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Prostate Biopsy Image Gleason Grading Classification using Machine Learning

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Abstract

Prostate cancer diagnosis utilizes Gleason grading to analyze biopsy images to establish cancer severity levels. The analysis of prostate biopsy images is an important step in automating the Gleason grading system, which helps in prostate cancer diagnosis and prognosis. The subjective evaluation of manual grading methods exposes vulnerabilities since they lead to inconsistent results so automated solutions have become essential for precision and reliability. Present machine learning algorithms show insufficient robustness because they incorporate inadequate feature extraction approaches together with inadequate classifier choices. An ensemble Extra Trees model with characteristics from prostate biopsy images serves as the proposal for Gleason grading classification. The HSV color space produces three statistics (Mean, Standard Deviation, and Skewness) from colors with addition of entropy alongside four texture features derived from GLCM analysis which includes Contrast, Energy, Homogeneity, and Correlation. The proposed model receives evaluation against several classifiers which include Nearest Neighbors, Linear SVM, Decision Tree, and Random Forest. The ensemble Extra Trees classifier reaches 99% accuracy during testing which proves better than baseline models thus indicating its potential in trustworthy prostate cancer grading. The significance of this research is to improve the accuracy and efficiency of Gleason grading in prostate biopsy images using machine learning, aiding in early diagnosis and better treatment planning for prostate cancer.

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1. Introduction

The diagnoses of prostate cancer occur in numerous men worldwide making it a common malignancy while the Gleason grading system performs examinations for severity evaluation. Medical staff can use this system to examine biopsy images for prostate architecture before identifying patterns which fall within six different grades that start at Gleason Grade 0 (benign) and finish at Gleason Grade 5 (highly aggressive cancer) [1-3]. The current manual approach used for pathologic assessment by physicians demonstrates subjective human interpretation and inconsistent results between different examiners. The field of automated classification now receives substantial attention because it overcomes existing limitations through machine learning methods. Current research in Gleason grading relies heavily on three distinct approaches which include manual feature extraction algorithms along with deep learning methods and their combination frameworks [5,6,11]. Existing handcrafted feature-based models demonstrate weak robustness while deep learning methods need large, labelled dataset collections, and hybrid approaches typically have high computational expenses. The present challenges demonstrate the requirement for developing an effective machine learning model with improved precision and ease of understanding as well as enhanced efficiency [12,13].

Researchers must evaluate multiple critical factors before selecting a research method to guarantee its reliability along with accurate data analysis and production feasibility. Data availability together with data quality stand as vital elements because the selected technique should efficiently handle noise and missing values as well as inconsistencies. The chosen approach for model development requires simultaneous optimization of performance accuracy and minimal error rate [14,15]. The method needs to execute computations efficiently to achieve both fast processing speed and reasonable resource consumption. Conventionally effective feature selection allows medical researchers to maintain the essential color-based features along with vital texture-based features without creating redundancy or developing overfitting. Medical applications require models that present interpretable and explainable decisions as clinicians need to understand the basis of their model outputs [16,17]. The technique needs to show its ability to generalize effectively across multiple datasets to prevent

overfitting the model and achieving robustness [18,19]. Real-world clinical workflow deployments require assessments of both scalability factors and practical implementation methods with ethical compliance and data protection of patient information according to regulatory standards [20]. The identified factors must be addressed to guarantee both the effectiveness and practicality of the technique that will be used for prostate biopsy Gleason grading [21,22].

1.1 Research Gap

The current methods for prostate biopsy Gleason grading are incomplete since they need a reliable machine learning-based algorithm to process both color-based and texture-based features properly for accurate classification [1,4,5]. The existing methods fail to employ ensemble classifiers such as SVM, KNN, and Decision trees while performing classification tasks [6,7,9]. Research findings demonstrate weaknesses in existing feature extraction approaches because they use only colors or textures not combination [12,15]. The development of a suitable model faces a significant challenge since it must balance accuracy performance with computational speed in medical image analysis.

1.2 Aim and Objective

The main purpose of this investigation involves creating a dependable machine learning-based algorithm to categorize prostate biopsy Gleason grades. The proposed ensemble Extra Trees classifier makes use of color-based features together with texture-based features for reliable image classification purposes. Combination of color and texture features are extracted. The extracted features consist of Mean, Standard Deviation, and Skewness values from HSV color space along with entropy and GLCM-based texture features with Contrast, Energy, Homogeneity, and Correlation measures. The integrated features between the proposed model ensemble extra tree intend to boost classification precision while retaining computational speed.

