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PREDICTING PROSTATE CANCER WITH MACHINE LEARNING: FINDING A BALANCE BETWEEN ACCURACY AND COMPUTATIONAL EFFICIENCY

[1*] Mr. Kallol Acharjee, [2] Dr. Kaushik Adhikary, [3] Dr. Sumit Das, [4] Dr. Dipankar Misra,

[5] Mr. Subhodip Koley

[1] Department of Information Technology, JIS College of Engineering, Kalyani, India

kallol.acharjee@jiscollege.ac.in, Orcid: https://orcid.org/0009-0006-9126-0925

[2] Department of Computer Science & Engineering, JIS University, Kolkata.

kaushik.adhikary@jisuniversity.ac.in Orcid: https://orcid.org/0000-0001-6514-0395

[3] Department of Information Technology, JIS College of Engineering, Kalyani, India

sumit.das @jiscollege.ac.in, Orcid: https://orcid.org/0000-0002-8018-9151

[4] Department of Computer Science & Engineering, JIS University, Kolkata.

dipankar.misra@jisuniversity.ac.in Orcid: 0000-0002-7880-3415

[5] Department of Computer Application, JIS College of Engineering, Kalyani, India

subhodip.koley@jiscollege.ac.in, Orcid: https://orcid.org/0009-0004-0262-0526

Abstract

Background: One of the most prevalent cancers in men is prostate cancer, and early identification is crucial to reducing death and enhancing treatment results. Traditional diagnostic methods could be laborious and imprecise. Machine learning (ML) techniques can reduce computer overhead and improve and automate prostate cancer prediction.

Methods: In this study, clinical criteria such as area, smoothness, texture, radius, and perimeter were incorporated in the improved prostate cancer dataset. Preprocessing techniques included label encoding, feature scaling, and mutual information to choose the top ten informative features. Several machine learning models, such as Extreme Gradient Boosting (XGBoost), Random Forest, K-Nearest Neighbours (KNN), Dark Gradient Boosting Machine (LightGBM), and Logistic Regression, were trained and assessed. To adjust the hyperparameters, the Optuna optimisation framework was employed. Computation time (training and testing) and accuracy were used to evaluate performance.

Results: Each model had outstanding forecasting ability. LightGBM fared better than KNN (98.33%) and XGBoost (99.16%) with an accuracy of 99.37%. KNN was the most efficient model with a total runtime of 0.038 seconds; LightGBM and XGBoost were somewhat slower but provided higher accuracy. Even with a moderate accuracy rate of 87.22%, logistic regression remained computationally efficient.

Conclusion: The findings demonstrate that KNN provides the best balance between accuracy and time efficiency, making it suitable for rapid diagnostic applications. However, LightGBM and XGBoost remain superior choices when accuracy is essential. The proposed approach demonstrates how well-suited optimised machine learning models may be as predictive tools for prostate cancer by encouraging early diagnosis and aiding therapeutic decision-making.

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1. Introduction:

One of the most common cancers to be diagnosed, prostate cancer (PCa) is a major cause of cancer-related mortality for men globally. Prostate cancer caused around 375,000 deaths and about 1.4 million new cases worldwide, according to the Global Cancer Observatory (GLOBOCAN 2022), demonstrating the disease's enormous health impact [1] . The likelihood of a successful prostate cancer (PCa) treatment is significantly increased by early and correct diagnosis. The histological examination of tissue removed from the prostate during a biopsy, usually guided by trans-rectal ultrasonography (TRUS), is currently the gold standard for the diagnosis and grading of PCa. The sensitivity of conventional ultrasonography in detecting malignant lesions is low [2]. ML in prostate MRI may be used for purposes other than diagnosis and image interpretation. For instance, accurate gland and region-of-interest segmentation and image co-registration between MRI and US are crucial for the best possible biopsy in MRI–US fusion targeted prostate biopsy. Image fusion and segmentation are typically done by hand, which can be tedious, time-consuming, and prone to inter-operator variation. ML has demonstrated promise in terms of accuracy and efficiency in gland segmentation and MRI–US fusion [3].

