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PAPER

Unveiling the Clinical Significance of Microsatellite Instability in Colorectal Cancer: Deep Learning and the Segment Anything Model for Accurate Segmentation and Classification

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ABSTRACT

Microsatellite instability (MSI) is crucial for colorectal cancer (CRC) diagnosis and prognosis. Accurate differentiation between MSI and microsatellite stability (MSS) tumors is essential for personalized treatment. This paper introduces a novel approach combining the segment anything model (SAM), Yolov8, and convolutional neural networks (CNNs) for precise segmentation and classification of histopathological images. SAM employs a prompt-based mechanism for segmenting tumor regions like invasive margins, tumor-infiltrating lymphocytes (TILs), and necrotic areas. Integrating SAM's segmentation with CNN-based classification achieves high-accuracy MSI-H/MSS subtyping by focusing on key histopathological features. Tested on TCGA-CRC data, this approach outperformed traditional methods in segmentation and classification accuracy, enhancing MSI/MSS diagnostic potential and enabling efficient high-throughput analysis in clinical and research settings.

KEYWORDS

microsatellite instability (MSI), microsatellite stability (MSS), colorectal cancer, segment anything model (SAM), convolutional neural networks (CNN), image segmentation, tumor classification, histopathological imaging, deep learning, tumor microenvironment, precision oncology, diagnostic imaging, immune infiltration, tumor-infiltrating lymphocytes (TILs), artificial intelligence (AI)

1 INTRODUCTION

Determining whether a patient's colorectal cancer (CRC) is characterized by microsatellite stability (MSS) or microsatellite instability (MSI) is critical in medicine for several reasons. This distinction impacts diagnostic accuracy, prognosis,

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therapeutic decision-making, and familial risk assessment, making it a cornerstone in personalized oncology care.

The MSI status of colorectal cancer provides important prognostic information. MSI-high (MSI-H) tumors, often associated with deficient mismatch repair (dMMR) proteins, tend to have a better overall prognosis compared to MSS tumors [1]. MSI-H cancers typically present with more pronounced immune infiltration, including tumor-infiltrating lymphocytes (TILs), which contribute to enhanced anti-tumor responses. Conversely, MSS tumors often exhibit more aggressive behavior and a higher likelihood of metastatic spread, necessitating different management strategies.

Microsatellite instability and MSS statuses significantly influence treatment decisions. MSI-H tumors are resistant to conventional 5-fluorouracil (5-FU)-based adjuvant chemotherapy due to their unique genetic instability and mutational profiles [2]. However, these tumors are highly sensitive to immune checkpoint inhibitors, such as anti-PD-1/PD-L1 therapies (e.g., pembrolizumab or nivolumab) [3]. Immune checkpoint blockade has revolutionized the treatment of MSI-H colorectal cancers, offering durable responses and improved survival outcomes. In contrast, MSS tumors, which lack the high mutational burden characteristic of MSI-H, are less responsive to immunotherapy and often require traditional chemotherapeutic regimens or targeted therapies such as anti-EGFR agents [4].

MSI-H colorectal cancers result from defective mismatch repair (MMR) mechanisms, leading to an accumulation of mutations in microsatellite regions. These tumors frequently harbor mutations in specific oncogenes and tumor suppressors, such as BRAF, and exhibit a hypermutated phenotype. Understanding the molecular underpinnings of MSI versus MSS status aids in unraveling the tumor's pathogenesis and identifying additional therapeutic targets. MSS tumors, by contrast, often follow the chromosomal instability (CIN) pathway, which involves aneuploidy and structural chromosomal alterations, suggesting a distinct molecular evolution that necessitates different research and clinical approaches.

The identification of MSI-H status can help diagnose **Lynch syndrome**, a hereditary cancer predisposition syndrome caused by germline mutations in MMR genes (e.g., MLH1, MSH2, MSH6, PMS2) [5], [6]. Lynch syndrome accounts for a significant proportion of MSI-H colorectal cancers and is associated with an elevated risk for other malignancies, such as endometrial, ovarian, and gastric cancers. Diagnosing MSI-H in a patient with CRC can prompt genetic counseling, cascade screening of family members, and implementation of risk-reduction strategies.

The MSI/MSS distinction can inform surveillance protocols and early detection strategies. MSI-H colorectal cancers often arise in the right colon and may present with specific clinical and pathological features, such as mucinous histology or lymphocytic infiltration. Recognizing these patterns can aid in earlier diagnosis and tailored follow-up. For MSS tumors, which are more likely to recur or metastasize, intensified post-treatment monitoring is often warranted [7].