1.3 Findings

The proposed model achieves effective results through experimental testing against various classification methods such as Nearest Neighbors, Linear SVM, Decision Tree, and Random Forest. The Extra Trees ensemble classifier delivers outstanding performance through its 99% accuracy which surpasses all baseline models. The research showcases the value of

using advanced ensemble learning approaches which provides reliable and accurate prostate cancer grading results beyond traditional manual methods. The presented research will support developers creating AI diagnostic systems that help pathologists reach better outcomes when assessing prostate cancer.

2. Related Work

Current developments in artificial intelligence (AI) have revolutionized prostate cancer diagnosis and treatment alongside prognosis evaluation thus improving diagnostic precision [1]. Various computational models enable machine learning techniques to improve cancer classification and detection practices according to research in broad clinical use [2]. Studies comparing multiple machine learning systems have proven that they can decrease the number of superfluous prostate biopsy procedures which results in better diagnostic outcomes [3]. Radiological and clinical data fusion proves highly beneficial for detecting prostate cancer of medical significance according to published research [4]. Machine learning methods aid in forecasting prostate cancer recurrence together with identifying biomarkers that support individualized treatment planning [5]. Researchers have examined predictive models for intermediate-risk prostate cancer assessment which provides important clinical decision-making solutions to medical practitioners [6].

Multiple investigations developed machine learning systems to detect prostate biopsy results across different PSA (Prostate-Specific Antigen) threshold values which improved early diagnosis methods [7]. An AI-based predictive model risk calculator operating online improves the accessibility of prostate cancer evaluation tools for clinical professionals [8]. The optimization process for machine learning models improved prostate cancer detection accuracy this makes AI-driven approaches suitable for practical applications [9]. A study showed how AI enhances clinical risk assessment along with treatment planning for patients who need prostatectomy [10]. Machine learning algorithms are currently used in prostate cancer MRI data analysis to decrease false-positive cases and lower diagnostic mistakes [11]. The combination of hybrid machine learning methods provides more effective predictions through a strengthened algorithm for prostate cancer assessment [12].

Using machine learning research has found success in cancer stem cell-related gene identification for both prognosis prediction and immunotherapy selection [13]. Research has utilized AI methodologies to identify genes that play a role in metastasis which both improve

diagnosis and treatment planning [14]. A set of machine learning pipelines exists to handle both clinical and proteomics data and enhance prostate cancer medical classification [15]. Various computational approaches based on AI have streamlined how doctors predict prostate cancer recurrence and demonstrated their capability to forecast outcomes [16]. The worldwide validation process of AI algorithms enhances their clinical utility for both prostate cancer detection and Gleason grading purposes [17]. Weakly supervised learning techniques apply automatic diagnosis and grading of prostate cancer through the use of complete slide images [18]. Research has shown that both quantitative parameters and radiomic features can succeed as inputs for machine learning models to forecast Gleason scores which proves AI's value in prostate cancer evaluation [19].

Scientific studies have evaluated machine learning approaches to enhance multiparametric MRI diagnostic measures for prostate cancer detection which resulted in better imaging-based performance measurements [20]. The Gleason grading system receives improved efficiency through AI-based methods which provide computerized systems to automate prostate cancer diagnosis [21]. Visual interpretation methods linked to machine learning models enable better predictions for prostate cancer diagnosis while producing transparent AI diagnostic solutions [22]. Multiphoton imaging teams up with automated image analysis and AI-based classification models to advance prostate cancer tissue classification according to research [23]. Radiomic machine learning methods analyzing multiparametric MRI data helped improve diagnosis accuracy of important prostate cancers as demonstrated in research [24]. The application of machine learning approaches allows doctors to forecast treatment responses of prostate cancer patients which supports the development of individualized medical care [25].

3. Proposed Work

In the following section proposed methodology and process working of each step are explained in detail.

