Machine Learning-Based Multi-Cancer Diagnostic System for Early Detection and Accurate Classification Across Diverse Cancer Types

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DOI: https://doi.org/10.51583/IJLTEMAS.2026.150600180

Received: 01 July 2026; Accepted: 06 July 2026; Published: 20 July 2026

ABSTRACT

Cancer is one of the major causes of death worldwide, mostly owing to late discovery and hence restricted treatment choices. Existing screening approaches are primarily invasive and often associated with complicated, long and expensive procedures. In biomedicine and bioinformatics, several research groups have examined the use of machine learning methods to solve the important challenge of categorizing cancer patients into high- and low-risk categories. These methodologies have thus been used to mimic the onset and treatment of cancer. The ability of ML algorithms to detect important characteristics in complex datasets further highlights their importance. Many of these approaches like as Decision Trees, Logistic Regression (LR), Support Vector Machines and K-Nearest Neighbours have been widely employed in cancer research to generate prediction models that aid decision makers to make better and more trustworthy decisions. ML methods are indeed able to improve our understanding of cancer formation, but need adequate validation to be regarded for application in ordinary clinical practice. Hence, an ML approach was utilized to simulate the progression of cancer. The prediction models shown here are based on several ML approaches and a broad variety of input features and Data Samples. The proposed framework incorporates data preprocessing, feature selection, and advanced classification algorithms to enhance diagnostic accuracy and facilitate timely clinical decision-making. The study emphasizes the potential of artificial intelligence in advancing precision oncology and improving healthcare outcomes.

Keywords: Machine Learning, Kaggle Multi Cancer Dataset, Predictive Models, Cancer Disease, Medical Images, Classification.

INTRODUCTION

Cancer is one of the leading causes of death worldwide. It is the second largest cause of mortality worldwide causing 9.7 million deaths in 2022 [1]. Cancer puts a tremendous economic burden on the worldwide population, impacting individuals, communities, health care systems, and national economies, along with its severe social and psychological effects on the lives of millions of people and their families [2]. Even with the finest therapeutic therapy, if the disease is detected only at an advanced stage, the survival rate is reduced by more than half [3]. This shows the significance of early detection, which may drastically improve the odds of survival for patients and decrease the expenses of therapy [4]. Only 39% of cancers are discovered early [5], according to research by the American Cancer Society in 2023. Cancer develops from the original location to the metastatic stage over time, and detection of cancer within this window is crucial to reduce the likelihood of death [7]. Many

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue VI, June 2026

tumours, for example, may not cause symptoms in the early stages or cause nonspecific, non-specific symptoms, such as tiredness or weight loss. There is consensus amongst USPSTF, ACS, ASCO (only on maximum and improved setting), CCA and EG to suggest screening with HPV DNA testing every 5 years for women 30–64 years of age. Cytology every 3 years (USPSTF, ACS, EG) or co-testing every 5 years (USPSTF, ACS) are also acceptable options. This is based on a study that compared screening strategies in terms of cervical cancer deaths per 1000 women and concluded that in women >30 years screened with HPV DNA [8] testing at 5-year intervals, the number of deaths was calculated at 0.29 per 1000 women versus a significantly higher 8.34 in women with no screening. The analysis of medical pictures plays an important role in the identification of disorders related to blood, skin, breast, brain, lungs, retina and other organs [9]. Due to the underlying organ dysfunction, tumours tend to grow fast. Today, 30 to 50 percent of cancers may be avoided by avoiding risk factors and using current evidence-based preventive strategies [10]. Timely cancer prevention and treatment [11] may also reduce the burden of the illness on the society. Early diagnosis and therapy are curative for many types of cancer [12,13].

