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# Novel prostate cancer detection and classification model using support vector machine

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**ABSTRACT**

Prostate cancer (PCa) is one of the most common and deadliest cancers that kill men worldwide with high mortality and prevalence especially in developed countries. PCa is regarded as one of the most prevalent cancers and is one of the main causes of deaths worldwide. Early detection of PCa diseases helps in making decisions about the progressions that should have occurred in high-risk patients decrease their risks. The recent developments in technology and methods have given rise to computer aided diagnosis (CAD). Early cancer detection can greatly increase the chance of survival through the administration of the proper treatment. Due to the emerging trends and available datasets in state-of-art machine learning (ML) and deep learning (DL) techniques, there has been significant growth in recent disease prediction and classification publications. This paper presents a unique support vector machine-based model for PCa detection and classification. This analysis aims to classify the PCa using ML algorithm and to determine the risk factors. Support vector machines (SVM) is used to identify and classify the PCa. Accuracy, sensitivity, specificity, precision, and F1-score are the measurements used to evaluate the performance of the presented method. This model will achieve accuracy, sensitivity, specificity, precision, and F1-score than earlier models.



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## 1. INTRODUCTION

The In the world, men are most commonly affected by prostate cancer (PCa), which is also the fifth leading cause of deaths related to cancer. It is extremely unusual in children and teenagers, with about 75% of cases detected being older than 65. The incidence and death rates typically increase with age. Age and family history are the two main risk factors [1]. Within the male reproductive system is the prostate, which is located in the pelvis in front of the rectum and under the bladder. It typically weighs 20 g in an adult male and is about 3 cm long, surrounding an area of the urethra. The human prostate is an organ that helps create and store seminal fluid. It also accumulates zinc and produces citrate. Twenty percent of seminal fluid is produced by the prostate glands, and diseases of the prostrates impair urination, ejaculation, and defecation. Particularly in the early stages, PCa symptoms frequently overlap with those of various diseases [2].

Indications and symptoms of PCa include bloody urine, pelvic pain, urination, and fatigue from low red blood cell counts. PCa is linked to risk variables such as race, age, and heredity. This suggests that because PCa is inherited, the risk is increased if a close relative has the disease. Furthermore, a number of

dietary and behavioral risk factors, PCa has been connected with factors like consuming too many milk products, processed meat, or diets lacking in certain vegetables [3].

Therefore, accurately diagnosing PCa as soon as possible is essential because it can improve therapy and reduce the risk of death. One of the main issues in research these days is accurately classifying cancer types and identifying the critical genes related to the disease [4]. With a patient's diagnosis of suspected PCa based on an abnormal screening digital rectal examination (DRE) or a high prostate-specific antigen (PSA) result, currently, random systematic (sextant) biopsies performed under the control of transrectal ultrasound (TRUS) is the accepted clinical procedure for diagnosing PCa. Depending on the number of biopsy sites, the physician usually divides the prostate into many regions. After that, a needle is placed into each area to extract tissue samples for further examination [5].

In order to increase the detection accuracy, in addition to the significant false-negative rate (i.e., the possibility of incorrectly diagnosing a patient with PCa as a normal subject), a TRUS-guided biopsy for prostate cancer detection (PCD) usually needs to be repeated 5-7 times. However, TRUS-guided biopsy is not suitable for screening a large number of patients for PCa diagnosis because it is an invasive procedure [6]. Better PCa diagnosis and therapy have been made possible by recent developments in complex computers and algorithms. The term "Computer-aided diagnosis" (CAD) describes the use of technology and computer algorithms are to help medical personnel diagnose and predict patients [7].

Precise diagnosis optimizes the healthcare of patient and avoids the unnecessary surgical treatments. Automatic CAD techniques help to improve the PCa diagnostic accuracy and reduce the differences between them. In addition, the CAD can result the improved reader interpretation of PCa [8]. In medical imaging fields of study, they are frequently used in the identification of anomalies or to help in the interpretation and analysis of medical images, such as computed tomography (CT), magnetic resonance imaging (MRI), X-ray, and mammography scans [9]. According to studies, MRI is an effective, the noninvasive imaging tool that can help consistently identify or diagnose a wide range of diseases by providing anatomical, functional, and metabolic MRI information, including Alzheimer's disease and PCa [10].

