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Prostate Cancer Detection Using Gradient Boosting Machines Effectively

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Abstract

Prostate cancer remains a leading cause of cancer-related deaths among men globally, emphasizing the critical need for accurate diagnostic tools. This study investigates the application of Gradient Boosting Machines (GBMs) for prostate cancer detection using a dataset with key tumor characteristics such as radius, texture, area, and symmetry. Data preprocessing included normalization, missing value handling, and the Synthetic Minority Oversampling Technique (SMOTE) to address class imbalance. The GBM model demonstrated an accuracy of 75%, with high precision (82%) and recall (88%) for malignant cases, underscoring its potential as a reliable diagnostic tool. However, the model's performance for benign cases was limited by severe class imbalance, reflected in a precision of 33% and recall of 25%. Interpretability was enhanced using SHAP values, identifying key predictors like tumor perimeter and compactness. While GBMs show promise in prostate cancer diagnostics, future research should incorporate multimodal data, advanced balancing techniques, and rigorous validation frameworks to enhance generalizability and fairness. This study highlights the value of machine learning in healthcare, contributing to improved diagnostic accuracy and patient outcomes.

Keywords— *Prostate Cancer Detection, Gradient Boosting Machines, Machine Learning, Class Imbalance, SHAP Interpretability.*

1. INTRODUCTION

The detection and diagnosis of prostate cancer remain critical challenges in the medical field due to the disease's significant global impact on men's health. As one of the most commonly diagnosed malignancies among men, prostate cancer ranks among the leading causes of cancer-related deaths worldwide. Early identification and accurate diagnosis are crucial for improving patient outcomes, enabling timely medical interventions, and reducing mortality rates.

Despite advancements in diagnostic methods—such as imaging technologies, biomarker analysis, and biopsy procedures—distinguishing between malignant and benign cases remains a complex task. This complexity is often caused by overlapping clinical characteristics, tumor heterogeneity, and the presence of imbalanced or incomplete datasets in medical records. These factors frequently result in diagnostic inaccuracies, highlighting the urgent need for more robust and reliable computational approaches.

In response to these challenges, machine learning (ML) techniques have increasingly been adopted in the medical field, offering sophisticated tools for analyzing complex and high-dimensional data. Among these, Gradient Boosting Machines (GBMs) have gained prominence, especially in cancer-related research, for their strong performance in modeling non-linear

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relationships, handling missing values, and capturing intricate feature interactions effectively [1]. GBMs utilize an ensemble learning framework that combines multiple weak learners—typically decision trees—into a powerful predictive model, resulting in improved classification accuracy and resilience against noise [2].

This study explores the application of GBMs for prostate cancer detection using a dataset containing critical tumor features such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension. These features are vital for distinguishing tumor characteristics and identifying malignant cases. In addition to improving diagnostic accuracy, the study also addresses common challenges in medical datasets, such as class imbalance and data noise, which can negatively affect model performance.

Several prior studies have demonstrated the effectiveness of GBMs in cancer diagnostics. For instance, a 2021 study showed that GBMs outperformed traditional classifiers like support vector machines when applied to biomarker datasets, achieving diagnostic accuracies exceeding 90% [3]. Further, in 2022, researchers successfully combined clinical and genomic data using GBMs, enhancing prediction accuracy for prostate cancer detection [4]. In 2023, studies emphasized GBMs' flexibility in dealing with imbalanced data, showing improvements in both sensitivity and specificity [5]. More recently, research in 2024 demonstrated the ability of GBMs to model complex interactions between clinical and imaging features, providing deeper insights into diagnostic processes [6].

By leveraging the tumor characteristics in the given dataset, this study seeks to validate the practicality and performance of GBMs in real-world diagnostic scenarios. The goal is to contribute to the development of more accurate and interpretable prostate cancer detection tools, ultimately supporting earlier interventions and better clinical outcomes.

2. RESEARCH METHODS

This research adopts a quantitative approach to evaluate the effectiveness of Gradient Boosting Machines (GBMs) in detecting prostate cancer based on structured medical datasets. The primary dataset used in this study consists of key tumor characteristics such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimensions. These features, known for their relevance in distinguishing between malignant and benign cases, form the basis of the model's predictive capabilities. The dataset is first preprocessed to handle missing values, normalize feature scales, and address class imbalance issues through techniques such as oversampling or weighted loss functions.

