



Neutrosophic Meta SHAP and Neutrosophic Meta LIME: An Efficient Framework for Explainable AI in Oral Cancer Detection

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Abstract

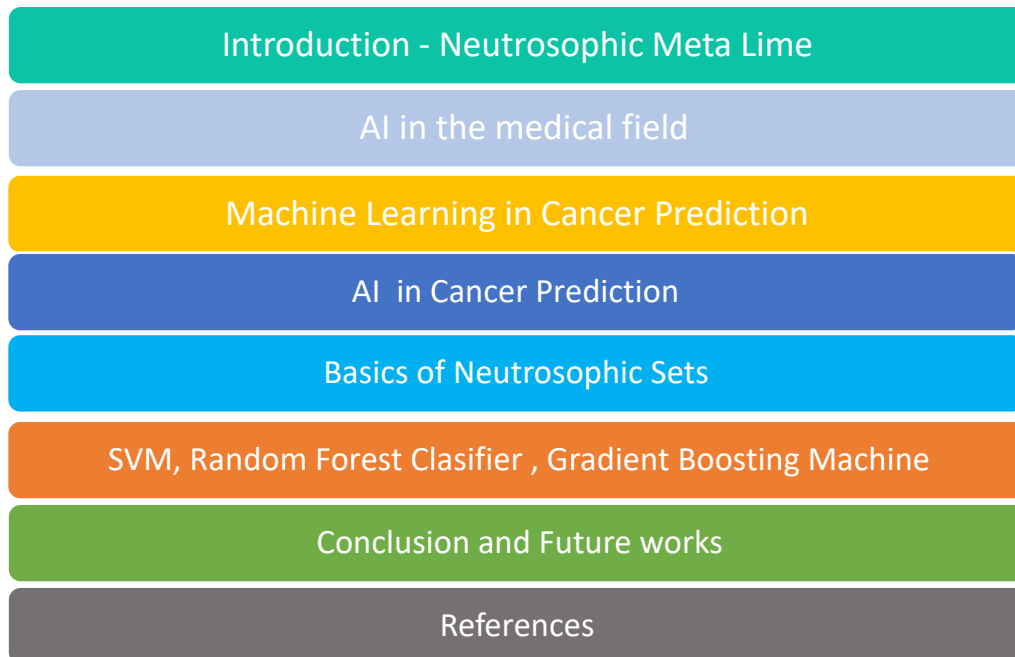
Among the current generation researcher, artificial intelligence has played vital role in various fields, including healthcare. One of the key areas where it has shown enormous potential is in cancer detection and treatment. AI and methods of machine learning algorithms have been applied to analyze large datasets, such as genomics, transcriptomic, and imaging data, to identify patterns and relationships that can help in cancer diagnosis and therapy. However, due to the inherent complexity and heterogeneity of tumors in individual patients, building a diagnostic and therapeutic platform that can accurately analyze outputs becomes a challenging task. To address this challenge, researchers have proposed the use of explainable AI frameworks in cancer detection. Explainable AI frameworks aim to provide transparency and comprehensibility to the decision-making process of AI algorithms, ensuring that the predictions or classifications generated by these algorithms can be understood and trusted by healthcare professionals. One popular explainable AI method is SHAP (SHapley Additive explanations). SHAP is a well-known XAI method that provides intuitive and interpretable feature importance [13] for individual predictions. Another explainable AI method is LIME (Local Interpretable Model-agnostic Explanations), which generates posthoc explanations and is suitable for quick and satisfactory explanations. These existing explainable AI methods, however, have limitations in their applicability to cancer detection. Therefore, in this research article, we propose the use of two novel frameworks: Neutrosophic Meta SHAP and Neutrosophic Meta Lime. Neutrosophic Meta SHAP and Neutrosophic Meta Lime are efficient frameworks specifically designed for the analysis and interpretation of AI models in oral cancer detection.

Keywords: Machine Learning in Disease prediction; ANN; SVM; GBM; Neutrosophic Meta SHAP; Neutrosophic Meta LIME; Oral Cancer

1. Introduction

Neutrosophic Meta SHAP and Neutrosophic Meta Lime are two novel frameworks that aim to enhance the explainability and interpretability of AI models in relation to the detection of oral cancer. These frameworks build upon the existing SHAP and LIME methods and overcome their limitations to provide more accurate and reliable explanations. Neutrosophic Meta SHAP incorporates the ideology of neutrosophic set theory, which allows for the representation and analysis of uncertain and conflicting information in the context of oral cancer. This framework utilizes the concept of neutrosophic meta-analysis, which combines multiple SHapley values from different AI models to generate a comprehensive and robust explanation of the feature importance in oral cancer detection. Neutrosophic Meta Lime, on the other hand, extends the capabilities of Local Interpretable Model-agnostic Explanations by incorporating the neutrosophic set theory, allowing for the interpretation of uncertain and conflicting information in the context of oral cancer detection. The proposed frameworks, Neutrosophic Meta SHAP and Neutrosophic Meta Lime, provide a more efficient and accurate approach to explain the predictions made by AI models in oral cancer detection. These frameworks not only enhance the interpretability of AI models, but also provide precious insights into the contribution and importance of each feature in the prediction. The utilization of

Neutrosophic Meta SHAP and Neutrosophic Meta Lime in oral cancer detection offers several benefits. First of all, these frameworks provide a more accurate and reliable explanation of the feature importance in oral cancer detection. This paper consisting of the following sections in which from introduction followed by AI in cancer prediction, Neutrosophic inventions in disease predictions finally Meta SHAP and Meta Lime methods have been implemented in Neutrosophic environment. The following diagram represents the outline of this article sections.



2. Preliminaries

2.1 AI in the Medical Field

In the realm of healthcare, AI encompasses the utilization of software, specifically ML algorithms, to mimic the thinking of humans in the analysis, presentation, and comprehension of intricate health & medical data. This approach aims to discern relationships between clinical processes and patient outcomes, distinguishing itself from traditional methods by its capacity to collect, process, interpret data, and yield definitive outputs. AI employs deep learning (DL) methods and ML techniques to identify behavioral patterns and autonomously generate reasoning. Presently, AI finds applications in diagnostic measures, medication growth, personalized drug, patient monitoring, and the formulation of treatment protocols. For instance, in coronary artery disease identification, AI algorithms serve as effective early triage tools. Gastroenterology benefits from AI in endoscopic examinations, expediting diagnoses and assessments of abnormal tissue. In infectious disease medicine, particularly artificial neural networks, aids in swiftly and accurately identifying host responses to viruses like COVID-19. The significant investment in AI-related research studies, particularly in the context of the ongoing pandemic, underscores its potential impact on healthcare, with applications extending to antibiotic resistance detection, malaria diagnosis, point-of-care diagnostics for Lyme disease, and improved diagnoses for conditions such as tuberculosis, meningitis, and sepsis. The rapid evolution of AI in healthcare signals a transformative era in medical research and practice.