These systems recognize specific features or patterns that might demonstrate the existence or absence of a disease or condition using machine learning (ML), deep learning (DL), and pattern recognition algorithms. According to research, PCa ranks as the fifth most prevalent cause of death worldwide and the second most common type of cancer in men. However, compared to all other cancer types, it is the one that is diagnosed in more men over middle age in both developed and developing countries [11]. However, still there are difficulties in MRI imaging of PCa. Some of these challenges include noise, blurring, rotation, low precision segmentation and classification approaches. These challenges could impact the exactness of the frameworks used to analyze PCa [12]. ML is a type of artificial intelligence that uses a particular algorithm or methodology to find patterns in unprocessed information. Allowing computer systems to learn from experience on their own, without the need for explicit programming or human interaction, is the main goal of ML. In multiple fields of medicine, ML techniques are frequently used since they are faster, more accurate, and less costly for diagnosing different diseases [13].

Because ML techniques can manage large amounts of data and integrate data from multiple sources, they improve prediction power. ML's classification is one of its key functions. When the output variable is categorical, classification includes methods for estimating it [14]. For the diagnosis of PCa, Trans-rectal ultrasonography guided biopsy (TRUS) is currently the accepted standard, however it exhibits high false-negative rate and propensity for causing discomfort, bleeding, and inflammation. Therefore, an automatic, -invasive and accurate PCa classification model is essential to save patients from invasive biopsies and to choose the best method of treatment [15].

A hierarchical classification and high-level representation were designed for MRI-based PCa diagnosis. A DL network uses multi-parametric MR images as input data to first learn high-level feature representation. Then, a method of hierarchical classification is developed by utilizing the high-level properties that have been learned, in which the PCa detection findings are iteratively refined by developing numerous random forest classifiers. An averaged section-based evaluation (SBE) of 89.90%, an averaged sensitivity of 91.51%, and an average specificity of 88.47% are obtained using the suggested procedure. The studies were conducted on 21 real patient subjects [16].

Cox regression was used to predict the chances of survival for PCa in patient data from public sector undertakings (PSU). This study contains a cohort of patients with ages ranging from 40 to 89. Between 2015 and 2018, the data was gathered from Songkhlanagarind Hospital in accordance with good clinical practice (GCP) standards. PCa patient's chances of survival are examined using COX regression. According to the results, in 2015, 78 people with PCa were treated by 22 patients, 63.636% were still alive and 36.364% had passed away. There were eighteen patients alive in 2016. With a doctor-friendly graphic user interface, this research aims to include targeted therapy features or real-time occurrences to display precise predicting results [17].

PCa28 gene Signature was used to be a predictor of PCa, protein-protein interaction network and genome-wide analysis to find potential genes for PCa early diagnostic biomarkers. First, using two separate sources, the authors gathered gene expression datasets of 145 PCa samples from the gene expression omnibus (GEO). These samples included both the tumor and the associated normal tissues. In tumor samples, the genes that were considerably strongly and weakly expressed, respectively, were found by the authors to be 158 and 268. Additionally, prediction scores (PS) and cluster scores (CS) are described to choose 28 genes (referred to as PCa28) associated with PCa. The findings show that PCa28 is specific to PCa has the ability to differentiate between normal and tumorous tissues [18].

PCa risk prediction using an enhanced hybrid algorithm was described. This study preprocesses the data, presents the clinical diagnosis features of PCa, and develops a law by examining the connection between PCa, PSA, and other indicators using patient data from patients with benign prostate disease and PCa from the National Center for Clinical Medical Science Data (301 Hospital) is contains a PCa dataset. As the prediction model, a classifier combining the AdaBoost and random forest algorithms are chosen based on cross-validation on the training set. The ratios of age, PSA (free), and PSA (total) have a great chance of detecting PC, according to research conducted by the authors. PCa is also affected differently by diagnostic features such as brain natriuretic peptide precursor, free calcium, apolipoprotein E ratio, apolipoprotein A1, and creatine protein T chloride [19].

The detection of prostate tumor Gleason scores and cancer treatment using real-time formal verification was described. This approach uses formal methods to differ the Gleason score and the PCa treatment. Because it doesn't involve a biopsy, the suggested procedure is thus non-invasive. Using a collection of temporal logic features, they assign the Gleason score and the relative treatment to patient magnetic resonance pictures by modeling them as timed automata networks. In the Gleason score inference, each assessed case had a sensitivity and specificity of 1, and in the therapy prediction, the corresponding values were 0.94 and 1, respectively, this suggested method's effectiveness is confirmed by the experimental study, which validates the qualities on 36 different patients [20].

