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Research article

Improving Prostate Cancer Classification with Random Forest Techniques

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ARTICLE INFO

Article history:
Received 1 November 2024
Revised 10 November 2024
Accepted 30 December 2024
Available online 31 December 2024

Keywords:
Prostate cancer, Random Forest, Classification, Machine Learning, Feature Selection

Please cite this article in IEEE style as:
I Gede Agus Krisna Warmayana, " Improving Prostate Cancer Classification with Random Forest Techniques," *JSIKTI: Jurnal Sistem Informasi dan Komputer Terapan Indonesia*, vol. 7, no. 2, pp. 53-63, 2024.

ABSTRACT

Prostate cancer is a leading cause of cancer-related mortality among men worldwide, necessitating accurate and efficient classification methods for improved diagnosis and treatment planning. This research explores the application of Random Forest algorithms to classify prostate cancer cases using a dataset comprising 100 samples with features such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension. The study emphasizes the integration of preprocessing, feature selection, model training, and evaluation to enhance classification performance. The model achieved a classification accuracy of 75%, with a high recall of 88% for malignant cases, demonstrating its potential in identifying high-risk patients. However, the model exhibited challenges in predicting benign cases due to class imbalance, as reflected in the low precision (33%) for this minority class. Addressing these limitations, techniques such as data balancing, advanced hyperparameter tuning, and enhanced feature engineering are suggested. This study provides valuable insights into key predictors of prostate cancer and highlights the potential of Random Forest techniques as a robust tool for clinical decision-making. Future work should focus on integrating additional clinical and genomic data to further improve classification accuracy and interpretability.

1. Introduction

Prostate cancer remains one of the leading causes of cancer-related morbidity and mortality among men worldwide, accounting for a significant proportion of cancer diagnoses annually. The disease's heterogeneity and variable progression rates make its accurate classification a crucial step in determining appropriate treatment strategies and improving patient outcomes. Despite advancements in diagnostic imaging and molecular profiling, traditional classification methods often struggle to handle the complexity and high dimensionality of prostate cancer datasets. Consequently, there is a growing need for robust computational approaches that can enhance classification accuracy and uncover meaningful patterns within the data. Machine learning techniques, particularly Random Forest algorithms, have emerged as promising tools for addressing these challenges. Random Forests, an ensemble learning method based on decision trees, excel at handling datasets with numerous features and complex interdependencies. Their ability to reduce overfitting, provide interpretable feature importance rankings, and achieve high predictive accuracy has made them increasingly popular in biomedical research. Recent studies, such as those by [1-3], have demonstrated the efficacy of Random Forests in improving cancer classification and identifying critical biomarkers.

This study leverages a dataset comprising 100 prostate cancer samples, characterized by attributes such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension. The target variable, "diagnosis_result," classifies samples as malignant or benign. By applying advanced Random Forest techniques to this dataset, the research aims to achieve higher

ISSN 2460-7258 (online) | ISSN 1978-1520 (print)
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classification accuracy compared to traditional methods, identify the most significant features contributing to prostate cancer classification, and provide actionable insights into the biological relevance of these features. Several recent investigations have explored the utility of machine learning in prostate cancer research. For instance, [4] demonstrated the potential of Random Forests in handling imbalanced datasets, while [5] highlighted the algorithm's ability to integrate clinical and molecular data for enhanced predictions. Furthermore, [6] and [7] explored feature importance rankings derived from Random Forest models, offering insights into critical predictors of prostate cancer. These studies, alongside others such as [8], [9], and [10], underscore the transformative potential of Random Forest techniques in cancer research.

Through the integration of state-of-the-art machine learning methodologies and domain-specific expertise, this study seeks to bridge the gap between computational advancements and clinical practice. By focusing on a dataset-specific approach, it aims to provide a detailed analysis of prostate cancer classification, contributing to both the academic literature and the practical understanding of this disease.

2. Materials and Methods

This study employs a machine learning framework to improve prostate cancer classification, with a primary focus on leveraging the Random Forest algorithm due to its robustness and versatility in handling complex datasets. The methodology is structured to incorporate preprocessing, feature selection, model training, and evaluation, ensuring a comprehensive approach to developing a reliable and interpretable classification model. This research builds on prior work highlighting the efficacy of Random Forests in medical applications, aiming to address specific challenges in prostate cancer diagnosis by employing advanced computational techniques.

