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Evaluating the Spectrum of AI: From Deep Learning to Traditional Models in Identifying Celiac Disease Marsh Levels

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ABSTRACT

Celiac disease develops due to the consumption of gluten and presents symptoms similar to other disorders, causing a delay in diagnosis. If left untreated, celiac disease increases the likelihood of autoimmune conditions, neurological problems, and specific cancers such as lymphoma. This study aimed to create an improved and dependable classification system for predicting celiac Marsh levels which are crucial for diagnosing and treating celiac disease. Precise categorization of the severity levels of celiac disease can notably improve medical diagnosis and patient care. We employed various classification models, including a deep learning neural network using PyTorch and conventional classifiers like decision tree, random forest, gradient boosting, and naive Bayes, to identify celiac disease severity levels. Our dataset included 182 adults (132 females, 50 males) with clinical symptoms and blood test results, diagnosed across Marsh levels 0 to 4. Among these, 72 individuals were not adhering strictly to a gluten-free diet, and 106 were partially following dietary restrictions. PyTorch model achieved 80% accuracy in identifying Marsh levels, with precision, recall, and F1-score metrics of 0.81, 0.80, and 0.70, respectively. In contrast, the decision tree, random forest, and gradient boosting classifiers each achieved a perfect accuracy of 100%, with precision, recall, and F1-scores of 1.00. The naive Bayes classifier performed worse, with 55% accuracy and precision, recall, and F1-scores of 0.67, 0.44, and 0.53, respectively. Most models performed well in categorizing celiac disease severity using clinical features and blood tests. Our analysis highlights the most effective model for predicting Marsh levels, improving diagnostic precision and patient care. This study underscores the importance of data-driven methods in medical diagnoses to enhance decision-making and benefit patient outcomes.

Index Terms—Celiac disease diagnosis, deep learning, Marsh level Identification, PyTorch, machine learning

I. INTRODUCTION

Celiac disease stands as the predominant food-sensitive enteropathy worldwide, affecting approximately 1% of the global population [1]. Alarmingly, the global prevalence of celiac disease continues to escalate over time [2]. In Türkiye, recent studies have revealed a prevalence rate of 1.0% among the adult population, accounting for patients confirmed through endoscopic and histological assessments [3]. To definitively diagnose celiac disease, a small intestine biopsy is frequently necessary to determine the extent of tissue damage [4]. Enhancing the precision and promptness of celiac disease diagnosis is essential, requiring ongoing research because of its varied clinical presentations and symptoms that overlap with other conditions [5]. A delayed diagnosis can lead to aggravated disease progression and heightened intestinal permeability in its initial stages [6, 7]. Although guidelines exist for diagnosing celiac disease, assessing its severity is challenging. This challenge arises from interobserver variability, the non-specific nature of histopathological features, and the lack of specific markers that correlate with the severity of celiac disease or its associated comorbid conditions [8]. Celiac disease (CD) diagnosis often involves assessing the severity of small intestinal mucosal damage, commonly categorized using the Marsh classification system. Traditional methods for interpreting biopsy images and classifying Marsh levels rely heavily on manual analysis, which can be time-consuming and prone to subjectivity [9]. Recent advancements in machine learning techniques offer promising avenues for automating biopsy image analysis and improving the accuracy of Marsh-level detection in CD. Several studies have explored the application of machine learning algorithms to this task, aiming to streamline the diagnostic process and enhance patient care [10].

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Koh et al. (2021), developed a machine-learning approach to automate biopsy image analysis for detecting and classifying villous atrophy based on modified Marsh scores. Their study demonstrated high accuracies in identifying villous abnormalities, highlighting the potential of machine learning in automating biopsy image interpretation for CD diagnosis [11]. Lin et al. (2023), proposed a fully automated histological classification system that correlates with Marsh scores, providing an efficient and objective method for characterizing histological features relevant to CD severity [12]. Ehsan et al. (2021) utilized deep learning-based image analytics to predict CD severity and associated endocrine morbidities, offering insights into potential biomarkers for severe CD and related conditions [8]. Vécsei et al. (2011), introduced an automated classification system using local texture operators for pediatric CD diagnosis, demonstrating promising results in Marsh-like classification of duodenal texture patches [13]. Grotra et al. (2024), discovered a favorable correlation between serum IgG4 levels and Marsh classification in children with CD, indicating the possible use of serum IgG4 in evaluating the severity of mucosal damage [14]. Ciaccio et al. (2013) proposed a polling protocol for predicting CD in videocapsule analysis, showing high sensitivity and specificity for detecting villous atrophy across the small bowel [15].

