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Identifying Key Features for Machine Learning Classification of COPD and Asthma Cough

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Abstract—**Chronic Obstructive Pulmonary Disease (COPD) and asthma remain diagnostically challenging in resource-constrained environments. Cough is a primary symptom of both COPD and asthma and is used to distinguish between these conditions. This paper identifies the cough sounds' key acoustic features that enhance the performance of the machine learning-based classification of COPD, asthma, and normal conditions. Forty-nine temporal, spectral, and cepstral features are derived from annotated cough sounds, and Analysis of Variance, Mutual Information, Kendall's Tau, ReliefF, Pearson's Correlation, and Gradient Boosting Machines (GBM) feature selection techniques are applied. The selected features are grouped into prioritized subsets of 10, 15, 25, 35, and all 49 features and the classification efficiency is evaluated using Convolutional Neural Networks, Transformers, and GBM models through cross-validation. The GBM model achieved optimal performance with 91.6% accuracy, 91.74% sensitivity, 95.64% specificity, and 91.71% F1-score using the top 25 features and attained 86.41% accuracy, 87.02% sensitivity, 93.07% specificity, and 86.59% F1-score using 19 overlapping features derived from all considered feature selection methods. The results emphasize that feature grouping significantly improves classification over single-feature approaches, offering a scalable solution for automated respiratory disease diagnosis.**

Index Terms—**Respiratory diseases, Cough sounds, Gradient Boosting Machines, Transformers, Convolutional Neural Networks, Machine Learning, Deep Learning.**

I. INTRODUCTION

CHRONIC Obstructive Pulmonary Disease (COPD) and asthma are among the most prevalent chronic respiratory disorders globally, affecting over 300 million [1] and 262 million [2] people, respectively, with significant morbidity and healthcare burdens. Despite overlapping symptoms like coughing, wheezing, and dyspnea, accurate differentiation is critical for tailored treatment [3], as misdiagnosis rates exceed 30% in primary care settings [4]. Traditional diagnostic tools such as spirometry [5], bronchoprovocation tests, and clinical assessments are often time-consuming, costly, and inaccessible in low-resource regions, highlighting the need for non-invasive, scalable alternatives [6]. Recent advances in machine learning (ML) and acoustic analytics have demonstrated the potential of cough sound analysis as a diagnostic tool [7]. Cough acoustics encode discriminative features reflecting airway obstruction, inflammation, and mucus retention, which differ between COPD and asthma [8]. For instance, time-frequency features like Mel-Frequency Cepstral Coefficients (MFCCs) [9] and non-linear dynamics have been shown to capture disease-specific patterns [10]. However, the efficacy of ML models hinges on optimal feature selection [11], as irrelevant or redundant features can degrade performance [12].

Previous research examined varied sets of features such as time-domain (eg., peak amplitude, zero-crossing rate) [13], frequency-domain (e.g., spectral centroid, harmonic-to-noise ratio) [14] and cepstral features [15]. However, there's no agreement on the discriminative features of COPD and asthma, in part because of inter-patient heterogeneity and environmental noise [16]. The public cough datasets (e.g., Hyfe and COUGHVID) [17] tend to be class imbalanced with a predominance of healthy controls. Methods such as synthetic minority oversampling technique or generative adversarial network-based augmentation are needed to counteract bias [18]. Most studies employ single-center, small datasets with low external validity [19]. However, standardized COPD and asthma cough sounds are not available.

While numerous studies have explored cough sound classification, many rely on hand-crafted or generalized feature sets that may overlook the nuanced acoustic characteristics inherent to different respiratory conditions [20]–[23]. These approaches often fail to account for the subtle temporal and spectral variations that distinguish diseases such as COPD and asthma from normal respiratory conditions [24]. As a result, there is a risk of misclassification and reduced model reliability, especially in real-world, heterogeneous data environments [25]. To bridge this gap, the present research identifies key acoustic features of cough sounds that capture pathophysiological differences among COPD, asthma, and healthy conditions, and evaluates Convolutional Neural Networks (CNNs), transformers, and Gradient Boosting Machines (GBM) to build a robust, interpretable framework for accurate, non-invasive and cost-effective cough sound classification in diverse healthcare sceneries.

The structure of this paper is as follows: Section I provides an overview of the research, including relevant background and a review of related literature. Section II outlines the methodology, dataset, extracting and selecting features, and applying both machine learning and deep learning models to distinguish between COPD and asthma coughs. Section III presents the evaluation outcomes, examining the effectiveness of different feature selection methods, analyzing feature significance through model performance, and identifying the most dominant features shared across techniques. Finally, Section IV summarizes the key findings and conclusions of the experimentations.

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II. MATERIALS AND METHODS

Fig. 1 presents the framework for classifying COPD, asthma, and normal/healthy cough sounds using ML algorithms. Cough recordings are collected from COPD, asthma, and healthy subjects and extracted 49 temporal, spectral, and cepstral features [26]. Feature selection prioritized subsets (49, 35, 25, 15, 10 features) for evaluation. Models are trained and tested across all feature combinations, with performance assessed via mean accuracy, sensitivity, specificity, and F1-score. The analysis identifies optimal feature groups and impactful shared features for respiratory classification.

A. Dataset

The absence of standardized cough sound databases requires curated datasets for reliable analysis. This research work collected 2142 cough recordings, including 629 COPD, 897 asthma, and 616 healthy samples, from participants aged 18 to 64 in a controlled environment using a Zoom H5 recorder at 44.1 kHz. The recordings, ranging from 380 to 970 milliseconds, are captured at distances ranging from 30 cm and 60 cm and stored in uncompressed WAV format.

B. Feature Extraction

Effective cough sound analysis for respiratory disease diagnosis relies on robust feature extraction techniques. This research employs 49 distinct features from temporal, spectral, and cepstral domains, extracted using a 50% overlapping frame approach to ensure signal integrity. Key spectral features include centroid (with minimum, maximum, mean, 25th percentile, median, 75th percentile, and standard deviation), roll-off (25th percentile), flatness (maximum and mean), flux (25th percentile), and bandwidth (median) [27]–[30]. Time-domain analysis incorporates zero-crossing rate (maximum and 75th percentile) and mean energy [20], [27]. Frequency characteristics are captured through the mean of formant frequencies (F1, F2, and F3) and fundamental frequency statistics (mean, median, and standard deviation) [31]–[33]. Sound eminence is assessed via jitter (local and RAP) and shimmer (local), while cepstral analysis utilizes MFCC0 to MFCC12 and Linear Prediction Coefficients(LPCs) LPC1 to LPC12 coefficients [34], [35]. This comprehensive feature set enables precise characterization of cough acoustics for diagnostic modeling.

C. Feature Selection techniques

The cough sound dataset consists of continuous numerical features capturing frequency patterns, energy distribution, and temporal variations, which serve as inputs for ML models, while the target variable is categorical indicating COPD, asthma, or normal cough forming a supervised classification problem. This distinction requires appropriate feature selection and classification techniques capable of handling continuous numerical inputs and categorical outputs. Filter-based and embedded methods [36] are well-suited for this task due to their model-agnostic nature and effectiveness. Accordingly, this research employs techniques such as ANOVA F-value, Mutual Information, Kendall's Tau, ReliefF, Pearson's Correlation, and GBM for feature selection [37], ensuring the chosen features enhance the ML model [38] performance by focusing on their relevance and contribution to classification performance [39].

The ANOVA F-value measures whether group means differ significantly by comparing variance between groups to variance within groups, as shown in Eq. 1. A high F-value suggests significant differences, while a low value indicates similarity among group means.

$$F = \frac{\frac{\sum_{i=1}^{k} n_i\left(\bar{X}_i - \bar{x}_{\text{overall}}\right)^2}{k-1}}{\frac{\sum_{i=1}^{k}\sum_{j=1}^{n_i}\left(x_{ij} - \bar{X}_i\right)^2}{N-k}} \tag{1}$$

Where F is the ANOVA F-value, which measures the ratio of variation between group means to the variation within the group, k is the number of groups, n_i is the number of observations in group i, $\bar{X}_i$ is the mean of group i, $\bar{x}_{\text{overall}}$ is the overall mean across all groups and observations, x_{ij} is the value of the j^{th} observation in the i^{th} group, and N is the total number of observations across all groups.

Mutual Information (MI) measures the dependency between features and target labels, capturing both linear and non-linear relationships. Features with higher MI scores share more information with the target, indicating greater relevance. Eq. 2 defines this dependency.

$$I(X;Y) = \sum_{x\in X}\sum_{y\in Y} P(x,y)\log\left(\frac{P(x,y)}{P(x)P(y)}\right) \tag{2}$$

Where $I(X;Y)$ is the MI between X features and Y targets, $P(x,y)$ is the joint probability distribution of X and Y, $P(x)$ and $P(y)$ are the marginal probabilities of X and Y.

Kendall's Tau (τ) measures the strength and direction of a monotonic relationship between variables. Higher absolute values indicate stronger associations, helping rank feature importance. Eq. 3 defines this rank-based correlation.

$$\tau = \frac{C - D}{\frac{1}{2}n(n-1)} \tag{3}$$

Where C is the number of concordant pairs, D is the number of discordant, and n is the total number of data points.

ReliefF Score evaluates feature relevance by comparing them to nearest neighbors, assigning scores based on their ability to distinguish between classes. Features that differentiate well are rewarded, as shown in Eq. 4.

$$W(f) = W(f) - \frac{1}{m}\sum_{i=1}^{m}[A - B] \tag{4}$$

Where,

$$A = \frac{1}{k}\sum_{j=1}^{k}\text{diff}\left(f, \text{instance}_i, \text{nearest\_hit}_j\right) \tag{5}$$

$$B = \frac{1}{k}\sum_{j=1}^{k}\text{diff}\left(f, \text{instance}_i, \text{nearest\_miss}_j\right) \tag{6}$$

$W(f)$ is the weight of feature f, m is the total number of sampled instances, k is the number of nearest neighbors considered for hits and misses, instance_i is a sampled data instance, nearest_hit_j is the j^{th} nearest neighbor of instance_i from the same class, nearest_miss_j is the j^{th} nearest neighbor of instance_i from a different class.