Related Work

Because these markers are released early by tumours, liquid biopsy may identify cancer even in the absence of symptoms or observable tumours [14]. Liquid biopsy also provides the benefit of real-time tumour information [15]. Therefore, the development of a single liquid biopsy test, which combines several indicators and may simultaneously identify many malignancies [16], will address the constraints highlighted in current clinical practice for cancer diagnosis [17]. The approach is referred to as a multi-cancer early detection (MCED) test and should be [18] highly sensitive for detection of early-stage cancers, highly specific to [19] avoid false positives, able to identify the tissue of origin (TOO) of the cancer, and cost effective [20].

This computational approach for autonomous breast cancer disease detection uses multilayer perceptron (MLP) neural network based on an improved non-dominated sorting genetic algorithm to optimize accuracy and network structure. The intelligent classification model for breast cancer detection proposed in [21] applies a genetic algorithm wrapper based on gain-directed simulated annealing to minimize redundant and unneeded features in the feature space to remove redundant information and reduce training cost. This results in an increase in classification accuracy and a decrease in computation costs. We test the effectiveness of this approach using Wisconsin's own breast cancer variations (WBCD and WBC). Researchers in [22] created a CAD for classifying mammography images, which employs a GA based feature selection strategy to reduce the feature vector and a semi-supervised support vector machine (SVM) to do classifications. This strategy enhances accuracy. The two machine learning techniques used in the automated system for breast tissues classification by the analyst of [23], i.e., a radial basis function network and a feed forward neural network with the back propagation learning algorithm (BPNN) (RBFN), were discussed. Breast cancer tissues were categorized into six types: adipose, glandular, glandular-like, connective, and cancer. Data were obtained via electrical impedance spectroscopy (EIS). The Radial basis function network fared better than the back propagation network in terms of accuracy, minimum error, maximum epochs and training time for classification of six different breast tissues. As a consequence, the training time has been reduced and the accuracy has been improved.

Neural network learning may suffer from problems of generalization and can become stuck in local optima. An SVM-based ensemble learning model for diagnosis of breast cancer is formed by a C-SVM and an SVM with six different kinds of kernel functions [24]. We offer a Weighted Area Under the Receiver Operating Characteristic Curve Ensemble (WAUCE) [25] approach for hybridization modelling based on the experience of several classifiers on diagnostics tasks. The model was evaluated on three datasets the Surveillance, Epidemiology, and End Results (Surveillance) dataset, the Wisconsin Breast Cancer [26] (WBC) dataset and the Wisconsin Diagnostic Breast Cancer [27] (WDBC) dataset (SEER). The total accuracy of this method is 98.08%. [28] described the experimental study and how sensitivity analysis was performed on two categories, Diameter and Pathological outcome using the multicentre data set. There were three subgroups in diameter; 0-10mm, 10-20mm, 20-30mm. Sensitivity was 85.7% (95% Cl, 70.8%-100.0%) and specificity was 91.1% (95% Cl, 86.8%-95.2%) in the 0-10mm group.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue VI, June 2026

The 10-20 mm group had a sensitivity of 85.7% (95% Cl, 77.1%-94.3%) and a specificity of 90.1% (95% Cl, 84.8%-95.4%). In the 20-30 mm group, sensitivity was 78.9% (95% Cl, 66.0%-91.8%) and specificity was 91.3% (95% Cl, 83.2%-99.4%) [29].

A machine learning study of MR radiology [30] that helps to improve PI-RADS performance in clinically significant PCA. This machine learning strategy, a machine aided system for PCA diagnosis, might improve the functionality of a PIRADS v2 structure design and therefore improve the quality of cancer consultation and therapy. A deep learning algorithm [32] enables guys to detect prostate cancer [31]. The findings were shown to be 93.5% accurate and 89% accurate for prostate cancer using 3D MRI images [33]. The [34] technique was used to identify prostate cancer in men and its findings were 84% accurate compared to semi-deep learning. The CNN algorithm for prostate cancer diagnosis.