Medical image processing was used to reconstruct tissue properties for cancer screening. A new approach for determining the relative tissue elasticity parameters is presented, based on both geometric and physical restrictions. A statistically based classifier that automatically generates a clinical T-stage and Gleason score based on the elasticity values reconstructed from CT images are proposed by the authors. Making use of a feature set including patient age information and reconstructed relative elasticity parameters, with up to 85% accuracy for cancer staging and up to 77% accuracy for cancer grading, the relative elasticity characteristics were utilized to predict cancer grading and staging [21].

A DL approach was employed to PCa detection using targeted contrast-enhanced ultrasound. In this study, a DL system for identifying PCa in consecutive Contrast- enhanced ultra-sound (CEUS) images is presented. Through three-dimensional convolution operations, the suggested method consistently recovers features from both the spatial and temporal dimensions, then capturing the dynamic information of the perfusion process stored in many adjacent frames for the identification of PCa. Tests demonstrated that the DL technique outperformed previously reported methods and implementations, obtaining approximately 91% specificity and 90% average accuracy for the diagnosis of PCa in the targeted CEUS images ($p<0.05$). The amount of the available data was constrained by the use of experimental targeted contrast agent in the CEUS videos used for this research [22].

A model was designed that can differentiates between PCa and benign prostatic hyperplasia using ML-based prostate-specific antigen density (PSAD) in a single-center retrospective research conducted in China. When combined with age and the prostate's opposite diameter, PSAD demonstrated a good ability to identify PCa, according to a decision tree prediction model that was developed to aid in the diagnosis of the disease. Patients with a small prostate transverse diameter should be closely monitored by physicians due to their increased risk of PCa. For PCa screening, diagnosis, prognosis, and follow-up, this work offered an excellent diagnosis and treatment method that supported medical professionals in making the best selection [23].

The application of the Bayesian network approach was designed to find the relationship between the morphological features taken from images of PCa. A Bayesian network analysis approach is used in this study to measure the strength of the relationship between various features and to summarize the imaging profile of patients from the PCa imaging database using a wide range of morphological features. Through the use of mutual information, Kullback-Liebler, and Pearson's correlation, an analysis was made to determine the nodes strength of association. Multiple feature connections were determined to be the strongest. Additionally, the impact of node connections and node force were calculated. This research can further improve detection performance by identifying the features that are more dominant in establishing the connection [24].

MRI-based computer-aided PCa identification was demonstrated. The two-stage completely automated computer-aided detection system was examined by the writers of this research. Using voxel

feature extraction, classification, local maxima detection, and multi-atlas-based prostate segmentation, they identify first candidates in the first step. The bases for performance evaluation are lesion-based free-response receiver operating characteristic curves and patient-based evaluations of receiver operating characteristics. Furthermore, a comparison is made between the system and radiologists predicted clinical performance. The sensitivity, for 0.1, 1, and 10 false positives per normal case, is 0.42, 0.75, and 0.89, according to the results [25].

Classification of PCa using wavelet neural network (WNN) was described. Morlet function was employed as an activation function of WNN and back propagation (BP) was applied for training the WNN. The WNN classified the PCa based on three factors such as prostate volume, age of patient and level of PSA. The performance results showed that the WNN has low mean square error (MSE) [26].

To address the above-mentioned limitation, this paper presents a novel PCa detection and classification model based on support vector machine. The section 2 presents, novel PCa detection and classification model using support vector machine. The section 3 evaluates the result analysis. Section 4 represents the work final conclusion.

## 2. NOVEL PCA DETECTIONAND CLASSIFICATION MODEL

In this section, novel PCa detection and classification model using support vector machine is presented. Figure 1 displays the presented model's block diagram. Firstly, the dataset is collected from kaggle healthcare repositiry as comma seperated values (.csv) files. Pretreatment data for PCa patients is included in the database. Serum, seledi lipid profile, and general background data were combined into one. This labelled dataset, which comprises 250 features and one class of features was extracted from medical examination records of patients who are suspected of having PCa. Patients background data included age, race, body mass index (BMI), and family history; other information included blood in semen, erectile dysfunction, urine difficulties, and urine stream force.