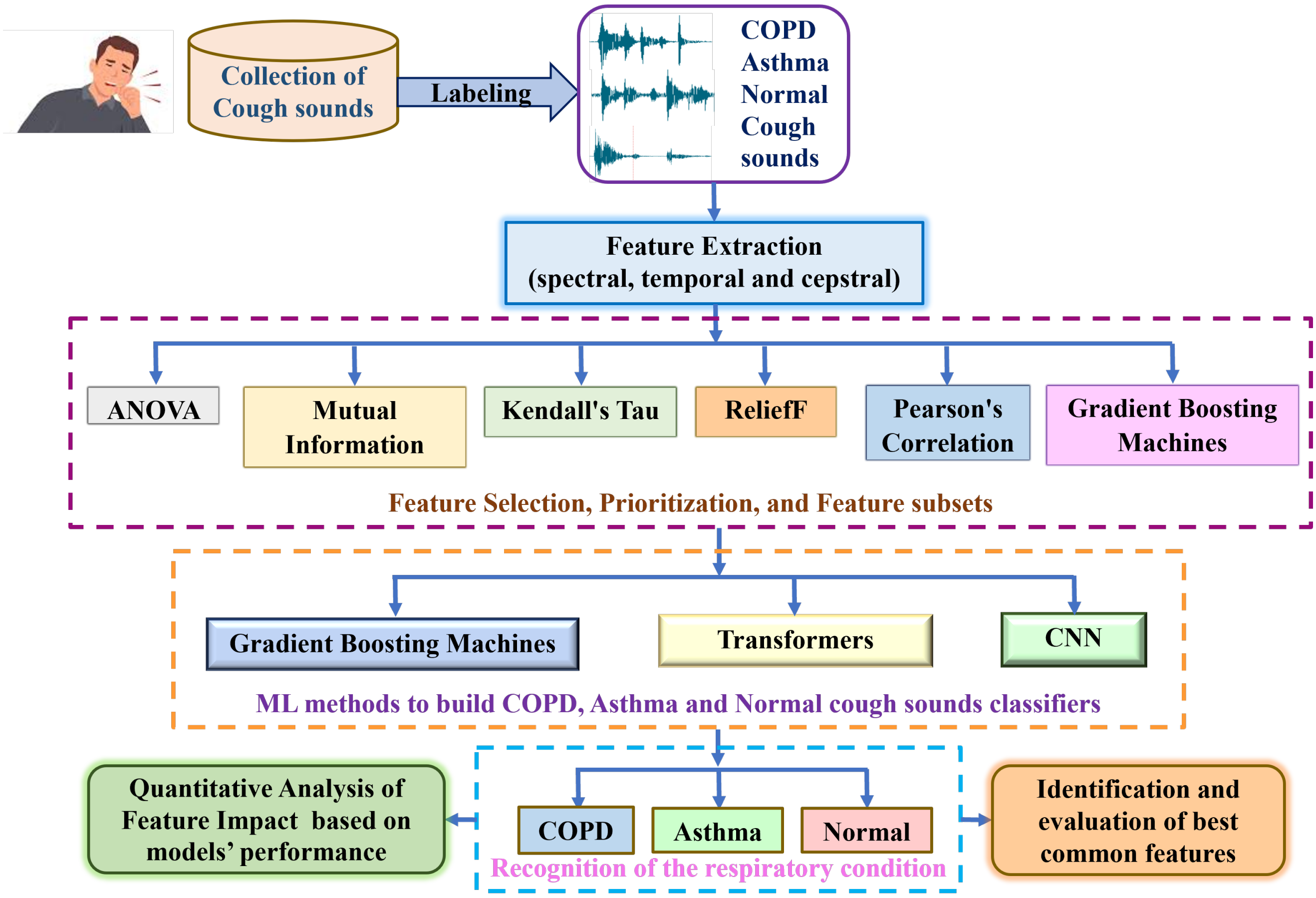

Fig. 1: Methodology for identifying discriminative features and classifying respiratory conditions.

Pearson's correlation coefficient (r) measures the linear relationship between features and the target variable, applicable to both continuous and classification tasks, as shown in Eq. 7.

$$r=\frac{\sum_{i=1}^{n}\left(X_i-\bar{X}\right)\left(Y_i-\bar{Y}\right)}{\sqrt{\sum_{i=1}^{n}\left(X_i-\bar{X}\right)^2}\sqrt{\sum_{i=1}^{n}\left(Y_i-\bar{Y}\right)^2}} \tag{7}$$

Where X_i and Y_i are individual data points, $\bar{X}$ and $\bar{Y}$ are mean values, and n is the number of data points.

GBM calculates feature importance by measuring each feature's contribution to reducing prediction errors, typically through improvements in loss functions during decision tree splits. Features are ranked based on their impact on accuracy, aiding in feature selection. The score of feature importance for a feature X_j, $FI\left(X_j\right)$ can be measured using Eq. 8.

$$FI\left(X_j\right)=\sum_{t=1}^{T}\sum_{s\in\text{ Splits }_t} 1\left(s\text{ uses }X_j\right)\cdot\Delta L(s) \tag{8}$$

Where T is the total number of boosting iterations, Splits_t splits in the t^{th} tree, $1\left(s\text{uses}X_j\right)$ is the indicator function that is 1 if the split s involves feature X_j, otherwise 0, and $\Delta L(s)$ is the reduction in the loss function achieved by split s.

D. Machine and Deep Learning Approaches for Classifying COPD and Asthma from Cough Sounds

A detailed evaluation is performed by grouping features into five ranked sets top 10, 15, 25, 35, and all 49 based on their importance, and testing these sets across various machine and deep learning models, including CNN, transformers, and GBM. Performance is assessed using cross-validated metrics such as mean accuracy, sensitivity, specificity, and F1-score, along with confusion matrices to evaluate classification results. The CNN model architecture includes two 1D convolutional layers with ReLU activation, max-pooling, a dense layer, and a softmax output for multi-class classification. It is trained with the Adam optimizer and categorical cross-entropy for 150 epochs. The Transformer model maps input features to a higher-dimensional space, processes them through self-attention-based encoder layers, and outputs predictions via a final dense layer. It is trained for 200 epochs using Adam and cross-entropy loss. The GBM model uses 100 estimators with a learning rate of 0.1 and a maximum depth of 7; after training, it outputs feature importance scores to identify the most impactful features. The architecture of GBM is demonstrated in Fig. 2.

III. RESULTS AND DISCUSSION

The results present the ranking of feature importance by various selection methods, the utilization of ML models to classify COPD and asthma cough sounds, and the evaluation of how feature significance impacts model performance.

A. Assessment of Feature Influence Under Various Selection Methods

The importance of individual features is assessed using ANOVA F-value, Mutual Information, Kendall's Tau,

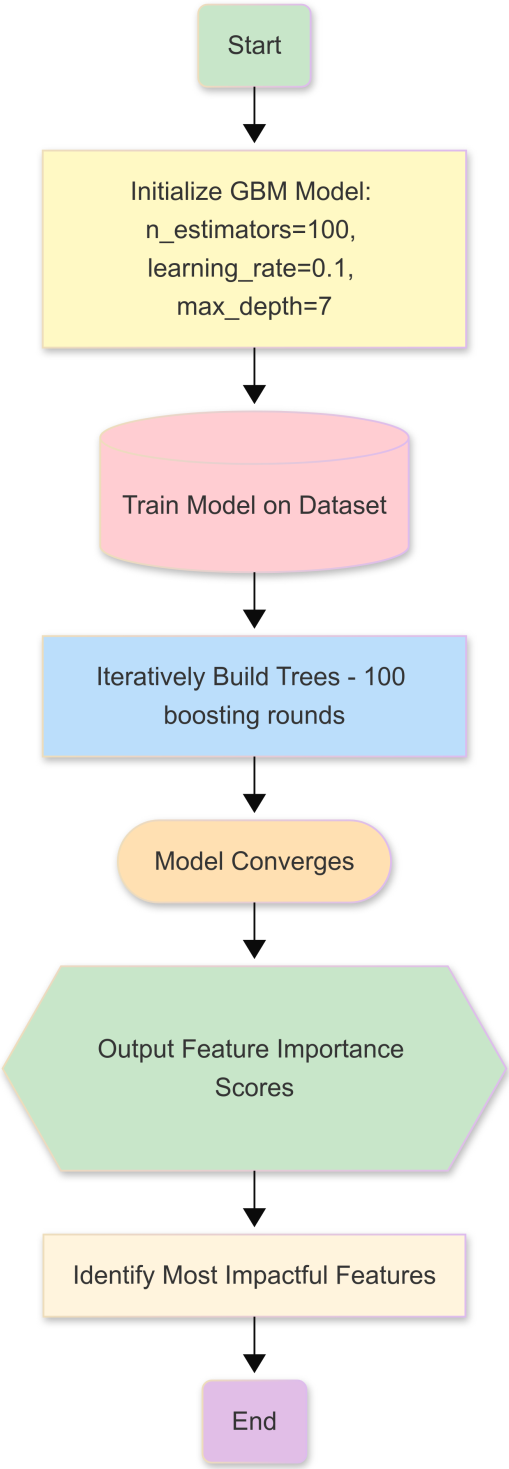

Fig. 2: The architecture of GBM.

ReliefF, Pearson's Correlation, and GBM feature selection techniques. These methods are well-suited for classifying COPD, asthma, and normal cough sounds using continuous numerical features and categorical labels. ANOVA F-value ranks features based on the variance between class means, identifying MFCC1 as most significant and shimmer local as least. Mutual Information evaluates feature-target dependency, highlighting LPC8 as the most important and the median fundamental frequency as the least important. Kendall's Tau assesses ordinal correlation, again ranking LPC8 high and shimmer local low. ReliefF measures a feature's ability to distinguish between similar and dissimilar instances, prioritizing LPC2 and minimizing shimmer local. Pearson's Correlation detects linear associations, ranking LPC11 highest and shimmer local lowest. GBM prioritizes features that most reduce loss across iterations. GBM ranked MFCC1 highest and Jitter (RAP) lowest. Collectively, these methods emphasize the value of integrating multiple features for improved classification of cough sounds. The importance of cough sound features using the GBM method is depicted in Fig. 3.

