

CANCER DETECTION AND CLASSIFICATION THROUGH TRANSFER LEARNING WITH RESNET18-BASED CONVOLUTIONAL NEURAL NETWORK

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ABSTRACT Cancer is a disease where some cells in the body grow destructively and, in most cases, spread to other body organs. Biologically, cell grows and expand through some natural processes to create new cells that replaces old and damaged ones, this process when distorted can result in abnormal cell growth thereby forming tumors that can harmful. Recently, the rapid advancements in deep learning have proffer solutions to the deadly disease by way of early detection and accurate classifications. This study explores the application of deep learning frameworks, specifically PyTorch, in developing a robust multi-cancer detection and classification system. The research focuses on creating an architecture capable of accurately diagnosing multiple cancer types, including brain, breast, bone, kidney, oral, lung/colon, cervical, and lymphoma cancers. The study employs a comprehensive methodology of obtaining large size of different cancer datasets which was preprocessed to ensure a clean, noiseless datasets, models development, and rigorous training and testing of the datasets and finally performance evaluation of the system were carried out. The results demonstrated significant improvements in diagnostic accuracy, highlighting the potential of machine learning in transforming cancer care. The proposed system offers promising prospects for enhancing early detection and personalized treatment, ultimately improving patient outcomes.

KEYWORDS: Cancer, Cell, Deep Learning, Machine Learning, Preprocessing, Pytorch, Tumor.

I. INTRODUCTION

Cancer, characterized by uncontrolled cell growth, is a leading cause of mortality worldwide. Early detection and accurate classification are crucial for effective treatment and improved survival rates. Traditional diagnostic methods often fall short in precision and efficiency. The integration of machine learning, particularly deep learning frameworks like PyTorch, has shown promise in overcoming these limitations [3]. Machine learning algorithms excel in analyzing complex medical data, identifying patterns, and making predictions with remarkable speed and accuracy [7]. Recent studies have demonstrated the potential of deep learning in various medical applications, including cancer detection and classification [1]. The convergence of machine learning and oncology provides an opportunity to revolutionize diagnostic practices, enhance treatment planning, and offer personalized patient care. This study delves into developing a multi-cancer detection and classification system using PyTorch, aiming to achieve superior diagnostic performance across various cancer types. It should be of interest that despite advancements in cancer research and treatment, a significant gap exists in the accurate and efficient detection of multiple cancer types. Most existing research has focused on single cancer detection, leaving a critical need for a multi-cancer detection framework. This study addresses the challenge of developing a system capable of discerning between various cancer types with high accuracy and efficiency [6]. The problem lies in creating a robust system that minimizes overfitting and generalizes well across diverse datasets [3].

II. Related Works

Recent advancements in the field of oncology have underscored the critical importance of early cancer detection and accurate classification in improving patient outcomes [11]. Various studies have highlighted the potential of machine learning techniques, particularly deep learning models implemented with frameworks like PyTorch, in enhancing the efficiency and precision of cancer diagnosis processes. One notable study by [6] demonstrated the efficacy of deep learning algorithms in multi-cancer detection by leveraging diverse datasets and sophisticated model architectures. The results indicated a significant improvement in classification accuracy across different cancer types, showcasing the potential of machine learning in revolutionizing diagnostic practices. [8] emphasized the role of feature extraction methodologies in optimizing the performance of cancer classification models. By integrating advanced feature engineering techniques with PyTorch-based models, the researchers achieved notable advancements in distinguishing between benign and malignant tumors, paving the way for more accurate diagnostic tools. Building on these advancements, recent studies by [9] and [16] have explored the potential of ensemble learning methods to improve the robustness and generalizability of cancer classification models. By aggregating predictions from multiple base learners, ensemble techniques showed enhancing model performance and mitigating over-fitting issues, thereby contributing to more reliable diagnostic systems.

The landscape of cancer detection and classification has witnessed a paradigm shift with the advent of machine learning technologies. Notable studies by [15] and [14] demonstrated the potential of convolutional neural networks (CNNs) in accurately identifying cancerous tissues from medical imaging data. Their findings underscore the efficacy of deep learning models in automating the detection process and improving diagnostic accuracy. The review conducted by [7] highlighted the significance of comprehensive evaluation metrics in assessing the robustness and generalizability of machine learning-based cancer detection systems. Their analysis emphasized the need for rigorous validation procedures and comparative studies to validate the effectiveness of novel methodologies against existing standards. [10] also explored the application of transfer learning techniques in cancer classification tasks by leveraging pre-trained models and fine-tuning them on specific cancer datasets and achieved remarkable results in differentiating between subtypes of cancer with high sensitivity and specificity, showcasing the versatility of machine-learning approaches in oncology. Furthermore, the work of [12] delved into the integration of multi-omics data for comprehensive cancer profiling by combining genomics, transcriptomics and proteomics data through advanced machine learning algorithms in which they uncover intricate molecular signatures associated with different cancer types that enabled more precise classification and personalized treatment strategies.

