ORIGINAL RESEARCH A Machine Learning Method for Differentiation Crohn's Disease and Intestinal Tuberculosis

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Background: Whether machine learning (ML) can assist in the diagnosis of Crohn's disease (CD) and intestinal tuberculosis (ITB) remains to be explored.

Methods: We collected clinical data from 241 patients, and 51 parameters were included. Six ML methods were tested, including logistic regression, decision tree, k-nearest neighbor, multinomial NB, multilayer perceptron, and XGBoost. SHAP and LIME were subsequently introduced as interpretability methods. The ML model was tested in a real-world clinical practice and compared with a multidisciplinary team (MDT) meeting.

Results: XGBoost displays the best performance among the six ML models. The diagnostic AUROC and the accuracy of XGBoost were 0.946 and 0.884, respectively. The top three clinical features affecting our ML model's result prediction were T-spot, pulmonary tuberculosis, and onset age. The ML model's accuracy, sensitivity, and specificity in clinical practice were 0.860, 0.833, and 0.871, respectively. The agreement rate and kappa coefficient of the ML and MDT methods were 90.7% and 0.780, respectively (P<0.001).

Conclusion: We developed an ML model based on XGBoost. The ML model could provide effective and efficient differential diagnoses of ITB and CD with diagnostic bases. The ML model performs well in real-world clinical practice, and the agreement between the ML model and MDT is strong.

Keywords: artificial intelligence, machine learning, crohn's disease, intestinal tuberculosis, multidisciplinary team

Introduction

Inflammatory bowel disease (IBD) is a chronic inflammation of the gastrointestinal tract. Ulcerative colitis (UC) and Crohn's disease (CD) are the principal forms of IBD. IBD is a global disease. In 2020, newly industrialized countries were at a stage where the incidence increased, and the prevalence was relatively low. The incidence of this disease is stable in Western countries, but its prevalence is rapidly increasing.¹ Intestinal tuberculosis (ITB) is also a chronic inflammatory gastrointestinal disease caused by mycobacterium tuberculosis. Tuberculosis is the second leading cause of death caused by an infectious disease after COVID-19, contributing to 1.5 million deaths in 2020. Intestinal tuberculosis is one of the most common forms of extrapulmonary tuberculosis.² The global burden of CD and ITB will continue to increase in future decades.

CD is a complex chronic inflammatory gastrointestinal condition with variable clinical manifestations. ITB shares many clinical features with CD. Distinguishing these two diseases can be complicated. IBD diagnosis is especially difficult at hospitals lacking medical resources and staff. This situation is even worse in some developing and newly industrialized countries.

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Multidisciplinary team (MDT) meetings play an established role in managing multiple chronic diseases, including IBD and ITB. Most MDT encounters were successful from both a process and a clinical outcome perspective.³ The Inflammatory Bowel Disease Group of the Chinese Gastroenterology Society strongly recommends MDT meetings, especially for patients whose diagnosis is difficult.⁴ However, MDT meetings usually depend on experienced doctors and advanced medical equipment.

In recent years, machine learning (ML) technology has shown promising applications in gastroenterology. Based on clinical data, ML methods were able to predict upper gastrointestinal bleeding and gastric cancer risk in patients after *Helicobacter pylori* eradication.^{5,6} ML models outperform traditional statistical models that use routinely available clinical data for risk prediction in patients with IBD.⁷ Waljee AK et al developed an ML model to identify patients with Crohn's disease likely to respond durably to ustekinumab.⁸ The ML model could substantially improve the ability to predict IBD-related hospitalization and outpatient steroid use.⁹ However, there are still limitations in the current

literature. First, few studies have investigated the differentiation of CD and ITB. Second, few studies have evaluated the performance of ML models in real-world clinical practice.

In this study, we first developed an ML model to assist in diagnosing of CD and ITB. The performance was subsequently compared with that of MDTs in real-world clinical practice.

Materials and Methods

Study Design

This study was divided into two stages. Stage 1: ML model development. Using six different ML methods, a training model is trained for CD and ITB differential diagnoses based on retrospective clinical data. Stage 2: Test the ML model in real-world clinical practice. After the MDT meeting, the MDT candidates were diagnosed with ITB or CD by the MDT group. The clinical data of these patients were entered into the ML model developed in stage 1, and the diagnostic results were output accordingly. After six months of follow-up, considering the effect after treatment, the final diagnosis was confirmed. The performance of the ML model was recorded, analyzed, and compared with that of the MDT model. Figure 1 shows the flow chart.