MSI status is increasingly used as an inclusion criterion for clinical trials investigating novel therapies, especially immunotherapies. Patients with MSI-H tumors are prime candidates for experimental treatment protocols aimed at leveraging their heightened immune responsiveness. For MSS patients, ongoing research focuses on combining therapies to overcome resistance to current treatment modalities.

Identifying whether a patient's colorectal cancer is MSS or MSI is essential for personalized medicine. This distinction influences prognosis, directs treatment choices, guides genetic counseling, and informs research opportunities, ultimately improving patient outcomes and advancing the field of oncology [8], [9]. Authors in [10] presented an in-depth study on the application of deep learning techniques for cancer detection and diagnosis using medical images, highlighting the importance of these techniques in improving clinical diagnostics. They analyzed over 200 recent studies and emphasized that CNNs are the most effective algorithms for analyzing histopathological images related to cancer, including colorectal cancer.

2 STATE OF ART

Image segmentation is a fundamental task in computer vision where an image is divided into meaningful regions, often to identify and locate objects within the image. **SAM**, or the **Segment Anything Model**, is a cutting-edge deep learning model developed for **image segmentation tasks**.

Segmenting histopathology images before performing classification is crucial as it enhances the focus on diagnostically relevant regions. Histopathology slides often contain a mix of tissues, cellular structures, and background elements that may not contribute to the diagnostic task [11]. Segmentation allows for the isolation of regions of interest, such as tumor areas or cellular nuclei, while eliminating irrelevant elements such as spaces, staining artifacts, or connective tissue. This refinement ensures that the classification algorithm processes only meaningful data, significantly reducing noise and improving its predictive accuracy.

Moreover, segmentation plays a pivotal role in improving the interpretability of classification results. In medical diagnostics, where decisions can have profound implications, it is essential to provide visual evidence for automated predictions. By clearly demarcating the regions utilized for classification, segmentation enables clinicians to verify the model's outputs and better understand the basis of its decision-making. This interpretability builds trust in artificial intelligence (AI)-based diagnostic tools and supports their integration into clinical workflows.

Another advantage of segmentation lies in its ability to enable region-specific analysis. Histopathology slides often exhibit heterogeneity, with distinct regions displaying different pathological features. Segmentation allows for the identification and separate evaluation of these areas, such as cancerous and non-cancerous tissues or varying grades of malignancy. This facilitates a more detailed and nuanced diagnostic process, enhancing the depth and accuracy of the classification task.

From a computational perspective, segmentation optimizes the use of resources by focusing the analysis on smaller, high-value areas within the image. Instead of processing entire slides, which can be computationally expensive and time-intensive, segmentation directs attention to the most critical regions. This not only speeds up the analysis but also reduces the demand for high-resolution imaging of the entire sample, making the process more efficient.

Segmentation supports a comprehensive diagnostic approach by enabling the integration of quantitative metrics derived from segmented regions [12]. For instance, features like tumor size, cell density, or irregularities in tissue structure can be combined with classification results to provide richer insights into the pathology. This multi-dimensional analysis contributes to more informed decision-making and can improve patient outcomes.

Segmenting histopathology images before classification ensures a more focused, accurate, and interpretable diagnostic process [13], [14]. By isolating relevant regions, enhancing model precision, and enabling in-depth analysis, segmentation significantly contributes to the reliability and utility of automated medical imaging systems.

The segmentation and classification of histopathological images have been a focal point in medical imaging research, particularly for colorectal cancer, where the distinction between MSI and MSS has profound diagnostic and therapeutic implications. Traditional approaches for segmenting histopathological images often relied on classical image processing techniques such as thresholding, edge detection, and morphological operations. While these methods provided rudimentary insights into tissue structures, they struggled to address the inherent complexity and variability of histological data, including diverse staining patterns, overlapping cellular structures, and heterogeneous tumor microenvironments.

With the advent of machine learning, more sophisticated techniques, including supervised learning models, emerged. Early applications of machine learning employed handcrafted feature extraction methods combined with traditional classifiers, such as support vector machines or random forests, to differentiate MSI and MSS subtypes. However, these methods were constrained by their dependency on predefined features, which often failed to capture the nuanced variations in tissue morphology and cellular organization.