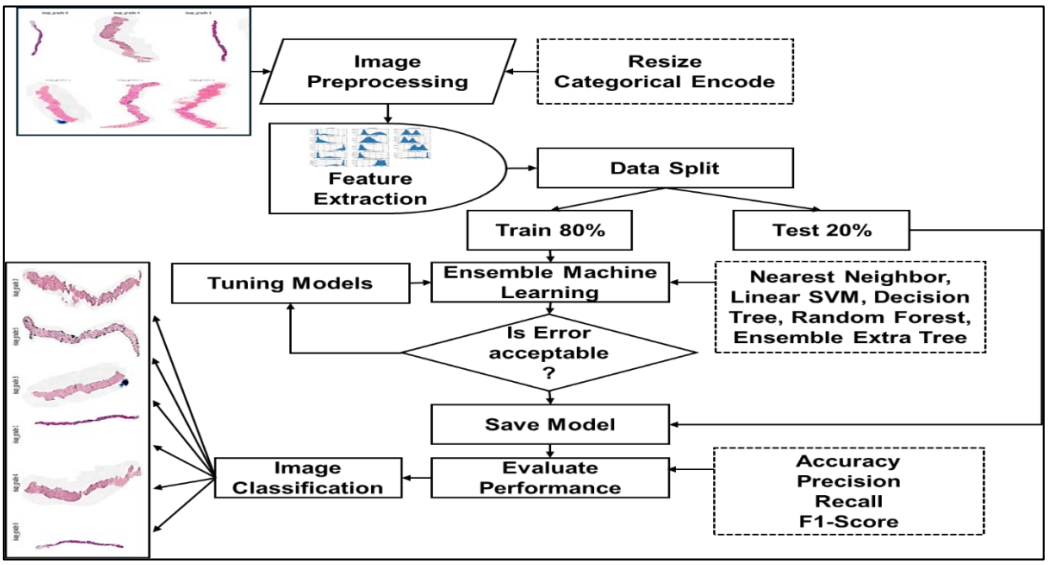


Figure 1. Proposed System Methodology Flow

Figure 1 demonstrate the procedure of classifying prostate biopsy images for Gleason grading through traditional machine learning techniques that involves combining meaningful feature retrieval from histopathological images with the use of k-Nearest Neighbors (k-NN), Linear Support Vector Machines (SVM), Decision Trees, and Random Forests classifiers. The Gleason grading system requires analysis of biopsy images to assess prostate cancer aggressiveness through the evaluation of microscopic patterns that generates a severity score. Traditional machine learning approaches need humans to determine features first before starting the classification process, but deep learning carries out these steps automatically. The extracted features commonly consist of Haralick features extracted from Gray-Level Co-occurrence Matrix and Local Binary Patterns together with glandular structure morphological characteristics and color histograms. Extracted features supply the information which classifiers use to learn Gleason grade assignment patterns. The different classifiers perform distinct operations where k-NN uses nearest training sample comparisons for classifying and Linear SVM establishes optimal hyperplanes and Decision Trees to construct hierarchical feature-split rules. Random Forests generate stable prediction models by combining multiple Decision Trees. Table 1 provides a clear connection between extracted features and classifiers, showing how different classification models utilize specific image properties for Gleason grading classification.

Table 1. Feature Extraction Methods

Feature Type	Feature Name	Description	Count	Supported Classifiers
Color Features (HSV Space)	Mean (H, S, V)	Average intensity of Hue, Saturation, and Value	3	SVM, Decision Trees, Random Forest
	Standard Deviation (H, S, V)	Spread of intensity values in each HSV channel	3	SVM, Decision Trees, Random Forest
	Skewness (H, S, V)	Asymmetry of intensity distribution	3	k-NN, SVM, Decision Trees, Random Forest
	Entropy	Measure of randomness in pixel intensity distribution	1	SVM, Decision Trees, Random Forest
Texture Features (GLCM-Based)	Contrast	Measures intensity variation between adjacent pixels	1	SVM, Decision Trees, Random Forest
	Energy	Sum of squared elements in GLCM (texture uniformity)	1	k-NN, SVM, Decision Trees, Random Forest
	Homogeneity	Closeness of element distributions in GLCM	1	k-NN, SVM, Decision Trees, Random Forest
	Correlation	Relationship between neighboring pixel intensities	1	SVM, Decision Trees, Random Forest

The classification accuracy together with robustness receives enhancement by using an ensemble model built with Extra Trees (Extremely Randomized Trees). Randomness levels in Extra Trees exceed Random Forest by allowing random feature selection for splitting which makes the model more resistant to noise and decreases prediction variance. The proposed ensemble process combines predictions from k-NN, SVM, Decision Tree, and Random Forest followed by Extra Trees to achieve better generalization performance. The training process includes biopsy image preprocessing followed by feature extraction and multiple classifier training that ends with combined output processing through weighted or majority voting schemes. The performance evaluation utilizes accuracy along with precision, recall, and F1-score through cross-validation for achieving robust results. Traditional machine learning benefits from this approach by providing interpretability along with efficiency which produces

a computationally fast method for prostate cancer grading and can replace deep learning techniques.