1. Dataset Descriptio : The dataset used in this study comprises 100 samples, each characterized by clinically relevant attributes such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension. These features, derived from biomedical imaging and diagnostic data, have been widely recognized as critical indicators of malignancy in prostate cancer [1][2]. The target variable, "diagnosis_result," provides a binary classification framework, distinguishing between malignant (M) and benign (B) cases. The small dataset size presents an opportunity to evaluate the Random Forest algorithm's performance in scenarios with limited data, a common challenge in medical research.
2. Preprocessing Steps : Effective preprocessing is crucial for ensuring the quality and reliability of the dataset. All numerical features are normalized to bring them onto a similar scale, preventing dominant attributes from disproportionately influencing the model. Missing values, if present, are handled using mean or median imputation to maintain the dataset's integrity. Additionally, outliers are identified and addressed through statistical methods or robust scaling techniques to minimize their impact on the model's learning process [4].
3. Feature Selection : Feature selection plays a vital role in identifying the most informative predictors of prostate cancer while reducing model complexity and improving interpretability. Techniques such as Recursive Feature Elimination (RFE) and Gini importance scores derived from the Random Forest algorithm are employed. These approaches prioritize features that significantly contribute to classification performance, ensuring the model focuses on biologically and diagnostically relevant data [6] [7].
4. Model Training and Optimization : The Random Forest algorithm is selected for its ensemble-based approach, which combines the predictions of multiple decision trees to deliver robust and accurate classifications. The dataset is divided into training and testing subsets using an 80-20 split to evaluate model performance effectively. Hyperparameter tuning is conducted using grid search to optimize key parameters, including the number of trees, maximum tree depth, and minimum samples per split. This ensures the model is fine-tuned for the specific dataset characteristics [5] [8].

 http://doi.org/10.26594/register.v8i2.XXX

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5. Model Evaluation : A variety of evaluation metrics are employed to comprehensively assess the model's performance. These metrics include accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic (ROC) curve. Cross-validation is also implemented to evaluate the model's generalizability and robustness. This step is critical in ensuring the algorithm performs consistently across different subsets of the dataset [3] [9].
6. Interpretability and Clinical Relevance : Beyond achieving high classification accuracy, the study emphasizes model interpretability. Feature importance rankings generated by the Random Forest algorithm are analyzed to uncover the most significant predictors of prostate malignancy. These findings are compared with existing medical literature to validate their clinical relevance and provide actionable insights for healthcare professionals. The interpretability of machine learning models is a key factor in bridging the gap between computational advancements and practical applications in clinical settings [6] [10].

2.1. Data Preprocessing

The first step in the methodology is data preprocessing to ensure the dataset is clean, consistent, and optimally structured for analysis. This process involves multiple stages designed to enhance the quality of the data and minimize potential biases, thereby improving the reliability of the subsequent machine learning model.

1. Normalization of Numerical Attributes : To prevent disproportionate influences of attributes with larger scales on the model, all numerical features, such as radius, texture, perimeter, area, smoothness, compactness, symmetry, and fractal dimension, are normalized to a standard scale. This step ensures that each feature contributes equally to the model's learning process. Min-max scaling, which maps all values to a [0, 1] range, and z-score normalization, which centers values around the mean with a unit standard deviation, are considered depending on the specific requirements of the model [5].
2. Handling Missing Values : Missing values in the dataset, if present, can compromise the integrity and reliability of the analysis. To address this, imputation techniques are employed. Depending on the nature and distribution of the data, missing values are replaced with the mean, median, or mode for numerical attributes or the most frequent category for categorical data. Advanced techniques, such as k-Nearest Neighbors (k-NN) imputation or multiple imputation, are also considered to preserve the dataset's variance and structure [3] [4].
3. Outlier Detection and Removal : Outliers are extreme values that can distort the model's understanding of the data, leading to reduced accuracy and performance. Statistical methods, such as the interquartile range (IQR) rule and Z-score analysis, are applied to identify and remove outliers. For more complex datasets, machine learning-based outlier detection techniques, such as Isolation Forests or Local Outlier Factor (LOF), are utilized to identify anomalies in the data. This ensures the dataset is representative of the underlying population and minimizes noise that could negatively impact model training [6].
4. Data Balancing : Prostate cancer datasets often exhibit imbalances between classes, such as a higher prevalence of benign (B) cases compared to malignant (M). Class imbalances can lead to biased models favoring the majority class. To address this, techniques such as oversampling (e.g., SMOTE – Synthetic Minority Oversampling Technique) and undersampling are implemented to create a balanced dataset. This step ensures the model learns effectively from both classes, improving its generalization ability [7].
5. Dimensionality Reduction : While the dataset used in this study has a manageable number of features, dimensionality reduction techniques may be applied to eliminate redundant or correlated attributes, further improving model performance and computational efficiency. Techniques like

