



Review

Oncology in the modern era: Artificial Intelligence is reshaping cancer diagnosis, prognosis and treatment

Mahda Delshad^{1,2}, Mohammad Amin Omrani³, Atieh Pourbagheri-Sigaroodi¹, Davood Bashash^{1,*}

¹Department of Hematology and Blood Banking, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

²Department of Laboratory Sciences, School of Allied Medical Sciences, Zanjan University of Medical Sciences, Zanjan, Iran.

³Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran.

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*Corresponding author:

Davood Bashash

Department of Hematology and Blood Banking, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Email: David_5980@yahoo.com

Abstract

The field of cancer research has been profoundly impacted by the utilization of artificial intelligence (AI), particularly through the analysis of medical records encompassing genomics, transcriptomics, proteomics, and imaging data. Subdomains of AI, such as machine learning (ML) and deep learning (DL), possess the capability to analyze intricate patterns within these records. This allows for groundbreaking advancements in cancer diagnosis, prognosis, and treatment by extracting valuable insights from sources such as histology and radiology imaging. The integration of AI-based models has led to improved prediction, diagnosis, and even treatment of various types of cancer, resulting in enhanced performance within the field of oncology. However, AI also faces challenges including ethical and legal considerations, data quality and accessibility, and issues pertaining to model interpretability. It is crucial to develop and evaluate AI-based systems in collaboration with clinicians and researchers to ensure their safety, reliability, and validity in cancer research.

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1. Introduction

Artificial Intelligence (AI) is a field focused on creating machines that imitate human intelligence. John McCarthy and his colleagues first introduced the term in 1956, envisioning the development of autonomous machines capable of emulating human thinking and behavior (1). AI aims to equip machines with the capacity to learn, problem-solve, and replicate human actions in order to address

complex challenges. AI can be categorized into four types: Reactive Machines, Limited Memory, Theory of Mind, and Self-awareness (2).

Machine learning (ML) is an algorithmic approach that improves its performance over time by accumulating knowledge from additional data (3). By leveraging both structured and unstructured data, ML algorithms can acquire insights and make predictions about future events. There are three primary types of ML algorithms: Supervised

Learning, Unsupervised Learning, and Reinforcement Learning. Deep learning (DL), a subset of ML, focuses on algorithms that mimic the structure and functioning of the human brain. These algorithms excel at processing large amounts of structured and unstructured data. At the core of DL are artificial neural networks (ANNs), which enable machines to make decisions. Within DL, there are various types of networks, with one prominent example being convolutional neural networks (CNNs), commonly employed for image analysis. Another type of network within DL is recurrent neural networks (RNNs), which utilize sequential information to build models and are particularly effective for tasks that involve storing and processing previous data. The third category is generative adversarial networks (GANs), which employ two neural networks to generate artificial data that appears authentic to humans. Lastly, deep belief networks (DBNs) are generative graphical models that consist of multiple layers of hidden units, also known as latent variables.

AI systems play a significant role in the healthcare industry, following a standardized process. They begin by analyzing a large volume of data using ML algorithms to extract meaningful insights. These insights are then utilized to generate valuable outputs that address specific challenges within the medical system. AI finds extensive applications in the healthcare domain, such as matching patient symptoms to appropriate doctors (4), discovering new drugs (5, 6), diagnosing patients (7), predicting patient outcomes (8), and employing AI-powered assistants for tasks like note transcription, image and file organization, and language translation. In recent years, AI systems have made remarkable progress in the domain of cancer diagnosis and prognosis. They have significantly simplified the process of diagnosing cancer and predicting tumor outcomes

and responses to different treatments (9). The purpose of this study is to underscore the importance and practicality of AI models in the field of cancer by emphasizing their critical role in diagnosis, prognosis, and treatment. The study aims to shed light on the valuable insights and support that AI can offer, showcasing its potential to revolutionize cancer care.

2. Artificial intelligence in the diagnosis of cancer

2.1. The application of artificial intelligence in cancer diagnosis using omics data

Next-generation sequencing (NGS) generates extensive data resources that hold critical insights into tumors. AI integration enables the utilization of this information to identify the causes and evolution of tumors, deliver accurate cancer diagnoses, analyze different disease subtypes, and assess risk stratification (10, 11). AI systems have a vital role in facilitating precision medicine for cancer patients by bridging the gap between omics data and clinical practice. However, the complex and high-dimensional nature of NGS data poses challenges for cancer diagnosis methods that rely on NGS. To improve the sensitivity and accuracy of AI algorithms in detecting minimal tumor cell mutations, it is necessary to enhance the depth and coverage of NGS data (12).

2.1.1. Using genomics to predict the diagnosis of cancer

The fusion of genomics and medical care has enhanced our understanding of cancer vulnerability and the effects of treatment on cancer patients (10). By employing spatial and single-cell genomics, we can reconstruct the progression of tumor formation, leading to a deeper comprehension of tumors and the creation of specialized medications that

specifically target their mechanisms (13-16). Wang et al. have created a sophisticated neural network model that integrates imaging and genomics data to effectively classify different subtypes of lung cancer and pinpoint potential targets for therapy (17). Similarly, Vanderbilt et al. have developed a groundbreaking technique to detect DNA viruses from NGS samples, allowing exploration of the relationship between viruses and specific tumor types without requiring additional sequencing. This approach has the potential to greatly aid in the diagnosis and management of patients with tumors (18).

2.1.2. Using transcriptomics to predict the diagnosis of cancer

Transcriptomics is a crucial component in the analysis of all transcripts produced during metabolism (10). It allows for the assessment of gene expression levels and the exploration of related molecular pathways. This field acts as a bridge connecting genomics and proteomics (19, 20). By harnessing methods such as data mining or advanced mathematical approaches like ML or DL, transcriptomics serves as a valuable tool in tumor screening and early detection, the discovery of new cancer biomarkers and therapeutic targets, drug prioritization, and the prediction of drug sensitivity and prognosis (19-22). Warnat-Herresthal et al. have made a noteworthy discovery by demonstrating the potential of ML-based transcriptomics in diagnosing acute myeloid leukemia (23). In a similar vein, Ben Azzouz et al. successfully utilized a ML approach to identify subtypes of triple-negative breast cancer, addressing the issue of heterogeneity in treatment (24). Furthermore, ML-based transcriptomics has been instrumental in the development of prognostic biomarkers for prostate cancer, the diagnosis of colorectal cancer (CRC), and the prediction of immune response (25). As miRNAs are important

parts of transcriptomics studies, **Figure 1** was designed to shed light on this context.

2.1.3. Using proteomics to predict the diagnosis of cancer

Proteomics offers a wealth of detailed and quantitative insights into proteins found in tissues, blood, and cell samples (26). Leveraging ML-based analysis of protein expression profiles obtained through proteomics, researchers can identify highly accurate and sensitive protein biomarkers, surpassing the capabilities of other single-omics approaches. This breakthrough enables the diagnosis of cancer, prognosis prediction (27), deciphering disease mechanisms (28, 29), uncovering new therapeutic targets, assessing drug effectiveness and toxicity (30), and predicting therapeutic responses, recurrence, and metastasis (31, 32). Henry et al. introduced a novel approach that utilizes ML to predict drug response based on proteomics data, thereby enabling the ranking and prioritization of drugs tailored to individual patients (33). In a similar vein, Federica et al. developed a decision support system specifically designed to assist in the diagnosis of high-grade serous ovarian cancer (34).

2.1.4. Using multi-omics to predict the diagnosis of cancer

While single-omics data have their merits in diagnosis, treatment, and prediction, they may not provide a comprehensive understanding of the molecular changes occurring in a tumor (35). This is where AI methods come into play, as they can assist in stratified medicine, biomarker discovery (36), pathway analysis, and even drug repurposing or discovery (37, 38). Ma et al. have introduced a groundbreaking approach that analyzes multi-omics data, revealing the intricate relationship between molecular features and clinical characteristics (39).