This paper investigates different machine learning algorithms, such as ensemble algorithms such as Extreme Gradient Boosting (XGBoost) and Light Gradient Boosting Machine (LightGBM) and classical algorithms such as K-Nearest Neighbors and Logistic Regression to make predictions based on the status of prostate cancer considering the balance between the predictive accuracy and the computational efficiency. The combination of automatic hyperparameter optimization and the assessment of model accuracy and runtime is the testimony to the continued necessity of practical and real-time solutions in clinical practices. The given approach highlights the possibilities of ML-based tools to enhance workflows and outcomes of prostate cancer patients.

2. Literature Review

Using the Kaggle Prostate Cancer Dataset and the SEER Database, the reviewed study compared a number of machine learning methods for prostate cancer detection, including Support Vector Machines (SVM), Random Forests, k-Nearest Neighbours (k-NN), and Neural Networks. With an accuracy rate of 91.1% and an AUC of 0.93, Random Forest outperformed the other models, followed by SVM with an AUC of 0.92, suggesting that it has excellent diagnostic potential. AUC, sensitivity, specificity, and accuracy were among the evaluation measures. Computational effectiveness, dataset biases, and the use of these models in clinical practice were not included in the study, though. To assist efficient management of prostate cancer, future research should concentrate on boosting interpretability, investigating deep learning and ensemble techniques, improving model generalisability, and testing these models in actual clinical settings [4].

This paper suggests a hybrid deep learning model for prostate cancer diagnosis that combines a Bidirectional Long Short-Term Memory (BiLSTM) and a 1D Convolutional Neural Network (1D-CNN). With 93.60% accuracy, 92.89% precision, 94.40% recall, 93.63% F1-score, and 94.96% ROC-AUC, the model demonstrated exceptional performance using the Kaggle prostate cancer dataset and an adaptive medical feature pruning (AMFP) technique for optimal feature selection. At 8.4 seconds for training and 0.0021 seconds for inference per sample, respectively, the times were remarkably efficient. Although the results surpass those of conventional classifiers like Random Forest, SVM, XGBoost, MLP, and Logistic Regression, the study does not analyse the constraints of the dataset, integrate clinical practice, or take ethical considerations into account.Enhancing model generalisability, incorporating a variety of clinical data, improving the AMFP approach, and

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investigating real-world deployment for wider clinical applicability should be the main goals of future study [5].

The study uses a dataset of 100 patient samples and the XGBoost algorithm to classify cases of prostate cancer based on clinical biomarkers like PSA levels, perimeter, radius, and texture. With a mean F1-score of 0.90 and a ROC-AUC of 0.93, the model demonstrated high predictive performance. SHAP value analysis revealed texture, PSA, and perimeter as important predictive parameters, indicating the model's interpretability and dependability. Despite the approach's potential to aid in clinical decision-making and early diagnosis, the study is constrained by its small sample size, lack of algorithmic comparison, and lack of validation across a range of groups. To improve patient outcomes and diagnostic accuracy, future research should concentrate on adding more clinical biomarkers, broadening datasets for generalisability, investigating different algorithms, and integrating such models into real-time clinical decision support systems [6].

The study looks into the classification of prostate cancer using Support Vector Machine (SVM) models based on clinical and demographic information such as patient age, tumour stage, PSA levels, and Gleason scores. By utilising preprocessing techniques including normalisation, handling missing values, and SMOTE for correcting class imbalance, the optimised SVM with an RBF kernel was able to attain a high accuracy of 94.2%. The most significant features in model projections, according to SHAP-based explainability analysis, were Gleason scores and PSA levels. Despite the model's impressive performance, handling unbalanced data and categorising minority cases continued to provide difficulties. SVM was not compared to other algorithms or its computational efficiency assessed in this study. To guarantee useful diagnostic application and patient benefit, future research should concentrate on strengthening interpretability techniques, increasing feature sets, improving imbalance handling, and confirming SVM integration into clinical workflows [7].

With an emphasis on prostate cancer, the reviewed paper examines developments in artificial intelligence applications, particularly machine learning (ML), artificial neural networks (ANN), and deep learning (DL), for the diagnosis and treatment of urologic tumours. The research uses clinical characteristics, genetic data, and medical imaging to illustrate the importance of ML and ANN in early diagnosis, prognosis, and personalised treatment. It draws data from Russian and worldwide scientific sources. Interestingly, DL enhanced tumour typing and treatment response predictions, while ML obtained 94% accuracy in bladder cancer identification. Notwithstanding encouraging findings, the review does not address issues of integration into clinical processes, ethical considerations, long-term clinical dependability, or computational efficiency. In order to increase diagnostic precision in genitourinary oncology, future research should focus on building strong, interpretable AI models employing a variety of datasets, improving real-world applicability, resolving data privacy and bias issues, and combining radiomics and neuro-fuzzy approaches [8].