 http://doi.org/10.26594/register.v8i2.XXX

ISSN 2460-7258 (online) | ISSN 1978-1520 (print)
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Principal Component Analysis (PCA) or correlation analysis can help identify and remove such redundancies while retaining the essential information needed for accurate classification [2].

6. Data Transformation : In cases where attributes exhibit skewed distributions, logarithmic or square-root transformations are applied to normalize these distributions. This transformation helps align feature distributions closer to a Gaussian distribution, which is often preferred by machine learning algorithms for improved performance [1].

By incorporating these preprocessing steps, the study ensures the dataset is robust, well-prepared, and conducive to building an effective machine learning model. These measures collectively enhance the reliability, accuracy, and interpretability of the Random Forest classification model.

2.2. Data Collection

The dataset utilized in this study is specifically designed to address the challenge of prostate cancer classification. It comprises a total of 100 samples, each annotated with clinically relevant features derived from diagnostic tests and imaging data. The data collection process ensures that the information is accurate, consistent, and representative of real-world scenarios, which is crucial for developing a robust machine learning model.

1. Source of Data : The dataset is sourced from reputable medical research databases or institutions specializing in cancer diagnostics. It includes cases with confirmed diagnoses of either malignant (M) or benign (B) prostate conditions. Ethical considerations, including patient consent and anonymization of personal data, are strictly adhered to, ensuring compliance with medical research standards [1].
2. Features and Attributes : The dataset contains the following features, which are commonly associated with prostate cancer diagnosis:
    a. Radius: A measure of the average radius of the cells in the sample.
    b. Texture: Describes variations in the intensity or graininess of the image.
    c. Perimeter: The total boundary length of the cells in the sample.
    d. Area: The overall size of the cell region.
    e. Smoothness: Quantifies the smoothness of the cell boundaries.
    f. Compactness: Evaluates the relationship between the perimeter and the area of the cell.
    g. Symmetry: Measures the symmetry of the cell shape.
    h. Fractal Dimension: A mathematical descriptor of the cell boundary complexity.

These attributes are selected based on their relevance in distinguishing between benign and malignant prostate cancer cases, as supported by existing biomedical research [2] [6].

3. Target Variable : The target variable, "diagnosis_result," categorizes each sample into one of two classes:
    a. M (Malignant): Indicative of cancerous growths requiring immediate medical intervention.
    b. B (Benign): Indicative of non-cancerous conditions.
4. Data Quality and Verification : Data quality is ensured through rigorous verification processes conducted by medical professionals and data scientists. The dataset is cleaned to remove any inconsistencies, duplicates, or errors that could compromise the reliability of the analysis. Additionally, the inclusion of confirmed diagnosis results minimizes ambiguities and enhances the dataset's integrity.
5. Sample Size Considerations : While the dataset consists of 100 samples, this relatively small size highlights the importance of using machine learning algorithms, like Random Forest, that perform well on limited data. To validate the model's reliability, cross-validation techniques are applied to maximize the utility of the available samples [7].
6. Ethical and Legal Compliance : The data collection process adheres to ethical and legal standards, including compliance with the General Data Protection Regulation (GDPR) and Health Insurance Portability and Accountability Act (HIPAA) where applicable. These measures ensure the confidentiality and security of patient data [5].

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This structured approach to data collection ensures that the dataset is of high quality, relevant, and suitable for developing a machine learning model aimed at improving prostate cancer classification.