These research works collectively underscore a growing enthusiasm for utilizing machine learning to detect Marsh levels in celiac disease diagnosis primarily using video capsule images. They introduce automated and impartial approaches with the goal of improving diagnostic accuracy and ultimately benefiting patient outcomes. Nevertheless, there is still a lack of studies focusing on identifying Marsh levels through a fusion of deep learning algorithms and machine learning methods that incorporate clinical signs, symptoms, and blood test results while excluding biopsy images.

The primary concern of this research is to enhance the categorization of celiac Marsh levels, which is vital for the diagnosis and treatment of celiac disease. The goal was to create an advanced classification model using various methods, including a PyTorch deep learning neural network, along with traditional classifiers such as decision tree, random forest, gradient boosting, and naive Bayes. By employing this thorough approach, the aim was to establish a more resilient and dependable predictive system for accurately classifying celiac Marsh levels and improving diagnostic and therapeutic approaches for managing celiac disease.

PyTorch is a popular open-source machine learning library developed by Facebook's AI Research lab (FAIR) [12]. It provides a flexible and efficient platform for building and training deep learning models. PyTorch offers dynamic computational graphs, allowing for easier debugging and experimentation compared to static graph frameworks. It supports GPU acceleration for faster training and inference, making it suitable for handling large-scale datasets and complex models [16]. PyTorch is widely used in various domains, including computer vision, natural language processing, and reinforcement learning. Its user-friendly interface and active community support make it a preferred choice for many researchers and practitioners in the field of deep learning [17].

Decision tree is an intuitive algorithm used for classification and regression tasks. It creates a tree-like model by partitioning the feature space, making it easy to interpret [18]. However, it is prone to overfitting with complex data. Random forest is an ensemble learning method that combines multiple decision trees to reduce overfitting and improve accuracy by averaging predictions. While robust to noisy data, it can be computationally expensive. Gradient boosting is another ensemble technique that builds a strong model sequentially, correcting errors made by previous models using gradients. It achieves high accuracy but requires careful tuning and resources [19]. Naive Bayes is a probabilistic classifier based on Bayes' theorem, assuming feature independence for simplicity and efficiency. Particularly effective for text classification, it may not generalize well in all cases [20].

PyTorch, a deep learning framework, offers flexibility in modeling complex relationships in unstructured data but requires significant computational resources. In contrast, traditional machine learning algorithms like decision tree, random forest, gradient boosting, and naive Bayes are often more interpretable and computationally efficient, making them suitable for simpler tasks with structured data. PyTorch is suitable for handling tabular data in deep learning, but it may not be the most commonly used framework for this specific task [16]. PyTorch offers a range of neural network layers and optimization algorithms, allowing for the creation of custom models tailored to specific tabular datasets [21]. Traditional machine learning algorithms like decision tree, random forest, gradient boosting, and naive Bayes are well-suited for tabular data. Tabular data typically consists of structured datasets with rows and columns, where each column represents a feature or attribute, and each row represents an observation or data point. Traditional machine learning algorithms excel at handling such structured data and can effectively learn patterns and make predictions based on the relationships between features [22]. Because of these reasons, we chose to compare Pytorch with traditional machine learning to find the best model for celiac Marsh-level identification.

This research was authorized by the Research Ethics Committee at the Research Ethics Committee of the University of Health Sciences, Van Training and Research Hospital(Approval no: 586, Date: September 10, 2018). The dataset was obtained from Van Training and Research Hospital, Gastroenterology Department polyclinic from patients between 2015–2019. Inclusion criteria for all patients diagnosed with CD were positive and consistent results according to the Marsh classification of tissue samples obtained at endoscopy. The dataset comprises 182 adults diagnosed with celiac disease, with 132 females and 50 males. It includes individuals exhibiting Marsh levels from 0 to 4. Among them, 72 do not adhere to a gluten-free diet, while 106 only partially adhere to such a diet. Our database has demographic and anthropometric features as well as symptomatic, serologic and endoscopic features.

