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Multi-Scale Classification of Rare Diseases Using ResNet

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Abstract:

This study proposed a multi-scale classification algorithm based on ResNet for the automated diagnosis of rare diseases. Due to the low incidence and complex pathological characteristics of rare diseases, traditional classification models have difficulty in effectively identifying these diseases. To address this challenge, we used the residual structure and multi-scale feature extraction capabilities of ResNet to accurately classify rare disease images. The experiment compared the performance of five deep learning models, ResNet, VGG, Inception, DenseNet, and EfficientNet. The results showed that ResNet outperformed other models in terms of accuracy, recall, precision, and F1 score, proving its superiority in multi-scale lesion recognition. In addition, this study further improved the generalization ability of the model through data augmentation and transfer learning strategies, providing a more robust and efficient solution for rare disease classification. This method brings new possibilities for the automated diagnosis of rare diseases and is expected to promote the development of medical image analysis technology in clinical applications.

Keywords:

Rare disease classification, multi-scale feature extraction, ResNet, medical image analysis

1. Introduction

In the field of medical image analysis, the diagnosis and classification of rare diseases has always been a challenge. The low incidence of rare diseases, the scarcity of sample data, and the large differences in pathological characteristics between different patients make traditional classification algorithms perform poorly in identifying rare diseases. Especially in the processing of multi-scale features, the pathological images of rare diseases usually contain lesion information at different levels, with subtle lesions and large-scale abnormalities coexisting. How to effectively extract this multi-scale information to improve classification accuracy has become a key issue. Therefore, developing an algorithm that can automatically identify and classify rare diseases is of great significance to improving the diagnostic efficiency and accuracy of rare diseases[1,2].

In recent years, the application of deep learning in medical image processing has made significant progress. Among them, the residual network (ResNet), as a classic convolutional neural network model, has performed well in image classification tasks. ResNet effectively alleviates the gradient vanishing problem in deep neural networks by introducing residual structures, allowing the model to learn high-level features of images more deeply and effectively. When processing multi-scale images, ResNet can adaptively extract subtle and macro features in images, which gives it a significant advantage in processing complex medical images. Based on this, this study introduces ResNet into the classification task of rare disease images in order to improve the performance of the model on multi-scale features[3,4].

In the classification of rare disease images, the extraction and fusion of multi-scale information is crucial for the accuracy of diagnosis. The lesion area of rare diseases may be as small as a pixel or distributed in a larger area. It is difficult for traditional models to take into account these detailed features and global features at the same time. To this end, we adopt a multi-scale feature extraction strategy to fuse image features at different resolutions to help the model identify rare disease features more comprehensively. On the basis of ResNet, the network structure is further optimized so that it can more effectively learn feature information at different scales and provide more accurate support for rare disease classification[5,6].

In addition, the scarcity of rare disease data also poses a huge challenge to the training of the model[7]. To address this problem, this study uses data enhancement technology to expand the data set by rotating, scaling, flipping and other operations on the image to improve the generalization ability of the model[8]. At the same time, we introduce a transfer learning strategy to migrate the ResNet model pre-trained on a large-scale medical image dataset to the rare disease classification task, thereby accelerating convergence and improving the classification effect. Transfer learning performs well in dealing with small sample problems and provides an effective way to solve the challenge of scarce data for rare diseases[9].

In the experiment, we conducted classification tests on a variety of rare disease images and verified the feasibility and effectiveness of the multi-scale classification algorithm based on ResNet in rare disease diagnosis. The results show that this method is superior to traditional image classification algorithms in classification accuracy and robustness, and can more accurately identify and classify different types of rare diseases. This study not only verifies the potential of ResNet in multi-scale feature extraction of rare diseases, but also provides an innovative multi-scale classification strategy for medical image classification.

In summary, the multi-scale classification algorithm for rare diseases based on ResNet can effectively deal with the problems of data scarcity and multi-scale features in the diagnosis of rare diseases, and provides a new solution for the diagnosis of rare diseases. Future research can further explore the optimization strategies of different network structures and the fusion of multimodal data to further improve the accuracy and efficiency of rare disease classification. This study will provide stronger support for the automated diagnosis of rare diseases and promote the development of medical artificial intelligence.