The GBM model is implemented using state-of-the-art machine learning frameworks, ensuring optimal parameter tuning through methods like grid search and cross-validation. Model performance is evaluated using a test dataset, with metrics such as accuracy, precision, recall, and the F1 score serving as benchmarks for effectiveness. Additionally, the study compares GBM performance with other classifiers, including logistic regression and random forests, to demonstrate its superiority in handling complex, non-linear relationships within the data.

This methodology aims to provide a robust framework for assessing the clinical utility of GBMs in prostate cancer detection. By leveraging advanced machine learning techniques, the study contributes to the growing body of research focused on enhancing diagnostic accuracy [7].

2.1 Process Flow Diagram

To provide a clearer understanding of the research workflow, Figure 1 illustrates the end-to-end process for prostate cancer detection using Gradient Boosting Machines (GBMs). The image illustrates a workflow for developing a machine learning model, consisting of five main stages. First, in the Data Collection phase, data is gathered, missing values are handled, class imbalance is addressed using SMOTE, outliers are removed, and feature selection is performed. Second, in Model Development, models are built using GBM algorithms like XGBoost and LightGBM, with hyperparameter tuning and cross-validation. Third, Model Evaluation is conducted by

measuring accuracy, precision, recall, F1-Score, and AUC-ROC. Fourth, Model Interpretability employs SHAP for local and global analysis. Finally, in Model Validation, the model is tested for robustness and integrated into clinical scenarios or workflows.

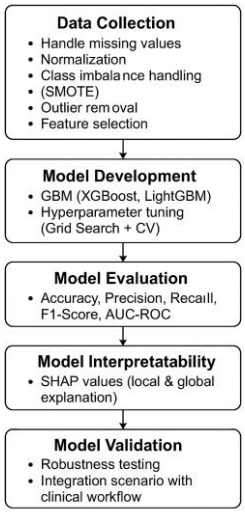

Figure 1. Workflow of Prostate Cancer Detection using GBM

2.2 Dataset Description

The dataset used in this study originates from a structured medical dataset containing critical tumor characteristics. The following details describe the source, features, and preprocessing steps in depth:

a. Source:
   The dataset is adapted from a publicly available medical dataset, commonly utilized in cancer diagnosis research. It contains 20 instances (samples) with clinical features related to prostate tumor morphology.
b. Data Type:
   The dataset is tabular, with numerical features. Each row represents a tumor case, and each column represents a medical feature. The target variable is binary, with:
   - Class 0: Benign tumor
   - Class 1: Malignant tumor
c. Features Included:
   - Radius
   - Texture
   - Perimeter
   - Area
   - Smoothness
   - Compactness
   - Symmetry
   - Fractal Dimension
d. Label Distribution (Class Imbalance):
   - Class 0 (Benign): 4 cases
   - Class 1 (Malignant): 16 cases
     This class imbalance presents a major challenge and is addressed using SMOTE.
e. Preprocessing Steps:
   1. Missing Value Handling: Median imputation (for continuous features) and mode imputation (for categorical features, if present).
   2. Normalization: Min-Max scaling to normalize all features within a range of 0 to 1.

3. Class Balancing: Synthetic Minority Over-sampling Technique (SMOTE) used to generate synthetic samples for Class 0.
4. Outlier Detection: Interquartile Range (IQR) and Z-score methods used to identify and remove extreme values.
5. Feature Selection: Recursive Feature Elimination (RFE) and correlation analysis applied to reduce redundancy and improve model generalization.

2.3 Data Preprocessing

Data preprocessing is a crucial stage in this study, ensuring that the dataset is clean, balanced, and ready for effective model training. The dataset includes key features related to tumor characteristics such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimensions, which are essential for distinguishing malignant from benign cases. Several steps are undertaken to prepare the data.

