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Evaluating the Effectiveness of Parameter Tuning for Support Vector Machine on Voice Pathology Database

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Abstract: This study explores the effectiveness of parameter tuning for Support Vector Machine (SVM) in the classification of voice pathologies using the Saarbrucken Voice Database (SVD). A balanced dataset consisting of 200 pathological and 200 non-pathological voice samples was used. Feature extraction was performed to derive key acoustic properties from the voice samples, and the SVM classifier was evaluated using four different kernel functions: linear, polynomial, radial basis function (RBF), and sigmoid. A grid search was employed to tune the hyperparameters, specifically focusing on the regularization parameter (C) and gamma (γ). The performance of each kernel was visualized using heatmaps that represent accuracy scores for different parameter combinations. Results demonstrated that the linear kernel, with $C = 0.1$ and $\gamma = 1$, achieved the highest accuracy of 64%, making it the most effective for this classification task. In contrast, the polynomial, RBF, and sigmoid kernels showed lower performance. These findings emphasize the importance of selecting appropriate kernels and parameters in SVM-based classification tasks for voice pathology detection.

Keywords: Feature Extraction, Kernel, SVD, SVM, Voice Pathology

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1. INTRODUCTION

Voice disorders are a prevalent health issue, significantly impacting individuals' ability to communicate effectively and reducing their quality of life. Accurate and early diagnosis of these pathologies is crucial for timely treatment and rehabilitation. However, traditional diagnostic methods largely depend on subjective evaluations by speech-language pathologists (SLPs), which are inherently prone to variability due to differences in expertise, fatigue, and human judgment [1], [2]. To overcome these challenges, machine learning (ML) techniques have emerged as promising alternatives, offering objective, reproducible, and efficient diagnostic solutions. Among these techniques, Support Vector Machines (SVM) have gained prominence in the automation of voice pathology detection, demonstrating substantial improvements in diagnostic precision [3].

SVM are a type of supervised learning algorithm renowned for their effectiveness in high-dimensional spaces and their robust performance in various medical diagnostic applications [4]. Their ability to model complex, non-linear relationships makes them well-suited for voice pathology classification, where distinguishing between healthy and pathological voices often requires sophisticated feature interactions. However, the success of SVM classifiers is highly dependent on the appropriate tuning of critical parameters: kernel type, regularization parameter (C), and kernel coefficient (γ) [5].

The kernel type determines how input features are transformed into a higher-dimensional space, facilitating the capture of non-linear patterns in the data. Common kernel choices include linear, polynomial, radial basis function (RBF), and sigmoid. Each offers unique capabilities, with RBF being particularly favored for non-linear datasets due to its flexibility [6]. The regularization parameter (C) controls the trade-off between model complexity and misclassification tolerance, while the gamma (γ) parameter, especially important in RBF and polynomial kernels, influences the reach of individual support vectors, thereby affecting model generalization [7].

Recent advancements in ML and artificial intelligence have expanded the use of automated voice pathology detection systems in clinical environments. These systems assist SLPs by reducing diagnostic time, minimizing human error, and enabling personalized treatment planning through detailed acoustic analysis [8], [9]. Previous studies have demonstrated the potential of combining SVM with optimized feature extraction techniques for accurate pathology detection. However, the effectiveness of SVM depends significantly on parameter optimization strategies, highlighting the need for a deeper investigation into how kernel selection, C, and γ influence classification performance [10].

In this study, the dataset will be taken from the Saarbrucken Voice Database (SVD), the feature extraction will be performed using Mel-Frequency Cepstral Coefficients (MFCC), and the classifier employed will be an SVM. The SVD is a well-established database that provides a comprehensive collection of voice samples from individuals with various voice disorders, making it an ideal resource for this research. By employing MFCC for feature extraction, this research ensure that the most relevant and discriminative features of the voice signals are captured [11]. These coefficients are widely used in speech and speaker recognition tasks due to their effectiveness in representing the short-term power spectrum of sound. The SVM classifier, with its robust theoretical foundation and practical success in various classification tasks, is expected to perform well in distinguishing between healthy and pathological voices. By systematically exploring the effects of kernel type, *C*, and gamma on the SVM's performance, this research aims to optimize the classifier and provide practical insights into its application in voice disorder diagnostics. This comprehensive approach will help to better understand the impact of these parameters and contribute to the development of more accurate and reliable diagnostic tools in the field of voice pathology.

