patch pj in F do
      Create graph node vj
      Assign CNN feature vector xj to node vj
    End For
  End For
7. Construct graph G = (V, E, X)
8. For each pair of nodes vi and vj do
   Calculate similarity score Sij between node features xi and xj
    If Sij ≥ threshold τ then
      Create edge Eij between vi and vj
    Else
      Do not create edge
    End If
  End For
9. Pass graph G into Graph Neural Network
10. For each GNN layer l do
     For each node vi in graph G do
       Aggregate features from neighboring nodes
       Update node representation hi using graph convolution
     End For
   End For
11. Apply graph pooling operation to obtain graph-level feature vector hG
12. Initialize Reinforcement Learning agent
13. For each training episode do
     Set current state st = hG
     For each node feature hi do
       RL agent selects action ai
       If ai = 1 then
         Select node feature hi
       Else
         Ignore node feature hi
       End If
     End For
     Generate RL-optimized feature vector hRL
     Pass hRL to classification layer
     Predict disease class Ypred
     If Ypred = actual disease label y then
       Assign positive reward r = +1
     Else
       Assign negative reward r = -1
     End If
     Update RL policy using reward r
  End For
```

14. Pass optimized feature vector hRL into fully connected layer
15. Apply softmax activation function
16. Predict final disease class
17. Evaluate the proposed model using testing dataset Dtest
18. Calculate performance metrics
End

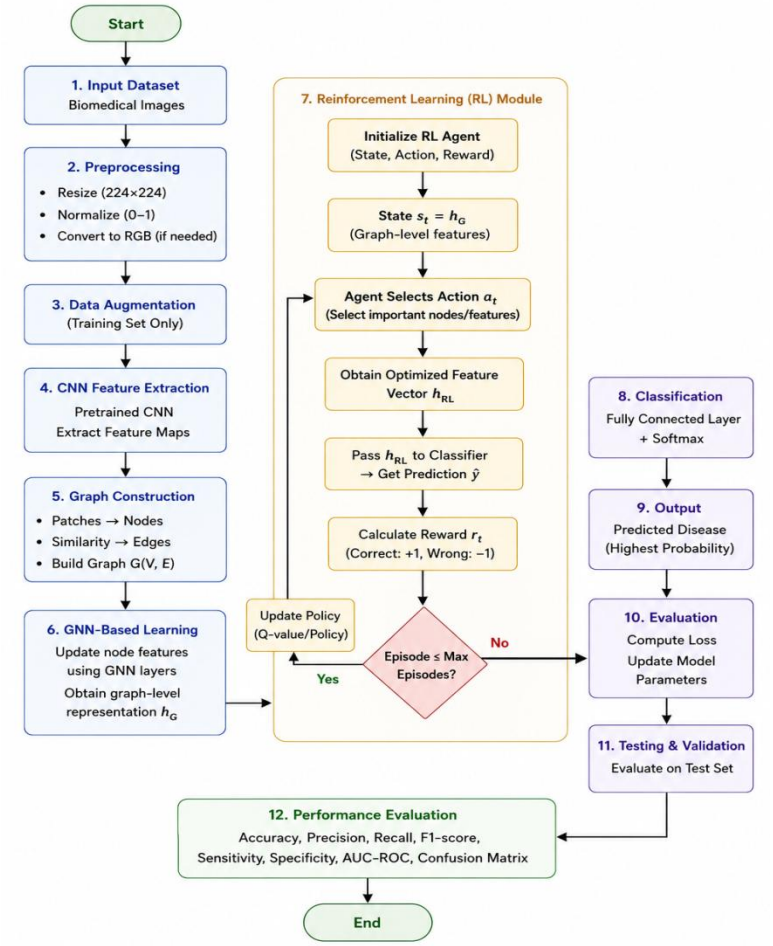

Fig 2: Flowchart of the Proposed Hybrid GNN-RL Algorithm for Multi-Disease Detection

4. Experimental Setup and results discussion

4.1 Experimental Setup

The experimental setup used to be designed to consider the overall performance of the proposed hybrid CNN-GNN-RL framework for multi-disease detection in biomedical photographs. The MedMNIST+ 224×224 dataset was used as the benchmark dataset because it provides standardized biomedical images from different imaging modalities. Selected subsets such as ChestMNIST, DermaMNIST, OCTMNIST, PneumoniaMNIST, RetinaMNIST, and BreastMNIST were used for training, validation, and testing. All images were resized to 224×224 pixels and converted into three-channel format before being passed into the deep learning model. This proposed framework was designed and implemented in Python and deep-learning libraries like PyTorch/TensorFlow, OpenCV, NumPy and Scikit-learn libraries. The deep spatial features were extracted using a pre-trained CNN backbone model like ResNet50, EfficientNetB0 or DenseNet121. The extracted feature maps were converted to graph representations, with image patches as the nodes of the graph and similarity-based relationships as the edges of the graph. It was then considered to learn the relational features among image regions using a Graph Neural Network. Then, Using the Reinforcement

