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Retrospective Study

**CT-Based Deep Learning for Preoperative Prediction of Tumor Immune
Microenvironment in Colorectal Cancer TSR, TILs, and IS Perspective**

Chuan Zhou *et al.* DL-CT for CRC TIME

Chuan Zhou, Yun-Feng Zhang, Zhi-Jun Yang, Yu-Qian Huang, Ming-Xu Da

Abstract

BACKGROUND

Colorectal cancer (CRC) is a leading cause of cancer-related death globally, with the tumor immune microenvironment (TIME) influencing prognosis and immunotherapy response. Current TIME evaluation relies on invasive biopsies, limiting its clinical application. This study hypothesizes that computed tomography (CT)-based deep learning (DL) radiomics can non-invasively predict key TIME biomarkers: Tumor-stroma ratio (TSR), tumor-infiltrating lymphocytes (TILs), and immune score (IS).

AIM

To develop a non-invasive DL approach using preoperative CT radiomics to evaluate TIME components in CRC patients.

METHODS

In this retrospective study, preoperative CT scans from 315 pathologically confirmed CRC patients (201 training, 95 validation cohorts) were analyzed. Manually delineated regions of interest (ROIs) were used to extract DL features. Predictive models (DenseNet-121/169) for TSR, TILs, IS, and TIME classification were constructed. Performance was evaluated *via* receiver operating characteristic (ROC) curves, calibration curves, and decision curve analysis (DCA).

RESULTS

The DL-DenseNet-169 model achieved ² area under the curve (AUC) values of 0.892 (95%CI: 0.828–0.957) for TSR and 0.772 (95%CI: 0.674–0.870) for IS. The DenseNet-121 model yielded ⁸ AUCs of 0.851 (95%CI: 0.768–0.933) for TILs and 0.852 (95%CI: 0.775–0.928) for IS. Calibration curves demonstrated strong prediction-observation agreement, and DCA confirmed clinical utility across threshold probabilities ($P < 0.05$ for all models).

CONCLUSION

CT-based DL radiomics provides a reliable non-invasive method for preoperative TIME evaluation, enabling personalized immunotherapy strategies in CRC management.

Key Words: Deep Learning; Radiomics; CT imaging; Colorectal cancer; Tumor immune microenvironment

Core Tip: This study introduces a novel computed tomography (CT)-based deep learning (DL) radiomics approach for noninvasive assessment of the tumor immune microenvironment (TIME) in colorectal cancer. By analyzing preoperative CT scans from 315 patients, DL models achieved high predictive accuracy (AUCs 0.851-0.892) for key TIME features: Tumor-stroma ratio, lymphocyte infiltration, and immune scoring. Clinical validation through calibration and decision curve analyses confirmed the utility of this approach in guiding immunotherapy strategies. This method eliminates invasive biopsy requirements while enabling personalized treatment planning and enhanced prognostic evaluation. The findings establish DL radiomics as a paradigm-shifting tool for precision oncology in gastrointestinal malignancies.

INTRODUCTION

Colorectal cancer (CRC) is one of the main causes of mortality and morbidity among cancers worldwide[1]. It is anticipated that by 2040, there will be 3.2 million new cases of CRC and 1.6 million deaths due to CRC[2]. The tumor immune microenvironment (TIME) has been identified as a significant factor influencing the development and progression of CRC. The use of immunotherapy such as immune checkpoint inhibitors (ICIs) therapy, has considerably transformed cancer treatment in recent decades[3,4]. ICI therapy has received approval for treating patients with CRC exhibiting molecular characteristics relating to DNA mismatch repair-deficient (dMMR)/microsatellite instability-high, MSI-H (MSI-H). However, it is crucial to acknowledge that the dMMR/MSI-H CRC subgroup accounts for only 15% of all CRC patients; as such, the

majority of CRC patients do not derive therapeutic advantages from ICI treatment[5]. Patients exhibit varying sensitivity to ICIs, which significantly limits their clinical application in CRC. Thus, identifying biomarkers that can accurately separate ICI-sensitive patients from those resistant to the drug is essential.