4. Results and Discussion

The Prostate Biopsy Image Gleason Grading Classification dataset was obtained from Kaggle through Dataset: xhlulu/panda-resized-train-data-512x512. The database contains 3,000 images arranged into six Gleason grade categories where each category contains 500 images among them 2400 is for training and 600 is for testing [26]. For processing purposes, the images received a 512x512 pixel resolution size. The section uses Google Colab for performing implementation tasks. Figure 2 demonstrates the distribution of the dataset whereby it includes 500 biopsy images for each Gleason grade from 0 to 5 for training along with evaluation purposes. Hodges designed Figure 3 to illustrate the feature extraction mechanism that converts images to HSV color space then computes mean, standard deviation, skewness along with entropy metrics while deriving four GLCM-based texture features that include contrast, energy, homogeneity, and correlation. Decision Tree and Random Forest show superior performance in Figure 4 which presents the confusion matrices of various machine learning models Nearest Neighbors and Linear SVM, Decision Tree, and Random Forest. Despite this performance advantage some variations in class prediction remains. The confusion matrix of the proposed ensemble Extra Trees model in Figure 5 shows 99% accuracy while maintaining a low number of misclassification errors thereby proving its excellent capability in Gleason grading classification. Classification error is a measure of how often a machine learning model incorrectly predicts the class labels of given data. For optimization of extra tree model performance, hyperparameter tuning is performed using Randomized Search Cross-Validation.

