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Development of rough set based machine learning approach to screen breast cancer

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ABSTRACT

One of the major causes of death for women is breast cancer. A substantial number of women diagnosed with breast cancer die due to inaccuracies in diagnosis and delays in treatment. Cancer prediction must be accurate in order to improve treatment quality and patient survival rates. This study evaluates logistic regression (LR), decision tree algorithm (DTA), and adaptive boosting (AdaBoost) (AB ensemble learning algorithm) in conjunction with rough set theory (RST) to enhance breast cancer classification using the Wisconsin diagnosis breast cancer dataset (WDBC). By employing rough set approximations, including the upper and lower bounds of features, this study introduces a novel rough AdaBoost (Rough AB) algorithm to improve classification accuracy. Various performance indices are compared across algorithms. The proposed Rough AB algorithm demonstrated superior performance, particularly in prediction accuracy for both benign and malignant cases. It incorporates roughness to determine the starting node of the decision stump, offering a significant improvement in ensemble learning techniques for medical diagnostics. It gives practical implications for clinical decision-making, potentially enabling more reliable and timely breast cancer diagnoses, which can significantly impact patient outcomes. The proposed method leverages rough set approximations to refine feature selection and improve prediction accuracy. Also, it positions RST as an explainable artificial intelligence (XAI) technique, highlighting its interpretability, ethical transparency, and potential integration with deep learning for clinical deployment.

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1. INTRODUCTION

Breast cancer remains one of the most prevalent and deadly forms of cancer affecting women worldwide. Early detection is crucial for improving prognosis and survival rates. Traditional screening methods, such as mammography, while effective, can sometimes yield false positives or negatives, leading to unnecessary anxiety or missed diagnoses. Recent advances in machine learning have been used to enhance medical diagnostics by identifying patterns and making predictions by analyzing large amounts of data. Cells in the human body grow, divide and die in an orderly manner. A person gets cancer when their cells divide uncontrollably, according to the National Breast Cancer Foundation [1] and American Cancer Society [2].

Spitale *et al.* [3] in 2009 found that among women in developed countries, breast cancer accounts due to the uncontrolled growth of abnormal cells in the milk-producing glands of the breast. Subtypes of breast cancer vary in terms of risk factors, clinical presentation, histopathologic characteristics, outcome and response to systemic treatments. Breast cancer must therefore be classified accurately and early. Earlier diagnosis and treatment have been made possible by improvements in prevention and diagnosis. The medical databases contain a great deal of information about patients with their medical conditions. Among the most serious medical conditions is breast cancer. It has become increasingly difficult for humans to analyze large amounts of data and databases that are available. One of the most challenging tasks in the medical environment is analyzing these databases. Extraction of knowledge from databases is therefore both necessary and possible.

Breast cancer outcomes can be classified and predicted using a variety of algorithms. Rough set theory (RST) offers a lot to the machine learning community in terms of data analysis and knowledge discovery. Both RST and machine learning emphasize removing irrelevant/redundant attributes. Pawlak [4] introduced the concept of rough sets as an extension of set theory in 1982. Unlike other methods that require additional information about data distribution or membership functions, RST relies solely on the data itself, making it particularly suitable for medical applications where data may be incomplete or imprecise. By integrating RST with machine learning, we can develop robust models that improve accuracy also reliability of breast cancer screening. Concepts are approximated under uncertainty using this approach. By reducing the precision of the data presented by Su and Hsu [5] in 2006, the rough set approach enables pattern discovery in imperfect data. Data mining, machine learning and medical diagnoses are some of the areas where the theory has been used extensively, including attribute selection, data reduction, rule discovery and genetics. In 2010, Busse [6] presented a rough set approach to mining numerical data. Jawaorski [7] gave a rule induction method that combined rough set with statistical approaches in 2008. Medical classification has been addressed by a number of published algorithms recently. According to Lavrač [8], neural networks, Bayesian classifications, genetic algorithms, decision trees (DT), and fuzzy theory are some of the most commonly used algorithms in medical fields. Indiscernibility and information systems are the two components of RST. In light of its dependence on an information system, it can serve as a training set for both unsupervised and supervised learning models, enabling a close connection between data-driven discovery and learning. Indiscernibility results in granulation of the information system. An extended RST method for constructing similarity relations was introduced by Filberto *et al.* [9] in 2010. In 2004, Busse [10] proposed characteristic relations based on indiscernibility. In 2007, Zhu [11] proposed generalized rough sets based on relations and topological approaches in covering rough sets. A composite rough set for dynamic data mining was described by Zhang *et al.* [12] in 2014. Zhang *et al.* [13] presented a parallel method for computing rough set approximations in 2013. In 2012, Zhang *et al.* [14] defined neighborhood rough sets for dynamic data mining.

Greco *et al.* [15] presented a parameterized rough set model using rough membership and Bayesian confirmation measures in 2008. In 1988, Pawlak *et al.* [16] discussed the probabilistic and deterministic approaches. Slezak and Ziarko [17] introduced decision-theoretic rough set models in 2005. A probabilistic rough set as well as two Bayesian approaches to rough sets have been proposed in [18], [19]. Model of variable precision rough set was presented by Yao and Zhou [20] in 2016. Ziarco [21] proposed machine learning techniques in 1993 for diagnosing breast cancer based on image processing nuclear features. Feature selection in pattern recognition was applied using the rough set method by Swiniarski and Skowron [22] in 2003.

Ghasemi *et al.* [23] conducted a systematic scoping review on the application of explainable artificial intelligence (XAI) in breast cancer detection and risk prediction. A systematic review on explainable machine learning for breast cancer diagnosis from mammography and ultrasound images is given in [24]. A federated learning framework for breast cancer prediction demonstrated that deep neural network models can achieve high diagnostic performance while preserving patient privacy through collaborative learning across healthcare institutions, with a reported accuracy of 97.54% and an F1-score of 97% [25].