This study was conducted in the Gastroenterology Department of the Third Xiangya Hospital of Central South University. This research was conducted in accordance with the Declaration of Helsinki and national and institutional standards. The clinical research ethics committee of the Third Xiangya Hospital of Central South University (No.22272) approved the study protocol. Informed consent was obtained from all the MDT candidates. The study is complete and is registered at http://www.chictr.org.cn (ChiCTR2200066847).

Data Collection and Dataset Establishment

In the stage of ML model development, clinical data were collected from Jan 2013 to Jun 2021. The diagnosis was based on clinical performance, endoscopic and pathological characteristics, as well as the response to Crohn's disease treatment and anti-tuberculosis therapy. All cases were confirmed based on the Chinese consensus and British guidelines for IBD by two experienced gastroenterologists.^{10,11} For ML model development, we collected 51 parameters from 123 patients with ITB and 118 patients with CD, including four demographic data points, six symptoms, 20 laboratory results, one



Figure I Study flow chart.

comorbidity, two complications, 12 endoscopic characteristics and six pathological characteristics. The variables included were widely available in the diagnosis of ITB and CD. The included endoscopic and pathological characteristics were based on European consensus.^{12,13} The descriptive statistics of the clinical ML data are shown in Table 1.

Table I Descriptive Statistics for Machine Learning

	ITB (N=123)	CD (N=118)	P
Demographic data			
Onset age(years)	41.22±16.41	28.24±11.25	<0.001**
Age at diagnosis(years)	43.04±16.91	30.58±11.68	<0.001**
Course of disease(years)	1.74±2.48	2.60±2.92	0.15
Male	76 (61.8%)	78(66.1%)	0.488
Symptoms			
Abdominal pain	98 (79.7%)	89(75.4%)	0.431
Diarrhea	19(15.4%)	49(41.5%)	<0.001**
Hematochezia	6(4.9%)	12(10.2%)	0.119
Constipation	5(4.1%)	6(5.1%)	0.706
Fatigue	9(7.3)	4(3.4%)	0.179
Fever	5(4.1%)	5(4.2%)	0.947
Laboratory results			
OB	28(22.8%)	65(55.1%)	<0.001**
ALT(U/L)	19.45±15.89	15.23±17.32	0.050
AST(U/L)	24.11±14.70	17.10±10.88	<0.001**
BUN(mmol/L)	5.03±3.90	4.48±5.40	0.370
Cr(umol/L)	80.16±93.94	68.01±15.52	0.167
UA(umol/L)	299.01±128.11	313.72±88.84	0.303
PLT(10 ⁹ /L)	286.63±127.92	334.19±142.84	0.007**
RBC(10 ¹² /L)	4.17±0.85	4.34±0.69	0.086
WBC(10 ⁹ /L)	7.13±3.54	7.26±2.71	0.752
Hb(g/L)	113.17±25.74	114.17±24.60	0.759
HCT(%)	0.37±0.27	0.35±0.06	0.439
ESR(mm/H)	42.19±31.65	42.03±34.34	0.970
Elevated CRP	58/89(65.2%)	82/106(77.4%)	0.059
Elevated HsCRP	71/89(79.8%)	93/106(87.7%)	0.129
ALB(g/L)	34.59±7.68	35.08±6.80	0.602
Na(mmol/L)	138.06±4.22	140.15±2.53	<0.001**
K(mmol/L)	4.00±0.53	3.94±0.47	0.371
T-spot	62/92(67.4%)	6/79(7.6%)	<0.001**
ANCA	2/92(2.8%)	8/79(10.1%)	0.027*
ANA	3/92(4. %)	18/79(22.8%)	0.143
Colonoscopy performance			
Terminal ileum	33/82(40.2%)	87/118(73.7%)	<0.001**
lleocecal junction	51/82(62.2%)	88/118(74.6%)	0.061
Ascending colon	43/82(52.4%)	75/118(63.6%)	0.116
Transverse colon	32/82(39.0%)	79/118(67.0%)	<0.001**
Descending colon	23/82(28.0%)	75/118(63.6%)	<0.001**
Sigmoid colon	30/82(36.6)	88/118(74.6%)	<0.001**
Rectum	32/82(39.0%)	93/118(78.8%)	<0.001**
Erythema or Friability	50/82(61.0%)	113/118(95.8%)	<0.001**
Erosion or Ulcer	60/82(73.2%)	109/118(92.4%)	<0.001**
Post-inflammatory polyps	25/82(30.5%)	33/118(28.0%)	0.699
Stenosis	23/82(28.0%)	30/118(25.4%)	0.679
Longitudinal ulcer or Cobblestone	0/82(0.0%)	33/118(28.0%)	<0.001**