B. Cough sound classification for COPD, asthma, and normal conditions

The classification of COPD, asthma, and normal cough sounds is performed using machine and deep learning models, including CNN, transformer, and GBM. To evaluate the impact of feature prioritization on model performance, features are grouped into five sets containing the top 10, 15, 25, 35, and 49 features. Each model is trained and tested using 5-fold cross-validation and evaluated using mean accuracy, sensitivity, specificity, and F1-score. Among all models and feature combinations, GBM consistently outperformed others, with the best results achieved using the top 25 features yielding a mean accuracy of 91.6%, sensitivity of 91.74%, specificity of 95.64%, and an F1-score of 91.71%. These findings emphasize the significance of targeted feature selection in enhancing model efficiency and diagnostic accuracy. The top 25 features identified using the GBM method include MFCC1, LPC4, MFCC9, LPC8, MFCC3, MFCC7, MFCC2, MFCC0, 25th percentile of spectral flux, MFCC8, mean energy, MFCC5, median of spectral bandwidth, MFCC10, LPC6, MFCC12, MFCC11, MFCC4, standard deviation in spectral centroid, LPC5, mean of first formant frequencies, mean of spectral flatness, 25th percentile of spectral centroid, LPC12, and mean of third formant frequencies.

The outcome of the analysis is tabulated in Table I to Table V, which gives the benchmarking CNN, transformers, and GBM on the top 10, 15, 25, 35, and 49 features for cough sound classification. Fig. 4 to Fig. 8 present the investigation of ML models using the top 10, 15, 25, 35, and 49 prioritized features, and the importance of the efficacy of different feature groups.

C. Quantification of feature importance driven by model performance

The quantification measures how feature subsets influence model performance by testing various feature-ML algorithm combinations. Key metrics including accuracy, sensitivity, specificity, and F1-score are recorded for each scenario. Comparisons are made between using all 49 features and smaller subsets. GBM shows the most significant improvement, performing best with 25 selected features.

Tables VI, VIII, X, and XII analyze variations in mean accuracy, sensitivity, specificity, and F1-score for models built using prioritized feature subsets comprising the top 35, 25, 15, and 10 features. Correspondingly, Fig. 9, 11, 13, and 15 present the trends in mean accuracy, sensitivity, specificity, and F1-score across models using these prioritized feature subsets. Tables VII, IX, XI, and XIII summarize the differences in mean accuracy, sensitivity, specificity, and

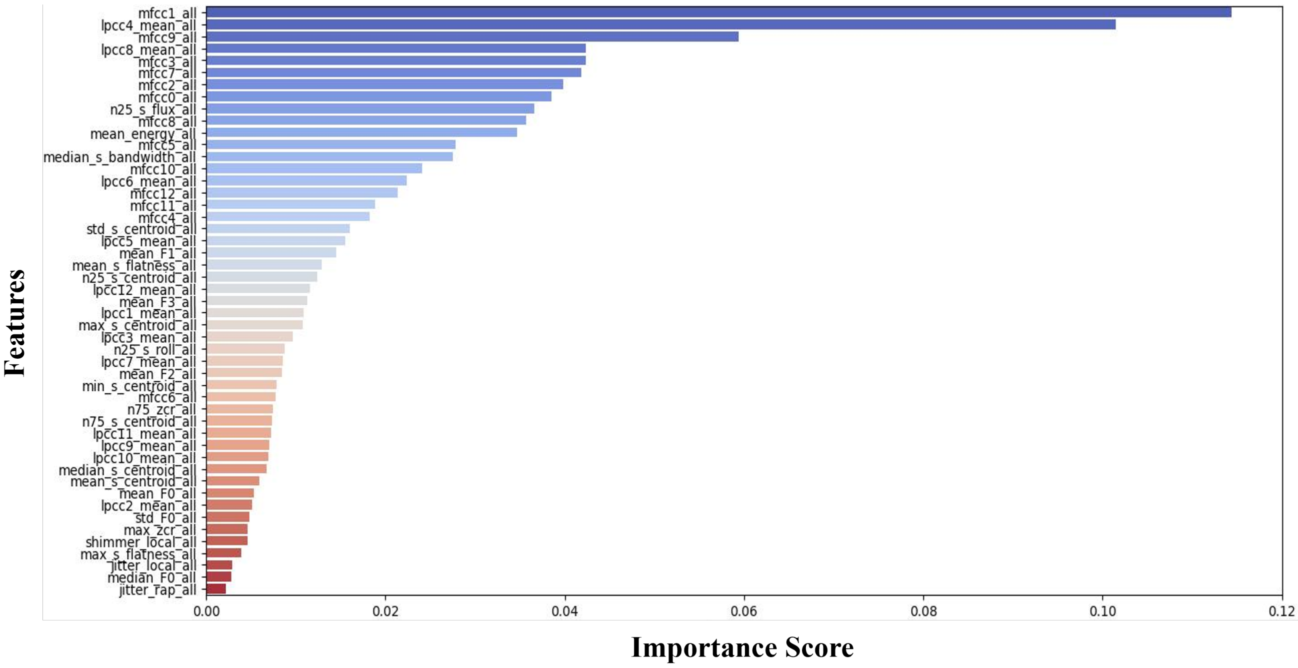

Fig. 3: Importance of cough sound features using the GBM method.

TABLE I: Benchmarking CNN, transformers, and GBM on top 10 features for cough sound classification

Feature Selection Method – **ML Technique**	**Mean Accuracy (%)**	**Mean Sensitivity (%)**	**Mean Specificity (%)**	**Mean F1-Score (%)**
ANOVA – CNN	72.78	72.69	85.83	72.8
ANOVA - Transformers	70.17	71.09	84.69	70.56
MI – CNN	70.31	71.12	84.75	70.23
MI – Transformers	71.01	72.26	85.25	71.4
Kendall's – CNN	70.03	70.32	84.33	70.04
Kendall's - Transformers	68.39	69.6	83.87	68.89
ReliefF – CNN	78.48	79.05	88.97	78.75
ReliefF - Transformers	77.17	77.78	88.29	77.46
Pearson's – CNN	72.22	73.53	85.96	72.32
Pearson's - Transformers	68.58	70.39	84.21	68.88
GBM	86.6	86.91	93.08	86.76

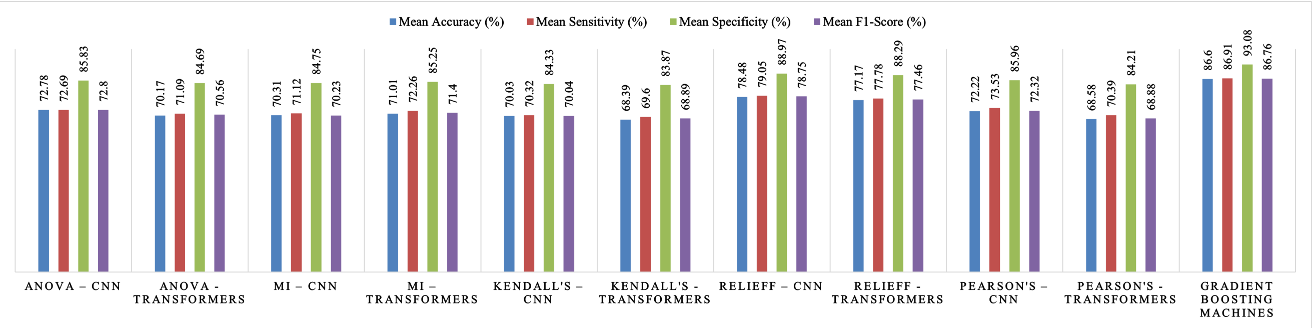

Fig. 4: Analyzing ML model performance using the top 10 prioritized features

F1 score for models built with 49 features compared to prioritized subsets containing 35, 25, 15, and 10 features. Fig. 10, 12, 14, and 16 demonstrate the trends in differences in mean accuracy, sensitivity, specificity, and F1 score for models using 49 features compared to prioritized subsets with 35, 25, 15, and 10 features.

As the feature count decreases from 49 to 35, mean accuracy drops by 0.94% to 3.64% across most feature-ML model combinations, except GBM, which improves slightly by 0.33%. This pattern persists at 25 features, where accuracy declines ranging from 1.08% to 13.92%, while GBM continues to improve by 0.61%. The disparity grows more evident with smaller feature sets: accuracy falls by 1.17% to 18.35% at 15 features and by 4.39% to 22.55% at 10 features, underscoring the strong influence of feature selection on model performance.

When decreasing from 49 to 35 features, mean sensitivity drops between 0.73% and 3.52% across most models, while GBM shows a slight improvement of 0.32%. At 25 features, the decline becomes more noticeable, ranging from 1.27%

TABLE II: Benchmarking CNN, transformers, and GBM on top 15 features for cough sound classification

Feature Selection Method – **ML Technique**	**Mean Accuracy (%)**	**Mean Sensitivity (%)**	**Mean Specificity (%)**	**Mean F1-Score (%)**
ANOVA – CNN	77.5	78.5	88.63	77.61
ANOVA - Transformers	75.07	75.92	87.21	75.38
MI – CNN	75.54	76.46	87.49	75.55
MI – Transformers	75.49	76.14	87.43	75.8
Kendall’s – CNN	75.49	76.72	87.57	75.73
Kendall’s - Transformers	74.46	75.34	86.95	74.8
ReliefF – CNN	83.1	83.6	91.28	83.16
ReliefF – Transformers	84.27	85	91.98	84.43
Pearson’s – CNN	76.89	77.24	88.08	76.79
Pearson’s - Transformers	74.7	75.41	87.04	74.93
GBM	89.82	89.94	94.69	89.95