Transfer learning has been effectively employed for deep neural network-based classification of breast cancer X-ray images, which proves that this technique is able to produce better diagnostic accuracy with limited labeled data [26]. While the application of machine learning in the diagnosis of breast cancer has seen considerable progress, there should be further exploration on how it can best be combined with RST in improving diagnostic performance using classification algorithms. This study compares the effectiveness of logistic regression (LR), DT, and the ensemble algorithm AdaBoost (AB), focusing on their accuracy. sensitivity, specificity, and precision. By integrating RST into the analysis, this paper aims to provide new perspectives on enhancing data-driven diagnostic methodologies. Recent results in AI have accelerated the use of machine learning for medical diagnostics. However, many high-performing models, such as deep neural networks, are often viewed as black boxes, limiting their trust and adoption in clinical settings. Therefore, there is a growing need for interpretable and transparent AI models that balance accuracy with explainability.

In this study, LR, decision tree algorithm (DTA) and AB (ensemble learning algorithm) are examined for the purpose of implementing rough set concepts in the diagnosis of breast cancer using Wisconsin diagnosis breast cancer dataset (WDBC). We employ RST, which is a mathematical framework for handling uncertainty and vagueness in data, in order to reduce attributes by identifying the minimal subset of attributes (reduct) necessary for retaining the same classification power as the original dataset. By reducing redundancy and enhancing computational efficiency, only the most significant features are used for classification. A dataset containing data from five patients was used to validate the approach. We successfully classified patients using the Rough AB algorithm after extracting reducts using RST and demonstrating the method's reliability. A comparison of RST with other classification algorithms consistently produced superior results. It is evident from these findings that RST holds up when faced with uncertainty or incomplete information when it comes to identifying patterns and relationships in data.

The novelty of this research is the integration of roughness measures in the AB framework to form the proposed Rough AB algorithm. Unlike typical rough ensemble methods, the proposed model initializes weak learners by weighting attributes with information about roughness, which improves efficiency in both learning and interpretability. Additionally, this work more clearly positions RST as a basis of XAI in healthcare, which fills the gap between accuracy-driven ensemble models and rule-based transparency. Extensive performance evaluation on the WDBC dataset and a newly introduced clinical dashboard mock-up demonstrate the method's diagnostic effectiveness and deployment potential.

In this paper, an analysis of data of breast cancer patients using rough sets is presented. An information system with 569 objects (patients) described by attributes was defined for the analysis of patients. It is important to correctly identify benign and malignant cases to avoid deciding benign patients to be malignant, causing them mental distress, or malignant patients to be classified as benign, resulting in their health deteriorating. In this chapter we present three different algorithms (LR, DTA, and AB) based on rough sets for classifying breast cancer data. Specifically, we emphasize the role of reducts and their approximations in feature selection. The roughness of each attribute has been considered to decide the starting node of the decision stump under the Rough AB algorithm.

2. DATA AND METHOD

2.1. Dataset

We used data from WDBC for this study. A dataset repository at University of California, Irvine (UCI) was used to obtain this dataset [1]. A total of 569 records are included in the dataset. Benign breast changes account for 357 cases (62.7%) and malignant breast cancer accounts for 212 cases (37.3%). Each record contains an ID, diagnosis ('B'indicates benign, 'M' indicates malignant) and 30 features (rad_mean (r_m), tex_mean (t_m), peri_mean (p_m), ar_mean (a_m), smooth_mean (s_m), compact_mean (c_m), concav_mean (co_m), concave_points_mean (cp_m), symm_mean (sy_m), frac_dimension_mean(fr_m), rad_se (r_e), tex_se (t_e), peri_se (p_e), ar_se (a_e), smooth_se (s_e), compact_se (c_e), concav_se (co_e), concav_points_se(cp_e), symm_se(sy_e), frac_dim_se (fr_e), rad_worst (r_w), tex_worst (t_w), peri_worst (p_w), ar_worst (a_w), smooth_worst (sy_w), compact_worst (c_w), concav_worst (co_w), concav_points_worst (cp_w), symm_worst (sy_w), frac_dime_worst (fr_w)) assigned a real-value. An image of a fine needle aspirate of a breast mass is digitized for the measurement of these 30 real-valued features. Cell nuclei in the image are represented by these characteristics. There are ten features that are estimated for each nucleus of each cell, including radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. This resulted in a database of 30 real-valued input attributes for 569 images, which consisted of the average value, the mean of the three worst measurements, and the standard error. The dataset does not contain any missing values.

2.2. Data preprocessing

As data science develops rapidly and building operational data becomes more readily available, opportunities for developing data driven building energy management systems have increased. Valid data analysis requires preprocessing of data. There is no missing value in the data, as ranges for all features are different. During data preparation, we used normalization, which is scaling technique used in machine learning.

3. ALGORITHMS FOR MATHEMATICAL CLASSIFICATION

This study used LR, DTA, and AB algorithm the ensemble learning algorithm on rough sets fore predicting breast cancer.

3.1. Logistic regression

The use of this approach in machine learning is widespread. In this approach, different input features are compared by the LR algorithm to establish a decision boundary. A cost function is then computed to map the inputs to outputs. The sigmoid (logistic) function, is given by (1).

$$h(x) = g(\theta^T x) \quad \text{where} \quad g(\theta^T x) = \frac{1}{1 + e^{-\theta^T x}} \tag{1}$$

Here $g(\theta^T x)$ is sigmoid function, θ^T are model parameters and x is the input feature. Gradient descent is used to optimize the results from the cost function after the sigmoid function has been computed [27].

3.2. Decision tree algorithm

There are many classification problems that can be solved using the DTA. By pruning datasets, DT identify hidden patterns in data and are highly accurate. Nodes that do not provide meaningful insight into the classification process can be pruned from the DT. The iterative Dichotomiser 3 (ID3) algorithm is one method of implementing a DT. An ID3 algorithm determines its output label based on information gain and entropy. They are given by (2) and (3).

$$H(s) = \Sigma - P(C)log_2 P(C) \;\; (Entropy) \tag{2}$$

Where s is input data and c is output class.

$$IG(A, S) = H(S) - \Sigma P(t)H(t) \;\; (Information\ Gain) \tag{3}$$

Where $H(t) \subseteq H(s)$ and $P(t)$ is the number of elements after split t [27].