2. RELATED WORKS

Voice pathology detection plays a crucial role in diagnosing various vocal disorders and diseases. Support Vector Machines (SVM) have emerged as a powerful machine learning technique for voice pathology detection due to their ability to handle high-dimensional data and nonlinear relationships. However, the effectiveness of SVM heavily relies on the appropriate selection of its parameters, such as the choice of kernel type, C, and γ. Recent research has focused on evaluating different parameter tuning strategies to enhance SVM performance for voice pathology detection. Studies have demonstrated that optimizing SVM parameters using evolutionary algorithms improves classification accuracy compared to manual selection methods [3], [4], [12]. Similarly, research combining feature selection techniques with SVM has highlighted the impact of selecting relevant features and tuning SVM parameters on performance enhancement [6], [13].

The choice of kernel type, *C*, and *γ* parameters significantly influences the performance of SVM in voice pathology detection. The kernel type determines the decision boundary's shape and flexibility, with popular options including linear, polynomial, radial basis function (RBF), and sigmoid kernels. Linear kernels are suitable for linearly separable data, while nonlinear kernels such as RBF can capture complex relationships in the data [6]. Next, the regularization parameter *C* controls the trade-off between maximizing the margin and minimizing the classification error. A smaller value of *C* leads to a larger margin and may prevent overfitting, while a larger *C* value allows the SVM to classify more training examples correctly but may lead to overfitting [7]. Gamma (γ) parameter determines the influence of each training example; low values of gamma indicate a far reach where points farther away from the decision boundary influence classification, while high values of gamma indicate a closer reach which only points close to the decision boundary influence classification [8].

In a comparative study, various parameter tuning techniques, including grid search and random search, were evaluated for SVM in voice pathology detection. The results indicated grid search was more effective in identifying optimal parameters than random search [5]. Moreover, advanced optimization techniques like genetic algorithms and particle swarm optimization (PSO) have been explored, with findings underscoring their effectiveness in boosting classification performance [3], [10], [14]. The kernel type significantly affects SVM's decision boundaries, with popular choices including linear, polynomial, radial basis function (RBF), and sigmoid kernels. Research has shown that RBF kernels often perform better due to their ability to capture complex relationships [12]. Additionally, the regularization parameter C balances margin maximization and classification error minimization, while γ controls the influence of training examples on decision boundaries [9], [11], [15].

Recent works have also examined the role of glottal source features and other specialized feature extraction methods in voice pathology detection. For example, [14] and [15] applied advanced feature engineering combined with machine learning to classify pathological and non-pathological voices effectively. These studies contribute to understanding how different parameter tuning approaches and feature sets influence classification outcomes. Unlike prior research, which often focused on one kernel or basic parameter settings, this study provides a comprehensive exploration of multiple kernel functions and parameter combinations on a balanced dataset of 200 pathological and 200 non-pathological samples, delivering practical insights for optimizing SVM-based models.

3. METHODOLOGY

3.1. Dataset Collection

The dataset used in this experiment is derived from the Saarbrucken Voice Database (SVD) which is a widely recognized resource for voice pathology research. The dataset includes recordings from both individuals with diagnosed voice pathologies and those with normal voices known as non-pathological which making it ideal for classification tasks.

For this research, a subset of the SVD was selected, consisting of 200 pathological voice samples and 200 non-pathological voice samples. The samples were balanced to ensure that both categories were equally represented, allowing for a fair comparison and reliable model training and evaluation.