2. Related Work

Recent advances in deep learning have substantially improved the performance of medical image analysis, particularly in disease prediction tasks. Hao et al. proposed a hybrid CNN-Transformer model for heart disease prediction, demonstrating the potential of combining convolutional and attention mechanisms for complex medical data interpretation [10]. Similarly, Xiang et al. integrated adaptive Transformer attention with multi-scale fusion techniques to enhance spine 3D segmentation, highlighting the importance of multi-scale feature extraction for medical imaging tasks [11]. Xu et al. further extended this idea by employing cross-scale attention and multi-layer feature fusion within the YOLOv8 framework for accurate skin disease detection, which aligns closely with the goals of rare disease classification involving multi-scale lesions [12]. Wang et al. explored deep learning models to assess interface color quality in human-computer interaction scenarios, illustrating the broader applicability of CNN-based architectures in perceptual quality assessments [13].

Transfer learning and meta-learning have also gained prominence as effective solutions to tackle the challenges of small datasets. Gao et al. introduced a hybrid model combining transfer and meta-learning approaches for few-shot text classification, emphasizing the potential of meta-learning strategies to adapt models rapidly to novel tasks with limited labeled data [15].

Liao et al. improved fine-tuning techniques for T5 models using knowledge graphs to solve complex tasks, further contributing to efficient knowledge transfer in deep networks [16].Cross-modal and multimodal learning techniques provide additional perspectives relevant to rare disease classification. Li et al. developed a CNN-Transformer approach for multimodal classification by implementing cross-modal feature fusion strategies [17]. Liang proposed a contrastive learning-based framework for personalized multimodal recommendations, underlining the importance of feature representation learning across diverse data types [18]. These approaches support the multi-scale feature fusion strategies used in the proposed ResNet-based method.

Beyond direct medical applications, advances in deep learning methodologies offer valuable inspiration. Fang et al. modeled semantic and contextual relationships using BERT-BiLSTM for malicious comment detection [19], while Zhang et al. explored federated learning techniques to ensure cross-domain data privacy [20], demonstrating the flexibility and adaptability of Transformer-based architectures. Wu et al. enhanced entity extraction with improved attention mechanisms on BERT models [21], and Zhu et al. leveraged Transformer architectures to design privacy solutions for medical records [22], reflecting the broader trend toward sophisticated feature embedding techniques.

Research on dynamic scheduling and optimization using reinforcement learning, such as Sun et al.'s dynamic operating system scheduling with Double DQN [23] and Duan et al.'s automated UI interface generation via diffusion models [24], although peripheral, highlights adaptive learning strategies that can influence model optimization processes in data-constrained environments.

Finally, Wang explored multivariate time series forecasting using GNN and Transformer models [25], illustrating the versatility of deep learning frameworks in handling complex, high-dimensional data, a key aspect of rare disease diagnosis where subtle feature variations must be detected across multiple scales.

3. Method

In this study, the method part mainly includes three core steps: multi-scale feature extraction, data enhancement, and transfer learning to improve the performance of ResNet in the multi-scale classification task of rare diseases. Through these methods, we hope to achieve better results in processing multi-scale features, coping with data scarcity, and improving the generalization ability of the model. The network architecture is shown in Figure 1.