Preprocessing is done on the dataset to get removal of noise, incompleteness, class imbalance, and other irregularities. The preprocessing involved the following steps: normalization, discretization, resampling, and data cleaning. In order to eliminate sparsely distributed records and columns fill in missing values, data cleaning was performed. Missing, inconsistent, and Incomplete values were successfully eliminated from the dataset by data cleaning, which addressed over- and undersampling problems connected to class imbalance, resampling was implemented. If characteristics of a class are distributed or represented differently, there is an imbalance. PCa and non-PCa were the target class features taken into consideration in this examination. The imbalanced dataset problem is solved by upsample the minority class and downsample the majority class. By substituting numerical equivalency for nominal values, the dataset was discretized. By performing this, the amount of data is decreased and the number of possible variations in each PCa feature is moderated. The missing values are filled in using this procedure. It also makes the ML work faster and easier.

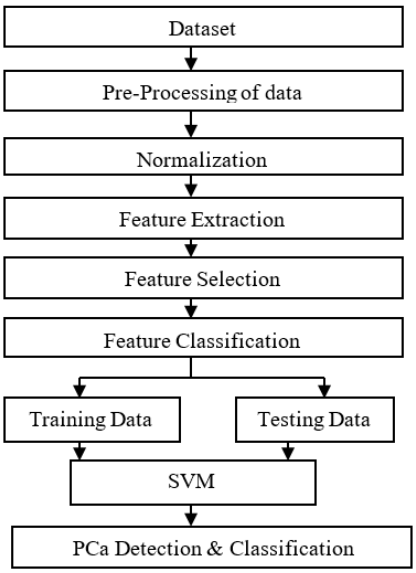


Figure 1. Block diagram of novel PCa detection and classification

In terms of distance measure, minimum-maximum normalization makes sure that the PCa dataset feature is not overwhelmed by other characteristics. The values are modified in this procedure to a range, which is typically between 0 and 1. The present study used the minimum-maximum (min-max) normalization approach, as shown in (1):

$$f(x) = \frac{x - min(x)}{\max(x) - \min(x)} \quad (1)$$

where min and max represent the variable's (feature x's) range's minimal and maximum values, respectively. When a dataset's values are simplified to a scale between 0 and 1, this is referred to as feature scaling. Preprocessing produces clean, noise-free, consistent, and normalized final output.

Relevant characteristics are found after the PCa clinical dataset has been cleaned, resampled, discretized, and normalized. Principal component analysis (PCA) is also used in feature extraction to prevent data loss. The target class is maintained and the dataset has less dimensions as the result. The 12 most relevant features were chosen after features were rated in relation to the PCa dataset. The process of choosing the subset of the most related and appropriate features to be included in the ML model's construction are known as feature selection. Adding the significant features to the dataset and removing the unimportant characteristics is the irrelevant feature selection is carried out. Wrapper and filter (one-way ANOVA) are two-step feature selection methods that are used to select important features from those extracted. There are instances in which learning algorithms perform poorly in terms of prediction because of insignificant input features. As a result, feature selection which chooses artificial intelligence (AI) -based classification identifying the most useful characteristics for a dataset. With the use of an recursive feature elimination (RFE) technique, which builds baseline models continuously and chooses the feature that performs the best each time until all features are classified, the best features are first selected. This study utilized a baseline model is a gradient boosting classifier, to perform the RFE procedure. Features thus get ordered from strongest to weakest in a descending order.

The feature significance (F-value and p-value) and effect size (eta squared) of the samples chosen using RFE is determined using a one-way analysis of variance (ANOVA) statistical test. Based on the eta squared and effective size, the magnitude differences between the two groups (malignant and benign) were examined. The difference between the two groups is shown to be insignificant, less relevant, important by the tiny, medium, and high effect sizes. Data used for testing and training are treated using the chosen features. Training and testing data is presented to the chosen features. A supervised ML approach called support vector machines (SVM) is finds the maximum-margin hyperplane for binary classification, separating known classified data points from unknown data points. Predicting new data sets is faster than with other predictive models, regardless of the size of the training set in the domain. When given an unknown PCa tuple without its corresponding output class, the SVM model looks for the K training tuples that are most similar to the unknown tuple in the pattern space. By applying classical statistical learning theory, the SVM produces a model that can be easily understood and provides good generalization of new information. Since they support the placement of the dividing hyperplanes, the closest points are known as support vectors. It also suggests that the hyperplanes cannot be changed by changing the nonsupport vectors, and vice versa. Finding the optimum hyperplane that maximizes the margin between two classes is the goal of supervised ML algorithms called supervised support vector machines, or SVMs. Because of their well-developed mathematical formulation, flexibility, high accuracy, strong theoretical support, direct geometric interpretation, and the number of software implementations, SVMs have been extensively used for the detection and classification of PCa.