The pathological voice samples include recordings from individuals with various disorders such as vocal fold paralysis, vocal nodules, and laryngeal cancer among others. Non-pathological samples were collected from individual with no history of vocal disorders and were recorded in similar conditions to those with pathologies to maintain consistency.

The balanced nature of the dataset provides an equal opportunity for the SVM classifier to learn from both classes, improving the model’s ability to generalize and perform well on unseen data.

3.2. Feature Extraction

In this research, feature extraction plays a crucial role in transforming raw voice data into a set of relevant characteristics, which serve as input for SVM classifier, The quality of these features directly impacts the classification performance, making the extraction process essential for accurate identification of voice pathologies.

The voice pathology dataset used in this experiment comprised voice recordings that contain various speech features indicative of pathological conditions. The main task during feature extraction was to isolate significant acoustic and physiological features from these recordings. To achieve this, several standard techniques were employed, focusing on both time-domain and frequency-domain characteristics.

Mel-Frequency Cepstral Coefficients (MFCCs**)** were primarily used for feature extraction, as they are highly effective in representing the power spectrum of audio signals, particularly for speech and voice data. MFCCs mimic the human ear's response to sound, making them ideal for voice analysis. A set of 12 – 13 MFCC coefficients was extracted from each voice sample, along with their first and second derivatives, to capture both the static and dynamic aspects of the voice signals.

The feature extraction process was automated using specialized speech analysis tools, ensuring consistency and reliability across all voice samples. After extracting these features, they were standardized and normalized to ensure compatibility with the SVM model, and to eliminate the influence of different units and scales.

In summary, the feature extraction methodology transformed raw voice recordings into a structured feature set that encapsulates key vocal characteristics. These extracted features provided a rich input for the classification stage, enabling the SVM model to detect subtle distinctions between pathological and non-pathological voice samples effectively.

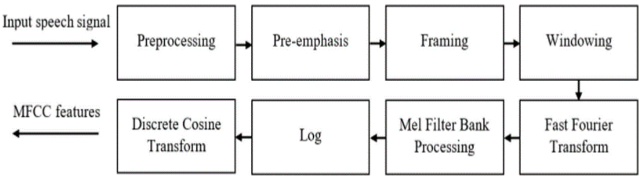

Figure 1. MFCC process

3.3. Classification

In this research, the Support Vector Machine (SVM) algorithm was chosen for the classification of voice pathology data due to its effectiveness in handling high-dimensional data and its ability to construct optimal decision boundaries between different classes. The SVM model is well-suited for binary classification tasks, making it ideal for the problem at hand—distinguishing between pathological and healthy voice samples.

The classification process began with the preparation of the voice pathology dataset, which was divided into training and testing sets using k-fold cross-validation to ensure that the model was evaluated consistently and without bias. The dataset features were standardized to ensure that all variables had the same scale, thus preventing larger values from dominating the learning process.

The SVM classifier was implemented with different kernel functions, including linear, polynomial, radial basis function (RBF), and sigmoid, to evaluate the performance of each kernel type. These kernels were chosen because they allow the SVM to capture various complexities in the data. The linear kernel provides a straightforward decision boundary, while the polynomial, RBF, and sigmoid kernels offer more flexibility in mapping the data into higher-dimensional spaces, enabling better separation of classes.

To optimize the model's performance, a grid search was conducted to tune the hyperparameters *C* (regularization) and *γ* (kernel coefficient) for each kernel. The grid search aimed to identify the best combination of *C* and *γ* that maximized the accuracy of the model. The performance of the SVM model was evaluated using accuracy as the main metric, and the results were visualized through heatmaps for each kernel, showing the impact of varying *C* and *γ* on the model's classification ability.

Through this systematic approach, the classification methodology allowed for a thorough evaluation of different kernel functions and parameter settings, leading to the identification of the most effective model configuration for the voice pathology classification task.