Recent studies have added more clarity on the impact of cells and molecules in the tumor stroma on tumor infiltration and metastasis through comprehensive investigations of the tumor microenvironment (TME) markers[6,7]. The tumor-stroma ratio (TSR) is a significant morphological parameter in the TIME and has been extensively validated as an independent prognostic factor for various solid tumors in numerous clinical studies[7,8]. A high abundance of tumor-stroma content (TSR > 50%) has been linked to adverse outcomes in relation to patient survival and prognosis[9,10].
6 Tumor-infiltrating lymphocytes (TILs) are crucial indicators of prognosis in CRC patients. The effectiveness of ICIs relies on the tumor-limiting actions of TILs[11]. Increased TILs levels are strongly associated with treatment outcomes[12,13]. The presence of immune cells, particularly the ratio of CD8+ and CD3+ T cells, in the TIME can serve as a prognostic marker for the efficacy of immunotherapy[14]. The studies propose the immune score (IS) as a tool for predicting recurrence and survival in CRC patients. It quantifies TIME features such as cell densities and locations. The IS outperforms TNM staging and MSI status in predicting patient survival and recurrence. Large-sample research also shows its ability to predict adjuvant chemotherapy efficacy in CRC[15,16]. Currently, the assessment of key biomarkers remains highly reliant on pathological techniques. The invasiveness of pathological testing, coupled with limitations and biases in obtaining tumor specimens, hinders the widespread application of TIME analysis and prognostic assessment. Hence, it is imperative to develop innovative non-invasive assessment methods to deepen our understanding of the TIME and accurately predict cancer prognosis.

Medical imaging provides detailed information on the overall structure of the tumor, including its microscopic variations and the functionality of the surrounding TME[17]. The application of radiomics in quantitative analysis of imaging data provides a more

comprehensive representation of tumors[18,19]. Consequently, a significant amount of research has focused on transforming specific regions of interest (ROIs) within images into quantitative radiomics features. These features are usually obtained through a high-throughput extraction process of information from the imaging data, and can be combined with the clinicopathological characteristics of the patient[20,21]. Subsequently, machine learning (ML) algorithms are employed to build a model using this amalgamated dataset.

Since its inception in 2012[22], radiomics has been widely applied in CRC research and has proven to be a promising tool that provides a risk-free and efficient method for diagnosis, classification, and prognostic prediction[23]. In the diagnostic research of CRC, Yang *et al* used a CT radiomics model to predict RAS and BRAF phenotypes[24]. Ma S *et al* developed and validated a DL model for tumor differentiation and lymph node metastases[25]. Prognostic models are being developed continuously. In a study involving 766 CRC patients, Li *et al* proposed that ML can predict lymph node metastasis[26]. In the ML model based on magnetic resonance imaging (MRI) images, Shu *et al* proposed a radiomics model that combined clinical risk factors and LASSO features, and demonstrated good predictive performance: AUC = 0.921[27]. Accurately predicting the efficacy of non-surgical treatment for CRC patients is also a hot issue in current ML model training. Giannini *et al* proposed that second-order texture features (five from positron emission tomography and one from MRI) could help distinguish responding and non-responding patients: Sensitivity = 86%; specificity = 83%; AUC = 0.860[28]. Regarding tumor response to anti-epidermal growth factor receptor therapy, Derclé *et al* established a relatively reliable ML model for predicting the response to targeted therapy based on 667 cases of CT imaging data[29]. In summary, radiomics can play a key role in CRC examination, serving as an additional tool in clinical settings to help clinicians identify patients with high-risk disease.

Based on the aforementioned research context, we have developed and validated a DL model that integrates CT imaging and histopathological images to predict immune-related indicators such as TSR, TILs, and IS in CRC patients.

MATERIALS AND METHODS

Study design and patients

The overall process of this study involves the integration of CT imaging and pathological data of CRC patients using DL to develop and validate a predictive model for the immune microenvironment of CRC patients (Figure 1)

This study was reviewed and approved by the Ethics Committee of Gansu Provincial Hospital Institutional Review Board (Approval No. 2023-604) with the requirement for informed consent being exempted. Prior to conducting the analysis, the patients' records were anonymized and stripped of any identifying information.

Patients

A total of 315 patients were successfully registered between January 2021 and September 2023. The recruitment process is shown in Figure 1. The recruited patients were randomly allocated to two separate groups, *viz.* the training cohort ($n = 220$) and the validation cohort ($n = 95$). The ratio of participants in the training cohort to the validation cohort was 7: 3.