2.2. Machine Learning in Cancer Prediction

The intricate task of accurately predicting optimal treatment regimens tailored to individual patients based on their unique molecular, hereditary, and tumor characteristics poses a significant challenge in cancer related care. Artificial Intelligence is positioned as a solution to this challenge. Numerous studies have explored AI applications in oncology, focusing on cancer risk stratification, diagnosis, advancement n medicines, and molecular tumor description. Through the analysis of pathology profiles, imaging investigations, and the conversion of visual data into mathematical sequences, machine learning (ML) plays a critical role in the prediction and diagnosis of cancer.

In January 2020, researchers introduced an AI system leveraging a Google Deep Mind (GDM) algorithm, surpassing human specialists in breast cancer detection. Similarly, the University of Pittsburgh developed a machine learning-based AI system in July 2020, exhibiting the greatest specificity and accuracy in identifying prostate cancer and sensitivity of 98%.

A recent study introduced an enhanced Vision Transformer (ViT) architecture, known as ViT-Patch, manipulated on a public dataset. Results demonstrated its effectiveness in malevolent detection and tumor localization. Another study employed ML to classify cancer-related data, generating breast cancer diagnoses. Support vector machine (SVM) classifiers showed the highest accuracy in breast cancer diagnosis. Rana et al. employed ML classification algorithms, with the random forest model exhibiting a 96% accuracy in detecting various cancers. The prediction accuracy of breast cancer by SVM, artificial neural networks (ANN), Naive Bayes classifier, and AdaBoost tree was examined through observational research. Principal component analysis reduced dimensionality, with ANN emerging as the most popular and reliable approach for real-time predictions and prognoses. Pulse-Coupled Neural Networks, particularly in image processing, were explored, revealing their utility. A comprehensive survey investigated various neural network designs, highlighting the strengths and weaknesses of multilayer auto-encoders and probabilistic neural networks, both achieving 96% accuracy in cancer dataset. Using the Wisconsin Diagnostic Breast Cancer dataset, another study assessed machine learning techniques, demonstrating their successful completion of the classification task with high precision in cancer prediction. This study emphasized the potential for improved prediction accuracy through more precise feature selection techniques incorporated into the proposed model. In essence, these studies collectively underscore the transformative role of AI and machine learning in revolutionizing oncologic care, offering unprecedented accuracy and efficiency in cancer prediction and diagnosis.

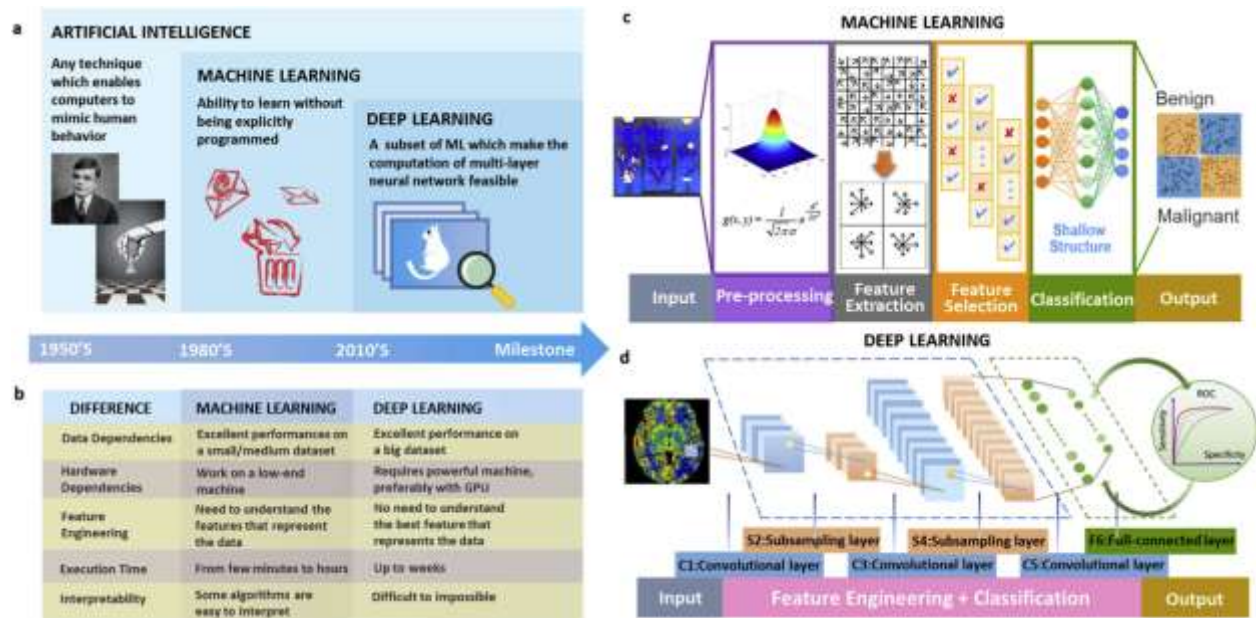


Figure 1: AI, ML and DL. (b) Timescale (c). workflow of ML and (d). Deep Learning Flow charts.

2.3. AI in Cancer Prediction

In recent decades, healthcare professionals across various fields, ranging from veteran to paramedics, took the challenge of predicting Cancer outcomes using their clinical judgement and expertise extensive experience. The advent of the digital data era has prompted clinicians to recognize the necessity of integrating artificial intelligence (AI) innovations, such as Deep Learning and Machine Learning, into their practices. Given the Extensive landscape of statistical tools and methodologies, predicting the progression of cancer poses significant challenges, prompting healthcare experts to seek more advanced solutions. Concerns about the risk of disease contraction, tumor recurrence post-treatment, or mortality further underscore the need for accurate prognostic tools, which significantly impact treatment decisions and outcomes. A substantial body of evidence in clinical cancer research focuses on predicting patient responses to therapy and establishing prognoses. Patients armed with more precise prognoses can benefit from more valuable and personalized treatment options. AI, leveraging its ability to analyze multi-factor data from

diverse patient assessments, emerges as a potent tool for providing precise information on patient endurance, prognosis, and predicting disease chain. Enshaei et al showcased how artificial intelligence plays a pivotal role in offering forecasting and predictive information to ovarian cancer patients. This was achieved through the integration of classifiers with conventional logistic regression techniques.