III. RESEARCH METHODOLOGY

A. DATA COLLECTION AND PREPROCESSING

The study utilizes a diverse dataset comprising high-resolution medical images from various cancer types, including brain, breast, bone, kidney, oral, lung/colon, cervical, and lymphoma cancers. The dataset was sourced from reputable platforms like Kaggle, ensuring a wide representation of different stages and subtypes. Data augmentation techniques, such as rotation, flipping, and scaling, were employed to expand

the dataset and enhance model generalization. The images were normalized to a consistent scale and pixel range, facilitating stable and efficient model training [2].

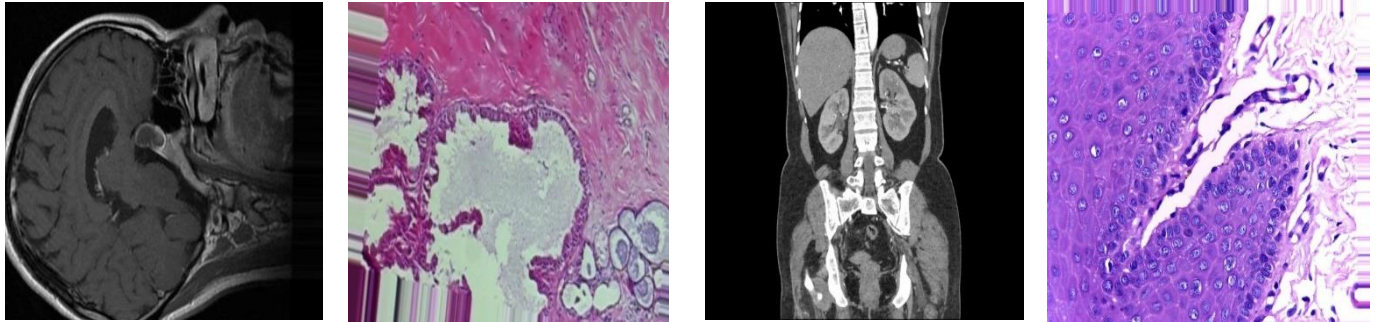


Figure 1: Sample Images from the Cancer Datasets.

The above images are the sample of different types of cancer, which the first image is brain glioma, the second image is breast benign, while the third sample image is kidney tumor, and the fourth image is oral SCC (squamous cell carcinoma) cases.

B. MODEL ARCHITECTURE

The proposed system is based on a Convolutional Neural Network (CNN) architecture shown in Figure 2. The CNN architecture is known for its effectiveness in image-based tasks. The ResNet-18 model, a widely used CNN architecture, was selected as the backbone due to its ability to capture and learn hierarchical features from complex medical images [2]. A transfer learning approach was employed, utilizing the pre-trained ResNet-18 model's base layers and fine-tuning the final fully connected layer on the target cancer dataset [5, 13].

C. MODEL TRAINING

The cross-entropy loss function was chosen as the primary objective for training, given its suitability for multi-class classification problems [3]. The Adam optimization algorithm was used to update the model parameters, offering adaptive learning rates for efficient convergence. A comprehensive hyperparameter tuning process was conducted, experimenting with various learning rates, batch sizes, and other relevant parameters to optimize model performance [2].

D. DESIGN AND IMPLEMENTATION

The implementation process involved several stages, from data preprocessing to model deployment. The architecture design focused on leveraging the strengths of CNNs, particularly ResNet-18, to extract relevant features from medical images [2]. The transfer learning approach allowed the model to utilize pre-trained features, reducing the computational load and improving training efficiency [5]. The model was trained on a powerful computational setup, ensuring high accuracy and efficiency.

E. DATA AUGMENTATION AND NORMALIZATION

To address data scarcity and enhance model robustness, various data augmentation techniques were applied. These included image rotations, flips, and scaling, creating diverse training examples and preventing overfitting. The images were normalized to ensure consistency, facilitating better convergence during training [2].