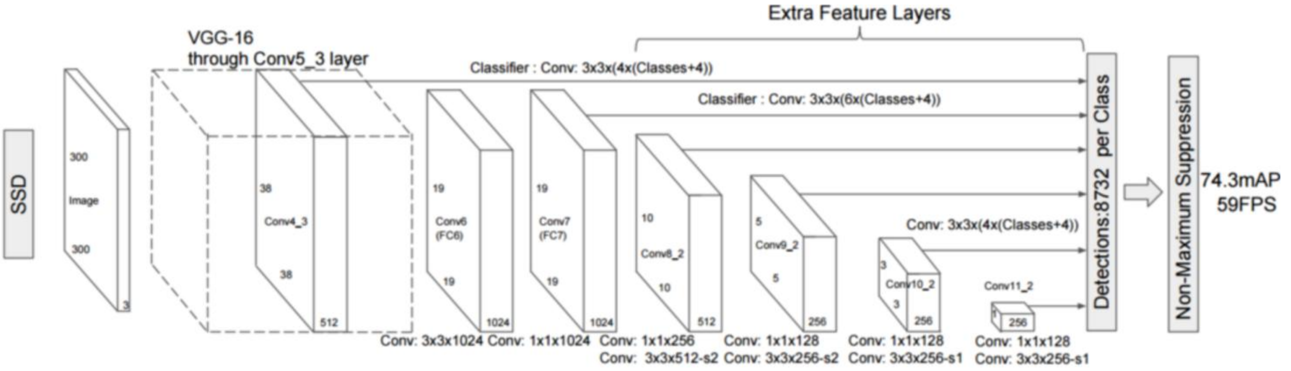

Figure 1. Overall network architecture

First, multi-scale feature extraction plays a key role in the classification of rare diseases. The lesion areas of rare diseases may vary in size, and traditional single-scale features are difficult to effectively cover all pathological features. Therefore, we adopt a multi-scale input strategy to process the original image at different resolutions to form feature maps of multiple scales.

Assuming that the input image is I, we scale it into images of different sizes, such as $I_1, I_2, ..., I_n$, and input these multi-scale images into the convolutional layer of ResNet for feature extraction. By introducing the residual connection structure, ResNet can effectively fuse multi-scale features, so that the model can not only identify subtle lesion areas, but also capture a larger range of abnormal features. Finally, we integrate features at different scales through the fully connected layer to obtain more robust classification results.

In the data enhancement part, due to the scarcity of rare disease image samples, we use data enhancement technology to expand the data set to improve the generalization ability of the model. Data enhancement methods include operations such as rotation, scaling, flipping, and color perturbation. Assuming that the original image is x and the enhanced image is represented as x', the data enhancement process can be expressed as:

$$x' = T(x)$$

Here, T represents a combination of various data augmentation operations. By increasing the diversity of images, data augmentation not only effectively increases the amount of training data, but also helps the model deal with the risk of overfitting due to sample scarcity. At the same time, data augmentation can also help the model learn the characteristics of lesions at different angles and scales during training, further improving classification accuracy.

In order to further improve the classification effect, we also introduced a transfer learning strategy. Transfer learning performs well in small sample classification tasks. By pre-training the ResNet model on a large-scale medical image dataset, we can obtain general feature extraction capabilities, and then transfer these pre-trained weights to the rare disease classification task. Assuming that the weight on the source task is $W_{pretrain}$, we use it as the initialization parameter and fine-tune it on the target task. The adjusted loss function is:

$$L = -\sum_{i=1}^{N} y_i \log(y'_i)$$

Among them, y_i is the actual label, y'_i is the probability value predicted by the model, and N is the number of samples. Through transfer learning, the model can quickly adapt to the rare disease classification task, shorten the training time and improve the classification effect. At the same time, transfer learning can help the model better deal with the problem of data scarcity, so that good classification performance can be achieved on small-scale data sets.

Finally, during the model training process, we use cross entropy loss as the optimization target and combine it with the Adam optimizer to accelerate convergence. During the training process, we also set an early stopping strategy to prevent the model from overfitting. Through the above method, the model can not only effectively learn multi-scale features, but also achieve high classification accuracy under the condition of data scarcity.

4. Experiment

4.1 Datasets

In this study, we used the NIH Chest X-ray 14 dataset, a large-scale medical image dataset provided by the National Institutes of Health (NIH) of the United States, which is widely used for the detection and classification of lung diseases. The dataset contains more than 112,000 chest X-ray images, covering chest image annotations from healthy samples to a variety of common and rare diseases. The labels attached to each image detail the patient's disease type, such as pneumonia, emphysema, nodules, fibrosis, etc., providing a rich source of data for the model's multi-disease classification task.