AI's proficiency in deciphering intricate datasets heralds a revolutionary shift in predicting cancer risk. These algorithmic approaches, often characterized as "agnostic," possess the capability to unveil concealed patterns, thereby enhancing risk stratification and refining screening recommendations. Notably, an AI model showcased superior performance compared to prevailing guidelines for colorectal cancer screening, presenting a paradigm shift towards early detection in individuals who might be overlooked by existing criteria, particularly for cancers devoid of well-defined screening protocols. The true prowess of AI emerges in its adeptness at personalized risk prediction, a critical facet for cancers like pancreatic cancer where early identification holds paramount importance. With an impressive accuracy rate, such as the 85% achieved by one model, AI enables targeted screening even in resource-constrained settings, amplifying its potential impact. In essence, AI's role in cancer risk prediction signifies a transformative tool. It lays the foundation for personalized healthcare strategies and facilitates early detection, especially in cases where established screening methods are lacking, ultimately contributing to life-saving interventions.

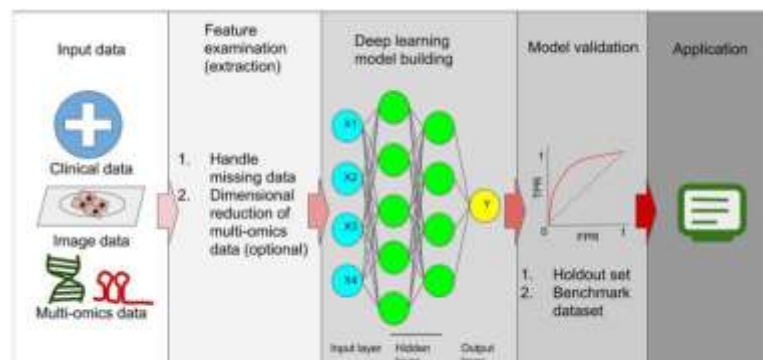


Figure 2: Workflow of building deep learning models for cancer prognosis

2.3.1 Artificial Neural Networks Interpretation Using LIME for Cancer Diagnosis

The intersection of artificial intelligence (AI) and healthcare has paved the way for groundbreaking advancements, particularly in the realm of cancer diagnosis. Artificial Neural Networks (ANNs) have emerged as powerful tools in this domain, utilizing complex algorithms to analyze intricate patterns within medical data. Understanding and interpreting the decisions made by ANNs is paramount for gaining trust and facilitating the integration of these models into clinical practice. This study focuses on leveraging LIME to augment the interpretability of ANNs in the context of oral cancer diagnosis. ANN, encouraged by the human brain's arrangement, have demonstrated remarkable accuracy in discerning subtle patterns indicative of various medical conditions, including cancer [19]. However, their inherently black-box nature raises concern about transparency and trust in their decision-making processes. LIME, as a model-agnostic interpretability technique, provides a valuable framework for probing and explaining the predictions made by complex models like ANNs. The primary objective of implementing artificial algorithms is to bridge the interpretability gap associated with ANNs in cancer diagnosis by employing LIME. By generating locally faithful and human-understandable explanations for individual predictions, LIME facilitates the elucidation of complex decision boundaries established by ANNs. This not only enhances clinicians' understanding of the diagnostic process but also allows them to contextualize and validate the model's predictions. The ensuing exploration delves into the application of LIME in the realm of cancer diagnosis using ANNs, aiming to provide a robust foundation for the interpretability of these sophisticated models. The significance of this study lies in its potential to foster trust and acceptance of AI-driven diagnostic tools in the healthcare community, thereby contributing to the broader integration of advanced technologies for more accurate and transparent oral cancer diagnoses.

2.3.2. Related Work

Considerable effort has been invested in interpreting Machine Learning (ML) models, with a notable shift towards emphasizing the explanation of features considered or disregarded by a model rather than merely focusing on parameter adjustments for increased accuracy. The significance of interpretability is particularly pronounced in high-stakes decision-making domains, such as healthcare. Explaining the decision-making process enhances the

trustworthiness of ML models, addressing concerns about their application, especially in critical areas like medicine. In 2002, Idri et al. explored the interpretability of neural networks in software cost estimation, utilizing a method to map Multilayer Perceptrons (MLP) to a fuzzy rule-based system. Despite some limitations, this approach aimed to express the information encoded in the network's architecture in an easily interpretable manner. More recently, the LIME framework has been employed across diverse domains, including medicine and finance. The Skater team utilized LIME for breast cancer diagnosis, demonstrating the varying sensitivity of different classifiers to attributes. This showcased the role of interpretation techniques in enhancing model understanding for selection. Furthermore, they expanded on LIME, presenting an approach that learns if-then rules to represent a model's global behavior in classification problems. Validating their approach using various datasets, including the Wisconsin Breast Cancer dataset, they trained a random forest classifier with an impressive 98% accuracy. Their technique generated rules that effectively imitated the model behavior across a substantial portion of the dataset. The comparison between model predictions and the resultant if-then rules was evaluated using a novel metric they introduced: Imitation@K, where K represents the number of rules. This approach not only enhances the interpretability of ML models but also provides insights into the alignment between model predictions and interpretable rules, fostering a deeper understanding of model behavior.

2.4 Neutrosophic in Disease Prediction

In 2005, Smarandache introduced neutrosophic sets which emerged as a framework designed to handle the interplay of indeterminacy and uncertainty. Subsequently, numerous authors and researchers have expanded this theory, yielding diverse applications across various domains such as mathematics, statistics, biomedical sciences, healthcare, image processing, and disease prediction. Recent innovations in neutrosophic environments included [13,14,17] et al.'s introduction of Heptagonal Neutrosophic Topology, Neutrosophic Topological Vector Space, and Neutrosophic Indefinite Integrals to address complex problems characterized by both indeterminacy and uncertainty. Bandera et al. [5,6] contributed to Neutrosophic Multi-criteria Decision-making, presenting a methodology for assessing and predicting Chronic Kidney using an enhanced Neutrosophic Artificial Intelligence model. Additionally, Rodríguez et al.[21,22] focused on Chronic Kidney prediction and Cancer Prediction, leveraging machine learning and Neutrosophic Multi-Criteria Decision-Making (MCDM) methodologies. Gupta et al.[10] explored deep learning techniques for cancer classification based on microarray gene expression data. Ahmed et al. [2] ventured into the realm of heart disease prediction [20] using machine learning within a neutrosophic environment Singh et al. [26] illustrated the Diagnosis of Skin Cancer Utilizing Neutrosophic Features via Deep Neural Network.. These advancements highlight the broad spectrum of applications for neutrosophic sets, showcasing their versatility in addressing challenges posed by indeterminacy and uncertainty across various scientific and medical disciplines.