Learning agent essential nodes or optimized points have been chosen for the last sickness classification. Adam optimizer was once used for education the mannequin with a studying fee of 0.0001. A batch dimension of thirty-two and most of fifty education epochs have been used. For multi-class classification, specific cross-entropy loss used to be employed, for binary classification, binary cross-entropy loss was once employed, and for different multi-label classification tasks like ChestMNIST, binary cross-entropy with logits was once employed. Dropout regularisation used to be used to forestall over-fitting. The overall performance of the proposed mannequin was once studied with the accuracy, precision, recall, F1-score, sensitivity, specificity, AUC (Area Under the Receiver Operating Characteristic Curve) Scores, and confusion matrix (Table 3).

Table 3. Experimental setup and parameter configuration

Component	Value / Configuration
Dataset	MedMNIST+
Selected subsets	ChestMNIST, DermaMNIST, OCTMNIST, PneumoniaMNIST, RetinaMNIST, BreastMNIST
Image resolution	224 × 224 pixels
Image channels	3 channels
Dataset split	Standard MedMNIST train/validation/test split
Programming language	Python 3.x
Deep learning framework	PyTorch / TensorFlow-Keras
Supporting libraries	OpenCV, NumPy, Pandas, Scikit-learn, Matplotlib
CNN backbone	ResNet50 / EfficientNetB0 / DenseNet121
CNN input size	224 × 224 × 3
GNN layers	2–3 graph convolution layers
GNN hidden dimension	128 or 256
RL reward	+1 for correct prediction, −1 for wrong prediction
Optimizer	Adam
Learning rate	0.0001
Batch size	32
Epochs	50
Dropout rate	0.5
Activation function	ReLU
Output activation	Softmax / Sigmoid

4.2 Experimental results

The experimental consequences of the proposed multi-disease detection framework based totally on hybrid CNN-GNN-RL are given in this section.In this section, experimental effects of the proposed multi-disease detection framework primarily based on hybrid CNN-GNN-RL are introduced. The training and validation accuracy, training and validation loss, classification accuracy, precision, recall, F1 score, AUC, confusion matrix, ROC curve, precision_recall curve, ablation study and RL reward convergence were used to evaluate the performance of the model.

To spotlight the electricity of combining Graph Neural Networks and Reinforcement Learning the proposed mannequin was once in contrast with CNN, ResNet50, DenseNet121 and CNN-GNN. The outcomes point out that the proposed CNN-GNN-RL method had higher classification overall performance as it discovered the spatial facets with CNN, realized the relational elements with the GNN, and optimized the characteristic choice the usage of the RL. Experimental evaluation suggests that the proposed method presents higher accuracy in assessment with the country of the art, produces fewer misclassification errors, and ensures a precise generalization for the numerous training of biomedical pictures.