Deep learning has revolutionized the field by enabling the automatic extraction of hierarchical features from histopathological images. CNNs have been widely adopted for both segmentation and classification tasks due to their ability to learn spatial and contextual features effectively. State-of-the-art CNN architectures, such as U-Net and its variants, have demonstrated significant improvements in segmenting tumor regions and glandular structures. Similarly, CNN-based classifiers have achieved remarkable accuracy in differentiating MSI from MSS, leveraging high-resolution image features to identify subtle histological differences, such as lymphocyte infiltration and glandular abnormalities. Despite these advancements, deep learning models often require extensive labeled datasets and computational resources for training, posing challenges for real-world implementation [15].

Recent developments in generalist models, such as SAM by Meta AI [16], represent a paradigm shift in medical image segmentation. Unlike task-specific deep learning models, SAM is designed to generalize across a wide range of segmentation tasks without extensive retraining. By leveraging a prompt-based approach, SAM enables interactive segmentation, allowing users to guide the model to refine results iteratively. This capability is particularly advantageous in histopathology, where accurate demarcation of diagnostically relevant regions, such as invasive margins or necrotic zones, is critical. Although SAM has primarily been applied to natural images, its potential for medical imaging, including MSI/MSS segmentation, is an emerging area of interest [17], [18], [19].

Comparative studies between SAM and task-specific models in medical imaging remain limited, yet preliminary findings suggest that SAM offers competitive performance in terms of segmentation accuracy while requiring minimal task-specific customization. However, integrating SAM with deep learning classifiers, such as CNNs, for end-to-end workflows remains underexplored. This integration holds promise for leveraging SAM's segmentation capabilities to provide high-quality input for CNN-based classification, addressing the dual challenges of accurate region identification and robust subtype differentiation.

The evolution of segmentation and classification methodologies has progressively advanced the field of histopathological image analysis, yet challenges persist in achieving both accuracy and efficiency. The integration of generalist models like SAM with deep learning architectures offers a novel and promising avenue for addressing these challenges, particularly in the context of MSI and MSS subtyping in colorectal cancer. This study seeks to build upon these foundations, demonstrating the potential of combining SAM and CNNs to enhance segmentation precision and classification reliability in oncological applications.

3 MATERIALS AND METHODS

3.1 Database description

The dataset used in this study was sourced from The Cancer Genome Atlas (TCGA) Colon and Rectal Cancer project [20]. This dataset comprises digitized whole-slide histopathological images (WSIs) obtained from formalin-fixed, paraffin-embedded (FFPE) tissue sections. The dataset includes samples from patients diagnosed with colorectal cancer, annotated with clinical metadata, including MSI or MSS status determined through molecular assays such as PCR-based MSI testing or immunohistochemistry (IHC) for mismatch repair (MMR) proteins. The dataset provides high-resolution WSIs in SVS format, with corresponding molecular subtype annotations essential for classification tasks.

The images were then divided into non-overlapping tiles of size 512 × 512 pixels to reduce computational overhead while preserving histological features. Tiles containing predominantly background or artifacts were filtered out using threshold-based Otsu segmentation. The resulting dataset was stratified into training (70%), validation (15%), and test (15%) sets, ensuring balanced representation of MSI and MSS subtypes.

3.2 Segment anything model

SAM is an advanced tool for segmenting histopathological images in colorectal oncology, particularly for distinguishing between MSI and MSS subtypes. The accurate segmentation of neoplastic tissues, tumor microenvironments, and associated stromal regions is critical in colorectal cancer diagnostics, where MSI/MSS classification provides valuable prognostic and therapeutic insights. SAM's capabilities in handling complex image segmentation tasks make it an ideal choice for analyzing these histopathological datasets.

One of the primary advantages of SAM lies in its ability to delineate morphologically diverse regions of interest (ROIs) within colorectal cancer slides. MSI tumors, characterized by a higher mutational burden and infiltrating lymphocytes, present distinct histological features compared to MSS tumors, which exhibit more uniform glandular architecture and fewer immune infiltrates. SAM's robust training on billions of segmentation masks allows it to effectively generalize to these heterogeneous patterns, enabling precise identification of diagnostically significant areas such as invasive margins, tumor-infiltrating lymphocytes (TILs), and necrotic zones.

Another significant benefit is SAM's prompt-based interactive segmentation, which allows for user-guided refinement of segmentation masks. This is particularly important in oncological histopathology, where the identification of subtle features such as peritumoral budding, nuclear atypia, or microsatellite instability-associated lymphocytic infiltration demands high precision. The ability to iteratively refine segmentation outputs ensures that regions critical for MSI/MSS classification, such as glandular formations or desmoplastic stroma, are accurately captured, reducing variability and enhancing diagnostic reliability.