In the realm of machine learning (ML) interpretability, the demand for robust and flexible methodologies has led to the development of innovative techniques which was implemented in Neutrosophic environment by Del Sol [9]. Two such methodologies, Neutrosophic Meta SHAP and Neutrosophic Meta LIME, have emerged to address the complexities associated with explaining ML model predictions, particularly in scenarios involving uncertainty and imprecision. Interpreting ML models is crucial for fostering trust and understanding, especially in high-stakes domains like healthcare and finance. Traditional approaches often fall short in handling the inherent uncertainties and vagueness present in real-world data. This is where Neutrosophic Meta SHAP and Neutrosophic Meta LIME step in, introducing a novel perspective by incorporating neutrosophic logic into the well-established SHAP and LIME frameworks. Neutrosophic logic extends the classical binary logic by introducing a third component—indeterminacy, which captures the degree of uncertainty or imprecision associated with a statement. Neutrosophic Meta SHAP leverages the principles of SHAP, a method based on cooperative game theory, to assign fair contributions of each attribute to a model's output. By introducing neutrosophic logic, this methodology accommodates uncertainty in feature attributions, providing a more nuanced thoughtful of the MCDM process. On the other hand, Neutrosophic Meta LIME builds upon the concept of local interpretability introduced by LIME. LIME generates locally faithful explanations for individual predictions, aiding in the interpretation of complex ML models. Neutrosophic Meta LIME enhances this by incorporating neutrosophic logic, allowing for the representation of uncertainty and imprecision in the local model approximations. This is particularly valuable when dealing with inherently uncertain or vague data, such as in medical diagnoses or financial predictions. Neutrosophic Meta SHAP and Neutrosophic Meta LIME represent a pioneering fusion of established interpretability frameworks with neutrosophic logic, catering to the need for more nuanced, flexible, and reliable explanations in the increasingly intricate landscape of machine learning. These methodologies hold promise in providing transparent and

interpretable insights into complex model predictions, ultimately fostering greater trust and adoption in critical decision-making scenarios.

Building upon theories like fuzzy [32] and intuitionistic fuzzy sets [4], Florentin Smarandache proposed Neutrosophic Set Theory in 1995 to handle uncertainty, ambiguity, and incompleteness in data [26]. This theory goes beyond simple true/false notions by introducing indeterminacy, allowing elements to possess degrees of truth (T), indeterminacy (I), and falsity (F), all ranging from 0 to 1. NS [25] in X is defined as $P = \{x: (T_P(x), I_P(x), F_P(x)) | x \in X\}$ where $T_P: X \rightarrow [0,1], I_P: X \rightarrow [0,1], F_P: X \rightarrow [0,1], 0 \leq T_P(x) + I_P(x) + F_P(x) \leq 3$.

The various operations on the two single-valued neutrosophic sets (SVNSs) represented below:

$$x_1 = (Tx_1, Ix_1, Fx_1), \text{ and } x_2 = (Tx_2, Ix_2, Fx_2)$$

$$x_1 + x_2 = (Tx_1 + T_2 - Tx_2Tx_1, Ix_1 + Ix_2 - Ix_1Ix_2, Fx_1 + Fx_2 - Fx_1Fx_2)$$

$$x_1x_2 = (Tx_1Tx_2, Ix_1Ix_2, Fx_1Fx_2)$$

$$\sigma x_1 = (1 - (1 - Tx_1)\sigma, 1 - (1 - Ix_1)\sigma, 1 - (1 - Fx_1)\sigma)$$

The power of SVNNS can be computed as:

$$x_1\sigma = (Tx_1\sigma, Ix_1\sigma, Fx_1\sigma)$$

The Analytic Hierarchy Process (AHP) is a widely used technique for comparing numerous variables and options by assigning weights based on a fundamental principle of arbitrary computation. When applied to decision-making, evaluation, and prioritization, AHP offers a robust framework for managing and structuring hierarchical models. Decision Trees (DT) iteratively select the explanatory variable that yields the most optimal split at each node, constructing regression or classification algorithms to predict the final outcome of the response parameter. While DTs are straightforward and easy to understand, their primary drawback is overfitting, which reduces generalization. Random Forest (RF) addresses this issue by aggregating multiple independent decision trees through the bootstrap aggregation method, resulting in a combined forecast that is more accurate than individual trees. Support Vector Machines (SVM) rely on the assumption that linearly separable patterns can be represented by a hyperplane, and non-linear patterns can be mapped onto a new space using a kernel function. Though SVM addresses overfitting, it is more complex than RF in terms of understanding and parameter tuning.

2.4.1 Interval Valued Neutrosophic Sets in RNN:

"Intelligent Neutrosophic Diagnostic System for Cardiotocography Data" introduces a novel framework for classifying fetal heart rate using machine learning algorithms. The proposed system leverages the WEKA application to analyze cardiotocography data and evaluate the performance of various algorithms, including neural network, decision table, nearest neighbor, and rough neural network. The study demonstrates the feasibility and efficiency of the proposed framework as a classifier, with a focus on classifying fetal states into normal, suspicious, and pathologic categories. Notably, the headset operation attributes (ROC) curve analysis showcases high area under the curve (AUC) values for the classification of pathologic, normal, and suspicious states, indicating the system's effectiveness in differentiating between these states. Furthermore, the research emphasizes the potential application of the proposed framework in real-life problems such as the classification of coronavirus, social media, and satellite images, highlighting its versatility and broader impact in various domains. Moreover, the study discusses the importance of addressing vagueness and ambiguity in medical data, emphasizing the critical role of fast and accurate decision-making in the medical field. By utilizing the projected neutrosophic diagnostic system, the research aims to provide an efficient framework for multi-classification of cardiotocography data related to fetal heart rate. The experimental results demonstrate the system's performance measurement in accuracy rate, precision, recall, and F-measure, showcasing its potential to aid doctors in prioritizing critical cases that require prompt intervention. Additionally, the article provides insights into the theoretical background of recurrent neural networks (RNN) and intelligent neutrosophic systems (INS) applied in constructing the diagnostic framework, offering a comprehensive understanding of the underlying methodologies. Overall, the research contributes to the advancement of medical data analysis and classification, with implications for improving decision-making processes and enhancing the diagnosis of fetal well-being based on cardiotocography data.

3. Proposed Methodology

In the setup phase, this study presents the Neutro-Meta LIME and Neutro-Meta SHAP as critical interpretability tools in the case of oral cancer recognition. The result of the oral cancer recognition model is more transparent because of Neutro-Meta SHAP, which is based on “Shapley Additive explanations”, and “Neutro-Meta LIME”, which employs Local Interpretable Model-agnostic Explanations (Welikala *et al.* 2020)[29]. This study establishes the model utilizing a binary classification framework, emphasizing the model's interpretability. This first step lays the framework for a comprehensive evaluation of the oral cancer detection model that highlights the importance and understandability of the elements involved in the detection technique (Abati *et al.* 2020) [1].

