# Multi Cancer Classification using Efficientnet-B3 Feature Extraction and UMAP-Optimized Traditional Machine Learning Models

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**Abstract.** Our work introduces the creation and testing of a multi-cancer classification system for histopathological images, with specific attention to the unique classification of Cervical Cancer, Acute Lymphoblastic Leukemia (ALL), Brain Cancer and Lung and Colon Cancer (handled as one group). Each of the cancer groups, with several stages or subclasses, was processed and modeled separately. The steps followed loading and pre-processing respective image datasets of each type of cancer, which was followed by feature extraction from using a pre-trained EfficientNetB3 model. To deal with dimensionality, UMAP (Uniform Manifold Approximation and Projection) was used for reducing the space of features into 128 features. The resulting lower-dimensional embeddings were subsequently employed in training and testing a collection of Machine learning classifiers: K-Nearest Neighbors (KNN), Random Forest, Logistic Regression (LR), Support Vector Machines (SVM), and XGBoost. The test accuracy of each model per cancer category indicated the following: In the classification of Cervical Cancer, KNN demonstrated the best performance with an accuracy of 95.84%, closely followed by SVM at 93.44%, XGBoost at 92.30%, Random Forest at 90.98%, and Logistic Regression at 90.70%. In the classification of ALL, XGBoost demonstrated the best performance with an accuracy of 93.73%, closely followed by Random Forest at 93.47%, KNN at 93.20%, SVM at 91.37%, and Logistic Regression at 91.17%. For Brain Cancer classification, Random Forest achieved the top accuracy of 92.33%, with KNN at 91.20%, XGBoost at 91.17%, Logistic Regression at 90.40%, and SVM at 88.80%. In the combined classification of Lung and Colon Cancer, Random Forest outperformed other models with an accu- racy of 97.78%, followed by XGBoost at 97.62%, KNN at 97.02%, Logistic Regression at 96.70%, and SVM at 95.36%.

**Keywords:** Cancer classification, deep learning, convolutional neural networks, transfer learning, multi-cancer classification, histopathological images, machine learning classifiers, Support Vector Machines (SVM), Random Forest, Logistic Regression, K-Nearest Neighbors (KNN), XGBoost, EfficientNetB3, UMAP, dimensionality reduction, feature extraction.

## 1 Introduction

Cancer is a major worldwide health problem that requires ongoing improvement in early and reliable diagnostic techniques to enhance patient survival rates [1], [16]. Conventional cancer screening methods tend to have drawbacks of being subjective, time-consuming, and dependent on the availability of experts [2], [18]. To address these challenges, the use of Artificial Intelligence (AI), specifically deep learning and machine learning methods, has become a revolutionary force in the analysis of medical images with the potential for

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automated, efficient, and objective detection and classification of various diseases, such as cancer [3], [9], [12].

The CNNs also exhibited a tremendous amount of success in learning intricate patterns from medical images and are crucial tools for the detection and classification of cancer [11], [12], [14]. The fact that CNNs can learn to automatically extract hierarchical features from raw pixels has contributed significantly to applications such as identifying medicinal mushrooms [5], skin cancer detection [1], [11], [14], and classifying different cancers [17], [23]. Transfer learning, a method that takes advantage of knowledge gained through training on big, varied datasets (e.g., ImageNet) and applies it to new, frequently smaller, datasets, has been shown to be particularly useful in medical imaging because large labeled medical datasets are not available [13], [15]. Pre-trained models such as EfficientNetB3 [20], used in our implementation, have the potential to offer strong initial feature representations, speeding up training and enhancing performance on particular medical image analysis tasks.

The high-dimensional feature vectors learned from CNNs are computationally demanding and can carry redundant in- formation. Dimensionality reduction Techniques, including UMAP (Uniform Manifold Approximation and Projection) [22], are essential to solve these problems through the projection of the data into a low-dimensional space while retaining key structural information, thus improving the efficiency and effectiveness of following classification models. In addition, using a variety of machine learning classifiers, such as SVM, Random Forest [8], Logistic Regression, KNN, and XGBoost, enables a thorough analysis of various learning paradigms and the selection of models most appropriate for the unique nature of each cancer type and stage [4], [21], [24].