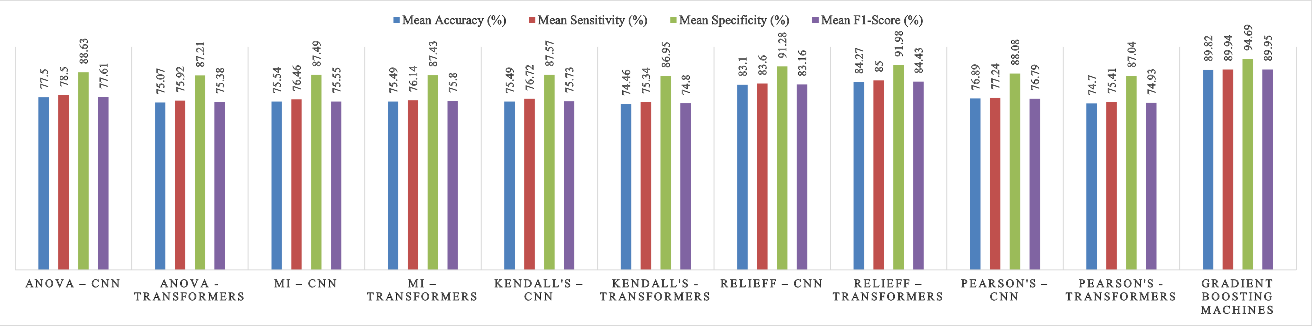

Fig. 5: Analyzing ML model performance using the top 15 prioritized features

TABLE III: Benchmarking CNN, transformers, and GBM on top 25 features for cough sound classification

Feature Selection Method – **ML Technique**	**Mean Accuracy (%)**	**Mean Sensitivity (%)**	**Mean Specificity (%)**	**Mean F1-Score (%)**
ANOVA – CNN	80.63	81.46	90.09	80.8
ANOVA - Transformers	82.35	83.51	91.13	82.58
MI – CNN	82.54	83.42	91.1	82.71
MI – Transformers	84.87	85.56	92.31	85.04
Kendall’s – CNN	81.84	82.33	90.64	81.93
Kendall’s - Transformers	83.38	84.14	91.57	83.55
ReliefF – CNN	87.3	87.77	93.49	87.41
ReliefF – Transformers	87.63	88.05	93.68	87.73
Pearson’s – CNN	79.79	81.09	89.8	79.99
Pearson’s - Transformers	81.89	83.11	90.9	82.12
GBM	91.6	91.74	95.64	91.71

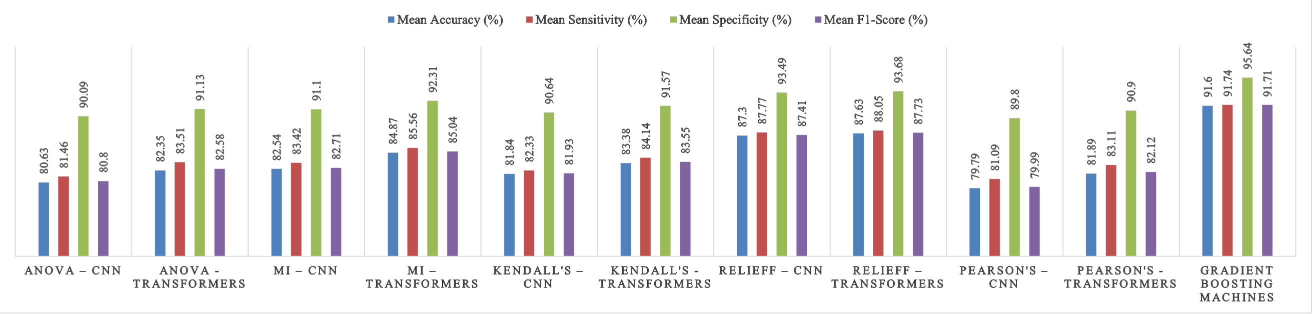

Fig. 6: Analyzing ML model performance using the top 25 prioritized features

to 13.65%, with GBM improving by 0.58%. The downward trend continues as sensitivity decreases between 1.12% and 18.11% at 15 features and between 4.25% and 21.59% at 10 features.

Between 49 and 35 features, mean specificity drops by 0.49% to 1.84% across models, while GBM slightly improves by 0.15%. At 25 features, specificity falls by 0.61% to 7.14%, with GBM showing a modest gain of 0.3%. The decline continues at 15 features, ranging from 0.65% to 9.51%, and becomes more pronounced at 10 features, with drops between 2.26% and 11.47%.

From 49 to 35 features, mean F1-scores decrease by 0.9% to 3.61% across models, while GBM improves slightly by 0.34%. At 25 features, the decline ranges from 1.15 to 13.74%, though GBM continues to improve with a 0.61% gain. The drop becomes steeper at 15 features, with F1 scores falling between 1.15% and 18.04%, and is most pronounced at 10 features, where the decrease is between 4.34% and

TABLE IV: Benchmarking CNN, transformers, and GBM on top 35 features for cough sound classification

Feature Selection Method – **ML Technique**	**Mean Accuracy (%)**	**Mean Sensitivity (%)**	**Mean Specificity (%)**	**Mean F1-Score (%)**
ANOVA – CNN	89.73	90.17	94.74	89.85
ANOVA - Transformers	88.61	89.37	94.24	88.87
MI – CNN	88.33	88.7	94	88.44
MI – Transformers	88.56	88.87	94.11	88.66
Kendall's – CNN	88.98	89.34	94.32	89.06
Kendall's - Transformers	88.47	89.11	94.14	88.7
ReliefF – CNN	90.05	90.52	94.96	90.08
ReliefF - Transformers	89.31	89.72	94.54	89.45
Pearson's – CNN	88.65	89.2	94.22	88.73
Pearson's - Transformers	87.67	88.17	93.67	87.87
GBM	91.32	91.48	95.49	91.44

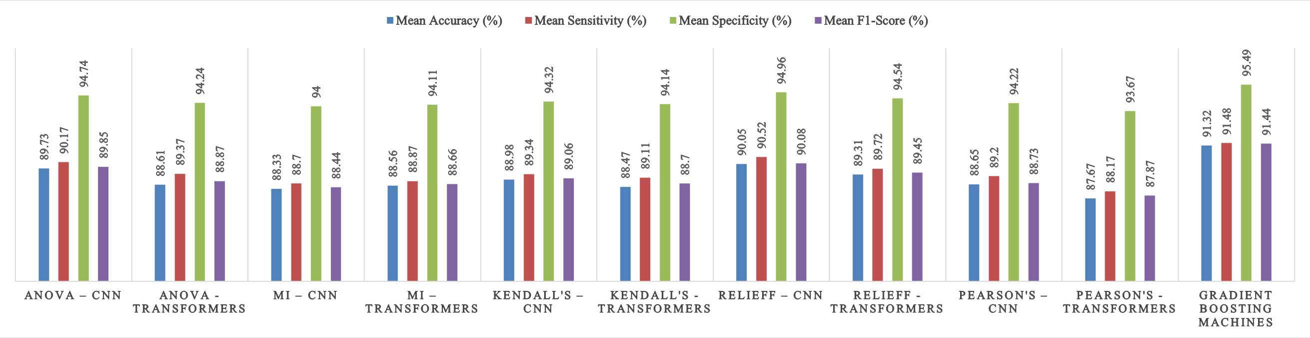

Fig. 7: Analyzing ML model performance using the top 35 prioritized features

TABLE V: Benchmarking CNN, transformers, and GBM on top 49 features for cough sound classification

Feature Selection Method – **ML Technique**	**Mean Accuracy (%)**	**Mean Sensitivity (%)**	**Mean Specificity (%)**	**Mean F1-Score (%)**
CNN	91.18	91.25	95.48	91.12
Transformers	90.94	91.19	95.34	91.03
GBM	90.99	91.16	95.34	91.1

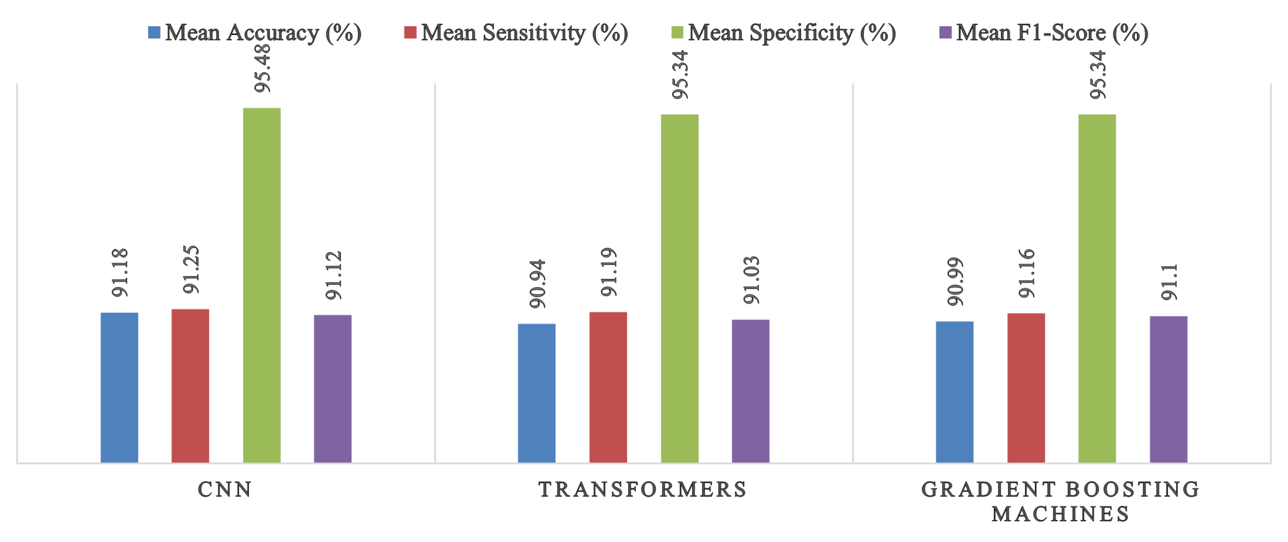

Fig. 8: Analyzing ML model performance using the top 49 prioritized features

22.14%.

D. Detection and assessment of top prioritized overlapping features

The analysis identified 19 key overlapping features among the top 35 priority features across all evaluated feature selection methods. These overlapping features include LPC1, 25th percentile of spectral flux, mean of third formant frequencies, LPC6, MFCC2, MFCC7, maximum spectral centroid, MFCC3, LPC8, LPC3, LPC4, MFCC4, LPC7, standard deviation of spectral centroid, 75th percentile of spectral centroid, mean of spectral flatness, LPC5, LPC12, and median of spectral bandwidth. The classification of cough sounds based on machine learning models CNN, transformers, and

TABLE VI: Evaluating mean accuracy variations across prioritized feature subsets.

