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Research Progress and Status of Radiomics and Deep Learning in Colorectal Cancer

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Abstract: Colorectal cancer (CRC) continues to be a major contributor to global cancer mortality. Within China, its incidence ranks second and its mortality ranks fourth. Under these conditions, improving early diagnosis and performing quantitative evaluation of treatment efficacy become essential priorities in both clinical practice and engineering development. Medical imaging offers indispensable non-invasive information. In routine diagnostics, however, assessment still depends largely on radiologists subjective visual interpretation, which does not provide sub-visual pathological and immunological phenotypes. Radiomics was introduced as an approach to quantify tumor microenvironments. Yet, early machine-learning-based pipelines encountered persistent obstacles, including biases introduced by manual feature engineering and limited generalization across different centers. Deep learning (DL) has altered this workflow in a fundamental way. With end-to-end nonlinear feature mapping, DL architectures can bypass conventional bottlenecks, leading to more reliable model behavior and improved robustness and reproducibility. This paper surveys recent developments in DL-empowered radiomics for CRC across five key areas: automated tumor segmentation, neoadjuvant therapy response prediction, risk stratification, lymph node metastasis evaluation, and microsatellite instability (MSI) status mapping. In addition, it points to emerging engineering directions—specifically multi-modal fusion and explainable DL—that are required to bring these computational models into standard clinical workflows.

1. Introduction

According to the 2022 global cancer statistics published by the International Agency for Research on Cancer (IARC)[1], cancer-related burden in China is especially high. In that context, colorectal cancer (CRC) incidence and mortality both move into the second and fourth positions, respectively, among all cancer types[2] . Addressing existing technical constraints to raise early detection rates and to enable dynamic efficacy evaluation is therefore presented as an urgent clinical requirement. Early screening programs and precision medicine strategies have been implemented in China, and these measures have managed—within the limits described in the source—to restrain these rates to some degree[3].

Radiomics is described as an interdisciplinary computational approach that uses machine learning or advanced statistical models to quantify macroscopic and microscopic tumor phenotypes. In practice, this method supports non-invasive, multi-dimensional tumor characterization, and it has been applied to predict staging, lymph node involvement, and overall prognosis, thereby supporting dynamic, personalized interventions[4]. At the same time, the text identifies constraints in conventional radiomics pipelines: they depend strongly on image data quality and sample size. Under conditions such as noise or small cohorts, model reliability is reported to deteriorate substantially[5]. In addition, the traditional workflow is stated to rely mainly on hand-crafted feature extraction, which creates a bottleneck related to "feature engineering"[6]. More recently, the integration of DL into CRC radiomics is described as having produced notable results. Deep neural networks are presented as using representation learning to implicitly reduce the influence of subjectivity in manual feature selection. When DL is coupled with radiomics, the source indicates improvements in data fitting and generalization in high-dimensional settings, along with faster translation toward clinical deployment[7]. This review is said to systematically examine current engineering applications of DL-empowered radiomics in CRC, covering five areas: automated region-of-interest (ROI) segmentation, neoadjuvant treatment response, prognostic risk stratification, lymph node metastasis, and microsatellite instability (MSI) prediction.

2. Technological Framework

2.1 The Radiomics Feature Engineering Pipeline

Over the last decade, Radiomics has become a mature element of digital medicine and is embedded in many predictive models across medical specialties [8]. In these settings, the extracted Radiomics features are used to translate the tumor microenvironment and related biomarkers into input variables for predictive modeling. [9] During the extraction stage, mathematically defined metrics are computed. The set includes first-order histogram statistics and 3D morphological measurements. It also covers higher-order texture descriptors such as Gray-Level Co-occurrence Matrices (GLCM) and Gray-Level Run Length Matrices (GLRLM). The resulting high-dimensional feature vectors are used to represent the ROI's topology, signal intensity, volume, and internal heterogeneity[10]. Through this mapping, sub-visual, pixel-level patterns are linked to disease subtyping, prognosis, and therapeutic sensitivity[11]. Overall, Radiomics is framed as constructing a "digital twin" of the tumor microenvironment, which enables longitudinal assessment of spatiotemporal heterogeneity. This capability is presented as useful for clinical phenotyping and for optimizing personalized chemo-immunotherapy regimens[12].