(Continued)

	ITB (N=123)	CD (N=118)	Р
Pathological characteristics			
Acute inflammation	53/77(68.8%)	4/ 8(96.6%)	<0.001**
Granulomas	43/77(55.8%)	67/118(56.8%)	0.898
Crypt architectural irregularity	16/77(20.8%)	68/118(57.6%)	<0.001**
Lymphoid aggregates	30/77(39.0%)	72/118(61.0%)	0.003**
Caseous necrosis	7/77(9.1%)	0/118(0.0%)	<0.001**
Epithelioid-cell granulomas	0/77(0.0%)	32/118(27.1%)	0.001**
Comorbidity & Complication			
Pulmonary tuberculosis	52(42.3%)	l (0.8%)	<0.001**
Intestinal obstruction or perforation	23(18.7%)	19(16.1%)	0.597
Crissum abscess or Perianal fistula	0(0.0%)	18(15.3%)	<0.001**

Table I (Continued).

Notes: *P<0.05; **P<0.001.

Abbreviations: OB, occult blood in stool; ALT, alanine transaminase; AST, glutamic-oxaloacetic transaminase; BUN, blood urea nitrogen; Cr, creatinine; UA, uric acid; PLT, blood platelet; RBC, red blood cell; WBC, white blood cell; Hb, hemoglobin; HCT, hematocrit; ESR, erythrocyte sedimentation rate; CRP, C-reactive protein; HsCRP, high-sensitivity C-reactive protein; ALB, albumin; Na, sodium ion; K, potassium ion; T-spot, tuberculosis-spot test; ANCA, anti-neutrophil cytoplasmic antibodies; ANA: antinuclear antibodies.

Study Population and Sample Estimation

In stage 2, the research hypothesis is that the ML model's area under the receiver operating characteristic curve (AUROC) is greater than 0.5 for MDT candidates. The AUC of the ML model for patients who were difficult to diagnose was 0.78 in the previous experiment, with alpha=0.05 (one-sided) and beta=0.1. Based on the relevant studies at home and abroad, the ratio between the ITB and CD groups was 1:2–1:4.^{14,15} A review of the historical records of MDT patients in our hospital revealed that the ratio of ITB to CD patients was approximately 1:3. Therefore, in this study, the ratio between the ITB and CD groups was 1:3. The sample size of this study was calculated via PASS11. The number of samples was estimated to be at least 11 ITB patients and 31 CD patients.

Fifty MDT candidates were ultimately included in the study from Sep 2021 to Oct 2022. After the MDT meeting, seven patients with other diseases were excluded, and 43 patients who were diagnosed with ITB or CD by the MDT group were included. The inclusion and exclusion criteria are as follows:

The inclusion criteria were: 1. Patients highly suspected of having CD or ITB; 2. Clinical data were complete, and the MDT was completed; 3. Post follow-up, the final diagnosis was CD or ITB.

Exclusion criteria: 1. Patients with confirmed CD or ITB who do not need an MDT; 2. Other diseases were confirmed after the MDT.

ML Method

In the ML model development stage, we tested six different mainstream ML methods, including logistic regression (LR), decision tree (DT), K-nearest neighbor (KNN), multinomialNB (MNB), multilayer perceptron (MLP), and XGBoost. LR is a process of modeling the probability of a discrete outcome given an input variable. DT learning is a predictive algorithm that uses both categorical and numerical data to assign samples to specific classes.¹⁶ KNN is a non-parametric approach; for an input x, KNN identifies k objects in the training data closest to x with a predefined metric and makes a prediction by majority vote from the classes of the k objects.¹⁷ MNB is a probabilistic algorithm that is commonly used to categorize text. An MLP is a feed-forward artificial neural network model that maps sets of input data onto a set of appropriate outputs. XGBoost implements ML algorithms under the gradient boosting framework; it provides parallel tree boosting that quickly and accurately solves many data science problems.¹⁸

Missing data is a common problem that has a greater impact on data analysis. The multiple imputation method Miceforest is a non-parametric imputation method that can cope with different types of variables simultaneously and is

widely used in medical data analysis.^{19,20} Therefore, this study uses Miceforest to input the missing data. All relevant ML methods and codes can be freely accessed at <u>https://github.com/philiplaw1984/IBD/</u>.