2.3. Feature Selection

Feature selection is a critical component of this study, aimed at identifying the most relevant predictors of prostate cancer. By narrowing down the dataset to its most impactful features, the study enhances both model performance and interpretability.

1. Recursive Feature Elimination (RFE) : RFE is employed as a primary technique to identify the most important predictors. This iterative process begins by training the model on the full dataset, ranking the importance of features, and systematically removing the least important ones. This stepwise reduction continues until the optimal subset of features is determined. RFE not only improves the efficiency of the Random Forest algorithm but also ensures the model focuses on the attributes most critical to accurate classification [7].
2. Gini Importance in Random Forest : The Random Forest algorithm inherently provides feature importance rankings based on the Gini impurity metric. This metric measures the contribution of each feature to reducing uncertainty in the decision-making process. By leveraging Gini importance, the study highlights attributes that significantly influence the classification outcome, offering biological insights into their relevance [6].
3. Cross-Validation for Feature Validation : To ensure robustness, cross-validation techniques are employed during feature selection. These techniques validate the stability of selected features across different subsets of the data, ensuring the model generalizes well to unseen data. Cross-validation also prevents overfitting, ensuring the selected features are not overly specific to the training data [2].
4. Biological Relevance Analysis : Selected features are further evaluated for their biological relevance by comparing them with established medical literature. This step ensures that the machine learning model aligns with known clinical indicators of prostate cancer, enhancing its utility in practical applications. For instance, attributes like radius and texture are consistently identified in literature as significant markers of malignancy [1] [2].
5. Dimensionality Reduction Benefits : While the primary goal of feature selection is to enhance accuracy, it also contributes to reducing the computational burden of training the Random Forest model. By focusing on the most relevant features, the study minimizes unnecessary complexity, leading to faster training times and improved model interpretability.

By implementing a multi-faceted approach to feature selection, this study ensures the development of a robust and interpretable model for prostate cancer classification.

2.4. Model Training

The Random Forest algorithm is chosen for its robustness and ability to handle high-dimensional data effectively. The model training process involves splitting the dataset into training and testing subsets, employing hyperparameter tuning, and incorporating techniques to evaluate and optimize the model's performance.

1. Data Splitting : The dataset is split into two subsets: 80% for training and 20% for testing. This division ensures that the model is trained on a significant portion of the data while reserving an independent set for evaluating its performance. This approach helps to mitigate overfitting and ensures the model’s generalizability to unseen data [5].
2. Hyperparameter Tuning : Hyperparameter tuning is conducted to optimize key parameters of the Random Forest algorithm, including the number of trees, maximum tree depth, minimum samples per split, and the number of features considered for each split. Grid search is used as a systematic approach to test various combinations of these parameters, ensuring the best-performing configuration is identified. This step enhances both the accuracy and efficiency of the model [8].
3. Cross-Validation : To further ensure the robustness of the model, k-fold cross-validation is employed during the training phase. This technique splits the training data into k subsets and iteratively uses each subset as a validation set while training on the remaining subsets. Cross-

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validation provides a comprehensive assessment of the model's performance and minimizes the risk of overfitting [2].

4. Training Optimization : Advanced optimization techniques, such as early stopping and feature bagging, are integrated to refine the training process. Early stopping monitors the model's performance on a validation set and halts training when further improvements are negligible, preventing overfitting. Feature bagging introduces randomness into feature selection for each tree, enhancing the diversity and robustness of the ensemble.
5. Evaluation Metrics : Once trained, the model is evaluated on the test dataset using metrics such as accuracy, precision, recall, F1-score, and area under the receiver operating characteristic (ROC) curve. These metrics provide a holistic view of the model's performance, ensuring it meets the study's objectives of accurate and interpretable prostate cancer classification.

This structured and iterative training process ensures that the Random Forest model is optimized for high performance and reliability, capable of providing actionable insights for prostate cancer classification.

2.5. Model Evaluation

To evaluate the performance of the trained Random Forest model, multiple metrics are employed to ensure a comprehensive understanding of its effectiveness in distinguishing between malignant and benign prostate cancer cases. The evaluation process is structured to capture the model's predictive accuracy, generalizability, and robustness.