Pathology

TSR measurements

Two pathologists, employing a blinded approach, identified the region of the tumor with the highest level of infiltration, using the method used to determine the T-stage. Subsequently, sequential 5- μ m sections were prepared using conventional hematoxylin-eosin (HE) staining. When observing at a lower magnification, it is crucial to identify the segment with the highest concentration of stroma content. It is also crucial to identify the specific area within that segment that has the highest stroma concentration. Accordingly, TSR evaluation was conducted when tumor cells were observed across the entire field of view. The TSR was calculated as $(\text{stromal area}/\text{total area}) \times 100\%$, ranging from 10% to 90% in 10% increments. Additionally, the TSR was computed for the 3 selected areas within the field of view, and the maximum value was finally selected. The high TSR group (Figure 3a) was defined as having a TSR greater than 50%,

while the low TSR group (Figure 3b) was defined as having a TSR less than or equal to 50%.

TILs infiltration determination

The pathological sections were analyzed under a microscope in the area with the most noticeable tumor infiltration, and the TILs were classified into four grades according to the level of infiltration. Herein, Grade 0 represents no lymphocyte reaction, Grade 1 indicates the presence of a few scattered lymphocytes, Grade 2 signifies a moderate lymphocyte reaction or infiltration of lymphocyte bands, and Grade 3 denotes a significant infiltration of lymphocytes that disrupts the continuity of the tumor cells. Utilizing infiltration status as the basis, the cases were then divided into two groups: The low TILs group (including cases graded 0-1, as shown in Figure 3c) and the high TILs group (consisting of cases graded 2-3, as shown in Figure 3d).

Immunohistochemistry staining and IS calculation

Immunohistochemistry (IHC) was used to identify CD3+ and CD8+ T cells[30,31]. Paraffin sections obtained from surgical tissue specimens were subjected to the Envision two-step staining procedure. The central area (CA) and invasive margin (IM) of the tumor were examined at a low magnification ($\times 100$) using an Olympus optical microscope. Two independent observers then selected eight representative fields of CA and IM, four each, which were photographed under high magnification ($\times 200$). The captured images were subsequently utilized to quantify the quantity of immune cells that exhibited positive staining for CD3 and CD8 (Figure 3e, f, g, h). The IS was determined based on previous studies[32,33]. The IS of each patient was aggregated by summing four binary scores (ranging from 0 to 4). A high-IS was defined as an IS of ≥ 3 , while a low-IS was defined as an IS of ≤ 2 .

Assessment of TIME

Using the divided data obtained through the mentioned methodology, we included the patients' TSR, TILs, and IS within a standardized assessment range of 0-3. More precisely, elevated levels of TSR, TILs, and IS were assigned a score of 3, while lower levels were given a score of 0. Consequently, a low TIME was indicated by scores of 0 or

1, while scores of 2 or 3 indicated a high TIME. Therefore, by utilizing this approach, the patient's TIME was approximated

Radiomics

CT imaging acquisition and image segmentation

Before the surgical procedure, all CRC patients were subjected to CT scanning; the specific CT parameters used are provided in the Supplementary Material (Table S1). In this study, CT plain images with a layer thickness of 5 mm were selected to delineate the ROI. Initially, the images of each patient were saved in DICOM format. To ensure the consistency of the image data, we performed normalization on all CT images. Two proficient radiologists delineated the ROI using ITK-SNAP software (version 3.6.0) employing a double-blind approach. Upon completion, the original and ROI images were stored in the nii.gz format. After completing the segmentation process, the crop tool was used to extract the largest ROI cross-section of the tumor. The designated section was preserved in the .png file format, specifically earmarked for the training phase of the DL model. **To ensure the consistency of the delineations made by the two radiologists (inter-observer variability), we used PyRadiomics (<http://www.radiomics.io/pyradiomics.html>) to extract the same radiomic features based on the ROIs delineated by the two physicians for statistical analysis. The results showed no statistically significant difference between the two sets of features ($P < 0.05$).**

Deep learning model construction

A cohort of 315 CRC patients who met the inclusion criteria were randomly divided into two groups: A training set ($n = 220$) and a test set ($n = 95$), with a 7: 3 ratio. The models selected for model pre-training included Resnet34, Resnet50, Resnet101, Resnet152, Densenet121, Densenet169, and Densenet201. The backbone employed for pre-training was the ImageNet dataset, which was initially trained and is accessible at <http://www.image-net.org>. The number of epochs was set to 100 and the batch size was set to 32. The normalize_method employed 'imagenet', and the initial learning rate was set to 0.01. **To improve the transparency of the model's decision-making, we employed the Gradient Weighted Class Activation Mapping (Grad-CAM) method to**

visualize and analyze the model. This method leveraged the gradient data derived from the final convolutional layer of a convolutional neural network to create a class activation map *via* weighted integration. The class activation map effectively pinpointed significant regions within the target image, thus aiding in a deeper comprehension of the model's decision-making process.