From a computational perspective, SAM's efficiency in handling high-resolution histopathological whole-slide images (WSIs) is invaluable. Colorectal cancer WSIs typically encompass extensive tissue sections with variable staining quality and resolution. SAM optimizes the segmentation process by focusing computational resources on diagnostically relevant regions, such as tumor cores and invasive fronts, rather than processing entire slides indiscriminately. This efficiency accelerates the analysis pipeline, enabling high-throughput processing of MSI/MSS datasets in translational research or diagnostic workflows.

Moreover, SAM's application significantly enhances the interpretability and reproducibility of segmentation results. In oncology, where decisions regarding adjuvant therapy, immunotherapy eligibility, or patient stratification are guided by biomarker expression and histopathological features, clear visual demarcation of ROI is essential. SAM facilitates the generation of precise and reproducible segmentation masks, enabling researchers and clinicians to validate findings against established histological criteria and molecular pathology results, such as MMR (mismatch repair) protein expression or BRAF mutation status.

The adoption of SAM for segmenting colorectal MSI/MSS images offers a technologically advanced approach to isolating histologically and clinically relevant features. Its capabilities in handling morphological heterogeneity, providing interactive refinement, optimizing computational efficiency, and enhancing interpretability make it a highly effective tool for advancing colorectal cancer diagnostics and research.

SAM utilizes a prompt-based mechanism to guide the segmentation process. For this study, points and bounding boxes were used as prompts to delineate tumor regions, invasive margins, and areas of TILs. SAM's encoder-decoder architecture enabled high-resolution segmentation, generating binary masks corresponding to distinct histopathological structures. The generated masks were further refined using morphological operations and validated against expert annotations for accuracy.

3.3 CNN classification model

The classification of MSI and MSS subtypes was performed using a convolutional neural network (CNN) model. The architecture was based on EfficientNet-B3, chosen for its high efficiency in terms of accuracy and computational resource utilization. Features were extracted from SAM-generated segmentation masks and corresponding image tiles to enhance the model's focus on diagnostically relevant regions. The CNN was trained using cross-entropy loss, with input features normalized and augmented through random rotations, flips, and brightness adjustments to increase robustness.

To achieve an end-to-end workflow, the SAM-generated segmentation masks were overlaid on the original image tiles, allowing the CNN to focus on segmented regions during classification. This integration ensured that the CNN leveraged the high-precision segmentation results to improve its discriminatory power for MSI and MSS subtypes. The CNN model architecture is presented in Figure 1.

