Chapter 6

Conclusion and Future Perspective

6.1 Conclusion

Pneumonia is one of the most common thoracic diseases that cause inflammation of the lungs and is considered one of the most common and potentially devastating medical complications after infection, resulting in hospitalization or death. Recently, after the COVID-19 invasion, pneumonia-caused deaths have drastically increased. Evaluation of patients with suspected thoracic disease and pneumonia usually begins with chest radiography. However, certain biochemical tests are required to detect unambiguous categories of pneumonia for specific treatment. RT-PCR is a commonly used method for detecting and quantifying the expression of viral genes in diagnostic samples. However, the technique is laborious, time-consuming, and costly, with a significantly high error rate. Additionally, the scarcity of test kits has become a significant challenge during the COVID-19 pandemic. This work developed multiple deep-learning models for the segmentation, classification, and detection of pneumonia, including COVID-19, in radiological images. Seven highly efficient pre-trained convolutional neural networks were designed and employed, namely, VGG16, VGG19, DenseNet201, Xception, InceptionV3, NasNetMobile, and ResNet152, for classification of up to five classes of pneumonia, i.e., COVID-19, viral pneumonia, bacterial pneumonia, tuberculosis, and control. For the first time, binary classification experiments were performed for COVID-19 vs. bacterial pneumonia and COVID-19 vs. tuberculosis disease classes. The best-performing accuracy was achieved for binary and five class classification tasks than any state-of-the-art methods. Further, a segmentation-based classification system was developed to improve the system's accuracy and preciseness. The segmentation experiments employed three versions of U-series networks: UNet, UNet+, and UNet++ models. Next, eight highly efficient convolutional neural networks were implemented, including VGG16, VGG19, Xception, InceptionV3, Densenet201, NASNetMobile, Resnet50, and MobileNet, respectively, to classify the segmented lung regions up to five classes. The system outperformed previous state-of-the-art methods in binary, three, and five-class classification experiments. Finally, three Ensemble models using four networks, including a hybrid model: Xception, MobileNet, NasnetMobile, and InceptionResNetV2, were designed and implemented to classify the segmented lung into five classes. For the first time, ensemble models were employed to classify pneumonia into five categories. The Ensemble model outperformed the previous experiments and state-of-the-art methods using chest X-rays and verified its efficacy and superiority for clinician precision in COVID-19 and pneumonia diagnosis. The visualization capabilities of the networks were also investigated using the Gradient-weighted Class Activation Mapping to view the abnormalities in chest X-rays and discuss them from radiological perspectives. The system algorithm's high accuracy and robustness raise the possibility of a valuable setup, particularly in environments with a scarcity of biochemical test facilities and radiological expertise.

6.2 Future perspective

Throughout this thesis, different research methodologies with inordinate potential to improve the contributions in abnormalities detection in radiological images were presented. The high-performing algorithms, CNNs, and ensembling methods were developed and tested on large datasets. However, more contributions will be made to enhance the system's performance in the future.

The first effort in extending this work will be implementing more extensive and diverse datasets to retrain the models. Adding more diverse pneumonia types and varied datasets will increase the system's capability. The different variants of SARS-COV-2 are evolving consistently. Their infection patterns may show a different pattern and could be detected by the AI-CAD system. Finding a specific causing variant of SARS-COV2 in COVID-19 will help the particular treatment selection and disease management. Also, implementing more large datasets will increase the robustness and stability of the system.

The next focus will be to improve the system's efficacy to detect more thoracic diseases such as lung nodules and cancer. To achieve this goal the radiological images of patients with lung nodules and those with both pneumonia and lung nodules will be employed to train the system. The involvement of more diseases other than pneumonia will help radiologists to diagnose such conditions present alone or in combination. It has been observed that patients coming to hospitals for COVID-19 or pneumonia were also diagnosed with lung nodules or other cancers; however, they never knew that before. The system, built with diverse detection types, will help patients significantly in the early diagnosis of such diseases and, thus, will enhance the possibility of getting cured.