Model evaluation

To evaluate the models' predictive accuracy, ROC curves were generated for each one, and the associated AUC values were calculated. Additionally, we utilized DCA curves and calibration curves to assess the joint model's net clinical benefit and goodness of fit.

Statistical analysis

The data underwent statistical evaluation utilizing version 30.0.0 of the Statistical Package for Social Sciences (SPSS) (<https://www.ibm.com/products/spss-statistics>) alongside R statistical software (version 4.2.2 R, <https://www.r-project.org/>). Additionally, the Kolmogorov–Smirnov test was employed to verify the normality of the data. Measures that adhered to a normal distribution were expressed as $x \pm s$, whereas those that did not fit a normal distribution were indicated by the median along with the upper and lower quartiles. To compare the measures, either an independent samples t-test – assuming normal distribution and equal variance – or a Mann-Whitney U-test was utilized for skewed distributions or cases with unequal variance. Multi-factor logistic regression (LR) analysis assisted in identifying independent predictors for the development of the prediction model and the creation of the nomogram. Furthermore, the AUC of the ROC curve was calculated to evaluate the model's capability to differentiate between various classes. A DCA curve was generated to assess and compare the clinical usefulness of the model. A P-value of less than 0.05 indicated a statistically significant difference.

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RESULTS

Patient characteristics

A total of 315 patients were included in the current study. In contrast, a total of 584 patients were excluded as they did not meet the inclusion criteria. The statistical analysis indicated that there were no significant differences in the clinical characteristics between the training and validation groups (Table 1).

DL model construction

Two-dimensional regions of interest (ROIs) with the largest cross-sectional areas were chosen, and different deep learning models were utilized for both pre-training and external validation. The assessment of these models showed that DenseNet-121 and DenseNet-169 demonstrated the best overall performance in the external validation dataset, as reflected by the minimum loss value. In addition, the validation set DenseNet-121,169, demonstrated superior overall performance, as indicated by its minimal loss value. Furthermore, the illustrated graph demonstrates that both models exhibited minimal fluctuations. These findings indicate that DenseNet-169 exhibits a reduced propensity for training errors and achieves quicker convergence in comparison to other convolutional neural networks (CNN) (Figure 4). The ROIs in CT images, specifically the areas of focus for CNN, are visualized in Figure 5 using Grad-CAM. As observed from the findings presented in Figure 5, when the images had high TIME scores, the CNN effectively focused on the most important areas within the tumor region, particularly in DenseNet-169 and -121. Conversely, when the TIME scores were low, the CNN's focus was spread more evenly across the ROI, leading to failure in accurately identifying the decisive region.

Performance evaluation and comparison of the models

ROC curve

The predictive performance of the models was assessed using ROC analysis. The DenseNet-169 model was chosen as the expected TSR DL model, with an AUC value of 0.939 (95%CI 0.908–0.970) for the training set and 0.892 (95%CI 0.828–0.957) for the validation set (Figure 6a). The TILs prediction model, which employed DenseNet-121, achieved an AUC of 0.86 (95%CI 0.815–0.911) for the training set and an AUC of 0.851 (95%CI 0.768–0.933) for the validation set, as shown in Figure 6b. Similarly, DenseNet-

121 was identified as the best model for predicting high and low IS scores, exhibiting AUC values of 0.885 (95%CI 0.842–0.928) for the training set and 0.852 (95%CI 0.775–0.928) for the validation set (Figure 6c). The specific performance of each model is shown in Table 2. In addition, Figure 7 (violin plot) displays the projected probability distributions in the four models, emphasizing the significant difference between the high scoring group and the low scoring group. This observation highlights the effectiveness of the predictive model in accurately classifying and detecting variations in the immune microenvironment within CT images with enhanced precision.

DCA and calibration curves

Upon analyzing the DCA curves, it was evident that all four models demonstrated a positive clinical utility. The calibration curves demonstrated a robust correlation among all four models, indicating their ability to accurately predict labeling (Figures 8, 9).