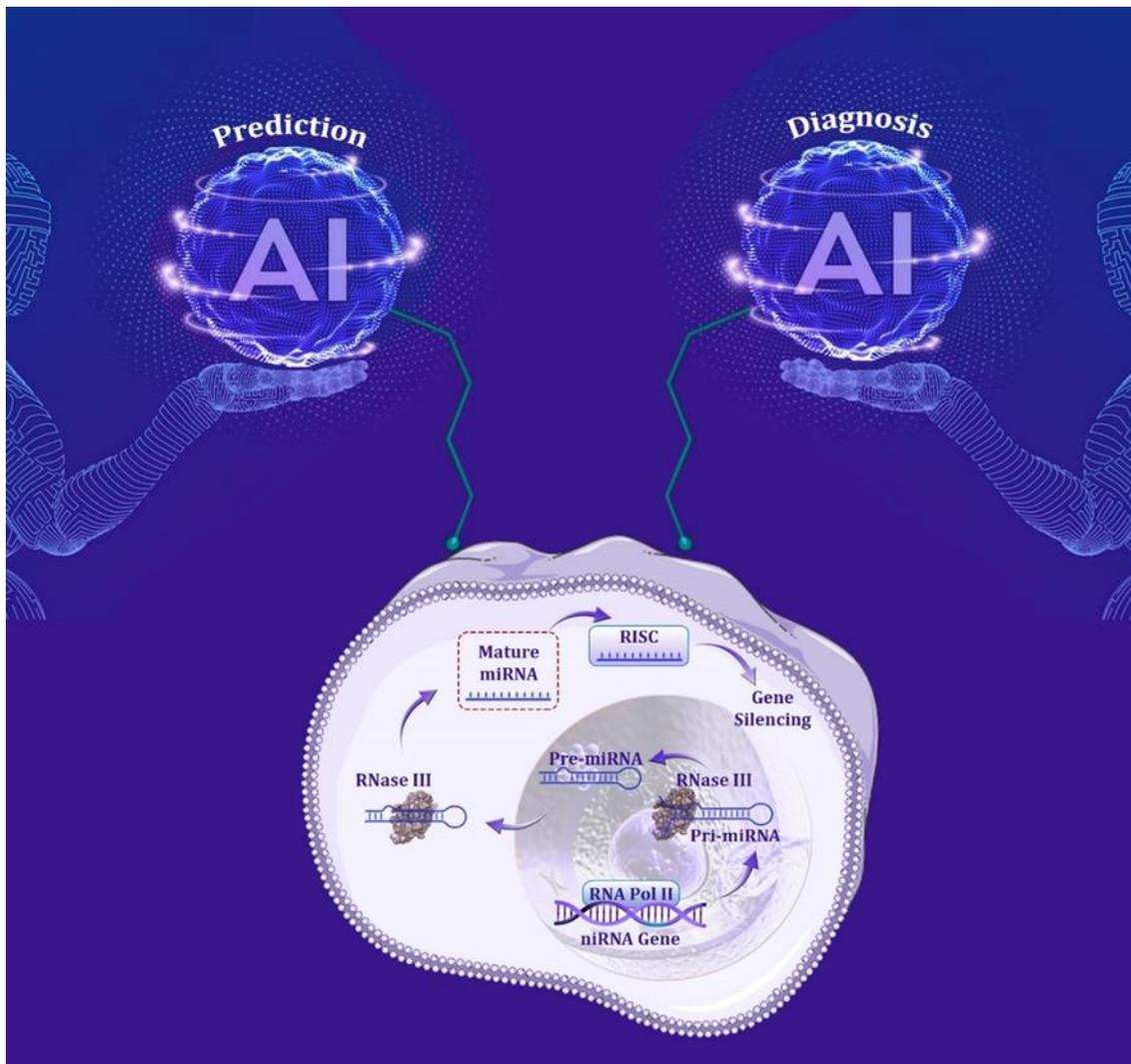


Figure 1. The role of miRNAs and their diagnosis in cancers. The transcription of miRNA genes by RNA polymerase II leads to the generation of large primary transcripts known as pri-miRNA. RNase III and RNA-binding protein DGCR8 compose a complex able to catalyze pre-miRNA and generate pre-miRNA. The pre-miRNA could be transported to the cytoplasm where it can undergo cleavage by another RNase III ending in the production of mature miRNA. By targeting mRNAs, mature miRNA is able to affect several cellular and molecular events, most of which are conducted via the incorporation of miRNA and a protein complex named RISC. Indeed, miRNA-RISC silences the genes via targeting and inhibiting mRNA transcripts or degrading mRNAs. Various miRNAs serve as oncogenic or tumor-suppressor agents in several cancers; therefore, their detection could provide predictive information. Actually, AI models are able to detect these miRNAs and estimate the diagnosis or prognosis of cancers. In this regard, several studies showed the role of ML models in detecting levels of specific miRNAs in the serum of cancer patients (like CRC, gastric cancer, and kidney malignancies) and predicting the diagnosis and prognosis of cancers.

Wang et al. have developed a molecular algorithm that detects early signs of cancer by examining changes in single-cell copy numbers (40). Olivier B

et al. have devised an integrated framework that leverages DL and ML to accurately predict survival and prognosis using multi-omics data (41).

2.2. The application of artificial intelligence in cancer diagnosis using image processing

2.2.1. Artificial intelligence and histology imaging

Histopathology involves the microscopic examination of tissue sections on glass slides, typically stained with haematoxylin and eosin or processed for immuno-histochemical or immuno-fluorescence labeling. Traditionally, pathologists visually inspect these slides, but this approach is subjective, lacks standardization, and can vary between individuals, even among experts. However, the advent of digital pathology and computer-assisted analysis has the potential to transform qualitative analysis into quantitative analysis. Advanced devices incorporating AI and ML, such as deep neural networks (DNN), can generate high-quality cancer images and identify unique biomarkers (42). Digital pathology is rapidly adopting advanced AI and ML technologies, with a particular emphasis on techniques like DNN, to generate cancer images of exceptional quality and identify distinct biomarkers (43). By digitizing histopathological slides into whole slide imaging (WSI), AI systems can analyze the genetic composition of cellular structures, potentially paving the way for the discovery of novel biomarkers that can greatly enhance cancer treatment (44). Researchers have already conducted extensive analyses in the field of digital pathology, utilizing digitized WSI approaches to identify and categorize various types of cancer (45).

2.2.1.1. Hematoxylin and Eosin (H&E)

Histopathologists traditionally rely on Hematoxylin and Eosin (H&E)-stained slides to diagnose solid tumors (46). However, the application of AI to pathology slides has revolutionized our understanding of cancer histology (47). In a groundbreaking study in 2016, Sirinukunwattana et

al. demonstrated the effectiveness of a spatially constrained CNN combined with a neighboring ensemble predictor in accurately detecting and classifying nuclei in routine colon cancer histology images. This breakthrough enabled the quantitative analysis of tissue constituents within WSIs. These findings highlight the potential of AI-based methods in identifying and locating abnormal histomorphology patterns in routine WSIs of cancer patients. This development opens up exciting possibilities for using ML techniques in histopathology analysis to predict the response to cancer immunotherapy (48). Numerous investigations have confirmed a positive correlation between heightened levels of T cell infiltration and increased counts of tumor-infiltrating lymphocytes with improved response to immune-checkpoint blockade. In a groundbreaking study, Saltz et al. found that the spatial arrangement and densities of tumor-infiltrating lymphocytes, which are closely linked to immunotherapy, can be extracted from H&E scanned images using a deep CNN model. These lymphocytes demonstrate diverse levels of enrichment across various tumor types, tumor molecular subtypes, and immune subtypes (49).