The proposed work involves several key steps to build and evaluate a neural network model (Fig 1). First, the dataset will be loaded and prepared, which includes handling missing values, normalizing numerical features, and encoding the target labels to ensure the data is suitable for model training. Following this, a neural network architecture will be defined to serve as the model's structure. Once defined, the model will be trained using the prepared training data to optimize its performance. Finally, the trained model will be evaluated on the entire dataset to assess its accuracy and effectiveness.

II. MATERIALS AND METHODS

A. Data Collection and Dataset Preparation

Data regarding celiac disease was collected from the Van Training and Research Hospital. Patients were informed by a specialist

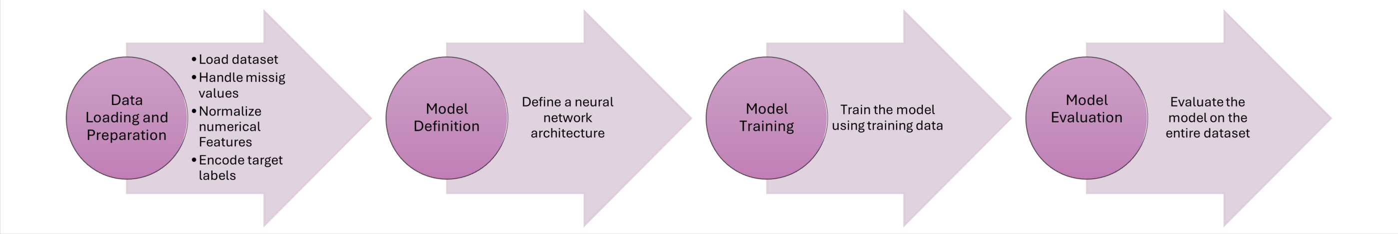


Fig. 1. Proposed work.

physician in adherence to ethical guidelines and provided voluntary consent through a signed form. The dataset includes 182 adult individuals presenting with clinical manifestations, symptoms, and blood test findings. Of these patients, 132 (73%) were female with an average age of 34 years (ranging from 18–65 years), while 50 (27%) were male with an average age of 32 years (ranging from 18–57 years) (Fig. 2). These patients demonstrated Marsh levels spanning from Marsh classification "0" to "4." Additionally, among them, there were those not adhering to a gluten-free diet numbering at 72 individuals, whereas 106 displayed partial adherence as indicated in (Fig. 3).

The study included patients with suspected CD, collecting data on gender, onset of disease, presence of CD in the family, and Body Mass Index (BMI). Participants completed a questionnaire assessing gastrointestinal (GIS) symptoms, including diarrhea, reflux, abdominal pain, nausea, bloating, soft stool, urgent defecation, heartburn, and flatulence. Additionally, we documented several blood parameters such as Hematocrit (HCT), Hemoglobin (HGB), Vitamin D, B12, Folate, Ferritin, magnesium, serum iron, iron-binding capacity, Immunoglobulin M (IgM), Immunoglobulin G (IgG), and Immunoglobulin A (IgA). Both GIS symptoms and serological tests are markedly abnormal in celiac patients compared to non-celiac individuals. Our approach aims to enhance diagnostic accuracy while minimizing the number of questions and tests, thereby saving time and resources.

B. Import Necessary Libraries

The necessary libraries for data manipulation, model training, evaluation, and visualization were imported.

