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Development of a Predictive Model for Prostate Cancer Using a Machine Learning Based Classification Algorithm

Akinrolabu, Olatunde David

Deep-Sight Research Group, Department of Computer Science, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria

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ABSTRACT

Prostate cancer remains one of the most prevalent malignancies among men worldwide, with early detection being crucial for effective treatment and improved survival outcomes. Traditional diagnostic procedures, such as prostate-specific antigen (PSA) testing, digital rectal examination (DRE), and biopsy, often suffer from limitations including subjectivity, low specificity, and inconsistent accuracy. This study presents the development of a predictive model for prostate cancer using a machine learning-based classification algorithm, specifically the Support Vector Machine (SVM). The dataset utilised was obtained from a publicly available prostate cancer repository, containing relevant biomedical and demographic features. Preprocessing procedures, including normalisation and data transformation, were applied to enhance model quality and ensure robustness. Experimental results revealed that the SVM model achieved a high predictive accuracy of 84.8% under crossvalidation and 87% on full dataset evaluation, with a corresponding error rate of less than 0.17. These results demonstrate the model's ability to accurately distinguish between malignant and non-malignant cases, validating its suitability for clinical decision support. The model's performance further confirms the potential of SVM as an effective classification technique for medical diagnostics, especially where datasets exhibit complex, nonlinear feature interactions. This study emphasises the significance of machine learning in enhancing diagnostic precision and reliability within the medical domain. The outcomes provide valuable insights into integrating artificial intelligence into healthcare systems for early cancer detection, reducing diagnostic delays, and supporting medical professionals in clinical decision-making.

Keywords: prostate cancer, support vector machine, machine learning, performance evaluation, classification

INTRODUCTION

Prostate cancer is one of the most prevalent malignancies among men and remains the second leading cause of cancer-related deaths worldwide (Zhang & Xiang, 2013). Globally, its incidence exhibits significant geographical variation, with the highest rates reported in the United States, Canada, and Scandinavian countries, while the lowest are found in Asian populations, particularly in China. In Nigeria, prostate cancer poses an increasingly serious public health challenge. Mohammed et al. (2020) reported approximately 161,360 diagnosed cases in 2017, resulting in an estimated 56,730 deaths. The risk of developing prostate cancer increases with age and is influenced by several factors such as genetic predisposition, ethnicity (notably higher among men of African descent), diet, and family history. Early detection of prostate cancer is crucial for improving survival outcomes, as timely intervention can enhance the five-year survival rate for up to nine out of ten patients (Abdel-Zaher & Eldeib, 2018). However, early detection remains a major clinical challenge due to the limitations of existing diagnostic methods. Traditional techniques such as the digital rectal examination (DRE), prostatespecific antigen (PSA) testing, transrectal ultrasound (TRUS), and biopsy procedures, although widely adopted, often yield inconsistent or inconclusive results. PSA testing, for instance, has been shown to reduce mortality by about 20%, yet it is associated with issues of overdiagnosis and overtreatment, as it cannot accurately predict tumour aggressiveness. Similarly, TRUS-guided biopsy lacks sufficient sensitivity to detect all clinically significant cases (Schröder et al., 2018).

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With advancements in medical imaging, multiparametric magnetic resonance imaging (MRI) has emerged as a more reliable diagnostic tool, offering improved sensitivity and specificity compared to TRUS, particularly for lesions in the transition zone (Abdelhamied, 2018). Nevertheless, despite these technological developments, challenges persist in differentiating between aggressive and indolent prostate cancers, emphasising the need for intelligent computational systems capable of enhancing diagnostic accuracy and risk stratification. In Nigeria, the burden of prostate cancer is further compounded by systemic health sector challenges, including inadequate diagnostic infrastructure, a shortage of trained medical personnel, limited access to advanced healthcare technologies, and insufficient data management systems. These factors collectively hinder timely detection and effective treatment, leading to higher morbidity and mortality rates. Addressing these limitations requires innovative and data-driven approaches capable of supporting medical decision-making and improving clinical outcomes. Motivated by these challenges, this study seeks to contribute to the advancement of intelligent healthcare systems through the development of a predictive model for prostate cancer detection using machine learning techniques. Specifically, this research aims to design a model capable of accurately classifying prostate cancer risk levels based on relevant clinical features to show how computational intelligence can enhance decision-making in prostate cancer management and boost early detection by combining machine learning with clinical diagnostic data, especially in healthcare systems with low resources like Nigeria's.

