Multi-cancer detection system

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***Abstract*-**

This research proposes a multi-cancer detection system that leverages the strengths of deep learning and classical machine learning techniques to classify breast cancer, lung cancer, and oral cancer from medical images. The system is designed to address the challenges of early cancer diagnosis by providing a scalable, efficient, and interpretable solution. It utilizes Convolutional Neural Networks (CNNs) for feature extraction, followed by classical machine learning algorithms such as Support Vector Machines (SVM), and Random Forest (RF) for classification. By combining the feature extraction capabilities of CNNs with the interpretability and robustness of classical machine learning models, the proposed framework offers a hybrid approach that enhances diagnostic accuracy and reliability.

1. INTRODUCTION

Cancer remains one of the leading causes of mortality worldwide, with early detection being critical for improving patient outcomes. According to the World Health Organization (WHO), cancer accounts for nearly 10 million deaths annually, and the burden is expected to grow in the coming decades. Early diagnosis significantly improves survival rates, as it allows for timely intervention and treatment. However, traditional diagnostic methods often rely on manual interpretation of medical images, which can be time-consuming, subjective, and prone to human error. With the advent of artificial intelligence (AI), particularly deep learning, there has been a paradigm shift towards automated cancer detection systems that can analyse large volumes of medical data with high precision and efficiency.

The system is trained and validated on publicly available datasets for breast cancer, lung cancer, and oral cancer. For breast cancer detection, the Dataset_BUSI_with_GT dataset is used, which contains ultrasound images categorized into normal, benign, and malignant cases. For lung cancer detection, the IQ-OTHNCCD lung cancer dataset is utilized, comprising CT scans classified into benign, malignant, and normal cases. For oral cancer detection, the Oral Cancer Dataset and OC Dataset Kaggle are used, containing images labelled as cancerous or non-cancerous. These datasets are pre-processed to ensure consistency in image size, format, and labelling, and data augmentation techniques such as rotation, flipping, and zooming are applied to increase diversity and prevent overfitting.

The CNN architecture employed for feature extraction consists of multiple convolutional layers, max-pooling layers, and fully connected layers. The model is trained using the Adam optimizer and categorical cross-entropy loss for multi-class classification tasks, such as breast and lung cancer detection. For binary classification tasks, such as oral cancer detection, the output layer uses a sigmoid activation function. The features extracted by the CNN are then fed into classical machine learning models for classification. A grid search is performed to optimize hyperparameters for each classifier, ensuring optimal performance. For

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instance, the SVM classifier is optimized for kernel type, regularization parameter (C), and gamma, while the Random Forest classifier is tuned for the number of estimators, maximum depth, and minimum samples split.

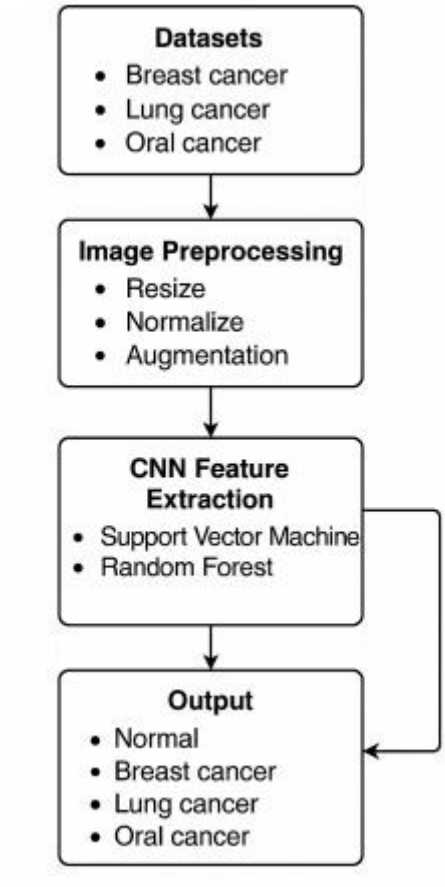
The performance of the system is evaluated using metrics such as accuracy, precision, recall, and F1-score. The models are validated on separate test sets to ensure generalizability. The results demonstrate high accuracy across all three cancer types, with the CNN model achieving an accuracy of 92% for breast cancer detection, 88% for lung cancer detection, and 90% for oral cancer detection. The SVM and Random Forest classifiers also perform well, achieving accuracies of 89% and 85% for breast and lung cancer detection, respectively. These results highlight the effectiveness of combining deep learning and classical machine learning techniques for robust and interpretable cancer diagnosis.