The SVM detects the presence and absence of PCa. If PCa is detected then it classifies the PCa asnadenocarcinomas, small cell carcinoma (small cell neuroendocrine carcinoma), other neuroendocrine tumors (including big cell carcinoma), transitional cell carcinoma, and sarcomas, the SVM detects PCa as either normal or PCa.

Adenocarcinomas account for nearly all cases of PCa. The prostate's gland cells, which produce the fluid that's added to semen, are the cause of these tumors. As a result, this analysis has extremely accurately recognized and classified. The model's performance is verified in terms of accuracy, sensitivity, specificity, precision and F1-score and are defined as follows: The (2) defines the accuracy as:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \times 100 \quad (2)$$

The percentage of those with the target condition and positive test results is referred to as sensitivity, or "positivity in PCa disease". The sensitivity is expressed in (3).

$$Sensitivity = \frac{TP}{TP+FN} \times 100 \quad (3)$$

The percentage among those without the target disease who had negative test results is known as specificity, or "negativity in PCa disease". The expression for Specificity is defined in (4).

$$Specificity = \frac{TN}{TN+FP} \times 100 \quad (4)$$

Precision: The precision can be defined as the sum of true positives and false positives, or the number of true positives divided by the total number of positive predictions. The (5) defines the precision.

$$Precision = \frac{TP}{TP+FP} \times 100 \quad (5)$$

The F1-score indicates that the model detects positive cases while reducing false positives and false negatives. The (6) expressed the F1-score.

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (6)$$

## 3. RESULTS AND DISCUSSION

This section, novel PCa detection and classification model using support vector machine is implemented. This part evaluates the model's results analysis that was presented. The performance metrics used to evaluate the proposed PCa model are F1-score, specificity, accuracy, sensitivity, and precision. The evaluation of performance is presented in Table 1.

Compared to Naïve bayes (NB) classifier, SVM classifier has obtained better performance. The Figure 2 shows the performance metrics comparative graphs. The Figures 2(a) and 2(b) shows sensitivity and specificity comparison respectively.

Table 1. Performance comparison

| Metrics/algorithm | Naïve bayes | SVM |
|---|---|---|
| Precision (%) | 91 | 95.23 |
| Sensitivity (%) | 90.23 | 94.57 |
| Specificity (%) | 92.3 | 95.9 |
| Accuracy (%) | 90.45 | 95.67 |
| F1-score (%) | 89.62 | 95.23 |

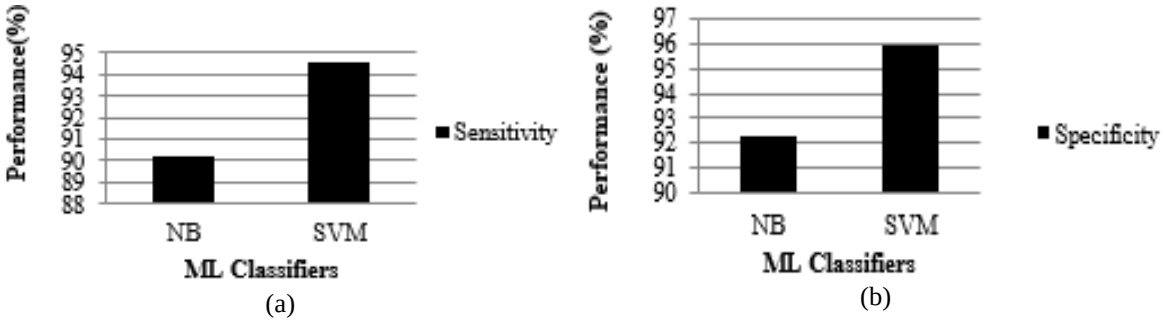


Figure 2. Performance comparative graph for (a) sensitivity and (b) specificity

In Figure 2(a), the x-axis indicates ML classifiers and y-axis indicates performance in terms of percentage. The SVM has shown better performance for sensitivity and specificity than NB classifier. The Figure 3 shows the performance comparison graphs. The Figures 3(a) and 3(b) shows precision and accuracy comparison. Compared to NB classifier, SVM has achieved better precision for PCa detection and classification. The SVM classifier has obtained better accuracy than NB. The Figure 4 shows F1-score comparison. From Figure 4, it is clear that, the SVM has high F1-score than other classifiers. Hence presented model has effectively detected and classified the PCa. When PCa is identified early on, various strategies for treatment can be implemented and the disease's progression may be prevented.

