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Artificial Intelligence for Automated Tumor Segmentation and Treatment Response Assessment

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ABSTRACT:

Cancer remains a leading cause of mortality worldwide, underscoring the urgent need for continuous innovation in diagnostic and therapeutic strategies. Medical imaging is a cornerstone of modern oncology, supporting tumor detection, delineation, staging, treatment planning, and longitudinal assessment of therapeutic response. Accurate tumor segmentation and treatment response evaluation are critical for effective clinical decision-making; however, conventional manual methods are often labor-intensive, time-consuming, and prone to considerable interobserver variability. The rapid advancement of artificial intelligence (AI), particularly machine learning and deep learning, has revolutionized medical image analysis by enabling automated, reproducible, and highly accurate interpretation of complex imaging datasets.

Recent progress in convolutional neural networks, transformer-based architectures, and foundation models has substantially improved the accuracy and robustness of tumor segmentation across diverse imaging modalities, including computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), and hybrid imaging techniques. Concurrently, AI-powered methodologies have enhanced treatment response assessment through radiomics, longitudinal image analysis, and predictive modeling, facilitating earlier detection of therapeutic effectiveness, disease progression, and treatment resistance. Furthermore, emerging multimodal AI frameworks that integrate imaging, digital pathology, genomic information, and clinical data are advancing precision oncology by providing comprehensive, patient-specific insights for personalized cancer management.

Despite these significant achievements, several challenges continue to limit the widespread clinical adoption of AI technologies. Data heterogeneity, limited availability of high-quality annotated datasets, model interpretability, regulatory and ethical considerations, and integration into existing clinical workflows remain important obstacles. Nevertheless, emerging paradigms—including foundation models, self-supervised learning, federated learning, and explainable artificial intelligence—offer promising solutions to improve model robustness, generalizability, transparency, and scalability across diverse healthcare environments.

This review provides a comprehensive overview of recent advances in AI-driven automated tumor segmentation and treatment response assessment. It examines current methodological developments, summarizes major clinical applications, critically discusses existing limitations, and highlights future research directions for successfully integrating artificial intelligence technologies into routine oncology practice, ultimately supporting more precise, efficient, and personalized cancer care.

Keywords: Artificial intelligence; Tumor segmentation; Treatment response assessment; Deep learning; Radiomics; Precision oncology; Medical imaging; Foundation models

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1. Introduction

Cancer continues to pose a major global health burden and remains one of the leading causes of mortality worldwide. According to recent global cancer statistics, both the incidence and prevalence of cancer are increasing steadily, driven by population aging, demographic expansion,

environmental exposures, and lifestyle-associated risk factors [1]. Although substantial advances in early detection, molecular diagnostics, targeted therapies, and immunotherapeutic strategies have significantly improved survival outcomes across many cancer types, optimizing treatment selection and accurately monitoring therapeutic response remain challenging aspects of contemporary oncology practice [2].

Medical imaging serves as a fundamental component of cancer diagnosis and management. Imaging modalities, including computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), PET/CT, PET/MRI, and ultrasound, provide critical information regarding tumor location, morphology, metabolic activity, vascular characteristics, and response to treatment [3]. These technologies contribute to virtually every stage of oncology care, encompassing cancer screening, diagnosis, staging, treatment planning, therapeutic monitoring, post-treatment follow-up, and long-term surveillance.

Among the numerous imaging-related tasks in oncology, tumor segmentation is particularly important because it provides the foundation for quantitative image analysis and precision treatment planning. Tumor segmentation involves accurately delineating tumor boundaries and identifying regions of interest within medical images. Precise segmentation facilitates tumor volume quantification, radiotherapy planning, surgical navigation, radiomics feature extraction, and longitudinal evaluation of disease progression and therapeutic response [4]. Traditionally, segmentation has been performed manually by radiologists and radiation oncologists. Although expert delineation remains the clinical reference standard, manual segmentation is labor-intensive, time-consuming, and susceptible to substantial intraobserver and interobserver variability, particularly when tumors exhibit irregular morphology, heterogeneous enhancement patterns, or poorly defined margins [5].

Treatment response assessment constitutes another essential aspect of modern oncology. Determining whether a tumor is responding to therapy, remaining stable, or demonstrating disease progression is critical for guiding subsequent clinical decision-making. Conventional evaluation systems, including the World Health Organization (WHO) criteria, Response Evaluation Criteria in Solid Tumors (RECIST), and Positron Emission Tomography Response Criteria in Solid Tumors (PERCIST), primarily rely on changes in lesion size or metabolic activity to assess therapeutic efficacy [6]. While these standardized frameworks have substantially improved consistency in clinical evaluation, they may not adequately capture the complex biological responses associated with immunotherapy, targeted therapies, or highly heterogeneous tumors [7].