2.2 Deep Representation Learning Mechanisms

DL, as an advanced subset of machine learning, is built on multi-layer artificial neural networks to realize powerful non-linear mapping. In this framework, features are learned in a complex and hierarchical manner from ultra-high-dimensional unstructured data. Weights are adjusted by forward and backpropagation algorithms, and the network produces probabilistic predictions[13]. For medical image analysis, Convolutional Neural Networks (CNNs), Deep Neural Networks (DNNs), and Recurrent Neural Networks (RNNs) are highlighted as the main computational engines. Compared with traditional shallow algorithms that depend on human priors, the major cited benefit of CNNs is end-to-end implicit feature extraction[14]. Because of this, CNNs are presented as the backbone of medical computer vision. A typical CNN design is described as consisting of an input layer, convolutional layers for feature extraction, pooling layers for spatial down-sampling, fully connected layers for global feature aggregation, and an output layer (Figure 1).

In CRC imaging tasks, CNNs are used for three core functions: classification, object detection, and semantic segmentation. For classification, classic models such as AlexNet, VGG, and ResNet are noted as using residual connections. For lesion detection, R-CNN variants and YOLO are described as relying on anchor mechanisms. For segmentation, Fully Convolutional Networks (FCNs) and U-Net variants are described as employing skip-connections to merge high-resolution spatial information with deep semantic contexts, which is stated to establish the gold standard for medical image segmentation[15]. By automating feature learning, DL is said to reduce both the time requirement and the subjectivity that come with manual contouring. Relative to traditional radiomics, deep networks are described as better suited for mining deep-level micro-patterns while also maintaining higher computational efficiency and reproducibility across heterogeneous cohorts[16]. Therefore, combining deep learning with radiomics is presented as improving model generalization and reliability, which in turn supports faster clinical translation of these fusion models for practical diagnosis and treatment.

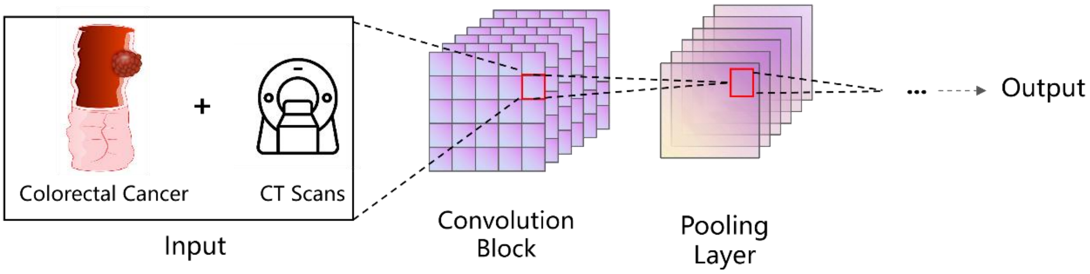

Figure 1 The structure of convolutional neural networks.

CNN extracts image features through stacked convolution and pooling operations. The features are then aggregated by the fully connected layer and converted into class probabilities in the output layer.

3. Algorithmic Breakthroughs in Automated CRC Segmentation

The computational goal of medical image segmentation is to separate target lesions and organs-at-risk (OARs) from complex anatomical background noise at the pixel level[17]. For CRC, generating precise 3D tumor masks is a prerequisite for capturing true tumor volume and assessing invasion depth; it is the critical anchor for downstream radiomics. Manual contouring is notoriously labor-intensive and suffers from high inter- and intra-observer variability. Evidently, developing DL segmentation networks with true 3D spatial awareness became a primary engineering focus.