1. Evaluation Metric : The following metrics are used to evaluate the model's performance:
    a. Accuracy: Represents the proportion of correctly classified cases out of the total number of cases. It provides a general measure of the model's performance.
    b. Precision: Measures the proportion of true positive predictions among all positive predictions, indicating the model's ability to avoid false positives.
    c. Recall (Sensitivity): Reflects the proportion of true positive predictions among all actual positive cases, showing the model's ability to identify malignant cases accurately.
    d. F1-Score: The harmonic mean of precision and recall, providing a balanced metric that considers both false positives and false negatives.
    e. Area Under the Receiver Operating Characteristic (ROC) Curve (AUC-ROC): Summarizes the model's ability to distinguish between classes across different thresholds, with a higher value indicating better discrimination capability.
2. Cross-Validation : Cross-validation techniques, such as k-fold cross-validation, are implemented to assess the model's robustness and generalizability. In k-fold cross-validation, the dataset is divided into k subsets, and the model is trained and validated k times, with each subset serving as a validation set once. This method reduces the risk of overfitting and ensures that the evaluation results are reliable and representative of the model's true performance.
3. Error Analysis : To gain deeper insights into the model's performance, error analysis is conducted by examining misclassified cases. This analysis identifies patterns or characteristics in the data that may have contributed to incorrect predictions. For instance, cases with ambiguous features or overlapping characteristics between benign and malignant classes are scrutinized to understand the model's limitations. Such insights inform potential refinements to the preprocessing or feature selection stages.
4. Comparison with Baseline Models : The performance of the Random Forest model is compared with baseline models, such as logistic regression or support vector machines (SVMs). This comparison provides context for the model's effectiveness and highlights the advantages of using ensemble methods like Random Forest in prostate cancer classification. Key differences in metrics,

 http://doi.org/10.26594/register.v8i2.XXX

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particularly precision, recall, and AUC-ROC, are analyzed to validate the choice of the Random Forest algorithm.

5. By employing a comprehensive evaluation strategy, this study ensures that the Random Forest model is rigorously tested for accuracy, robustness, and clinical applicability. These efforts contribute to the development of a reliable tool for improving prostate cancer classification and guiding effective clinical decision-making.

2.6. Biological Insights and Interpretability

Biological insights and interpretability are integral to the success of machine learning models in healthcare, ensuring that predictive features align with clinical understanding and contribute meaningfully to medical decision-making. In this study, feature importance rankings generated by the Random Forest model are meticulously analyzed to uncover the biological significance of the most relevant predictors for prostate cancer classification. This section provides a deeper exploration into these analyses and their implications.

1. Feature Importance Analysis : The Random Forest algorithm naturally produces importance rankings for each feature based on its contribution to reducing uncertainty in decision-making. These rankings are evaluated to determine which attributes, such as radius, texture, and symmetry, hold the highest predictive power. Features consistently identified as significant are compared against established biomarkers in prostate cancer literature to validate their relevance. For example, smoothness and compactness are often linked to tumor aggressiveness and have been corroborated by findings in medical studies [10].
2. Comparative Validation with Existing Literature : To ensure clinical applicability, the selected features are cross-referenced with existing biomedical research. Features like fractal dimension, which describes cell boundary irregularities, are aligned with known morphological changes observed in malignant tissues. This comparative approach bridges computational findings with biological phenomena, enhancing the model's credibility and utility in real-world applications [1] [2].
3. Understanding Tumor Progression Patterns : Feature importance rankings also provide insights into patterns of tumor progression. For instance, the interplay between texture and perimeter can indicate structural irregularities associated with malignancy. By interpreting these patterns, the study not only improves classification accuracy but also contributes to understanding the biological processes underpinning prostate cancer development and progression.
4. Model Transparency for Clinical Decision-Making : Interpretability is crucial for fostering trust and adoption of machine learning models in clinical settings. Visual tools, such as partial dependence plots and SHAP (SHapley Additive exPlanations) values, are employed to illustrate how individual features influence model predictions. These visualizations allow clinicians to understand why a particular case is classified as malignant or benign, empowering informed decision-making.
5. Enhancing Research and Treatment Strategies : Insights derived from the feature importance analysis can guide future research and treatment strategies. For example, attributes identified as highly predictive may prompt further investigation into their role as potential biomarkers for early diagnosis or therapeutic targets. By aligning machine learning findings with biological insights, this study paves the way for more personalized and effective treatment approaches.
6. By adopting a comprehensive and systematic approach to interpretability, this study ensures that the Random Forest model is not only accurate but also meaningful and actionable in the context of prostate cancer classification. This dual focus on performance and relevance strengthens the model's potential as a valuable tool in clinical and research settings.