[35] [36] After replicating the approach, the accuracy for diagnosing prostate cancer was around 86%. For women who do not have access to pelvic examination or are unwilling to undergo pelvic examination, self-collected vaginal samples may be utilized for HPV testing [37,38]. Specifically, patients may get specimens from the vagina by using a tampon, cotton swab, cytobrush, or cervicovaginal lavage, and self-collection can be conducted under supervision in a clinic setting or at home [39]. However, statistics suggest that the sensitivity of this approach is much lower than clinician-collected specimens (76% vs. 91%) [40], and EG suggests that this method should not be favoured over clinician-collected samples.

Cancer Disease

Cancer is a disorder in which the body produces aberrant cells that multiply without control. Everyone is born with some risk of cancer. No one can get it like a cold or flu. Disruption in the programming of a cell or of a population of cells may lead to out-of-control proliferation [41]. Age, sex, race, heredity, radioactive substances, chronic inflammation, cigarettes, smoke and dust may all cause changes to the code. As seen in Figure 1, cancer may afflict men, women and children, young and old, affluent and poor. You can’t get cancer from someone else, nor transmit it to someone else.

Now there are new ways of treating cancer and a lot of individuals become well [42]. You may get cancer anyplace in the body including the bones and the skin depicted in figure1. Of course, many of these are beyond of our control, but we need to be aware of those we can control. Of all the diseases, cancer is one for which prevention is a better cure. It's a tough question.

It depends on the stage of cancer and the organs where the disease has appeared. Yes, if cancer is identified in its early stages, cancer is totally curable for forms like breast cancer. But in general, early identification is very important in the effective treatment of cancer. The survival rate of the cancer patient is always greater with early identification, low grade and early stage of cancer. Studies [43] suggest that hormonal, behavioural and environmental factors may all be involved in an increased risk of breast cancer. But why some women with no conceivable hazards at all end up with cancer while others with risk factors never do is unclear. Breast cancer is likely caused by a mix of hereditary and environmental factors.

Research says that India would have roughly 1,70,000 new instances of breast cancer by 2024. It also shows that 1 in 28 women will be diagnosed with the malignancy. The incidence of breast cancer is higher in females, but men have a 1-2% risk of having the illness [44].

Many men will be diagnosed with prostate cancer throughout the course of their lives. Prostate cancers usually grow slowly and remain confined, and may not cause any visible symptoms. Some types of prostate cancer grow slowly and may not need treatment. Other types grow quickly and are far more deadly. The early identification of prostate cancer enhances [45] the possibility that the illness may be effectively treated if it remains localized to the gland. Most prostate cancers grow slowly, but others might advance fast [46]. Postmortem studies revealed that many older men (and some younger men) dying of unrelated causes were in fact afflicted with prostate cancer.

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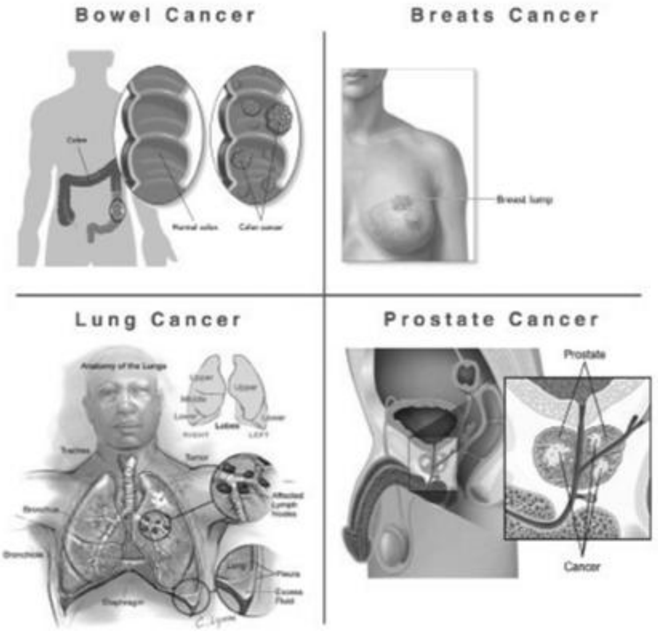