Artificial intelligence (AI) has emerged as a transformative technology capable of overcoming many of the limitations associated with conventional medical image interpretation. Recent developments in machine learning, deep learning, computer vision, and multimodal data integration have enabled automated extraction of clinically meaningful information from large-scale imaging datasets [8]. Across a broad range of malignancies, AI-driven systems have demonstrated exceptional performance in tumor detection, segmentation, classification, prognostic prediction, treatment planning, and therapeutic response assessment, highlighting their growing importance in precision oncology [9].

The development of advanced deep learning architectures, including convolutional neural networks (CNNs), U-Net variants, transformer-based models, and foundation models, has substantially improved both segmentation accuracy and predictive performance across diverse imaging applications [10]. Moreover, the integration of radiomics, radiogenomics, digital pathology, and clinical information has expanded the scope of artificial intelligence beyond image interpretation toward comprehensive precision oncology frameworks capable of supporting individualized cancer diagnosis, prognosis, and treatment planning [11].

This review provides a comprehensive overview of the current landscape of artificial intelligence for automated tumor segmentation and treatment response assessment. It critically discusses recent methodological advances, summarizes major clinical applications, examines emerging foundation models, evaluates current challenges and limitations, and highlights future research directions

that are expected to shape the next generation of AI-enabled precision oncology and routine clinical cancer care.

2. Fundamentals of Artificial Intelligence in Medical Imaging

Artificial intelligence (AI) comprises computational methodologies designed to perform tasks that traditionally require human cognitive abilities, including pattern recognition, learning, reasoning, and decision-making [12]. Within medical imaging, AI has emerged as a transformative technology capable of extracting clinically meaningful information from increasingly large and complex imaging datasets, thereby supporting more accurate and efficient diagnostic decision-making.

Machine learning, a major branch of artificial intelligence, enables computational algorithms to identify patterns directly from data without requiring explicit rule-based programming. Conventional machine learning methods typically depend on handcrafted imaging features that are subsequently analyzed using classifiers such as support vector machines, random forests, and logistic regression models [13]. Although these approaches have demonstrated effectiveness in selected applications, their performance is often constrained by the need for manual feature engineering and limited scalability when applied to complex imaging datasets.

Deep learning has addressed many of these limitations by enabling automatic hierarchical feature extraction directly from raw medical images. Through multiple interconnected neural network layers, deep learning models progressively learn increasingly sophisticated feature representations, resulting in superior performance across image recognition, segmentation, and classification tasks [14]. Among these architectures, convolutional neural networks (CNNs) have become the cornerstone of medical image analysis owing to their ability to effectively capture spatial relationships and local image patterns. By automatically learning highly discriminative imaging features without manual feature selection, CNNs have substantially improved performance across a broad spectrum of oncology imaging applications [15].

Among CNN-based architectures, U-Net has emerged as one of the most influential models for biomedical image segmentation. Specifically developed for medical imaging applications, U-Net employs an encoder–decoder architecture with skip connections that preserve fine spatial information while enabling precise localization of anatomical structures and tumor boundaries [16]. Building upon this foundation, several enhanced variants—including Attention U-Net, U-Net++, and nnU-Net—have further improved segmentation accuracy and robustness across multiple cancer imaging applications [17].

V-Net extends these principles to volumetric three-dimensional medical imaging and has demonstrated exceptional performance in CT- and MRI-based tumor segmentation tasks [18]. Similarly, ResNet architectures introduce residual learning mechanisms that facilitate the training of substantially deeper neural networks, improving feature representation while mitigating optimization challenges such as vanishing gradients [19].

More recently, transformer-based architectures have revolutionized medical image analysis. Vision Transformers (ViTs) utilize self-attention mechanisms to capture long-range dependencies and global contextual relationships within medical images, thereby overcoming several limitations associated with conventional convolutional neural networks [20]. Swin Transformers further improve computational efficiency through hierarchical feature extraction and shifted-window self-attention mechanisms, making them particularly well suited for analyzing high-resolution medical imaging datasets [21].

Graph Neural Networks (GNNs) represent another promising class of deep learning architectures that is gaining increasing attention in oncology research. GNNs model complex relationships among imaging features, anatomical structures, molecular pathways, and patient populations using graph-based representations [22]. Their ability to capture relational information makes them especially valuable for integrating heterogeneous biomedical data within precision oncology frameworks.