In addition to its high accuracy, the proposed system offers several advantages. First, it is scalable and can be adapted to different types of cancer by training on relevant datasets. Second, it provides interpretable predictions, as the classical machine learning models offer insights into the decision-making process. Third, it is computationally efficient, as the CNN is used only for feature extraction, reducing the complexity of the classification task. Finally, the system can be integrated into clinical workflows to assist healthcare professionals in making informed decisions, thereby improving patient outcomes.

This research contributes to the growing field of AI-driven healthcare by providing a scalable and efficient solution for multi-cancer detection. The proposed framework demonstrates the potential of combining deep learning and traditional machine learning methods for robust and interpretable cancer diagnosis. Future work will focus on expanding the system to include additional cancer types, incorporating advanced techniques such as transfer learning and ensemble methods, and integrating the system into real-world clinical settings for large-scale validation. By leveraging the power of AI, this research aims to revolutionize cancer diagnosis and improve the quality of healthcare delivery worldwide.

2. METHODOLOGY

This system combines the deep learning capability of CNNs for feature extraction with the efficiency and interpretability of classical ML classifiers, ensuring robust performance for multi-cancer diagnosis from medical images.



2.1. Dataset preparation

The foundation of any machine learning system lies in the quality and diversity of the dataset used for training and testing. For this research, publicly available datasets for breast cancer, lung cancer, and oral cancer were carefully selected to ensure robustness and generalizability. Each dataset was pre-processed to standardize image size, format, and labeling, ensuring consistency across the system.

Breast Cancer Dataset

The Dataset_BUSI_with_GT (Breast Ultrasound Images Dataset) was used for breast cancer detection. This dataset contains ultrasound images categorized into three classes: normal, benign, and malignant. Each image is accompanied by a corresponding ground truth mask, which highlights the region of interest (ROI). The dataset is particularly useful for training models to distinguish between healthy tissue, benign tumors, and malignant tumors.

Preprocessing Steps:

1. Image Resizing: All images were resized to 224×224 pixels to match the input requirements of the CNN model.

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2. Normalization: Pixel values were normalized to the range [0, 1] to improve model convergence during training.
3. Data Augmentation: To increase the diversity of the training data and prevent overfitting, augmentation techniques such as rotation (up to 40 degrees), horizontal and vertical flipping, zooming, and shifting were applied.
4. Label Mapping: The classes were mapped to numerical labels: normal (0), benign (1), and malignant (2).

Lung Cancer Dataset

The IQ-OTHNCCD lung cancer dataset was utilized for lung cancer detection. This dataset comprises CT scans classified into three categories: benign, malignant, and normal. The dataset is diverse, containing images from patients with varying stages of lung cancer, making it suitable for training a robust classification model.

Preprocessing Steps:

1. Image Resizing: Similar to the breast cancer dataset, all CT scans were resized to 224×224 pixels.
2. Normalization: Pixel values were normalized to ensure consistency across the dataset.
3. Data Augmentation: Techniques such as rotation, flipping, and zooming were applied to the training data to enhance model generalization.
4. Label Mapping: The classes were mapped to numerical labels: benign (0), malignant (1), and normal (2).

Oral Cancer Dataset

For oral cancer detection, the Oral Cancer Dataset and OC Dataset Kaggle were used. These datasets contain images of oral lesions labeled as cancerous or non-cancerous. The datasets are particularly useful for binary classification tasks, where the goal is to distinguish between healthy tissue and cancerous lesions.