F. TRANSFER LEARNING AND FINE-TUNING

The pre-trained ResNet-18 model provided a solid foundation for the system, with its base layers frozen to retain learned features. The final fully connected layer was fine-tuned on the target dataset, enabling the model to specialize in detecting and classifying multiple cancer types [5].

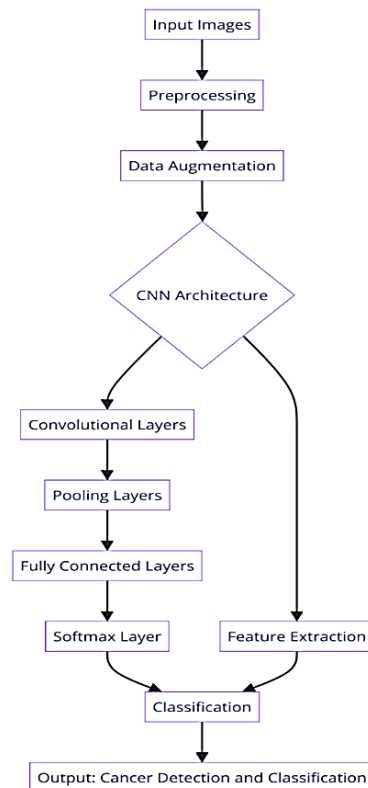


Figure 2: Diagram of the Convolutional Neural Network (CNN) Architecture

IV. RESULTS AND DISCUSSION

The model's performance was evaluated using various metrics, including accuracy, precision, recall, and F1-score. The results showed high accuracy across most cancer types, particularly in breast, lung/colon, kidney, and acute lymphoblastic leukemia (ALL), where accuracy exceeded 95%. The models for oral cancer and lymphoma showed relatively lower accuracy, indicating the need for further fine-tuning and possibly more data.

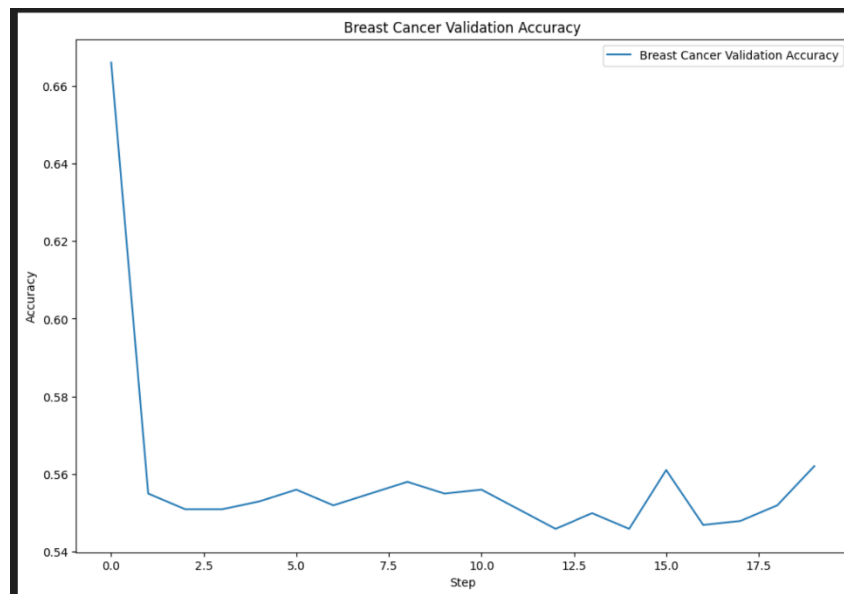


Figure 3: Graphs showing Accuracy and Loss Curves for the Validation Sets of Breast Cancers

Figure 3 shows a line graph depicting the "Breast Cancer Validation Accuracy" over time. The x-axis represents the step or iteration, while the y-axis shows the validation accuracy. The line graph fluctuates between around 0.54 and 0.64, indicating the model's performance in validating breast cancer cases. The graph suggests that the model's accuracy varies throughout the training or validation process, with peaks and valleys in the validation accuracy.

A. MODEL DEVELOPMENT AND TRAINING

To build the multi-cancer classification models, we utilize the pre-trained ResNet18 architecture from PyTorch's torch vision library. The training process and performance metrics for each cancer type are presented in table 1.