FCN and U-Net topologies currently dominate this space[18], with performance routinely benchmarked using the Dice Similarity Coefficient (DSC). Long et al.[19]introduced the FCN, replacing dense layers with convolutions to enable end-to-end pixel-wise predictions. Adapting this for 3D data. Soomro et al.[20]built a hybrid 3D-FCNNs+3D model incorporating level-set evolution, achieving a testing DSC of 93.78% on MRI multi-planar reconstructions. Later, Ronneberger et al.[21]introduced U-Net, whose symmetric encoder-decoder structure and skip connections perfectly balanced global context with local texture. U-Net variants have since proliferated in CRC research. Huang et al.[22]proposed 3-D RU-Net, pairing a global encoder for rough ROI localization with a local decoder for feature pyramids, achieving a mean DSC of 75.5% on T2WI sequences. To leverage multi-modal data, Chen C[23]designed TMSF-Net, utilizing a parallel three-branch encoder to extract and fuse multi-scale features across modalities, pushing the DSC to 0.976. Addressing the ambiguous boundaries between rectal tumors and adjacent soft tissue, Chen S. et al.[24]developed TdDS-UNet with a deep supervision strategy, optimizing boundary loss via multi-scale gradient backpropagation to reach a DSC of 0.805. More recently, attention mechanisms have been integrated; Yao et al.[25]built the DeepCRC model on the nnU-Net framework, embedding self-attention modules in down-sampling layers to capture global receptive fields while retaining CNN inductive biases (mean DSC: 61.90% ±24.90% on highly complex CTs).Table1 details these architectural innovations.

In summary, U-Net and its 3D derivatives demonstrate excellent robustness against irregular intestinal deformations. As algorithms transition from 2D to 3D, and from pure convolutions to hybrid CNN-Transformer architectures, automated target delineation is approaching attending-physician-level accuracy, significantly streamlining radiologic workflows.

Table 1. Core Network Innovations and Performance of CRC Automated Segmentation Models

Model	Modality	Backbone	Innovations	Dataset	Best Performance
3DFCNNs[20]	MRI	3D-FCN	Hybrid Topology	N=70	93.78%
3DRUNet[22]	MRI	U-Net	Dual-Pathway Design	N=64	75.50% ± 10.70%
TMSFNet[23]	CT	Custom3D CNN	Multi-Scale Fusion:	N=22	52.51% ± 10.41%
TdDSUNet[24]	MRI	DeepU-Net	Boundary Optimization	N=144	80.50% ± 5.30%
DeepCRC[25]	CT	nnU-Net	CNN-Transformer Hybrid	N=227	61.90% ± 24.90%

4. Engineering Applications Across the CRC Clinical Lifecycle

4.1 High-Dimensional Mining for Lymph Node Metastasis(LNM)

Accurate LNM staging dictates the extent of surgical resection and the necessity of adjuvant chemotherapy in locally advanced CRC[26]. Addressing this, Zhao et al.[27]proposed a joint framework using autoencoders and deep residual networks to filter 20 highly expressive deep features from venous-phase CTs. The combined model (merging DL features with CEA/CA199 markers) achieved an Area Under the Curve (AUC) of 0.770. Using multi-parametric MRI from a large cohort (n=611), Wan et al.[28]compared various 2D and 3D ResNet variants. Their 3D ResNet101 achieved a testing AUC of 0.790, statistically outperforming senior radiologists (AUC: 0.540). In a multi-modal approach, Wang et al.[29]built a cross-modality network combining 18F-FDG PET metabolic features, CT density, and clinical labels, maintaining a robust external validation AUC of 0.836. Pushing for lightweight deployment, Yang et al.[30]utilized MobileNet-V3-large to extract deep MRI features, applying early fusion with traditional radiomics to achieve an external AUC of 0.752—boosting diagnostic accuracy by 0.113 over human baselines. Because pixel-level lymph node annotation is prohibitively expensive, Xia et al.[31]implemented a weakly-supervised multi-instance learning framework. By training imaging features against coarse postoperative pathology labels across 1014 patients, the model achieved an overall AUC of 0.810, significantly outperforming senior radiologists.