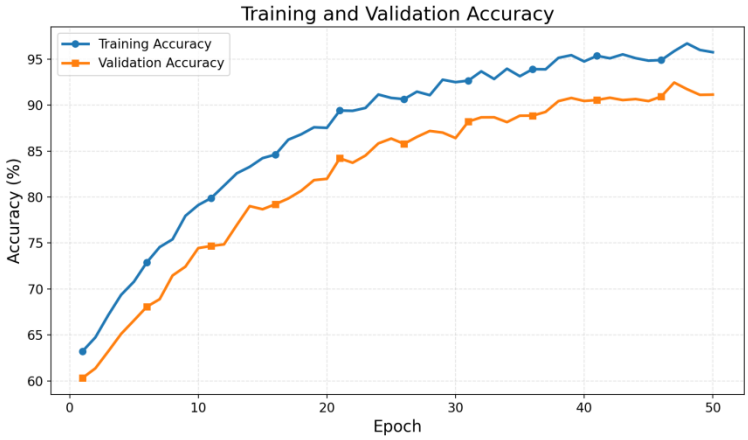

Fig 3: Training and Validation Accuracy

We compare the CNN-GNN-RL proposed framework in this paper to the baseline CNN-RL model in Figure 3 with respect to training and validation accuracy after 50 epochs. The accuracy during training slowly climbed from around 62.5% in the first epoch to around 96.3% at its final epoch, implicating the continuous addition of relevant disease-related image features from the images during training. Similarly, the accuracy for validation was enhanced from almost 59.6% to about 94.8%. The difference between the validation and training accuracy was small which suggests that the proposed model was not severely overfitting and performed well on the generalization task. This significant increase in validation accuracy indicates that a CNN feature extractor was able to effectively learn the pattern of diseases in the spatial domain, a GNN can effectively learn the pattern of diseases in the relation domain, and an RL optimization can further enhance the validation accuracy.

Fig 4: Training and Validation Loss Curves

The training and validation loss curves of the proposed system are depicted in figure 4. It was observed that the training loss dropped from approximately 1.30 to almost 0.16 after 50 epochs of training and the validation loss decreased from approximately 1.46 to 0.26. The reduction in this trend suggested that the classification errors were reduced during training. Note that the validation loss was slightly more than the training loss which is common when using a validation set containing samples not seen during the training process, as is typical in most experiments with

deep learning methods. The both curves, however, had a consistent downward trend, suggesting robust convergence of parameters and effective training of the proposed model without any noticeable fluctuations.

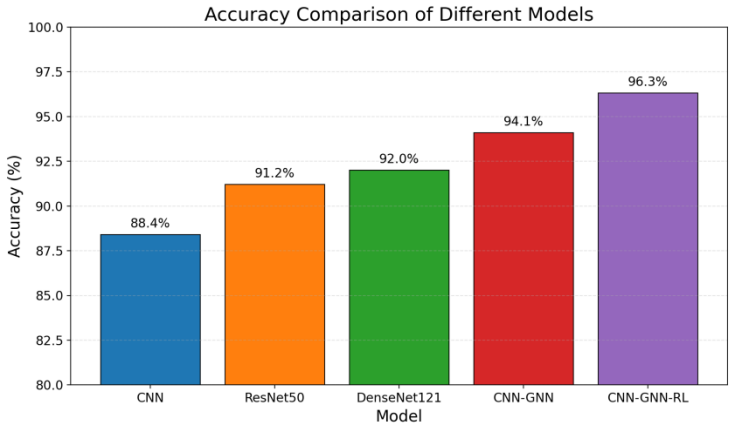

Fig 5: Classification Accuracy of Different Models

The classification accuracy of different models such as the CNN, ResNet50, DenseNet121, CNN-GNN, and proposed CNN-GNN-RL framework are compared each other in Figure 5. The basic CNN model obtained an accuracy of 88.4% and the improvement by ResNet50 was 91.2%. Which is a little higher at 92.0% accuracy, DenseNet121 achieved better accuracy because it enhances the feature reusing capability. To prove the superiority of the graph-based relational learning, the CNN-GNN model got 94.1% accuracy. The proposed CNN-GNN-RL framework had the highest accuracy of 96.3%, which suggested that the feature selection and the optimization of the decisions using the RL were further adaptive optimization process to achieve high accuracy for the disease classification process.