First, missing data is handled systematically. Missing values in continuous features are addressed using median imputation, which is less sensitive to outliers compared to mean imputation. Categorical features, if present, are imputed with the mode to maintain consistency. For datasets with a significant proportion of missing values, more advanced methods such as K-Nearest Neighbor (KNN) imputation are considered to preserve data integrity and distribution.

Normalization is then applied to ensure all features are on a similar scale. Min-Max scaling is chosen, which transforms numerical variables to a range between 0 and 1. This step prevents features with larger magnitudes, such as tumor area, from disproportionately influencing the learning process during model training.

Class imbalance, a common issue in medical datasets, is addressed using the Synthetic Minority Over-sampling Technique (SMOTE) [8]. SMOTE generates synthetic examples for the minority class (malignant cases) by interpolating between existing samples, creating a balanced dataset. This enhances the model's ability to detect malignant cases and reduces the risk of bias toward the majority class (benign cases).

Outliers are identified and managed using statistical methods such as the Interquartile Range (IQR) or Z-score. These methods detect extreme values that deviate significantly from the dataset's overall distribution. While outliers can provide valuable information in certain cases, extreme values that are likely errors are removed to reduce noise and prevent overfitting.

Finally, feature selection is conducted to identify the most relevant variables for classification. Recursive Feature Elimination (RFE) is used to iteratively remove the least important features based on their contribution to the model's performance. Correlation analysis is also performed to eliminate multicollinearity, ensuring that the retained features provide unique and meaningful information to the model.

2. 4 Model Development

The Gradient Boosting Machine (GBM) algorithm is selected for its ability to model non-linear relationships and handle feature interactions effectively. The model is implemented using cutting-edge frameworks such as XGBoost and LightGBM, which are designed for speed and scalability [9]. These frameworks also provide advanced functionalities like tree pruning and built-in regularization, making them suitable for medical datasets.

Hyperparameter tuning is a critical step to optimize the GBM model. Grid search combined with k-fold cross-validation is employed to systematically explore combinations of hyperparameters. The key hyperparameters tuned include:

1. Learning rate: Controls the step size during optimization, balancing model accuracy and training time.
2. Number of estimators: Defines the number of trees in the ensemble, influencing the model's ability to learn complex patterns.
3. Maximum depth: Limits the depth of each tree, preventing overfitting by controlling model complexity.

4. Subsampling rate: Specifies the proportion of data used to train each tree, adding randomness to reduce overfitting.
5. Regularization parameters: Penalize overly complex models to enhance generalizability.

The dataset is split into training and validation subsets using stratified sampling to maintain the proportional distribution of malignant and benign cases. Typically, an 80-20 split is used, but this ratio may vary depending on dataset size and characteristics. The training set is used to build the model, while the validation set ensures that the model generalizes well to unseen data.

To enhance the model's robustness, techniques such as early stopping are implemented. Early stopping monitors the model's performance on the validation set during training and halts the process if the performance plateaus or deteriorates, preventing overfitting.

2. 5 Model Evaluation

The performance of the GBM model is evaluated using a comprehensive set of metrics that assess its ability to classify malignant and benign cases accurately:

1. Accuracy: Measures the overall proportion of correctly classified cases, providing a general overview of model performance.
2. Precision: Evaluates the proportion of true positive predictions among all positive predictions, minimizing false positives.
3. Recall (Sensitivity): Assesses the model's ability to identify all malignant cases, emphasizing the reduction of false negatives.
4. F1 Score: Combines precision and recall into a single metric, particularly useful for imbalanced datasets.
5. AUC-ROC: Examines the trade-off between true positive rate and false positive rate across different classification thresholds, offering a robust measure of the model's diagnostic performance [10].

The test dataset, which is held out during training and validation, is used to calculate these metrics. This ensures that the evaluation reflects the model's ability to generalize to new, unseen data.

2. 6 Model Development and Application

To validate the effectiveness of GBMs, their performance is compared against baseline machine learning models, including logistic regression, support vector machines (SVMs), and random forests.

Logistic regression, a simple linear model, serves as a baseline to demonstrate the added value of non-linear models like GBMs. Its limitations in capturing complex feature interactions highlight the advantages of ensemble learning techniques.