This work revolves around the crucial assignment of categorizing the varying stages in a number of significant cancer types based on histopathological images. Rather than classifying broadly categorized cancers, our work explores the internal categorization of stages for:

- Cervical Cancer, encompassing the stages: cervic_dyk, cervic_koc, cervic_mep, cervic_pab, and cervic_sfi.
- Acute Lymphoblastic Leukemia (ALL), classifying be- tween: all_benign, all_early, all_pre, and all_pro.
- Brain Cancer, differentiating between: brain_glioma, brain_menin, and brain_tumor.
- Lung and Colon Cancer, classifying the stages: colon_aca, colon_bnt, lung_aca, lung_bnt, and lung_scc.

A significant feature of our methodology is independent processing and modeling of each of these cancer types, considering the distinct visual patterns that accompany each disease and the way it advances through various stages. The approach entails using the feature extraction capability of a pre-trained EfficientNetB3 model on histopathological images for each type of cancer, and then dimensionally reducing the features extracted using UMAP to 128 components. The resultant lower-dimensional embeddings are subsequently used to train and test a set of varied machine learning classifiers: SVM, Random Forest, Logistic Regression, KNN, and XGBoost. Each model is thoroughly tested on each of the four cancer types and their corresponding internal stages using primary evaluation criteria such as accuracy, classification reports, and confusion matrices. The conclusions of this research add to an

enhanced understanding of the relevance of AI methods for the subtle categorization of cancer development within certain cancer subtypes, with the ultimate goal of enhancing diagnostic accuracy and guiding more specific treatment plans.

## 2 Related Work

The Convolutional Neural Networks (CNNs) has greatly improved Artificial Intelligence (AI) in applications such as image identification, detection, and classification [12], [19]. CNNs acquire knowledge from examples, identify patterns, and make choices with a small amount of human intervention and have been highly successful in diverse real-world applications, including in agriculture. Deep learning techniques, particularly Convolutional Neural Networks (CNNs), have become extensively used in medical imaging for tasks such as automatically identifying, detecting, and classifying diseases, including cancer. [3], [9], [11].

A number of studies have also investigated the application of deep learning to cancer-related applications. For example, studies have aimed at classification of wild mushrooms through ensemble image processing learning combined with bagging algorithms and have shown high accuracy rates [8]. Other studies have implemented CNN architectures like Inception-V3, VGG-16, and ResNet50 to determine edible, inedible, and toxic mushrooms [5]. These studies demonstrate the ability of CNNs to undertake image classification tasks in biological contexts.

In the particular case of cancer detection and classification, several CNN architectures and machine learning methodologies have been explored [1], [14]. In one, MobileNetv2 was compared with VGG-16 for classifying medicinal mushrooms and was found to perform superior to VGG-16 [5]. This highlights the significance of using proper CNN architectures for certain image classification tasks.

The MCED concept has drawn the focus, where multiple cancers are detected at an early stage of development [15], [17], [23]. Various CNN models, such as EfficientNet, MobileNetV3, DenseNet, VGG, and ResNet, are frequently investigated for their effectiveness in various studies, frequently using ensemble methods for better outcomes in cancer detection from digital histopathology images [3]. Visualization methods such as grad-CAM are frequently used in these studies for increasing explain ability in CNN-based cancer detection systems.

Transfer learning, by which pre-trained models are fine- tuned to new tasks, has also been used in cancer detection [13]. Pre-trained CNN models like ResNet50, MobileNet, DenseNet, and VGG have been used by research work by tapping knowledge from large image datasets like ImageNet for classification of various cancer types [2]. The ResNet50 model has performed well in multi-cancer classification [15]. Additionally, studies have examined the utilization of ensemble learning by aggregating diverse machine learning models to enhance precision and resilience in cancer diagnosis [4]. Ensemble techniques such as stacking have yielded improved performance relative to standalone models in predicting cardiovascular disease [4]. In the case of cancer diagnosis operations such as identification of wild mushrooms, ensemble

CNN models have outperformed single CNN models [3]. Dimensionality reduction methods such as UMAP (Uniform Manifold Approximation and Projection) and PCA (Principal

Component Analysis) are essential when handling high- dimensional data derived from CNNs [22]. These reduce the computational intensity and could, in theory, enhance the performance of subsequent classification models.

Most research targets detecting the existence of cancer or classifying general cancer types, but there is some research that has gone further and attempted to classify stages in particular cancers:

- Lung cancer stage prediction using Multi-Layer Perceptron (MLP) and deep learning classifiers [10].
- Machine learning techniques such as Support Vector Ma- chines (SVM), Decision Tree, and K-Nearest Neighbor (KNN) for multi-cancer early detection and classification [21].
- TNM stage classification from free-text histology reports using SVM.

