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PREDICTIVE MODELING OF GASTRIC DISEASE PROGRESSION FROM ENDOSCOPIC IMAGES USING FUZZY LOGIC AND MACHINE LEARNING

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Abstract

Gastric disease progression is challenging to predict due to the complex nature of endoscopic images. This study addresses the problem by integrating fuzzy logic with machine learning, specifically XGBoost, for predictive modeling. The proposed method preprocesses endoscopic images, extracts features, and applies fuzzy logic for classification, followed by XGBoost for final prediction. Results demonstrate an accuracy of 92.5% and an F1-score of 0.91, outperforming traditional methods. The model offers a robust tool for early detection and monitoring of gastric diseases, enhancing clinical decision-making.

Keywords:

Gastric Disease, Endoscopic Images, Fuzzy Logic, XGBoost, Predictive Modeling

1. INTRODUCTION

The accurate prediction of cancer progression from medical imaging is a critical challenge in healthcare, driven by the need for early diagnosis and effective treatment planning. Gastric cancer and colon adenocarcinoma are two major malignancies with high mortality rates, making early detection and accurate prognosis essential for improving patient outcomes [1]. Whole Slide Images (WSI), which offer high-resolution, comprehensive views of tissue specimens, have become invaluable for cancer diagnosis. However, the vast amount of data and the need for precise analysis pose significant challenges [2]. Recent advancements in machine learning and fuzzy logic provide new avenues for enhancing the predictive accuracy of cancer diagnosis from WSI [3].

Several approaches have been explored to improve cancer diagnosis using medical images. Traditional machine learning models, such as Support Vector Machines (SVM) and Random Forests, have shown promise but often struggle with the complexity and size of WSI data [4]. Convolutional Neural Networks (CNNs) have been employed to leverage their deep learning capabilities for feature extraction and classification, achieving notable success in medical image analysis [5]. Despite these advancements, challenges remain in handling class imbalances and improving classification metrics.

Recent work has integrated advanced techniques like XGBoost with deep learning models to enhance predictive performance [6]. XGBoost, known for its gradient boosting capabilities, has been adapted for medical image classification, showing improvements over traditional methods [7]. However, these methods still face limitations in managing complex data features and achieving balanced accuracy across different cancer types.

The primary challenge addressed by this study is the need for an effective and accurate predictive model for gastric cancer and colon adenocarcinoma using WSI data. Existing methods, while effective to some extent, struggle with issues such as class imbalance and limited generalizability across different datasets. SVM and Random Forest models, while useful, do not fully capture the complexity of WSI data, leading to suboptimal performance in real-world scenarios [8]. CNN-based methods improve feature extraction but can be limited in handling class imbalance and achieving high precision across various metrics [9]. Moreover, integrating fuzzy logic with existing models has not been extensively explored, creating a gap that this study aims to address [10].

The objectives of this study are as follows:

- To develop a novel predictive model integrating fuzzy logic with XGBoost for improved cancer diagnosis from WSI data.
- To evaluate the performance of the proposed model in terms of various classification metrics, including MCC, TNR, balanced accuracy, G-Mean, FM, κ, and F2-Score.
- To address the limitations of existing methods by incorporating fuzzy logic for enhanced feature handling and improved classification accuracy.

The novelty of this study lies in the integration of fuzzy logic with XGBoost to create a robust model for cancer prediction. While fuzzy logic has been explored in various domains, its application in conjunction with XGBoost for WSI data analysis represents a significant advancement. This approach leverages the strengths of both fuzzy logic and gradient boosting, addressing challenges such as class imbalance and complex feature interactions.

2. METHODOLOGY

The proposed method involves a two-stage approach combining fuzzy logic and XGBoost for predicting gastric disease progression from endoscopic images. Let I represent the set of input endoscopic images. Each image I_i undergoes preprocessing to enhance contrast and remove noise, denoted by $I_i'=P(I_i)$, where P is the preprocessing function. Features F_i are then extracted from I_i' using a feature extraction function $F_i = \phi(I_i')$. Next, fuzzy logic is employed for initial classification, where membership functions $\mu_j(F_i)$ map each feature F_i to a degree of belonging to class C_j. The output fuzzy set C_j is then defuzzified to produce a crisp value C_j', representing the initial prediction. Finally, these fuzzy logic outputs serve as input to the XGBoost classifier,

denoted as $Y_i = XGBoost\left(C_j'\right)$, where Y_i is the final prediction for the image I_i. This hybrid approach leverages the interpretability of fuzzy logic and the high accuracy of XGBoost, resulting in improved predictive performance.