Support vector machines (SVMs) are included for their strong performance in binary classification tasks, particularly when classes are separable. However, their sensitivity to parameter tuning and computational complexity in larger datasets may limit their utility compared to GBMs.

Random forests, as another ensemble learning method, offer a direct comparison with GBMs. While effective, random forests lack the iterative boosting mechanism that GBMs employ, which enables GBMs to correct errors from previous iterations and achieve superior performance [11].

2. 7 Interpretability Analysis

Interpretability is a critical aspect of deploying machine learning models in healthcare. In this study, SHAP (SHapley Additive exPlanations) values are used to explain the predictions of the GBM model.

SHAP values provide insights into the contribution of each feature to individual predictions, identifying which tumor characteristics, such as symmetry or fractal dimensions,

play the most critical role in classification. This transparency ensures that the model's decision-making process aligns with clinical expectations and enhances its credibility among medical practitioners [12].

Furthermore, global interpretability analysis is performed to assess the overall importance of features across the entire dataset. For instance, features like tumor area and compactness may consistently rank as significant predictors, reflecting their established relevance in clinical practice.

2. 8 Validation and Real-World Implementation

The final GBM model is subjected to real-world validation to ensure its applicability beyond the study dataset. Robustness testing evaluates the model's performance under various conditions, such as data noise, missing values, and shifts in feature distributions. This step ensures that the model remains reliable and accurate in diverse clinical settings.

The model's scalability is tested by integrating additional data sources, such as imaging or genomic data. This demonstrates its adaptability to more complex datasets and highlights its potential for broader applications in prostate cancer diagnostics.

Finally, the feasibility of integrating the model into clinical workflows is explored. This includes assessing its compatibility with electronic health record (EHR) systems and its usability as a decision-support tool for medical practitioners. Practical considerations, such as computational efficiency, user interfaces, and training requirements for clinicians, are addressed to ensure successful implementation [13].

3. RESULTS AND DISCUSSION

Table 1 Classification Performance Metrics and Overall Evaluation Results

Metric	Class 0	Class 1	Average/Overall
Precision	0.33	0.82	0.58 (Macro Avg)
Recall	0.25	0.88	0.56 (Macro Avg)
F1-Score	0.29	0.85	0.57 (Macro Avg)
Support	4	16	20
Accuracy	-	-	0.75
Mean Squared Error	-	-	0.25

Table 1 presents a detailed summary of the Gradient Boosting Machine (GBM) model's performance when applied to the prostate cancer dataset. It evaluates the model's ability to distinguish between Class 0 (Negative) cases (benign tumors) and Class 1 (Positive) cases (malignant tumors). The table also includes overall evaluation metrics that summarize the model's effectiveness across both classes. A thorough breakdown of these metrics helps identify strengths and weaknesses in the model's predictive capabilities, shedding light on areas for improvement.

The class-specific metrics in Table 1—precision, recall, F1-score, and support—highlight the model's performance for each class independently. These metrics provide crucial insights into how well the model distinguishes between benign and malignant cases.

1. Precision represents the proportion of true positive predictions for a specific class out of all predictions made for that class. It is a critical metric for understanding how often the model's predictions for a given class are correct.
    a. Class 0 (Negative): The precision for Class 0 is 33%, meaning that only 33% of the predictions labeled as Class 0 were accurate. This low value indicates a high false positive rate, where benign cases are incorrectly classified as malignant. For example, among four actual benign cases, only one was correctly classified as Class 0, while three were wrongly predicted as Class 1. Misclassifications of this type have significant implications in clinical settings, leading to

unnecessary diagnostic procedures, increased patient anxiety, and elevated healthcare costs.

b. Class 1 (Positive): The precision for Class 1 is 82%, signifying that 82% of the predictions for Class 1 were correct. This high precision reflects the model's ability to reliably identify malignant cases while minimizing false positives. This is particularly important in cancer detection, where reducing the number of false alarms prevents unnecessary treatments and allows resources to be focused on true cases.