Our work focuses on multi-class cancer stage classification from histopathological images for Cervical, ALL, Brain, and Lung/Colon Cancers. Using pre-trained EfficientNetB3 for feature extraction [20], UMAP for dimensionality reduction [22], and evaluating various classifiers (SVM, Random Forest, Logistic Regression, KNN, XGBoost), our research contributes to AI's practical application in complex cancer stage classification.

Modelling each cancer type separately to predict its internal stages distinguishes our approach from general multi-cancer detection or binary cancer classification. Fig. 1 shows the Block Diagram.

## 3 Block Diagram

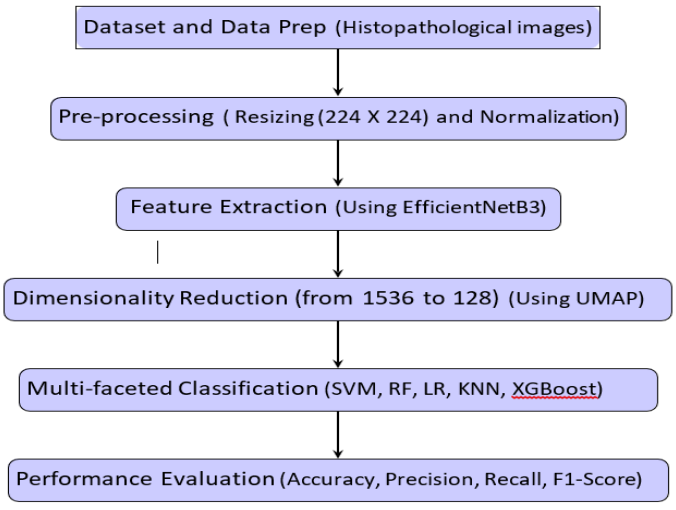



**Fig. 1.** Block Diagram.

## 4 Methodology

The main aim of this work is to classify the various phases within particular cancer types precisely using histopathological images. In this regard, we have employed an extensive method- ology including data preparation, feature extraction via a pre- trained Convolutional Neural Network (CNN), dimensionality reduction, multi-perspective classification with various ma- chine learning models, and careful performance analysis.

### 4.1 Dataset and Data Preparation

The study utilizes a dataset of histopathological images corresponding to four distinct cancer types: Cervical Cancer, Acute Lymphoblastic Leukemia (ALL), Brain Cancer, and Lung and Colon Cancer. For each cancer type, the dataset is further categorized into specific stages:

- Cervical Cancer: cervic_dyk, cervic_koc, cervic_mep, cervic_pab, and cervic_sfi.
- Acute Lymphoblastic Leukemia (ALL): all_benign, all_early, all_pre, and all_pro.
- Brain Cancer: brain_glioma, brain_menin, and brain_tumor.
- Lung and Colon Cancer: colon_aca, colon_bnt, lung_aca, lung_bnt, and lung_scc.

**Table 1**. Multi Cancer Dataset Overview.

| | |
|---|---|
| **Dataset Name** | Multi Cancer Dataset |
| **Source** | Kaggle |
| **Author** | Obuli Sai Naren |
| **Total Images** | 130,000 |
| **Image Format** | JPEG |
| **Image Dimensions** | 512px × 512px |

**Table 2.** Dataset Details by Cancer Type.

| Cancer Type | Number of Classes | Number of Images |
|---|---|---|
| Cervical Cancer | 5 | 25,000 |
| ALL Cancer | 4 | 20,000 |
| Brain Cancer | 3 | 15,000 |
| Lung and Colon Cancer | 5 | 25,000 |

Folder Structure and Class Names: The dataset is organized into folders, with each subclass folder containing 5,000 images. The naming format for each image is

<subclass>_<serial_number>.jpg for easy refer ence.

Notes on Images:

- All subclass folders contain 5,000 images each.
- Each image follows the naming format <subclass>_<serial_number>.jpg.

The dataset is pre-processed to ensure uniformity and suit- ability for the deep learning model. This may involve resizing images and normalization to standardize pixel values. For each cancer type, the prepared dataset is split into training and testing sets to train the models and evaluate their performance on unseen data. A common split ratio, such as 80% for training and 20% for validation/testing, is employed.