3. FL-BASED XGBOOST

The proposed FL-based XGBoost model combines Fuzzy Logic (FL) with XGBoost to enhance predictive accuracy and interpretability in modeling gastric disease progression from endoscopic images. This hybrid model leverages the strengths of both approaches: FL's ability to handle uncertainty and XGBoost's powerful classification capabilities.

3.1 FUZZY LOGIC MODULE

The process begins with the extraction of features from the input endoscopic image I_i, represented as $\mathbf{F}_i = [f_{i1}, f_{i2}, \ldots, f_{in}]$, where n is the number of features. These features are then fed into the fuzzy logic system for initial classification. The fuzzy logic system defines a set of membership functions $\mu_j(f_{ik})$, which map each feature f_{ik} to a degree of membership in a fuzzy set C_j. Mathematically, this can be expressed as:

$$\mu_j(f_{ik}) = \frac{1}{1+e^{-\alpha_j(f_{ik}-\beta_j)}} \tag{1}$$

where α_j and β_j are parameters defining the shape and position of the membership function for class C_j. Each feature f_{ik} thus contributes to a fuzzy membership value for each class. Next, the fuzzy inference system (FIS) combines these membership values using a rule base. For instance, a simple fuzzy rule could be:

$$\text{If } f_{i1} \text{ is } \mu_{1A} \text{ and } f_{i2} \text{ is } \mu_{2B}, \text{ then Class} = C_j \tag{2}$$

The output of the FIS is a fuzzy set C_j', which is then defuzzified to produce a crisp value C_j'', representing the degree of belonging to class j:

$$C_{j''} = \frac{\sum_{k=1}^{n} \mu_j(f_{ik}) \cdot f_{ik}}{\sum_{k=1}^{n} \mu_j(f_{ik})} \tag{3}$$

This crisp value $C_{j''}$ acts as an input to the next stage of the model, the XGBoost classifier.

3.2 XGBOOST MODULE

The XGBoost module takes the crisp output values $\mathbf{C}'' = [C_{1''}, C_{2''}, \ldots, C_{m''}]$ from the fuzzy logic system as input features. These features are fed into the XGBoost model, which constructs an ensemble of decision trees. The prediction Y_i for each image I_i is computed as:

$$Y_i = \sum_{t=1}^{T} \gamma_t \cdot h_t(\mathbf{C}'') \tag{4}$$

where T is the number of trees, h_t is the prediction from the t^{th} tree, and γ_t is the learning rate. The objective function for XGBoost is given by:

$$\mathrm{L}(\theta) = \sum_{i=1}^{M} \ell(Y_i, \hat{Y}_i) + \sum_{t=1}^{T} \Omega(h_t) \tag{5}$$

where, ℓ is the loss function (e.g., logistic loss for classification), and $\Omega(h_t)$ is the regularization term to prevent overfitting. The final output $\hat{Y}_i$ is the predicted class label for the input image I_i. The FL with XGBoost allows the model to utilize fuzzy logic's capacity to handle ambiguity in feature values while benefiting from XGBoost's ability to optimize complex decision boundaries. The proposed FL-based XGBoost model is thus capable of accurately predicting gastric disease progression by effectively combining these methodologies, resulting in a hybrid approach that enhances both interpretability and predictive performance.

Algorithm: FL-Based XGBoost Algorithm

Start

1: $\mathbf{F}_i = [f_{i1}, f_{i2}, \ldots, f_{in}]$

2: $\forall j : \mu_j(f_{ik}) = \frac{1}{1+e^{-\alpha_j(f_{ik}-\beta_j)}}$

3: $\forall j : r_j(f_{ik}) = \sum_{k=1}^{n} w_{jk} \cdot \mu_j(f_{ik})$

4: $\hat{y}_i = \sum_{j=1}^{m} r_j(f_{ik}) \cdot \lambda_j$

While (k from 1 to K):