Table 1: Hyperparameter Tuning Results

Cancer Type	Batch Size	Learning Rate	Epochs	Validation Accuracy	Test Accuracy
Breast Cancer	32(train), 16(Val/test)	0.001	4	98.5%	98.3%
Oral Cancer	32(train), 16(Val/test)	0.001	4	83.5%	80.5%
Lymphoma	32(train), 16(Val/test)	0.001	4	88.3%	86.9%
Cervical Cancer	32(train), 16(Val/test)	0.001	4	95.3	94.9
Lung and Colon Cancer	32(train), 16(Val/test)	0.001	4	97.8%	98.1%
Brain Cancer	32(train), 16(Val/test)	0.001	4	92.2%	92.9%
Kidney Cancer	32(train), 16(Val/test)	0.001	4	98.0%	98.0%
Acute Lymphoblastic Leukemia (ALL)	32(train), 16(Val/test)	0.001	4	99.0%	99.1%

The table above shows the hyperparameter values used for each cancer type, including the batch size, learning rate, and number of training epochs. It also summarizes the performance of the models on the validation and test sets, as measured by the validation and test accuracy, respectively. The results indicate that the models generally achieved high validation and test accuracy, with the Breast Cancer, Lung and

Colon Cancer, Kidney Cancer, and Acute Lymphoblastic Leukemia (ALL) models performing particularly well, reaching over 95% accuracy on the test set. The Oral Cancer and Lymphoma models had lower test accuracy compared to the other cancer types, suggesting that further hyperparameter tuning or model architecture adjustments may be needed to improve their performance.

B. CONFUSION MATRICES

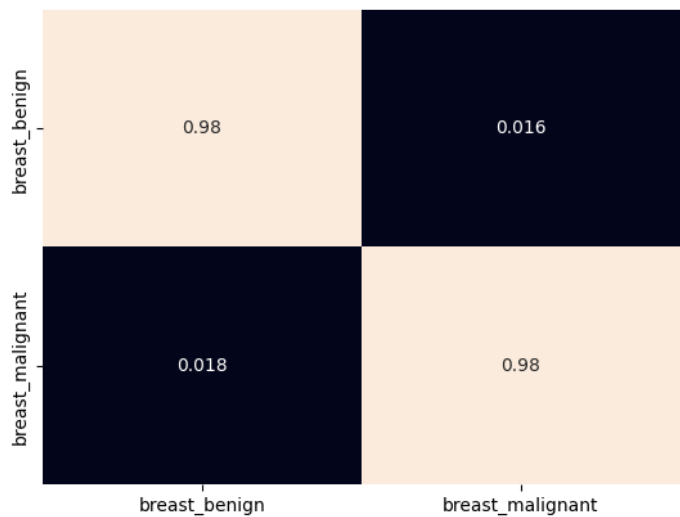


Figure 5: Heatmap Shows a Confusion Matrix for a Breast Cancer.

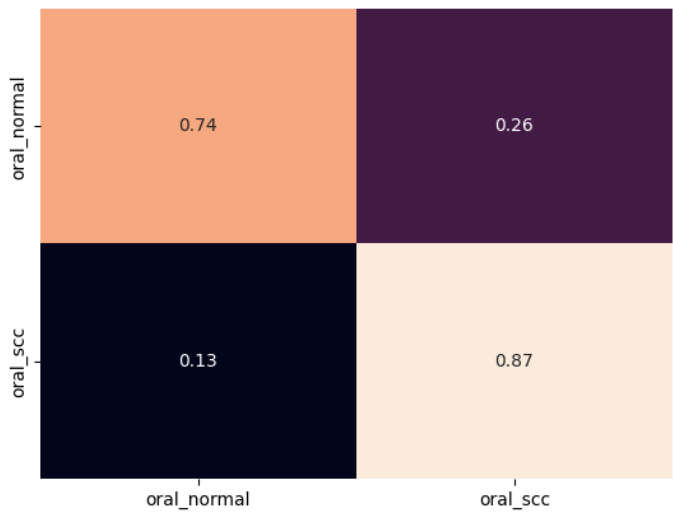


Figure 6: Heatmap Shows a Confusion Matrix for an Oral Cancer.

Figure 5 shows the model accurately classifies 98% of both benign and malignant cases, with minimal misclassification rates. While figure 6 shows the model correctly identifies 74% of normal oral cases and 87% of oral SCC (squamous cell carcinoma) cases, with misclassification rates of 26% for normal as SCC and 13% for SCC as normal.