### 4.2 Feature Extraction using Transfer Learning

ZTransfer learning is used to take advantage of the knowledge acquired by a pre-trained CNN on a large, general- purpose image dataset. This is especially useful in medical imaging where the availability of large, labeled datasets may be restricted. A pre-trained EfficientNetB3 model is used as the feature extractor. Efficient Net models are recognized for their efficiency and robust performance on a variety of image recognition tasks. For each histopathological image in the dataset (for each of the four types of cancer), the EfficientNetB3 model reads the image and produces a high- dimensional feature vector that encodes the learned properties of the image. The convolutional layers in the pre-trained model are responsible for automatically learning hierarchical features of interest for image classification.

### 4.3 Dimensionality Reduction with UMAP

The feature vectors of high dimensionality obtained from the CNN can be costly in computation and might have redundant information. Uniform Manifold Approximation and Projection (UMAP), a non-linear dimensionality reduction method, is utilized to lower the dimension of the computed feature vectors to 128 dimensions. UMAP tries to preserve data structure in the lower space such that vital discriminatory information useful for classifying stages of cancer is preserved and noise and computational load are decreased.

### 4.4 Multi-faceted Classification

After feature extraction and dimensionality reduction, a set of varied machine learning classifiers is used to construct the predictive models for every one of the four cancer types. The classifiers used in this implementation are:

1. **Support Vector Machines (SVM):** SVM is a robust classification method capable of working in high-dimensional spaces.
2. **Random Forest:** Random Forest is an ensemble learning approach that builds many decision trees and combines their predictions.
3. **Logistic Regression:** Logistic Regression is a linear classifier for binary and multi-class classification by modeling the probability of an instance being in a certain class.
4. **K-Nearest Neighbors (KNN):** KNN is a non-parametric method that assigns a class

to a sample based on the most common class among its k nearest neighbors in the feature space.

5. **XGBoost:** XGBoost is a high-performance optimized gradient boosting algorithm known for efficiency.

For each of the four cancer types, each of these five classifiers is independently trained on the reduced-dimensional feature vectors and the respective stage labels within that particular cancer type. This independent modeling strategy enables the classifiers to learn the specific characteristics and patterns involved in the stage progression of each unique cancer.

### 4.5 Performance Evaluation

The performance of every trained classifier for every one of the four types of cancer is thoroughly tested using the held-out testing set. Major evaluation metrics are employed to test the effectiveness of the models, including:

1. Accuracy: The ratio of correctly classified instances to the total number of instances.
2. Classification Reports: These give a detailed assessment, such as precision (the classifier's ability not to mark as positive a negative sample), recall (the classifier's ability to identify all the positive samples), F1-score (the harmonic mean of precision and recall), and support (the number of actual instances of the class in the given dataset) for each phase in each cancer type.
3. Confusion Matrices: These give a visual overview of the predictions of the model, displaying the number of true positives, true negatives, false positives, and false negatives for each phase, enabling a thorough analysis of the types of classification errors.

## 5 Results and Evaluation

The models were tested and developed with a uniform approach, including 5-fold stratified cross-validation on training data to estimate generalization and final testing on a reserved test set. Final evaluation metrics used are precision, recall, accuracy wqand F1-score, which are aggregated in classification reports. Confusion matrices were also created to give a better picture of the classification performance by classes. Table 1 to Table 8 provide a comprehensive overview of the dataset and performance metrics for multi-cancer classification.

**Table 3.** 5-Fold Cross-Validation Accuracy Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.9557 | 0.9380 | 0.9287 | 0.9643 | 0.9453 |
| | - | - | - | - | - |
| | 0.9695 | 0.9493 | 0.9420 | 0.9688 | 0.9603 |
| ALL | 0.9113 | 0.9387 | 0.9057 | 0.9287 | 0.9360 |
| | - | - | - | - | - |

| | | | | | |
|---|---|---|---|---|---|
| | 0.9259 | 0.9500 | 0.9187 | 0.9353 | 0.9467 |
| | 0.8900 | 0.9333 | 0.9073 | 0.9173 | 0.9213 |
| Brain Cancer | - | - | - | - | - |
| | 0.9080 | 0.9427 | 0.9200 | 0.9253 | 0.9307 |
| | 0.9587 | 0.9830 | 0.9710 | 0.9697 | 0.9820 |
| L/C Cancer | - | - | - | - | - |
| | 0.9613 | 0.9857 | 0.9737 | 0.9731 | 0.9847 |