The study assesses several supervised machine learning algorithms for prostate cancer detection, with a high accuracy of 96.25%: Support Vector Machine (SVM), K-Nearest Neighbours (KNN), Naive Bayes (NB), and Random Forest (RF). The results show that machine learning techniques may detect problems early and accurately, outperforming traditional diagnostic techniques. Nevertheless, neither computing efficiency, dataset biases, model interpretability, cost-effectiveness, nor integration with current clinical workflows are investigated in this study. Incorporating more clinical and radiological data, improving model generalisability and reliability across a range of populations, and exploring ensemble or hybrid approaches should all be goals of future study. Furthermore, assessing these machine learning-based systems' practicality and potential to minimise intrusive diagnostic procedures will be crucial to their clinical implementation [9].

The study looks into advanced tabular deep learning techniques, such as transfer learning and convolutional neural networks, as well as conventional, tree-based, and advanced methods for diagnosing prostate cancer. Utilising an F1-score of 0.907 and an AUC of 0.911, the suggested

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approach demonstrated its efficacy in predictive modelling. The study does not, however, address computational effectiveness, the Tab2Visual framework's shortcomings in terms of turning tabular data into graphical representations, or the models' applicability in various clinical contexts. Further restricting the approach's clinical application is the lack of discussion regarding ethical issues, data bias, and interaction with current diagnostic workflows. Future studies should concentrate on increasing interpretability, testing models across broader and more varied populations, boosting prediction accuracy, and investigating how these cutting-edge techniques might support traditional diagnostic systems in the identification of prostate cancer [10].

According to the study, the Gradient Boosting Machine (GBM) algorithm is the best at predicting the Gleason grade of prostate cancer, with an accuracy of 93%, sensitivity of 92%, specificity of 94%, and AUC-ROC of 0.95. The study shows good diagnostic performance using a modified ResNet50 model for feature extraction and fuzzy C-Means segmentation for tumour identification. It does not, however, address the drawbacks of MRI, model bias, cost-effectiveness, or interaction with existing clinical workflows. Additionally, its practical usefulness is limited by the lack of long-term patient outcome analysis. To improve the clinical uptake and dependability of AI-based prostate cancer grading systems, future studies should concentrate on multi-modal imaging integration, deeper neural architectures, real-time diagnostic tools, and validation across a range of populations [11].

This paper offers an ensemble model for prostate cancer detection that combines Support Vector Machine (SVM), AdaBoost, Decision Tree (DT), and Random Forest (RF). It outperforms earlier techniques and achieves 96% accuracy. Despite showing good classification performance, the study ignores MRI scan restrictions, algorithm parameter optimisation, and processing efficiency. Furthermore, there is no assessment of long-term clinical benefit, integration with other imaging modalities, or generalisability across varied populations. Future research should look towards adding more deep learning and machine learning methods, growing datasets for wider applicability, allowing real-time MRI processing, and working with doctors to improve models for useful diagnostic applications [12].

In this study, 200 patients and 200 healthy controls' clinical and radiological data are used to assess several machine learning models for prostate cancer diagnosis, including logistic regression, decision trees, random forests, support vector machines, and neural networks. Outperforming the other examined algorithms, the random forest model showed the best performance with 0.92 accuracy, 0.95 sensitivity, and 0.89 specificity. The study does not address computational efficiency, interpretability, integration with other data types, or long-term success in clinical practice, despite highlighting machine learning's diagnostic potential. To increase diagnostic accuracy and patient outcomes across a range of groups, future research should concentrate on integrating genetic and lifestyle data, assessing real-world application, testing cutting-edge machine learning approaches, and creating clinician-friendly tools [13].