DISCUSSION

The present study suggests that radiomics features extracted from CT scans may potentially contribute to predicting the immune microenvironment of CRC patients prior to surgery, although further validation is required to confirm the robustness of this approach. To the best of our knowledge, this is the first radiomics study to include TSR, TILs, and IS in order to predict the preoperative TIME in CRC.

Previous research has shown that radiomics is capable of predicting various key factors during the preoperative period, thus enhancing the assessment and outcomes of immunotherapy for patients. In this regard, Cai *et al.* used MRI-derived radiomic features to evaluate the tumor response (TSR) in rectal cancer prior to surgery. Their results indicate that the radiomics features surpassed the apparent diffusion coefficient in terms of accurately differentiating the TSR in rectal cancer[34]. Similarly, Meng *et al.* employed an XGBoost classifier that combined CT and MRI radiomics to forecast the TSR and improve patient risk classification in cases of pancreatic ductal adenocarcinoma[35]. Notably, our study achieved an AUC of 0.892 for the TSR model, suggesting that our findings align with earlier investigations.

In addition, Li *et al*, utilized a preoperative T2-weighted MRI radiomics model to effectively predict the survival outcomes of glioma patients, as well as assess the extent of macrophage infiltration before surgery[36]. Sun *et al*, developed a radiomics signature consisting of eight variables to identify CD8+ T cells, which was subsequently validated against the gene expression signature of CD8+ T cells in the TCGA dataset, resulting in an AUC value of 0.67. This marker showcased its capacity to differentiate between inflammatory and immune wild-type tumors in groups of individuals with presumed immunophenotypes[37]. In addition, three radiomics features were selected in the study of breast cancer to construct a prognostic radiomics model for TILs[38]. In contrast to analogous research endeavors, our developed model exhibited notably enhanced efficacy within the validation dataset, evidenced by an AUC metric of 0.790. It is our conviction that leveraging a DL framework, specifically employing the DesenNet-121 algorithm, has the potential to markedly augment the prognostic accuracy concerning TILs. Consequently, this advancement suggests that in forthcoming clinical practices, medical professionals could ascertain insights into the TME immune cell infiltration profiles of CRC patients prior to surgical intervention.

In addition to the above, Xue *et al*, developed a model to predict IS in CRC patients using multimodal MRI and applying an MR-radiomics methodology[31]. Herein, Spearman correlation analysis, as well as the Gradient Boosting Decision Tree (GBDT) algorithm was used to determine the most influential features, resulting in an AUC value of 0.768. This study also utilized CT, a widely accessible and cost-effective imaging modality that accommodates a wide range of subjects. Accordingly, the DL model was utilized to enable the accurate prediction of IS. Notably, the validation set AUC of 0.851 exceeded the findings of previous studies. The integration of the aforementioned crucial immune indicators in a simultaneous manner resulted in a favorable model efficacy, as demonstrated by an AUC value of 0.772. Based on this we suggested a hypothesis regarding the possibility of combining the three immunological indicators to gain a more comprehensive understanding of DesenNet-169. The corresponding findings offered a more thorough representation of the TIME in patients

with CRC. The model's performance was confirmed by the satisfactory results obtained from the DCA and calibration curves. These findings are highly significant for clinicians, as they can assist in the preoperative evaluation and the development of immunotherapy strategies. However, characterizing the biological aspects of the TME cannot be sufficiently achieved by relying on a single or limited set of immune microenvironment indicators. Therefore, in order to reflect the situation of the TME as comprehensively as possible, the development and validation of integrated models that incorporate more effective indicators are urgently needed[39]. In this study, we chose Densnet-121 and Densnet-169 as the models based on their AUC performance on the validation set and the closeness between the AUC values of the training and validation sets. However, this approach may have certain limitations, such as the observation that the accuracy (ACC) in the validation set was higher than that in the training set (Table 2). This may be due to the data split between the training and validation sets, where the distribution of a few outlier samples could affect the model's parameter performance on the training set. Future studies could involve multiple data splits or 10-fold cross-validation to enhance the scientific and objective nature of the model and address this issue.