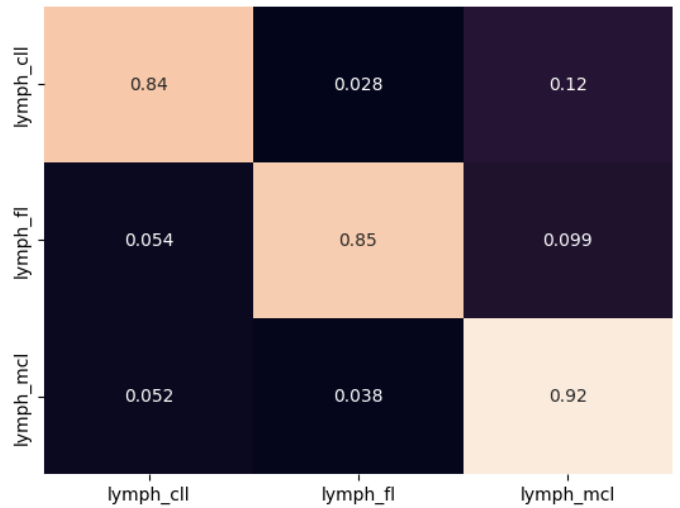


Figure 7: Heatmap Shows a Confusion Matrix for Lymphoma Cancer.

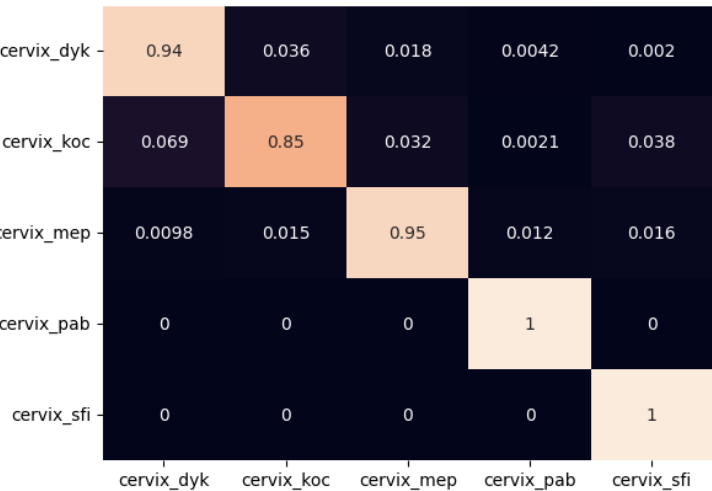


Figure 8: Heatmap Shows a Confusion Matrix for Cervix Cancer.

Figure 7 shows high accuracy for lymph disease types, with over 80% correct classifications. While figure 8 also shows high accuracy for cervix types, with perfect scores for cervix PAB and SFI, and some misclassification for cervix KOC.

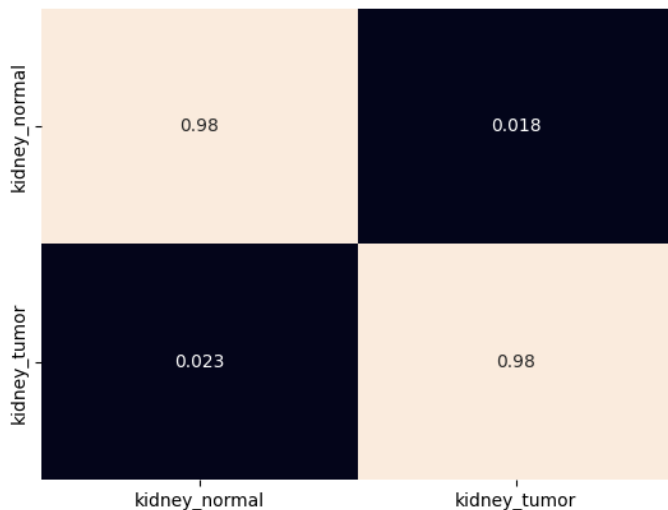


Figure 9: Heatmap Shows a Confusion Matrix for Kidney Cancer.



Figure 10: Heatmap Shows a Confusion Matrix for Acute Lymphoblastic Leukemia (ALL) Cancer.