LITERATURE REVIEW

In recent years, computational intelligence has emerged as a transformative approach for addressing complex problems in various domains, including healthcare. Techniques such as fuzzy logic, expert systems, neural networks, and machine learning algorithms have been widely applied to medical diagnostics, demonstrating promising results in decision support and disease classification (Samy & Naser, 2018). technologies aim to reduce diagnostic errors, improve efficiency, and enhance accessibility to quality healthcare, particularly in developing countries where medical expertise and infrastructure are limited.

A. Expert Systems and Fuzzy Logic in Medical Diagnosis

Expert systems have played a vital role in medical diagnostics by simulating the reasoning capabilities of human experts. Samy and Naser (2018) developed an expert system using the CLIPS programming language to assist in the analysis of cancer-related conditions. The system demonstrated encouraging preliminary results, receiving positive feedback from users. Similarly, Abdelhamied et al. (2021) designed an expert system to assist healthcare workers in overcrowded Egyptian outpatient clinics by encoding medical knowledge of over 300 common diseases into a rule-based system. The system utilised production rules triggered by specific symptom combinations to provide diagnostic hypotheses and treatment recommendations. Although effective, the system faced challenges such as selection bias due to specific imaging requirements and underfitting during model testing.

Fuzzy logic has also been applied successfully in medical diagnosis, offering a mechanism for reasoning under uncertainty. Mohammed (2018) developed a fuzzy expert system for diagnosing back pain diseases using parameters such as body mass index, age, gender, and physical symptoms. The system achieved 90% diagnostic accuracy, highlighting the potential of fuzzy logic in handling vague or imprecise medical data. These developments underscore the importance of hybrid intelligent systems in clinical decision-making, although their rule-based structures often limit scalability and adaptability to larger, more diverse datasets.

B. Machine Learning and Deep Learning Applications

Machine learning (ML) has gained considerable attention for its ability to learn complex patterns from medical data without explicit programming. Ertosun and Rubin (2020) employed three architectures of convolutional neural networks (CNNs) to identify malignant masses in mammography images from the DDSM dataset. Their data augmentation techniques cropping, translation, rotation, and scaling—improved model generalisation, although CNN-based methods require extensive computational resources and large datasets. Abdel-Zaher and Eldeib (2020) proposed a deep learning framework that initialised neural network parameters using a pre-trained deep belief network (DBN). The approach demonstrated enhanced classification performance but was limited by

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the curse of dimensionality, emphasizing the need for efficient dimensionality reduction strategies in medical image analysis.

In another study, Priya et al. (2019) proposed a colour-based image segmentation framework for breast thermography analysis using the k-means clustering algorithm. Their model effectively detected abnormal thermal patterns indicative of tumours. However, k-means clustering faced limitations such as difficulty in predicting the optimal number of clusters (k), inconsistent results across runs, and poor performance with nonglobular cluster distributions. Sadhana et al. (2021) compared several supervised learning classifiers, including Decision Trees and Support Vector Machines (SVMs), on three breast cancer datasets—Wisconsin Breast Cancer (WBC), Wisconsin Diagnostic Breast Cancer (WDBC), and Wisconsin Prognostic Breast Cancer (WPBC). The SVM achieved the highest classification accuracy, reinforcing its robustness and reliability in biomedical data classification tasks.