Feature Selection – ML/DL	**mean accuracy (%) using 35 Prioritized Features**	**mean accuracy (%) using 25 Prioritized Features**	**mean accuracy (%) using 15 Prioritized Features**	**mean accuracy (%) using 10 Prioritized Features**
ANOVA – CNN	89.73	80.63	77.5	72.78
ANOVA – Transformers	88.61	82.35	77.56	70.17
MI – CNN	88.33	82.54	75.54	70.31
MI – Transformers	88.56	81.64	75.47	71.01
Kendall's – CNN	88.98	81.84	75.49	71.17
Kendall's – Transformers	88.91	82.43	78.37	68.39
ReliefF – CNN	90.05	83.43	81.27	75.81
ReliefF – Transformers	89.5	83.48	84.47	77.72
Pearson's – CNN	88.65	79.79	76.89	69.88
Pearson's – Transformers	88.58	82.37	83.97	68.32
GBM	**91.32**	**91.6**	**89.82**	**86.6**

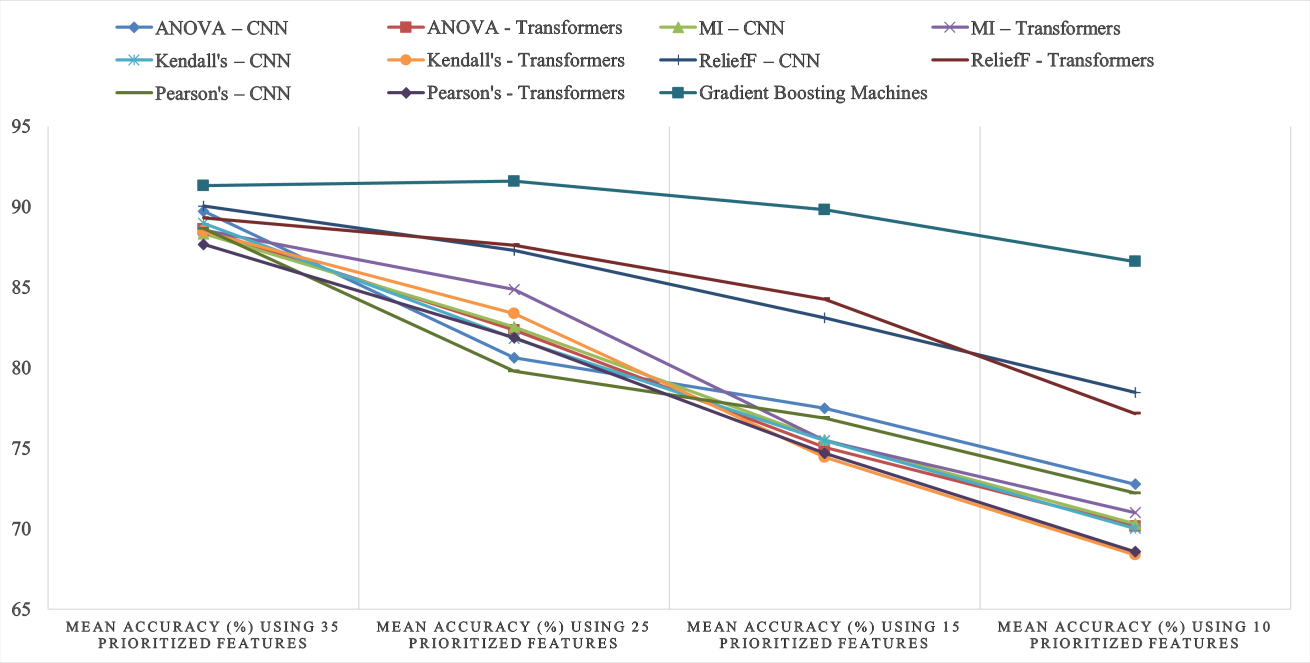

Fig. 9: Assessment of mean accuracy trends across models using prioritized feature subsets

TABLE VII: Analysis of mean accuracy differences in models built with selected feature subsets

Feature Selection – ML/DL	**mean accuracy (%) difference (%) using 35 Prioritized Features**	**mean accuracy (%) difference (%) using 25 Prioritized Features**	**mean accuracy (%) difference (%) using 15 Prioritized Features**	**mean accuracy (%) difference (%) using 10 Prioritized Features**
ANOVA - CNN	1.45	10.55	13.68	18.4
ANOVA - Transformers	2.33	8.59	15.87	20.77
MI - CNN	2.85	9.87	13.95	18.93
MI - Transformers	2.38	9.07	14.16	19.13
Kendall's - CNN	2.2	9.17	14.33	21.55
Kendall's - Transformers	2.47	9.56	16.08	21.5
ReliefF - CNN	1.6	3.4	8.18	12.76
ReliefF - Transformers	1.63	3.31	6.97	11.27
Pearson's - CNN	2.25	8.43	11.6	18.96
Pearson's - Transformers	3.27	9.06	16.24	22.36
GBM	-0.33	-0.61	1.17	4.39

GBM are developed using this optimized 19-feature set and evaluated through 5-fold cross-validation. Among these, the GBM model demonstrated the best performance, achieving a mean accuracy of 86.41%, sensitivity of 87.02%, specificity of 93.07%, and an F1-score of 86.59%, outperforming the other models across all evaluation metrics. The results are summarized in Table XIV and demonstrated in Fig. 17.

The GBM-based cough sound classification model demonstrated substantial performance gains using its optimized set of 25 selected features, achieving impressive metrics across all evaluation criteria. It attained a mean accuracy of 91.6%, a mean sensitivity of 91.74%, a mean specificity of 95.64%, and a mean F1-score of 91.71%. These results represent a significant improvement over previous configurations, highlighting the effectiveness of the feature selection approach. When the GBM applied their feature selection techniques and utilized their top 25 selected features, they achieved significantly improved performance metrics. For GBM, the mean accuracy reaches 91.6%, the mean sensitivity is 91.74%, the mean specificity is 95.64%, and the mean F1-

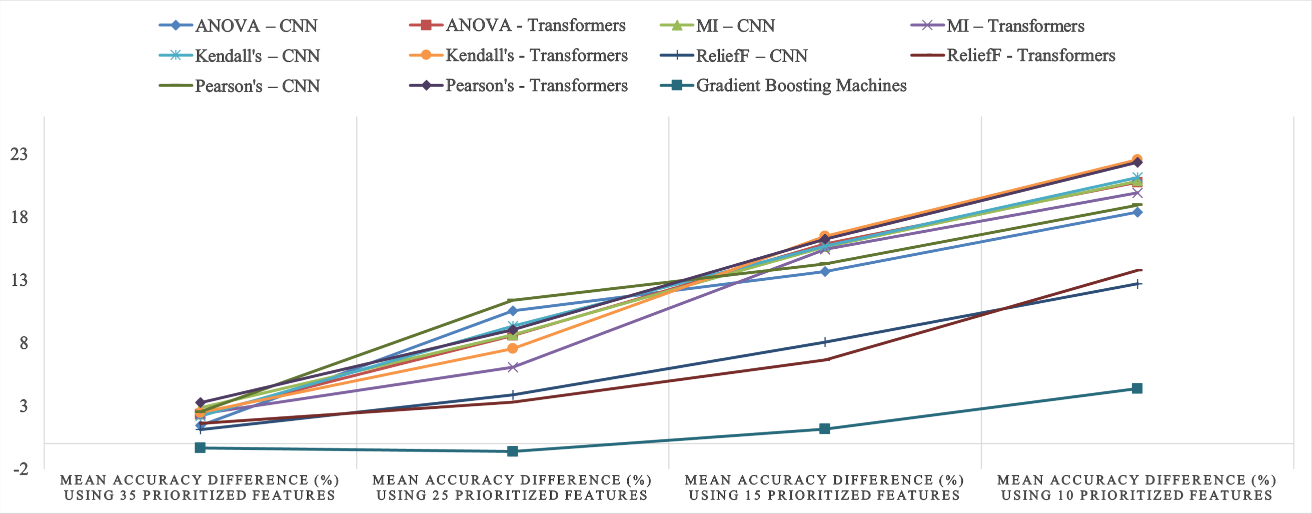

Fig. 10: Trends of mean accuracy difference in models using prioritized feature subsets.

TABLE VIII: Evaluating mean sensitivity variations across prioritized feature subsets.

Feature Selection – ML/DL	mean sensitivity(%) using 35 Prioritized Features	mean sensitivity(%) using 25 Prioritized Features	mean sensitivity(%) using 15 Prioritized Features	mean sensitivity(%) using 10 Prioritized Features
ANOVA – CNN	90.17	81.46	78.5	72.69
ANOVA – Transformers	89.37	83.51	75.92	71.09
MI – CNN	88.7	83.42	76.46	71.12
MI – Transformers	88.87	85.56	76.14	72.26
Kendall’s – CNN	89.34	82.33	76.72	70.32
Kendall’s – Transformers	89.11	84.14	75.34	69.6
ReliefF – CNN	90.52	87.77	83.6	79.05
ReliefF – Transformers	89.72	88.05	85	77.78
Pearson’s – CNN	89.2	81.09	77.24	73.53
Pearson’s – Transformers	88.17	83.11	75.41	70.39
GBM	**91.48**	**91.74**	**89.94**	**86.91**

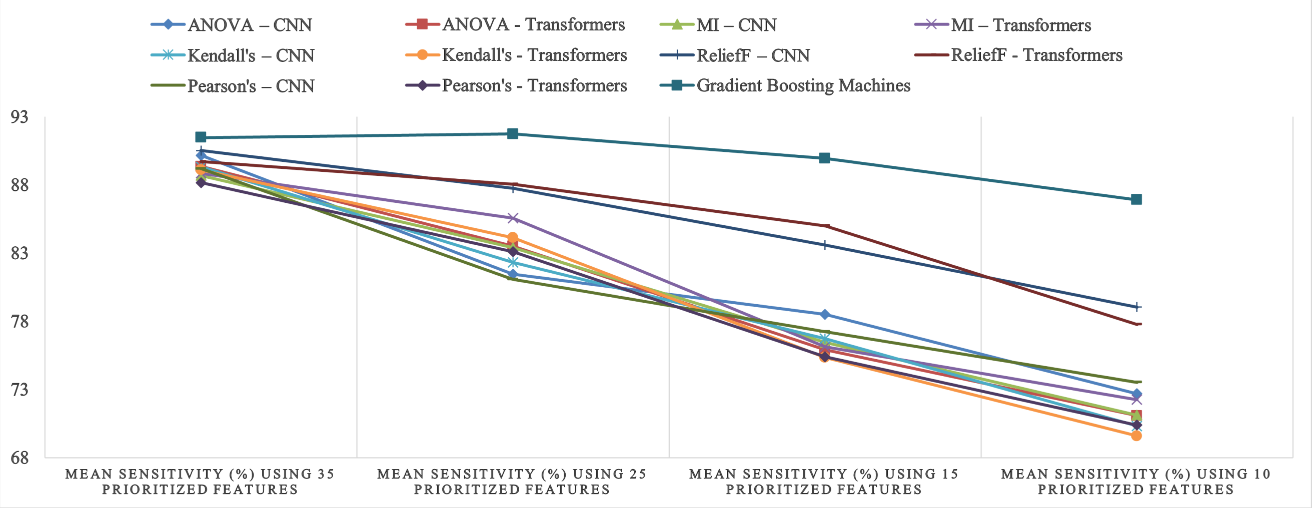

Fig. 11: Assessment of mean sensitivity trends across models using prioritized feature subsets.

score achieves 91.71%. Table XV and Fig. 18 presents the performance comparison of models built with 19 common features identified by all feature selection methods and the top 25 features from GBM.