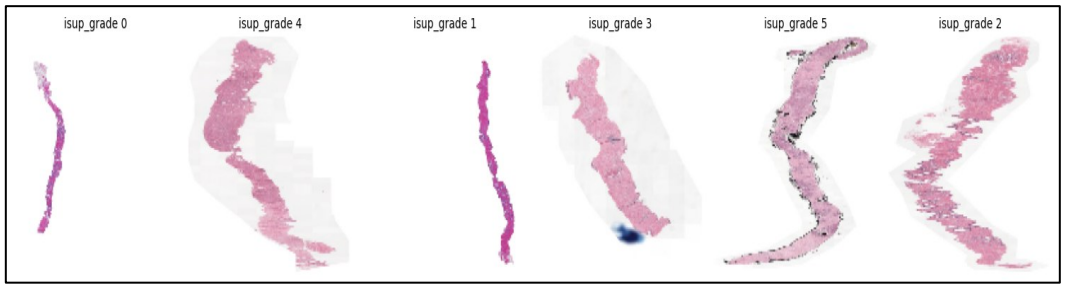


Figure 2. Dataset Reading

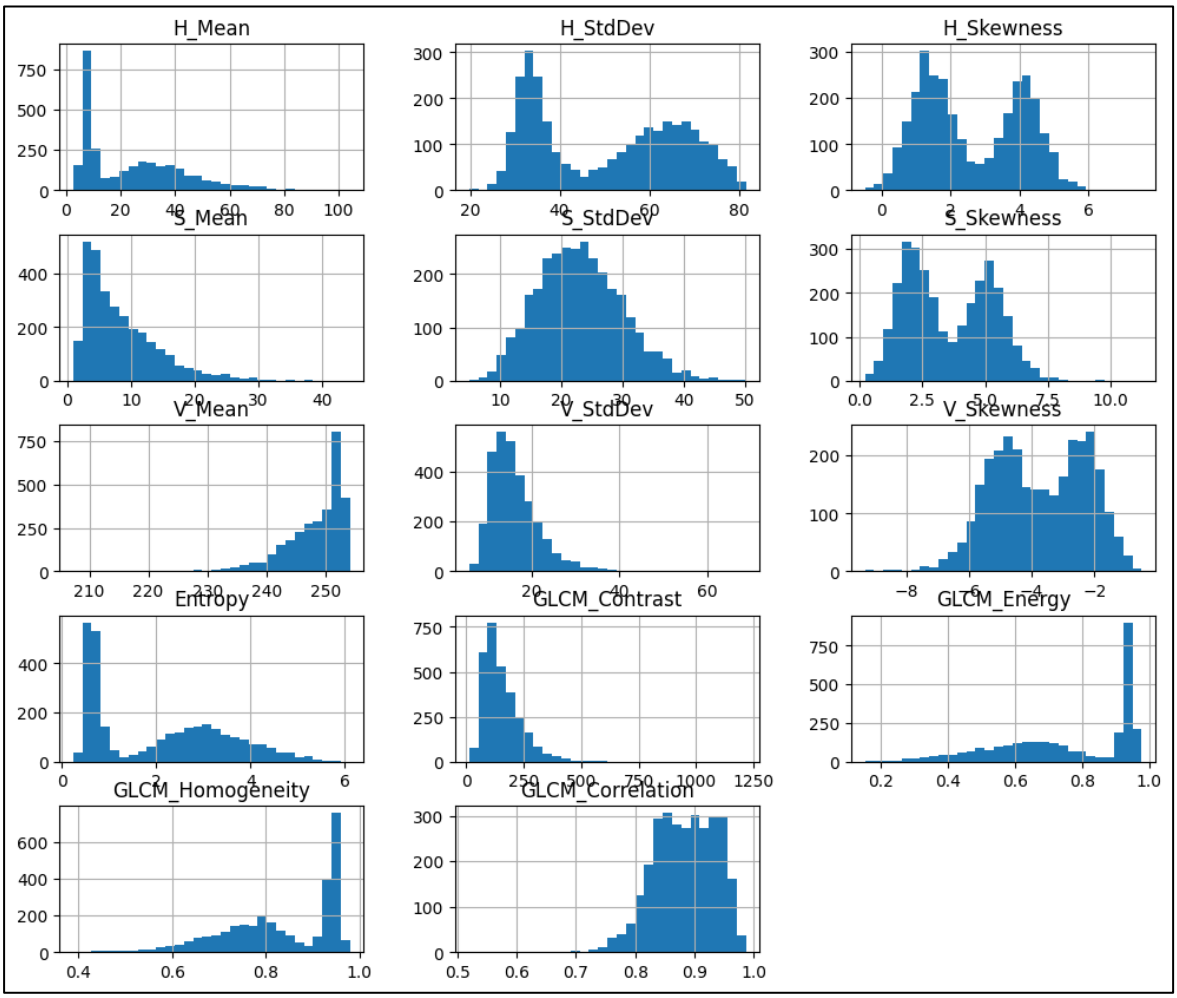
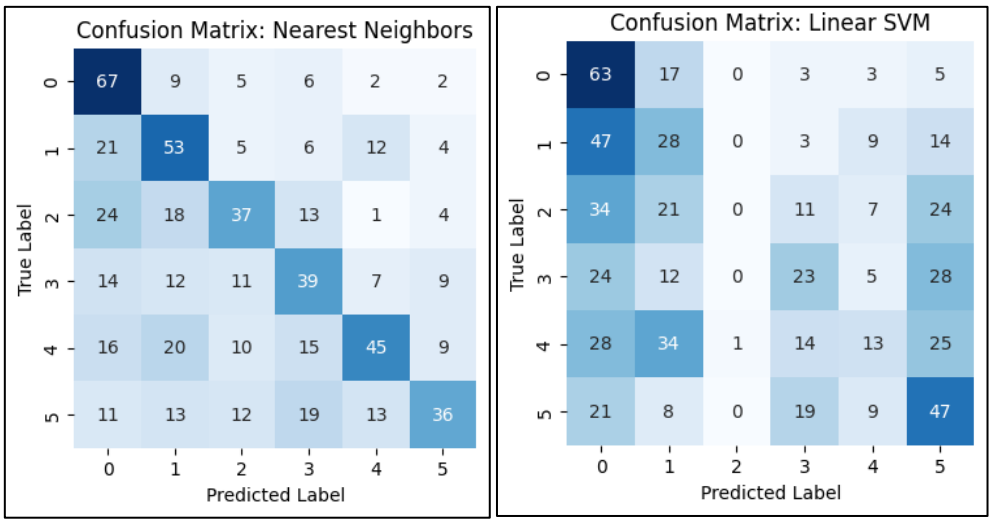