A variety of imaging modalities support AI-driven oncology applications. Computed tomography (CT) remains the most widely utilized modality for

cancer detection, staging, treatment planning, and therapeutic monitoring because of its high spatial resolution and widespread clinical availability. Magnetic resonance imaging (MRI) offers superior soft-tissue contrast together with functional imaging capabilities, making it indispensable for evaluating malignancies of the brain, breast, prostate, and liver. Positron emission tomography (PET) provides complementary metabolic and molecular information, while hybrid imaging platforms such as PET/CT and PET/MRI integrate functional and anatomical data within unified diagnostic systems [23]. Ultrasound continues to play a vital role in breast, thyroid, liver, and gynecological oncology owing to its accessibility, cost-effectiveness, portability, and capability for real-time image acquisition [24].

Radiomics has emerged as a powerful computational framework for transforming medical images into high-dimensional quantitative biomarkers. By extracting shape, texture, intensity, and spatial characteristics from imaging data, radiomics enables objective characterization of tumor heterogeneity beyond conventional visual interpretation [25]. Extending this concept, radiogenomics establishes associations between imaging phenotypes and underlying genomic and molecular characteristics, thereby providing valuable insights that support precision oncology and personalized therapeutic decision-making [26].

Collectively, these technological advances constitute the foundation of contemporary AI-driven tumor segmentation and treatment response assessment. The continued evolution of advanced deep learning architectures, multimodal data integration strategies, and quantitative imaging methodologies is enabling increasingly sophisticated analysis of cancer imaging data and accelerating the transition toward more precise, personalized, and data-driven oncology care.

3. Artificial Intelligence for Automated Tumor Segmentation

Tumor segmentation is one of the most critical tasks in oncologic imaging because it forms the basis for diagnosis, treatment planning, radiotherapy contouring, surgical navigation, radiomics analysis, and longitudinal disease monitoring. Accurate delineation of tumor boundaries allows clinicians to quantify tumor burden, evaluate spatial heterogeneity, monitor treatment-induced changes, and estimate prognosis. However, manual segmentation remains labor-intensive and subject to substantial interobserver variability, particularly in tumors exhibiting infiltrative growth patterns, heterogeneous enhancement characteristics, or poorly defined margins [27,28]. Consequently, automated tumor segmentation has emerged as one of the most active areas of artificial intelligence research in medical imaging.

Deep learning has revolutionized tumor segmentation by enabling direct learning of hierarchical image features from raw imaging data. Unlike conventional image processing techniques that rely on handcrafted features, deep neural networks automatically learn complex representations that can capture tumor morphology, texture, intensity variations, and contextual anatomical information [29]. These capabilities have led to remarkable improvements in segmentation accuracy across multiple cancer types and imaging modalities.

Tumor segmentation approaches can generally be categorized into semantic segmentation, instance segmentation, and panoptic segmentation. Semantic segmentation assigns each pixel or voxel to a predefined class, such as tumor or background. This approach is widely used in radiotherapy planning and volumetric tumor assessment because it provides comprehensive delineation of tumor regions [30]. Instance segmentation extends semantic segmentation by distinguishing individual tumor lesions belonging to the same class. This capability is particularly useful in metastatic disease where multiple lesions may coexist within the same anatomical region [31]. Panoptic segmentation combines semantic and instance segmentation by simultaneously identifying lesion categories and individual tumor instances, thereby providing more comprehensive scene understanding [32].

The introduction of U-Net marked a major breakthrough in biomedical image segmentation. U-Net employs a symmetric encoder-decoder architecture connected through skip pathways that preserve fine-grained spatial information lost during feature extraction [16]. This design enables precise localization while maintaining contextual understanding. Since its introduction, U-Net has become the foundation for numerous segmentation algorithms and remains one of the most widely adopted architectures in medical imaging.

Several enhanced variants of U-Net have subsequently emerged. Attention U-Net incorporates attention mechanisms that selectively emphasize relevant image regions while suppressing irrelevant background structures [33]. This modification improves segmentation performance in anatomically complex regions where tumors may exhibit low contrast relative to surrounding tissues. U-Net++ introduces nested and dense skip connections that reduce the semantic gap between encoder and decoder feature maps, resulting in improved feature fusion and segmentation accuracy [34].

Among contemporary approaches, nnU-Net has gained particular attention because of its self-configuring framework. Unlike manually optimized architectures, nnU-Net automatically adapts preprocessing, network architecture, training strategies, and postprocessing procedures to specific datasets. Extensive benchmarking studies have demonstrated that nnU-Net achieves state-of-the-art performance across numerous public medical imaging challenges while requiring minimal manual intervention [17].