E. Comprehensive results and evaluations

The identification of significant features and classification of COPD, asthma, and normal cough sounds is thoroughly evaluated using CNN, Transformer, and GBM models with five-fold cross-validation. Features are grouped into sets of 10, 15, 25, 35, and all 49, and each model’s performance is assessed using mean accuracy, sensitivity, specificity, and F1-score. Among the models, GBM consistently outperformed the others, achieving its best results with the top 25 features, where it reached a mean accuracy of 91.6%, a sensitivity of 91.74%, a specificity of 95.64%, and an F1-score of 91.71%. While CNN and Transformer models showed performance degradation as the number of features decreased, GBM exhibited improvements, indicating its robustness to feature reduction. Even with only 19 overlapping features selected

TABLE IX: Analysis of mean sensitivity differences in models built with selected feature subsets

Feature Selection – ML/DL	**mean sensitivity(%) difference (%) using 35 Prioritized Features**	**mean sensitivity(%) difference (%) using 25 Prioritized Features**	**mean sensitivity(%) difference (%) using 15 Prioritized Features**	**mean sensitivity(%) difference (%) using 10 Prioritized Features**
ANOVA – CNN	1.08	9.79	12.75	18.56
ANOVA - Transformers	1.82	7.68	15.27	20.1
MI – CNN	2.55	7.83	14.79	20.13
MI – Transformers	2.32	5.63	15.05	18.93
Kendall’s – CNN	1.91	8.92	14.53	20.93
Kendall’s - Transformers	2.08	7.05	15.85	21.59
ReliefF – CNN	0.73	3.48	7.65	12.2
ReliefF - Transformers	1.47	3.14	6.19	13.41
Pearson’s – CNN	2.05	10.16	14.01	17.72
Pearson’s - Transformers	3.02	8.08	15.78	20.8
GBM	-0.32	-0.58	1.22	4.25

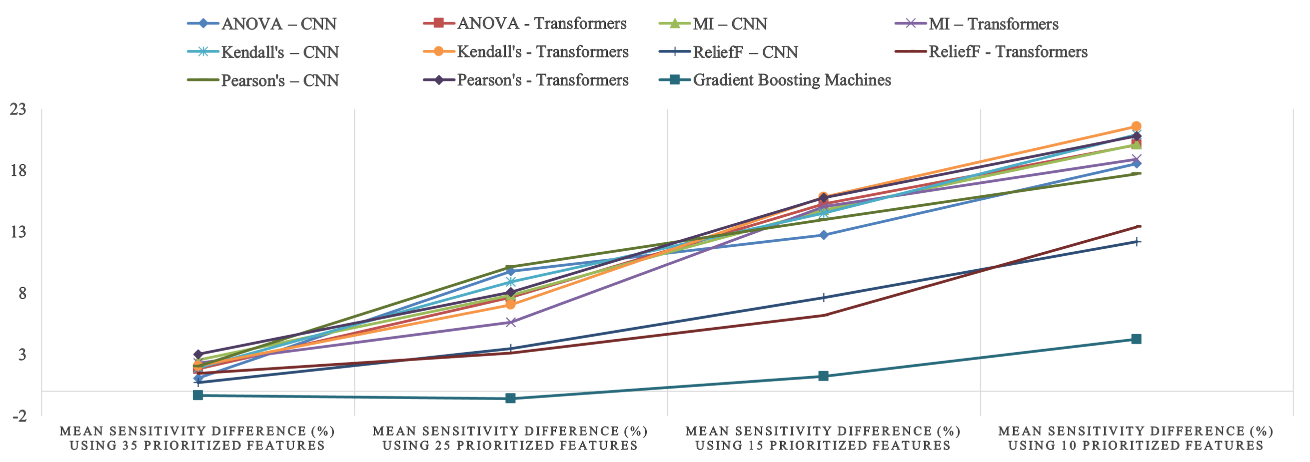

Fig. 12: Trends of mean sensitivity difference in models using prioritized feature subsets.

TABLE X: Evaluating mean specificity variations across prioritized feature subsets.

Feature Selection – ML/DL	**mean specificity(%) using 35 Prioritized Features**	**mean specificity(%) using 25 Prioritized Features**	**mean specificity(%) using 15 Prioritized Features**	**mean specificity(%) using 10 Prioritized Features**
ANOVA – CNN	94.74	90.09	88.63	85.83
ANOVA - Transformers	94.24	91.13	87.21	84.69
MI – CNN	94	91.1	87.49	84.75
MI – Transformers	94.11	92.31	87.43	85.25
Kendall’s – CNN	94.32	90.64	87.57	84.33
Kendall’s - Transformers	94.14	91.57	86.95	83.87
ReliefF – CNN	94.96	93.49	91.28	88.97
ReliefF - Transformers	94.54	93.68	91.98	88.29
Pearson’s – CNN	94.22	89.8	88.08	85.96
Pearson’s - Transformers	93.67	90.9	87.04	84.21
GBM	95.49	95.64	94.69	93.08

TABLE XI: Analysis of mean specificity differences in models built with selected feature subsets

Feature Selection – ML/DL	**mean specificity(%) difference (%) using 35 Prioritized Features**	**mean specificity(%) difference (%) using 25 Prioritized Features**	**mean specificity(%) difference (%) using 15 Prioritized Features**	**mean specificity(%) difference (%) using 10 Prioritized Features**
ANOVA – CNN	0.74	5.39	6.85	9.65
ANOVA - Transformers	1.1	4.21	8.13	10.65
MI – CNN	1.48	4.38	7.99	10.73
MI – Transformers	1.23	3.03	7.91	10.09
Kendall’s – CNN	1.16	4.84	7.91	11.15
Kendall’s - Transformers	1.2	3.77	8.39	11.47
ReliefF – CNN	0.52	1.99	4.2	6.51
ReliefF - Transformers	0.8	1.66	3.36	7.05
Pearson’s – CNN	1.26	5.68	7.4	9.52
Pearson’s - Transformers	1.67	4.44	8.3	11.13
GBM	-0.15	-0.3	0.65	2.26

across all feature selection techniques, GBM maintained high performance, achieving 86.41% mean accuracy and an F1-score of 86.59%. These results highlight the effectiveness of prioritized feature selection in improving diagnostic accuracy

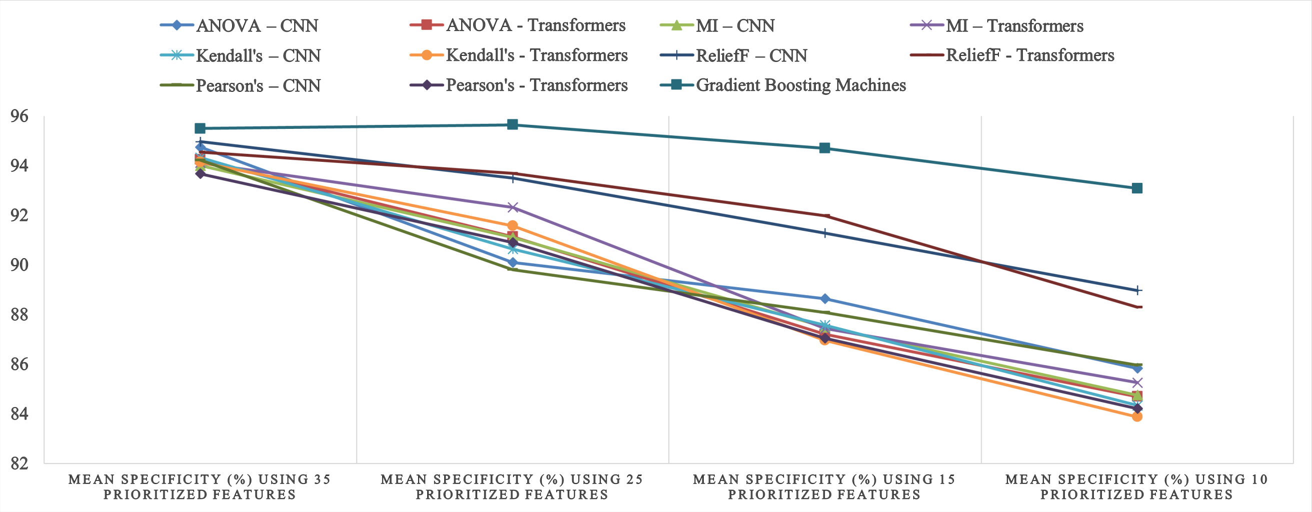

Fig. 13: Assessment of mean specificity trends across models using prioritized feature subsets.