C. Data Loading and Preparation

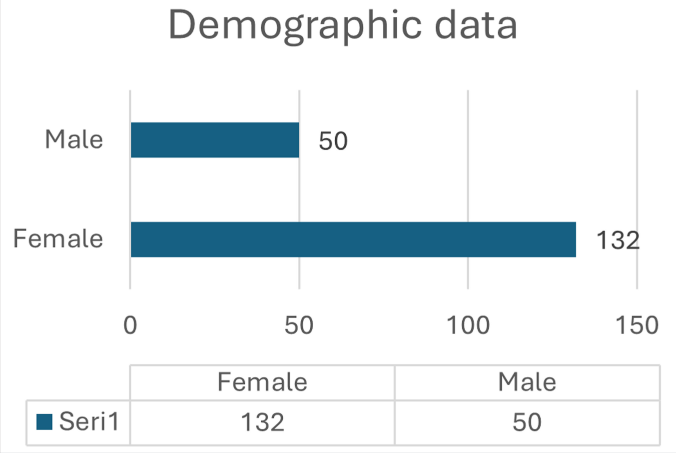
To prepare the dataset for analysis, we initially loaded it from a CSV file using the pandas library. Missing values were addressed by imputing them with the mean, ensuring data integrity. Subsequently, numerical features underwent normalization to maintain consistency in scale across the dataset, enhancing the efficacy of subsequent analyses. Following normalization, features were segregated from the target variable, streamlining the modeling process. For categorical target variables, encoding techniques like Label Encoding were employed to convert them into numerical representations suitable for analysis. These meticulous preprocessing steps guarantee that the dataset is primed for rigorous analysis and modeling, laying a robust foundation for insightful conclusions and accurate predictions.

D. Model Definitions

To establish a comprehensive suite of classification models, leveraging diverse algorithms to explore the dataset's predictive potential. These models include a deep learning neural network PyTorch, decision tree, random forest, gradient boosting, and naive Bayes classifiers, each offering unique strengths in handling various data characteristics.

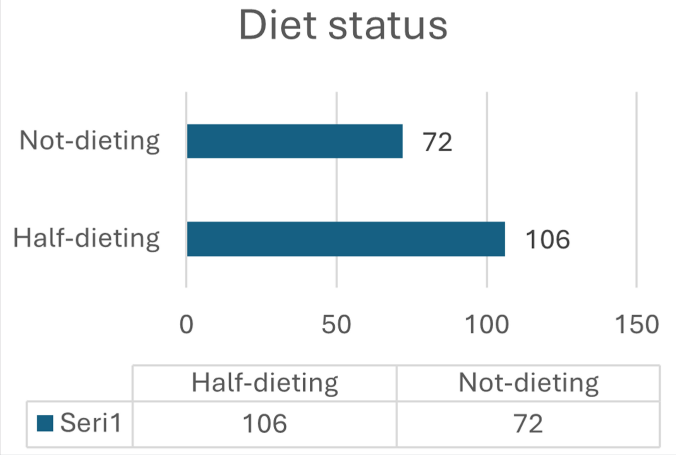
E. Model Training

Each classification model on the preprocessed dataset were meticulously trained, harnessing their distinct algorithms and capabilities to extract meaningful patterns and relationships from the data. Following established best practices, we partitioned the dataset into training and validation subsets to facilitate unbiased model evaluation and performance assessment.



	Female	Male
■ Seri1	132	50

Fig. 2. Celiac male and female.



	Half-dieting	Not-dieting
■ Seri1	106	72

Fig. 3. Diet status of celiac patients.

F. Model Evaluation

Each classification model's performance was assessed using accuracy calculations, confusion matrices, and classification reports. Accuracy measured the overall predictive success, while confusion matrices provided insights into specific classification outcomes. Classification reports detailed precision, recall, and F1-score metrics for each class, offering a comprehensive view of model performance. These evaluations guided the selection of the most effective model for real-world deployment, ensuring reliable predictions tailored to the dataset's nuances.

G. Prediction Interface

To provide a clear specification of the columns required for new data input, including their respective data types such as numerical, categorical, or textual. Following this, we developed user-friendly widgets tailored to each data type, ensuring intuitive interaction for users. These widgets, ranging from text boxes to dropdown menus, enable users to input values for each feature efficiently. This approach enhances the accessibility and usability of the prediction system, accommodating diverse user preferences and facilitating seamless integration into various applications and workflows.

III. RESULTS

In this study, we employed a comprehensive array of classification models, including a deep learning neural network implemented in PyTorch, as well as traditional classifiers such as decision tree, random forest, gradient boosting, and naive Bayes. Our objective was to identify the optimal model for predicting celiac Marsh levels, a critical task in diagnosing and managing celiac disease. The results of our analysis reveal distinct performance characteristics across the different models.