Figure 1: The Different Types of Cancer Disease

Cancer occurs in the lung. Inhalation is the introduction of air from the nasal cavity down the trachea into the lungs, into the bronchi. These cells that line the tubes are where the great majority of lung malignancies begin. Lung cancer may be split into 2 categories: Non-small cell lung cancer (NSCLC) accounts for around 80% and small cell lung cancer (SCLC) for 20% [47]. The most prevalent kind of mixed small cell/large cell lung cancer is when there are both types of lung cancer cells present. Prostate cancer will be diagnosed in a substantial proportion of males. Prostate cancers frequently grow slowly and remain localised, where they may not cause any apparent symptoms [48]. Some prostate cancers are slow growing and may not need any treatment, while others may grow quickly and are far more deadly. Early identification of prostate cancer improves the success rates of treatment while the illness is still confined to the gland [49]. In most instances, prostate cancer grows slowly, but sometimes it progresses quickly.

Proposed Framework

The approach used for the extraction of information from the dataset of the patients whether it was benignant or malignant growth. In this method the datasets are trained and tested with different testing rate and test rate by different classifiers. We used the classification learner app for this technique which is a machine learning methodology [50] that assists in the simple prediction of the illnesses. Under Machine Learning, on the Apps tab, select Classification Learner. Click New Session > From Workspace in the File section of the Classification Learner tab. In this box click new session, then choose from file, start a new session by importing data from file and set a validation scheme. Then pick the information to be imported and another window opens, in that window in upper right corner we have an import selection click on it. Then at this moment another window is launched with a name new session from file, in that window we obtain the data set variables, validation schemes replies and predictors for the prediction model [51]. Then click on the start session as shown in figure 2.

After clicking on the start session then at that moment window shown with a scalar plot drawn with malignant and benignant cancer from the transferred dataset. In that window we have a predictor of the scalar plot on x and y axis and classifications displaying benignant and malignant malignancy. The produced scalar plot is used to determine which predictors are utilized to forecast the replies. Now we need to test and train the data using several classifiers which are present in the model session. All the Machine learning [52] classifiers are present in the model but we are using four classifiers for testing and training the data. The classifiers employed include support vector machine, decision tree, Logistic Regression (LR) and k-nearest neighbour classifiers. These classifiers are evaluated with varied testing and training rates for improved performance assessment. We choose the classifier that we want to train and test the data and click on the train all button. Then to see the output of the

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model, pick the model in the model's pane and check the summary tab [53]. The summary page presents the training results meretrices, computed on the validation set.

Evaluate the accuracy of the prediction within each class of the selected model. On the Classification Learner tab, in the Plots section, click the arrow to view the gallery, and then select Confusion Matrix in the Validation Results group. The matrix provides us the outcomes of the real class and the anticipated class. In the model pane, we can try to experiment with multiple models to pick the best model, we can add different characteristics for the model we can reject the features that have poor prediction value [54]. In the model pane click on downward arrow, in that pick support vector machine classifier and then click on train all. Then the model is trained and the prediction model is formed according to the characteristics chosen in the next session from the file window. This window itself we may split the data set into two pieces, one for training and another for evaluating the data. The training of the model was provided with more data and testing was provided with less data as per the need to fulfil each point in the prediction model. The model is trained and tested; from this we receive the accuracy results and confusion matrix. The confusion matrix is used to calculate the values of precision, recall and F-1 score.

Similarly, several classifiers in the model pane were picked such Decision Tree, Logistic Regression (LR) and K-Nearest Neighbour classifiers are trained and evaluated at varied rates [55]. The prediction model, accuracy and confusion matrix we achieved from the training and testing the model. The confusion matrix is used to extract the precision, recall and F-1 score values of the selected classifier. Machine learning enables us to analyse and apply large datasets faster and more efficiently than previous techniques. For cancer diagnosis a dataset and a machine learning approach [56] may be used. The dataset is used for developing the supervised machine learning model for detecting cancer with the help of classification methods. This collection contains features of malignant and benign tumours. The initial step of the conceptual model considers data purification (filtering) and data augmentation for processing.