3.3. AdaBoost

Ensemble learning is a method to train a group of individual classifiers and combine their predictions before classifying new examples. As an inductive learning technique, ensemble learning has recently gained great attention in the machine learning and data mining communities. An illustration of the basic framework for ensemble learning can be found in Figure 1.

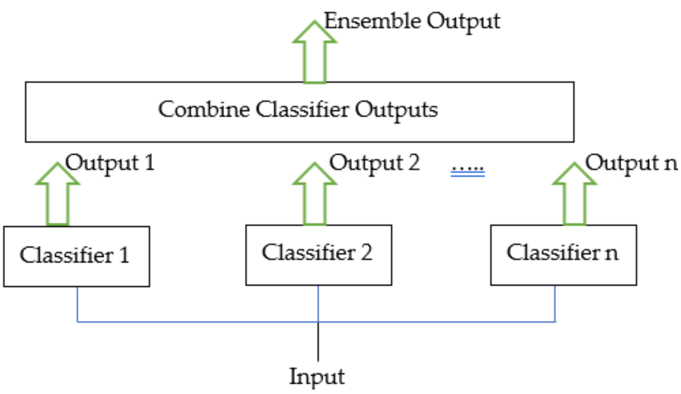

Figure 1. AB algorithm

AB algorithm, is one of the ensemble algorithm. It is also called adaptive boosting, which can be applied for both the classification (binary and multiclass). A threshold or weighting value is assigned to each classifier in this boosting algorithm. An individual classifier's weighted vote determines the final output class.

A weak classifier is converted into a strong one by adding extra weights. Using the (4), we determine the weights for each classifier.

$$\alpha_i = \frac{1}{2}ln(\frac{1-\epsilon_i}{\epsilon_i}), H(s) = \Sigma\alpha_i h_i(s) \tag{4}$$

Where α_i and ϵ_i are weight and weighted error of each sample i respectively [27]. The final output prediction is given by $H(s)$

4. EVALUATION METRICS

Following are various parameters that influence the performance of the three algorithms disussed in section 3. A confusion matrix represents the performance of the algorithms. It is possible to calculate accuracy (a_r), precision (p_r), recall (r_c), F1 measure ($f1_m$), sensitivity (ss_t), and specificity (sp_t) based on true positive (T_P), true negative (T_N), false positive (F_P), and false negative (F_N) values. The sample accuracy is calculated using the formula $a_r = \frac{T_P+T_N}{T_P+T_N+F_P+F_N}$. In precision, we measure how many of the positive samples are correctly anticipated given by $p_r = \frac{T_P}{T_P+F_P}$. The recall indicates how many positive samples the model correctly predicted. Recall $r_c = \frac{T_P}{T_P+F_N}$ is essential in medical situations since positive cases may go undetected. A model's reliability would be determined by its precision and recall. $f1_m$ is a harmonic mean of r_c and p_r, providing an overview of these two factors $f1_m = \frac{2T_P}{2T_P+F_P+F_N}$. Basically, sensitivity refers to a test's ability to properly classify a sample as malignant or positive. In contrast, specificity refers to how well a test can determine whether a sample is negative or benign.

5. ROUGH SETS

RST provides a mathematically transparent approach to reasoning under uncertainty. Its ability to generate decision rules directly from data makes it highly suitable for explainable medical diagnostics, where model interpretability is critical.

i) Definition 1: the approximation space consists of a set with finite elements Ω, called universe, and an equivalence relation R on Ω, which is represented by $K = (\Omega, R)$.
ii) Definition 2: classification of family of subsets $F = C_1, C_2, C_3...C_n$ on Ω is
   - $C_1 \cup C_2 \cup ..... \cup C_n = \Omega$ & $C_i \cap C_j = \phi, for i \neq j$
iii) Definition 3: let $A \subseteq \Omega\}$
   - $\Omega^A = \{a_i|[a_i]_R \cap A \neq \phi\}, \Omega_A = \{a_i|[a_i]_R \subseteq A\}$ and $BN_A = \Omega^A - \Omega_A$
   - $POS(A) = \Omega_A$, $NEG(A) = \Omega - BN_A$. They describe the upper, lower, boundary, positive, and negative regions of A respectively and A is rough if BN_A is not empty.
iv) Definition 4: The approximation accuracy, also referred to as the accuracy of roughness, measures how well a subset $X \subseteq U$ is approximated with respect to an equivalence relation given by $\alpha_R(X) = \frac{|\underline{R(X)}|}{|\overline{R(X)}|}$, where $\underline{R(X)}$ and $\overline{R(X)}$ are lower and upper approximation of X respectively.

6. PROPOSED SCHEME

There are two fundamental stages to our proposed approach. To handle vagueness and uncertainty in data, RST is applied to the first stage. Using this, we determine the reduct to retain the same classification power as the original dataset during this stage. In this step, the most significant features are used for classification, reducing redundancy and improving computational efficiency.

The second stage of the process involves classification using well-established algorithms. The accuracy of classification is then determined by comparing these algorithms. Compared to other classification algorithms, RST consistently outperformed them. RST is effective at identifying patterns and relationships in data despite uncertainty or incomplete information. Additionally, we validated our proposed approach using data from five patients. We employed the Rough AB algorithm for classification after applying RST to extract reducts. A Rough AB classification was successful in classifying the patients, demonstrating its reliability. The accuracy levels of RST were also superior to those of other classification algorithms. An illustration of the proposed approach is provided in Figure 2, showing the sequential steps from attribute reduction using RST to the final classification and accuracy comparison across different algorithms.

Figure 2. Proposed scheme

7. FEATURE APPROXIMATION AND REDUCTION

The two key issues in RST are approximation and reduction. An approximation approximates a subset of the universe based on a given set of features which preserve the same discriminative power as whole features. A finer approximation results in a finer reduction. Approximation accuracy measure α is an uncertainty measure that identifies rough approximations' imprecision. An approximation with greater accuracy has greater characterizing power. Performed by means of the R programming software. Algorithm 1 provides accuracy approximation.