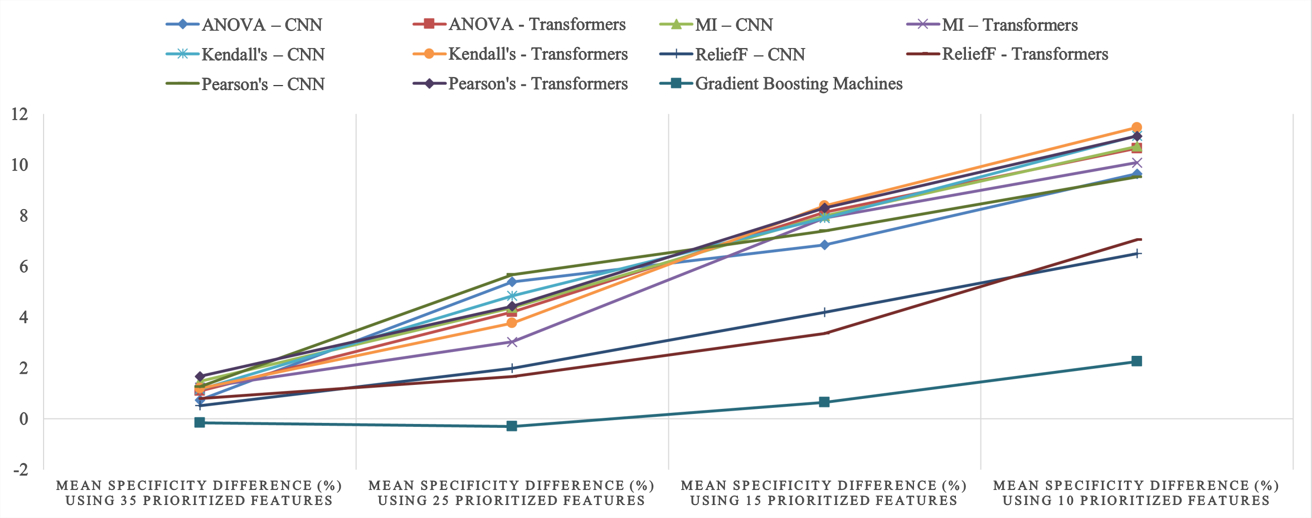

Fig. 14: Trends of mean specificity difference in models using prioritized feature subsets.

TABLE XII: Evaluating mean F1-score variations across prioritized feature subsets.

Feature Selection – ML/DL	**mean F1-score(%) using 35 Prioritized Features**	**mean F1-score(%) using 25 Prioritized Features**	**mean F1-score(%) using 15 Prioritized Features**	**mean F1-score(%) using 10 Prioritized Features**
ANOVA – CNN	89.85	80.8	77.61	72.8
ANOVA - Transformers	88.87	82.58	75.38	70.56
MI – CNN	88.44	82.71	75.55	70.23
MI – Transformers	88.66	85.04	75.8	71.4
Kendall’s – CNN	89.06	81.93	75.73	70.04
Kendall’s - Transformers	88.7	83.55	74.8	68.89
ReliefF – CNN	90.08	87.41	83.16	78.75
ReliefF - Transformers	89.45	87.73	84.43	77.46
Pearson’s – CNN	88.73	79.99	76.79	72.32
Pearson’s - Transformers	87.87	82.12	74.93	68.88
GBM	91.44	91.71	89.95	86.76

and enhancing model efficiency for the classification of respiratory diseases.

F. Comparison with existing models

Most existing research analyzes respiratory conditions using a combination of cough sounds, symptoms, lung sounds, spirometry, clinical tests, and radiology images. However, only a few researchers focus exclusively on the sounds of coughing. The proposed approach aligns with state-of-the-art methods that rely solely on cough sounds. Table XVI presents a comparative analysis of the proposed method with several leading approaches from the literature. The table summarizes various studies on respiratory condition classification using cough sounds. Most approaches utilize a mix of hand-crafted and/or deep features (e.g., MFCCs, spectrograms), with classifiers like CNNs, Support Vector Machines (SVMs), and Transformers. Reported accuracies range from 74% to 91.6%. The proposed method outperforms others, achieving the highest accuracy (91.6%) and strong

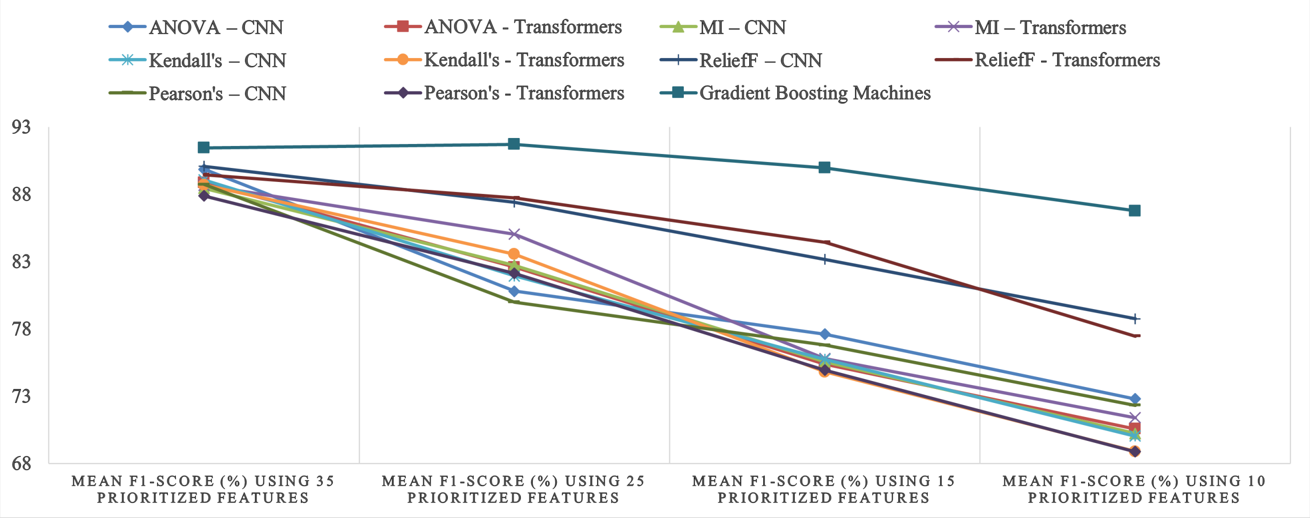

Fig. 15: Assessment of mean F1-score trends across models using prioritized feature subsets.

TABLE XIII: Analysis of mean F1-score differences in models built with selected feature subsets

Feature Selection – ML/DL	**mean F1-score(%) difference (%) using 35 Prioritized Features**	**mean F1-score(%) difference (%) using 25 Prioritized Features**	**mean F1-score(%) difference (%) using 15 Prioritized Features**	**mean F1-score(%) difference (%) using 10 Prioritized Features**
ANOVA – CNN	1.27	10.32	13.51	18.32
ANOVA - Transformers	2.16	8.45	15.65	20.47
MI – CNN	2.68	8.41	15.57	20.89
MI – Transformers	2.37	5.99	15.23	19.63
Kendall's – CNN	2.06	9.19	15.39	21.08
Kendall's - Transformers	2.33	7.48	16.23	22.14
ReliefF – CNN	1.04	3.71	7.96	12.37
ReliefF - Transformers	1.58	3.3	6.6	13.57
Pearson's – CNN	2.39	11.13	14.33	18.8
Pearson's - Transformers	3.16	8.91	16.1	22.15
GBM	-0.34	-0.61	1.15	4.34

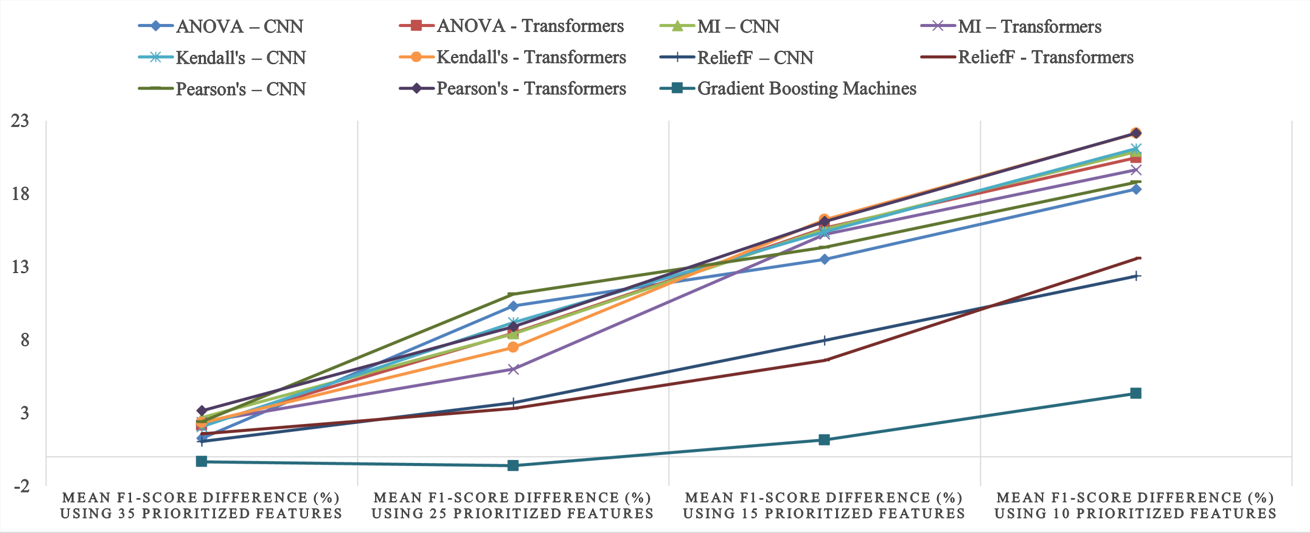

Fig. 16: Trends of mean F1-score difference in models using prioritized feature subsets.

TABLE XIV: Model evaluation with 19 overlapped features from top-ranked subsets.

ML/DL Models	Mean Accuracy (%)	Mean Sensitivity (%)	Mean Specificity (%)	Mean F1-Score (%)
CNN	83.71	84.55	91.7	83.89
Transformers	80.63	81.46	90.09	80.8
GBM	86.41	87.02	93.07	86.59

performance across all metrics using GBM with selected hand-crafted features.