C. Hybrid and Knowledge-Based Diagnostic Systems

Several researchers have explored the integration of rule-based reasoning with learning algorithms to enhance diagnostic precision. Roventa et al. (2022) developed an expert system designed to identify major cancerous diseases using clinical and paraclinical data. The system contained a structured knowledge base encompassing 27 diseases across nine categories, thereby improving the diagnostic reasoning process for cases with overlapping symptoms. Nonetheless, the study's scope was limited to a small patient population, restricting its generalizability.

Similarly, Qeethara-Kadhim et al. (2018) evaluated the effectiveness of artificial neural networks (ANNs) in disease diagnosis, applying feed-forward backpropagation networks to detect acute nephritis and heart disease. The model achieved impressive classification accuracies of 99% and 95% respectively, demonstrating the potential of ANNs in clinical classification problems. However, such models often face challenges related to overfitting, explainability, and the need for large, annotated datasets to ensure robust performance across diverse patient populations.

Freasier et al. (2019) constructed a medical expert system using a multiplication model of support logic programming to determine the dominant stenosis in coronary arteries based on preprocessed myocardial perfusion images. Using a Prologue-based knowledge base, the system correctly identified the location of arterial stenosis in over 90% of cases, underscoring the efficiency of hybrid symbolic–statistical systems in diagnostic inference.

3.4 Summary and Research Gap

From the reviewed literature, it is evident that computational intelligence and machine learning techniques have significantly contributed to the automation of medical diagnosis across various disease domains. However, most existing studies either focus on specific cancers, such as breast or skin cancer, or rely on small datasets that limit model generalisation. Moreover, few studies have explored the application of advanced machine learning techniques, particularly Support Vector Machines (SVMs), in prostate cancer prediction within low-resource healthcare contexts.

Problem Statement

Despite the growing global attention on prostate cancer, effective early detection remains a significant challenge, particularly in developing nations such as Nigeria. The conventional diagnostic process for prostate cancer heavily relies on the availability of qualified specialists and the use of standard clinical procedures, including PSA testing, digital rectal examination, and biopsy. However, these methods are often limited by subjectivity, high false-positive rates, and dependence on expert interpretation. In many healthcare facilities, especially in resource-constrained settings, the absence of specialized oncologists or radiologists further delays diagnosis and treatment, resulting in poor patient outcomes. Moreover, manual diagnostic procedures are timeconsuming, prone to human error, and difficult to scale in regions with limited healthcare infrastructure. These systemic challenges highlight the need for intelligent, data-driven diagnostic systems that can assist medical practitioners by providing accurate and rapid prediction of prostate cancer risk. Such systems could serve as complementary diagnostic tools, particularly in settings where access to medical expertise is restricted. Therefore, the core problem addressed in

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this study is the lack of an automated, machine learning–based predictive framework capable of supporting early and accurate detection of prostate cancer. Developing such a computational model has the potential to enhance diagnostic precision, reduce dependence on specialist availability, and contribute to more efficient and equitable healthcare delivery.

RESEARCH METHODOLOGY

This study adopts a quantitative research approach, leveraging computational intelligence techniques to develop a predictive model for prostate cancer diagnosis. Quantitative methods are particularly suited for data-driven investigations, as they enable statistical evaluation of model performance and reproducibility of results. The research process involves four key phases: data collection, preprocessing, model development, and performance evaluation. This study adopts a support vector machine supervised learning approach. For the aim of this research work to be achieved, the following procedures/processes shall be done to achieve the aforementioned specific objectives.

1. To collect and preprocess prostate cancer datasets containing clinically relevant features from diverse patient samples;

2. To design a predictive model employing the Support Vector Machine (SVM) algorithm for accurate classification of prostate cancer, and

3. To evaluate the model's performance using standard machine learning metrics such as accuracy, precision, recall, F-measure, and error rate.