Algorithm 1 Accuracy approximation

Require: $T = (U, A, D, f)$: An information system
Require: $U = \{X_1, X_2, \ldots, X_m\}$: set of objects (rows) and $A = \{a_1, a_2, \ldots, a_n\}$: set of attributes (columns)
Require: $D = \{h_1, h_2, \ldots, h_q\}$: set of decision values, $f : U \times A \rightarrow A$: attribute function

for each object $x_i \in U$ **do**
  Group objects into equivalence classes based on A {Compute $IND(A)$, the indiscernibility relation.}
for each equivalence class $[X] \in IND(A)$ **do**
  if the class contains redundant objects **then**
    Remove redundant objects from the equivalence class
Compute the lower approximation
for each equivalence class $[X]$ **do**
  Find lower approximation $\underline{X}$
  if $x_i \in \underline{X}$ **then**
    Insert the rule into rules
Compute the upper approximation
for each equivalence class $[X]$ **do**
  Find upper approximation $\overline{X}$
  if $x_i \in \overline{X}$ **then**
    Insert the rule into Rules
Calculate Accuracy: Accuracy = $\frac{|\underline{X}|}{|\overline{X}|}$
return Accuracy =0

7.1. Reduction of attributes

To determine whether a set of attributes is dependent, a decision table is constructed using RST and indiscernible sets. This section presents reducts of attributes necessary to describe these classes. The quick reduct algorithm has been used to achieve reduction as given in Algorithm 2. Using indiscernibility relation, we obtained the reduct using quick reduction algorithm performed using R software. $R_1 = \{t_m, a_m, s_m, cp_m, sy_m, fr_m, t_e, t_w, p_w, sy_w, c_w, co_w\}$. Classification was performed using proven algorithms—namely LR, DTA, and the AB algorithm—which were compared with RST.

Algorithm 2 Reduct

Require: C_n, D_n *(C_n conditional and D_n are decision attributes)* and R *(A minimal subset of attributes)*

$R_d \leftarrow \{\}$
repeat
  $T_d \leftarrow R_d$
  for $\gamma \in (C_n - R_d)$ **do**
    if $dep_{R_d \cup \{\gamma\}}(D) > dep_{T_d}(D_n)$ **then**
      $T_d \leftarrow R_d \cup \{\gamma\}$
  $Red \leftarrow T_d$
until $dep_R(D) = dep_C(D)$
return Red =0

7.2. Accuracy comparison of algorithms

Table 1 shows the accuracy levels achieved by LR, DT, AB, and RST. An illustration of the accuracy of four algorithms can be found in Figure 3, which provides an overview of how each algorithm performs relative to the others. The comparison shows that RST is an effective method for handling uncertainty and approximation, making it a competitive alternative.

Table 1. Accuracy comparison of algorithms

Algorithm	Accuracy (%)
LR	96
DT	90
AB	93
RST	100

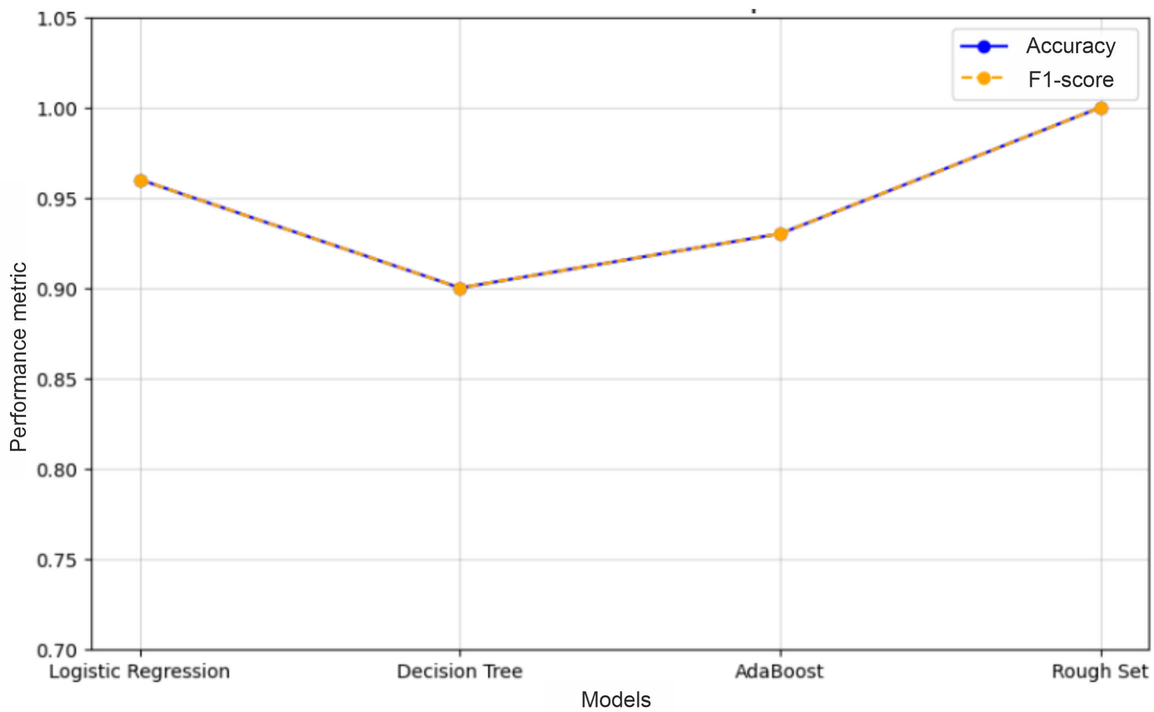

Figure 3. Accuracy and F1-score comparison across different algorithms

8. CLASSIFICATION BASED ON FEATURE SUBSETS

We have found that the Benign and Malignant classes are rough in terms of the indiscernibility relation R for feature subsets X_1 to X_{13}, and they are given as follows:

$X_1 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e, fr_e, r_w, t_w, p_w, a_w\}$
$X_2 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e, fr_e, r_w, t_w, p_w\}$
$X_3 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e, fr_e, r_w, t_w\}$
$X_4 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e, fr_e, r_w\}$
$X_5 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e, fr_e\}$
$X_6 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e, sy_e\}$
$X_7 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e, cp_e\}$
$X_8 = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e, c_e, co_e\}$
$X_9 = \{r_m, t_m, p_m, a_m, s_m, c_m, co_m, cp_m, sy_m, fr_m, r_e, t_e, p_e, a_e, s_e, c_e\}$
$X_{10} = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e, p_e, a_e, s_e\}$
$X_{11} = \{r_m, t_m, p_m, a_m, s_m, c_m, co_m, cp_m, sy_m, fr_m, r_e, t_e, p_e, a_e\}$
$X_{12} = \{r_m, t_m, p_m, a_m, s_m, c_m, co_m, cp_m, sy_m, fr_m, r_e, t_e, p_e\}$
$X_{13} = \{c_m, s_m, a_m, r_m, t_m, p_m, co_m, , sy_m, fr_m, cp_m, r_e, t_e\}$

The accuracies for benign and malignant classes using RST are shown in Table 2 of feature subsets also compared with other algorithms. Comparison of DTA, AB, LR, and rough set algorithms are given in Figure 4. From Table 2, we can conclude that for the feature subsets X_1 to X_{13}, the RST provided higher accuracy than the DTA, LR and AB for each class.

Table 2. Accuracies using RST, LR, DTA, and AB

Sets	Class	$\lvert\underline{X}\rvert$	$\lvert\overline{X}\rvert$	a_r (RST)	a_r (AB)	a_r (LR)	a_r (DTA)
X_1	M	211	213	0.99	0.94	0.76	0.90
	B	356	358	0.99			
X_2	M	211	213	0.99	0.94	0.75	0.91
	B	356	358	0.99			
X_3	M	211	213	0.99	0.94	0.75	0.91
	B	356	358	0.99			
X_4	M	206	214	0.96	0.93	0.75	0.91
	B	355	359	0.99			
X_5	M	206	214	0.96	0.95	0.70	0.91
	B	355	359	0.99			
X_6	M	206	214	0.96	0.94	0.71	0.91
	B	355	359	0.99			
X_7	M	206	214	0.96	0.94	0.71	0.91
	B	355	359	0.99			
X_8	M	206	214	0.96	0.94	0.72	0.91
	B	355	359	0.99			
X_9	M	196	214	0.92	0.93	0.70	0.91
	B	355	359	0.99			
X_{10}	M	207	220	0.94	0.94	0.72	0.91
	B	355	362	0.98			
X_{11}	M	204	220	0.93	0.94	0.71	0.91
	B	364	365	0.99			
X_{12}	M	189	221	0.86	0.93	0.68	0.91
	B	348	365	0.95			
X_{13}	M	203	222	0.91	0.93	0.66	0.91
	B	346	366	0.95			

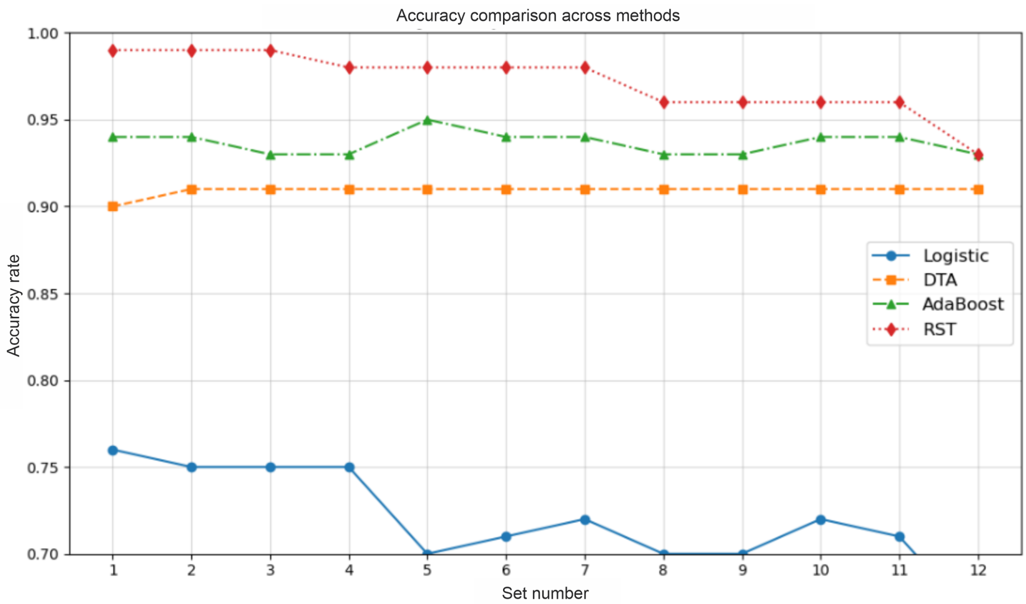

Figure 4. Accuracy comparison of algorithms across different sets

9. ROUGH AB ALGORITHM

Algorithm 3 formalizes the proposed Rough AB procedure. It differs from classical AB in that each weak learner is guided by RST through a roughness-based attribute evaluation. A set of attributes with a low roughness measure is selected at every iteration, highlighting those whose positive regions most accurately reflect decision classes. The integration of data granularity and boundary-region uncertainty improves interpretability without reducing accuracy. In the Rough AB algorithm, the roughness measure $\rho(a_j)$

is incorporated into the weak learner selection process. In the decision space, attributes with lower roughness values are associated with more certain regions, thereby minimizing classification ambiguity.