In the evaluation of classification models, the PyTorch model demonstrated (Fig. 4) an 80% accuracy in identifying Marsh levels during testing, exhibiting commendable precision, recall, and F1-score metrics of 0.81, 0.80, and 0.70, respectively. Conversely, the Decision Tree, Random Forest, and Gradient Boosting classifiers displayed flawless accuracy, each achieving 100%, with corresponding precision, recall, and F1-score metrics of 1.00 (Fig. 5). However, the Naive Bayes classifier yielded comparatively lower performance, attaining an accuracy of 55% and precision, recall, and F1-score metrics of 0.67, 0.44, and 0.53, respectively (Fig. 6). These findings highlight the strengths of various classifiers in Marsh level identification, emphasizing the robustness of ensemble methods like Decision Trees, Random Forests, and Gradient Boosting, while also

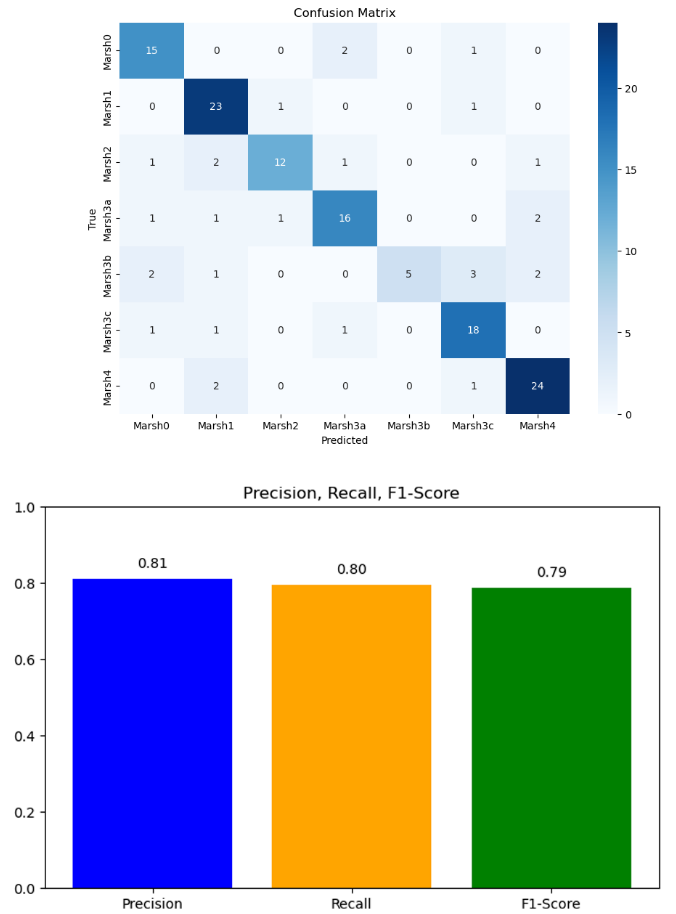
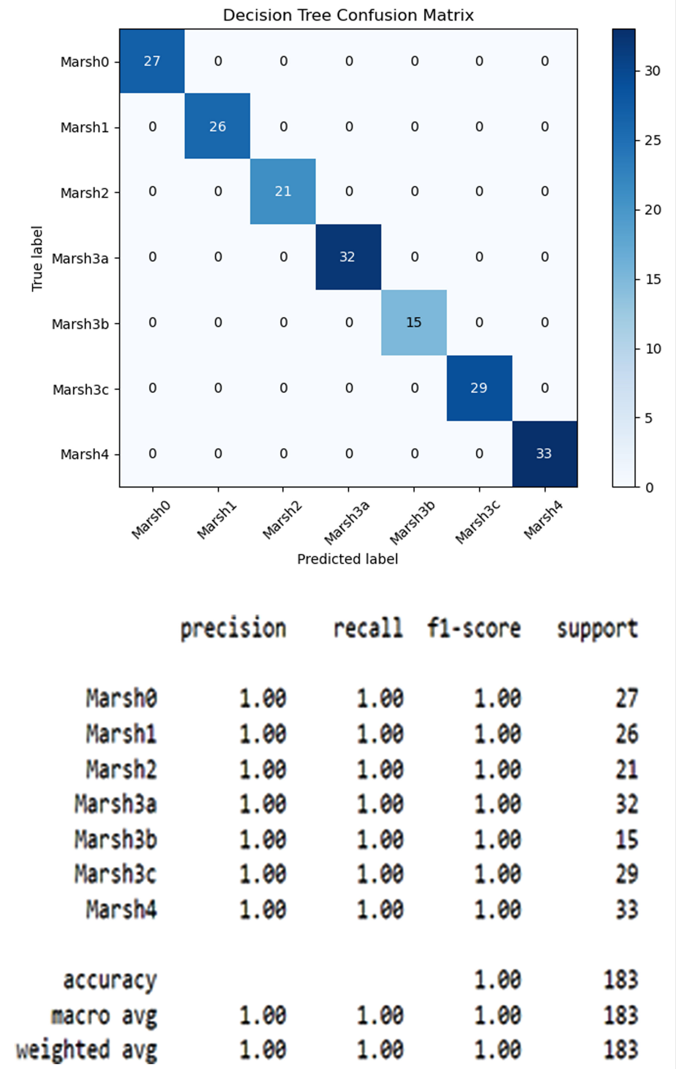