Linyan Wang et al. have devised an advanced DL system that can automatically identify malignant melanoma (MM) in eyelid histopathological sections with dense information. The DL system achieved remarkable results, attaining an impressive AUC of 0.989 for patch diagnosis, with an accuracy, sensitivity, and specificity of 94.9%, 94.7%, and 95.3% respectively. When applied to WSI, the DL system exhibited a sensitivity, specificity, and accuracy of 100%, 96.5%, and 98.2% respectively, with an impressive AUC of 0.998. By utilizing artificial intelligence, the DL system can effectively detect MM in histopathological slides and highlight the specific lesion area on whole slide images using a probabilistic heatmap. This innovative approach

holds promising potential for application in histopathological sections of other tumor types (50). Iizuka et al. employed CNN and RNN to train models using biopsy histopathology WSI of the stomach and colon. The objective was to classify the images into adenocarcinoma, adenoma, and non-neoplastic categories. Their models were rigorously tested on three independent test sets, yielding impressive AUC values. For gastric adenocarcinoma and adenoma, the AUC values reached up to 0.97 and 0.99 respectively. Similarly, for colonic adenocarcinoma and adenoma, the AUC values were 0.96 and 0.99 respectively. These findings indicate that the trained models have the potential to be integrated into practical histopathological diagnostic workflows and demonstrate their ability to generalize effectively (51).

2.2.1.2. Immunohistochemistry (IHC)

Immunohistochemical characterization can include the phenotyping of immune cells, such as quantifying the density of CD3 and CD8 positive cells in the tumor core and invasion margin (52). Viktor H. Koelzer and his team delved into the possibilities of using immunoprofiling to understand how cancer treatment affects patients. They used advanced techniques to analyze the interactions between tumors and immune cells, looking for patterns that could predict how patients would respond to treatment. The researchers proposed using ML and artificial intelligence tools to sift through complex datasets, as well as utilizing DL methods to analyze how the immune system affects patient survival. They emphasized the importance of combining the expertise of surgical pathologists with computational analyses to better categorize patients in the field of immune-oncology. According to the authors, in order to meet the evolving needs of clinical practice, it is crucial to conduct focused

research that combines pathology and bioinformatics. They also suggest that professional societies should support these efforts. Additionally, they emphasize the importance of integrating data sciences and digital image analysis into the education of pathologists to stay up-to-date with advancements in the field (53).

Assessing the presence of HER2 in invasive breast cancer is a critical part of diagnostic evaluation. However, the subjective nature of visually examining immunohistochemistry (IHC) for HER2 scoring can introduce variability between different observers. Talha Qaiser and colleagues conducted a competition to evaluate and improve the current state-of-the-art automated methods for HER2 scoring using artificial intelligence. This study established a benchmark for comparing the effectiveness of automated algorithms in HER2 scoring and showcased their potential in assisting pathologists with more objective IHC scoring (54).

2.2.1.3. Pap Smear

Cervical cancer poses a major health risk for women, and early detection plays a crucial role in saving lives. Regular screenings are vital for preventing cervical cancer. The Pap test is a widely employed technique for identifying any abnormal or precancerous alterations in cervical cells. However, manually examining Pap smear images is subjective and can lead to inconsistent outcomes. In order to establish a dependable and automated approach for detecting cervical cancer, it is necessary to accurately segment and classify Pap smear cell images. To tackle this challenge, researchers have developed a computer-assisted screening system that utilizes digital image processing to analyze Pap smear images. The system is composed of six sequential steps, including acquiring the images, enhancing their quality, segmenting the cells, extracting relevant features,

selecting the most important features, and finally, classifying the cells. To achieve cell segmentation, the proposed system utilizes an iterative method based on shapes and a marker-control watershed technique. Three crucial features are extracted from the segmented nuclei and cytoplasm. For classification, a bagging ensemble classifier is employed, which combines the results of five classifiers. The experimental findings demonstrated high classification accuracies of 98.47% and 98.27% for the two-class problem, and 90.84% (seven-class) and 94.09% (five-class) for the multi-class problem, using the Herlev dataset and SIPaKMed dataset respectively (55).

According to histology staining, **Table 1** provided details of studies that utilized AI systems to diagnose cancers.

2.2.2. Artificial intelligence and radiology imaging

2.2.2.1. Magnetic resonance imaging (MRI)

Determining the size and extent of a brain tumor is a complex undertaking that poses challenges in planning and evaluating treatment options. Magnetic resonance imaging (MRI) is a valuable non-invasive diagnostic tool for brain tumors as it does not involve ionizing radiation. Gliomas, which are the most common and aggressive brain tumors, have a relatively short life expectancy when they reach their highest grade. Currently, the clinical approach to segmenting brain tumors relies on manual segmentation, which is not only time-consuming but also subject to the expertise and variability of the operator. An intriguing research study introduced an entirely automated technique for segmenting brain tumors using CNNs and high-grade glioma brain images from the BRATS 2015 database. The proposed method successfully segmented brain tumors into four distinct classes,

including edema, non-enhancing tumor, enhancing tumor, and necrotic tumor. Accurate tumor segmentation is essential for distinguishing healthy tissues from tumor regions like advancing tumor, necrotic core, and surrounding edema (66).

In a recent investigation, researchers set out to create a quick and automated technique for identifying brain tumors in T2-weighted MRI brain images. They developed a modified MET approach that proved to be more accurate and efficient than traditional FCM and k-means clustering methods. This proposed method not only achieved higher predictive accuracy and dice coefficient values, but also required less processing time. In fact, it outperformed existing segmentation methods when it came to swiftly detecting tumor regions in T2-weighted MRI brain images. The researchers in this study introduced a modified segmentation method based on MET, aiming to swiftly and effectively identify brain tumor regions in T2-weighted MRI brain images. They compared the outcomes of this new approach with the results obtained from traditional FCM and k-means techniques. The findings revealed that the proposed method successfully and promptly extracted tumor regions, ultimately reducing the time required for medical experts to make diagnoses (67).

A recent research project aimed to explore the potential correlation between ML models utilizing features from MRI and ODX test recurrence scores in women with breast cancer. The study involved 261 female patients with invasive breast cancer who underwent dynamic contrast-enhanced MRI before surgery and had accessible ODX scores. A computer algorithm was employed to extract a total of 529 characteristics from the MRI images. The patients algorithm was employed to extract a total of 529 characteristics from the MRI images. The patients were divided into a training set and a test set to evaluate the performance of the ML models. Two ML

Table 1. Details of studies used AI systems to diagnose cancers based on histology staining

Patient samples	Healthy samples	Disease	Technique	Model	Description	Ref.
20*	20*	GC	H&E	CNN	The experiments resulted in the detection of the disease with an accuracy of up to 89.72% implying that the AI model can be a promising tool to assist in pathological diagnosis.	(56)
5461*	NA	TC	NA	NA	The algorithm has the potential to be used as a screening and assistive tool based on WSI for improved diagnosis of indeterminate cases comparably to human experts.	(57)
378	NA	GC, CRC, Endometrial	H&E	DRL	The DRL predicted microsatellite instable directly from H&E-stained histology slides.	(58)
NA	NA	BC	H&E	CNN	The model achieved accuracies of 77.8% for four classes and 83.3% for carcinoma/non-carcinoma. The method had a high sensitivity for cancer cases at 95.6%, making it useful for pathologists.	(49)
68	71	CRC	H&E	SVM, CNN	By using the best alignment metric, they showed that a strong correlation between glandular shape and tumor grade was present. They achieved a tissue classification accuracy of 95.3% and specificity of 95.2%.	(59)
1584*	509*	RCC	H&E	CNN	CNN distinguished clear cell, chromophobe, and papillary RCC and achieved a classification accuracy of 94.07%.	(60)
502*	NA	CC	H&E	CNN	The model was able to diagnose CC with 93.3% accuracy which could be useful to assist pathologists in classifying CCs from cytological images.	(61)
5429*	2480 (s)	BC	H&E	CNN	The model achieved accuracy between 98.87% and 99.34% for binary classification and between 90.66% and 93.81% for multi-class classification.	(62)
39*	NA	LC	IHC	CNN	By staining variation and artifacts the model showed performance as precise as humans with a low cell count difference of 0.033 cells on average.	(63)
83*	NA	BC, PCa, Colon	IHC	U-Net	U-Net based method showed satisfactory performance which exceeded humans in identifying lymphocytes	(64)
675	242	CC	Pap smear	KNN	The accuracy of the cancer diagnosis method was found to be 98.31% for the KNN model.	(65)