Feature Clarification

In the feature clarification phase, this research identifies crucial attributes pivotal for oral cancer detection. A comprehensive examination is conducted, meticulously assessing factors that significantly impact the decision-making process of the model. The objective is to pinpoint and comprehend specific features from the secondary dataset that wield substantial influence on accuracy and effectiveness of oral cancer diagnosis (Tseng *et al.*, 2020)[27]. The study aims to enhance model accuracy by ensuring alignment with the intricate patterns of oral cancer, thereby contributing to the interpretability and overall effectiveness of the detection methods employed (Inchingolo *et al.*, 2020)[11].

Model Development

In this study model development endeavour to build the oral cancer detection model, Neutro-Meta SHAP and LIME increase its interpretability. Through enhanced interpretability tools, the study provides transparency in the model's decision-making process and highlights the various factors that affect its results. Similar methods are used to construct a complete model for oral cancer diagnosis using cutting-edge methods (Rymarczyk *et al.* 2023) [24]. In a similar way, improves detecting accuracy. In order to construct a model that works well, is clear, and accessible, various algorithms and parameters must be fine-tuned. This will boost oral cancer detection techniques (Irani *et al.* 2020) [12].

Random Forests

The Random forests have been a specific learning strategy which help to reveal feature relevance as well as model predictions. It has various benefits from Neutro-Meta SHAP as well as LIME interpretability (Bouvard *et al.* 2022)[7].

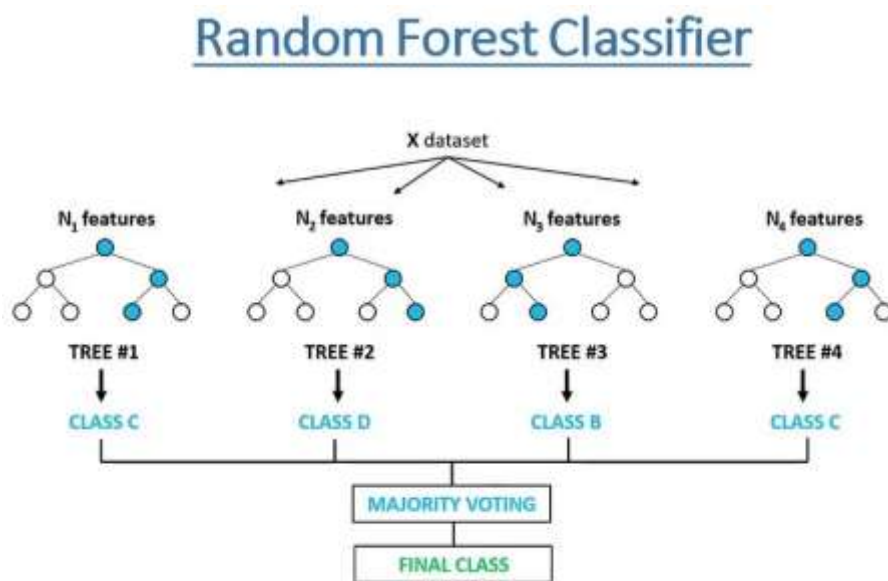


Figure 3: Random forest

Support Vector Machines (SVM)

The SVM is crucial in case of “Neutro-Meta SHAP” as well as “Neutro-Meta LIME’s” interpretability which has some benefit for the Random Forests, and it is a useful learning technique that evaluates features as well as model predictions (Mohammadi *et al.* 2021)[18].

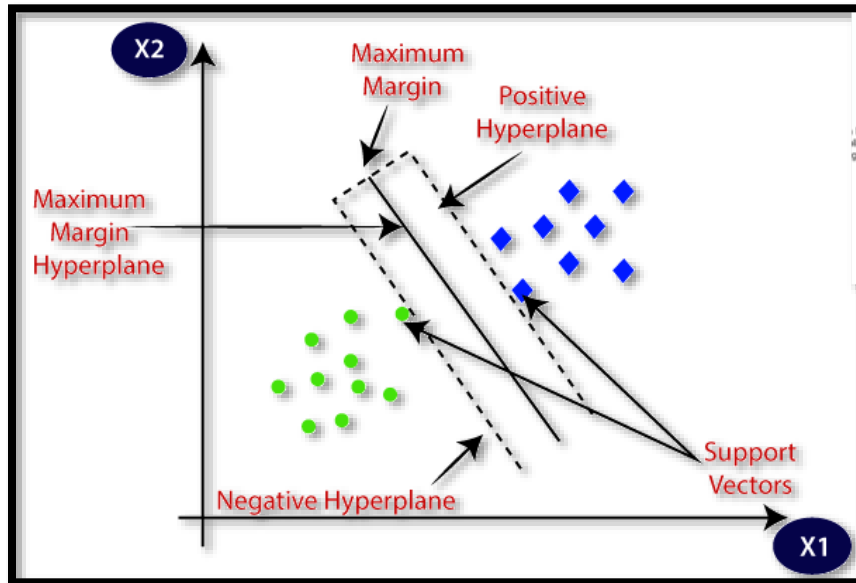


Figure 4: Support Vector Machine Algorithm

Gradient Boosting Machines

The gradient boosting algorithms such as “XGBoost and LightGBM” can combine with Neutro-Meta SHAP as well as LIME in order to analyse weak learners for this study along with useful information on the case of gradient boosting-based performance (Rufu *et al.* 2021)[23].



Figure 5: Gradient Boosting (XGBoost and LightGBM) Machines

Logistic Regression

The two process such as “Neuro-Meta SHAP” and “Neuro-Meta LIME” can perform logistic regression after completely checking how specific all the parameters affect on the specific class.

Performance Evaluation

The performance evolution for this study takes some values which are False Positive (FP), True Positive (TP), True Negative (TN), as well as False Negative (FN). This step is meticulously executed using the interpretable model (Warnakulasuriya et al. 2022)[28]. False positives are faulty positive identifications, whereas True Positives are model-correct positive identifications. It has been seen that accurate diagnosis requires both positive identifications. True Negative accounts for properly recognized negative cases, where False Negative compensates for scenarios in which the model is unable to identify positive cases (Chattopadhyay et al. 2019) [8]. This study can discover the model's strengths and potential areas for improvement by thoroughly examining these indications, which helps to improve and optimize the algorithm for detecting oral cancer (Sarode et al. 2020) [25].

4. Experimental results and calculation

It has been seen that in this study, deep learning models using ML algorithms with binary classification have been notified to show significant performance such as false positive, true positive, false negative, and true negative.