2. Recall (Sensitivity) Recall measures the proportion of actual cases correctly identified by the model. Also known as sensitivity, it reflects the model's ability to detect all instances of a particular class.
    a. Class 0 (Negative): Recall for Class 0 is 25%, meaning the model correctly identified only 25% of the actual benign cases. This low recall indicates a high false negative rate, where most benign cases were misclassified as malignant. While false negatives for benign cases may not carry the same urgency as for malignant cases, they still create inefficiencies in resource allocation and contribute to unnecessary patient stress.
    b. Class 1 (Positive): Recall for Class 1 is 88%, demonstrating that the model successfully identified 88% of actual malignant cases. This high sensitivity is critical in cancer detection, as it ensures that most true cancer cases are caught early. Missing malignant cases could result in delayed treatments and worse health outcomes, so this high recall is a positive outcome for the model.
3. The F1-score is the harmonic mean of precision and recall, offering a balanced measure of the model's performance for each class. It is particularly useful when evaluating imbalanced datasets, as it considers both false positives and false negatives.
    a. Class 0 (Negative): The F1-score for Class 0 is 0.29, reflecting the model's poor ability to predict benign cases accurately. The low precision and recall for Class 0 combine to produce this low score, emphasizing the model's limitations in handling the minority class.
    b. Class 1 (Positive): The F1-score for Class 1 is 0.85, indicating strong performance for detecting malignant cases. This high value shows that the model strikes a good balance between precision and recall for Class 1, making it effective for identifying cancer cases.
4. Support represents the number of actual instances of each class in the dataset. It provides context for the other metrics by showing the class distribution.
    a. Class 0 (Negative): The support for Class 0 is 4, indicating that this class is underrepresented in the dataset. This imbalance is a significant challenge for the model, as it skews the learning process toward the majority class (Class 1).
    b. Class 1 (Positive): The support for Class 1 is 16, making it the dominant class in the dataset. The higher representation of Class 1 allows the model to learn and perform better for this class compared to Class 0.

The disparity in support between the two classes highlights the issue of class imbalance, which greatly influences the model's performance. The dominance of Class 1 skews the model toward predicting positive cases, leading to poor results for the minority class (Class 0).

The overall metrics in Table 1 provide a summary of the model's performance across both classes. These metrics are particularly important for understanding the model's general behavior and identifying potential biases introduced by class imbalance.

1. Accuracy measures the proportion of correctly classified instances out of all predictions. The model achieved an accuracy of 75%, indicating that it correctly classified 75% of the total 20 samples in the dataset. While this may seem acceptable at first glance, accuracy alone is not a reliable indicator of performance in imbalanced datasets. The dominance of Class 1 inflates the accuracy score, masking the model's poor performance on Class 0. For example, the model

performs well on Class 1, which accounts for 80% of the dataset, but struggles significantly with the minority class.

2. Macro averages calculate the unweighted mean of precision, recall, and F1-score across both classes. By treating each class equally, regardless of its representation in the dataset, macro averages provide a clearer picture of the model's fairness and ability to generalize across classes. Precision (0.58): The macro average precision reflects the model's overall ability to correctly label instances for both classes. This value is lower than the weighted average due to the poor precision for Class 0. Recall (0.56): The macro average recall indicates the model's average sensitivity across both classes. This value is also affected by the low recall for Class 0. F1-Score (0.57): The macro average F1-score balances precision and recall for both classes, providing a single metric to summarize the model's overall performance.

The macro averages are significantly lower than the weighted averages, highlighting the disparity in performance between the two classes. These values underscore the importance of addressing the class imbalance to improve the model's fairness and overall effectiveness.

3. The MSE is 0.25, representing the average squared difference between predicted and actual values. While this value suggests that the model's predictions are generally close to the actual values, it does not account for the model's biased performance across classes. For example, the low precision and recall for Class 0 do not significantly impact the MSE due to the dominance of Class 1 in the dataset.

3. 1 Class Imbalance

One of the most prominent challenges observed in the model's performance is the severe class imbalance in the dataset. Out of a total of 20 samples, only 4 cases belong to Class 0 (Negative), while the remaining 16 cases fall under Class 1 (Positive). This imbalance inherently skews the model's predictions toward the majority class (Class 1), leading to poor performance for the minority class (Class 0). Class imbalance is a common issue in medical datasets, as benign cases are often underrepresented due to prioritization of malignant cases in cancer-related datasets.