3. Methodology:

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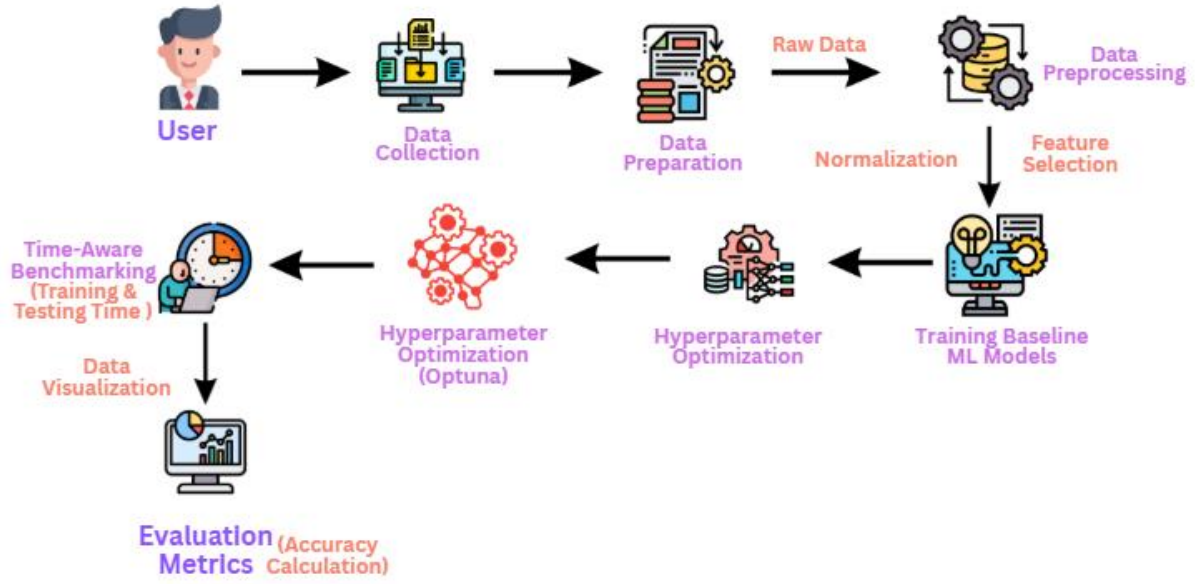

Fig 1: How model will predict

3.1 Dataset

A supervised learning dataset for prostate cancer prediction is represented by the dataset notation provided. A quick explanation is as follows:

3.1.1 Dataset definition:

$$D = \{(X_i, y_i)\}_{i=1}^{N} \tag{1}$$

According to this equation, the dataset D has Nsamples, or roughly 1200 records. Each sample has:
Feature vector X_i: a set of measurable traits that characterise each tissue or cell sample.
The corresponding class or diagnosis result for that sample is denoted by the label y_i

Feature vector:

$$X_i = [\text{radius, texture, perimeter, area, smoothness, compactness, symmetry, fractal\_dimension}] \tag{2}$$

These quantitative features help describe the size, shape, and texture of the cell nucleus. They are derived from diagnostic tests or medical imaging.

Target variable:

$$y_i \in \{\text{"benign","malignant"}\} \tag{3}$$

The output class is represented by this, where:
"benign" → non-cancerous tumor
"malignant" → cancerous tumor
Dataset D consists of pairs of input features and corresponding labels that are used to train a classification model to identify whether a tumour is benign or malignant.

3.2 Preprocessing

Feature Selection (using Mutual Information):

$$f_k = \arg\max I(X_k, y) \tag{4}$$

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This step selects the top Kmost informative features based on mutual information $I(X_k, y)$, which measures how much knowledge of a feature X_k reduces uncertainty about the goal y. To put it another way, it only keeps the traits that are most closely linked to a cancer diagnosis.

Z-score Normalization:

$$X_i' = \frac{(X_i - \mu_X)}{\sigma_X} \tag{5}$$

Each characteristic is standardised to have a zero mean (0) and unit variance (1). This ensures that all features are on a same scale, preventing large-valued features from dictating the learning process.

Train–Test Split (80:20 Stratified):

20% of the dataset is used for testing, and the remaining 80% is used for training. A stratified split preserves the same proportion of benign and malignant cases in both sets, ensuring fair model evaluation and avoiding class imbalance bias.

3.3: Baseline Models

Implemented Classifiers:

To establish a benchmark and evaluate performance, five different machine learning techniques were used as baseline models: Logistic Regression (LR), Random Forest (RF), K-Nearest Neighbours (KNN), LightGBM, and XGBoost.