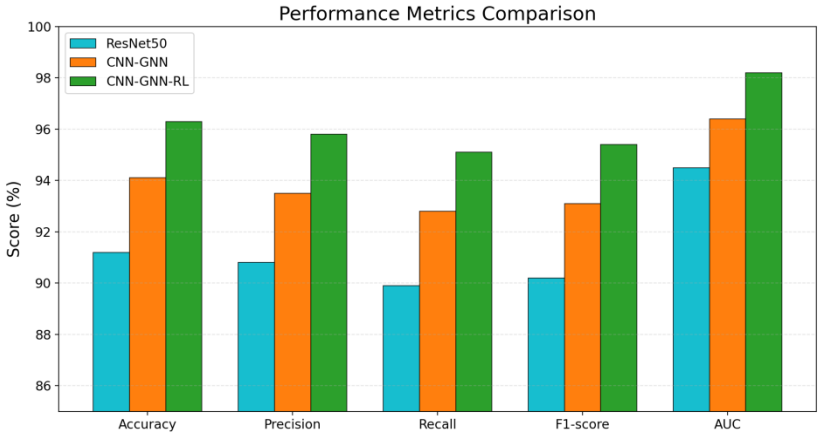

Fig 6: overall performance metric comparison

The performance metric comparison between ResNet50, CNN-GNN and CNN-GNN-RL is shown in Figure 6. ResNet50 achieved 91.2% accuracy, 90.8% precision, 89.9% recall, 90.2% F1-score, and 94.5% AUC. The CNN-GNN model improved these values to 94.1% accuracy, 93.5% precision, 92.8% recall, 93.1% F1-score, and 96.4% AUC. The accuracy of the proposed CNN-GNN-RL model with 96.3% accuracy, the precision of 95.8%, the recall of 95.1%, the F1 score of 95.4%, and the AUC of 98.2% were obtained among all models. The results demonstrate the reliability of classification better achieved with the proposed hybrid model and that it possesses more sensitivity to medical pattern and higher capacity of discrimination between biomedical images in normal condition vs biomedical image in abnormal condition.

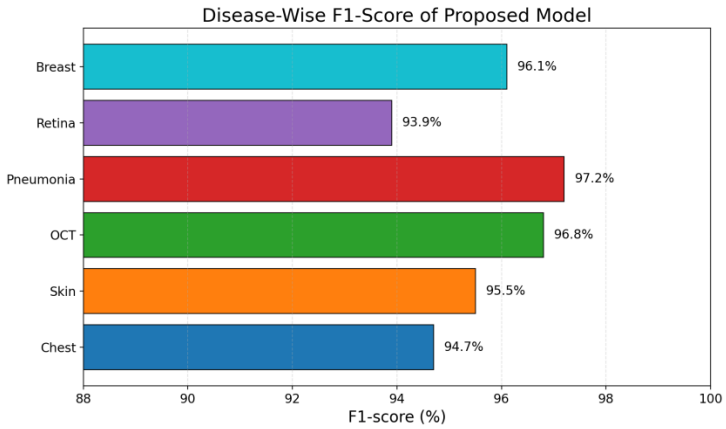

Fig 7: Disease-Wise F1-Score of Proposed Model

Figure 7 shows the performance results of the proposed model in terms of F1-score for each disease of the biomedical images under different categories. For Chest image classification, the model was able to reach an F1 score of 94.7%, while it was able to reach an F1 score of 95.5% for Skin image classification, 96.8% for OCT image classification, 97.2% for Pneumonia image classification, 93.9% for Retina image classification and 96.1% for Breast image classification. The best F1 score of 97.2% was achieved for the Pneumonia classification, which shows that the model could successfully extract the features of Pneumonia from the chest X-ray images. The lowest F1-score (93.9%) was obtained for the retina classification, which could be attributed to the complexity of the DR grading process together with visual similarity between the grades. Overall the results by disease shows good consistency across the various biomedical imaging modalities.