**Table 4.** Train Accuracy Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.9673 | 0.9466 | 0.9386 | 0.9885 | 0.9575 |
| ALL | 0.9219 | 0.9520 | 0.9157 | 0.9444 | 0.9507 |
| Brain Cancer | 0.9043 | 0.9475 | 0.9148 | 0.9263 | 0.9275 |
| L/C Cancer | 0.9619 | 0.9857 | 0.9734 | 0.9758 | 0.9849 |

**Table 5.** Test Accuracy Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.9344 | 0.9098 | 0.9070 | 0.9584 | 0.9230 |
| A.L.L. | 0.9137 | 0.9347 | 0.9117 | 0.9320 | 0.9373 |
| Brain Cancer | 0.8880 | 0.9233 | 0.9040 | 0.9120 | 0.9117 |
| L/C Cancer | 0.9536 | 0.9778 | 0.9670 | 0.9702 | 0.9762 |

**Table 6.** precision Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.90-0.97 | 0.82-0.97 | 0.84-0.98 | 0.94-0.98 | 0.88-0.98 |

| | | | | | |
|---|---|---|---|---|---|
| A.L.L. | 0.86-0.96 | 0.88-0.97 | 0.85-0.97 | 0.89-0.97 | 0.90-0.97 |
| Brain Cancer | 0.85-0.93 | 0.89-0.95 | 0.87-0.94 | 0.88-0.94 | 0.88-0.94 |
| L/C Cancer | 0.92-0.98 | 0.97-0.99 | 0.95-0.98 | 0.94-0.99 | 0.96-0.99 |

**Table 7.** Recall Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.88-0.98 | 0.82-0.97 | 0.84-0.98 | 0.94-0.98 | 0.88-0.98 |
| A.L.L. | 0.86-0.96 | 0.87-0.97 | 0.85-0.97 | 0.89-0.97 | 0.90-0.97 |
| Brain Cancer | 0.86-0.93 | 0.89-0.95 | 0.87-0.94 | 0.88-0.94 | 0.88-0.94 |
| L/C Cancer | 0.93-0.98 | 0.97-0.99 | 0.95-0.98 | 0.94-0.99 | 0.96-0.99 |

**Table 8.** F1-Score Comparison Across Cancer Types and Models.

| Cancer Type | SVM | RF | LR | KNN | XGB |
|---|---|---|---|---|---|
| Cervical Cancer | 0.89-0.97 | 0.82-0.97 | 0.84-0.98 | 0.94-0.98 | 0.88-0.98 |
| A.L.L. | 0.86-0.96 | 0.87-0.97 | 0.85-0.97 | 0.89-0.97 | 0.90-0.97 |
| Brain Cancer | 0.85-0.93 | 0.89-0.95 | 0.87-0.94 | 0.88-0.94 | 0.88-0.94 |
| L/C Cancer | 0.93-0.98 | 0.97-0.99 | 0.95-0.98 | 0.94-0.99 | 0.96-0.99 |