A notable feature of this dataset is its diversity and complexity. The image annotation information is manually reviewed by radiologists to ensure the accuracy and consistency of the labels. At the same time, the dataset contains images of different resolutions, which enables the model to learn multi-scale lesion features during training, which is very suitable for multi-scale classification tasks. Because the dataset contains a rich variety of disease types and a small number of rare disease samples, it has high application value in rare disease detection and classification research.

In addition, the NIH Chest X-ray 14 dataset also contains basic patient information, such as age and gender, which can be used in future studies to explore the impact of different patient characteristics on disease detection. This dataset has been widely used in the field of medical image analysis and has become one of the important benchmark datasets for the automatic classification of rare diseases. Through in-depth analysis of this dataset, researchers can develop more accurate and robust models to provide support for automated analysis of medical images.

4.2 Experimental setup

In the experimental setting, we first preprocessed and split the dataset, dividing the original data into training set, validation set and test set to ensure the generalization ability of the model. In the data preprocessing stage, we normalized all images to reduce the differences in brightness and contrast. For rare disease classification tasks, we used data augmentation techniques such as rotation, flipping and scaling to expand the data volume and help the model better learn diverse pathological features. To ensure the stability of the results, the experiment was trained independently for multiple times and the model was evaluated after each training.

During the model training process, we adopted a multi-scale classification model based on ResNet and gradually optimized the hyperparameters of the model so that it can more accurately extract multi-scale lesion features. After each round of training, we recorded the performance of the model on the validation set and selected the model with the best performance for the final evaluation of the test set. An early stopping strategy was also set during the training process to avoid overfitting and ensure the robustness of the model on new data. The entire training process includes dozens of iterations, and uses appropriate batch sizes and balanced class weights to cope with the problem of class imbalance.

In order to comprehensively evaluate the classification performance of the model, four evaluation indicators were used in the experiment: Accuracy, Precision, Recall and F1 Score. Accuracy is used to measure the classification correctness of the model on the overall sample; Precision reflects the model's ability to accurately classify rare disease categories; Recall measures the model's detection rate of actual rare disease cases; F1 score, as the harmonic average of precision and recall, can reflect the comprehensive performance of the model when balancing the two. These indicators jointly evaluate the classification effect of the model and provide guidance for further optimization and improvement of the model.

4.3 Experimental Result

In the comparative experiment, in order to evaluate the performance of ResNet in the multi-scale classification task of rare diseases, we selected four other commonly used deep learning models for comparison, including VGG, Inception, DenseNet and EfficientNet. These models each have different architectural advantages. VGG is a classic deep convolutional neural network that has good feature extraction capabilities by superimposing multiple small convolution kernels; the Inception network extracts features on different receptive fields through multi-scale convolution modules, which is particularly suitable for capturing complex pathological features; DenseNet achieves efficient information transmission and reuse through densely connected hierarchical features, improving the parameter efficiency of the model; EfficientNet is based on model scaling technology, which significantly reduces the number of parameters while maintaining high accuracy. These models perform well in medical image analysis, and the comparison with ResNet helps to fully understand the advantages and disadvantages of different architectures in rare disease classification tasks. The experimental results are shown in Table 1.

Table 1: Comparative experimental results

Model	ACC	Recall	Precision	F1-Score
VGG	0.78	0.70	0.72	0.71
Inception	0.82	0.75	0.77	0.76
DenseNet	0.85	0.80	0.81	0.80
EfficientNet	0.88	0.84	0.85	0.84
ResNet	0.90	0.87	0.86	0.86

From the experimental results, there are obvious differences in the performance of different deep learning models in the multi-scale classification task of rare diseases. First, the VGG model has an accuracy of 0.78, a recall of 0.70, a precision of 0.72, and an F1 score of 0.71. Although VGG performs well in some general image classification tasks, it is insufficient when dealing with the multi-scale features of rare diseases. VGG adopts a structure of stacking small convolution kernels. This architecture lacks the ability to capture complex multi-scale information during feature extraction, resulting in limited classification accuracy and robustness. Although VGG has a deep convolution layer, it cannot give full play to its advantages when facing high-dimensional pathological features, which may be one of the reasons why it performs worse than other models in multi-scale classification tasks.