4.2 Virtual Biopsy for Microsatellite Instability(MSI)

MSI is a crucial genetic classification in CRC and a definitive biomarker for the efficacy of PD-

1/PD-L1 immune checkpoint inhibitors[32]. Traditional immunohistochemistry and PCR sequencing are constrained by tumor spatial heterogeneity and the invasive nature of biopsies[33]. Radiomics acts as a "virtual biopsy," decoding sub-voxel spatial heterogeneity to predict MSI non-invasively.

Zhang et al.[34]applied LASSO dimensionality reduction and XGBoost to extract six core radiomic features from MRI data (n=491), achieving a validation AUC of 0.895. Enhancing clinical interpretability, Peng et al.[35]integrated multi-parametric MRI (T2WI and ADC maps) to construct a radiomics nomogram, which hit an extreme testing AUC of 0.984. Exploring advanced topologies, Chen X. et al.[36]used Genetic Algorithms (GA) to auto-tune an Artificial Neural Network (ANN) on CT data, yielding an external AUC of 0.775, far surpassing clinical baselines (0.623). Acknowledging microenvironmental heterogeneity, Cai et al.[37]applied unsupervised clustering to divide tumors into sub-regional “habitats.” They extracted features specifically from high-risk MSI regions, and reported an external AUC of 0.830. With the shift toward foundational models, Chen W. et al.[38] used a Vision Transformer (ViT) together with a CNN in a two-stream architecture, evaluated on a large 2180-patient cohort. In this design, the ViT was used to capture global context, while the CNN processed local textures. The reported outcome was an end-to-end MSI prediction AUC of 0.830.

4.3 Dynamic Prediction of Neoadjuvant Treatment Response

For locally advanced rectal cancer (LARC), neoadjuvant chemoradiotherapy (nCRT) is presented as the key frontline approach for achieving macroscopic tumor downstaging and eliminating potential micro-metastases[39]. The morphological regression caused by nCRT is described as creating more favorable anatomical conditions for surgery, which supports higher rates of sphincter-preserving procedures[40] . The morphological regression caused by nCRT is described as creating more favorable anatomical conditions for surgery, which supports higher rates of sphincter-preserving procedures[41]. Deep radiomics is indicated as suitable for non-linear time-series prediction[42]. Liu et al.[43]constructed a deep feedforward network using baseline MRI features to forecast distant metastasis after nCRT, reporting a 3-year survival AUC of 0.894. Feng et al.[44]emphasized multi-scale information and matched macroscopic MRI deep features with microscopic Whole Slide Imaging (WSI) features. With evaluation on more than 1,000 patients, the multi-omics model is reported as robust, with Validation Cohort 1 AUC: 0.860 and Cohort 2 AUC: 0.872. After shifting away from radiation-based inputs, Qin et al.[45]trained a Multi-Layer Perceptron (MLP) on low-cost ultrasound imaging and achieved a joint model AUC of 0.893.

For colorectal liver metastases (CRLM)[46], quantifying spatial heterogeneity before treatment is described as important for determining chemotherapy response[47]. Wei et al.[48], quantifying spatial heterogeneity before treatment is described as important for determining chemotherapy response[49]proposed DERBY, a knowledge-graph-style model that used DNNs to cross-reference PET-CT data with deep features and clinical metrics. The improved DERBY+ variant, incorporating histopathological markers, is reported to keep high stability in external validation, with AUC values ranging from 0.77 to 0.83.