### 5.1 Train and Test Accuracies for Different Cancer Types

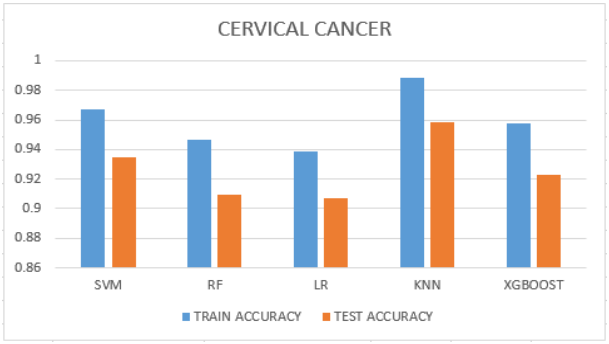



**Fig. 2.** Cervical.

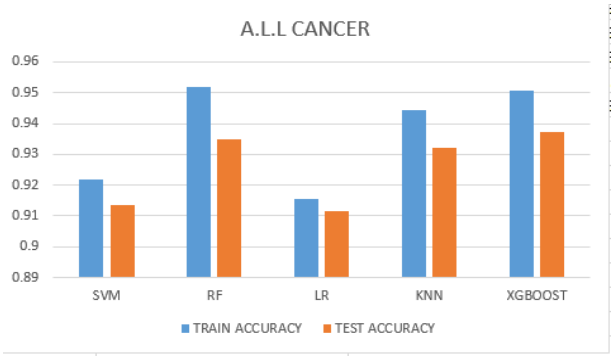



**Fig. 3.** All.

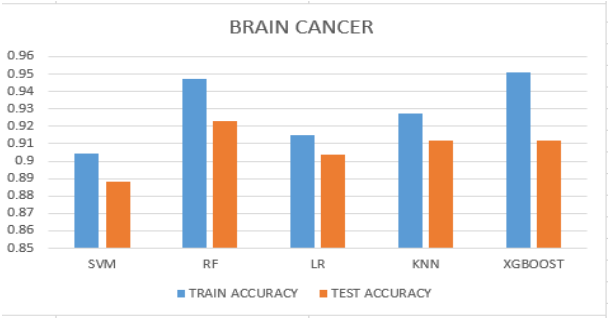



**Fig. 4.** Brain.

Fig. 2 to Fig. 5 illustrate the classification accuracy outcomes for Cervical Cancer, Acute Lymphoblastic Leukemia (ALL), Brain Cancer, and Lung/Colon Cancer, respectively. Each figure showcases performance across five models: SVM, Random Forest, Logistic Regression, KNN, and XGBoost, using UMAP-reduced features from EfficientNetB3.

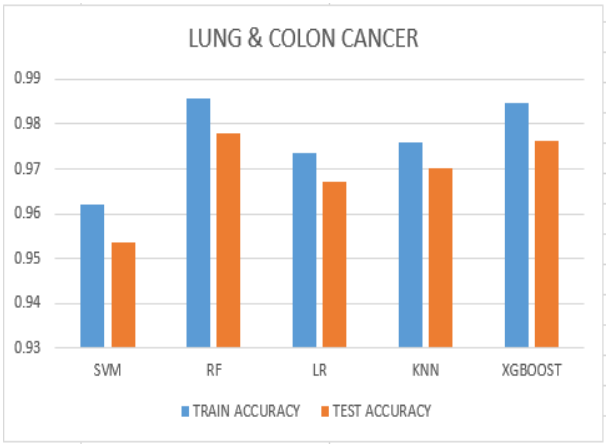
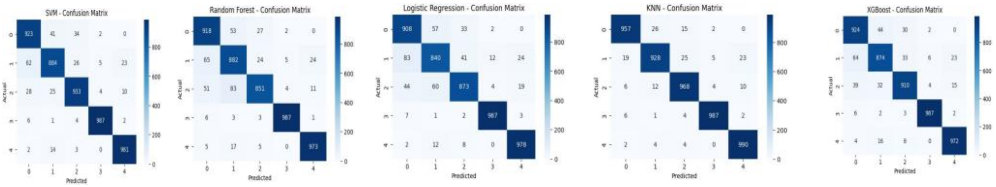
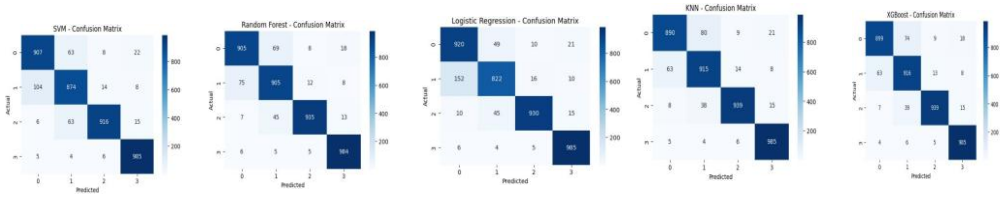



**Fig. 5.** Lung/Colon.



(a): SVM (b): Random Fores (c): LR (d): KNN (e):XGBoost

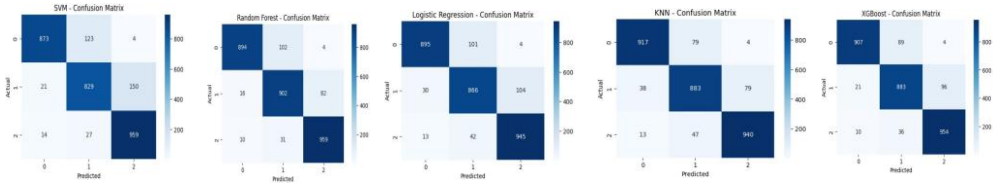
**Fig. 6.** Confusion Matrices for Different Models (Cervical Cancer)