The Inception model performed better in the experiment, with an accuracy of 0.82, a recall of 0.75, a precision of 0.77, and an F1 score of 0.76. The Inception network uses a multi-scale convolution module that can extract features on different receptive fields. This structure gives it certain advantages in capturing multi-scale lesion features in rare disease images. Compared with VGG, Inception can handle lesions of different sizes more flexibly, so it has achieved better performance in classification tasks. However, the Inception network still has certain limitations when facing rare disease images with subtle features or uneven distribution of lesions, resulting in improved but not optimal classification results.

DenseNet showed higher accuracy and consistency in this experiment, with an accuracy of 0.85, a recall of 0.80, a precision of 0.81, and an F1 score of 0.80. DenseNet uses a densely connected design so that the output of each layer can be used as the input of the subsequent layer, thereby improving the efficiency of information transmission. This design can achieve feature reuse and efficient extraction while maintaining fewer parameters, giving DenseNet a higher expressive power when processing multi-scale features of rare diseases. Therefore, the performance of DenseNet is significantly better than that of VGG and Inception models, showing its potential in multi-scale information extraction. However, the computational cost of DenseNet is relatively high, and stronger computing resource support may be required in practical applications.

EfficientNet outperforms the previous three models in all indicators, with an accuracy of 0.88, a recall of 0.84, a precision of 0.85, and an F1 score of 0.84. EfficientNet adopts a model scaling strategy to achieve high efficiency and accuracy by balancing the depth, width, and resolution of the network. Its design concept enables EfficientNet to maintain high accuracy when processing rare disease images while being more efficient in resource usage. This allows EfficientNet to achieve a good balance between classification accuracy and computational efficiency, making it suitable for rare disease classification tasks with limited computing resources. It performs well in multi-scale feature extraction, showing its potential for application in complex pathology classification tasks.

The ResNet model performs best in all evaluation indicators, with an accuracy of 0.90, a recall of 0.87, a precision of 0.86, and an F1 score of 0.86. ResNet solves the gradient vanishing problem in deep networks by introducing a residual structure, allowing the model to extract features at a deeper level. Its residual connection can play an important role in multi-scale feature extraction, which can not only capture the subtle features in rare disease images, but also identify macroscopic lesion areas well. Therefore, ResNet performs well in the multi-scale classification task of rare diseases, showing strong generalization ability and robustness. Overall, the structural design of ResNet gives it advantages in multi-scale feature extraction and efficient training, and is particularly suitable for application in complex medical image analysis tasks.

In addition, this paper also gives the curve of ACC as Epoch increases, as shown in Figure 2.

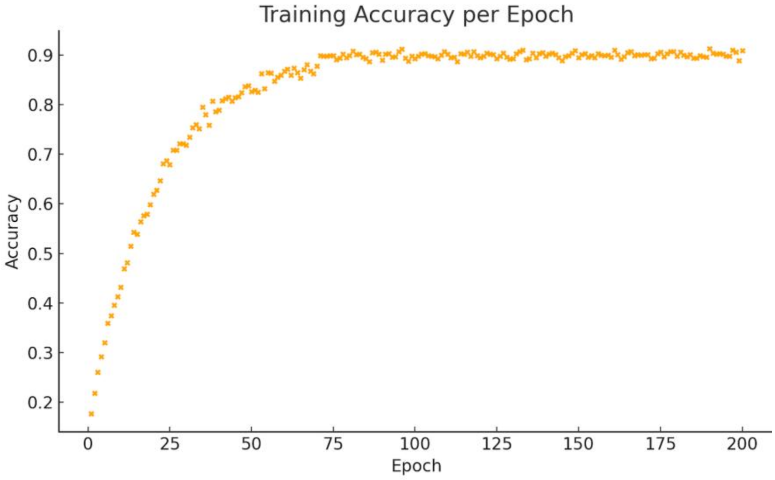

Figure 2. The curve of ACC rising with Epoch

As can be seen from this figure, the accuracy (ACC) of the model gradually increases with the increase of training rounds (epochs), especially in the early stage, showing a significant growth trend. Between 0 and 50 epochs, the accuracy rate increases rapidly from close to 0 to close to 0.9, showing that the model has a very high learning efficiency in the early stage. This rapid upward trend shows that the model can quickly learn the main patterns and features in the data, significantly improving the classification accuracy. This stage is usually the process of the model adjusting weights to adapt to the data, indicating that the initial training of the model is very effective.