GC: Gastric cancer, **CNN:** Convolutional neural network, **TC:** Thyroid cancer, **WSI:** Whole slide imaging, **CRC:** Colorectal cancer, **DRL:** Deep residual learning, **BC:** Breast cancer, **SVM:** Support vector machine, **RCC:** Renal cell carcinoma, **CC:** Cervical cancer, **LC:** Lung cancer, **PCa:** Prostate cancer, **KNN:** K-nearest neighbors, **NA:** Not available, *****: Number of slides.

models were specifically developed to differentiate between high and low/intermediate ODX scores. These models were then assessed using independent data, revealing a moderate association between the imaging results and ODX scores. However, despite these findings, the study concluded that the current ML models are not yet capable of replacing the ODX test solely based on imaging (68).

2.2.2.2. Computed tomography (CT)

CT scan is a medical imaging method that utilizes X-rays and computer analysis to generate detailed images of the body. AI systems have shown promise in improving disease diagnosis using various approaches (69, 70). In order to address this challenge, image processing techniques and DL algorithms, such as CNN, are employed. In the specific context of this study, each image undergoes a preprocessing step to remove air-filled dark areas,

which typically include the colon and lungs. The study revealed that the proposed approach, utilizing CNN, achieved remarkable accuracy rates of 87% in segmenting the colon and 88% in detecting polyps. This performance exceeded that of traditional ML algorithms such as random forest (RF) and K-nearest neighbors (KNN). The findings of the study lay the groundwork for future research in leveraging DL algorithms for automated diagnosis of colon cancer, establishing a benchmark for further advancements in the field (71).

In the aforementioned research conducted by Yeshwant Reddy Chillakuru et al., an automated nodule detector was created and assessed. This detector used the axial-slice number of nodules recorded in radiology reports to generate highly accurate predictions. By leveraging this approach, the study successfully developed a lung nodule detector with a significantly lower false positive rate compared to previous methods that involved feature engineering and traditional ML techniques. The development of the high precision nodule detector has the potential to significantly decrease the time and effort required for re-identifying previous nodules during lung cancer screenings. Additionally, it enables the creation of new institutional datasets, fostering the exploration of innovative applications of computer vision in lung cancer imaging. By utilizing axial-slice information, the proposed lung nodule detector enhances the efficiency of radiology workflows during lung nodule screenings and supports research endeavors in applying DL to detect lung cancer. Future studies could concentrate on improving the detector's performance in detecting ground glass nodules and utilizing temporal lung nodule screening data to predict malignancy (72).

In their research, Grzegorz Chlebus et al. presented an intriguing approach for automatically segmenting liver tumors in abdominal CT scans.

Their method utilized a 2D deep DNN along with object-based postprocessing, which achieved the third-place ranking in the second LiTS round at the MICCAI 2017 conference. Automatic segmentation of liver tumors in CT images has the potential to greatly impact liver therapy planning and follow-up assessments by incorporating standardized and comprehensive volumetric information. In this study, a fully automatic method for liver tumor segmentation was developed using a 2D CNN paired with an object-based postprocessing step. By cascading two models that worked at both the voxel- and object-levels, the researchers were able to greatly reduce the number of false positive findings by 85% compared to the raw neural network output. The proposed method achieved a segmentation quality for identified tumors that was comparable to that of a human expert, and it successfully detected 77% of potentially measurable tumor lesions in the LiTS reference dataset according to the RECIST 1.1 guidelines. The neural network demonstrated greater reliability in detecting larger lesions (with the longest axial diameter ≥ 10 mm) compared to smaller ones (< 10 mm). Furthermore, the research study emphasized the significance of accounting for the variability in imaging techniques and annotations across multiple sites in the LiTS challenge data collection. This observation underscores the importance of addressing and understanding such variations when developing and evaluating liver tumor segmentation methods (73).

2.2.2.3. Ultrasound

Ultrasound is a medical imaging technique that employs high-frequency sound waves to generate internal body images. The potential of AI to detect intricate patterns and analyze them using quantitative parameters has been explored in the context of ultrasound detection methods (74). One particular area of interest is the segmentation and

volume computation of the thyroid gland, as these tools play a crucial role in assessing the thyroid's condition over time. However, many existing approaches for thyroid segmentation are not fully automatic and often require a significant amount of time to accurately segment the thyroid gland. In a recent study conducted by Prabal Poudel et al., three non-automatic segmentation algorithms (active contours without edges, graph cut, and pixel-based classifier) were compared in the context of three-dimensional ultrasound imaging. The evaluation considered various aspects such as accuracy, robustness, ease of use, level of human interaction required, and computation time. The study highlighted that these methods lacked automation and exhibited limitations in terms of accuracy. In order to address these shortcomings and enhance accuracy while providing automation, two ML approaches (RF and CNN) were implemented. The primary objective of the study was to discuss and analyze the advantages and disadvantages of different algorithms. In the final step, the volume of the thyroid was computed using the segmentation results obtained, and the performance of all algorithms was analyzed by comparing the segmentation outcomes with the ground truth (75). Under the leadership of Hang-Tong Hu, a team of researchers has successfully developed an AI system that harnesses contrast-enhanced ultrasound (CEUS) to distinguish between benign and malignant focal liver lesions (FLLs). This AI system surpassed the accuracy of radiologists and minimized the variation in diagnoses among different observers. To train the AI system, the researchers collected data from 363 patients for training and 211 patients for testing. The system was trained using a DL architecture on four-phase CEUS images from the training dataset. The performance of the AI system was evaluated by comparing it to

radiologists with varying levels of expertise. The findings revealed that utilizing the AI system as an assistant improved the performance of less experienced radiologists to the level of expert radiologists and reduced diagnostic variability. Overall, the CEUS-based AI system proved to be an effective tool in distinguishing between benign and malignant FLLs, enhancing diagnostic accuracy in the process.

The application of AI models in the context of other imaging techniques such as mammography, colonoscopy, endoscopy, and dermoscopy was illustrated in **Figure 2**. Moreover, **Table 2** provided details of studies that used AI models to analyze radiology data regarding cancer diagnosis.