Three-dimensional segmentation has also benefited from specialized architectures such as V-Net. By operating directly on volumetric data, V-Net captures spatial relationships across image slices and provides more anatomically coherent segmentations compared with two-dimensional approaches [18]. This capability is particularly valuable in CT and MRI applications where tumors extend across multiple imaging planes.

Recent advances in transformer-based architectures have further enhanced segmentation performance. TransUNet integrates convolutional neural networks with transformer encoders, enabling simultaneous capture of local image details and global contextual information [35]. Comparative studies have demonstrated superior performance of TransUNet compared with conventional CNN-based approaches in brain tumor, liver tumor, and prostate cancer segmentation tasks [36].

Similarly, Swin-UNet incorporates hierarchical vision transformers into a U-Net-like architecture. Through shifted-window self-attention mechanisms, Swin-UNet effectively captures long-range dependencies while maintaining computational efficiency [37]. Several investigations have reported improved segmentation accuracy compared with CNN-based architectures, particularly in challenging tumor segmentation scenarios characterized by heterogeneous morphology and complex anatomical backgrounds [38].

The emergence of foundation models has introduced a new paradigm in medical image segmentation. The Segment Anything Model (SAM), originally developed for general computer vision applications, demonstrated unprecedented zero-shot segmentation capabilities across diverse image domains [39]. Building upon SAM, specialized medical adaptations such as MedSAM and SAM-Med2D have been developed to address the unique characteristics of medical imaging datasets [40,41]. These foundation models leverage large-scale pretraining and prompt-based interaction to facilitate robust segmentation across multiple imaging modalities and anatomical sites. Early evidence suggests that medical foundation models may significantly reduce annotation requirements while improving generalizability across institutions and patient populations [42].

Brain tumor segmentation represents one of the most extensively studied applications of AI. The Brain Tumor Segmentation (BraTS) challenges have driven substantial methodological innovation over the past decade. Deep learning architectures including U-Net, nnU-Net, TransUNet, and transformer-based models have achieved Dice Similarity Coefficient (DSC) values exceeding 0.90 for whole-tumor segmentation in many benchmark datasets [43]. These advances have improved radiotherapy planning and facilitated quantitative assessment of glioblastoma progression and treatment response.

Breast cancer segmentation has also benefited significantly from AI-driven approaches. Automated segmentation of breast lesions on MRI, ultrasound, and mammography enables more accurate lesion characterization and supports radiomics-based biomarker development [44]. Deep learning models consistently outperform traditional image processing methods, particularly in dense breast tissue where lesion boundaries are difficult to delineate manually [45].

In lung cancer, segmentation of primary tumors and metastatic lesions plays a critical role in staging, radiotherapy planning, and treatment monitoring. AI-based systems have demonstrated robust performance in CT-based lung tumor segmentation despite challenges associated with respiratory motion, heterogeneous tumor appearance, and proximity to mediastinal structures [46]. Several multicenter studies have reported segmentation

accuracies comparable to expert thoracic radiologists [47].

Liver tumor segmentation remains particularly challenging because of variable tumor morphology, low lesion contrast, and underlying liver disease. Nevertheless, deep learning approaches have achieved substantial improvements compared with traditional methods. Transformer-based architectures have shown particular promise in capturing complex spatial relationships within hepatic imaging datasets [48].

Similarly, AI-driven segmentation has demonstrated significant clinical value in prostate cancer and head-and-neck oncology. Automated delineation of prostate lesions on multiparametric MRI supports targeted biopsy planning and focal therapy selection, while head-and-neck segmentation facilitates efficient radiotherapy contouring and reduces clinician workload [49,50].

Performance evaluation of segmentation algorithms relies on several quantitative metrics. The Dice Similarity Coefficient remains the most widely used metric and measures overlap between predicted and reference segmentations. Values approaching 1.0 indicate excellent agreement [51]. Intersection over Union (IoU), also known as the Jaccard index, evaluates segmentation overlap from a complementary perspective and is frequently used in benchmarking studies [52]. Hausdorff Distance measures boundary agreement by quantifying the maximum distance between corresponding contour points and is particularly useful for assessing clinically relevant contour accuracy [53].

Despite remarkable progress, several limitations remain. Most segmentation models require large annotated datasets, and expert annotation remains expensive and time-consuming. Performance may deteriorate when applied to external datasets due to domain shift and differences in imaging protocols [54]. Furthermore, segmentation accuracy may be reduced in rare tumor types, small lesions, or tumors exhibiting extensive heterogeneity. Foundation models and self-supervised learning approaches may help address these challenges by improving generalizability and reducing dependence on large annotated datasets [55].