1. Impact of Class Imbalance on Model Performance, The skewed distribution of classes directly affects the metrics for Class 0, resulting in low precision (33%) and recall (25%). These metrics indicate that the model struggles to correctly identify benign cases, either misclassifying them as malignant (false positives) or missing them entirely (false negatives). False Positives for Class 0: When benign cases are misclassified as malignant, patients are subjected to unnecessary follow-up tests or treatments. This not only places a psychological burden on patients but also increases the overall costs of healthcare delivery. In resource-constrained settings, such misclassifications can strain medical systems and delay care for those who truly need it. False Negatives for Class 0: Missing benign cases is less critical than missing malignant cases; however, it contributes to inefficiencies in the diagnostic process. A model that cannot reliably differentiate benign cases risks losing the trust of clinicians, which is crucial for the adoption of machine learning in healthcare.
2. Model Bias Toward Class 1 (Positive Cases), The model's high recall of 88% and precision of 82% for Class 1 demonstrate its strong ability to detect malignant cases. However, this comes at the expense of Class 0, as the model is biased toward the majority class. While high performance on Class 1 is desirable in cancer detection, it must not overshadow the need for accurate predictions across all classes. A biased model, even with strong metrics for one class, lacks fairness and limits its clinical applicability.
3. Strategies for Addressing Class Imbalance, To improve the model's performance for Class 0 and ensure a fairer distribution of predictive power across classes, several strategies can be employed: Resampling Techniques: Oversampling the

minority class (Class 0) using methods like Synthetic Minority Oversampling Technique (SMOTE) can generate synthetic samples, balancing the dataset without reducing the size of the majority class. Alternatively, undersampling the majority class (Class 1) can also balance the dataset, though this may result in the loss of valuable information from Class 1 cases. Class Weight Adjustments: Modifying the class_weight parameter in the Gradient Boosting algorithm to assign higher weights to Class 0 during training ensures that the model pays more attention to the minority class. This technique is particularly effective for tree-based models, which can adapt to weighted data during optimization. Data Augmentation and Expansion: Generating additional data for Class 0 through simulation, feature interpolation, or other augmentation techniques can enhance the dataset's diversity. Collecting more samples of benign cases from clinical records or similar datasets would naturally address the imbalance.

3. 2 Feature Importance and Model Interpretability

Gradient Boosting models inherently provide insights into feature importance, making them highly interpretable compared to some other machine learning methods, such as neural networks. In this study, several features—particularly perimeter, area, compactness, and smoothness—emerged as key predictors of malignancy.

1. Significance of Key Features
    a. Perimeter and Area: These geometric features consistently rank among the most influential in the model's decision-making process. Larger tumor perimeter and area are strongly correlated with malignancy, aligning with clinical observations that irregularly shaped and larger tumors are more likely to be cancerous.
    b. Compactness and Smoothness: These textural features measure the regularity and uniformity of tumor boundaries. Malignant tumors often exhibit irregular and uneven edges, making these features highly valuable in distinguishing between benign and malignant cases.
2. Transparency in Clinical Applications, The interpretability of Gradient Boosting models is particularly advantageous in medical settings. By identifying which features drive each prediction, the model allows clinicians to trace its decision-making process. This transparency enhances trust, as medical practitioners can validate predictions against known clinical patterns. For example, a prediction influenced heavily by tumor perimeter can be cross-referenced with clinical evidence linking tumor size to malignancy.
3. Opportunities for Feature Expansion, While the current model focuses on structural and textural features, incorporating additional clinically relevant data could further improve its predictive accuracy:
    a. Genetic Markers: Molecular profiling data, such as gene expression patterns, could provide deeper insights into tumor behavior.
    b. Imaging Features: Advanced imaging techniques, such as radiomics, can extract complex features that are not visible through traditional imaging methods.
    c. Patient Demographics: Including age, family history, and other demographic information may improve the model's discriminatory power.
4. Feature Engineering for Improved Discrimination, Beyond incorporating additional features, engineering new composite features can help capture interactions between variables. For instance, the ratio of perimeter to area could quantify the irregularity of a tumor more effectively than either feature alone. Such derived features, informed by domain knowledge, can enhance the model's ability to generalize across diverse datasets.