3. Artificial intelligence in the prognosis of cancers

AI-driven predictive models have become integral in cancer treatment, offering the ability to identify an individual's probability of developing a specific type of cancer by analyzing risk factors. With this capability, AI can identify individuals who are at a high risk of developing the disease before it becomes apparent. This allows healthcare professionals to closely monitor these patients and intervene promptly when necessary. Notably, researchers at the University of Hawaii have discovered that DL algorithms can effectively distinguish between mammograms of women who will later develop breast cancer and those who will not. Additionally, researchers at MIT have developed a DL model that predicts cancer risk based on mammogram images. These advancements in AI are revolutionizing cancer risk assessment and aiding in early detection and intervention. The developed model underwent validation using data from multiple hospitals located on different continents. It successfully identified 30% of future breast cancer patients as being part of a

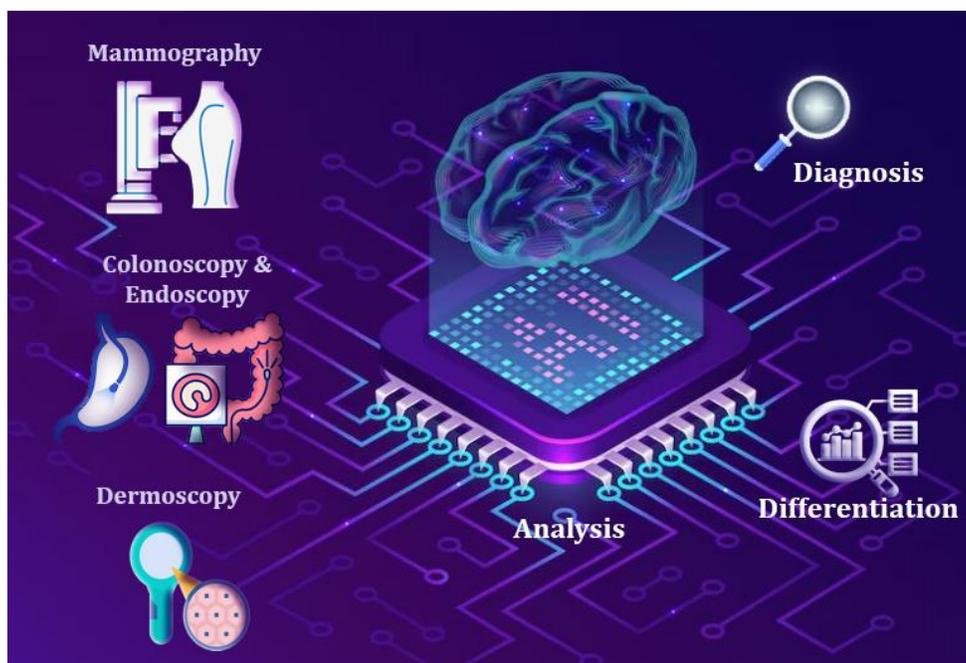


Fig. 2. The application of AI models in mammography, endoscopy, colonoscopy, and dermoscopy. AI systems could be utilized to analyze various medical images in order to predict the diagnosis of cancers and the differentiation of various stages or types of the disease. As mammography is currently the gold standard for screening breast cancer, its images could be evaluated by AI models by using simple texture descriptors, appropriate filtering, and enhancement techniques based on self-examination and mammography data. Similarly, AI models are able to interpret images and records of endoscopy and colonoscopy with satisfactory accuracy and AUC. Concerning the gaps in colonoscopy skills among endoscopists due to lack of experience, AI models could be a promising approach to diagnose and differentiate CRC as well as gastric cancer. Furthermore, in the context of melanoma and skin disorders, dermoscopy is used to capture skin images for computer-aided diagnosis of melanoma. The skin image undergoes pre-processing and is then classified as normal or melanoma. As melanoma is an aggressive form of skin cancer, accurately and rapidly identifying skin lesions is an essential step.

high-risk group. In comparison, human doctors utilizing the conventional Tyrer-Cuzick methodology only flagged 18% of these cases (107). Predicting cancer survival can greatly contribute to tailoring treatment plans, enhancing treatment strategies for high-risk patients, and avoiding therapies with limited efficacy (108). Furthermore, AI models exhibit superior accuracy compared to traditional statistical models in predicting the risk of disease recurrence after a specific treatment option. This enables the optimization of clinical follow-up plans (109, 110). The integration of AI technologies

in cancer care holds significant potential for personalized and optimized treatment approaches. Radiomics is an advanced technique that combines DL with medical imaging analysis to extract numerous disease-related patterns and characteristics that may not be visible to the human eye (111). By merging radiomics with clinical genomic data, it becomes possible to inform cancer treatment models and make accurate predictions about treatment effectiveness or potential adverse effects (112). Radiomics has proven to be a valuable tool in the prediction of lung, brain, and liver cancer.

Table 2. Details of studies used AI systems to diagnose cancers based on radiology data.

Patient samples	Healthy samples	Disease	Technique	Model	Description	Ref.
274	NA	Glioma	MRI	CNN	U-Net based deep convolution networks showed an automatic detection and segmentation for brain tumors according to MRI imaging.	(76)
44	22	BrC	MRI	DNN, DWT	The model classified brain MRIs into normal and three types of malignant brain tumors glioblastoma, sarcoma, and metastatic bronchogenic carcinoma tumors.	(77)
40	NA	BrC	MRI	Template-based K-means, FCM	The proposed algorithm achieved satisfactory detection of abnormal and normal tissues in the human brain with small detachment of gray-level intensity. Additionally, it detected human brain tumors within seconds, which is faster than other algorithms that take minutes	(78)
25	NA	LiC	MRI	SLFN	The model was accurate and efficient, compared to manual ground-truth segmentation and significantly reduced the time required for liver tumor segmentation. The accuracy was also comparable or better than existing semi-automatic methods. The proposed scheme	(79)
341	NA	PCa	MRI	CNN	XmasNet outperformed 69 methods and had the AUC of 0.84 and a high sensitivity and specificity.	(80)
175	252	PCa	MRI	CNN	The detection of prostate cancer was conducted by CNN with an AUC of 0.87.	(81)
5	NA	RCC	CT	RUSBoost, Decision tree	According to CT data sets the segmentation effectiveness in terms of Dice coefficient was 0.85 ± 0.04 . The overall accuracy of the proposed classification model was 92.1%.	(82)
169	NA	RCC	CT	CNN	The model showed an AUC close to 0.9 concerning renal cell subtype classification.	(83)
20*	NA	LC	CT	Various	Regarding the detection of tumors, GCP SO showed the best performance with 96.8% accuracy.	(84)
154	93	LC	X-ray	DenseNet-121	The developed model was able to detect lung tumors with accuracy, sensitivity, and specificity of 74.43%, 74.68%, and 74.96%, respectively.	(85)
659	NA	LC	X-ray	YOLOv4	The sensitivity of the model was found to be the best at 79%. The median time from detection to diagnosis for radiologists assisted with AI was 46 (3–523) days, longer than that for radiologists (8 (0–263) days.	(86)
1090	NA	TC	Ultrasound	Inception-v3	The study found that Inception-v3 can achieve excellent diagnostic efficiency. Nodules that are 0.5–1.0 cm in size and have microcalcification and a taller shape can be more accurately diagnosed using Inception-v3.	(87)
131	NA	TC	Ultrasound	SVM, MLP	The diagnosis of thyroid cancer was carried out based on AI algorithms which achieved accuracy, sensitivity, and specificity of 97.78%, 100%, and 95.45%.	(88)
NA	NA	BC	Mammography	AlexNet	The highest AUC achieved is 88% for samples obtained from both segmentation techniques. When using samples from the CBISDDSM dataset, the model accuracy increases to 73.6%. The SVM accuracy is 87.2% with an AUC of 94%.	(89)
115	NA	BC	Mammography	CellSearch system	The study concludes that pretreatment CTC detection is an independent and strong prognostic factor for overall survival in non-metastatic breast cancer.	(90)
18	23	BC	Mammography	Various	The experimental results show that MSVM outperforms the decision tree model, with average accuracy rates of	(91)