Overall, artificial intelligence has transformed tumor segmentation from a labor-intensive manual process into an increasingly automated and reproducible workflow. Continued advances in deep learning architectures, foundation models, and multimodal integration are expected to further improve segmentation accuracy and facilitate broader clinical adoption in precision oncology.

4. Artificial Intelligence for Treatment Response Assessment

Treatment response assessment is a cornerstone of modern oncology because it determines therapeutic effectiveness, guides clinical decision-making, and influences long-term patient outcomes. Accurate evaluation of response allows clinicians to distinguish responders from non-responders, identify disease progression at an early stage, optimize treatment strategies, and avoid unnecessary toxicity associated with ineffective therapies [56]. Traditionally, response assessment has relied on standardized imaging-based criteria; however, the increasing complexity of contemporary cancer therapies has exposed limitations in conventional approaches. Artificial intelligence (AI) has emerged as a promising solution capable of providing more comprehensive, quantitative, and personalized evaluation of treatment response.

Historically, tumor response has been assessed using morphologic changes observed on medical imaging. The World Health Organization (WHO) criteria, introduced in the late twentieth century, relied on bidimensional measurements of tumor lesions to classify treatment response [57]. Subsequently, the Response Evaluation Criteria in Solid Tumors (RECIST) were developed to standardize response assessment by measuring the longest diameter of selected target lesions [6]. RECIST 1.1 remains the most widely adopted framework in clinical trials and routine oncology practice. More recently, the Positron Emission Tomography Response Criteria in Solid Tumors (PERCIST) incorporated metabolic imaging parameters derived from fluorodeoxyglucose (FDG)-PET to assess treatment-induced changes in tumor metabolism [58].

Although these criteria have improved standardization, they possess several limitations. Tumor size changes often occur relatively late during treatment and may not accurately reflect underlying biological alterations. Targeted therapies and immunotherapies frequently induce atypical response patterns, including pseudoprogression, hyperprogression, and delayed responses that are inadequately captured by size-based criteria [59]. Furthermore, conventional assessment methods evaluate only a limited number of lesions and may fail to account for intratumoral heterogeneity and

dynamic biological changes occurring during therapy [60].

Artificial intelligence offers the potential to overcome these limitations by extracting quantitative information from medical images that extends beyond visual interpretation. AI-based response assessment integrates radiological, clinical, pathological, and molecular data to identify subtle imaging biomarkers associated with treatment outcomes. These approaches leverage machine learning and deep learning techniques to analyze high-dimensional datasets and generate predictive models capable of anticipating therapeutic response before macroscopic changes become apparent [61].

Radiomics has emerged as one of the most widely investigated approaches for treatment response prediction. Radiomics converts medical images into quantitative descriptors that characterize tumor shape, intensity, texture, spatial heterogeneity, and temporal evolution [25]. Numerous studies have demonstrated associations between radiomic features and therapeutic outcomes across multiple cancer types. For example, texture-based radiomic signatures extracted from pretreatment CT and MRI scans have shown predictive value for chemotherapy response in breast cancer, non-small cell lung cancer (NSCLC), and colorectal cancer [62,63].

Compared with traditional radiomics, deep learning-based approaches automatically learn predictive imaging representations directly from raw image data without requiring handcrafted feature engineering. Convolutional neural networks (CNNs) have demonstrated superior performance in identifying complex imaging patterns associated with treatment response [64]. Recent studies have shown that deep learning models outperform conventional radiomics in predicting pathological complete response following neoadjuvant therapy in breast cancer patients [65]. Similar findings have been reported in rectal cancer, where AI models successfully predicted treatment response following chemoradiotherapy, facilitating personalized treatment planning and organ-preserving therapeutic strategies [66].

Longitudinal imaging analysis represents another important application of AI in treatment response assessment. Traditional response criteria typically compare baseline and follow-up imaging studies at predefined intervals. In contrast, AI systems can analyze temporal imaging trajectories across multiple time points, capturing dynamic changes in tumor morphology, texture, vascularity, and metabolic activity [67]. Recurrent neural networks (RNNs), long short-term memory (LSTM) networks, and transformer-based architectures have demonstrated substantial promise in modeling longitudinal imaging data and predicting future disease behavior [68].

Early response prediction is particularly valuable because it enables treatment adaptation before disease progression becomes clinically apparent. Several investigations have demonstrated that AI-derived imaging biomarkers can identify responders and non-responders after only one or two treatment cycles [69]. Such early prediction may facilitate personalized treatment modification, reduce exposure to ineffective therapies, and improve overall outcomes. In neoadjuvant breast cancer treatment, AI models incorporating MRI-derived imaging features have successfully predicted pathological complete response weeks before surgery [70].