Fig. 4. PyTorch model's confusion matrix and precision, recall, and F1-score metrics.



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              precision    recall  f1-score   support

      Marsh0       1.00      1.00      1.00        27
      Marsh1       1.00      1.00      1.00        26
      Marsh2       1.00      1.00      1.00        21
     Marsh3a       1.00      1.00      1.00        32
     Marsh3b       1.00      1.00      1.00        15
     Marsh3c       1.00      1.00      1.00        29
      Marsh4       1.00      1.00      1.00        33

    accuracy                           1.00       183
   macro avg       1.00      1.00      1.00       183
weighted avg       1.00      1.00      1.00       183
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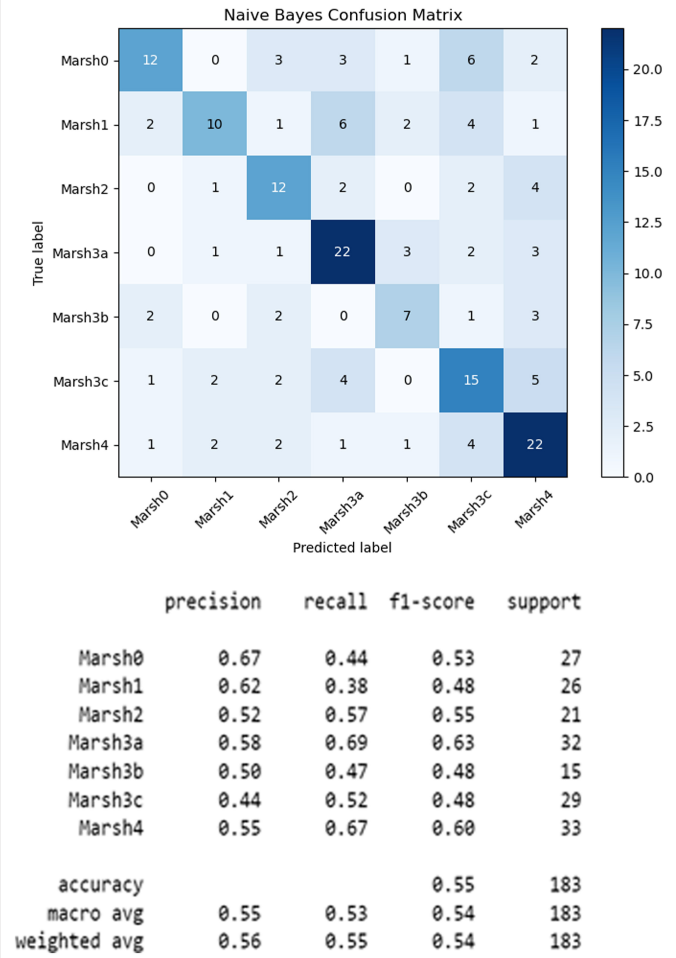
Fig. 5. Decision trees, random forests, and gradient boosting's confusion matrix and precision, recall, and F1-score metrics.