					95%, 94%, and 98% for normal, benign, and malignant cancer classes, respectively. The sensitivity rate is increased by 3%, specificity by 2%, and receiver operating characteristics (ROC) area is 0.99 using SVM.	
30	NA	BC	Mammography	CNN, RNN	The results show that the operation of two classifier outputs yields overall diagnostic accuracy, which outperforms conventional models.	(92)
136	221	BC	Mammography	Various CNNs	According to the results, the models were able to identify tumors with an accuracy of 84.5%, an AUC of 0.88, a sensitivity of 89.7%, and a specificity of 78.1%.	(93)
112	NA	LC	PET-CT	CNN	The AI-based model showed a high sensitivity (90%) in detecting lung lesions but its high negative predictive value on a patient basis (100%) could be important in actual scenarios.	(94)
956	NA	LC	PET-CT	CNN	The combination of PET and CT showed an accuracy of 79% and an AUC of 87% to predict progression of lung tumors which was near the performance of CT alone and over the outcome of PET alone.	(95)
52	NA	CRC	PET-CT	NA	The study concluded that their ML model, based on restaging [18F]-fluorodeoxyglucose (FDG)-PET-CT, was feasible and potentially useful in predicting disease progression.	(96)
NA	NA	CRC	Colonoscopy	Supervised neural network, Multiple layers	The AI system has a sensitivity and specificity of 97.3% and 99.0%, respectively. The system predicted cancerous regions in 21.9 milliseconds per image which is sufficient to support endoscopists in high detection against non-polypoid lesions that are frequently missed by optical colonoscopy.	(97)
826*	1104*	CRC	Colonoscopy	CNN	Compared with endoscopists, the AI model showed similar precision (87.3%) but higher accuracy (85.9%) and recall rate (87.6%) in distinguishing polyp images from non-polyp ones.	(98)
NA	NA	CRC	Colonoscopy	CNN	The proposed system showed superior detection performance in terms of precision, recall, and reaction time in both image and video databases.	(99)
119*	312*	GC	Endoscopy	CNN	The algorithm was able to detect gastric lesion with a mean average precision of 0.87.	(100)
533	1208	GC	Endoscopy	CNN	The proposed method was evaluated using five-fold cross-validation, and the results showed a sensitivity of 96.0% and 0.10 false positives per image.	(101)
228*	698*	GC	Endoscopy	CNN	By performing transfer learning with two classes (cancer and normal), the accuracy of the model was 87.6% for the detection of early gastric cancerous lesions.	(102)
NA	NA	Melanoma	Dermoscopy	SVM	After extracting unique features from segmented lesions, the SVM model classify cancerous and healthy lesions with an accuracy of 92.3%.	(103)
3000*	NA	Melanoma	Dermoscopy	GAN	By evaluating pigmented and non-pigmented lesion segmentation the model could correctly identify about 92% of the lesions.	(104)
NA	NA	Melanoma	Dermoscopy	CNN	The model achieved an accuracy of 89.5% by applying a publicly available dataset.	(105)
95	508	Melanoma	Dermoscopy	NA	The AI system showed a promising sensitivity (96.8%); however, the specificity was 37.4%.	(106)

CNN: Convolutional neural network, **BrC:** Brain cancer, **DNN:** Deep neural network, **DWT:** Discrete wavelet transform, **FCM:** Fuzzy C-means, **LiC:** Liver cancer, **SLFN:** Single hidden layer feedforward neural network, **PCa:** Prostate cancer, **RCC:** Renal cell carcinoma, **LC:** Lung cancer, **GCPSO:** Guaranteed convergence particle swarm optimization, **TC:** Thyroid cancer, **SVM:** Support vector machine, **MLP:** Multilayer perceptron, **BC:** Breast cancer, **MSVM:** Multiclass support vector machine, **RNN:** Recurrent neural network, **CRC:** Colorectal cancer, **GC:** Gastric cancer, **GAN:** Generative adversarial network, **NA:** Not available, *****: Number of images.

By utilizing radiomic brain features extracted from MRI scans, DL techniques can accurately differentiate between brain gliomas and brain metastases, achieving comparable accuracy to expert neuroradiologists (113). Additionally, AI-based "cancer survival prediction" models have been demonstrated superior accuracy when compared to conventional analytic methods (114). In a recent research endeavor, an advanced ANN was employed to make predictions about mesothelioma with an outstanding accuracy of 96%. Moreover, ML techniques have been effectively utilized to diagnose both blood and colon cancer, achieving a remarkable detection rate of 0.96 and an accuracy rate of 0.95, respectively. These findings highlight the potential of ML in aiding accurate cancer diagnosis based on gene expression data (115). Furthermore, in an innovative breakthrough, researchers accomplished a remarkable accuracy rate of 97% in diagnosing lung cancer. They achieved this by analyzing tissue sample slides using an algorithm that examined cancer tissue imaging and identified genetic alterations linked to the disease. This cutting-edge technology proves capable of differentiating between various types of lung cancer, a task that even experienced pathologists find challenging (116). Numerous research projects have utilized ANNs in the field of survival analysis. ANNs have the unique ability to capture variable interactions and build sophisticated prediction models that go beyond linear relationships. This allows for more flexible and accurate predictions of survival time compared to conventional methods. A notable example is the work of Ching et al., who introduced an innovative

ANN framework called Cox-nnet. By leveraging high throughput transcriptomics data, this framework enables the prediction of patient prognoses. Notably, it unveils valuable biological insights at both the pathway and gene levels, providing a deeper understanding of the underlying mechanisms (118). In their research, Bomane et al. utilized three classifiers and carefully selected relevant features to establish connections between cytotoxic-drug sensitivities, patient prognosis, and breast cancer. Their objective was to optimize the administration of paclitaxel therapies in real-world clinical settings (119).

The objective of a research study was to create a two-stage fuzzy neural network (FNN) that can provide prognoses for prostate cancer. This network has the ability to learn the correlation between clinical features and the prognosis of prostate cancer, enabling accurate predictions once the patient's clinical data is available. Unlike conventional ANN, the training results of this proposed network are presented as fuzzy IF-THEN rules. These rules are easier to interpret, which is crucial for medical doctors. The network's interpretability can greatly support medical doctors in making informed treatment decisions for patients with prostate cancer (120). In the same research study, the authors conducted a screening of 43 abnormal genes to construct a SVM model for predicting the prognosis of prostate cancer. The model achieved an average accuracy of 66% and 64% when evaluated through 5-fold cross-validation or training-testing methods, respectively. However, when combined with the features from the National Institute for Health and Care Excellence (NICE), the model's accuracy improved significantly. The 5-fold cross-validation accuracy reached around 71%, surpassing the accuracy of NICE alone (62%). This groundbreaking

study not only explored the relationship between genome-wide somatic mutations and prostate cancer prognosis but also successfully developed an effective prognostic prediction model using unique genetic signatures (atypical genes) (121).

4. Artificial intelligence in treatment of cancers

4.1. The development of anti-cancer drugs

AI has demonstrated its potential in predicting the effectiveness of anticancer drugs and supporting drug development processes. By utilizing high-throughput screening techniques, researchers can uncover the connection between the genomic variations of cancer cells and drug activity. ML techniques can then integrate the screening data to develop models that predict drug activity based on the mutation profiles of cancer cell genomes (122). Remarkably, AI models have achieved success in forecasting drug sensitivity in various types of cancer, including ovarian (122-124), gastric (125-127), and endometrial cancer (128, 129). In addition to its role in predicting drug activity, AI can play a crucial role in addressing the challenge of drug resistance in cancer treatment. By analyzing extensive data on drug-resistant cancers, AI algorithms can uncover insights into the mechanisms through which cancer cells develop resistance. This knowledge can then inform and guide the development of new drugs to overcome resistance (130, 131). Additionally, scientists are leveraging ML to generate reverse synthesis pathways for molecules, which accelerates the process of drug discovery. By processing chemical data, ML algorithms can generate valuable results that assist in the development of new drugs (132, 133).

ML techniques have the remarkable ability to rapidly process vast amounts of data accumulated over

extensive periods. (134). Within the ML domain, DL stands out as a powerful algorithm that has exhibited exceptional performance across various fields, including drug discovery (135, 136). Its potential in this area holds promise for advancing the development of new drugs and enhancing our understanding of complex biological processes. DL models possess unique characteristics that make them well-suited for complex tasks, particularly those involving the modeling of drug reactions based on biological and chemical data. Although the application of DL in drug response prediction is a relatively new field, it has shown remarkable progress. DL has revolutionized image analysis and is now being extended to explore novel opportunities in drug repurposing. In a notable study, Kadurin et al. developed a DL model utilizing an antagonistic autoencoder and large-scale datasets of full dose-response data obtained from the NCI-60 cell line. This research serves as an illustrative example of how DL can be effectively applied in drug development processes (137).