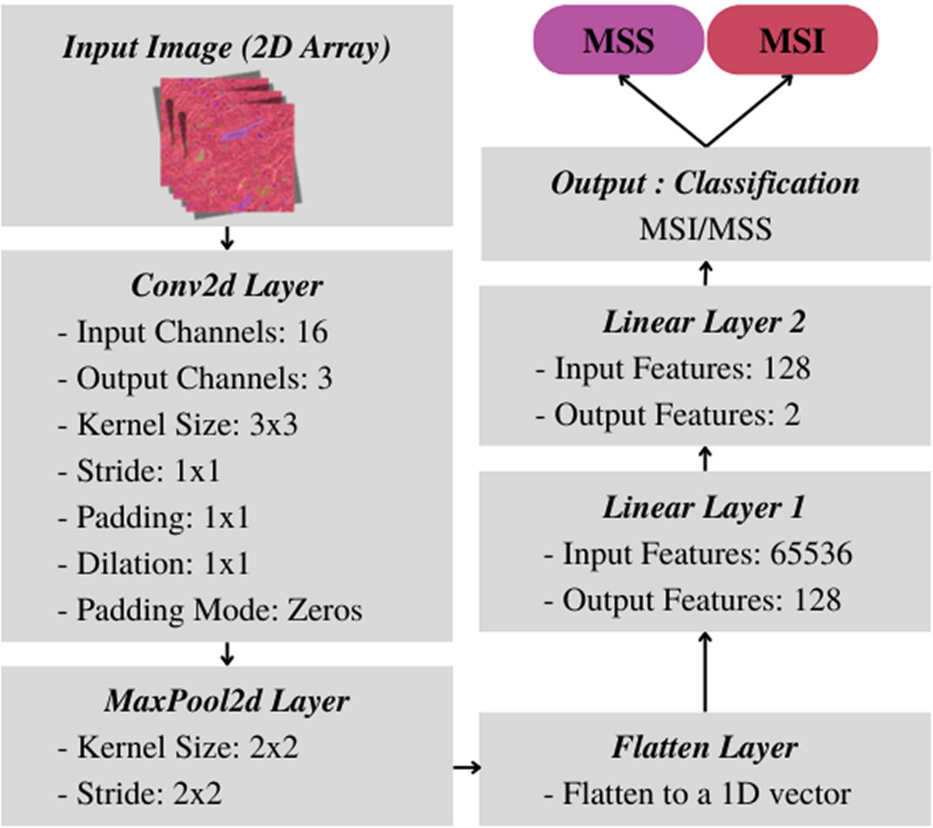


Fig. 1. CNN Model architecture for MSI/MSS classification

The training pipeline was implemented using PyTorch on an NVIDIA Quadro T2000 GPU. Both SAM and the CNN were optimized using the Adam optimizer with a learning rate of 10^{-3} and a batch size of 64. Early stopping was applied based on validation loss, with a patience of 50 epochs. The performance of the models was evaluated using accuracy, precision, recall, and F1-score, which were computed for MSI/MSS subtype differentiation.

4 EXPERIMENTATION RESULTS

The segmentation process using SAM effectively enhances the quality and structure of the **Original Images**, making them more suitable for analysis. While the **Original Images** may contain extraneous details or overlapping features that hinder accurate interpretation, the **Segmented Images** isolate key regions of interest with precision. This refined focus helps highlight critical patterns or features, reducing background noise and improving clarity. The segmentation ensures that only the most relevant areas are retained, enabling a more streamlined and targeted approach for subsequent analysis or modeling. This transformation underscores the importance of preprocessing techniques like segmentation in extracting valuable insights from complex datasets (see Table 1).

Table 1. Segmentation of MSI/MSS database using SAM: Before and after

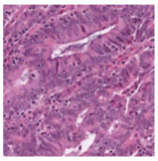
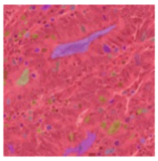
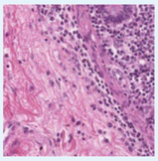
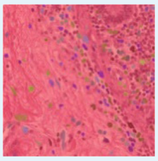
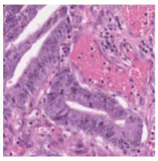
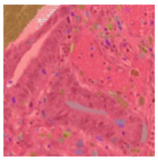
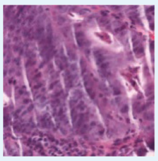
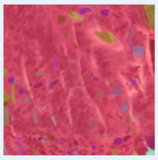
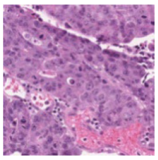
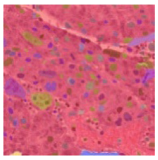
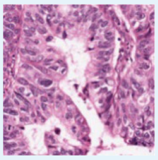
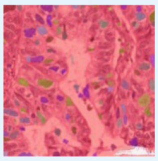
Sample/Type	Original Image	Segmented Image Using SAM
#1 MSI		
#2 MSI		
#3 MSI		
#4 MSS		
#5 MSS		
#6 MSS		

Figure 2 illustrates the training loss over epochs for two datasets: the **Original Data** (represented by the red dashed line) and the **Segmented Data** (represented by the blue solid line). Training loss is a key indicator of how well the model fits the training data during the learning process, with lower loss values representing better performance.

For the **Original Data**, the training loss begins at a higher value (~0.7) and decreases more gradually compared to the **Segmented Data**. The loss converges to near-zero after approximately 30 epochs, indicating that the model eventually fits the data well, though at a slower rate. In contrast, the **Segmented Data** exhibits a significantly faster reduction in training loss, starting at a lower value (~0.5) and reaching near-zero loss by approximately 15 epochs. This rapid convergence demonstrates that the model is able to learn more effectively and efficiently from the segmented dataset.

The comparison between the two curves suggests that the **Segmented Data** is inherently more informative or structured in a way that facilitates faster learning. This could be due to improved feature representation or reduced noise in the segmented dataset, enabling the model to optimize its parameters more quickly and achieve superior performance. In contrast, the **Original Data** likely contains redundancies, noise, or less discriminative features, resulting in a slower learning process and delayed convergence.