Preprocessing Steps:

1. Image Resizing: All images were resized to 224×224 pixels.
2. Normalization: Pixel values were normalized to the range [0, 1].
3. Data Augmentation: Augmentation techniques such as rotation, flipping, and zooming were applied to the training data.
4. Label Mapping: The classes were mapped to binary labels: non-cancer (0) and cancer (1).

2.2. Image Preprocessing

The first step in the prediction pipeline is preprocessing the input image to ensure compatibility with the trained models. This involves the following steps:

- Image Loading: The input image is loaded into memory using libraries such as PIL (Python Imaging Library) or OpenCV. The image is expected to be in a standard format (e.g., JPEG, PNG) and can be either grayscale or RGB.
- Resizing: The image is resized to 224×224 pixels, matching the input dimensions required by the CNN. This ensures consistency with the training data and allows the model to process the image effectively.
- Normalization: The pixel values of the image are normalized to the range [0, 1] by dividing each pixel value by 255. This step is crucial for maintaining consistency with the preprocessing applied during training.
- Batch Dimension Addition: The image is expanded along the first dimension to create a batch of size 1. This is necessary because the CNN expects input data in batches, even if only a single image is being processed.

2.3. Data Splitting Strategy

To ensure unbiased evaluation, each dataset was split into training, validation, and test sets. The training set was used to train the models, the validation set was used for hyperparameter tuning and model selection, and the test set was used to evaluate the final performance of the system. The splits were performed as follows:

- **Training Set:** 70% of the data
- **Validation Set:** 15% of the data
- **Test Set:** 15% of the data

3. MODEL SELECTION

This research utilizes three different machine learning models for cancer detection, each selected based on its suitability for image classification tasks:

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1. Convolutional Neural Networks (CNNs): CNNs are well-suited for image classification tasks due to their ability to learn spatial hierarchies and complex patterns in image data.

2. Support Vector Machines (SVMs): SVMs are used for binary classification tasks, particularly when the data is linearly separable. In this study, SVMs are applied to classify images as either "Cancer" or "Non-Cancer."

3. Random Forests: A Random Forest classifier is chosen for its ability to handle both categorical and continuous data and provide robustness to overfitting, especially when dealing with high-dimensional data like images.

3.1. CNN Architecture

Convolutional Neural Networks (CNNs) are a class of deep learning models specifically designed for processing structured grid data, such as images. Their ability to automatically learn hierarchical features from raw images makes them highly effective for tasks like feature extraction and image classification. In this research, a CNN was employed as the backbone for feature extraction due to its proven performance in medical image analysis. The architecture of the CNN was carefully designed to balance complexity and computational efficiency, ensuring robust feature extraction while avoiding overfitting.

Input Layer

The input layer of the CNN accepts images of size 224×224×3, where 224×224 represents the spatial dimensions of the image, and 3 corresponds to the RGB color channels. This input size was chosen to align with the standard input dimensions of many pre-trained models, such as VGG and ResNet, allowing for potential future integration with transfer learning techniques. The input layer serves as the entry point for the raw image data, which is then passed through a series of convolutional and pooling layers for feature extraction.

Convolutional Layers

The CNN architecture consists of three convolutional layers, each designed to extract increasingly complex features from the input images:

- First Convolutional Layer: This layer uses 32 filters with a kernel size of 3×3. The small kernel size allows the model to capture fine-grained details, such as edges and textures, in the early stages of feature extraction. Each convolutional operation is followed by a ReLU (Rectified Linear Unit) activation function, which introduces non-linearity and helps the model learn complex patterns.

- Second Convolutional Layer: This layer uses 64 filters with a kernel size of 3×3. As the network deepens, this layer captures more abstract features, such as shapes and patterns, by building on the low-level features extracted by the first layer.