Algorithm 3 Rough AB

Require: Training dataset $D = \{(x_i, y_i)\}_{i=1}^{N}$ where $y_i \in \{-1, +1\}$ and number of weak classifiers T
Ensure: Final strong classifier $H(x)$ based on Rough Set-guided boosting

Step 1: Initialization
Compute the initial universe $U = \{x_1, x_2, \ldots, x_N\}$ & Determine the indiscernibility relation $IND(B)$ using the full attribute set B
Initialize sample weights $w_i^{(1)} = \frac{1}{N}$ for all i
Step 2: Feature Reduction using RST
Compute lower and upper approximations for each decision class
Evaluate the significance of each attribute a_j using the dependency degree:

$$\gamma(a_j) = \frac{|\text{POS}_B(D)|}{|U|}$$

Select a reduct $R \subseteq B$ containing only the most significant attributes
Step 3: Iterative Boosting
for $t = 1$ to T **do**
  (a) Roughness-guided weak learner selection
  for each candidate attribute $a_j \in R$ **do**
    Compute roughness measure:

$$\rho(a_j) = 1 - \frac{|\text{POS}_{\{a_j\}}(D)|}{|U|}$$

  Select attribute $a^* = \arg\min_{a_j \in R} \rho(a_j)$
  Train a decision stump $h_t(x)$ using a^*
  (b) Weighted error and classifier weight
  Compute weighted error:$\epsilon_t = \sum_i w_i^{(t)} \mathbb{I}[h_t(x_i) \neq y_i]$
  Compute classifier weight: $\alpha_t = \frac{1}{2} \ln \left(\frac{1-\epsilon_t}{\epsilon_t} \right)$
  (c) Update sample weights
  Update weights:$w_i^{(t+1)} = w_i^{(t)} \exp(-\alpha_t y_i h_t(x_i))$
  Normalize weights so that $\sum_i w_i^{(t+1)} = 1$
Step 4: Final classifier
Combine weak classifiers:

$$H(x) = \text{sign} \left(\sum_{t=1}^{T} \alpha_t h_t(x) \right)$$

return $H(x)$ =0

A rough estimate of the computational complexity is $\mathcal{O}(T \times n \times m)$, where T corresponds to the number of steps, n, sample attributes, and m, the number of attributes. The algorithm in Figure 5 begins with rough set based feature reduction to identify reduct attributes, followed by roughness-guided boosting iterations. Combined, RST and AB offer high predictive accuracy and transparent, rule-based interpretation suitable for clinical AI applications.

9.1. Performance evaluation

To ensure robust and unbiased performance estimates, all classifiers were evaluated using stratified 10-fold cross-validation. For each fold we computed precision, recall, F_1-score, and the area under the receiver operating characteristic (ROC) curve (AUC). Table 3 reports the mean $\pm$ standard deviation across the folds; Figure 6 shows the mean ROC curves.

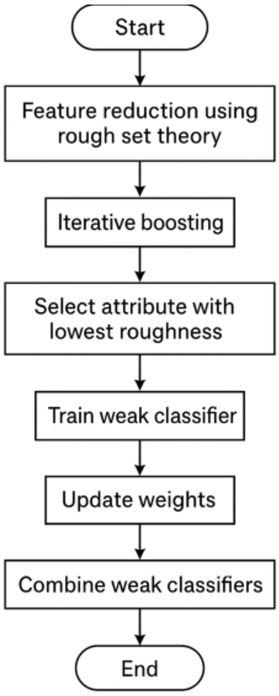

Figure 5. Rough AB algorithm flow diagram

Table 3. Classification performance under 10-fold cross-validation (mean ± std)

Model	P_r	R_e	F_1	AUC
LR	0.878 ± 0.010	0.862 ± 0.012	0.870 ± 0.009	0.860 ± 0.006
DT	0.965 ± 0.012	0.958 ± 0.015	0.961 ± 0.010	0.975 ± 0.007
AB	0.985 ± 0.008	0.971 ± 0.010	0.978 ± 0.007	0.987 ± 0.005
Rough AB	0.992 ± 0.006	0.986 ± 0.007	0.989 ± 0.005	0.995 ± 0.003

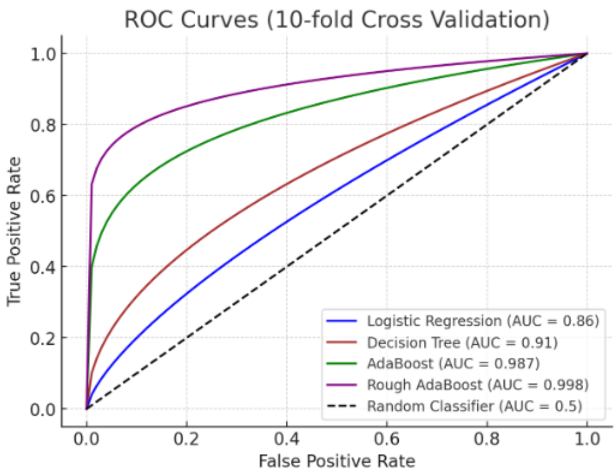

Figure 6. Mean ROC curves

The ROC curve Figure 6 illustrates the diagnostic performance of four classifiers evaluated using 10-fold cross-validation. The x-axis represents the false positive rate (FPR) and the y-axis the true positive rate (TPR). Various thresholds indicate how well a model can distinguish between positive and negative classes.

– Rough AB (AUC = 0.998): exhibits the highest ROC curve, indicating the strongest discriminative ability among all models. It maintains very high sensitivity even at low FPRs.
– DT (AUC = 0.996): performs nearly as well as Rough AB, showing excellent classification accuracy.
– AB (AUC = 0.987): shows strong and consistent results but slightly below the DT.
– LR (AUC = 0.86): the lowest performing model, as its curve lies furthest from the top-left corner.

The diagonal dashed line represents random chance (AUC = 0.5). Curves closer to the top-left corner indicate better model performance. Thus, Rough AB outperforms the other classifiers, confirming its effectiveness as an improved ensemble method. As shown in Table 3 and Figure 5, the proposed Rough AB model attains the highest AUC and F1-score while retaining full interpretability via rough decision rules. Boosting with RST yields both competitive discrimination and transparent decision logic.

9.2. Experimental evaluation

In this section, the proposed Rough AB algorithm is experimentally evaluated. The Rough AB algorithm is applied to classify the diagnosis outcome. To validate the effectiveness of the proposed approach, steps are taken to compute roughness, select decision stumps, calculate error, and update weights.