Logistic Regression (LR):

$$\hat{y} = \sigma(w^T X + b), \sigma(z) = \frac{1}{1+e^{-z}} \tag{6}$$

It is a linear model that predicts whether a sample will be benign or malignant using the sigmoid activation function $\sigma(z)$. The sample is classified as either benign or malignant if $\hat{y}$>0.5.

RF, KNN, LightGBM, XGBoost:

These classifiers capture complex relationships between features and can be ensemble, tree-based, or non-linear. The formula represents the generic model.

$$\hat{y} = f(X) \tag{7}$$

where $f(X)$ represents the learnt decision function. RF employs multiple decision trees and bagging, KNN classifies data using the closest neighbours, LightGBM and XGBoost build a potent prediction model, and integrate several weak learners using gradient boosting. When used as baselines to evaluate cancer classification skills, these models perform admirably.

3.4 Hyperparameter Optimization

Purpose:
The objective of hyperparameter optimisation is to find the optimal set of model parameters (such as learning rate, depth, and number of estimators) that maximises model accuracy on the training data.

Using Optuna:

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Optuna is an autonomous optimisation system that efficiently determines the optimal hyperparameter values.
The search space includes:

$$\theta^* = \arg\max_{\theta \in \Theta} \mathcal{L}\left(f_\theta(X_{\text{train}}), y_{\text{train}}\right) \quad (8)$$

Where:

$\theta = \{\eta, d, n\}\rightarrow$ set of hyperparameters
η: learning rate
d: maximum depth
n: number of estimators
Θ: search space (all possible combinations of hyperparameters)
$f(X_{\text{train}}, \theta)$: model trained with parameters θ
$\mathcal{L}(\cdot)$: loss function (e.g., RMSE, log-loss, accuracy error)
θ^*: optimal hyperparameter set found by Optuna
The goal is to find the optimal parameters θ^* that yield the best accuracy on the training data. To sum up, this step uses Optuna to automatically modify model settings for the best classification results.

3.5 Time-aware Benchmarking

3.5.1 Purpose:
This step evaluates each model's accuracy as well as its computing efficiency, or how quickly it trains and makes predictions.

3.5.2 Training and Testing Time:

The average testing time for each sample is determined as follows to ensure fair comparisons:

$$T_{\text{test/sample}} = \frac{T_{\text{test}}}{N_{\text{test}}} \quad (9)$$

T_{train}: total amount of time spent training the model.
T_{test}: total amount of time spent testing the model.
where the number of test samples is denoted by N_{test}.

3.5.3 Speed–Accuracy Tradeoff:

Each model's accuracy and execution time are assessed to determine which provides the optimum speed-performance trade-off. Less accurate are quick methods like logistic regression. Complex models (like XGBoost or LightGBM) take longer to train and assess even though they are more accurate. In summary, this phase aids in identifying the model that functions effectively and precisely, suitable for real-world medical prediction scenarios.

3.6 Evaluation Metric

Purpose:
The model's performance is assessed using accuracy, which quantifies how frequently the model correctly predicts the class labels (benign or malignant).

Formula:

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$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Samples}} = \frac{\sum_{i=1}^{N_{\text{test}}} \mathbf{1}(\hat{y}_i = y_i)}{N_{\text{test}}} \quad (10)$$

$\hat{y}_i$: The predicted label for the i^{th}test sample
y_i: true label
$1(\hat{y}_i = y_i)$: indicator function, which equals 1 if the prediction is correct and 0 otherwise.
N_{test}: the total quantity of test samples.

Interpretation:
Accuracy quantifies how accurate the model is overall; higher accuracy means that the model correctly classifies more data. In summary, by measuring the proportion of correctly predicted cases among all test cases, this statistic offers a simple yet practical evaluation of model performance.

4. Result:

	Model	Accuracy (%)	Train Time (s)	Test Time (s)	Total Time (s)
0	KNN	98.333333	0.016021	0.022100	0.038121
1	LogisticRegression	87.222222	0.041554	0.003859	0.045412
2	LightGBM	99.375000	0.282680	0.007440	0.290120
3	XGBoost	99.166667	0.374672	0.002320	0.376992
4	RandomForest	96.250000	0.436735	0.056329	0.493065

Fig 2: Summary Table

According to this summary table, LightGBM produced the best overall performance with the highest accuracy of 99.38% and a moderate training time; XGBoost performed nearly as well with 99.17% accuracy but needed a little longer to train; KNN was the most time-efficient model with the fastest total computation time of just 0.0381 seconds and strong accuracy of 98.33%; Random Forest demonstrated good accuracy at 96.25% but had the highest overall processing time, indicating limited suitability for more complex decision boundaries.