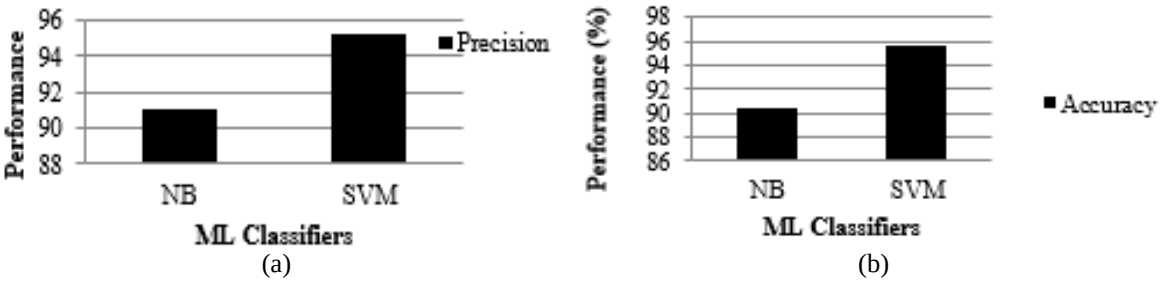


Figure 3. Performance comparative graphs (a) precision performance comparison and (b) accuracy performance comparison

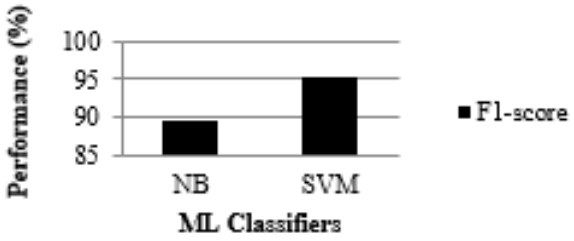


Figure 4. F1-score performance comparison

## 4. CONCLUSION

In this work, novel PCa detection and classification model using support vector machine is presented. The SVM is utilized in the early stages of PCa differential diagnosis. To identify and categorize people with and without PCa, SVM is utilized. Among the variables taken into consideration in this study are race, age, Body mass index (BMI), obesity, family history, problems trouble urinating, blood in semen, urine stream force, bone pain, and erectile dysfunction. Preprocessing is done on the dataset to address dimensionality reduction and class imbalance. Analyzing and categorizing the important features in order to detect PCa is the aim of feature selection. To choose essential characteristics, the two-step feature selection method is used. The effectiveness of this system is measured in terms of F1-score, Precision, Sensitivity, Accuracy, and Specificity. The SVM classifier has achieved improved accuracy in PCa detection and classification when compared to previous models. Medical professionals can use this approach for early detection and classification of PCa, minimizing death rate, saving time and cost. In future, hybrid ML techniques will be used to further improve the performance of PCa cancer detection and diagnosis.

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## AUTHOR CONTRIBUTIONS STATEMENT

| Name of Author | C | M | So | Va | Fo | I | R | D | O | E | Vi | Su | P | Fu |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kandukuri Sujata | ✓ | ✓ | ✓ | ✓ | | ✓ | | | ✓ | ✓ | | | ✓ | |
| Bokka Sridhar | | ✓ | | ✓ | | ✓ | ✓ | ✓ | | ✓ | | ✓ | | |
| Avala Mallikarjuna Prasad | ✓ | | ✓ | ✓ | ✓ | ✓ | | | ✓ | | ✓ | | ✓ | |

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

## CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

## DATA AVAILABILITY

- The data that support the findings of this study are openly available in [Siti Sarah *et. al.*,] at http:// 10.11591/ijece.v13i6.pp6862-6871.org/[10.11591/ijece.v13i6.pp6862-6871], [4].
- The data that support the findings of this study are openly available in [Hamza Abu *et. al.*,] at http:// 10.11591/ijece.v14i2.pp2234-2241.org/[10.11591/ijece.v14i2.pp2234-2241], [6].
- The data that support the findings of this study are openly available in [Kim CH *et. al.*,] at http:// 10.3390/cancers13071524.org/[10.3390/cancers13071524], [14].
- The data that support the findings of this study will be available in [IEEE] [DOI: 10.1109/ACCESS.2023.3326882] allow for the commercialization of research findings.

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