Figure 9 and figure 10 confusion matrices, show high model accuracy in distinguishing between normal and tumor kidney samples and in classifying various stages of acute lymphoblastic leukemia, with minimal misclassification

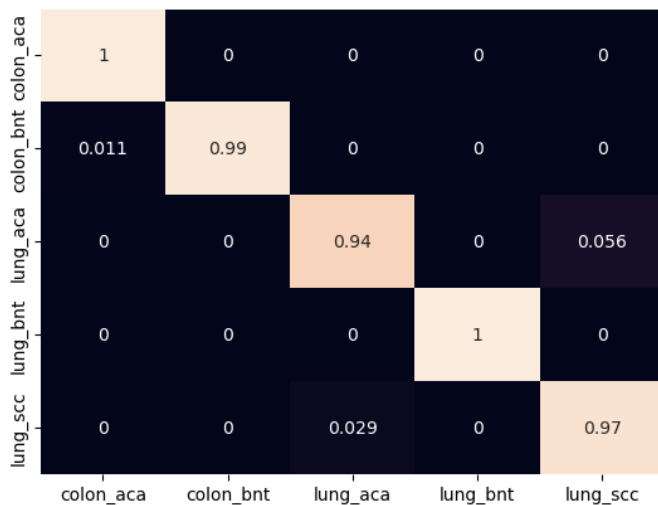


Figure 11: Heatmap shows a Confusion Matrix for Lung and Colon Cancer.

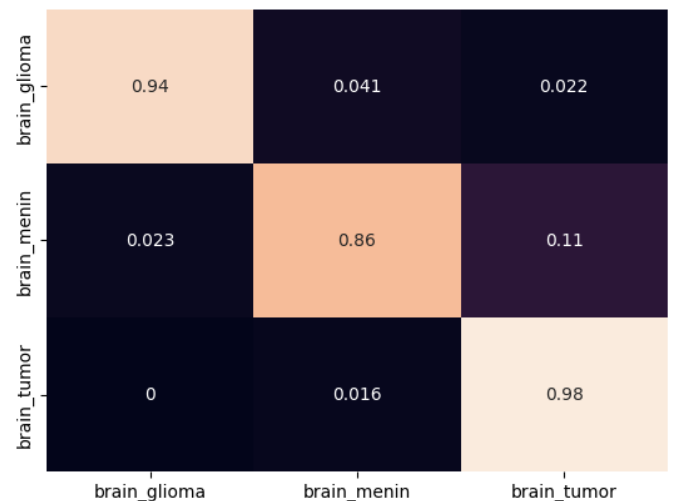


Figure 12: Heatmap Shows a Confusion Matrix for Brain Cancer.

The above images of Confusion matrices show the performance of the model across different cancer types. Fig 11 and 12 shows the classification performance for different types of lungs, colon and brain cancers and the models achieves high accuracy with each having classifications accuracies close to 1