Let, True Positive (TP): 80

False Positive (FP): 10

True Negative (TN): 120

False Negative (FN): 20

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + TN + FP + FN)}$$

$$= (80+120) / (80+120+10+20) = 200 / 230 \approx 0.8696$$

$$\text{Precision} = TP / (TP + FP)$$

$$= 80 / 80+10$$

$$= 80 / 90 \approx 0.8889$$

$$\text{Recall} = TP / (TP + FN)$$

$$= 80 / (80+20) = 80 / 100$$

$$= 0.8$$

$$\text{Specificity} = TN / (TN + FP)$$

$$= 120 / (120+10)$$

$$= 120 / 130 \approx 0.9231$$

$$\text{F1 Score} = 2 \times (\text{Precision} + \text{Recall}) / (\text{Precision} \times \text{Recall})$$

$$= 2 \times (0.8889 \times 0.8) / (0.8889 + 0.8) \approx 0.8421$$

SVM

1. Initialize:

Set $w=0$ and $b=0$

2. For $=1$ to T :

a. Select a random sample (x_i, y_i) from the training dataset.

b. Compute the decision function:

$$f(x_i) = w \cdot x_i + b$$

c. Update the parameters:

$$w = w + \eta \cdot (C \cdot y_i \cdot x_i - w)$$

$$b = b + \eta \cdot C \cdot y_i$$

3. Output:

Final hyperplane parameters: w, b

Step 1: Initialization

In the oral cancer detection investigation, it set the regularization parameter (C) and initialize the weight vector (w), as well as bias (b), and SVM algorithm.

Step 2: Define the Objective Function

After the first step need to create an objective function, whose purpose is to discipline inaccurate classifications with the specific loss while reducing the Euclidean norm of w.

Step 3: Optimization Setup

Then set in for optimization by creating the SVM optimization problem and including the objective function and constraints.

Step 4: Training Iterations

In the training samples, it updates w and b to find the ideal hyperparameters for properly identifying oral cancer.

Step 5: Regularization Impact

The regularization (C) influences SVM optimization for oral cancer diagnosis by balancing model accuracy and complexity.

Step 6: Model Evaluation

It analyzes the trained SVM model's performance in case of identifying oral cancer for interpretability with the help of criteria such as accuracy and recall.

Step 7: Neutro-Meta SHAP Integration

In this study "Neutro-Meta SHAP" in used to increase interpretability and learn about feature importance and decision-making techniques for detecting oral cancer.

Step 8: Neutro-Meta LIME Integration

In order to give local interpretability and individual prediction grounds for the SVM model for oral cancer diagnosis, it used "Neutro-Meta LIME".

Step 9: Model Validation

In order to guarantee that the SVM model performs effectively in practice, validate it with clinical data and solicit feedback from medical professionals on how to improve it.

Step 10: Results Analysis

The performance of SVM model findings for accuracy and transparency, helps to make decisions on the performance and interpretability of Neutro-Meta SHAP and LIME in identifying oral cancer.

Step 11: Conclusion

We analysed in this study that perform the implications of SVM results, which highlighting the contributions of “Neutro-Meta SHAP and LIME” to model interpretability and their significance in oral cancer detection.

Gradient Boosting Machines

1. $F_0(x) = \text{mean}(y)$

2. For $t = 1$ to T :

a. Computation of the negative gradient of the loss function:

$$r_{ti} = -\partial F_t - 1(x_i) \partial L(y_i, F_t - 1(x_i))$$

b. Fit a weak-learner (e.g., decision tree) to the negative gradient:

$$f_t(x) = \arg \min f \left(\sum_{i=1}^n L(y_i, F_t - 1(x_i) + \eta \cdot f(x_i)) \right)$$

c. Determine the optimal step size: $\gamma_t = \arg \min \gamma \left(\sum_{i=1}^n L(y_i, F_t - 1(x_i) + \gamma \cdot f_t(x_i)) \right)$

d. Update the model: $F_t(x) = F_t - 1(x) + \eta \cdot \gamma_t \cdot f_t(x)$

3. Output:

Final ensemble of weak learners: $F(x) = \sum_{t=1}^T \eta \cdot f_t(x)$

Step 1: Initialization

The initialization of the gradient boosting algorithm, setting the initial prediction for each sample and specifying the number of gradient boosting classifiers.

Step 2: Loss Function Definition

After the initialization, the loss function shows the difference involving forecasts and actual results in case of the oral cancer detection.

Step 3: Negative Gradient Calculation

It calculates the negative gradient of the loss function to determine the direction of improvement for each sample's subsequent boosting rounds.

Step 4: Learning Rate Adjustment

Change the learning rate to control each weak learner's contribution to the overall oral cancer detection model.

Step 5: Update Predictions

This model helps to update predictions by adding the product of the learning rate and the predictions generated by the weak learner to increase the accuracy of oral cancer diagnosis.

Step 6: Residual Calculation

The residual calculation helps to guide the subsequent gradient-boosting iterations for better oral cancer detection. These residuals are the differences between current projections and actual results.

Step 7: Neutro-Meta SHAP Integration

It integrates Neutro-Meta SHAP in order to interpret the ensemble model, which provides an understanding of feature importance and decision processes for oral cancer detection.

Step 8: Neutro-Meta LIME Integration

Neuro-Meta LIME is incorporated for local interpretability; it explains individual forecasts within the gradient-boosting model for detecting oral cancer.

Step 9: Model Validation

The model validation in the gradient boosting along with clinical data, gives assurance about its efficacy in real-world scenarios in case of oral cancer detection.

Step 10: Results Analysis

The result of this study is that using a gradient boosting model highlights the transparency as well as accuracy, by outlining conclusions based on the detection of oral cancer along with Neuro-Meta SHAP as well as LIME.

Neuro-Meta SHAP

$$\phi_i(f) = \sum_{k=0}^n S \subseteq N \setminus \{i\} \frac{|N|! |S|}{|N|! (|N| - |S| - 1)!} [f(S \cup \{i\}) - f(S)]$$

$$\phi_1(f) = B_1 \sum b = 1 B \phi_i(b)(f) = N = \{x_1, x_2, x_3\},$$

$$\phi_2(f) = 3! 1 [f(\{x_1, x_2, x_3\}) - f(\{x_1, x_3\})] + (f(\{x_1, x_2\}) - f(\{x_1\})) + (f(\{x_2, x_3\}) - f(\{x_3\}))]$$