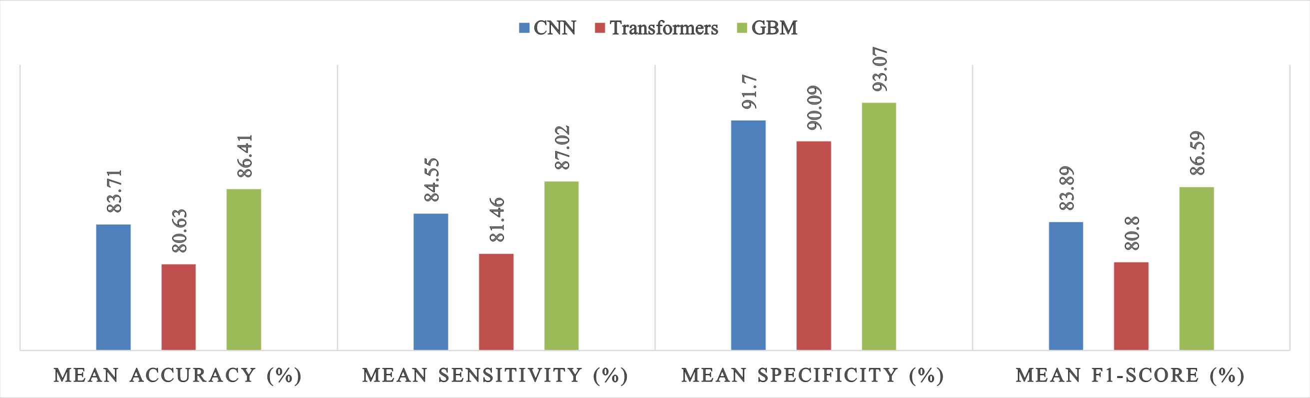

Fig. 17: Performance comparison of models built with 19 overlapped Features.

TABLE XV: Performance comparison of the GBM-based model using 19 overlapped and 25 prioritized features.

Performance metrics	GBM built with 19 overlapped features	GBM with its top 25 features
Mean Accuracy (%)	86.41	91.6
Mean Sensitivity (%)	87.02	91.74
Mean Specificity (%)	93.07	95.64
Mean F1-Score (%)	86.59	91.71

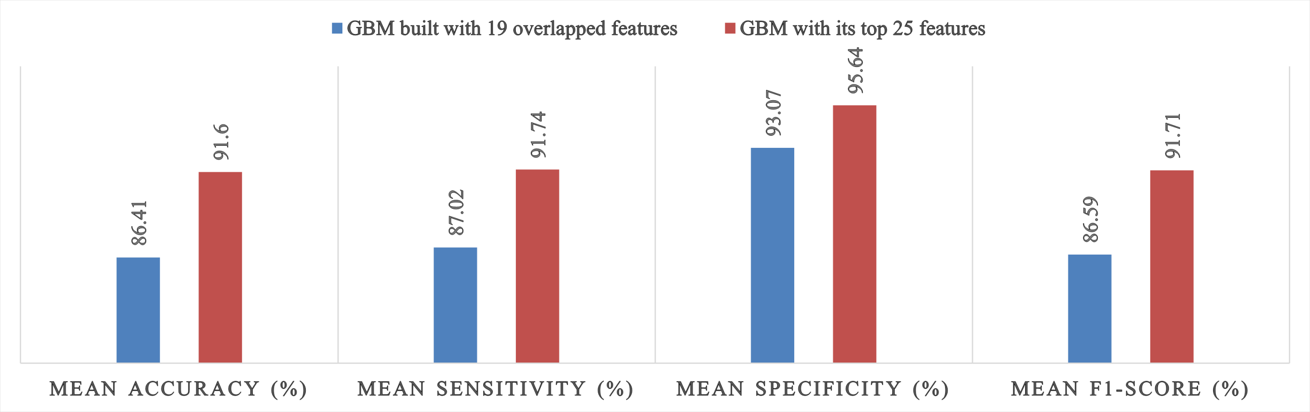

Fig. 18: Performance evaluation of GBM using 19 overlapping and top 25 features.

G. Extensions and Future directions

To extend the proposed work of COPD, asthma, and health classification using cough sound features, various deep audio representation models and hybrid feature strategies have been evaluated. Table XVII compares various combinations of feature extraction techniques and classification methods for cough-based classification tasks. The highest accuracy of 91% is achieved using a combination of WavLM, log mel spectrogram, and multiple handcrafted features (spectral centroid, rolloff, flatness, ZCR, MFCC, LPC) with a SVM classifier. Using the same rich feature set with BiLSTM with Attention yielded a slightly lower accuracy of 89%, while Transformer and EfficientFormer models using only WavLM and log mel spectrogram achieved 90% and 88% accuracy, respectively. A model based on HuBERT and BiLSTM with Attention reached an accuracy of 88%, showing that WavLM-based features combined with handcrafted features and SVM outperform other configurations in this comparison. Integration of self-supervised pretrained models such as WavLM with handcrafted acoustic features to further enhance performance and support the development of more robust and reliable classification systems.

The proposed work demonstrates robust ML and DL methods for distinguishing COPD, asthma, and normal respiratory conditions using handcrafted cough sound features. To further advance this work, future research should explore integrating pre-trained self-supervised audio models like WavLM [45], wav2vec 2.0 [46] and HuBERT embeddings [47], which have shown superior performance in pathological sound recognition by capturing complex temporal and spectral nuances. Additionally, feature fusion approaches that combine acoustic data with other physiological signals such as spirometry, respiration rate, or imaging (e.g., X-rays) [48], [49] have been shown to significantly improve diagnostic accuracy in clinical AI applications [50]. Improvement in pulmonary disease classification [51] when multimodal features [52] are combined with DL models [53]. Edge deployment also represents a promising avenue, as low-cost devices using EfficientFormer [54] and TinyML solutions have been proven for real-time health diagnostics [55] in rural areas. Explainable AI tools [56] like SHAP and LIME can build clinician trust by visualizing how input features influence predictions, aiding in the adoption of AI diagnostics. To address limited labeled data, contrastive learning [50], and few-shot methods have shown promise in improving model generalization, particularly in health-

TABLE XVI: Comparison with state-of-art models

Study	Classes	Features extraction and selection techniques	Classification methods	Performance
S.Xu *et al.* [40]	Asthma vs Healthy; COPD vs Healthy	Gabor time-frequency transformation; Neighborhood Component Analysis for feature selection	RF, SVM, Decision Trees, k-nearest neighbor (KNN); majority-voting ensemble	Majority-voting ensemble with Accuracy: 83.31%, Sensitivity: 82.8%, Precision: 83.0%, F1 score: 82.9%.
S.Ghrabli *et al.* [28]	Pneumonia and Asthma	Power spectral density in segmented coughs	LDA and KNN	Accuracy: 78%
M.Ghourabi *et al.* [41]	Wet vs Dry cough	STFT spectrogram images from cough audio;time mask and classical image transforms	Swin Transformer, 2D CNN baseline	Accuracy: 88.37% (Swin Transformer), 90.87% (CNN baseline on classically augmented data)
P.Miotła *et al.* [42]	cough vs non-cough	Spectrogram	MobileNet, ResNet 50, DenseNet121	MobileNet with Accuracy: 84%, Precision: 80.8%, Recall: 88.7%, F1-score: 84.6%
B.T.Balamurali *et al.* [43]	Healthy vs Pathological coughs in children	MFCCs and log-compressed mel-filterbanks	Transformers with self-supervised contrastive pre-training (Transformer-CP); VGGish, GRU, and ensemble methods	Transformer-CP) + fine-tuning + Ensemble with Accuracy: 84.3%, Recall: 73.1%, Precision: 82%, F1 Score: 77.3%
E.A.Mohammed *et al.* [44]	COVID-19 positive, negative, and healthy coughs	spectrograms Pre-trained CNNs combined with ensemble of top performing classifiers	Precision: 80% Sensitivity: 71%	F1-score: 75%
O.Zealouk *et al.* [31]	TB-positive vs negative	23 MFCC features selected using Recursive feature elimination using RF	Logistic Regression (LR), SVM, KNN, and CNN	LR with Accuracy:81.5% ± 7.7%, Sensitivity: 74.5% ± 13.7%, Specificity: 86.5% ± 7.5%, F1-Score: 76.0% ± 11.7%
Proposed Model	COPD, Asthma, and Healthy	25 features (refer section III-B) selected using GBM from 49 hand-crafted features	GBM, CNN, Transformer	GBM with 25 prioritized features with Accuracy: 91.6%, Sensitivity: 91.74%, Precision:95.64%, F1 score: 91.71%

TABLE XVII: Classification performance of COPD, asthma, and normal cough sounds using self-supervised pre-trained audio models

Features extraction	Classification methods	accuracy (in %)
WavLM + Log melspectrogram + [spectral centroid, spectral roll-off, spectral flatness, ZCR, MFCC, LPC]	SVM	91
WavLM + Log melspectrogram	Transformer	90
WavLM + Log melspectrogram	EfficientFormer	88
WavLM + Log melspectrogram + [spectral centroid, spectral roll-off, spectral flatness, ZCR, MFCC, LPC]	BiLSTM with Attention	89
HuBERT	BiLSTM with Attention	88

related acoustic benchmarks [57]. Evaluating models on diverse, longitudinal datasets such as Coswara [58] can further ensure consistent performance across age, gender, and comorbidities. Ultimately, aligning with regulatory standards and validating through clinical trials will be crucial for ensuring the safe and effective deployment in the real world.

IV. CONCLUSION

This paper presents that the machine learning model GBM effectively differentiates between COPD, asthma, and healthy individuals using optimized cough sound features. By systematically evaluating temporal, spectral, and cepstral features through multiple selection techniques, the research identifies an optimal subset of 25 features that achieves high diagnostic accuracy of 91.6%, sensitivity of 91.74%, specificity of 95.64%, and F1-score of 91.71%. Additionally, the 19 overlapping features derived from consensus across selection methods maintain robust performance. The findings highlight that the group of features significantly enhances classification efficiency compared to single-feature approaches. This automated, feature-driven diagnostic framework presents a scalable and cost-effective solution for COPD and asthma disease screening, particularly beneficial in resource-limited settings where early and accurate diagnosis remains challenging.

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