4.2. Improving surgery

Computer vision technology has made notable advancements in the field of surgery, particularly in designing navigation systems and robotic-assisted surgical tools. These innovations have significantly improved the safety and efficiency of oncological surgery by reducing the potential for human error. Surgeons can enhance the quality of care for cancer patients by embracing AI and actively participating in this transformative revolution. DL models, a prominent subset of AI, have demonstrated exceptional capabilities in recognizing high-risk cancer lesions during fine needle biopsies. DL models outperform traditional methods in terms of accuracy, thereby influencing surgical procedures. Accurate diagnosis of benign neoplasms can effectively prevent or limit unnecessary surgical

excisions, reducing the risks of complications and unnecessary harm to patients. An intriguing study showcased the impact of AI assistance in reducing mastectomies by a significant 30.6%. This reduction was achieved by enhancing the detection of benign lesions during core biopsies, which were previously only diagnosed after extensive surgeries (138).

The integration of AI in CAS has gained widespread adoption in clinical settings, leading to enhanced efficiency and effectiveness of surgical procedures for oncologic diseases (139). In particular, computer vision technology is extensively utilized in image guidance and navigation. This assists surgeons in both pre-operative planning and intra-operative navigation, leveraging radiological CT images (139). By leveraging computer vision, surgeons can accurately identify and analyze pathological or critical structures within the patient's body. This aids in the careful planning and execution of surgical interventions, enabling precise removal or preservation of these structures as required (139). Through the integration of radiological imaging and tracking technologies within surgical instruments, CAS systems can effectively identify and highlight structures of interest, even if they are not visually apparent. This capability greatly aids surgeons in safely navigating towards their targeted operative areas (139). Notably, computer-assisted liver map creation has proven to be successful in liver cancer surgery, offering valuable guidance during the procedure (140). Furthermore, ongoing advancements are being made to develop techniques that provide insights and orientation for concealed anatomical features, such as determining the position of the aorta and ureter in laparoscopic rectal surgery (141). These innovations contribute to improved surgical precision and patient outcomes. In a research study, a publicly accessible dataset was utilized to classify kidney cancers by employing a

combined approach that incorporates both clinical data and image analysis. By leveraging ML techniques and clinical information, the researchers were able to predict the specific surgical procedure that would be most suitable for individual kidney cancer patients. Interestingly, the study revealed that aside from cancer stage and tumor volume, common demographic features also played a significant role in determining the chosen surgical procedure for nephrectomy. These findings highlight the potential of AI-based smart systems in assisting healthcare professionals in determining the appropriate therapy or surgical approach for patients diagnosed with kidney cancer (142). Robotic-assisted surgery has emerged as a prominent area within computer-assisted surgery (CAS). The concept of using robotics in surgical procedures was initially introduced in 1964. However, it took over three decades for the technology to gain approval from the United States Food and Drug Administration (FDA) for medical use (143). Presently, robotic surgery is widely embraced in pelvic surgeries, including prostatectomy and hysterectomy, owing to its numerous advantages. These advantages include improved visualization with 3D vision, elimination of hand tremors, and enhanced maneuverability facilitated by the expanded degrees of freedom offered by robotic surgical tools. These factors contribute to the popularity of robotic-assisted surgery in the field of CAS (144). Recent meta-analyses have revealed the benefits of robotic prostatectomy compared to laparoscopic techniques. These benefits include improved urinary function, lower rates of intraoperative complications, and better outcomes in terms of positive surgical margins (144). These findings suggest that robotic prostatectomy has the potential to become the gold standard for surgical treatment of prostate cancer. The field of robotic surgery holds

great promise, and there are ongoing plans to integrate assistance systems with surgical robots in the near future. By incorporating computer vision technologies, these systems will be capable of addressing surgeons' uncertainties regarding anatomical structures and resection margins. This will be achieved by comparing intraoperative data with a vast library of millions of inventory images, allowing for real-time guidance and precise decision-making during surgery (145).

4.3. Optimizing chemotherapy

In the realm of cancer treatment using chemotherapy, artificial intelligence plays a crucial role in anticipating how patients will respond to various drugs. AI is employed in several ways, such as helping healthcare professionals regulate the administration of chemotherapy drugs, foreseeing patients' ability to tolerate those drugs, and refining chemotherapy protocols (146-148). An intriguing experiment showcased the effectiveness of "CURATE.AI," an AI platform that utilizes DL and other advanced technologies. This platform successfully determined the most effective dosage of zen-3694 and enzalutamide, resulting in enhanced treatment efficiency and patient tolerance when used together (149). PARP inhibitors have shown promise in targeting breast cancer cells with homologous recombination (HR) deficiencies. To identify cancer cells with HR defects and predict which patients would benefit from PARP inhibitors, Gulhan et al. devised a screening system utilizing DL. This system achieved an impressive 74% accuracy in detecting such cells (150). Furthermore, Dorman et al. developed a ML algorithm that predicts the tolerance of breast cancer towards chemotherapy. By analyzing the correlation between patients' genetic information and the effects of chemotherapy drugs, the study successfully differentiated between the impacts of taxol and

gemcitabine. Moreover, research has demonstrated that the use of DL surpasses the Epstein-Barr Virus-DNA-based model in effectively assessing risk and providing guidance for induction chemotherapy in cases of nasopharyngeal carcinoma (151). This suggests that the DL method's guiding capability can serve as a valuable tool for predicting the success of single induction chemotherapy in advanced nasopharyngeal carcinoma (152).

4.4. Improving radiotherapy

In the past few decades, radiotherapy has witnessed advancements in beam delivery techniques, leading to increased precision and conformity. Techniques like intensity-modulated radiotherapy (IMRT) (153), volumetric modulated arc therapy (VMAT) (154, 155), and stereotactic ablative radiotherapy (SABR) (156, 157) have significantly enhanced the ability to administer radiation doses that conform closely to the tumor volume while minimizing the impact on surrounding healthy tissues. These advancements have revolutionized radiotherapy by enabling highly precise and targeted treatment delivery.

Image-guided radiotherapy (IGRT) has revolutionized the field by providing knowledge about the precise location of the target area for irradiation and enabling effective management of organ motion during treatment (158, 159). In comparison to traditional 2D IGRT methods, AI-based algorithms for 3D volumetric imaging in IGRT offer superior capabilities in detecting geometric uncertainties and motion that occur during treatment. These algorithms also enhance the accuracy of tumor localization and facilitate measurements of changes in size, shape, and position (160). With AI-based volumetric imaging in IGRT, real-time soft-tissue registration becomes possible without the need for fiducials, making the practical implementation of soft-tissue image

guidance for target volumes and organs-at-risk (OARs) more feasible in routine clinical practice. By utilizing AI-based 2D imaging in IGRT, it becomes feasible to monitor and track both the planning target volume (PTV) and the gross tumor volume (GTV) in real-time. This advancement allows for a substantial reduction in the safety margin required to account for motion, effectively minimizing radiation exposure to healthy tissue and reducing the likelihood of adverse effects. Additionally, with real-time AI-based IGRT approaches, treatment confidence can be enhanced by improving the probability of delivering the prescribed dose, regardless of whether there is a need for dose escalation or a reduction in the target margin (161). AI technology has found valuable applications in the field of cancer radiotherapy, aiding radiologists in accurately identifying target areas and automating the planning of radiation treatment regimens (162, 163). Lin et al. successfully employed a 3D CNN to achieve automatic delineation of nasopharyngeal carcinoma, achieving an impressive accuracy of 79%, comparable to that of specialized radiotherapy experts (164). This demonstrates the potential of AI in assisting healthcare professionals in the precise and efficient planning of radiotherapy for cancer patients. In their study, Cha et al. integrated DL technology with radiomics, a technique for extracting image features from radiographic images. This integration allowed them to construct a predictive model capable of assessing the response to treatment in cases of bladder cancer (165). On the other hand, Babier et al. developed automation software utilizing DL technology, significantly reducing the time required for radiation therapy planning to just a few hours (166).