Assuming

$$f(\{x_1, x_2, x_3\}) = 10,$$

$$f(\{x_1, x_3\}) = 7,$$

$$f(\{x_1, x_2\}) = 9,$$

$$\phi_2(f) = 1/6 [(10 - 7) + (9 - 3) + (8 - 5)] = 1/6 (9 + 6 + 3) = 3$$

$$\phi_i(f) = \frac{1}{B} \sum_{b=1} \phi_i(b)(f)$$

$$\phi_2(f) = \frac{1}{100} \sum_{b=1} 100 \phi_2(b)(f)$$

$$\phi_2(f) = \frac{1}{100} \sum b = \frac{1}{100} \phi_2(b)(f)$$

$$\phi_2(1)(f) = 3, \phi_2(2)(f) = 2, \phi_2(3)(f) = 4, \dots$$

$$\phi_2(f) = 1/100 \sum b = 1/100 \phi_2(b)(f)$$

$$\phi_2(f) = 1/100 (3 + 2 + 4 + \dots)$$

$$\phi_2(f) = 1/100 \times 250 = 2.5$$

$$\phi_2(f) = 1/100 \sum b = 1/100 \phi_2(b)(f)$$

$$\phi_2(1)(f) = 3, \phi_2(2)(f) = 2, \phi_2(3)(f) = 4,$$

$$\phi_2(f) = \frac{1}{100 \sum b} = \frac{1}{100} \phi_2(b)(f)$$

$$\phi_2(f) = 1/100 \times 250 = 2.5$$

$$\phi_2(f) = 1/100 \sum b = 1/100 \phi_2(b)(f)$$

$$\phi_2(1)(f) = 3, \phi_2(2)(f) = 2, \phi_2(3)(f) = 4, \dots$$

Substitute these values into the equation,

$$\phi_2(f) = \frac{1}{100} \sum b = 100 \phi_2(b)(f)$$

So, the SHAP value $\phi_2(f)$ for feature $f(2)$ is approximately 2.5.

$$\phi_2(f) = 1001 \times 250 = 2.5$$

Now, considering another feature, $\phi_1(f) = 4.0$ and $\phi_3(f) = 1.5$.

The overall SHAP values vector for the prediction is given by:

$$[\phi_1(f), \phi_2(f), \phi_3(f)] = [4.0, 2.5, 1.5]$$

$$\phi_1(f) = f(\{x_1\}) - f(\{0\}) = 3 - f(\{0\})$$

Similarly,

$$\phi_2(f) = f(\{x_1, x_2\}) - f(\{x_1\})$$

$$\phi_3(f) = f(\{x_1, x_2, x_3\}) - f(\{x_1, x_2\})$$

Assuming $f(\{0\}) = 1, f(\{x_1\}) = 3, f(\{x_1, x_2\}) = 9, f(\{x_1, x_2, x_3\}) = 10$

$$\phi_1(f) = 3 - 1 = 2$$

$$\phi_2(f) = 9 - 3 = 6$$

$$\phi_3(f) = 10 - 9 = 1$$

So, for this specific permutation, the SHAP values are [2,6,1] [2,6,1].

Weighted Average Calculation

$$SHAP(f) = \sum_{b=1}^B \phi_b(f)$$

$$SHAP(f) = 1/5 \sum b = 1/5 [2,6,1] = 1/5 \sum b = 1/5 [2,6,1]$$

Neutro-Meta LIME:

$$L(f, g, \pi x) = \sum_{i=1}^n \pi x(i) [f(x_i) - g(x_i)]^2$$

$$\text{Min } w_0, w_1, \dots, w_n, L(f, g, \pi x) + \lambda \Omega(g)$$

$$f^{(x)} = g(x) = w_0 + w_1 x_1 + w_2 x_2 + \dots + w_n x_n$$

$$w_i = \sum_{j=1}^n \frac{\exp(-\sigma_2 d(x, x_j)^2)}{\exp(-\sigma^2 d(x, x_i)^2)}$$

where, $d(x, x_i)$ is a distance measure between instances x and x_i , σ is a smoothing parameter controlling the locality of the explanation.

$$g(x) = w_0 + w_1 x_1 + w_2 x_2$$

$$L(f, g, \pi x) = \pi x(1) [f(x_1) - g(x_1)]^2 + \pi x(2) [f(x_2) - g(x_2)]^2$$

$$d(x, x_1) = (2 - 1)^2 + (3 - 4)^2 = 2$$

$$d(x, x_2) = (2 - 3)^2 + (3 - 4)^2 = 2$$

$$\frac{\left(\frac{\partial w_1}{\partial \sigma}\right)}{\left(-\frac{d(x, x_1)^2}{\sigma}\right)} = \frac{-\sigma d(x, x_1)}{\exp(-\sigma^2 d(x, x_1)^2)}$$

Min $w_2, w_3, \dots, w_n L(f, g, \pi x) + \lambda \Omega(g)$

$F(x) = g(x) = w_n + w_2 x_2 + w_3 x_3 + \dots + w_n x_n$

$$\frac{\frac{\partial}{\partial x} w_j}{\left(-\frac{d(x, x_j)^2}{\sigma^2}\right)} = -\frac{2 \sum_j \sigma^2 d}{(x, x_j)} (-\sigma^2 d(x, x_j)^2)$$

$$\phi_2(f) = f(\{x_1, x_2\}) - f(\{x_1\})$$

$$\phi_3(f) = f(\{x_1, x_2, x_3\}) - f(\{x_1, x_2\})$$

Step 11: Discussion

This step discusses the implications of gradient-boosting performance, and it highlights the assistance of Neuro-Meta SHAP and LIME in order to model interpretability in oral cancer detection.

Logistic Regression:

1. Initialize:

Set $w = 0$

2. For $t = 1$ to T :

a. Compute the log-odds: $z = w \cdot x_i$

b. Apply the sigmoid function to get the predicted probability: $y = \frac{1}{1 + e^{-z}}$

c. Compute the gradient of the loss function: $\nabla J(w) = -n \sum_{i=1}^n (y_i - y^{\wedge}) \cdot x_i$

d. Update the parameters: $w = w - \eta \cdot \nabla J(w)$

3. Output:

Final model parameters: w

SVM

The purpose of SVM is to find the hyper plane that best splits data elements into different groups. The optimization problem includes a margin term and a cost function that penalizes misclassifications.

Objective function:

$$(x + a)^n = 1/2 \|w\|^2 + C \sum_{i=1}^n \max(0, 1 - y_i(w \cdot x_i + b))$$

1. When $1 - y_i(w \cdot x_i + b) > 0$:

$$(\partial/\partial w) \max(0, 1 - y_i(w \cdot x_i + b)) = (\partial/\partial w)(1 - y_i(w \cdot x_i + b)) = -y_i x_i$$

2. When $1 - y_i(w \cdot x_i + b) \leq 0$:

$$(\partial/\partial w) \max(0, 1 - y_i(w \cdot x_i + b)) = 0$$

Now, substitute these derivatives back into the main equation

$$n(x + a)^{n-1} = w - C \sum_{i=1}^n y_i x_i \cdot I(1 - y_i(w \cdot x_i + b) > 0)$$

Derivatives = $\partial / \partial w$ and $\partial / \partial b$

$\|w\|^2$ represents the Euclidean norm (magnitude) of the weight vector w .