Architecture

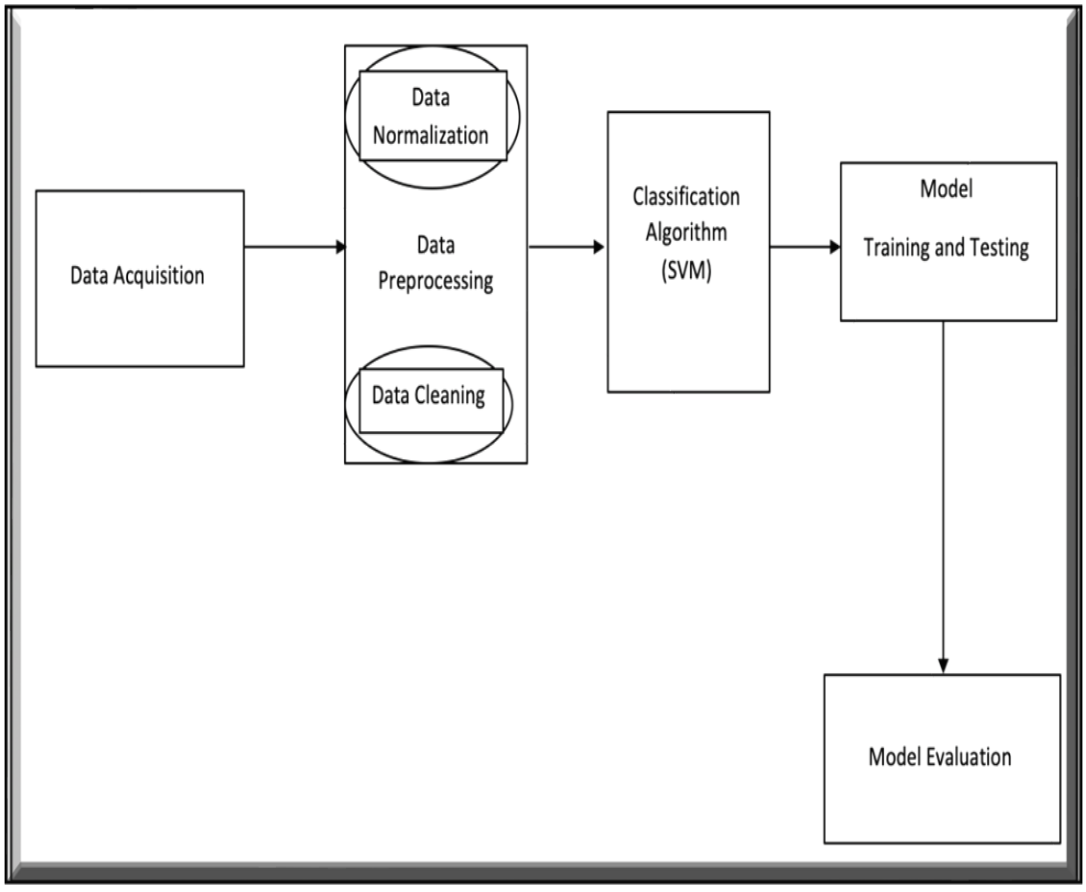

Figure 1: System Architecture

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Detailed Analysis of the Architecture

Data Collection

The dataset used in this study was obtained from an open-access repository, specifically curated for prostate cancer classification tasks. The dataset comprises clinically relevant features, including demographic, genetic, and diagnostic parameters, which were manually imported into Microsoft Excel and subsequently processed in Python. Each record in the dataset represents an individual patient sample with corresponding feature attributes and diagnosis labels. The data were prepared for analysis and then fed into a Support Vector Machine (SVM) classifier to develop a model capable of distinguishing between benign and malignant prostate conditions. The quantitative approach was chosen to facilitate measurable and objective analysis of the model's predictive accuracy, enabling empirical evaluation through standard performance metrics.