Figure 3. Feature Distribution



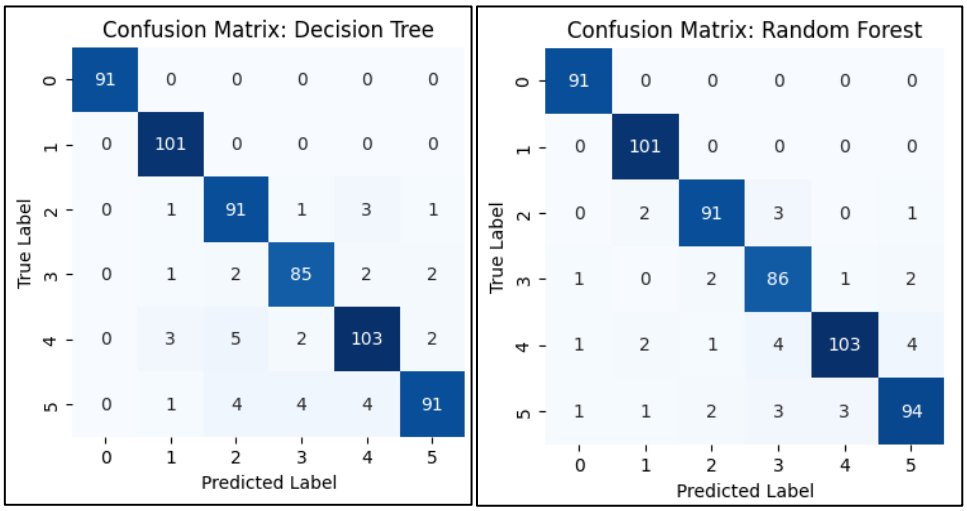


Figure 4. Confusion Matrix of Different Model Evaluation

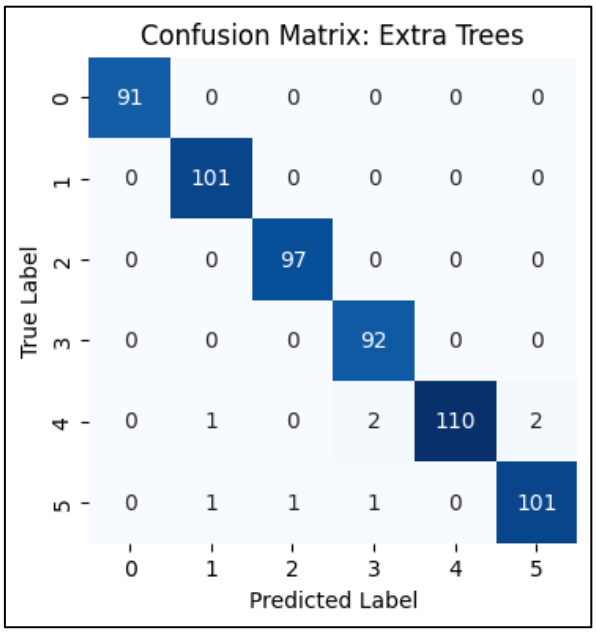


Figure 5. Confusion Matrix of Proposed Ensemble Extra Tree Model Evaluation

Table 2 demonstrates the different machine learning models for Gleason grading classification based on their accuracy, precision, recall, and F1-score performance metrics. The Nearest Neighbors method delivers results that align with the accuracy of 46% but establishes identical precision and recall values that reflect moderate performance. The Linear Support Vector Machine (SVM) achieves the lowest performance since it reaches an accuracy score of only 29% because it struggles to handle complex histopathological features. Random Forest and Decision Tree models accomplish high accuracy rates at 94% while Random Forest proves superior in recall performance at 95% which indicates improved predictive abilities. The

proposed ensemble Extra Trees model shows the peak performance by attaining 99% accuracy in all evaluation metrics thus validating its remarkable ability to identify errors in prostate biopsy images. The execution time depends on the algorithm's complexity; its suitability depends on whether it meets real-time constraints and accuracy requirements. Here for proposed model, it takes 2.04 second.

Table 2. Comparative Analysis

Model	Accuracy	Precision	Recall	F1-score	Time
Nearest Neighbour	0.46	0.47	0.47	0.46	3.35 Second
Linear Support Vector Machine	0.29	0.24	0.30	0.25	4.65 Second
Decision Tree	0.94	0.94	0.94	0.94	3.23 Second
Random Forest	0.94	0.94	0.95	0.94	2.19 Second
Ensemble Extre Tree	0.99	0.99	0.99	0.99	2.04 Second

5. Conclusion

Traditional machine learning techniques prove highly effective for performing Gleason grading classifications of prostate biopsy images through evaluation of features extracted from the data and classifier assessment. Linear SVM and Nearest Neighbors perform inadequately yet Decision Tree and Random Forest exhibit better accuracy with enduring differences between classes. An ensemble Extra Trees model established itself as the top performer with 99% accuracy which makes it an effective solution for automated Gleason grading. Additional work should pursue both built-in features and optimal selection techniques along with the deep learning hybrid models to boost accuracy results. Adding more clinical datasets containing diverse histopathological images as well as conducting validation across multiple test in clinics will enhance general diagnostic applicability in real diagnostic settings.

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