Survival prediction represents another major area of clinical interest. While conventional prognostic models often rely on clinical staging and pathological variables, AI systems can integrate imaging biomarkers with clinical and molecular information to generate more accurate prognostic estimates [71]. Deep learning frameworks have demonstrated superior performance in predicting overall survival, progression-free survival, and disease-specific survival across multiple cancer types [72]. Such models may support risk stratification and individualized treatment planning.

Glioblastoma remains one of the most extensively studied malignancies for AI-driven response assessment. The highly infiltrative nature of glioblastoma and the occurrence of treatment-related imaging changes such as pseudoprogression complicate conventional response evaluation [73]. Deep learning models integrating multiparametric MRI features have shown improved accuracy in distinguishing true progression from treatment-related effects compared with traditional imaging interpretation [74]. Several studies have also reported successful prediction of survival outcomes and molecular biomarkers using longitudinal imaging data [75].

In breast cancer, AI-based response assessment has focused extensively on neoadjuvant chemotherapy. Dynamic contrast-enhanced MRI provides rich information regarding tumor vascularity and treatment-induced changes. Deep learning models

combining imaging biomarkers with clinical variables have achieved high predictive accuracy for pathological complete response, potentially enabling individualized treatment adaptation [76]. Comparative studies consistently demonstrate superior performance of AI-driven approaches relative to conventional imaging assessment alone [77].

Lung cancer represents another important application area. In NSCLC, radiomic and deep learning models have demonstrated predictive value for chemotherapy response, targeted therapy outcomes, and immunotherapy efficacy [78]. AI-derived imaging biomarkers associated with epidermal growth factor receptor (EGFR) mutations, programmed death-ligand 1 (PD-L1) expression, and tumor mutational burden have further enhanced treatment stratification [79]. These advances support the integration of imaging biomarkers into precision oncology workflows.

In colorectal cancer, response assessment following neoadjuvant chemoradiotherapy remains clinically important because accurate prediction of complete response may allow selected patients to avoid radical surgery. AI-based MRI analysis has demonstrated encouraging performance in identifying complete responders and predicting recurrence risk [80]. Similar approaches have been applied successfully in hepatocellular carcinoma, where AI systems predict treatment outcomes following transarterial chemoembolization, radiofrequency ablation, and systemic therapies [81].

Lymphoma provides a unique setting in which PET imaging plays a central role in treatment monitoring. Deep learning approaches analyzing FDG-PET/CT images have shown improved prediction of treatment response and survival outcomes compared with conventional metabolic assessment methods [82]. These systems may facilitate more accurate risk stratification and individualized therapeutic decision-making.

Despite impressive advances, several challenges remain. Most AI models are developed using retrospective datasets and require prospective multicenter validation before widespread clinical adoption [83]. Variability in imaging protocols, treatment regimens, and patient populations may affect model performance and generalizability. Furthermore, integration of AI systems into clinical workflows requires careful consideration of interpretability, regulatory compliance, and clinician acceptance [84].

Nevertheless, the growing body of evidence suggests that AI-driven treatment response assessment may fundamentally transform oncology practice. By providing earlier, more accurate, and biologically informed evaluation of therapeutic effectiveness, AI has the potential to support precision medicine and improve patient outcomes across diverse cancer types.

5. Integration of Multimodal Data for Precision Oncology

Precision oncology aims to tailor therapeutic strategies according to the unique biological characteristics of individual patients and tumors. While medical imaging provides valuable information regarding tumor morphology, metabolism, vascularity, and treatment response, cancer is fundamentally a complex biological disease influenced by genomic, transcriptomic, proteomic, pathological, and clinical factors. Consequently, reliance on a single data modality may fail to capture the complete disease landscape. The integration of multimodal data has therefore emerged as a critical strategy for advancing personalized cancer care [85].

Recent developments in artificial intelligence have facilitated the integration of heterogeneous datasets, including radiological images, digital pathology slides, genomic sequencing results, laboratory parameters, electronic health records (EHRs), and clinical outcomes. Multimodal deep learning enables simultaneous analysis of these diverse information sources, allowing models to uncover relationships that may not be apparent when modalities are analyzed independently [86].

Several data fusion strategies have been proposed for multimodal learning. Early fusion combines features from multiple modalities at the input stage before model training. This approach enables direct interaction among different data types but may be vulnerable to missing data and dimensionality mismatches [87]. Intermediate fusion integrates modality-specific representations within hidden network layers, allowing models to learn complex cross-modal interactions while preserving modality-specific information [88]. Late fusion combines independent predictions generated by separate models and is generally more robust to missing modalities but may fail to fully exploit synergistic relationships among data sources [89]. Hybrid

fusion approaches combine multiple fusion strategies and increasingly represent the preferred methodology for complex oncology applications [90].