	AGE	RACE	DRE	PSA	VOL	GLEASON	COMPACTNESS	SYMMETRY	FRACTAL_DIMENSION	LABEL
2	65	1	2	1.4	0	6	0.278	0.242	0.079	0
3	72	1	3	6.7	0	7	0.079	0.181	0.057	0
4	70	1	1	4.9	0	6	0.16	0.207	0.06	0
5	76	2	2	51.2	20	7	0.284	0.26	0.097	0
6	69	1	1	12.3	55.9	6	0.133	0.181	0.059	0
7	71	1	3	3.3	0	8	0.17	0.209	0.076	1
8	68	2	4	31.9	0	7	0.109	0.179	0.057	0
9	61	2	4	66.7	27.2	7	0.165	0.22	0.075	0
10	69	1	1	3.9	24	7	0.193	0.235	0.074	0
11	68	2	1	13	0	6	0.24	0.203	0.082	0
12	68	2	4	4	0	7	0.067	0.153	0.057	1
13	72	1	2	21.2	0	7	0.129	0.184	0.061	1
14	72	1	4	22.7	0	9	0.246	0.24	0.078	1
15	65	1	4	39	0	7	0.1	0.185	0.053	1
16	75	1	1	7.5	0	5	0.229	0.207	0.077	0
17	73	1	2	2.6	0	5	0.16	0.23	0.071	0
18	75	2	1	2.5	0	5	0.072	0.159	0.059	0
19	70	1	2	2.6	11.8	5	0.202	0.216	0.074	0
20	54	1	1	2.8	0	6	0.103	0.158	0.054	0
21	67	2	3	8.6	25.5	7	0.081	0.189	0.058	1
22	58	1	2	3.1	0	7	0.127	0.197	0.068	1
23	70	0	4	67.1	0	7	0.065	0.182	0.069	1
24	74	1	3	12.7	27.5	7	0.214	0.252	0.07	1

Figure 2: Data downloaded directly from an open-access repository

Data Preprocessing: Data preprocessing was a crucial step in ensuring data quality, consistency, and suitability for machine learning analysis. The preprocessing pipeline involved several operations aimed at minimising noise and improving model reliability. The key steps are outlined as follows:

a) Feature Scaling: After the label encoding, that is, all the texts are converted into numerical values, feature scaling is necessary to normalise the range of independent variables.

The following are the steps involved in data pre-processing:

1. Read the data
2. Derive the class labels for each sample
3. Check out the missing values
4. Convert the Categorical Values
5. Split the dataset into the Training and Test Set

Model Development (Support Vector Machine)

Model Development: The Support Vector Machine (SVM) algorithm was employed for the predictive modelling phase. SVM is a robust supervised learning algorithm that constructs optimal hyperplanes for classification in

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high-dimensional feature spaces. It is particularly effective in medical diagnosis tasks where class boundaries are nonlinear and datasets are moderately sized. The dataset was divided into training and testing subsets using an 80:20 ratio. The training set was used to optimise the model parameters, while the testing set evaluated the model's generalisation capability. Kernel functions were explored to enhance non-linear classification performance, and hyperparameter tuning was applied to achieve optimal model accuracy. The mathematical model for the proposed system, as adopted from Josepth and Fonten is as follows:

The SVM algorithm builds a binary classifier by constructing a hyperplane, separating class members from nonmembers in the input space and finally finds a nonlinear decision function in the input space by mapping the data into a higher-dimensional feature space and separating by means of a maximum margin hyperplane. The system automatically identifies a subset of informative points called support vectors and uses them to represent the separating hyperplane, which is essentially a linear combination of these points. This machine is presented with a set of training examples, (x_i, y_i), where the x_i are the real-world data instances and the y_i are the labels indicating which class the instance belongs to.