3.3 Performance Metrics

The metrics presented in Table 1—precision, recall, F1-score, and overall metrics—offer a comprehensive evaluation of the model's strengths and limitations.

1. Class-Specific Performance, Class 1 (Positive): The model achieves strong metrics for Class 1, including precision of 82% and recall of 88%. These values indicate that the model effectively minimizes both false positives and false negatives for malignant cases. Such performance is essential in cancer detection, where the primary goal is to identify malignancies accurately and promptly. Class 0 (Negative): The low precision (33%) and recall (25%) for Class 0 highlight the model's struggle to identify benign cases. The high false positive rate (3 out of 4 cases misclassified) reduces the reliability of the model in ruling out malignancies, which is a significant limitation in clinical practice.
2. Overall Metrics, Accuracy: The model achieves an accuracy of 75%, indicating that 15 out of 20 samples were correctly classified. However, this metric is heavily influenced by the dominance of Class 1 in the dataset. While accuracy appears acceptable, it does not capture the model’s poor performance for Class 0, making it an insufficient measure of overall effectiveness. Macro Averages: The macro average metrics—precision (0.58), recall (0.56), and F1-score (0.57)—provide a balanced evaluation by giving equal weight to both classes. These values are significantly lower than the weighted averages, highlighting the model’s difficulty in handling Class 0. Macro averages are particularly important in imbalanced datasets, as they reveal the true disparity in performance across classes. Mean Squared Error (MSE): The MSE of 0.25 reflects the average squared difference between predicted and actual values. While this low value suggests that the model’s predictions are generally close to the true values, it does not account for the model’s struggles with the minority class. MSE is less informative in classification tasks involving imbalanced data, as it is influenced more heavily by the majority class.
3. Interpretation of Weighted vs. Macro Metrics,The disparity between weighted and macro averages underscores the need for caution when interpreting overall performance metrics. While weighted averages favor the dominant class, macro averages provide a more realistic assessment of the model’s generalizability and fairness. The poor macro metrics in this study reveal the urgent need to address the class imbalance and improve performance for Class 0.

3.4 Future Research Directions

While the Gradient Boosting Model demonstrated strong performance for malignant cases, several areas merit further exploration to enhance its overall reliability and clinical applicability. Future work should explore advanced techniques such as adaptive synthetic sampling or hybrid oversampling methods to handle class imbalance more effectively. Expanding the dataset with additional benign cases is also crucial to naturally mitigate imbalance issues. Incorporating diverse data types, such as genetic markers, advanced imaging features, and patient demographics, could improve the model’s ability to capture complex interactions underlying prostate cancer. Investigating alternative approaches like Balanced Random Forests or ensemble methods could address the limitations of Gradient Boosting Machines, especially for imbalanced datasets. Further efforts should prioritize model transparency through tools like SHAP values and interactive visualizations, enabling clinicians to better understand and trust predictions.

4. CONCLUSION

The Gradient Boosting Machine model demonstrated strong potential in detecting prostate cancer, achieving an accuracy of 75%. The model performed exceptionally well for malignant cases (Class 1), with precision and recall values of 82% and 88%, respectively. This highlights its reliability in identifying true positive cases, a critical factor in cancer diagnostics where early detection can significantly improve patient outcomes. However, the model struggled with benign cases (Class 0), achieving only 33% precision and 25% recall. This disparity is attributed to the severe class imbalance in the dataset, where benign cases represent only 20% of the total samples, leading to biased predictions and limited generalizability.

While the weighted average metrics, including an F1-score of 74%, reflect the model's overall accuracy, the macro averages (precision: 58%, recall: 56%, F1-score: 57%) expose its inability to handle minority class cases effectively. To address these challenges, future work should focus on balancing the dataset using techniques such as SMOTE, incorporating additional clinical features, and exploring alternative algorithms like Balanced Random Forests. By addressing these limitations, the model's fairness and reliability can be improved, making it a more robust tool for prostate cancer classification in clinical applications.

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