Several studies have demonstrated that multimodal AI models outperform unimodal systems in cancer diagnosis, prognosis prediction, and treatment response assessment. Integration of radiomic features with genomic signatures has improved prediction of molecular subtypes and survival outcomes in glioblastoma, breast cancer, lung cancer, and colorectal cancer [91,92]. Similarly, multimodal frameworks incorporating pathology images and genomic data have shown enhanced performance in tumor classification and biomarker discovery [93].

The emergence of foundation models and large multimodal models (LMMs) has further accelerated progress in precision oncology. These models are pretrained on massive datasets and subsequently adapted to specific clinical tasks using relatively limited labeled data. By learning generalized representations across multiple modalities, foundation models may enable more robust and scalable deployment of AI systems in clinical practice [94].

From a clinical perspective, multimodal AI has the potential to transform cancer management by supporting personalized diagnosis, treatment selection, risk stratification, and longitudinal monitoring. As data integration technologies mature, multimodal systems are expected to become central components of precision oncology workflows.

6. Emerging Technologies and Foundation Models

The rapid evolution of artificial intelligence has given rise to several transformative technologies that are reshaping oncologic imaging and treatment assessment. Among these developments, self-supervised learning has emerged as a particularly important approach for addressing the scarcity of annotated medical imaging data. Unlike conventional supervised learning, self-supervised methods learn meaningful representations from unlabeled datasets through pretext tasks, thereby reducing dependence on expert annotations [95].

Contrastive learning has become one of the most successful self-supervised paradigms. By learning relationships between similar and dissimilar image pairs, contrastive models generate highly transferable feature representations that improve downstream segmentation, classification, and prognostic prediction tasks [96]. These methods have demonstrated impressive performance across various oncologic imaging applications.

Vision-language models represent another major advance. Inspired by large-scale models developed in natural language processing, vision-language systems integrate image and text information to enable multimodal reasoning and clinical decision support [97]. Such models can analyze radiology images while simultaneously incorporating radiology reports, pathology descriptions, and clinical notes, creating more comprehensive patient representations.

The Segment Anything Model (SAM) has introduced a foundation-model paradigm for image segmentation. SAM demonstrated unprecedented generalization capabilities across diverse image domains and inspired several medical adaptations, including MedSAM and related oncology-specific frameworks [40]. These models facilitate prompt-based segmentation and may substantially reduce annotation burdens in clinical settings.

Recent years have also witnessed growing interest in medical foundation models specifically designed for healthcare applications. These models leverage large-scale imaging repositories to learn generalizable medical representations that can be adapted to multiple cancer-related tasks [98]. Similarly, generative artificial intelligence has demonstrated potential for image synthesis, data augmentation, reconstruction, and simulation of rare clinical scenarios [99].

Large language models (LLMs) are increasingly being integrated into oncology workflows. Beyond generating clinical documentation, LLMs may support decision-making, literature synthesis, patient communication, and multimodal clinical reasoning when combined with imaging and genomic data [100]. Although still in early stages of development, these technologies may contribute significantly to future precision oncology ecosystems.

Collectively, foundation models, self-supervised learning, vision-language architectures, and generative AI represent a paradigm shift toward more generalized and scalable medical AI systems capable of addressing multiple clinical tasks within unified frameworks.

7. Challenges and Limitations

Despite remarkable advances, several barriers continue to impede widespread clinical adoption of AI-driven tumor segmentation and treatment response assessment systems. One of the most significant challenges is the limited availability of large, high-quality annotated datasets. Medical image annotation requires extensive expert involvement, making dataset generation expensive and time-consuming [101].

Class imbalance represents another major obstacle. Many oncology datasets contain disproportionately fewer examples of rare tumors, uncommon molecular subtypes, or treatment-resistant disease states. Consequently, AI models may perform suboptimally in clinically important but underrepresented patient populations [102].

Data heterogeneity further complicates model development and deployment. Variations in scanner manufacturers, acquisition protocols, reconstruction algorithms, image quality, and institutional practices can significantly influence model performance [103]. Such variability contributes to domain shift, whereby models trained on one dataset experience reduced accuracy when applied to external populations [104].

Annotation variability also affects model reliability. Even among experienced radiologists, substantial differences may exist in tumor contouring and response assessment. Since AI systems learn from human-generated labels, inconsistencies in annotation quality can propagate into model predictions [105].