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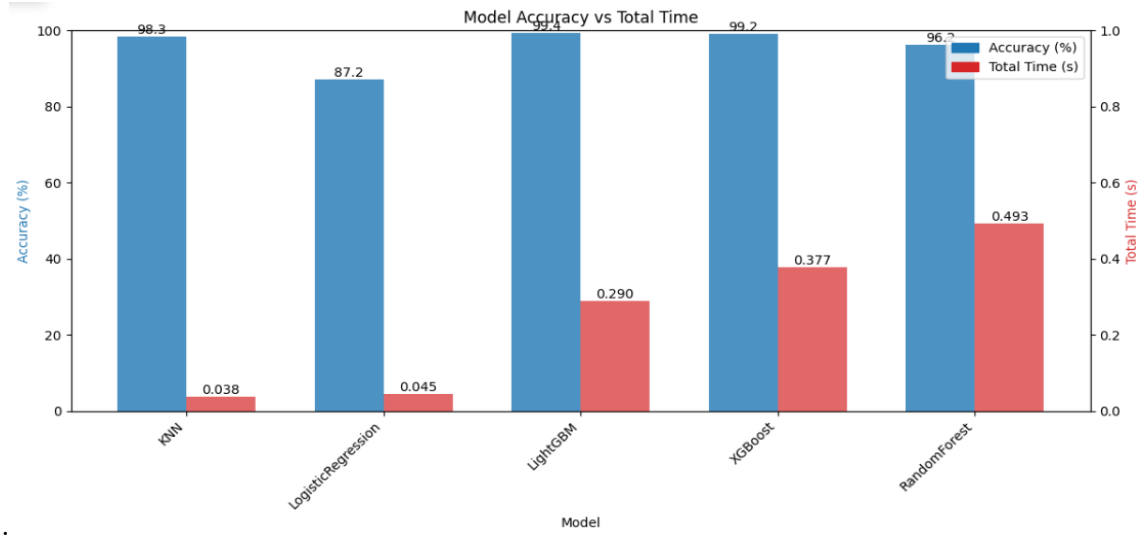

Fig 3: Accuracy & Time Comparison Plot with Labels

The accuracy (%) and total processing time (s) of various machine learning models are compared in this bar graph, where red bars indicate total processing time and blue bars indicate accuracy; While KNN is the fastest and most efficient model overall, achieving an excellent accuracy of 98.3% with the lowest total time of just 0.038 seconds, LightGBM and XGBoost stand out with the highest accuracies of about 99%; Logistic Regression operates quickly but records the lowest accuracy at 87.2%; and Random Forest, despite delivering strong accuracy at 96.2%, has the highest processing time at 0.493 seconds, reflecting its higher computational complexity.

5. **Explanation:**

```
Best Model by Less Time:
Model: KNN
Accuracy (%): 98.33333333333333
Train Time (s): 0.016021251678466797
Test Time (s): 0.022099852561950684
Total Time (s): 0.038121104240417 48
```

Fig 4: Best Model Predict

The K-Nearest Neighbours (KNN) algorithm exceeded all other models in terms of accuracy and computational cost. It achieved 98.33% accuracy, correctly classifying almost all test samples; its incredibly quick training time of 0.016 seconds reflects KNN's simplicity because it primarily stores the training data; its testing time of 0.022 seconds—slightly slower

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because it compares each test point with stored samples—still results in a total runtime of just 0.038 seconds, demonstrating KNN's remarkable efficiency.

6. **Conclusion**

The technique showed that KNN offered the best compromise between speed and accuracy (~98.3% accuracy in just 0.038 s total time), whereas tree-based ensembles (LightGBM and XGBoost) obtained the highest accuracy (~99%) but with longer training times. KNN or Logistic Regression is advised for deployments needing real-time performance, whereas LightGBM/XGBoost is better for diagnostic accuracy.

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