4.4 Granular Risk Stratification and Survival Analysis

Translating high-dimensional imaging data into risk coefficients for Disease-Free Survival (DFS) or Overall Survival (OS) represents the ultimate goal of AI in precision medicine[50]. Wang et al.[51]conducted a pioneering multi-modal study: they fused weakly-supervised CNN features from WSI, traditional CT radiomics, and a CD3+, CD8+ lymphocyte density immune score using an SVM. This panoramic model achieved DFS and OS validation AUCs of 0.875 and 0.860, respectively, enabling true dual molecular imaging risk stratification. Jiang et al.[52]developed a deep regression network based on 3D tumor segmentation to predict 1-, 3-, and 5-year OS directly from baseline

T2WI (AUCs: 0.65, 0.64, 0.74). Focusing on the internal microenvironment, Cai et al.[53]utilized deep networks to quantify the Tumor-Stroma Ratio (TSR) in rectal cancer, proving that AI-extracted TSR correlates strongly with long-term survival (joint model AUC: 0.76). Deep radiomics is actively dismantling the broad generalizations of the traditional TNM staging system, driving oncology toward highly quantified, individualized care.

5 Summary and Engineering Trajectories

DL–based radiomics has demonstrated practical advantages for CRC modeling across the full care pathway. Rather than depending on manually designed features, deep architectures learn hierarchical representations directly from imaging inputs. This capability helps quantify tumor phenotypes and subtle intratumoral heterogeneity that are often difficult to assess consistently by visual inspection. In addition, AI-derived imaging biomarkers support standardized prediction of risk and disease status, which may facilitate earlier detection and more timely treatment decisions. Such tools can be particularly valuable in settings where expert interpretation is limited, because they provide reproducible estimates that can improve access to consistent clinical decision support. Ultimately, improved prediction and risk stratification can enable more individualized therapeutic planning.

Despite these benefits, several issues remain before widespread clinical adoption is realistic. A major limitation is limited interpretability: deep models are often treated as “black boxes,” which can hinder clinician confidence and complicate verification of whether the model reasoning reflects plausible tumor biology. Emerging engineering solutions have been adapted to address this issue in medical imaging. Attention mechanisms can help identify informative regions in images and improve the transparency of model analysis. Grad-CAM can further support interpretation by visualizing the image areas associated with a given prediction. Concept-based explainable models offer another direction by linking model outputs to higher-level, clinically meaningful concepts. Second, training and deployment commonly require substantial computational resources, including high-end GPUs and high-capacity storage, increasing technical and financial barriers. Third, model generalization can degrade when testing data differ from training cohorts, such as variations in scanner hardware, imaging protocols, and patient mix across centers. Finally, the need for large volumes of labeled data—with consistent annotations, segmentation protocols, and reliable endpoints—creates additional practical constraints for model development.

Looking forward, progress will likely depend on bridging prediction performance with biological and clinical interpretability. Combining deep radiomics with multi-omics information can provide complementary evidence from genomics, transcriptomics, proteomics, and immune-related markers, improving both robustness and clinical relevance. Explainable AI methods (e.g., Grad-CAM and SHAP) can further help translate model outputs into features that are more understandable for clinicians. Beyond visualization, biological interpretability strategies—such as connecting imaging-derived signals to tumor microenvironment mechanisms—may strengthen the evidentiary basis for using these tools in decision-making. In parallel, building larger, more diverse datasets is essential for stable external validity and for the development of clinically reliable medical foundation models.

A decisive step toward real-world impact is the expansion and harmonization of training databases. Multi-center, large-scale datasets covering diverse populations, scanners, and acquisition protocols form the backbone of credible validation and fair performance evaluation. Therefore, a collaborative global effort among institutions is recommended to construct a consortium-level database with standardized annotation guidelines and privacy-preserving data governance. Shared benchmarks and harmonized data standards can reduce dataset bias, improve cross-domain robustness, and accelerate model iteration. In the long run, such a globally driven data infrastructure will help ensure that deep radiomics supports earlier diagnosis, more accurate risk stratification, and more personalized treatment choices for CRC patients worldwide.

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