Retinal images also have lots of information about physiology rather than vision only. In very recent studies, extracting features from retinal or fundus images has significantly helped to get information about several diseases like diabetic retinopathy, glaucoma, diabetes, cardiovascular, and even cancers [220, 221]. Developing powerful algorithms to extract features from retinal images may also help to detect COVID-19 and lung cancers. In the further extension of this work, The retinal images from COVID-19, pneumonia, and lung cancer patients will be collected and employed to train the CNN models. This will help the quick, cost-effective, and radiation-free diagnosis of thoracic diseases, as no chest X-ray, CT, or MRI will be required.

Genomic studies focus on genomes' structure, function, evolution, mapping, and editing. This field of study attempts to understand the structure and function of genetic or epigenetic sequence information of organisms and downstream biological products. Genomics, the study of an organism's whole genetic material, has contributed significantly to our understanding of cancer [222]. The Human Genome Project, which produced a high-quality version of the human genome sequence, has allowed researchers to identify genetic changes that can lead to cancer, such as gene alterations that instruct cells to grow and divide. Understanding the genetic changes in cancer cells has led to new treatments targeting specific genetic mutations.

Artificial intelligence (AI) is increasingly used to extract knowledge from complex and large data sets such as those generated by high-throughput molecular technologies. AI methods are becoming ubiquitous in various fields related to genetics and genomics, including those that classical statistical modeling approaches have long dominated [223, 224]. AI algorithms are used in clinical genomics to target tasks impractical to perform using human intelligence and error-prone when addressed with standard statistical methods. Deep learning has found several applications in genomics and cancer research [225]. In cancer pathology, deep learning has been used for tumor detection, grading, and subtyping, where every solid tumor sample undergoes detailed analysis by a trained pathologist who confirms the presence of cancer. Deep learning has also been used in cancer diagnosis, prognosis, and developing decision support tools for omics data types, such as genomic, methylation, and transcriptomic data, as well as histopathology-based genomic inference. Additionally, deep learning is increasingly used in single-cell genomics, predicting cancer outcomes from histology and genomics using convolutional networks. In genomics, deep learning has been applied to functional genomics, such as predicting the sequence specificity of DNA- and RNA-binding proteins, methylation status, gene expression, and control of splicing. Advances in deep learning have enabled extracting previously hidden information directly from routine histology images of cancer, allowing for a more accurate diagnosis and better classification of cancer pathology. The advent of deep learning has also seen rapid advances in regulatory genomics modeling efforts, particularly rich sequence models based on convolutional neural networks that learn the mapping.

In the future, the DL and ML techniques will be employed on omics datasets to understand and discover new cancer biomarkers and a more precise prediction of patient prognosis. The image and omics data will be combined for deep learning implementation to find the best results. The deep learning classification approaches will be employed on omics data of healthy and diseased patients. The correlation of genes, mRNA, and proteins in healthy and cancerous persons could be found with several ML and DL approaches that will significantly add to the prediction, diagnosis, and prognosis of the patients.

The algorithmically related extension of the work will focus on developing more powerful CNN models, especially employing unsupervised learning. Unsupervised learning is a type of machine learning where the algorithm learns patterns and relationships in data without being explicitly trained with labeled examples [226]. Unlike supervised learning, where the algorithm is provided with labeled data to learn from, unsupervised learning is used when the data is unlabeled, and the algorithm must find structure and patterns on its own. Standard unsupervised learning techniques include clustering, anomaly detection, and dimensionality reduction. Unsupervised learning is more complex; however, it has several benefits over supervised learning. The first benefit is that no labeled datasets are required. Labeling datasets always needed lots of input from expert radiologists. That's why scarcity is frequently observed in labeled datasets. Also, there is a high possibility of manual errors in labeled datasets, which may reduce the efficiency and accuracy of the deep learning model. These limitations may be superseded by employing unsupervised learning, and also, the large datasets could be easily made available to train the system. The next benefit of unsupervised learning is that it can identify hidden patterns and relationships in data that may not be apparent in a labeled dataset. This is particularly useful in multifaceted imaging systems, where the underlying data structure may be complex and poorly understood. Another benefit of unsupervised learning is that it can discover new categories or clusters within a dataset, which can be helpful for image classification tasks. Overall, unsupervised learning has the potential to uncover valuable insights and patterns in data that may be difficult or impossible to discover using other methods.