Minimize ½||W||2 (1)

Subject to Dii (WTXi -) ≥1,i=1,…….,I (2)

where Dii are the class labels

The parameter C is a regularisation parameter that controls the trade-off between the two terms in the objective function. The following decision rule is used to correctly predict the class of a new instance with a minimum error. The dual formulation permits an efficient learning of non–linear SVM separators, by introducing kernel functions which calculate a dot product between two vectors that have been nonlinearly mapped into a highdimensional feature space. Since there is no need to perform this mapping explicitly, the training is still

Ƒ(x)=sgn[WT X-Y] (5)

The real feature space can be very high or even infinite. The parameters are obtained by solving the following nonlinear SVM dual formulation (in Matrix form),

Minimise LD(U)=1/2 uTQu – et u (6)

By performing computations in the input space. The decision function in this nonlinear case is given by:

Ƒ(x)=sgn[(K(x_i * T) * u – y (7)

where u is the Lagrangian multiplier.

Minimize ½ $\sum^{n}_{k=1}(w^{t}_{k})w_k + C\sum_{i}^{l}=E^{i}$ (8)

Subject to the constraints:

$W_{t\ wi}(x_i) - W_{tt}(x_i) \geq e_{tk}$ - £I * k where k ≠ k_i (9)

where k_i is the class to which the training data x_i belong,

$e_{tk} = 1 - c_{tk}$ (10)

1if ki = k

$c^{t}_{k} = 1(0\text{if } ki \neq k)$ (11)

The decision function for a new input data x_i given by

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$J_i = \arg\max (F_x(x_i))$ (12)

$F_k(x_i) = W_{kt}(x_i) - Y_k$ (13)

Model Training and Testing

Model training represents the learning phase in which the predictive framework iteratively adjusts its internal parameters to minimise classification error. During this process, the Support Vector Classifier (SVC) model is exposed to input features along with their corresponding target labels, allowing it to learn the underlying patterns and relationships between predictors and prostate cancer outcomes. The training process continues until convergence is achieved that is, when further iterations yield minimal improvement in the loss function, ensuring an optimal balance between bias and variance. Following the training phase, model evaluation is conducted using an independent test dataset to assess its generalisation capability on unseen data. The test set provides an unbiased estimate of the model's predictive performance based on standard evaluation metrics. To prevent data leakage and ensure model robustness, no instance from the training set is included in the test set. In this study, due to the moderate size of the available dataset, the data were partitioned into two subsets: 80% (937 samples) for training and 20% (313 samples) for testing. This stratified split ensures that both subsets maintain similar class distributions, thereby enhancing the reliability of model performance assessment.

```
 Training set and Testing set after splitting
(313, 9) data test
(937, 9) data train
(937,) label train
(313,) label test
```

Figure 3: Dataset Split

Model Evaluation and Result

This is the last phase of the experimental implementation. The developed SVM model was evaluated using standard machine learning performance metrics, including: Accuracy, Precision, Recall (Sensitivity), F1-Score and Error Rate

These metrics collectively assess the model's ability to distinguish between malignant and benign cases, ensuring clinical reliability and robustness.

```
SVC score:  0.8753993610223643 or 87 %

confusion_matrix:
 [[166  13]
 [ 26 108]]

classification_report:
              precision    recall  f1-score   support

         0.0       0.86      0.93      0.89       179
         1.0       0.89      0.81      0.85       134

    accuracy                           0.88       313
   macro avg       0.88      0.87      0.87       313
weighted avg       0.88      0.88      0.87       313


"
A SVM APPROACH TO THE DETERMINANT OF PROSTATE CANCER IN HUMAN <O-
"
```

Figure 3: Accuracy Score, Classification Report (Precision, Recall and F-Measure)

The error generated for the epoch is calculated by taking the sum of the false negatives and false positives of the confusion matrix (misclassified samples) and dividing it by the test data. Therefore, to calculate the total error generated by the model the calculation is done below:

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$$\text{Error Rate(Full Set)} = \frac{13+26}{313} = 0.1246 = 1.24\%$$