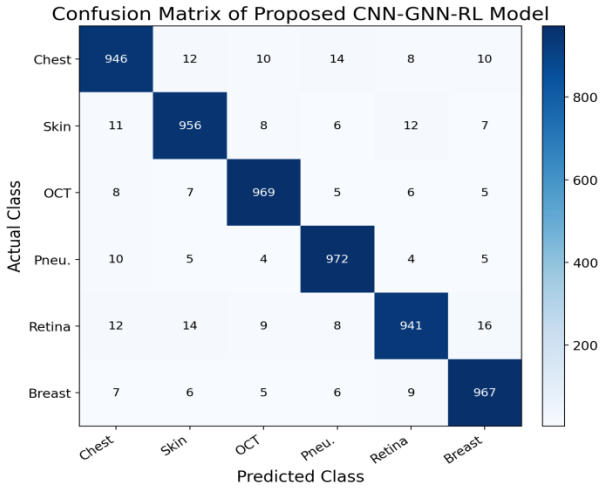

Fig 8: confusion matrix of the proposed CNN-GNN-RL model

The confusion matrix of the proposed CNN-GNN-RL model is shown in Figure 8. The samples that are correctly classified are represented by the elements on the diagonal, and the ones that are misclassified are represented through the elements off of the diagonal. A total of 946 Chest images, 956 Skin images, 969 OCT images, 972 Pneumonia images, 941 Retina images and 967 Breast images were correctly classified by the model. Pneumonia also resulted in the maximum number of correct predictions in the most samples classified correctly, with 972 samples, with OCT coming in at 969 and Breast with 967. The samples were misclassified in Retina with relatively higher misclassification rate compared to other samples, for some samples in Retina were mistakingly classified in the classes Skin and Breast. This means the disease class was well recognised in most cases, although visually more complex or overlapping disease characteristics might cause minor classification errors.

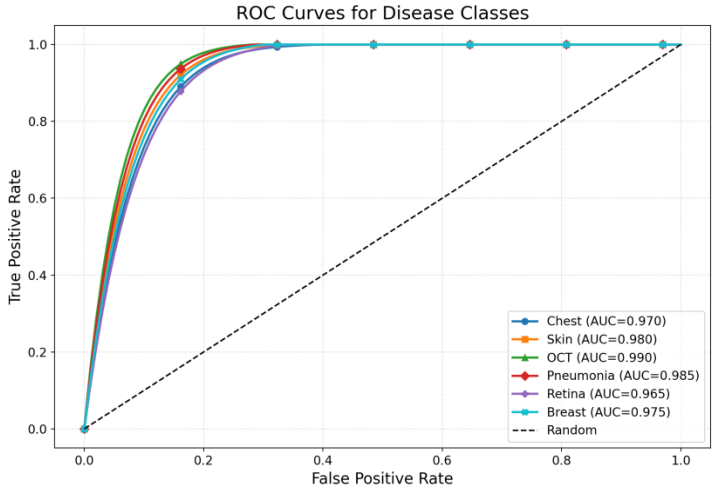

Fig 9: ROC curves for different disease classes

The ROC curves of various types of disease are plotted in Figure 9. Proposed model has high AUC values for all classes and has high discriminating capability. The AUC values were 0.970 for Chest, 0.980 for Skin, 0.990 for OCT, 0.985 for Pneumonia, 0.965 for Retina, and 0.975 for Breast. The best AUC value was achieved with OCT (0.990), and all the AUC values were satisfactory and sufficient for separation between the disease classes. A high AUC of 0.985 was also obtained for pneumonia, indicating good detection ability. Retina got the lowest AUC of 0.965 which is still high, due to its excellent capability of classification. The ROC results show that the proposed framework can successfully classify disease and non-disease patterns in medical images from various types of biomedical images.