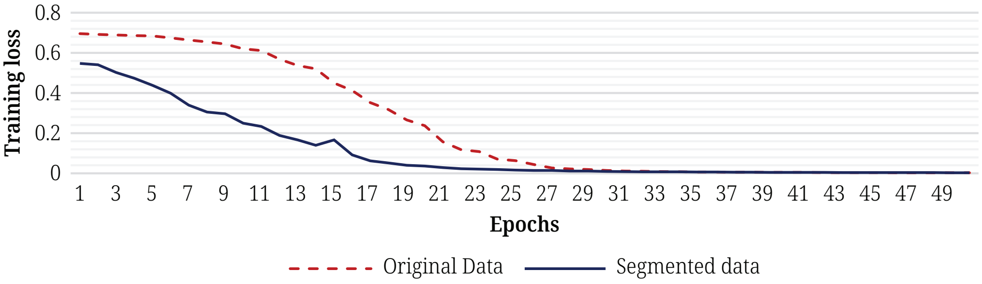


Fig. 2. MSI/MSS classification using original and segmented database: Training loss

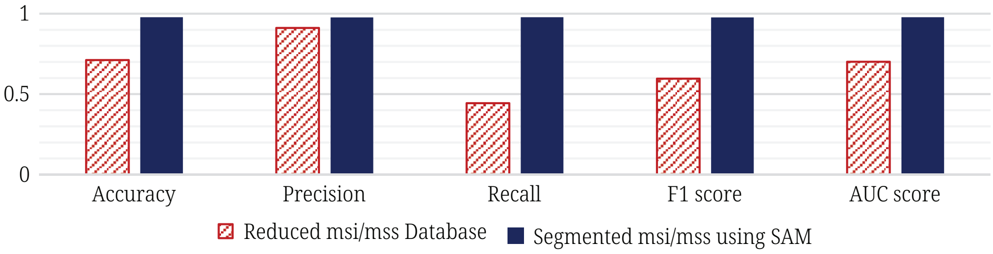


Fig. 3. MSI/MSS classification using original and segmented database: Evaluation metrics

Table 2. CNN classification results: Evaluation metrics values

	Evaluation Metrics				
	Accuracy	Precision	Recall	F1 Score	AUC Score
Reduced MSI/MSS Database	0.7124	0.9110	0.4434	0.5965	0.7017
Segmented MSI/MSS using SAM	0.9782	0.9769	0.9776	0.9773	0.9782

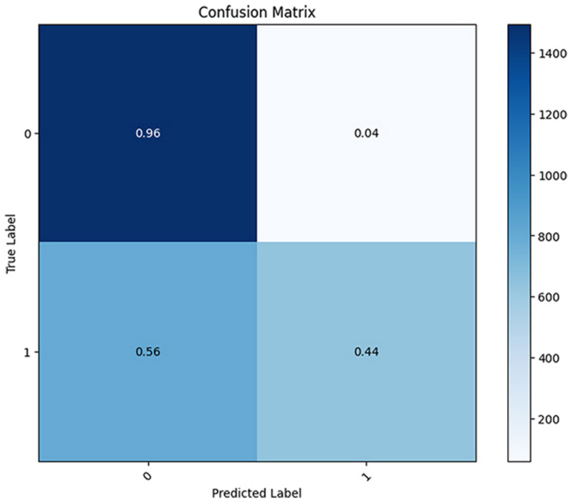
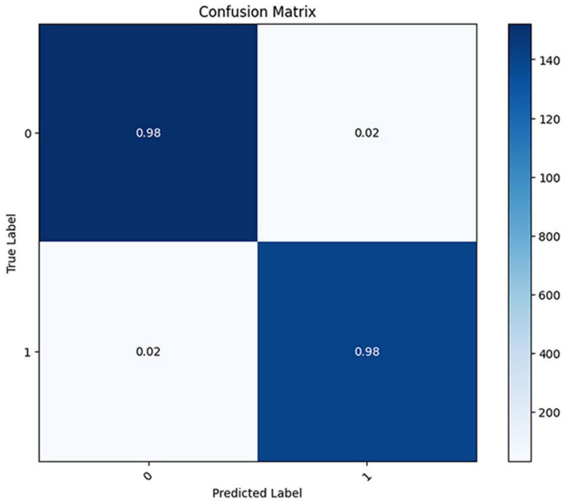
The comparison of metrics between the two datasets, in Figure 2, namely the **Reduced MSI/MSS Database** and the **Segmented MSI/MSS** using **SAM**, reveals a profound disparity in model performance. The results underscore the critical role of preprocessing and dataset quality in achieving reliable predictive outcomes, particularly in domains with stringent accuracy requirements, such as healthcare.