True label \ Predicted label	Marsh0	Marsh1	Marsh2	Marsh3a	Marsh3b	Marsh3c	Marsh4
Marsh0	12	0	3	3	1	6	2
Marsh1	2	10	1	6	2	4	1
Marsh2	0	1	12	2	0	2	4
Marsh3a	0	1	1	22	3	2	3
Marsh3b	2	0	2	0	7	1	3
Marsh3c	1	2	2	4	0	15	5
Marsh4	1	2	2	1	1	4	22

```
              precision    recall  f1-score   support

      Marsh0       0.67      0.44      0.53        27
      Marsh1       0.62      0.38      0.48        26
      Marsh2       0.52      0.57      0.55        21
     Marsh3a       0.58      0.69      0.63        32
     Marsh3b       0.50      0.47      0.48        15
     Marsh3c       0.44      0.52      0.48        29
      Marsh4       0.55      0.67      0.60        33

    accuracy                           0.55       183
   macro avg       0.55      0.53      0.54       183
weighted avg       0.56      0.55      0.54       183
```

Fig. 6. Naive Bayes's confusion matrix and precision, recall, and F1-score metrics.

underscoring the importance of considering model suitability for specific datasets and tasks.

IV. DISCUSSION

In our investigation, we explored a range of classification techniques, including advanced deep learning approaches like PyTorch neural networks and traditional methods such as decision trees, random forests, gradient boosting, and naive Bayes. Our primary aim was to determine the most efficient model for forecasting celiac Marsh levels in the diagnosis and management of celiac disease. Our findings demonstrate the unique performance characteristics exhibited by each model. The intricate architecture and sophisticated features of the PyTorch neural network yielded promising predictive accuracy by recognizing complex patterns within the data. Meanwhile, conventional classifiers such as decision trees, random forests, gradient boosting, and naive Bayes also achieved competitive results with strengths in various aspects of interpreting and categorizing datasets.

The PyTorch neural network exhibited high accuracy in prediction, but it requires extensive and diverse datasets for effective training as well as significant computational resources. On the other hand, Naive Bayes assumes feature independence, which may not be valid for all datasets and has limited capacity to handle numerical or continuous data. This limitation could potentially result in lower predictive accuracy when dealing with complex datasets such as ours. Our comparative evaluation yielded valuable insights into the strengths of each model, providing important guidance for selecting an appropriate method for predicting celiac Marsh levels. This supports informed decision-making in clinical practice and contributes to refining patient management strategies by enhancing diagnostic precision specific to celiac disease through evidence-based approaches outlined in our study.

VI. CONCLUSION

Our research thoroughly assessed various classification models, encompassing contemporary deep learning methods like the PyTorch neural network and conventional techniques such as decision trees, random forests, gradient boosting, and naive Bayes, to forecast celiac Marsh levels. Despite distinct strengths and weaknesses in each model's performance, our results offer valuable insights into their relative effectiveness and applicability for this essential diagnostic purpose. Our comparison study acts as a reference for choosing the most appropriate model to predict celiac Marsh levels, thus improving diagnostic precision and guiding patient management strategies in clinical settings. Future research may investigate combining methods or using ensemble approaches to capitalize on the advantages of multiple models and enhance predictive accuracy. Concisely, our research highlights the significance of embracing data-driven techniques in medical diagnosis, enabling informed decision-making and advancing patient outcomes by leveraging diverse modeling approaches.

Availability of Data and Materials: The data that support the findings of this study are available on request from the corresponding author.

Ethics Committee Approval: This research was authorized by the Research Ethics Committee at the Research Ethics Committee of the University of Health Sciences, Van Training and Research Hospital (Approval no: 586, Date: September 10, 2018).

Informed Consent: Patients were informed by a specialist physician in adherence to ethical guidelines and provided voluntary consent through a signed form.

Peer-review: Externally peer-reviewed.

Author Contributions: Concept – İ.Z.G., E.K.B.; Design – İ.Z.G., E.K.B.; Supervision – İ.Z.G.; Resources – E.K.B.; Materials – E.K.B., İ.Z.G., Y.K.; Data Collection and/or Processing – Y.K.; Analysis and/or Interpretation – E.K.B.; Literature Search – E.K.B.; Writing – E.K.B.; Critical Review – E.K.B.; İ.Z.G.

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