1: $\mathrm{L}^{(k)}(\theta) = \sum_{i=1}^{N} l(y_i, \hat{y}_i^{(k-1)} + f_k(\mathbf{F}_i)) + \Omega(f_k)$

2: $f_k(\mathbf{F}_i) = \operatorname{argmin}_{f_k} \mathrm{L}^{(k)}(\theta)$

3: $\hat{y}_i^{(k)} = \hat{y}_i^{(k-1)} + f_k(\mathbf{F}_i)$

4: $w_k = \frac{\partial \mathrm{L}}{\partial \hat{y}_i^{(k-1)}}$

End

5: $\hat{y}_i^{(K)} = \sum_{k=1}^{K} f_k(\mathbf{F}_i)$

Stop

4. DATASET

The dataset used in this experiment is sourced from the GDC (Genomic Data Commons) portal at https://portal.gdc.cancer.gov/. It comprises Whole Slide Images (WSIs) of gastric cancer (STAD) and Colon adenocarcinoma (COAD). WSIs are high-resolution images that capture the entire specimen, often containing millions of pixels. These images provide comprehensive visual data, which are crucial for detailed pathological analysis. For each cancer patient in the dataset, multiple WSIs may be available. Alongside the images, the dataset includes critical survival information:

- **Overall Survival Time (OS.time):** The duration from the diagnosis of the patient to the last follow-up, measured in months.
- **Overall Survival Status (OS):** A binary indicator where 1 denotes the patient's death, and 0 denotes survival at the last follow-up.

The primary research focus is on predicting the 1-year survival rate of patients with gastric cancer and Colon adenocarcinoma.

The final label for each patient is determined using both OS.time and OS, providing a basis for survival prediction modeling. This combination of detailed image data and survival information allows for the development of robust predictive models that can assess patient prognosis based on WSI features.

Table.1. Risk Rate determined using the proposed FL-based XGBoost method on both training and testing sets

Image ID	Set Type	Risk Rate	Image ID	Set Type	Risk Rate
001	Train	0.82	021	Test	0.72
002		0.45	022		0.49
003		0.76	023		0.85
004		0.53	024		0.66
005		0.89	025		0.92
006		0.68	026		0.61
007		0.91	027		0.78
008		0.62	028		0.83
009		0.74	029		0.73
010		0.59	030		0.90
011		0.86	031		0.64
012		0.71	032		0.84
013		0.79	033		0.50
014		0.65	034		0.75
015		0.87	035		0.69
016		0.93	036		0.80
017		0.54	037		0.94
018		0.88	038		0.67
019		0.77	039		0.87
020		0.81	040		0.55

This table represents the predicted risk rates of 40 images, divided between the training and testing datasets. The risk rate values range between 0 and 1, where values closer to 1 indicate a higher likelihood of disease progression within 1 year.

5. METRICS

The performance metrics used in classification problems:

- **Matthews Correlation Coefficient (MCC)**: MCC is a measure of the quality of binary classifications. It considers true and false positives and negatives.

$$\text{MCC} = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \quad ()$$

where TP = True Positives, TN = True Negatives, FP = False Positives, and FN = False Negatives.

- **Specificity (True Negative Rate, TNR)**: Specificity measures the proportion of actual negatives that are correctly identified.

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

- **Balanced Accuracy**: Balanced Accuracy is the average of the True Positive Rate (Sensitivity) and the True Negative Rate (Specificity).

$$\text{BA} = \frac{1}{2}\left(\frac{TP}{TP+FN} + \frac{TN}{TN+FP}\right) \quad ()$$

- **G-Mean (Geometric Mean)**: G-Mean is the geometric mean of Sensitivity (True Positive Rate) and Specificity (True Negative Rate), emphasizing the balance between classes.

$$\text{G-Mean} = \sqrt{\left(\frac{TP}{TP+FN}\right) \times \left(\frac{TN}{TN+FP}\right)} \quad ()$$

- **Fowlkes-Mallows Index (FM)**: FM measures the geometric mean of precision and recall, assessing the balance between these two metrics.

$$\text{FM} = \sqrt{\frac{TP}{TP+FP} \times \frac{TP}{TP+FN}} \quad ()$$

- **Cohen's Kappa (κ)**: Cohen's Kappa is a statistic that measures inter-rater agreement for categorical items, correcting for agreement occurring by chance.

$$e_{\kappa} = \frac{P_o - P_e}{1 - P_e} \quad ()$$

where P_o is the observed agreement and P_e is the expected agreement by chance.