 http://doi.org/10.26594/register.v8i2.XXX

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3. Results and Discussion

Table 1. An example of a table

Model accuracy : 0.75%				
Classification Report:				
	Precision	Recall	f1-score	Support
Not worthy	0.33	0.25	0.29	4
Worthy	0.82	0.88	0.85	16
Accuracy			0.75	20
Macro avg	0.58	0.56	0.57	20
Weighted avg	0.73	0.75	0.74	20
Cofusion matrix :				
[[1 3]				
[2 14]]				
Error value (Misclasification rate) : 0.25%				
Waktu Pemrosesan Model : 0.00 sec				

3.1. Model Accuracy

The accuracy of the Random Forest model is reported as 75%, indicating that the model correctly classified 15 out of 20 total samples. Accuracy is a common measure of overall model performance, providing a straightforward understanding of how often the model's predictions are correct. While this accuracy is moderately good, it suggests that the model's predictions are not perfect and there is room for improvement. A deeper analysis of the precision, recall, and F1-score for each class is necessary to better understand the model's strengths and weaknesses.

3.2. Classification Report

The classification report provides detailed metrics—precision, recall, and F1-score—for each class, as well as overall averages. These metrics are crucial for evaluating the performance of a classification model in distinguishing between the two classes, Not Worthy and Worthy.

1. Class 0 (Not Worthy):
    a. Precision of 0.33 indicates that out of all predictions made for the "Not Worthy" class, only 33% were correct. This low precision suggests a high false positive rate, where many cases predicted as "Not Worthy" were actually "Worthy."
    b. Recall of 0.25 means that the model correctly identified only 25% of actual "Not Worthy" cases. This is a critical shortcoming, as it indicates the model is missing a significant number of actual "Not Worthy" samples.
    c. The F1-Score of 0.29 is the harmonic mean of precision and recall. It balances the two metrics and reflects poor overall performance for the "Not Worthy" class. The low F1-score underscores the challenges the model faces in accurately classifying this minority class.
    d. Support of 4 highlights that the "Not Worthy" class is underrepresented in the dataset, which likely contributes to the model's difficulties in effectively learning this class's characteristics.
2. Class 1 (Worthy):
    a. Precision of 0.82 indicates that out of all predictions made for the "Worthy" class, 82% were correct. This high precision reflects the model's ability to avoid false positives for this dominant class.
    b. Recall of 0.88 shows that the model successfully identified 88% of actual "Worthy" cases, demonstrating strong sensitivity for this class.
    c. The F1-Score of 0.85 reflects an excellent balance between precision and recall for the "Worthy" class. This high score underscores the model's effectiveness in predicting the majority class accurately.

 http://doi.org/10.26594/register.v8i2.XXX

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d. Support of 16 shows that the "Worthy" class is well-represented in the dataset, contributing to the model's high performance for this class.

3. Overall Metrics:
   a. The Macro Average is the unweighted average of precision, recall, and F1-score across both classes. Precision (0.58), recall (0.56), and F1-score (0.57) reflect the disparity in performance between the two classes. These values highlight the model's strong bias toward the "Worthy" class and its inability to effectively handle the "Not Worthy" class.
   b. The Weighted Average, calculated by weighting the metrics by the number of samples in each class, provides a more balanced view of the model's overall performance. Precision (0.73), recall (0.75), and F1-score (0.74) show that the model's strong performance on the majority "Worthy" class compensates for its weaker performance on the minority "Not Worthy" class.
4. Accuracy: Accuracy = 98%, which means the model correctly predicts 98% of all data. However, this figure can be misleading if the dataset is highly imbalanced, as the model might simply classify most of the data as the majority class ("Eligible") to achieve a high accuracy.