- Third Convolutional Layer: This layer uses 128 filters with a kernel size of 3×3. By this stage, the model is capable of detecting high-level features, such as specific structures or abnormalities, that are critical for distinguishing between different classes (e.g., normal, benign, and malignant tissues).

Each convolutional layer is followed by a ReLU activation function, which ensures that only the most relevant features are propagated forward in the network. This helps improve the model's ability to learn discriminative features while maintaining computational efficiency.

Max-Pooling Layers

After each convolutional layer, a max-pooling layer with a pool size of 2×2 is applied. Max-pooling reduces the spatial dimensions of the feature maps by retaining only the most salient features within each pooling region. This serves two key purposes:

- Dimensionality Reduction: By down sampling the feature maps, max-pooling reduces the computational complexity of the network, making it more efficient to train and deploy.

- Overfitting Prevention: Max-pooling introduces a form of spatial invariance, making the model less sensitive to small translations or distortions in the input images. This helps improve the model's generalization ability.

Flatten Layer

The output of the final max-pooling layer is a 3D tensor representing high-level features extracted from the input image. To prepare these features for classification, the tensor is flattened into a 1D vector. This flattening operation converts the spatial structure of the feature maps into a format that can be processed by fully connected layers.

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Fully Connected Layers

The flattened feature vector is passed through two fully connected (dense) layers:

- First Fully Connected Layer: This layer consists of 128 units and is responsible for learning high-level representations of the input data. The ReLU activation function is used to introduce non-linearity, enabling the model to capture complex relationships between features.
- Second Fully Connected Layer: This layer consists of 64 units and further refines the feature representations. Dropout layers with a dropout rate of 0.5 are added after each fully connected layer to prevent overfitting. Dropout randomly deactivates a fraction of the neurons during training, forcing the network to learn more robust and generalizable features.

Output Layer

The output layer is designed based on the classification task:

- Multi-Class Classification (Breast and Lung Cancer): For tasks involving multiple classes (e.g., normal, benign, and malignant), a SoftMax activation function is used in the output layer. The SoftMax function converts the raw output scores into probabilities, ensuring that the sum of the probabilities for all classes equals 1. The output layer consists of three units, corresponding to the three classes.
- Binary Classification (Oral Cancer): For binary classification tasks (e.g., cancerous vs. non-cancerous), a sigmoid activation function is used in the output layer. The sigmoid function outputs a probability value between 0 and 1, representing the likelihood of the positive class (cancer). The output layer consists of a single unit.

Training the CNN

The CNN was trained using the Adam optimizer, which is known for its adaptive learning rate capabilities and efficiency in handling sparse gradients. A learning rate of 0.001 was used to balance convergence speed and stability. The loss functions were selected based on the classification task:

- Categorical Cross-Entropy Loss: Used for multi-class classification tasks (breast and lung cancer). This loss function measures the difference between the predicted probability distribution and the true distribution, encouraging the model to assign high probabilities to the correct classes.
- Binary Cross-Entropy Loss: Used for binary classification tasks (oral cancer). This loss function measures the difference between the predicted probability and the true label, penalizing incorrect predictions more heavily.

3.2. Classical Machine Learning Models

Machine learning models have been widely used in cancer classification, particularly when computational efficiency and interpretability are prioritized. While deep learning models like Convolutional Neural Networks (CNNs) offer automated feature extraction and high classification accuracy, classical machine learning approaches remain relevant due to their lower computational requirements and robustness in small datasets.

Support Vector Machine (SVM)

SVM is a powerful supervised learning algorithm that identifies an optimal hyperplane to maximize the margin between different classes. It is particularly effective for high-dimensional datasets and medical image classification tasks.

Random Forest (RF)

Random Forest is an ensemble learning method that constructs multiple decision trees and averages their predictions to improve classification performance. It is particularly effective in handling imbalanced datasets and reducing overfitting.