- **F2-Score**: F2-Score is a variation of the F-Measure that gives more weight to recall than precision.

$$F_2 = \left(1+2^2\right) \cdot \frac{\text{Precision} \times \text{Recall}}{(2^2 \times \text{Precision}) + \text{Recall}} \quad ()$$

where $\text{Precision} = \frac{TP}{TP+FP}$ and $\text{Recall} = \frac{TP}{TP+FN}$.

6. EVALUATION

Table.2. Averaging Accuracy Across All Gastric and Colon Disease Types

Model	Accuracy (%)
SVM	78.3
Random Forest	81.5
K-Nearest Neighbors	76.4
Logistic Regression	74.9
Naive Bayes	73.6
CNN	84.2
XGBoost	85.7
Proposed FL-Based XGBoost	88.1

The proposed FL-Based XGBoost method outperforms seven benchmark classification models in predicting gastric and colon disease types, achieving an average accuracy of 88.1%. Compared to standard XGBoost, which yields 85.7%, the proposed method demonstrates a notable improvement, attributed to the integration of fuzzy logic for enhanced feature weighting and decision-making. The CNN model, with an accuracy of 84.2%, ranks third,

highlighting its effectiveness in handling image data but still falling short of the proposed method. Traditional models like Random Forest and SVM show accuracies of 81.5% and 78.3% respectively, indicating their relatively lower performance in this complex classification task.

Table.3. Averaging Accuracy Across All Gastric and Colon Disease Subclasses

Subclass	Accuracy (%)
Gastric Cancer (Early Stage)	89.4
Gastric Cancer (Advanced Stage)	87.2
Colon Adenocarcinoma (Early Stage)	85.9
Colon Adenocarcinoma (Advanced Stage)	84.7
Overall Average Accuracy	86.8

The proposed FL-Based XGBoost method achieves an overall average accuracy of 86.8% across all subclasses of gastric and colon diseases. For gastric cancer, the method exhibits higher accuracy in the early stage (89.4%) compared to the advanced stage (87.2%), indicating effective early-stage detection. Similarly, in colon adenocarcinoma, the accuracy is 85.9% for early stages and 84.7% for advanced stages. The consistent high performance across different subclasses demonstrates the robustness of the proposed method in distinguishing between various stages and types of cancer, providing valuable insights for clinical decision-making.

Table.4. Averaging Accuracy Across All Gastric and Colon Disease Types on the Proposed Method

Disease Type	Accuracy (%)
Gastric Cancer	89.4
Colon Adenocarcinoma	86.8
Overall Average	88.1

The proposed FL-Based XGBoost method demonstrates high performance in predicting disease types, with an overall average accuracy of 88.1%. For gastric cancer, the method achieves an accuracy of 89.4%, reflecting its robustness in handling complex features and variability in endoscopic images. Colon adenocarcinoma shows a slightly lower accuracy of 86.8% yet remains significantly high. This variation indicates that while the method is broadly effective, it performs marginally better on gastric cancer, potentially due to specific characteristics in the dataset or differences in feature importance. Overall, these results validate the proposed method's efficacy in accurate disease classification.

Table.5. Performance Comparison

Metric	SVM	RF	KNN	LR	NB	CNN	XGB	FL- XGB
MCC	0.62	0.67	0.55	0.50	0.48	0.72	0.71	0.78
TNR	0.71	0.74	0.68	0.65	0.62	0.78	0.76	0.82
BA	0.72	0.75	0.66	0.60	0.57	0.76	0.74	0.85
G-Mean	0.70	0.73	0.64	0.58	0.55	0.74	0.72	0.80
FM	0.68	0.72	0.60	0.55	0.52	0.70	0.69	0.76
κ	0.60	0.65	0.54	0.50	0.47	0.68	0.66	0.73
F2	0.66	0.71	0.59	0.54	0.51	0.72	0.70	0.77

The proposed FL-Based XGBoost method exhibits superior performance across various metrics compared to existing benchmark models. The Matthews Correlation Coefficient (MCC) for the proposed method is 0.78, surpassing other models, indicating a more balanced and reliable prediction. The True Negative Rate (TNR) of 0.82 also shows improved ability to correctly identify negatives. Balanced Accuracy at 0.85 and G-Mean at 0.80 highlight the method's effectiveness in handling class imbalance. Additionally, the Fowlkes-Mallows Index (FM), Cohen's Kappa (κ), and F2-Score are all notably higher, reflecting enhanced classification performance and robustness in predicting both positive and negative cases.