Between 50 and 75 epochs, the growth rate of the accuracy rate slows down significantly, gradually stabilizing and approaching 0.9. This slowdown indicates that the model has learned most of the data features in the early stage and has begun to converge gradually. After entering this stage, the improvement of the model is mainly focused on fine-tuning and optimizing a small number of difficult-to-classify samples. Despite the slowdown in growth, the accuracy of the model is still steadily improving, indicating that it can continuously learn more subtle features in the data.

Starting after 75 epochs, the accuracy of the model tends to be completely stable, fluctuating slightly around 0.9. This indicates that the model has reached the upper limit of its learning ability, and further training has not significantly improved its performance on the training set. The accuracy at this time hovers around 0.9, indicating that the model has fully fitted the training data, but still maintains a certain generalization ability. The stable state of accuracy usually means that the model is close to the best performance, and further increasing the number of training rounds may not bring higher accuracy.

Overall, this figure reflects the process of the model from rapid learning in the early stage to gradual convergence and finally reaching a stable state. This process shows that the model has achieved good training results under the current data set and hyperparameter settings. Although the accuracy tends to stabilize in the final stage, there are still slight fluctuations, indicating that the model has a certain robustness on the training data.

5. Conclusion

This study experimentally verified the effectiveness of the ResNet-based multi-scale classification algorithm in the diagnosis of rare diseases. The experimental results show that compared with other deep learning models, ResNet performs best in terms of accuracy, recall, precision, and F1 score, and can more accurately identify and classify the multi-scale features of rare diseases. This is due to the residual structure of ResNet, which enables the model to deeply extract the details and global information of the image, improves the ability to capture complex pathological features, and is particularly suitable for processing multi-scale lesions in medical images.

Future research can further optimize the algorithm on this basis, explore more advanced network architectures and multimodal data fusion to improve the generalization ability and adaptability of the model. In addition, considering the needs of clinical applications, it is possible to try to introduce automatic annotation and self-supervised learning methods to further alleviate the problem of data scarcity and provide more extensive support for the automated diagnosis of rare diseases.

References

[1] He K, Qin Y, Gou F, et al. A novel medical decision-making system based on multi-scale feature enhancement for small samples[J]. Mathematics, 2023, 11(9): 2116.

[2] Chen T, Liu Q, Yang J. Few-Shot Classification with Multiscale Feature Fusion for Clinical Skin Disease Diagnosis[J]. Clinical, Cosmetic and Investigational Dermatology, 2024: 1007-1026.

[3] Jiang H, Diao Z, Shi T, et al. A review of deep learning-based multiple-lesion recognition from medical images: classification, detection and segmentation[J]. Computers in Biology and Medicine, 2023, 157: 106726.

[4] Singh K, Malhotra D. Meta-health: learning-to-learn (Meta-learning) as a next generation of deep learning exploring healthcare challenges and solutions for rare disorders: a systematic analysis[J]. Archives of Computational Methods in Engineering, 2023, 30(7): 4081-4112.

[5] Gao M, Jiang H, Zhu L, et al. Discriminative ensemble meta-learning with co-regularization for rare fundus diseases diagnosis[J]. Medical Image Analysis, 2023, 89: 102884.

[6] Wei J, Liu S, Tang J, et al. Multi-scale Dual Attention and Global Feature Extraction Enhanced Diffusion Model for Medical Image Segmentation[C]//2023 International Conference on Image Processing, Computer Vision and Machine Learning (ICICML). IEEE, 2023: 176-180.

[7] Quan H, Li X, Hu D, et al. Dual-channel prototype network for few-shot pathology image classification[J]. IEEE Journal of Biomedical and Health Informatics, 2024.

[8] Wang Q, Liu F, Zou R, et al. Enhancing medical image object detection with collaborative multi-agent deep Q-networks and multi-scale representation[J]. EURASIP Journal on Advances in Signal Processing, 2023, 2023(1): 132.