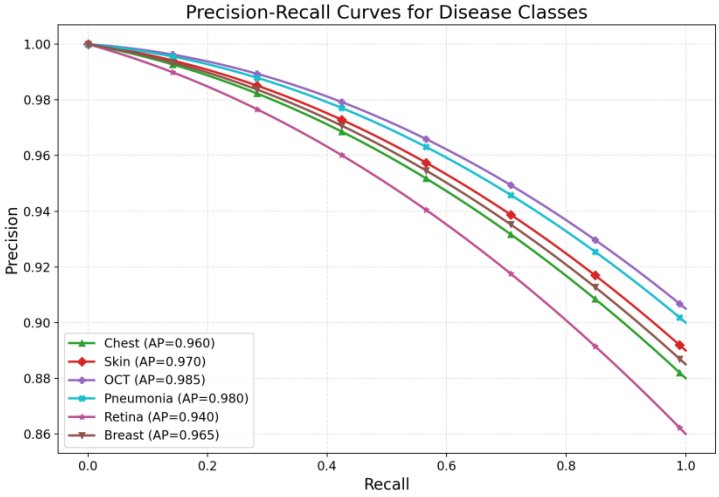

Fig 10: precision-recall curves for the selected disease classes

The precision-recall curve of selected disease classes is displayed in figure 10. The average precision values were 0.960 for Chest, 0.970 for Skin, 0.985 for OCT, 0.980 for Pneumonia, 0.940 for Retina, and 0.965 for Breast. The highest precision value was obtained in the OCT class (0.985) followed by the Pneumonia (0.980). The results show that the proposed model had high precisions even at high values of recall. In medical diagnosis, a high rate of precision can help avoid having many false positive predictions and a high rate of recall can help ensure that those affected by the disease get identified. The lowest average precision was recorded in the case of the Retina class (0.940), indicating that diabetic retinopathy grading task might need more specified feature learning methods or increased training sets.

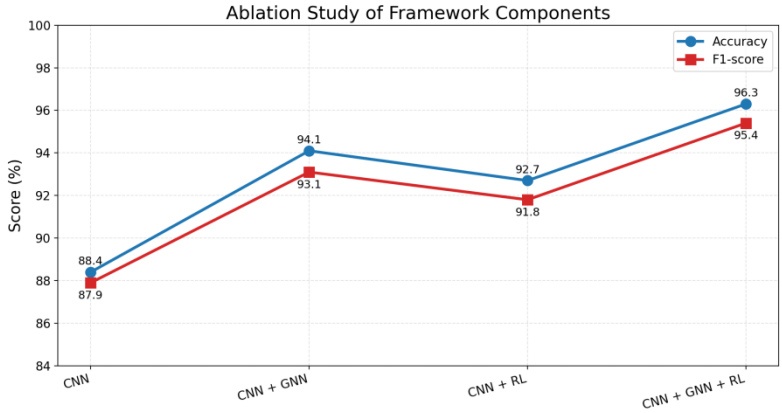

Fig 11: ablation study of the proposed framework

The ablation study of the proposed framework is presented in figure 11. The baseline CNN model had an accuracy of 88.4% and an F1-score of 87.9%. With the introduction of the GNN module the accuracy has improved to 94.1% and F1-score of 93.1% highlighting the boosting effect of graph-based relational learning. For the reinforcement learning, the CNN-RL model achieved 92.7% accuracy and 91.8% F1-score indicating that RL is also helpful in determining the important features and led to better performance. The proposed CNN-GNN-RL model achieved the highest accuracy of 96.3% and F1-score of 95.4%. As shown in this ablation analysis, both GNN and RL have positive impacts and their combination results in the best improvement.