Interpretability remains a critical concern. Many deep learning systems function as "black boxes," making it difficult to understand the rationale underlying specific predictions. Lack of transparency may reduce clinician trust and hinder regulatory approval [106]. Explainable AI techniques have emerged as potential solutions; however, achieving meaningful interpretability without sacrificing performance remains challenging.

Generalizability represents another major limitation. Many published studies rely on retrospective single-center datasets and may not adequately reflect real-world clinical diversity. Prospective multicenter validation studies remain relatively uncommon, limiting confidence in clinical applicability [107].

Regulatory considerations present additional challenges. AI systems intended for clinical use must satisfy stringent requirements related to safety, effectiveness, reproducibility, and post-deployment monitoring. Regulatory frameworks continue to evolve in response to adaptive learning systems capable of continuous performance modification [108].

Data privacy and security concerns are particularly important in healthcare environments. Large-scale AI development often requires access to sensitive patient information, creating potential risks related to confidentiality breaches and cybersecurity threats [109]. Federated learning and privacy-preserving machine learning approaches have been proposed as potential solutions.

Ethical considerations must also be addressed. Algorithmic bias may contribute to healthcare disparities if training datasets inadequately represent diverse populations. Ensuring fairness, equity, transparency, and accountability remains essential for responsible AI implementation [110].

Finally, integration into existing clinical workflows presents practical challenges. Successful deployment requires clinician acceptance, interoperability with hospital information systems, cost-effectiveness, and demonstration of measurable improvements in patient outcomes [111]. Overcoming these barriers will be essential for translating AI innovations into routine oncology practice.

8. Future Perspectives

The future of AI in oncology is likely to be shaped by increasingly sophisticated multimodal systems capable of integrating imaging, pathology, genomics, and clinical information within unified analytical frameworks. Explainable AI will play an important role in enhancing clinician trust and facilitating regulatory approval by providing transparent and interpretable decision-support mechanisms [112].

Federated learning offers a promising strategy for overcoming data-sharing restrictions while preserving patient privacy. By enabling collaborative model training across multiple institutions without transferring raw data, federated learning may facilitate development of more robust and generalizable oncology AI systems [113].

Foundation models are expected to become increasingly influential. Similar to large language models in natural language processing, future oncology foundation models may support a broad range of clinical tasks, including segmentation, diagnosis, prognosis prediction, treatment selection,

and outcome forecasting using a single adaptable architecture [114].

The concept of digital twins is also gaining attention. Digital twins are computational representations of individual patients that continuously integrate clinical, imaging, molecular, and therapeutic data. AI-driven digital twins may enable simulation of treatment strategies, prediction of disease progression, and personalized optimization of therapeutic interventions [115].

Adaptive radiotherapy represents another promising application. Real-time AI-guided segmentation and response monitoring could facilitate dynamic treatment adaptation based on evolving tumor characteristics throughout the treatment course [116].

Increasing availability of real-world evidence datasets and prospective multicenter validation studies will further enhance clinical translation. Future systems are likely to function as integrated clinical decision-support platforms that augment clinician expertise rather than replace human judgment [117].

Ultimately, the convergence of multimodal learning, foundation models, federated learning, explainable AI, and digital health technologies may substantially advance precision oncology and improve outcomes for cancer patients worldwide.

9. Conclusion

Artificial intelligence has emerged as a transformative force in oncology, fundamentally reshaping approaches to tumor segmentation and treatment response assessment. Deep learning architectures, transformer-based models, and foundation models have achieved remarkable improvements in segmentation accuracy across multiple cancer types and imaging modalities. Simultaneously, AI-driven response assessment systems have demonstrated significant potential for predicting therapeutic outcomes, identifying disease progression, and supporting personalized treatment strategies.

The integration of radiological, pathological, genomic, and clinical data through multimodal learning frameworks represents a major step toward precision oncology. Emerging technologies such as self-supervised learning, foundation models, vision-language systems, and federated learning are addressing longstanding challenges related to data scarcity, generalizability, and scalability.

Despite substantial progress, important limitations remain, including dataset heterogeneity, annotation variability, interpretability concerns, regulatory challenges, and the need for prospective multicenter validation. Addressing these issues will be essential for successful clinical implementation.

Future oncology workflows are likely to incorporate AI as an integral decision-support tool that enhances diagnostic accuracy, optimizes treatment planning, and facilitates individualized patient management. Continued collaboration among clinicians, data scientists, engineers, regulatory authorities, and healthcare organizations will be critical for realizing the full potential of artificial intelligence in precision cancer care.

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