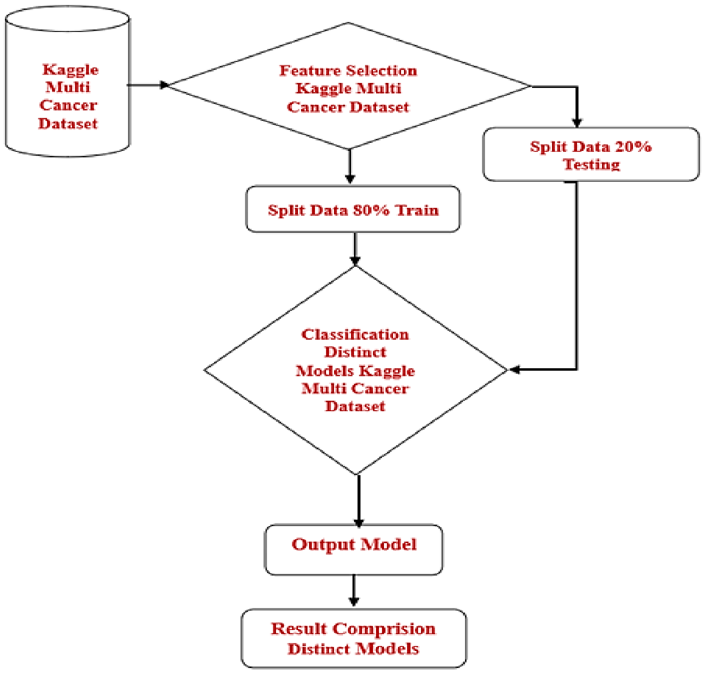

Figure 2: The Proposed Architecture

The suggested conceptual paradigm is built on four pillars: preprocessing, feature extraction, classification, and performance analysis. From the beginning the conceptual model takes into consideration data augmentation and data purification (filtering) prior to processing [56]. In the second step, features are extracted. In medical datasets, this is the process of extracting features and constructing a collection of descriptors. The aim is to identify certain properties of the sample that may predict consistently whether it is benign or cancerous. The classifiers may be realized using several machines learning based classification algorithms. A classifier was trained on 3 cancers like breast cancer, Lung & Colon cancer and Cervical cancer to control samples as a whole model for each

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue VI, June 2026

sample. Here we have used 3 various classifiers like Decision tree, Logistic Regression (LR), Support Vector Machines (SVM), KNN and choose the best model whose accuracy is larger and producing better result [57].

Kaggle Multi Cancer Dataset

Images illustrating of different forms of cancer have been accumulated for the sake of study and analysis, and this collection comprises such photographs. Figure 3 illustrates how the dataset, which consists of 130,000 histopathological pictures representing eight main cancer types and twenty-six subclasses, offers a wealth of resources for medical image classification and machine learning applications. For the purpose of increasing both variety and resilience, the dataset was expanded with the use of Keras' Image Data Generator. Subfolders that are named after the eight primary cancer classes are located at the base of the dataset. Each of these subfolders [58] includes photos that are grouped into further subclasses. The framework makes it possible for people to simply browse to the sort of cancer that they are interested in looking at.