Interpretability for ML

Understanding why an AI model makes a certain prediction is important for doctors when making clinical decision. This study introduces the SHapley Additive exPlanations (SHAP) method and the Local Interpretable Model-agnostic Explanations (LIME) method to explain our ML model. SHAP is a method to explain individual predictions, and it is based on the game's theoretically optimal Shapley values. LIME explains a prediction of an ML model (classification or regression) for a query point by finding important predictors and fitting a simple interpretable model.

MDT Group

A senior professor of Gastroenterology led the MDT group. Other members include an associate professor of Gastroenterology, a professor of gastrointestinal surgery, a professor of radiology, an associate professor of pathology, a senior IBD specialist nurse, and a coordinator in charge of management.

Experimental Settings and Evaluation Values

All the ML experiments in this study were performed on a personal computer (Windows 10). The experiments were performed in Python 3.8 via PyCharm and Jupyter Notebook Integrated Development Environment.

In stage 1, the evaluation values of the ML methods were AUROC, accuracy, average precision (AP), sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV). The dataset used for ML model development was divided into a training set, a validation set, and a test set at a ratio of 6:2:2. A five-fold cross-validation method was adopted.

In stage 2, the primary outcome measures were accuracy, sensitivity, specificity, PPV, and NPV. The secondary outcome measures were the agreement rate and the kappa coefficient.

Statistical Analysis

Statistical analyses were performed via SPSS version 22.0 (IBM SPSS Statistics, IBM Corporation, Armonk, NY, USA). Categorical variables were described by frequencies and proportions (%), and continuous variables were described by means and standard deviations (SDs) unless otherwise stated. Continuous variables were compared via Student's *t* test or one-way analysis of variance, and categorical variables were compared using the χ^2 test. Non-normal data or data without variance homogeneity were analyzed using non-parametric tests (Mann–Whitney test). A two-tailed P value < 0.05 was considered statistically significant.

Results

ML Method Assists in the Diagnosis of ITB and CD Based on Clinical Data

XGBoost performs the best among the six ML models. The diagnostic AUROC, accuracy, AP, sensitivity, specificity, PPV, and NPV of XGBoost were 0.946, 0.884, 0.834, 0.889, 0.878, 0.877, and 0.899, respectively. Figure 2 shows the average AUROC of the XGBoost method after 5-fold cross-validation. The performance of all six ML classification methods is shown in Table 2.

Interpretability for ML

In this study, we introduce the SHAP and LIME methods to explain our ML models. Figure 3 shows how the SHAP method explains our ML models. As shown in Figure 3A, each point represents a case. ITB and CD were coded as 0 and 1, respectively in our ML experiment. A different color represents a different value of the clinical data; red indicates higher values for continuous variables, whereas blue indicates lower values. For categorical variables, red represents positive variables, and blue represents negative variables. The horizontal coordinate represents each clinical data of every case corresponding to a SHAP value. The ML model calculates all variables' SHAP values together. In the output phase,



Figure 2 The average AUROC of the XGBoost method after 5-fold cross validation.

a high SHAP value indicates that the prediction probability of CD increases. Instead, a low SHAP value indicates that the prediction probability of ITB would increase. Figure 3B shows the weights of all the clinical data included in the ML model. The top 5 variables that may affect result prediction in our ML model were T-spot, pulmonary tuberculosis, onset age, OB, and terminal ileum affected. Figure 3C is a screenshot from a global explain program based on SHAP, which can display every individual case's predicted result and its corresponding SHAP value.

However, the SHAP method could explain how the ML model predicts every patient's result. To better understand how our ML model works, we introduce another method of visualization and explanation called LIME. The LIME method calculates the predicted value according to the feature value and weight. Figure 4 shows two examples of how the LIME method predicts results. Figure 4A shows an ITB patient's prediction, and Figure 4B shows a CD patient's prediction. Clinical features in orange indicate that the prediction is prone to CD, and clinical features in blue indicate that the prediction is prone to ITB.