The extraction of radiomic features inherently exhibits sensitivity to specific instrument parameters[40]. Essentially, the selection of CT machines and imaging techniques affects the representation of these characteristics, with texture attributes being especially dependent on scanning parameters[41]. Accordingly, this investigation solely utilized imaging information from one CT scanner to guarantee uniformity. To ensure consistency, only images possessing the same scanning parameters and a slice thickness of 5 mm were used in the stages of feature extraction and post-processing. Multiple factors can impact the stability of functional performance, particularly the region of interest (ROI), especially concerning its size and extent. Subsequently, the segmentation outcomes were corrected and reviewed by two clinical radiologists experienced in abdominal imaging to ensure inter-rater reliability. In our endeavor to characterize the TIME heterogeneity among CRC lesions, we focused on extracting DL

features directly from the textures of CT images. In the study by Lin P *et al*, a joint model was established by integrating ML features and DL features derived from 2D CT images. Specifically, based on manually annotated ROIs, the ROIs were expanded to surrounding areas by 10 and 20 pixels to construct a DL model, namely ResNet-19[42]. This approach also demonstrated considerable predictive potential. The shape features related to the geometric attributes of the ROI, along with first-order statistical features that describe the distribution of single pixel values, also provided additional support to our model. As the accuracy of imaging technologies improves, issues concerning the stability of radiomic features are expected to gradually resolve[43]. On the other hand, although the characterization of tumor heterogeneity still relies on molecular and cellular biology, the evolution of imaging modalities has shown great potential in this regard[44]. However, further research is needed to reliably detect different tissue textures and establish connections with singular molecular causes, such as tumor-associated immune cells, which were the focus of this study.

The present study utilized ten DL models to perform visual training and evaluate factors such as specificity, sensitivity, and potential overfitting. Finally, the DenseNet model was selected, as it shares a fundamental concept with ResNet but forms dense connections between previous and subsequent layers[45,46]. DenseNet achieves feature reuse by establishing connections between features across channels, resulting in superior performance compared to ResNet employing fewer parameters and lower computational cost[47]. In accordance with previous investigations employing DL-based CT radiomics in CRC, our findings may contribute to the understanding of TME information, offering certain benefits. From this perspective, Wu *et al*, employed CNN models to predict the presence of KRAS non-invasively[48], while Wei *et al*, employed ResNet10 to predict the response to chemotherapy in patients with colorectal liver metastases[49]. The study utilized a large sample size of 1028 cases and employed the CNN+[Recurrent Neural Network\(RNN\)](#) model to predict the initial response to treatment in metastatic CRC. Accordingly, the study yielded a C-index value of 0.649. However, unlike our findings, these studies do not offer personalized information on

the TME, the integration of different types of data modalities, and a comprehensive understanding of the TIME in CRC patients, even though they may offer certain insights into the patient's reaction to chemotherapeutics. Thus, the biological characteristics of the TIME cannot be adequately represented by individual, or a comprehensive understanding of the TIME indicators. As a result, there is a growing inclination towards the development of a thorough evaluation system that includes various indicators to fully describe the TME[50,51].

Although we recognize the potential clinical importance of our findings, it is crucial to acknowledge the presence of certain limitations and unexplored aspects that require further investigation in the future. Firstly, we observe a lack of adequate external validation, which limits the availability of easily accessible single-center retrospective studies. Therefore, there is a need for comprehensive, standardized prospective studies that include patient groups from multiple centers in future research efforts. Furthermore, this study did not provide a thorough classification of TSR and TILs. Consequently, additional investigations are necessary to elucidate the complex and extensive roles of TILs, specifically B cells, in combination with thorough analyses of cellular components within the tumor stroma. Furthermore, the research revealed that the procedure of image segmentation and pathology slice evaluation for radiomics was significantly time-intensive. The model exhibited low reproducibility and the findings of the study lacked generalizability. Therefore, it is essential to prioritize the advancement of automated image segmentation techniques in order to establish a consistent and standardized study process. Moreover, the inclusion of external validation is crucial to ensure the strength and dependability of the results.

In this study, a radiomics prediction model was developed using a DL approach to predict preoperative TSR, TILs, and IS in CRC patients based on CT images. Moreover, the integrated model may provide potential assessment capabilities for TIME, thereby potentially offering guidance for immunotherapy in CRC.

CONCLUSION

This study developed a DL-based radiomics prediction model using preoperative CT images to non-invasively evaluate TSR, TILs, and IS in CRC patients. The integrated model demonstrated potential for assessing the TIME, offering a novel tool to guide immunotherapy strategies and improve personalized treatment planning in CRC management.

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