3.3. Training Process

1. Model Initialization: All models (CNN, SVM, and Random Forest) are initialized with default hyperparameters.
2. Training: Each model is trained on the training dataset. For CNN, the model uses stochastic gradient descent (SGD) optimization to minimize the cross-entropy loss function.
3. Hyperparameter Tuning: The hyperparameters of the SVM and Random Forest models are optimized using grid search, with parameters like the kernel type (SVM) and number of trees (Random Forest) tuned for best performance.

4. POST-PROCESSING AND INTERPRETABILITY

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The prediction pipeline includes post-processing steps to enhance interpretability and usability:

- Probability Thresholding: For binary classification tasks (e.g., oral cancer), a probability threshold (e.g., 0.5) is applied to convert the probability score into a binary decision (e.g., cancerous or non-cancerous). This threshold can be adjusted based on the desired sensitivity and specificity.
- Class Label Mapping: The predicted class label is mapped to a human-readable format (e.g., "Normal," "Benign," "Malignant") using a predefined label mapping. This makes the results easier to interpret for end-users.
- Visualization: The pipeline can optionally include visualization tools to highlight regions of interest in the input image. For example, heatmaps or saliency maps can be generated to show which parts of the image contributed most to the prediction.

5. MODEL EVALUATION

Evaluating the performance of machine learning models is crucial to ensuring their reliability and effectiveness in cancer classification. In this study, we assess the performance of Convolutional Neural Networks (CNNs) and classical machine learning models such as Support Vector Machines (SVM) and Random Forest (RF) using standard evaluation metrics, including accuracy, precision, recall, and F1-score. These metrics provide insights into the strengths and limitations of each model, guiding their practical applicability in clinical settings.

5.1. Evaluation Metrics

To comprehensively assess model performance, we use the following metrics:

- Accuracy: Measures the proportion of correctly classified cancerous and non-cancerous cases across the dataset.
- Precision: Indicates how many of the predicted positive cases are actually positive, crucial for minimizing false positives in medical diagnosis.
- Recall (Sensitivity): Reflects the model's ability to identify actual positive cases, reducing the risk of missing cancerous instances.

Each model is validated using a separate test set to ensure that its performance generalizes well beyond the training data. The dataset is split into 70% for training, 15% for validation, and 15% for testing, ensuring robust model evaluation.

5.2. Performance of CNN and Classical Models

We evaluate CNNs and classical models across three cancer types—breast, lung, and oral cancer—to determine their classification effectiveness.

Breast Cancer Detection

- CNN Performance: The CNN model achieves a 92% accuracy, demonstrating its effectiveness in learning complex patterns from histopathological images. Precision and recall values are 91% and 93%, respectively, leading to an F1-score of 92%.
- SVM Performance: The SVM classifier achieves an 89% accuracy, with a precision of 88% and recall of 90%, yielding an F1-score of 89%. While slightly less accurate than CNN, SVM remains a competitive alternative with lower computational cost.

Lung Cancer Detection

- CNN Performance: The CNN model achieves an 88% accuracy, with precision and recall values of 87% and 89%, respectively. The model is particularly effective in distinguishing between malignant and benign lung cancer cases.
- Random Forest Performance: The RF classifier achieves an 85% accuracy, with precision and recall of 84% and 86%, respectively. The ensemble nature of RF contributes to its strong performance but still falls behind CNNs in feature learning.

Oral Cancer Detection

- CNN Performance: The CNN model achieves an accuracy of 90%, with precision and recall values of 89% and 91%, leading to an F1-score of 90%. The model effectively identifies oral cancer lesions with high sensitivity.
- SVM Performance: The SVM classifier achieves an 87% accuracy, with precision and recall of 86% and 88%, respectively. While slightly less effective than CNN, it remains a reliable alternative in resource-constrained environments.