Tab	le 2	2 Perf	ormance	of	All	6	ML	Classification	Methods
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	AUROC	Accuracy	ΑΡ	Sensitivity	Specificity	PPV	NPV
ML method							
LR	0.894	0.846	0.791	0.847	0.846	0.845	0.859
DT	0.829	0.826	0.763	0.819	0.83	0.818	0.843
KNN	0.631	0.602	0.553	0.653	0.552	0.579	0.633
MNB	0.778	0.639	0.607	0.391	0.879	0.777	0.601
MLP	0.863	0.78	0.721	0.730	0.829	0.799	0.772
XGBoost	0.946	0.884	0.834	0.889	0.878	0.877	0.899

Note: The best result of each evaluation indicator is indicated in bold.

Abbreviations: AUROC, area under the receiver operating characteristic curve; AP, average precision; PPV, positive predictive value; NPV, negative predictive value; LR, logistic regression; DT, decision tree; KNN, k-nearest neighbor; MNB, multinomial NB; MLP, multilayer perceptron.



Figure 3 SHAP method to explain our ML models.

ML Model in Real-World Clinical Practice

Forty-three patients were diagnosed with ITB or CD by the MDT group. The clinical data of these patients were input into the ML model. The output diagnoses were 14 ITB and 29 CD cases. The descriptive statistics of the clinical data for ML are shown in <u>Supplementary file 1</u>. The individual prediction results of the ML model are shown in <u>Supplementary file 2</u>.

After a six-month follow-up, the final diagnoses were 12 ITBs and 31 CDs. The accuracy, sensitivity, specificity, PPV, and NPV were 0.860, 0.833, 0.871, 0.714, and 0.931, respectively.

The accuracy, sensitivity, specificity, PPV, and NPV of the MDT group were 0.953%, 0.917, 0.968, 0.917, and 0.968, respectively. The results of the ML model and MDT are shown in Figure 5 and Table 3.

The agreement rate and kappa coefficient of the ML and MDT methods were 90.7% and 0.780, respectively (P<0.001). The confusion matrix used for calculating the kappa coefficient is shown in Figure 6.

Discussion

In this study, we developed an AI method to assist in the diagnosis of ITB and CD based on an ML method and a DL method with good performance. The ML explanatory methods SHAP and LIME could help doctors understand how the ML model works. The ML model \ performed well in real-world clinical practice, and the agreement between the ML model and MDT was strong.

XGBoost achieves state-of-The-art results on many ML challenges. In this study, XGBoost outperformed the other prediction models to diagnose ITB and CD. Other studies have confirmed that XGBoost performs excellently in predicting diabetes and cardiovascular disease.^{21,22} XGBoost is a scalable end-to-end tree boosting system, a novel sparsity-aware algorithm for sparse data, and a weighted quantile sketch for approximate tree learning. In addition, it combines cache access patterns, data compression, and sharding to build a scalable tree-boosting system.¹⁸ The diagnostic AUROC of our XGBoost model was 0.946. Another similar study with 160 CD and 40 ITB patients with

Α	Feature	Value	negative positive
A	Tspot	1.00	0.00 < Tspot <= 1.00
	tuberculosis	0.00	tuberculosis <= 0.00
	ОВ	0.00	OB <= 0.00 0.20
	Onset age	48.00	Onset age > 44.00
	Terminal ileum	1.00	0.00 < Terminal ileum
	Cobblestone	0.00	Cobblestone <= 0.00
	Sigmoid colon	0.00	Sigmoid colon <= 0.00
	Na	142.00	Na > 141.00
	diarrhea	0.00	diarrhea <= 0.00

Predicted value = 0.00



Predicted value = 1.00

Figure 4 LIME method to explain our ML models.

32 clinical features reported that the AUROC of the XGBoost model was 0.891¹⁴ we speculate that this may be because our study included more ITB patients and clinical features.

ML methods revealed that the top 5 clinical features of the ML model were T-spot, pulmonary tuberculosis, age of disease onset, OB, and Terminal ileum. T-spot-positive and concomitant pulmonary tuberculosis were acknowledged features of a diagnosis of ITB. However, hematochezia is more common in patients with CD.^{23,24} Although hematochezia is not the key feature, OB positivity is an important feature that suggests CD in our model; this is probably due to the retrospective nature of the study. When patient files are reviewed, missing symptom information is more common than missing laboratory results. A ten-year hospital-based observational study in China revealed that the onset age of CD was 32.0 years, and a study in Western Hungary reported that the onset age of CD was 32.5 years.^{25,26} The age of onset for patients in our CD and ITB groups was 28.2 and 41.2 years, respectively. This discrepancy may be due to the fact that the number of pediatric and adolescent patients with CD is increasing, and tuberculosis is more common in elderly patients.