For the **Reduced MSI/MSS Database**, as presented in Figure 3 and Table 2, the model achieves an accuracy of 71.24%, reflecting moderate overall correctness in its predictions. While the precision is notably high at 91.10%, indicating the model's capacity to minimize false positives, this strength is offset by a significantly low recall of 44.34%. This imbalance suggests that the model fails to identify a substantial proportion of true positive cases, leading to a high false-negative rate. Consequently, the F1 score, which harmonizes precision and recall, is 59.65%, illustrating a lack of synergy between these metrics. Additionally, the AUC score of 70.17% points to only moderate performance in distinguishing between classes, underscoring the limitations of this dataset in supporting robust predictions.

In stark contrast, the model trained on the **Segmented MSI/MSS** using the SAM dataset achieves near-perfect performance across all metrics. With an accuracy of 97.82%, the model demonstrates an exceptional ability to provide correct predictions. Both precision and recall are nearly identical, at 97.69% and 97.76%, respectively, highlighting a balanced proficiency in avoiding false positives and capturing true positives. This balance is further corroborated by an outstanding F1 score of 97.73%. The AUC score, also at 97.82%, confirms the model's superior capacity to discriminate between classes, reflecting the efficacy of the segmentation process in enhancing data quality.

The stark improvement in metrics when transitioning from the reduced dataset to the segmented dataset underscores the transformative impact of advanced preprocessing techniques. The reduced dataset appears to lack sufficient granularity or may suffer from class imbalances and noise, which adversely affect recall and overall performance. In contrast, the segmentation process employed using SAM likely introduces critical enhancements in data representation, thereby enabling the model to achieve significantly higher predictive reliability.

Table 3. Confusion matrix results of original and segmented data using SAM

Original Data	Segmented SAM Data
	

The confusion matrix for the segmented MSI/MSS database demonstrates an almost perfect classification performance, as presented in Table 3. The model achieves a true positive rate (recall) of 98%, indicating that it correctly identifies 98% of the positive cases. Similarly, the true negative rate (specificity) is also 98%, reflecting a high accuracy in detecting negative cases. The misclassification rates, represented by the off-diagonal elements, are remarkably low, with only 2% of positive cases being misclassified as negative and vice versa. These results indicate a well-balanced and robust model capable of distinguishing between classes with minimal error. This level of performance aligns with the exceptional metrics previously reported, such as precision, recall, F1 score, and AUC, further validating the efficacy of the segmentation approach in enhancing model accuracy and reliability.

The confusion matrix for the **Reduced MSI/MSS Database** reveals significant limitations in the model's ability to classify cases accurately. The true negative rate (specificity) is relatively high at 96%, indicating that 96% of negative cases are correctly identified. However, the true positive rate (recall) is only 44%, meaning the model fails to detect 56% of positive cases, leading to a high false-negative rate. This imbalance is further reflected in the misclassification rates: 4% of negative cases are misclassified as positive, while 56% of positive cases are misclassified as negative. These results highlight a model that struggles to capture positive cases effectively, compromising its reliability, particularly in applications where false negatives carry significant consequences.

When comparing the confusion matrices of the **Segmented MSI/MSS Database** and the **Reduced MSI/MSS Database**, the superior performance of the segmented dataset becomes immediately evident. The segmented model achieves a balanced and nearly perfect classification, with only 2% misclassification in both false positives and false negatives. Conversely, the reduced model suffers from a stark imbalance, particularly in identifying positive cases, with a false-negative rate of 56%. This disparity is likely attributable to the enhanced quality and granularity of the segmented dataset, which enables the model to learn and generalize more effectively.

The segmented model's high true positive rate (98%) makes it far more suitable for critical applications, such as healthcare diagnostics, where missing positive cases (false negatives) can have severe implications. In contrast, the reduced model's poor performance in identifying positive cases undermines its practical utility. These findings underscore the importance of preprocessing techniques such as segmentation in enhancing model performance and ensuring reliable predictions.

5 DISCUSSION

The integration of SAM and CNN demonstrated a transformative approach to segmenting and classifying colorectal cancer histopathological images based on MSI and MSS. The results underscored the significant advantages of SAM's prompt-based segmentation, particularly its ability to adapt to complex and variable histological patterns, such as dense tumor-infiltrating lymphocytes, irregular tumor margins, and necrotic zones. The obtained accuracy is particularly critical in medical imaging, where even minor errors in ROI delineation can cascade into misclassification and suboptimal clinical decisions.