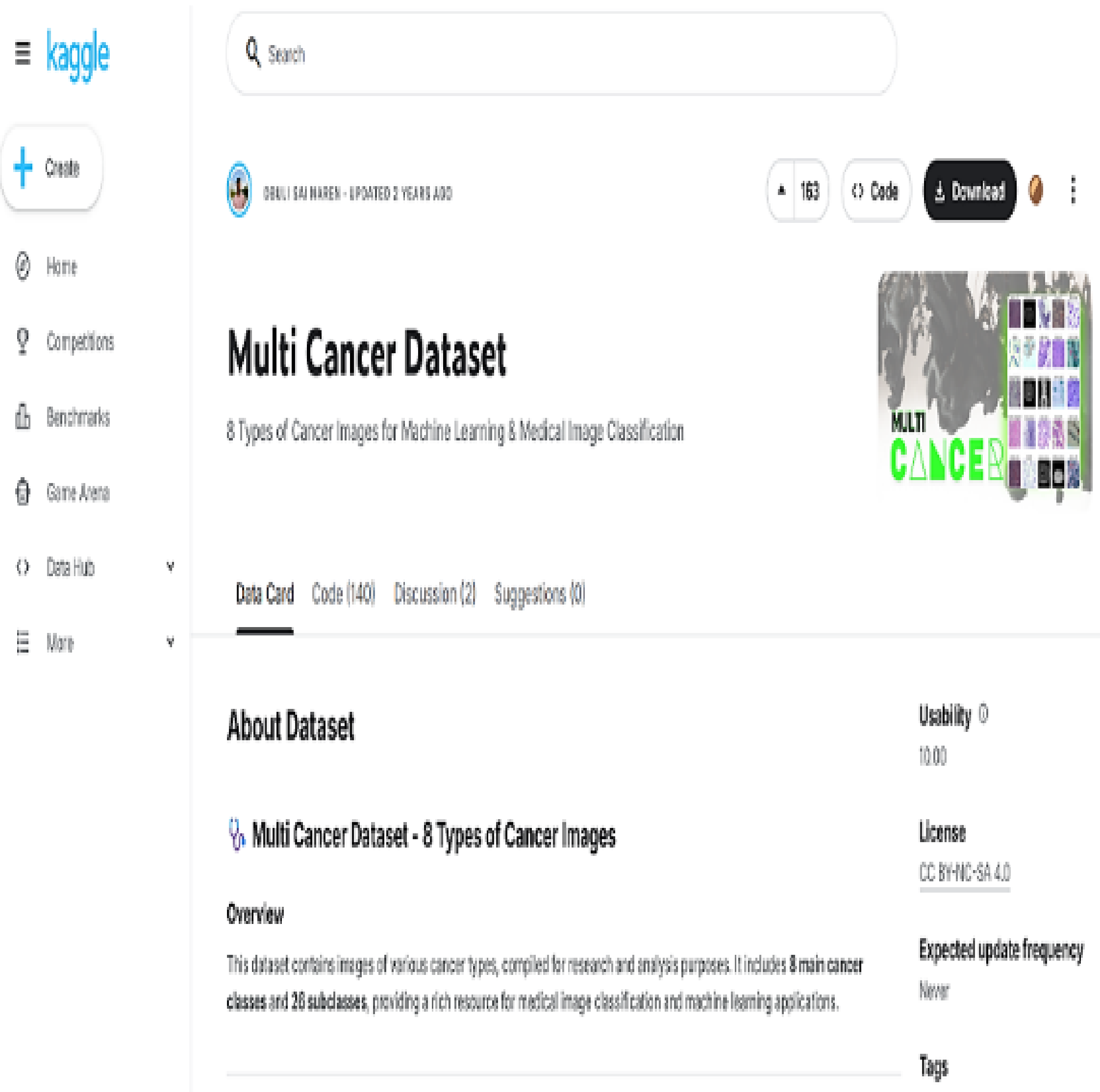

Figure 3: Kaggle Multi Cancer Dataset

Outcome

The multi-cancer diagnostic method that was developed and was based on machine learning obtained a high level of accuracy in identifying and categorizing a wide variety of cancer types, which allowed for earlier detection and enhanced clinical decision-making [59]. This framework highlighted the promise of AI-driven precision medicine for scalable, rapid, and accurate cancer detection. It also improved the reliability of predictions, decreased the number of diagnostic mistakes, supported efficient healthcare delivery, and supported efficient healthcare delivery. A variety of classifiers, which are shown in tables 1, 2, and 3, are used in the

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue VI, June 2026

training and testing of the datasets. A prediction model for the classifier is formed by selecting two features during the feature selection stage [59]. These characteristics are chosen for the creation of the model. As can be seen in figures 4, 5, and 6, the performance analysis was carried out using a training rate of 80% and a testing rate of 20% using the Kaggle Multi Cancer Dataset that was used.