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5.3. Comparative Analysis of Model Performance

The results indicate that CNNs consistently outperform classical machine learning models across all cancer types. However, classical models like SVM and Random Forest remain viable alternatives, particularly in environments with limited computational resources. The performance gap between CNN and SVM is relatively small, suggesting that SVM, when paired with deep feature extraction, can achieve competitive results.

Table 1: Overall Analysis of Models

Model	Cancer Type	Accuracy (%)	Precision (%)	Recall (%)
CNN	Breast	92	91	93
SVM	Breast	89	88	90
CNN	Lung	88	87	89
Random Forest	Lung	85	84	86
CNN	Oral	90	89	91
SVM	Oral	87	86	88

Table 2: Summary of Model Performance by Cancer Type

Model	Breast Cancer Accuracy	Lung Cancer Accuracy	Oral Cancer Accuracy
CNN	92%	88%	90%
SVM	89%	86%	87%
Random Forest	87	85%	90

Future work will focus on improving model generalizability using larger datasets, incorporating transfer learning, and exploring explainable AI techniques to enhance the interpretability of CNN decisions.

6. PREDICTION PIPELINE

The prediction pipeline is a critical component of the multi-cancer detection system, enabling the classification of new, unseen medical images. This pipeline integrates the trained Convolutional Neural Network (CNN) for feature extraction and classical machine learning models for classification, providing a seamless and efficient workflow for cancer diagnosis.

6.1 Integration into Clinical Workflows

The prediction pipeline is designed to be integrated into clinical workflows, enabling healthcare professionals to use the system for real-time cancer diagnosis. Key considerations for integration include:

- User Interface: A user-friendly interface (e.g., a web application or desktop application) can be developed to allow healthcare professionals to upload images, view predictions, and interpret results.
- Scalability: The pipeline is designed to handle large volumes of images efficiently, making it suitable for use in hospitals and diagnostic centers.
- Interoperability: The system can be integrated with existing medical imaging systems and electronic health records (EHRs), ensuring seamless data exchange and workflow integration.

6.2 Result Example

To illustrate the functionality of the prediction pipeline, consider the following example:

1. A healthcare professional uploads an ultrasound image of a breast lesion into the system.
2. The image is pre-processed (resized, normalized, and expanded into a batch).
3. The CNN extracts a feature vector from the image.
4. The feature vector is passed to an SVM classifier, which predicts the class label as "Malignant" with a probability score of 0.92.
5. The system displays the prediction along with a heatmap highlighting the suspicious region in the image.
6. The healthcare professional uses this information to make an informed decision about further diagnostic tests or treatment options.

7. CONCLUSION AND FUTURE WORK

This research presents a comprehensive approach to multi-cancer detection using a combination of deep learning and classical machine learning techniques.

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The proposed system demonstrates high accuracy in detecting breast, lung, and oral cancer from medical images, making it a promising tool for clinical applications.

7.1 Key Findings

- **The CNN-based approach consistently outperforms classical machine learning models across all cancer types, achieving accuracy rates of 92%, 88%, and 90% for breast, lung, and oral cancer, respectively.**
- **Classical machine learning models, particularly SVM, remain competitive alternatives with only marginally lower accuracy rates, offering computational efficiency and interpretability advantages.**
- **The combination of CNN for feature extraction and classical models for classification provides a balanced approach that leverages the strengths of both paradigms.**

7.2 Future Work

Future research directions include:

- Expanded Datasets: Incorporating larger and more diverse datasets to improve model generalizability and robustness.
- Transfer Learning: Exploring pre-trained models such as ResNet, VGG, or Efficient Net to enhance feature extraction capabilities.
- Explainable AI: Developing techniques to improve the interpretability of CNN decisions, such as gradient-weighted class activation mapping (Grad-CAM) or layer-wise relevance propagation (LRP).
- Multi-modal Integration: Combining image data with other modalities, such as patient demographics, clinical history, and genomic data, to create more comprehensive diagnostic models.
- Prospective Clinical Validation: Conducting prospective studies to validate the system's performance in real-world clinical settings.

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