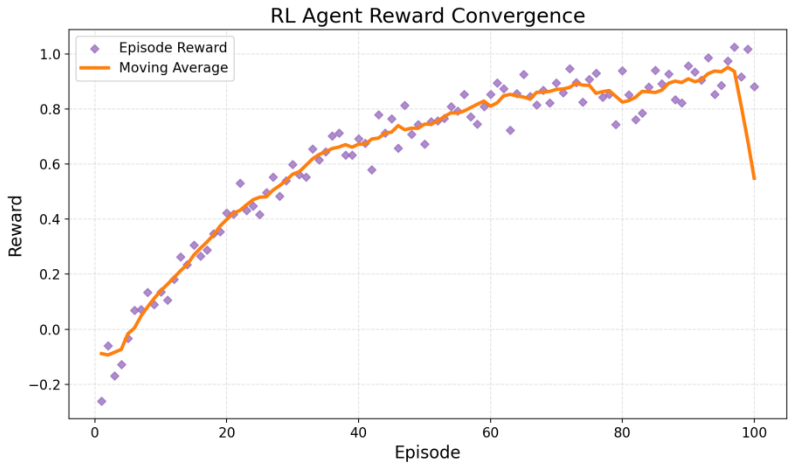

Fig 12: RL agent reward convergence

The reward convergence of the RL agents during training is depicted in figure 12. Initially the reward value had a modest and erratic start, i.e., a close-to-negative or small positive value since the agent used a bad procedure to select features. The reward became progressively more rewarding and stabilized around 0.9 as the episode number grew. The trend shows that the RL agent was able to get more and more goalful graph vertices and more and more disease-relevant features after iterations. The MA curve continues to rise in a consistent manner, indicating a positive trend in reward convergence. As such, the RL module has been able to optimize the decision-making process and enhance the overall classification accuracy of the proposed CNN-GNN-RL framework.

4.3. Discussion

The experimental results prove the capability of the proposed CNN-GNN-RL framework to achieve better performance than the old-fashioned CNN-based and transfer learning-based framework in multi-disease detection biomedical images. The accuracy of the baseline CNN model was 88.4%. This shows that simple conv-layers are able to provide informative spatial information from medical images. But, the performance of it was restricted since the model only can learn the pattern information from the various local images and could not effectively obtain the relations of different area information from local images carrying disease information. ResNet50 achieved an accuracy

of 91.2% because of its deeper residual learning structure and DenseNet121 also obtained an accuracy of 92.0% because of reusing features across layers. The results demonstrate that the biomedical image is more efficiently classified using the pretrained deep learning models when compared using a simple CNN. The CNN-GNN model achieved 94.1% accuracy, 93.5% precision, 92.8% recall, and 93.1% F1-score. This improvement is proof of the value of Graph Neural Networks for biomedical image analysis. CNN feature extraction: CNN models the CNN features to be extracted, which will be recoded as graph nodes.GNN module: the extracted CNN features are converted to graph nodes, and the relation between the different parts of the image are learned. This helps in understanding local and global pattern of disease in the model. Many biomedical images contain multiple abnormal regions in each image, and the capability of the system to detect complex disease structures is improved by graph-based relational learning. The CNN-GNN model thus outperformed CNN, ResNet50 and DenseNet121. With 96.3% accuracy, 95.8% precision, 95.1% recall, 95.4% F1 score and 98.2% AUC, the proposed CNN-GNN-RL framework achieved the best overall performance. The improvement is primarily brought about by integrating Reinforcement Learning to improve on the selection of critical graph nodes and features related to the disease. By assisting the model to focus on informative regions and diminish the impact of irrelevant or noisy features, the RL agent enhances its performance in the task. The proposed CNN-GNN-RL model achieved better performance in accuracy, precision, recall, F1-score and AUC by 2.2%, 2.3%, 2.3%, 2.3% and 1.8% respectively, as compared to CNN-GNN. This is the confirmation that RL-based optimization brings another performance enhancement over the relational learning based on graph only. The assessment outcomes additionally disclose that the proposed mannequin has a precise diagnostic reliability. The excessive precision price potential that the mannequin has fewer false predictions and the excessive recall price skill that the mannequin is capable to efficiently become aware of the greater wide variety of instances of diseases. A properly stability between precision and recall is additionally established through the F1 rating (95.4%). The AUC fee of 98.2% suggests appropriate capacity of the proposed mannequin to discriminate between the special training of a disease. Based on these results, the aggregate of CNN + GNN + RL looks to be splendid for multi-disease detection as it includes a spatial characteristic extraction, relational learning, and wise selection optimization (Table 4).