Algorithm 1. The proposed method

```
FUNCTION SVM_Classification(data, labels)
        // 1. Split data into training and testing sets
        (X_train, X_test, y_train, y_test) = train_test_split(data, labels, test_size = 0.2)

        // 2. Scale the data using standard scaling
        X_train_scaled= StandardScaler.fit_transform(X_train)
        X_test_scaled= StandardScaler.transform(X_test)

        // 3. Define the parameter grid for Grid Search
        parameter_grid =
                {
                'C': [0.1, 1, 10, 100],
                'gamma': [1, 0.1, 0.01, 0.001],
                'kernel': ['linear', 'rbf', 'poly', 'sigmoid']
                }
        // 4. Initialize the SVM classifier
        model = SVM()

        // 5. Perform Grid Search with Cross Validation
        best_model=GridSearchCV(model, parameter_grid, cv = 5, scoring = 'accuracy')
        best_model.fit(X_train_scaled, y_train)

        // 6. Get the best parameters and model
        best_parameters= best_model.best_params()
        best_classifier= best_model.best_estimator()

        // 7. Make predictions on the test set
        y_pred= best_classifier.predict(X_test_scaled)

        // 8. Calculate accuracy and performance metrics
        accuracy = Accuracy_Score(y_test, y_pred)

        // 9. Return best parameters and accuracy
        RETURN best_parameters, accuracy

END FUNCTION
```

3.4 Performance Metrics

The performance of the SVM models is evaluated using accuracy as the primary metric. Accuracy measures the proportion of correctly classified instances to the total number of instances, providing a straightforward metric for assessing model performance. To better visualize the results, a heatmap was utilized to display the grid search scores corresponding to various combinations of SVM parameters of C and γ. The heatmap effectively illustrates the impact of parameter tuning on model performance.

The x-axis of the heatmap represents different values of the γ parameter while the y-axis corresponds to varying values of the C parameter. The accuracy scores are represented by a color gradient where the darker shades indicate lower accuracy, and lighter shades represent higher accuracy. This visualization aids in identifying the optimal combination of parameters that yield values consistently provide strong or weak performance. By utilizing the heatmap, the experiment can clearly demonstrate how different kernels react to changes in C and γ, guiding the selection of the most effective parameter values for each kernel type.

4. RESULTS AND DISCUSSION

In this section, the performance of various kernel functions within the SVM framework for voice pathology detection is evaluated. The primary goal is to identify the most effective kernel and parameter combination in achieving the highest classification accuracy. This analysis provides insights into the strengths and weaknesses of each kernel type (Linear, RBF, Polynomial, and Sigmoid) when applied to voice pathology data. Moreover, parameter tuning, particularly the C and γ is explored in depth. This exploration is crucial, as optimal parameter selection is essential for enhancing the performance of SVM models. The subsequent subsections focus on comparing the performance of the four kernels and investigating the effect of various C and γ values on classification accuracy.

4.1 Kernel Performance Comparison

From this research, Table 1 presents the performance of SVM models with varying parameters C and γ across four different kernels: Linear, RBF, Polynomial, and Sigmoid. The results reveal that the Linear kernel performs the best overall, maintaining a stable accuracy between 0.6344 and 0.6406 across different parameter combinations. The highest accuracy of 0.6406 is observed when $C = 0.1$and $\gamma = 1$. This stability across various settings indicates that the Linear kernel is well-suited for this dataset, even with minimal parameter tuning.

In contrast, the RBF kernel performs poorly for most combinations, with an accuracy of 0.5125 across most of the C and γ values. However, a notable improvement is seen when $C = 1$, $\gamma = 0.001$ or $C = 100$, $\gamma = 0.001$, where the accuracy reaches 0.5969 and 0.6062, respectively. This suggests that the RBF kernel may benefit from higher C values and smaller γ values but requires more precise tuning to outperform other kernels.

The Polynomial kernel shows moderate performance, with accuracy ranging between 0.5531 and 0.5719. The best result is observed when $C = 0.1$ and $\gamma = 0.1$, as well as when $C = 10$ and $\gamma = 0.1$, both yielding an accuracy of 0.5719. Although the polynomial kernel performs slightly better than the RBF kernel, it does not surpass the accuracy achieved by the Linear kernel.