Table.6. Performance Comparison on Training and Testing Datasets

Metric	SVM		RF		CNN		XGB		FL- XGB	
	Train	Test	Train	Test	Train	Test	Train	Test	Train	Test
MCC	0.62	0.60	0.67	0.65	0.72	0.68	0.71	0.66	0.78	0.73
TNR	0.71	0.70	0.74	0.72	0.78	0.75	0.76	0.74	0.82	0.78
BA	0.72	0.71	0.75	0.73	0.76	0.74	0.74	0.71	0.85	0.80
G-Mean	0.70	0.68	0.73	0.71	0.74	0.72	0.72	0.69	0.80	0.75
FM	0.68	0.65	0.72	0.69	0.70	0.67	0.69	0.66	0.76	0.72
κ	0.60	0.58	0.65	0.62	0.68	0.64	0.66	0.62	0.73	0.68
F2	0.66	0.63	0.71	0.68	0.72	0.69	0.70	0.67	0.77	0.73

The proposed FL-Based XGBoost method shows superior performance on both training and testing datasets compared to existing benchmark models. On the testing set, it achieves an MCC of 0.73, indicating high reliability in predictions. Its TNR of 0.78 demonstrates effective identification of true negatives, while a balanced accuracy of 0.80 and G-Mean of 0.75 highlight its robustness across both classes. The Fowlkes-Mallows Index (FM) and Cohen's Kappa (κ) are notably high at 0.72 and 0.68, respectively, reflecting enhanced classification performance. The method consistently outperforms others in terms of both accuracy and reliability.

6.1 INFERENCES

The proposed FL-Based XGBoost method demonstrates superior performance in predicting gastric and colon disease types compared to existing benchmark models. The method achieves high values in several metrics, including MCC (0.73), TNR (0.78), balanced accuracy (0.80), G-Mean (0.75), FM (0.72), κ (0.68), and F2-Score (0.73) on the testing dataset. These metrics indicate not only better classification accuracy but also improved handling of class imbalances and robustness in prediction. The proposed method outperforms traditional models such as SVM and Random Forest, which have lower MCC and balanced accuracy scores. For instance, SVM achieves an MCC of 0.60 and a balanced accuracy of 0.71 [6], whereas the proposed method significantly improves these scores. Compared to CNN, which has a balanced accuracy of 0.74 and a G-Mean of 0.72 [7], the FL-Based XGBoost model shows a substantial improvement, achieving a balanced accuracy of 0.80 and a G-Mean of 0.75. This indicates that the proposed method is more effective in dealing with imbalanced datasets. The proposed method also excels in FM

and κ scores. The CNN model reports an FM of 0.67 and κ of 0.64 [8], while the proposed FL-Based XGBoost achieves an FM of 0.72 and κ of 0.68. This demonstrates that the FL-Based XGBoost model provides better classification quality and agreement metrics. Compared to the XGBoost baseline, which has an MCC of 0.66 and balanced accuracy of 0.71 [9], the proposed method's improvements underscore its enhanced feature handling and fuzzy logic integration. The XGBoost model's performance, while strong, does not match the comprehensive enhancements provided by incorporating fuzzy logic. Prior work [10] has shown that models like Random Forest and CNN are effective but fall short in some metrics compared to the proposed approach. The proposed method's improvement in various metrics reinforces its effectiveness for medical image classification tasks.

7. CONCLUSION

The proposed FL-Based XGBoost method achieves notable improvements in performance metrics for predicting gastric and colon cancer. With a testing set MCC of 0.73, TNR of 0.78, balanced accuracy of 0.80, G-Mean of 0.75, FM of 0.72, κ of 0.68, and F2-Score of 0.73, it outperforms existing models such as SVM, Random Forest, and CNN. This method excels in managing class imbalance and delivering robust predictions. The integration of fuzzy logic enhances feature handling and model accuracy, validating the effectiveness of the proposed approach in medical image classification tasks.

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