Table 1. Performance Metrices of Breast Cancer

Models	Accuracy	Recall	F1 Score	Precision
K- Nearest Neighbour	95.9	96.17	96.12	96.17
SVM	98.89	97.67	97.78	98.78
Logistic Regression (LR)	89.6	88.1	88.13	87.8
Decision Tree	93.37	97.15	93.1	91.46

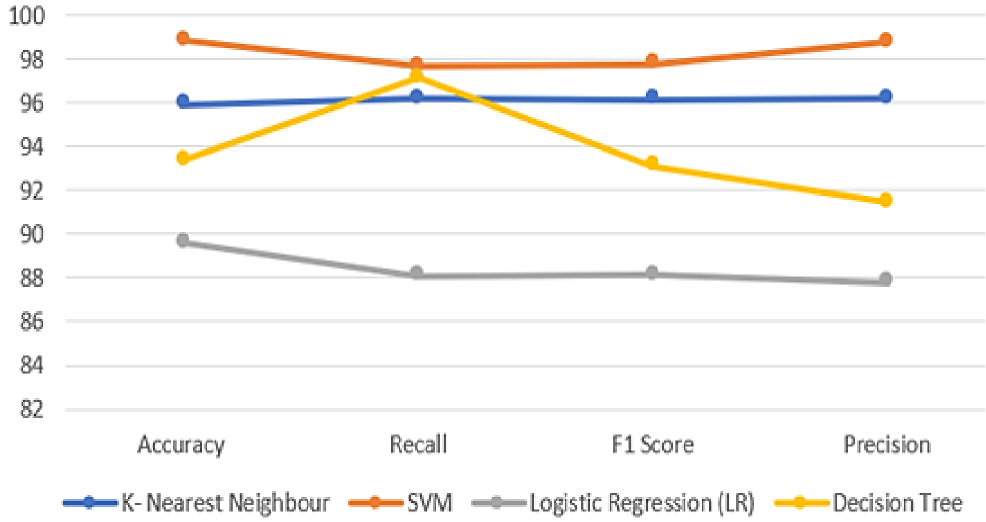

Figure 4: The Prediction Breast Cancer Using Four Distinct Models

Table 2. Performance Metrices of Lung & Colon Cancer

Models	Accuracy	Recall	F1 Score	Precision
K- Nearest Neighbour	79.17	99.1	87.56	77.78
SVM	82.34	89.61	99.12	80.46
Logistic Regression (LR)	79.6	78.1	78.13	77.8
Decision Tree	79.23	87.86	86.11	84.52

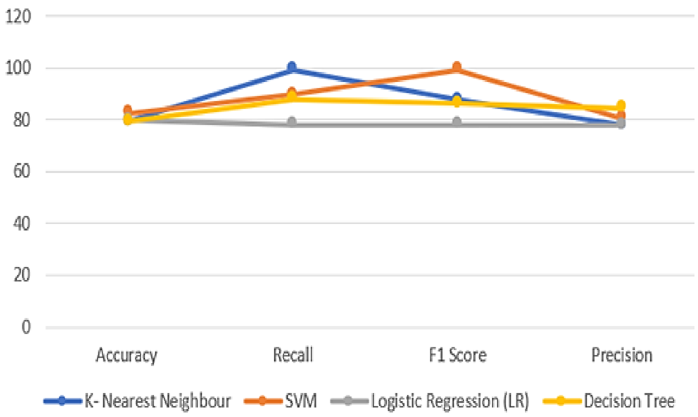

Figure 5: The Prediction Lung & Colon Cancer Using Four Distinct Models

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Table 3. Performance Metrices of Cervical Cancer

Models	Accuracy	Recall	F1 Score	Precision
K- Nearest Neighbour	88.21	96.13	91.2	86.75
SVM	87.27	89.68	89.81	89.67
Logistic Regression (LR)	69.67	68.41	68.33	67.34
Decision Tree	78.84	78.58	81.27	85.62