Next, the Sigmoid kernel consistently underperforms across all parameter values, with an accuracy fixed at 0.5125 for most combinations. This suggests that the Sigmoid kernel is not effective for this dataset, as it fails to produce competitive results regardless of the parameters used.

Therefore, the Linear kernel emerges as the best-performing kernel for this dataset, especially at lower C values. The RBF and Polynomial kernels show potential in performing good kernel but require more careful parameter tuning, while the Sigmoid kernel is the least effective for this dataset.

Table 1. Summarize of SVM on each kernel

C	**γ**	**Linear**	**RBF**	**Poly**	**Sigmoid**
0.1	1	0.6406	0.5125	0.5656	0.5125
0.1	0.1	0.6406	0.5125	0.5719	0.5125
0.1	0.01	0.6406	0.5125	0.5531	0.5125
0.1	0.001	0.6406	0.5125	0.5687	0.5125
1	1	0.6344	0.5125	0.5656	0.5125
1	0.1	0.6344	0.5125	0.5719	0.5125
1	0.01	0.6344	0.5125	0.5531	0.5125
1	0.001	0.6344	0.5969	0.5625	0.5125
10	1	0.6344	0.5125	0.5656	0.5125
10	0.1	0.6344	0.5125	0.5719	0.5125
10	0.01	0.6344	0.5125	0.5531	0.5125
10	0.001	0.6344	0.6062	0.5625	0.5125
100	1	0.6375	0.5125	0.5656	0.5125
100	0.1	0.6375	0.5125	0.5719	0.5125
100	0.01	0.6375	0.5125	0.5531	0.5125
100	0.001	0.6375	0.6062	0.5625	0.5125

4.2 Parameter Tuning Analysis

The results show using heatmap to see the relationship between correlation of parameters between C and γ for each kernel. Based on Figure 2, the heatmap for the linear kernel shows that the accuracy remains consistently high at 0.64 across all values of C and γ. Specifically, the highest accuracy is observed with $C = 0.1$, regardless of the value of γ. This suggests that the linear kernel is effective for this dataset and that lower values of C are optimal. The stability in performance across different γ values indicates that the choice of γ has minimal impact on the accuracy when using a linear kernel.

Next, as shown in the heatmap in Figure 3, the highest accuracy achieve for polynomial kernel shows is 0.57 with $C = 0.1$ and $\gamma = 0.1$. There is a noticeable variation in accuracy across different combination of C and γ, with the lowest performance at 0.55 for some combinations. This kernel shows a moderate level of effectiveness; however, it does not reach the performance levels of the linear kernel. The polynomial kernel might benefit from further tuning or a different approach to achieve better results.

Moreover, the RBF kernel heatmap shown in Figure 4 demonstrates a peak accuracy of 0.61 with C =10 and γ = 0.001. This suggests that a higher C value combined with a very small γ value yields better performance for this kernel. However, the accuracy significantly drops to 0.51 for other combinations of C and γ. This indicates that the

RBF kernel is sensitive to parameter changes and requires precise tuning to achieve optimal performance.

Furthermore, Figure 5 depicts poor performances of sigmoid kernel across all tested parameters with a constant accuracy of 0.51 regardless of the value of C and γ. This suggests that the sigmoid kernel is not suitable for this dataset or that the range of parameters tested is not appropriate for this kernel. The lack of variation in accuracy indicates that the sigmoid kernel is not effective for distinguishing voice pathology.

Thus, the linear kernel with C = 0.1 and γ values of 0.1 or other tested values provides the highest and most consistent accuracy of 0.64 for the voice pathology dataset. The polynomial and RBF kernels shows moderate performance, with the polynomial kernel peaking at 0.57 and the RBF kernel at 0.61 under specific parameter combinations. However, both require careful tuning to achieve their best performance. The sigmoid kernel performs the worst, with a constant accuracy of 0.51, indicating its unsuitability for this dataset. Therefore, the linear kernel is the best choice for this application, offering robust and reliable performance.