Table 4. Performance comparison of different models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
CNN	88.4	87.6	86.9	87.9	91.8
ResNet50	91.2	90.8	89.9	90.2	94.5
DenseNet121	92.0	91.4	90.8	91.1	95.1
CNN-RL	92.7	92.1	91.5	91.8	95.6
CNN-GNN	94.1	93.5	92.8	93.1	96.4
Proposed CNN-GNN-RL	**96.3**	**95.8**	**95.1**	**95.4**	**98.2**

The performance of the proposed CNN-GNN-RL model is compared to the performance of the already proposed deep learning models and hybrid models as shown in Table 3. The proposed model achieved the highest accuracy of 0.963 which is 7.9% higher than the basic CNN model, 5.1% higher than ResNet50, 4.3% higher than DenseNet121, 3.6% higher than CNN-RL and 2.2% higher than CNN-GNN. Likewise, the proposed model had the highest precision, recall, and F1 scores as well as AUC values. All these enhancements show that the fusion of CNN, GNN and RL has proven to be effective for the multi-disease classification task. The CNN module learns the deep spatial features, the GNN module is used to learn relationship among disease region, and for final classification the most informative features are selected by the RL module. Thus the proposed framework is more effective as compared to conventional and single-hybrid techniques for multi-disease detection using biomedical image based techniques.

5. Conclusion

This study introduced a hybrid framework based on CNN-GNN-RL approach for multiple diseases detection in biomedical images. Convolutional Neural Networks (CNNs) are used to identify the spatial features with depth, Graph Neural Networks (GNNs) to learn from relations and finally Reinforcement Learning (RL) for the optimal feature selection and decision making. In biomedical image processing systems, images typically present intricate disease

patterns with an unstable image quality and similar disease areas in different images, thus candidates may be hard to classify. Hand-crafted features are required for traditional machine learning techniques and standard CNN based models may fail to capture the relation between abnormal regions. To address such challenges, the proposed framework aims to overcome them by representing CNN-extracted features with graph structures and enabling the GNN module to capture the structural and contextual relationships between the image regions. The RL module also increases the performance by identifying the most informative features and minimizing the influence of irrelevant or noisy regions. The experimental results proved that the CNN-GNN-RL model had an improved classification performance than the conventional CNN, ResNet50, DenseNet121, CNN-RL, and CNN-GNN models. The proposed model achieved 96.3% accuracy and 95.4% F1-score indicating its suitability for multi-disease detection in biomedical images. High precisions, recalls and AUCs also suggest that the model could be easily used to differentiate the categories of diseases. The findings show better classification accuracy, fewer misclassifications and enhanced robustness of automated disease detection systems when integrating spatial feature extraction, graph-based information on the relationship between the parts and reinforcement learning (RL) optimization. As a result, it seems that the proposed framework is a potentially useful method of computer-aided diagnosis that can provide assistance to doctors for rapid and accurate disease diagnosis. For future research, the proposed model can be further expanded by working with a larger real-time clinical data of hospital from various clinical settings. This would help to enhance the generalization capability of the model and also to validate the results of the same with real-world biomedical images. Usually, more image categories could be collected and more types of image modalities like CT, MRI, ultrasound, X-ray, OCT and histopathology images could be added to make a more comprehensive multi-disease detector system. In addition, E-AI methods like grad-cam, attention heatmap and graph visualisation can be combined with the model to visually demonstrate which part of the image the model looks at for the disease classification. This would help the system to be clear and be trusted by the patients. Enhancing the Reinforcement Learning part by employing advanced techniques like Deep Q-Networks, Actor-Critic or Proximal Policy Optimization for more accurate feature selection and decision optimization can also be an area of future research.

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