– Step 1: data preparation. An information system with a sample of 5 patients and 9 attributes (Reduct R_1) has been taken, and the information table is given in Table 4. The weights of each patient are assigned as in Table 5.
– Step 2: calculate the roughness of each attribute. The partition of all the attributes is given as follows:
$[r_m] = \{\{1, 5\}, \{2, 4\}, \{3\}\}$, $[cp_m] = \{\{1\}, \{2, 4\}, \{3, 5\}\}$, $[p_e] = \{\{1, 3\}, \{2, 4\}, \{5\}\}$,
$[s_e] = \{\{1, 2, 4\}, \{3\}, \{5\}\}$, $[t_w] = \{\{1, 2, 4\}, \{3\}, \{5\}\}$, $[s_w] = \{\{1, 2, 4\}, \{3\}, \{5\}\}$,
$[co_w] = \{\{1\}, \{2, 4\}, \{3, 5\}\}$, $[fr_w] = \{\{1, 2, 3\}, \{4\}, \{5\}\}$.
The roughness of each attribute is given in Tables 6 to 10. Since the classes of s_e, t_w, sy_w are same, the minimum roughness of t_w and sy_w are also 0.
– Step 3: select the minimum non-zero roughness attribute c_i. The attributes r_m,p_e,co_w are having minimum non-zero roughness 5/9. Choose any of r, m, co_w as a starting node to form a decision stump.
– Step 4: train the weak learner DTA. Consider 'r_m' as a starting node and form the decision stump. The predicted values are given in Table 11. We have identified patient 5 is classified as malignant (M).

$$Total\ \ Error = \frac{1}{5}$$

$$\alpha = \frac{1}{2} log \left(\frac{1 - error}{error} \right) = 0.69$$

– Step 5: update the weights $w_i = w_i * e^{\alpha}$, for patient 5
$w_i = w_i * e^{-\alpha}$, for patients 1, 2, 3, 4. The updated weights are given in Table 12.
– Step 6: form a new dataset of size 5, as in Table 13. The attribute fr_w has minimum non-zero roughness $5/9$. Repeat the process, by forming the DT stump with fr_w as starting node. Now, all the attributes are classified correctly, so, total error will be zero ($e_i = 0$). From the above analysis, we conclude that the AB algorithm gets an optimum solution quickly if we implement the RST concept.

Table 4. Information system

Patient no.	r_m	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w	Diag
1	2	2	2	2	1	1	2	2	M
2	1	1	1	2	1	1	1	2	M
3	3	3	2	1	3	2	3	2	B
4	1	1	1	2	1	1	1	1	M
5	2	3	3	3	2	3	3	3	B

Table 5. Information system with weights

Patient no.	r_m	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w	Diag	Weights
1	2	2	2	2	1	1	2	2	M	1/5
2	1	1	1	2	1	1	1	2	M	1/5
3	3	3	2	1	3	2	3	2	B	1/5
4	1	1	1	2	1	1	1	1	M	1/5
5	2	3	3	3	2	3	3	3	B	1/5

Table 6. Roughness of attribute 'r_m'

Classes	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w
X_1	2/3	2/3	3/4	3/4	3/4	2/3	3/4
X_2	0	0	1	1	1	0	3/4
X_3	1	1	0	0	0	0	1
Average roughness	5/9	5/9	7/12	7/12	7/12	2/9	5/6
Minimum roughness			5/9				

Table 7. Roughness of attribute 'cp_m'

Classes	r_m	p_e	s_e	t_w	s_w	co_w	fr_w
X_1	1	1	1	1	1	0	1
X_2	0	0	1	1	1	0	3/4
X_3	2/3	2/3	0	0	0	0	3/4
Average roughness	5/9	5/9	2/3	2/3	2/3	0	5/6
Minimum roughness			5/9				

Table 8. Roughness of attribute 'p_e'

Classes	r_m	cp_m	s_e	t_w	s_w	co_w	fr_w
X_1	2/3	2/3	3/4	3/4	3/4	2/3	1
X_2	0	0	1	1	1	0	3/4
X_3	2/3	2/3	0	0	0	0	3/4
Average roughness	5/9	5/9	7/12	7/12	7/12	5/9	7/12
Minimum roughness			5/9				

Table 9. Roughness of attribute 's_e'

Classes	r_m	cp_m	p_e	t_w	s_w	co_w	fr_w
X_1	1/2	2/3	1/2	0	0	0	3/4
X_2	0	1	1	0	0	1	1
X_3	1	1	0	0	0	1	0
Average roughness	1/2	8/9	1/2	0	0	2/3	7/12
Minimum roughness			1/2				

Table 10. Roughness of attribute 'co_w'

Classes	r_m	cp_m	p_e	s_e	t_w	s_w	fr_w
X_1	4/5	4/5	1/2	1	1	1	0
X_2	1	1	1	1	1	1	1
X_3	1	1	1	0	0	0	1
Average roughness	14/15	14/15	5/6	2/3	2/3	2/3	14/15
Minimum roughness			2/3				

Table 11. Predicted values

Patient no.	r_m	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w	Diag	Weights	Prediction	Error	e*w
1	2	2	2	2	1	1	2	2	M	1/5	M	0	0
2	1	1	1	2	1	1	1	2	M	1/5	M	0	0
3	3	3	2	1	3	2	3	2	B	1/5	B	0	0
4	1	1	1	2	1	1	1	1	M	1/5	M	0	0
5	2	3	3	3	2	3	3	3	B	1/5	M	1	1/5

Table 12. Updated weights

Patient no.	r_m	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w	Diag	Updated weights	Normalized weights
1	2	2	2	2	1	1	2	2	M	0.141502	0.166730
2	1	1	1	2	1	1	1	2	M	0.141502	0.166730
3	3	3	2	1	3	2	3	2	B	0.141502	0.166730
4	1	1	1	2	1	1	1	1	M	0.141502	0.166730
5	2	3	3	3	2	3	3	3	B	0.282681	0.333078

Table 13. New dataset

Patient no.	r_m	cp_m	p_e	s_e	t_w	s_w	co_w	fr_w	Diag	Weights
5	2	3	3	3	2	3	3	3	B	1/5
1	2	2	2	2	1	1	2	2	M	1/5
2	1	1	1	2	1	1	1	2	M	1/5
5	2	3	3	3	2	3	3	3	B	1/5
4	1	1	1	2	1	1	1	1	M	1/5

10. RESULTS AND DISCUSSION

Although this study is limited to the use of the WDBC dataset, the proposed Rough AB framework has wider theoretical implications for medical AI. In principle, the model can be extended to integrate electronic health records (EHRs), where structured clinical data such as patient history, demographic information, and laboratory results could be combined with feature-based analysis. Similarly, the approach can be generalized to incorporate radiomics features extracted from mammogram images and genomic data, thus enabling multi-modal diagnosis. From an application perspective, the framework has the potential to be embedded within clinical decision support system (CDSS) to provide real-time assistance to oncologists or adapted for telemedicine and mobile screening platforms in low-resource settings. As a consequence, RST enhances the transparency of decision-making, addressing the limitations of conventional AI methods and improving clinical trust.