4.5. Optimizing immunotherapy

In the realm of cancer immunotherapy, AI plays a crucial role in assessing treatment effectiveness and aiding physicians in refining treatment plans (167, 168). Sun et al. have developed an AI platform utilizing ML that shows remarkable accuracy in predicting the therapeutic outcomes of programmed cell death protein 1 (PD-1) inhibitors. This platform proves to be valuable in evaluating the efficacy of immunotherapy in patients with advanced solid tumors who demonstrate sensitivity to PD-1 inhibitors (169). Bulik-Sullivan et al. have developed a ML (ML) approach that harnesses a database of human leukocyte antigen (HLA) mass spectrometry. This innovation enhances the identification of cancer neoantigens, thereby improving the effectiveness of cancer immunotherapy (170). The identification and quantification of various immune signatures associated with immunotherapeutic responsiveness pose significant challenges. Nevertheless, the advancements in AI offer a promising avenue for addressing this research challenge. In a separate study, ML was employed to identify the factors influencing tumor immunogenicity and quantify the immunophenoscore, a unique predictor that aids in recognizing the treatment response to anti-PD-L1 and CTLA-4 therapies using an established scoring system (171).

Integrating RNA-Seq and imaging data is crucial in predicting patients' response to cancer immunotherapy, particularly within a clinical setting. To analyze the infiltration of immune cell types in the tumor microenvironment and assess immune-related gene expression in colorectal cancer (CRC), a deconvolution algorithm known as cell type identification by estimating relative subsets of RNA transcripts was employed (172). ML through ANN has proven valuable in identifying tumor

antigen T-cell epitopes from melanoma patients, a crucial step in personalized cancer immunotherapy. Moreover, ML techniques for microarray deconvolution have enabled the identification and assessment of the abundance of blood-derived TCRV γ 9V δ 2+ γ δ lymphocytes as tumor infiltrating lymphocytes in various types of solid and hematological malignancies. These lymphocytes hold promise as effective agents for cancer immunotherapy (173, 174).

5. Challenges and limitations

The application of AI technology in cancer diagnosis, prognosis, and treatment encounters various challenges that must be overcome to maximize its effectiveness (175). One such challenge is the inability to directly utilize medical imaging data as input, necessitating the development of robust feature extraction and processing techniques (176). Furthermore, there is a requirement to refine and popularize the technology, conduct thorough testing, determine optimal weight coefficients in neural network models, and undertake further research on medical interpretation (177). The utilization of computerized calculations has shown a notable increase in the volume of "big data" and the associated expenses. The implementation of AI techniques, while effective in providing precise information and image assessments, can be costly due to the computational requirements for efficient data processing (178). However, it is important to note that the value of AI-generated data lies in its medical relevance and accurate interpretation. For the successful implementation of AI-driven methodologies in routine medical practice, it is essential that the intended users receive adequate training and possess a comprehensive understanding of the techniques involved (179). As the era of big data continues to expand, it becomes increasingly crucial to address the ethical challenges

associated with utilizing patient information, particularly in cases where explicit consent may not be obtained. The development of ethical strategies and protocols is vital to safeguard patient confidentiality and ensure their protection (180).

In the years ahead, the clinical validation of emerging concepts and tools in AI for medical applications poses a significant challenge. Three commonly reported limitations are frequently encountered, along with potential approaches to overcome them. Firstly, many studies comparing the effectiveness of AI against human clinicians often suffer from unreliable design and a lack of primary replication. This means that the algorithms developed have not been validated using data from sources other than the ones used for their training (181). To address this issue, the open science era offers a potential solution, where open data and open methods are emerging as best practices in research. Next, there are some challenges when it comes to studying the use of AI in healthcare. Many of these studies are based on looking back at past data and involve small groups of patients, which can introduce biases in the findings. AI models are typically designed to work well with specific datasets, but this can cause them to become too specialized and not perform as well when applied to different datasets (182). To address this issue, it's important to regularly reassess and fine-tune the algorithms to ensure they can adapt to changes in patient characteristics (179). Additionally, there have been limited studies that directly compare the performance of AI systems and human clinicians using the same datasets. In some cases where such studies have been conducted, concerns have been raised about the AI systems achieving lower diagnostic accuracy rates than anticipated, particularly when compared to specialized doctors (183). However, there is growing interest in investigating how clinicians and algorithms can

work together, as the combination of human expertise and AI has shown promising results that surpass the capabilities of either alone (179). Ultimately, the real-world application of AI models in clinical settings must be thoroughly validated to provide medical practitioners with reliable support in making accurate diagnoses (184).

6. Conclusion and future prospects

Through the utilization of advanced ML and DL techniques, AI has the ability to harness diverse data sources in cancer research, including genomics, transcriptomics, proteomics, and various types of medical imaging and histologic data. By analyzing these data, AI can uncover valuable patterns and insights that contribute to the advancement of cancer screening, diagnosis, treatment, and patient monitoring. In the field of oncology, AI has demonstrated its potential to revolutionize traditional approaches. Specifically, AI can aid in the detection and diagnosis of cancer by examining medical images such as histology images, H&E images, MRI, CT scans, PET scans, ultrasound, mammography, endoscopy, and colonoscopy. It can accurately identify malignant lesions, classify tumor subtypes, and detect genomic alterations, leading to improved accuracy and efficacy in cancer diagnosis. AI has proven to be valuable in predicting the prognosis of cancer by assessing the likelihood of recurrence, metastasis, survival, and response to treatment. It achieves this by analyzing a range of biomarkers and clinical characteristics. Additionally, AI can support cancer treatment decisions by recommending the most suitable therapy for individual patients, taking into account their molecular profile, disease stage, and personal preferences. Furthermore, ML and DL techniques can be employed to enhance the efficacy of various treatment modalities such as chemotherapy,

immunotherapy, surgery, and radiotherapy. This can be done by optimizing factors like dosage, timing, and target specificity to maximize treatment effectiveness.

However, there are various challenges and limitations that AI encounters when applied to oncology. These include ethical and legal concerns regarding the use of AI in decision-making, the absence of standardized and well-annotated datasets, the necessity for models that are explainable and interpretable, and the integration of AI with human expertise and judgment. Therefore, it is crucial to consider AI as a supportive tool rather than a substitute for human oncologists. It is imperative to develop and assess AI-based systems in close collaboration with clinicians and researchers to ensure their safety, validity, and reliability in the context of cancer care.

Like in other areas of healthcare, the incorporation of AI in the field of cancer is predicted to bring about significant transformations in the future (185). AI has the potential to advance predictive modeling and early detection by analyzing diverse data sources, such as electronic health records, genetic data, and environmental information. By leveraging this analysis, AI can provide insights into an individual's likelihood of developing cancer and enable personalized prevention strategies (9, 186, 187). The application of AI is expected to have a beneficial influence on different aspects of cancer care, including cancer radiology and clinical oncology (185).

Once the challenges are addressed and AI algorithms are thoroughly validated through future research, the field of oncology is expected to become more specialized, leading to more frequent and precise treatment for individuals. Additionally, the integration of risk assessment tools into smartphone applications will enable the general public to receive

immediate estimates of their cancer risk. Algorithms will also assist physicians in determining whether patients should be referred to specialized healthcare centers from primary care settings. Integrating algorithms with electronic health record (EHR) systems can support healthcare facilities by providing alternative approaches for better allocation of resources, focusing on individual subgroups with a higher risk of cancer progression or related complications (188).

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Conflicts of interest

The authors declare that they have no conflict of interest.

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