C. PREDICTING NEW IMAGES

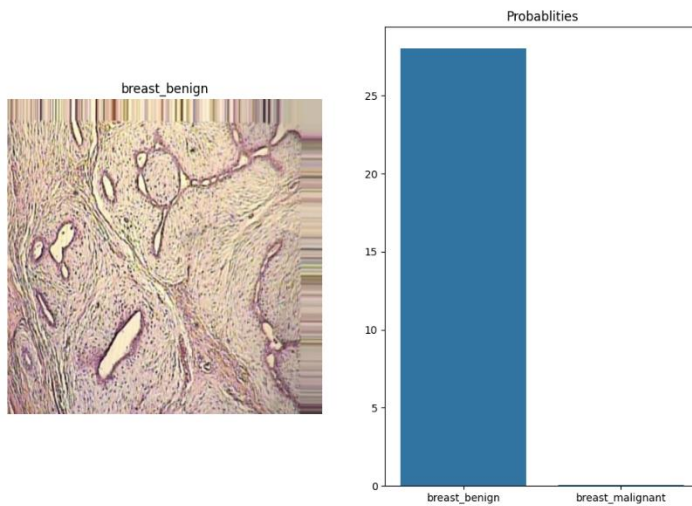


Figure 13: Visualizations of Breast Cancer

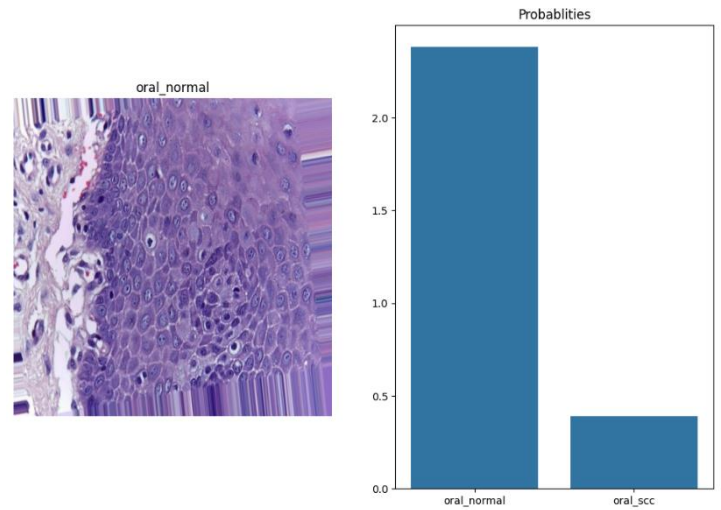


Figure 14: Visualizations of Oral Cancer

Figure 13 and figure 14 images show model predictions confidently classifying a breast tissue sample as benign and an oral tissue sample as normal, with high probabilities for the correct classes and minimal likelihood for cancerous categories.

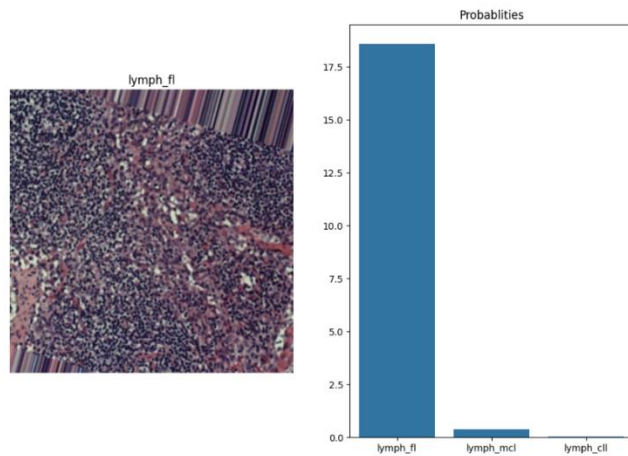


Figure 15: Visualizations of Lymphoma Cancer

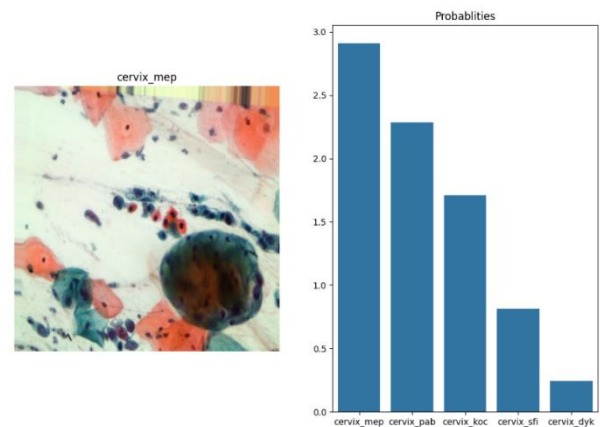


Figure 16: Visualizations of Cervix Cancer

Fig 15 and 16 confidently classifies a lymph node sample as follicular lymphoma (lymph_fl), and the right image shows a cervical sample identified as metaplastic epithelium (cervix_mep) with varying probabilities for other cervical conditions, indicating some uncertainty in classification.