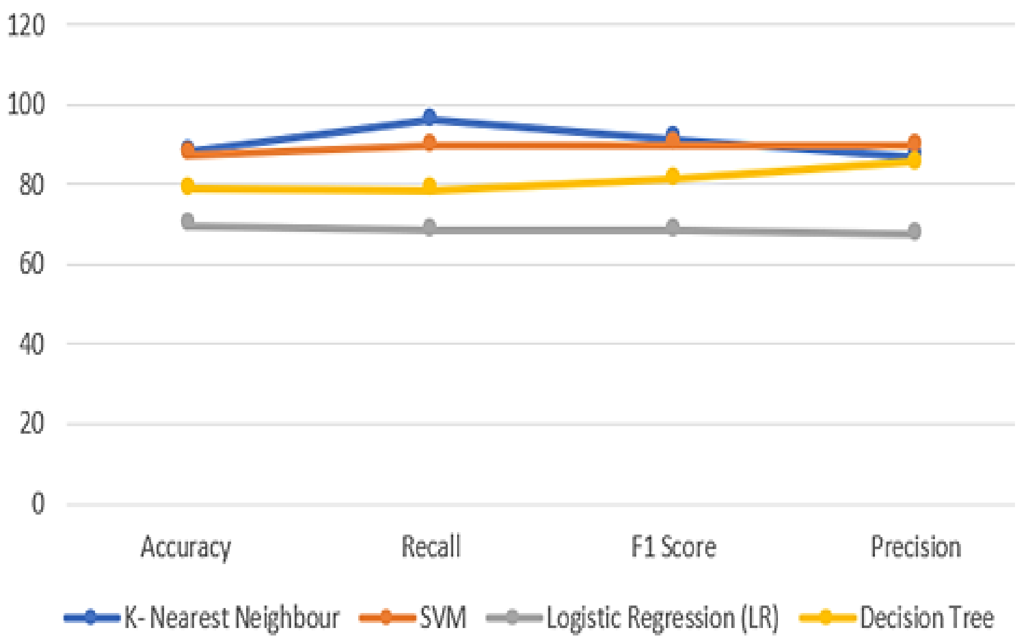

Figure 6: The Prediction Cervical Cancer Using Four Distinct Models

CONCLUSION

The research performed binary classification of healthy persons and those with a certain kind of Cancer sickness. The research highlights the importance of accurate, non-invasive approaches for early cancer diagnosis in reducing mortality. The suggested Machine Learning-Based Multi-Cancer Diagnostic System illustrates the potential of artificial intelligence to greatly enhance early detection and accurate categorization of several cancer kinds. It employs powerful machine learning techniques and extensive clinical or medical images databases to efficiently discover intricate illness patterns that may be difficult to detect using standard diagnostic methods. Early and accurate detection of cancer allows prompt clinical intervention, improves treatment planning and patient outcomes while minimizing diagnostic delays and the expense of health care. The research emphasizes the significance of suitable data preprocessing, feature selection, and model tuning to get good predictive performance. Explainable AI and multimodal healthcare data may help improve the reliability and interpretability. However, there are still obstacles, such as data quality, class imbalance, and clinical validation. In conclusion, this system offers a viable option for the intelligent, scalable and precision-driven detection of cancer, eventually leading to improved patient outcomes and healthcare efficiency.

Future Work

Further studies should concentrate on combining multimodal healthcare data, such as medical pictures, genetic profiles, lab findings and electronic health records, to improve the accuracy and robustness of diagnosis. Moreover, designing lightweight, real-time and cloud-enabled diagnostic frameworks might encourage practical deployment in hospitals and distant healthcare settings. Overall, the suggested approach is a promising step

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue VI, June 2026

towards the construction of intelligent, scalable and reliable multi-cancer detection systems that supports precision medicine and improves worldwide cancer treatment.

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