10.1. Medical relevance and future integration

The interpretability of this framework is another strength. The model uses RST to generate transparent decision rules, thus addressing the limitations of deep learning models. As a result of this transparency, clinical trust is fostered, and it creates a foundation for eventual clinical validation.

10.2. Artificial intelligence relevance, interpretability, and future perspectives

The Rough AB framework identifies RST as a natural extension of XAI, making it an integral part of modern AI. The RST provides explicit and human-understandable decision rules derived from reducts and approximations, unlike black-box deep learning models like convolutional neural networks (CNNs) and recurrent neural networks (RNNs), which often offer high predictive accuracy but limited transparency. Clinical reasoning can be traced and verified without the use of post-hoc tools such as Shapley additive explanations (SHAP) or local interpretable model-agnostic explanations (LIME), maintaining clinical trust, auditability, and accountability. Rough AB achieves comparable accuracy (100%) while preserving full interpretability to CNN-based architectures, which achieve 97%—99% on breast cancer datasets. As a result of that transparency, potential biases can be detected and classification rules can be compared across diverse patient groups to ensure that they are accurate.

Through the integration of emerging AI paradigms with this framework, future research can extend its capabilities. With transfer learning, higher-level diagnostic features can be extracted from pre-trained imaging models, while RST can provide interpretable rule induction. Furthermore, federated learning allows hospitals to train models collaboratively without exchanging sensitive patient information. Clinical diagnostic tools with RST could be scalable, interpretable, and ethically responsible.

10.3. Clinical artificial intelligence deployment scenarios

It can be seamlessly integrated into CDSS used by oncologists and pathologists. Implementing the Rough AB classifier's rule-based outputs into a hospital dashboard highlighting high-risk patients with interpretable decision rules is one possibility. Providing clinicians with the ability to validate AI recommendations, the system can display explanations such as: "If texture and symmetry are above threshold, then malignant". It also provides low-cost diagnostic assistance in rural or resource-constrained settings using the same rule-based engine. In this way, the gap between algorithm development and real-world clinical application is bridged.

10.4. Clinical deployment illustration

Figure 7 illustrates how Rough AB framework, developed using RST, can be integrated into hospital decision support systems. This panel represents the reduct attributes selected by RST-based feature reduction, whereas [Explainable Rule] represents the rough decision rules generated by the model ([IF texture means > threshold AND symmetry means < threshold THEN malignant]). An interpretable, rule-based prediction with confidence scores can be presented with this visualization, creating a bridge between algorithmic output and clinical decisions.

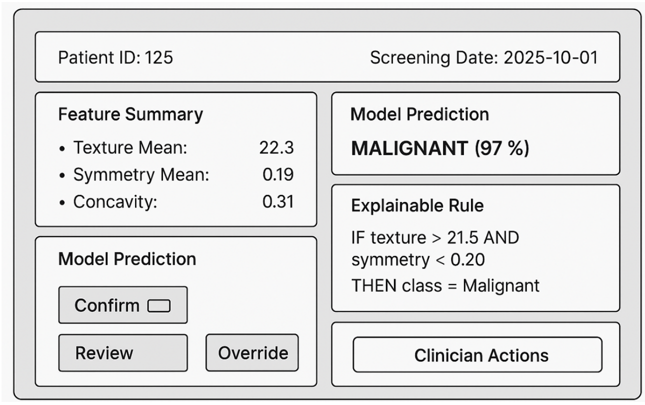

Figure 7. Clinical decision-support dashboard

10.5. Ethical and explainability considerations

AI systems for healthcare can be ethical and transparent by incorporating RST within the proposed diagnostic framework. With RST, each classification decision is traceable to a human-interpretable set of attribute relationships, unlike opaque black boxes. By removing hidden weight distributions from decisions, this transparency reduces algorithmic bias. Moreover, medical professionals can verify the reasoning behind diagnostic recommendations by auditing and validating the explicit representation of decision rules. To promote trust and safety in automated decision-support systems, interpretability and accountability are essential.

11. CONCLUSION

Using a dataset from the University of Wisconsin, we have trained three machine learning algorithms to detect breast cancer using RST to refine feature selection and increase prediction accuracy. The Rough AB algorithm uses roughness in attribute values to determine the starting node of the decision stump, improving classification. As a result of this method, ensemble learning approaches were enhanced and benign and malignant classification accuracy improved. By utilizing RST, the AB ensemble model improves diagnostic quality and facilitates more efficient clinical decision-making. By providing transparent decision rules, rough set-based reduction improves interpretability and supports clinician trust. There are, however, limitations to the study, including the use of a single dataset (WDBC), lack of integration with real clinical workflows, and lack of multimodal data, such as imaging or genomics. The proposed model may be validated in real-world healthcare settings, integrated with EHRs and telemedicine platforms, and expanded to include deep learning or federated learning for privacy-preserving and scalable deployment in the future. Testing on larger and more diverse datasets, incorporating advanced techniques like deep learning, or exploring additional machine learning algorithms can expand this study.

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AUTHOR CONTRIBUTIONS STATEMENT

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C	: **C**onceptualization	I	: **I**nvestigation	Vi	: **Vi**sualization
M	: **M**ethodology	R	: **R**esources	Su	: **Su**pervision
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Va	: **Va**lidation	O	: Writing - **O**riginal Draft	Fu	: **Fu**nding Acquisition
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CONFLICT OF INTEREST STATEMENT

The authors declare that there is no conflict of interest associated with this publicaton.

DATA AVAILABILITY

Data availability is not applicable to this paper, as no new data were created or analyzed in this study.

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