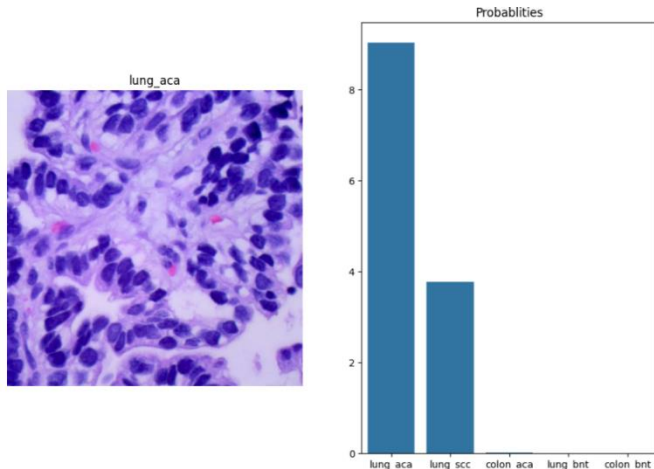


Figure 17: Visualizations of Lung and Colon

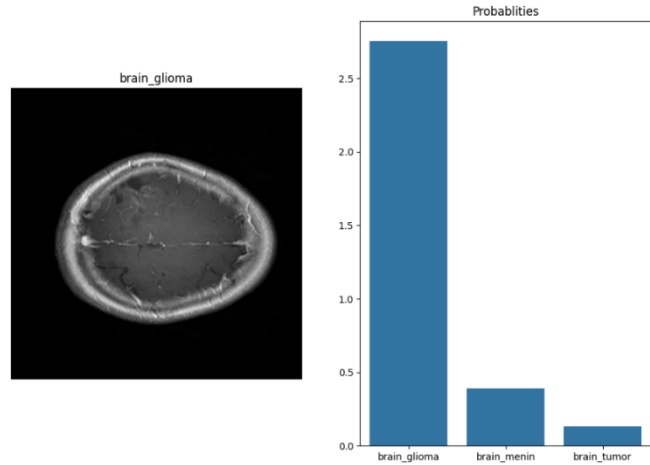


Figure 18: Visualizations of Brain Cancer

Figure 17 is a histological image of lung tissue, likely from a lung adenocarcinoma (lung_aca) sample, while figure 18 is a magnetic resonance imaging (MRI) scan of a brain, likely showing a brain glioma (brain_glioma), as confirmed by the bar charts on the right showing the probabilities of different classifications.

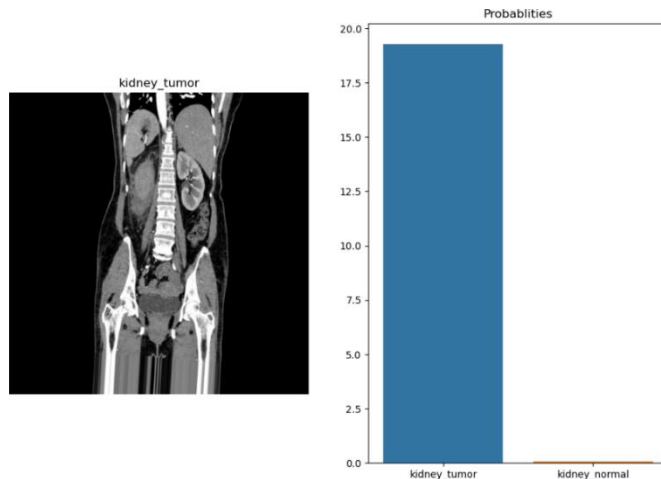


Figure 19: Visualizations of Kidney Cancer

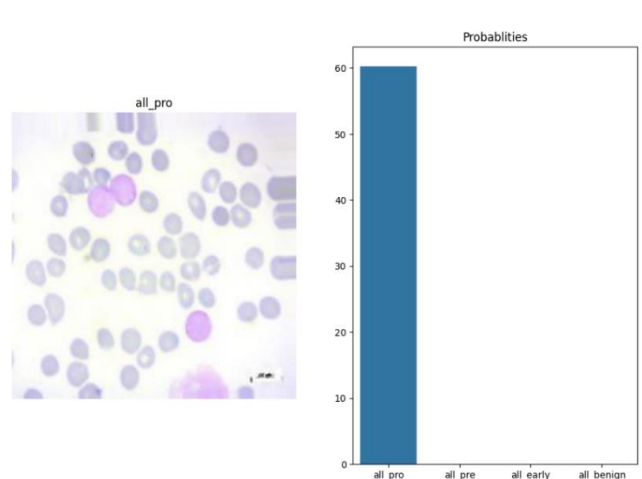


Figure 20: Visualizations of ALL Cancer

Figure 15 and 16 below illustrate the model's predictions for kidney and leukemia samples. On the left, the kidney tumor is confidently classified as "kidney_tumor" with almost no probability for "kidney_normal." On the right, the leukemia sample is confidently identified as "all_pro" (acute lymphoblastic leukemia in the proliferative stage) with minimal probability for other classes. This indicates strong model confidence in correctly identifying these specific conditions. The discussion also highlights the potential of machine learning in oncology, emphasizing the model's capability to improve early cancer detection and personalized treatment. The system's ability to handle multiple cancer types simultaneously marks a significant advancement in cancer diagnostics, offering a comprehensive tool for healthcare professionals [1].

V. CONCLUSION

The study successfully developed a robust multi-cancer detection and classification system using PyTorch. The proposed model demonstrated high accuracy in diagnosing various cancer types, proving the efficacy of deep learning in medical applications [6]. The research contributes to the ongoing efforts to improve cancer care, offering a promising tool for early detection and personalized treatment [1]. The study's findings underscore the importance of integrating machine learning into healthcare, paving the way for future research and innovation. Future work could explore more advanced architectures, larger datasets, and the inclusion of additional cancer types. The ethical considerations of AI in healthcare and its integration into clinical workflows remain crucial aspects to address as the technology advances.

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