Next, the results also shown using Receiver Operating Characteristics (ROC) curves for linear, polynomial, RBF and sigmoid kernel. Each curves evaluates the true positive against the false positive rate. For Figure 6, it shows the ROC curve for the linear kernel creates a hyperplane as a decision boundary and making it most suitable for linearly separable data. The ROC curve reaches a moderate value of 0.75 which indicates a balance between sensitivity and specificity. It suggests that while the linear kernel performs well for some threshold values, it may fail to perfectly separate pathological and non-pathological samples. For Figure 7, its shows the ROC curve for polynomial kernel remains 0.75, indicating no significant performance advantage in this case. The ROC curve's gradual rise, rather than a steep ascent near the origin which suggest that while the polynomial kernel can fit some nonlinear patterns, its degree of complexity may not be optimal for the dataset used. Next, Figure 8 shows RBF kernel where with AUC of 0.75. The curve's progression indicates that the RBF kernel can distinguish between classes, however, it does not achieve an ideal balance with some misclassification affecting sensitivity and specificity. In Figure 9, it shows the ROC curve for sigmoid function, with AUC score of 0.75 similar to other kernels. The ROC curve's gradual slope suggests that the model performs well for some thresholds but struggles to fully separate the classes across all thresholds. The performance may be constrained from suboptimal parameters tuning and lack of suitability for the underlying dataset characteristics. Thus, as all three kernel shows an AUC of 0.75, it suggests moderate classification performance and the differences in the curve shapes highlight variations in how well each kernels separates pathological and non-pathological samples. Linear kernel shows its computationally efficient, polynomial kernel shows its flexibility, RBF kernel shows capability to capture complex and nonlinear relationship in data and sigmoid kernel shows its ability to captures some nonlinearity. The best choice of the best kernel for a given problem may not depend on AUC only but other factors as well.