(f): SVM (g): Random Forest (h): LR (i): KNN (j):XGBoost

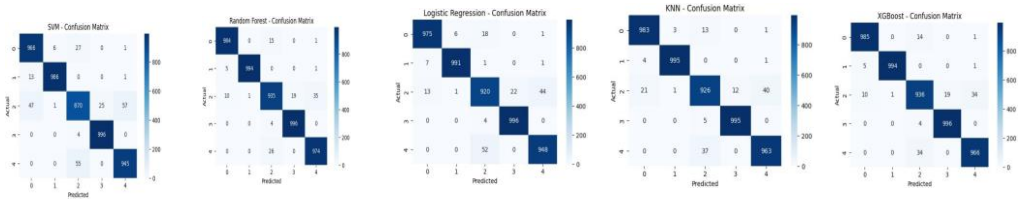
**Fig. 7.** Confusion Matrices for Different Models (All Cancer)

Fig. 6 to Fig. 9 present confusion matrices for Cervical Cancer, ALL, Brain Cancer, and Lung/Colon Cancer, respectively.



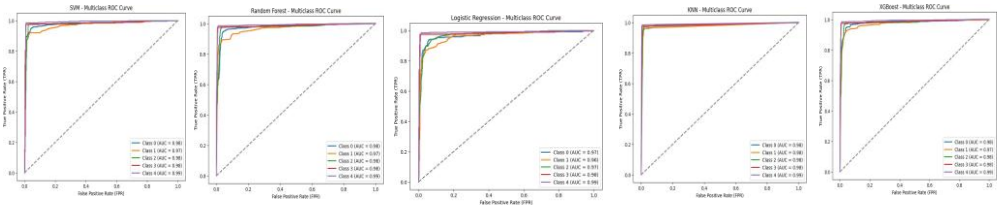

(k): SVM (l): Random Forest (m): LR (n): KNN (o): XGBoost

**Fig. 8.** Confusion Matrices for Different Models (Brain Cancer)



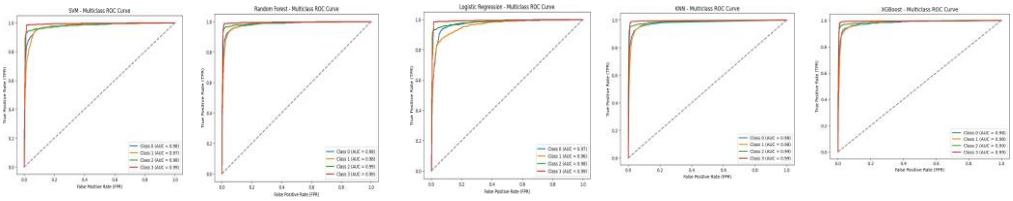

(p): SVM (q): Random Forest (r): LR (s): KNN (t): XGBoost

**Fig. 9.** Confusion Matrices for Different Models (Lung/Colon Cancer).




(a): SVM (b): Random Forest (c): LR (d): KNN (e): XGBoost

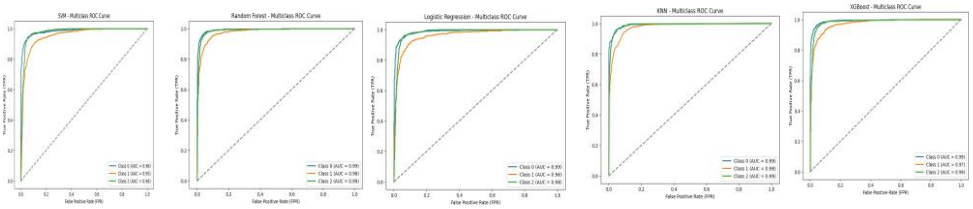
**Fig. 10.** ROC Curves for Different Models (Cervical Cancer).