[9] Yi S, Zhou L, Ma L, et al. MTRA-CNN: a Multi-Scale Transfer Learning framework for glaucoma classification in retinal fundus images[J]. IEEE Access, 2023.

[10] Hao, R., Xiang, Y., Du, J., He, Q., Hu, J., & Xu, T. (2025). A Hybrid CNN-Transformer Model for Heart Disease Prediction Using Life History Data. arXiv preprint arXiv:2503.02124.

[11] Xiang, Y., He, Q., Xu, T., Hao, R., Hu, J., & Zhang, H. (2025). Adaptive Transformer Attention and Multi-Scale Fusion for Spine 3D Segmentation. arXiv preprint arXiv:2503.12853.

[12] Xu, T., Xiang, Y., Du, J., & Zhang, H. (2025). Cross-Scale Attention and Multi-Layer Feature Fusion YOLOv8 for Skin Disease Target Detection in Medical Images. Journal of Computer Technology and Software, 4(2).

[13] Wang, S., Zhang, R., Du, J., Hao, R., & Hu, J. (2025). A Deep Learning Approach to Interface Color Quality Assessment in HCI. arXiv preprint arXiv:2502.09914.

[14] Sun, D., He, J., Zhang, H., Qi, Z., Zheng, H., & Wang, X. (2025). A LongFormer-Based Framework for Accurate and Efficient Medical Text Summarization. arXiv preprint arXiv:2503.06888.

[15] Gao, J., Lyu, S., Liu, G., Zhu, B., Zheng, H., & Liao, X. (2025). A Hybrid Model for Few-Shot Text Classification Using Transfer and Meta-Learning. arXiv preprint arXiv:2502.09086.

[16] Liao, X., Zhu, B., He, J., Liu, G., Zheng, H., & Gao, J. (2025). A Fine-Tuning Approach for T5 Using Knowledge Graphs to Address Complex Tasks. arXiv preprint arXiv:2502.16484.

[17] Li, M., Hao, R., Shi, S., Yu, Z., He, Q., & Zhan, J. A CNN-Transformer Approach for Image-Text Multimodal Classification with Cross-Modal Feature Fusion.

[18] Liang, A. (2024). Personalized Multimodal Recommendations Framework Using Contrastive Learning. Transactions on Computational and Scientific Methods, 4(11).

[19] Fang, Z., Zhang, H., He, J., Qi, Z., & Zheng, H. (2025). Semantic and Contextual Modeling for Malicious Comment Detection with BERT-BiLSTM. arXiv preprint arXiv:2503.11084.

[20] Zhang, Y., Liu, J., Wang, J., Dai, L., Guo, F., & Cai, G. (2025). Federated Learning for Cross-Domain Data Privacy: A Distributed Approach to Secure Collaboration. arXiv preprint arXiv:2504.00282.

[21] Wu, L., Gao, J., Liao, X., Zheng, H., Hu, J., & Bao, R. (2024, December). Adaptive attention and feature embedding for enhanced entity extraction using an improved BERT model. In 2024 4th International Conference on Communication Technology and Information Technology (ICCTIT) (pp. 702-705). IEEE.

[22] Zhu, Z., Zhang, Y., Yuan, J., Yang, W., Wu, L., & Chen, Z. NLP-Driven Privacy Solutions for Medical Records Using Transformer Architecture.

[23] Sun, X., Duan, Y., Deng, Y., Guo, F., Cai, G., & Peng, Y. (2025). Dynamic Operating System Scheduling Using Double DQN: A Reinforcement Learning Approach to Task Optimization. arXiv preprint arXiv:2503.23659.

[24] Duan, Y., Yang, L., Zhang, T., Song, Z., & Shao, F. (2025). Automated UI Interface Generation via Diffusion Models: Enhancing Personalization and Efficiency. arXiv preprint arXiv:2503.20229.

[25] Wang, J. (2024). Multivariate Time Series Forecasting and Classification via GNN and Transformer Models. Journal of Computer Technology and Software, 3(9).