Table 1: Evaluation Metrics (SVC Full Epoch)

Model	Accuracy Score	Precision	Recall	F1-Score	Error Rate
SVM	**88%**	**87.5%**	**87%**	**87%**	**1.24%**

Cross Validation

```
cross validation scores:  [0.8   0.84  0.744 0.888 0.816 0.888 0.856 0.888 0.8   0.896]

mean =  0.8416
```

Figure 8: Cross Validation Scores

Table 2: Evaluation Metrics (Cross Validation Scores)

Epoch	Accuracy Score	MEAN ACCURACY SCORE
1	80%	84.2%
2	84%	
3	74%	
4	88%	
5	81%	
6	88%	
7	86%	
8	88%	
9	80%	
10	89%	

DISCUSSION

The Support Vector Classifier (SVC) model was trained and evaluated using the preprocessed prostate cancer dataset to predict the likelihood of cancer occurrence based on the extracted clinical and demographic attributes. The model's objective was to effectively distinguish between positive (cancer) and negative (non-cancer) cases by learning the optimal decision boundary that maximises class separation within the feature space. During experimentation, the dataset was partitioned using an 80:20 train-test split, and cross-validation techniques were employed to assess the model's stability and generalisation performance. The SVC demonstrated consistent

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predictive accuracy across both evaluation settings. Specifically, the model achieved an average classification accuracy of 84.8% during cross-validation, corresponding to a mean error rate of 0.162, indicating minimal variance across folds. When evaluated on the complete test set, the model's accuracy further improved to 87%, with only 39 misclassifications out of 313 total test samples. These results confirm that the SVC effectively captured the discriminative patterns within the data, achieving strong generalisation capability despite the relatively limited sample size. The low error rate demonstrates the model's robustness and ability to minimise both false positives and false negatives, a critical factor in clinical applications where diagnostic precision directly influences treatment outcomes. The observed performance validates the suitability of Support Vector Machines for medical diagnosis tasks, particularly in conditions where the dataset exhibits non-linear relationships and limited dimensionality. Furthermore, the findings suggest that integrating more diverse patient data and additional clinical biomarkers could further enhance predictive accuracy and support broader deployment of the model as a clinical decision-support tool for early prostate cancer detection.

CONCLUSION, CONTRIBUTION AND RECOMMENDATION

The development and evaluation of a predictive model for prostate cancer using a Support Vector Machine (SVM) classifier yielded promising results. The study demonstrated that the model effectively classified input data with an accuracy exceeding 84%, supported by strong precision, recall, and F1-score metrics. The model's performance across both train-test split and cross-validation techniques confirmed its robustness, reliability, and minimal error convergence. These findings highlight the potential of machine learning-based systems, particularly SVMs, to support medical practitioners in the early detection and diagnosis of prostate cancer, especially in healthcare environments with limited specialist availability. The results also reaffirm the importance of data quality and preprocessing in achieving high prediction accuracy and generalizable model performance.

This research contributes significantly to the growing field of computational intelligence in healthcare by establishing the efficacy of SVM as a dependable classification approach for medical diagnosis. It further introduces a novel Python-based implementation framework for prostate cancer prediction, offering reproducibility and flexibility beyond traditional platforms such as MATLAB, WEKA, and RapidMiner. The study reinforces the value of supervised machine learning models in identifying complex, nonlinear relationships among biomedical features, demonstrating how iterative optimisation of model parameters minimises classification error and enhances predictive accuracy. Thus, the study extends empirical knowledge on the application of SVMs to oncological datasets and provides a foundation for future research on intelligent diagnostic systems.

In light of these findings, future studies should focus on expanding the dataset to include more diverse and clinically validated samples, as larger datasets often yield better generalisation and improved model robustness. Further exploration of advanced algorithms such as ensemble learning, deep neural networks, and reinforcement learning could enhance predictive performance.

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