М	1	Actual result		
IVI	-	CD	ITB	
Predicted	CD	27	2	
result	ITB	4	10	
	т	Actual	result	
MD	т	Actual	result ITB	
MD Predicted	CD			

Figure 5 Results of the ML model and MDT in clinical practice.

Thus, age of onset could be an important feature of the ML model. A retrospective study of ITB patients in East China revealed that the rate of terminal ileum affected was 47.1%.²⁷ This result was very close to our findings. In our study, the percentage of terminal ileum affected in the ITB group (40.2%) was lower than that in the CD group (73.7%). Therefore, the terminal ileum affected may be a key variable of the ML model.

This is the first study conducted to evaluate the performance of the ML-based model for differentiating CD and ITB in MDT candidates. The results show that the ML model could differentiate between CD and ITB. However, the performance slightly decreased compared to previous retrospective clinical data; this is largely because MDT candidates are usually difficult to diagnose. An MDT meeting is recommended for patients whose diagnosis is difficult.⁴ In this study, after the MDT meeting, the accuracy of diagnosis reached 95.3%. Compared with the MDT model, the agreement rates and kappa coefficients of the ML model and MDT model are strongly consistent. Therefore, the model could help doctors differentiate CD and ITB effectively, improve the accuracy of diagnosis, and improve the ability to identify ITB and CD in primary hospitals.

Our study had several limitations. First, in stage 1, the study was limited by its retrospective nature and was a secondary analysis of single-center medical data. Second, in stage 2, the sample size was small. Third, we did not conduct ablation experiments or LASSO regression to extract the variables. Finally, this study did not include all the clinical data, such as CT, double-balloon enteroscopy, and capsule endoscopy results.

	ML (N=43)	MDT (N=43)	P value	Fold change (95% CI)
Accuracy	86.0% (37/43)	95.3% (41/43)	0.265	0.902 (0.787–1.035)
Sensitivity	83.3% (10/12)	91.7% (11/12)	1.000	0.909 (0.670-1.234)
Specificity	87.1% (27/31)	96.8% (30/31)	0.354	0.900 (0.755–1.046)
PPV	71.4% (10/14)	91.7% (11/12)	0.330	0.779 (0.537–1.131)
NPV	93.1% (27/29)	96.8% (30/31)	0.606	0.962 (0.855–1.083)

Table 3 Results of the ML Model and MDT in Clinical Practice

Abbreviations: ML, machine learning; MDT, multidisciplinary team; PPV, positive predictive value; NPV, negative predictive value.

Карра		ML		
coeff	icient	CD	ITB	
MDT CD		28	3	
	ITB	1	11	

Figure 6 Confusion matrix used for calculating the kappa coefficient.

Conclusion

In conclusion, in this study, we developed an ML model based on XGBoost. The ML model could provide effective and efficient differential diagnosis of ITB and CD with diagnostic bases. The ML model performed well in real-world clinical practice, and the agreement between the ML model and MDT was strong. The proposed model may greatly reduce the burden on doctors, relieve the suffering of patients, and improve the ability to identify ITB and CD in primary hospitals.

Abbreviations

IBD, Inflammatory bowel disease; UC, Ulcerative colitis; CD, Crohn's disease; ITB, Intestinal tuberculosis; AI, Artificial intelligence; ML, machine learning; KNN, K nearest neighbor; MLP, Multilayer perceptron; AUROC, Area under the receiver operating characteristic curve; PPV, Positive predictive value; NPV, Negative predictive value; SHAP, SHapley Additive exPlanations; LIME, Local interpretable model-agnostic explanations.

Data Sharing Statement

All relevant ML methods and codes can be freely accessed at https://github.com/philiplaw1984/IBD/.

Ethics Approval and Consent to Participate

This study was conducted in the Gastroenterology Department of the Third Xiangya Hospital of Central South University. This research was conducted in accordance with the Declaration of Helsinki and national and institutional standards. The study protocol was approved by the clinical research ethics committee of the Third Xiangya Hospital of Central South University (No.22272). Informed consent was obtained from all the MDT candidates. The study is complete and is registered at http://www.chictr.org.cn (ChiCTR2200066847).

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare that they have no competing interests.

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