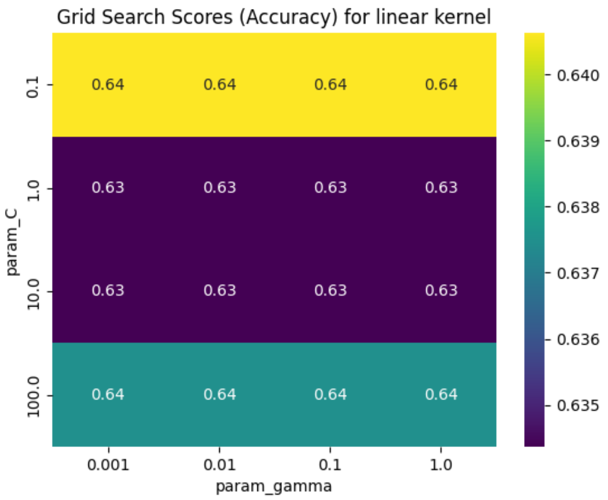

Figure 2. Heatmap of Linear Kernel

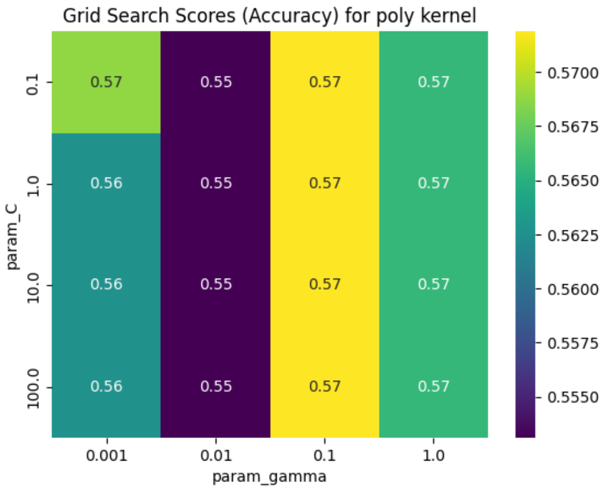

Figure 3. Heatmap of Polynomial Kernel

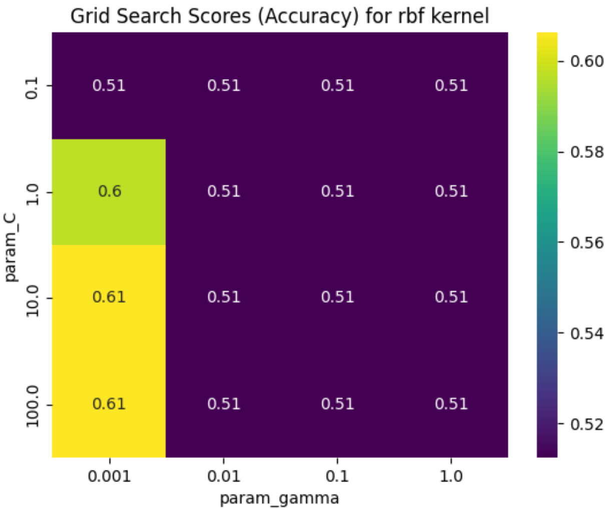

Figure 4. Heatmap of RBF kernel

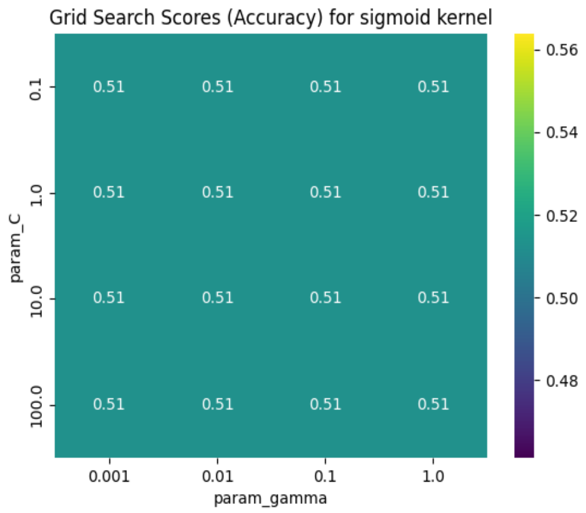

Figure 5. Heatmap of Sigmoid kernel

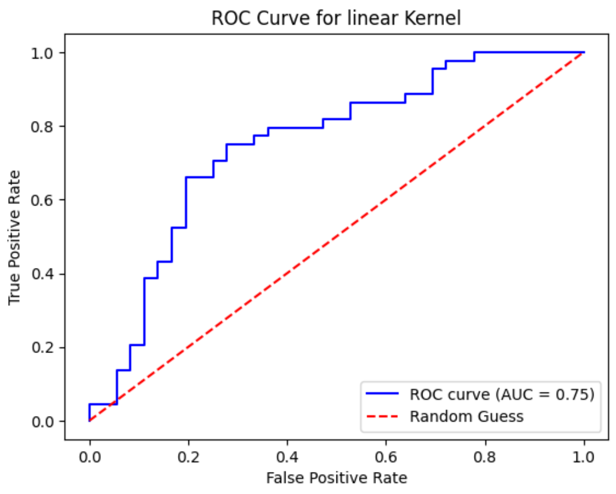

Figure 6. ROC Curve for linear kernel

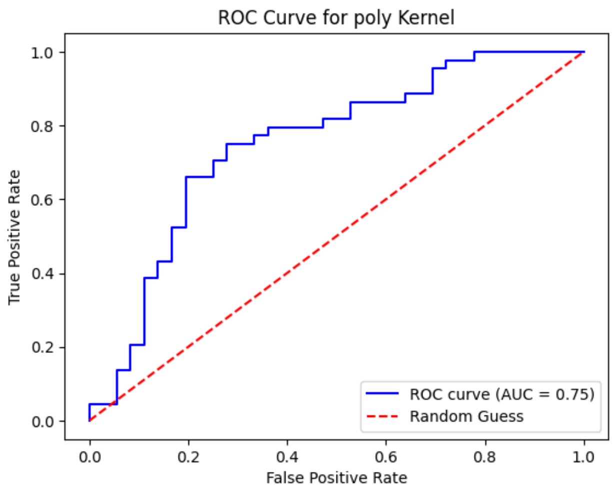

Figure 7. ROC Curve of poly kernel

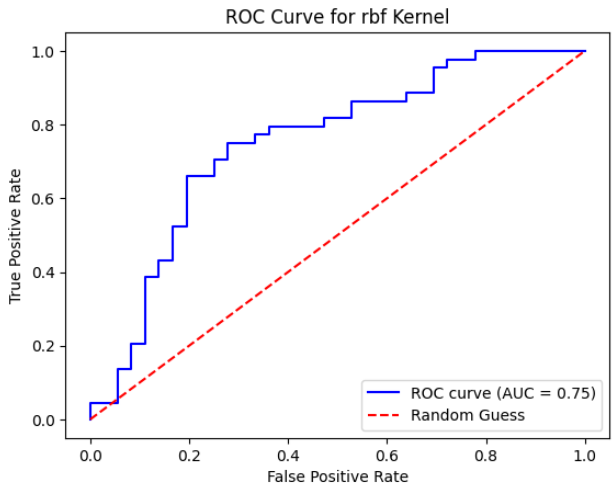

Figure 8. ROC Curve for RBF kernel

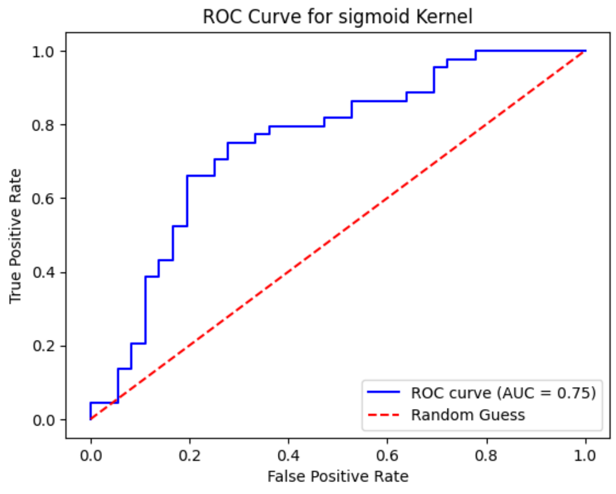

Figure 9. ROC Curve for Sigmoid kernel

5. CONCLUSION AND FUTURE WORKS

In conclusion, this study evaluates the effectiveness of parameter tuning for SVM classifiers applied to a voice pathology database, with a focus on the impact of different kernels which are linear, polynomial, radial basis function (RBF) and sigmoid and their corresponding parameters C and γ. Among the four kernels, the linear kernels consistently outperformed the others, achieving the highest accuracy of 0.64 across various parameter combinations. The polynomial and RBF kernels exhibited moderate performance, with the RBF kernel performing slightly better at specific parameter settings, though both kernels required more precise tuning to achieve optimal results. The sigmoid kernel proved ineffective for this dataset, consistently showing the lowest accuracy. Based on the findings, the linear kernel with $C = 0.1$ emerges as the most effective choice for voice pathology classification using SVM. This demonstrates the significance of selecting the right kernel and parameters to maximize the performance of machine learning models on medical datasets.

In enhancing the findings of this study, further tuning of the polynomial and RBF kernels could be conducted by expanding the range of C and γ values or employing advanced optimization techniques like Bayesian optimization or genetic algorithms. Additionally, the inclusion of other SVM kernels or hybrid models, such as combining SVM with deep learning approaches, may offer improved additional features or using dimensionality reduction techniques like Principal Component Analysis (PCA) to improve model performance. Lastly cross-validation techniques could be applied to ensure the generalizability of the results across different subsets of the dataset, providing a more robust assessment of the model's real-world applicability.

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