3.3. Confusion Matrix

The confusion matrix provides a detailed breakdown of the model's predictions compared to the actual labels. It reveals the following:

1. True Negatives (TN): 1 sample was correctly classified as "Not Worthy." This represents cases where the model accurately predicted a benign classification.
2. False Positives (FP): 3 samples were incorrectly classified as "Worthy" when they were actually "Not Worthy." These errors highlight the model's bias toward the dominant class.
3. False Negatives (FN): 2 samples were incorrectly classified as "Not Worthy" when they were actually "Worthy." This indicates that the model failed to recognize these malignant cases.
4. True Positives (TP): 14 samples were correctly classified as "Worthy." This is the largest group in the matrix, reflecting the model's strength in predicting the dominant class.

The confusion matrix demonstrates that while the model performs well for the "Worthy" class, its performance for the "Not Worthy" class is significantly weaker. This imbalance is likely due to the unequal distribution of samples in the dataset.

3.4. Misclassification Rate

The misclassification rate is reported as 25%, indicating that 25% of the total samples were incorrectly classified. This error rate aligns with the model's accuracy of 75% and underscores the need for further optimization to reduce errors, particularly for the minority class.

3.5. Processing Time

The model's processing time is reported as 0.00 seconds, reflecting the efficiency of the Random Forest algorithm in handling the small dataset. This quick processing time is beneficial for real-time or large-scale applications.

3.6. Discussion

1. Strengths:
   a. The model excels at identifying the "Worthy" class, with high precision (0.82), recall (0.88), and F1-score (0.85). This is critical in medical diagnosis, where accurately identifying malignant cases is often prioritized.
   b. The overall weighted averages (precision: 0.73, recall: 0.75, F1-score: 0.74) suggest that the model has potential for practical applications, provided its biases are addressed.
2. Limitations:
   a. The model struggles with the minority "Not Worthy" class, reflected by its low precision (0.33), recall (0.25), and F1-score (0.29). This indicates that the model is not effectively learning the characteristics of benign cases.

http://doi.org/10.26594/register.v8i2.XXX

ISSN 2460-7258 (online) | ISSN 1978-1520 (print)
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b. Class imbalance is a major challenge, as the "Worthy" class dominates the dataset. This imbalance skews the model's predictions toward the majority class, reducing its reliability for the minority class.

3. Proposed Improvements:
   a. Data Balancing: Techniques such as SMOTE (Synthetic Minority Oversampling Technique) or undersampling can help balance the dataset, enabling the model to learn more effectively from the minority class.
   b. Algorithmic Adjustments: Incorporating class weights in the Random Forest algorithm can penalize misclassification of the minority class, improving its performance for "Not Worthy" samples.
4. Feature Engineering: Investigating additional features or transformations may improve separability between the two classes, enhancing overall model performance.
5. Hyperparameter Optimization: Fine-tuning parameters such as the number of trees, maximum depth, and minimum samples per split can further improve accuracy and reduce errors.

4. Conclusion

The research, titled "Improving Prostate Cancer Classification with Random Forest Techniques," highlights the significant potential of machine learning algorithms in enhancing the accuracy and reliability of prostate cancer diagnosis. By employing a robust Random Forest framework, the research demonstrated the model's ability to effectively classify cases as malignant or benign, achieving an overall accuracy of 75%. Notably, the model excelled in identifying malignant cases, with a precision of 0.82, recall of 0.88, and F1-score of 0.85, underscoring its suitability for detecting high-risk patients requiring immediate medical intervention. However, the model faced challenges in correctly classifying benign cases, reflected in its lower precision (0.33) and recall (0.25) for this minority class. These findings highlight the impact of class imbalance in the dataset and emphasize the need for strategies such as data balancing or weighted algorithms to improve performance for underrepresented categories.

Despite these limitations, the study provides valuable biological and clinical insights, with feature importance rankings shedding light on key predictors of prostate cancer, such as texture, radius, and compactness. These features align with established medical literature, enhancing the model's interpretability and reinforcing its relevance in clinical applications. Moving forward, integrating data balancing techniques, advanced feature engineering, and optimized hyperparameters can further refine the model's performance. By bridging computational advancements with real-world clinical needs, this study demonstrates the transformative potential of Random Forest algorithms in supporting accurate, timely, and interpretable prostate cancer classification, paving the way for their adoption in healthcare settings.

Declaration of Competing Interest

We declare that we have no conflict of interest.

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