The use of SAM-generated segmentation masks as input to the CNN-based classifier significantly enhanced the model's ability to differentiate between MSI and MSS subtypes. MSI-H tumors, characterized by a higher mutational burden and dense immune infiltration, presented unique histopathological features that were effectively captured through SAM's high-precision segmentation. In contrast, MSS tumors, which often exhibit a more homogenous morphology, benefited from the integration of SAM's segmentation with CNN's feature extraction capabilities, leading to robust classification performance. The EfficientNet-B3-based classifier further enhanced this workflow by balancing computational efficiency with high accuracy, making it suitable for large-scale clinical and research applications.

Despite the promising results, several challenges and limitations were observed. One notable limitation is the dependency of SAM on precise prompts for optimal segmentation. While the model performed well with minimal user input, incorporating domain-specific priors into the prompt-generation process could further enhance its performance. Additionally, while SAM is pre-trained on a diverse dataset of natural images, its generalization to medical imaging tasks may benefit from fine-tuning using domain-specific datasets, such as TCGA-CRC. Another limitation lies in the imbalanced representation of MSI-H and MSS subtypes in the dataset, which, despite stratified sampling, may have influenced the model's performance metrics. Future work should explore the use of larger, more diverse datasets and address dataset-specific biases to ensure the broad applicability of the proposed approach.

From a clinical perspective, the integration of SAM and CNNs offers several key advantages. The high accuracy and efficiency of this approach could streamline histopathological workflows, reducing the burden on pathologists and enabling high-throughput analysis. Furthermore, the precise identification of MSI status has direct implications for patient management, as MSI-H tumors are more responsive to immune checkpoint inhibitors, while MSS tumors require alternative therapeutic strategies. By improving the reliability and scalability of MSI/MSS classification, this study contributes to advancing precision oncology in colorectal cancer.

6 CONCLUSION

This study presents a novel framework for segmenting and classifying colorectal cancer histopathological images by integrating the SAM with a CNN-based classifier. The results demonstrate the effectiveness of SAM's prompt-based segmentation in delineating diagnostically relevant regions and its synergy with CNNs for accurate MSI/MSS subtype differentiation. The proposed approach achieved state-of-the-art performance, significantly improving segmentation precision and classification accuracy compared to traditional methods.

By leveraging SAM's adaptability and the CNN's robust feature extraction, this study highlights a scalable, efficient, and clinically relevant solution for advancing personalized medicine in colorectal cancer. Future research should focus on refining prompt-generation techniques, incorporating additional histopathological features, and validating the approach across larger, multi-institutional datasets. The integration of SAM and deep learning models in oncology represents a significant step toward enhancing diagnostic precision, therapeutic decision-making, and ultimately, patient outcomes.

The adaptation of SAM and CNN workflows for real-time applications in clinical settings is another promising direction. This requires optimizing the computational efficiency of the models to enable deployment on edge devices or within cloud-based platforms. Such advancements would facilitate high-throughput, real-time analysis of histopathological slides, directly aiding pathologists in routine diagnostics.

Another critical perspective is the development of semi-supervised or unsupervised learning techniques to address the limited availability of labeled histopathological datasets. Leveraging generative adversarial networks (GANs) or self-supervised pre-training could reduce the dependency on extensive manual annotations, thereby accelerating the adoption of SAM-based workflows in data-scarce environments.

Furthermore, the integration of explainable AI (XAI) techniques into the proposed framework would enhance its clinical utility by providing transparent and interpretable insights into the decision-making process. This is particularly important in a medical context, where understanding the rationale behind model predictions is essential for building trust among clinicians and ensuring patient safety.

Lastly, the extension of this methodology to other cancer types and histopathological subtypes represents a significant opportunity for generalizing the proposed approach. Conducting multi-institutional validation studies across diverse patient populations would ensure the robustness, reproducibility, and generalizability of the framework, thereby paving the way for its widespread adoption in precision oncology. By addressing these future perspectives, the integration of SAM and deep learning models could redefine the landscape of histopathological image analysis, enabling breakthroughs in cancer diagnostics, therapeutic decision-making, and personalized patient care.

The perspectives of this study highlight the transformative potential of integrating the SAM with AI for broader cancer management. These include enhancing radiotherapy precision by accurately targeting tumor regions while sparing healthy tissues, identifying radioresistant cells to optimize combined therapies, and mapping metastatic sites for improved treatment strategies. Additionally, this approach can reduce challenges related to treatment resistance and be generalized to other cancer types, such as lung, breast, and prostate cancers, enabling early detection, patient stratification, and personalized treatments. This work paves the way for advancing cancer care through AI-driven precision medicine.

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