C serves as a regularization parameter, striking a balance between minimizing training error and keeping the weight vector small.

$\sum_{i=1}^n$ – denotes the sum over all training instances.

$\max(0, 1 - y_i(W \cdot X_i + b))$ represents the hinge loss, penalizing deviations from correct classifications.

Gradient Boosting Machines

In this study, gradient Boosting reduces a loss function by constructing a collection of weak learners progressively. At each iteration, a weak learner is fitted to the loss function's negative gradient in respect to the ensemble's most recent prediction.

Objective function:

$$(x + a)^n = \sum_{i=1}^n L(y_i, y_i) + \sum_{i=1}^n \Omega(fk)$$

Derivative with respect to x : $1 dx dF = n(x+a)^{n-1}$

Derivative of $L(y_i, y_i)$ with respect to x :

For simplicity, let $g(x) = L(y_i, y_i)$,

Then, $\frac{dx}{dg} = dy^i dg \cdot \frac{dx}{dy^i}$

Derivative of $\Omega(fk)$ with respect to x :

Similar to the above, let $h(x) = \Omega(fk)$,

Then, $\frac{dx}{dh} = \frac{df_k}{dh} \cdot \frac{dx}{df_k}$

Combine the derivatives:

$$\frac{Dx}{dF} = \sum_{i=1}^n \left(\frac{dx}{dg} + \frac{dx}{dh} \right)$$

Derivatives: $\frac{\partial L(y_i, y^i)}{\partial y^i}$

Logistic Regression

In this study logistic regression is used to model the likelihood of a binary outcome. As part of the optimization problem, the probability function needs to be maximized, and optimization algorithms make use of its derivatives.

Function:

$$L(w) = \prod_{i=1}^n [n_i = 1 \cdot P(Y = y_i | x_i)]^{y_i} \cdot [1 - P(Y = y_i | x_i)]^{1 - y_i}$$

Derivatives = $\frac{\partial l(w)}{\partial w}$

In case of these models which has been used in this study, has their specific derivatives formulas along with third specific functions. The derivatives of the cost function for SVM model with respect to the parameters are used in gradient descent and other optimization approaches. The probability function for logistic regression has derivatives based on the weight vector. The output of the above by SVM and logistic regression is depicted below.

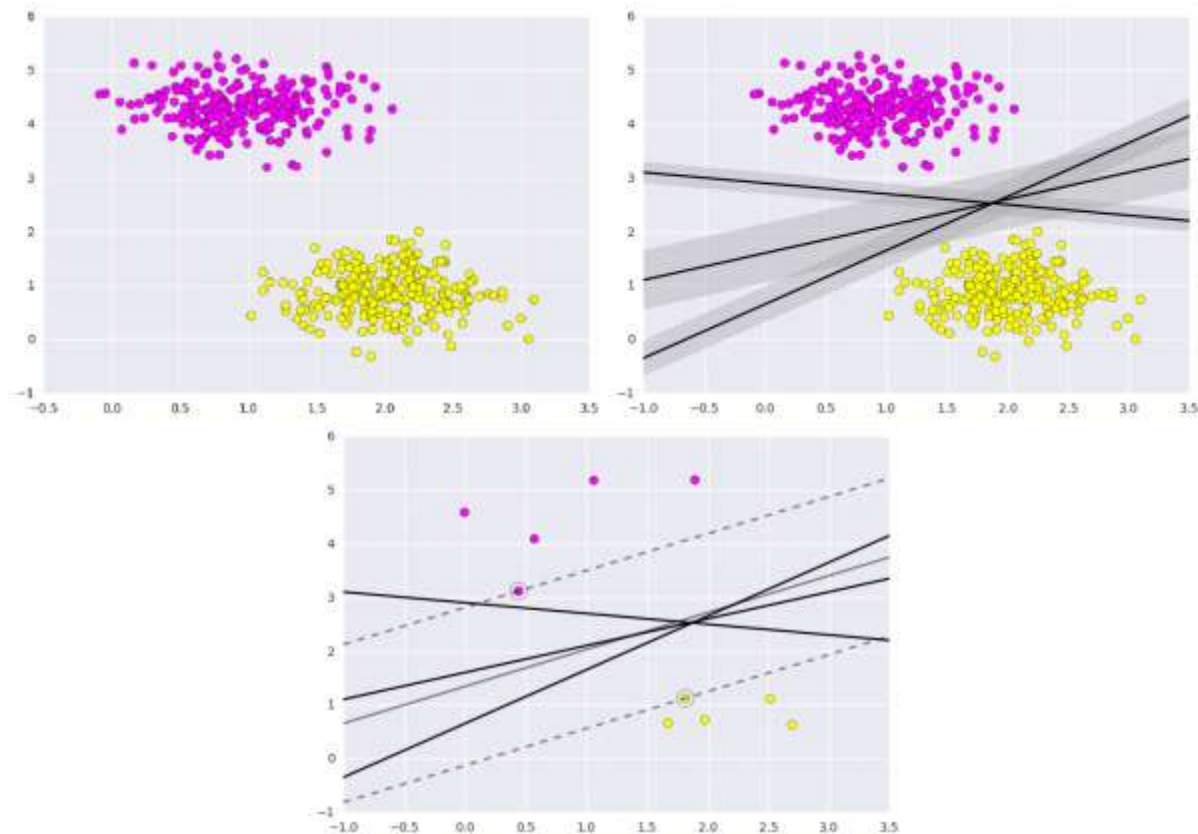


Figure 6: Output

5. Conclusion

The performance of Neutro-Meta SHAP and LIME in oral cancer detection is a significant step in order to improve the weak matches and transparency along with ML models. This study highlights the critical significance of earlier detection in case of handling the global health limitation generated by oral cancer. On the basis of the utilization in the case of advanced ML methods as well as deep learning processes, this study indicates a dedication to improving diagnostic precision and gives valuable ideals during the time of model development. The development of model performance, as remembered in metrics which are accuracy, recall, precision, as well as specificity, which shows the possibility of the proposed approaches. The interpretability tools of this study, such as Neutro-Meta SHAP and Neutro-Meta LIME, donate to unravelling the decision-making procedures along with its complex algorithms, which fosters a more explicit understanding of the features that influence the predictions of oral cancer. In a similar way, this study develops its effect on the current world healthcare applications along with the interpretability model that enhances with patient data as well as getting feedback from medical experts. This step supports the practical utility of the created model for this study in the case of healthcare purposes, and also finds the research gap under the advanced technology as well as healthcare practice.

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