(f): SVM (g): Random Forest (h): LR (i): KNN (j): XGBoost

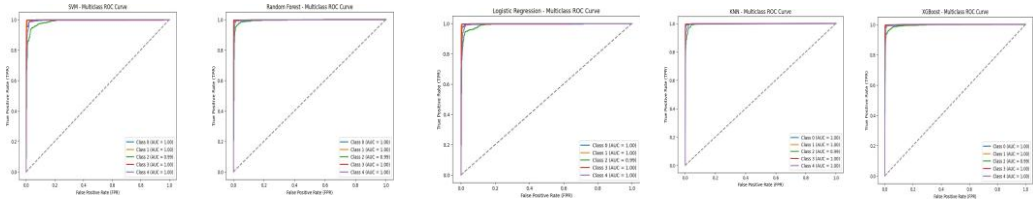
**Fig. 11.** ROC Curves for Different Models (All Cancer).

Fig. 10 to Fig. 13 present ROC curves for Cervical Cancer, ALL, Brain Cancer, and Lung/Colon Cancer, respectively.



(k): SVM (l): Random Forest (m): LR (n): KNN (o): XGBoost

**Fig. 12.** ROC Curves for Different Models (Brain Cancer).



(p): SVM (q): Random Forest (r): LR (s): KNN (t): XGBoost

**Fig. 13.** ROC Curves for Different Models (Lung/Colon Cancer).

### 5.2 General Comparative Observations

- **Random Forest and XGBoost:** These algorithms are consistently among the strongest performers on the can- cer classification tasks, frequently hitting the highest or second-highest test accuracies.
- **K-Nearest Neighbor (KNN):** KNN gives competitive results, achieving the highest accuracy in classifying cervical cancer and demonstrating good performance in ALL and brain cancer classification.
- **SVM and Logistic Regression:** These algorithms tend to deliver decent results but generally fall behind the top performance achieved by KNN, Random Forest, and XGBoost across these datasets.
- **Effect of Number of Classes:** Accuracy is affected by class count. Brain cancer (3 classes) often shows higher accuracy than cervical (5) and ALL (4) for most models.
- **Optimal Model Choice:** The best model is indeed a function of the specific cancer type and the underlying patterns present in the image data.

Overall, Random Forest and XGBoost consistently demonstrate strong performance across these cancer classification problems, frequently achieving high test accuracies. K-Nearest Neighbors (KNN) also performs remarkably well, notably achieving the highest accuracy for cervical cancer. However, it's crucial to emphasize that solely relying on accuracy might not be sufficient. Further evaluation using other relevant metrics, such as precision, recall, F1-

score, and considering the specific context and requirements of the application (e.g., the cost of false positives vs. false negatives), is essential for determining the most suitable model for each cancer type.

## 6 Conclusion

In summary, this research probed the performance of various machine learning algorithms—Support Vector Ma- chines (SVM), Random Forest, Logistic Regression, K- Nearest Neighbors (KNN), and XGBoost in classifying four types of cancer based on image data: cervical cancer, ALL (Acute Lymphoblastic Leukemia), brain cancer, and lung and colon cancer. Our comparative performance across these varied datasets revealed nuanced differences in model effectiveness.

Our results suggest that XGBoost and Random Forest demonstrated consistently strong performance, frequently achieving the best or second-best test accuracies across the four types of cancers. This indicates their robust applicability to complex medical image classification tasks.

KNN also performed well, securing the highest accuracy in cervical cancer classification and exhibiting competitive outcomes for ALL, brain cancer, and lung and colon cancer. This suggests that instance-based learning algorithms hold promise for this application area.

Although SVM and Logistic Regression yielded com- parable accuracies, they generally did not reach the peak performance levels observed with XGBoost, Random Forest, and KNN in these specific experiments.

It is important to note that the optimal model's accuracy appeared to be influenced by the specific characteristics of the cancer type and the nature of the classification task, as reflected in the different number of classes. For instance, the general accuracy for brain cancer classification (3 classes) was often higher than that for cervical cancer (5 classes) and ALL (4 classes) for several models.

While our primary comparison focused on accuracy, a comprehensive evaluation of these models necessitates an in- depth analysis of other crucial metrics such as precision, recall, and F1-score, as well as the examination of confusion matrices to gain insights into the types of classification errors made. These metrics would provide a more holistic understanding of each model's strengths and weaknesses in a clinical setting.

Future work could explore the impact of diverse feature extraction techniques, further model hyperparameter optimization, and the potential benefits of ensemble methods that integrate the strengths of multiple models. Additionally, investigating the interpretability of these models could offer valuable insights for clinical decision-making. The final choice of which machine learning model works best for cancer classification will be driven by various considerations, notably the specific needs of the diagnosis and the features of the data being analyzed.

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