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Application of Artificial Intelligence in Cancer Management with a Personalized Medicine Approach

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Abstract

Recently, the medical profession has seen an accelerated integration of devices equipped with artificial intelligence (AI) technology, thanks to significant advancements in this area. Over 60 medical devices integrated with AI have already received approval from the Food and Drug Administration (FDA) in the United States. The widespread use of AI technology in medicine is seen as an unavoidable trend soon. AI technology is now being used in the area of cancer, particularly in radiology, for clinical use of medical equipment. It is anticipated that AI technology will become a crucial core technology in this industry. Precision medicine, which involves selecting the most suitable treatment for each patient based on extensive medical data like genome information, has gained global popularity. AI technology is anticipated to play a crucial role in extracting valuable data from vast medical datasets and applying it to medical care. Cancer is the second most prevalent global illness that relies on oncogenic mutations and non-mutated genes for its survival. The significant variability of tumors may result in varying curative results when using the same medications or surgical procedures in people with the same tumor. This highlights the need for more precise treatment approaches for tumors and personalized therapies tailored to individual patients. We summarize current and noteworthy AI advances in cancer research in this report. We also discuss AI's limitations, challenges, and potential effects on cancer therapy. We also explored AI in omics, pathology, and medical imaging.

Keywords: Artificial intelligence, Cancer therapy, Precision medicine, Machine learning.

Introduction

Cancer poses a significant risk to human well-being, resulting in a substantial number of deaths and an increasing occurrence rate. Early diagnosis and treatment may lead to the successful cure of several forms of cancer. Nevertheless, the current state of cancer therapy is suboptimal. The death rates for cancer, particularly prostate, colorectal, and cervical cancer, are persistently high and are still increasing (1). These tumors have no reliable means for screening and therapy, leading to patients not receiving prompt and effective treatment. Furthermore, tumors exhibit a significant degree of heterogeneity, posing considerable obstacles in their management. Hence, there is a want for novel diagnostic and therapeutic approaches that are customized to suit the specific

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needs of each patient (2).

Precision medicine (PM) is an auspicious methodology that considers a person's genetics, environment, and habits, with a focus on elucidating, identifying, and addressing diseases. It aims to develop a personalized treatment plan for patients by gathering multi-omics or multi-mode information from individuals. Moreover, artificial intelligence (AI) employs computers or robots to execute tasks by imitating or replicating human intellect, primarily via machine learning (ML) and deep learning (DL) (3). Artificial intelligence can analyse a vast quantity of data to facilitate the groundbreaking discovery of PM. Artificial intelligence has shown exceptional capabilities in efficiently processing, extracting valuable insights from, and comprehensively analyzing data. It may use this data to create various models that contribute to the attainment of project management objectives (3).

The term "artificial intelligence" was first used at the Dartmouth Summer Workshop in 1956, when it was often referred to as "thinking machines. AI may be described as the capacity of a computer to acquire knowledge and identify patterns and connections via a sufficient number of representative instances (4). It then applies this information successfully to make decisions when faced with unfamiliar data. AI is a broad concept that includes and is often used interchangeably with, machine learning and deep learning. Machine learning is a branch of AI, whereas deep learning is a specific subset of machine learning that emphasizes the usage of deep artificial neural networks. These neural networks include numerous completely hidden layers (4). Deep learning has been more popular in recent years because of its remarkable achievements in computer vision applications, including face recognition and picture categorization. The versatility of deep learning has expanded its potential applications in cancer research and medicine. It can effectively and precisely identify cancer from stained tumor slides or radiology images, offering the possibility of relieving pathologists and radiologists from monotonous and repetitive duties (4).

Tumors are often detected in two scenarios: one is via screening of high-risk populations. Another aspect is the identification of tumors that exhibit clinical symptoms. Once cancer is found, patients will have further exams, including a physical examination, imaging tests, pathology analysis, and serum tumor marker testing. These discoveries will enable precise diagnosis, staging, and classification of tumors, hence facilitating precision therapy for the patient's benefit (5). AI may contribute to several aspects of tumor management, including prevention, screening, diagnosis, therapy, and prognosis prediction. Once AI is integrated into the clinical process, it will enhance the accuracy of lesion identification and optimize the screening procedure. Furthermore, AI may enhance the accuracy of medical diagnosis by assisting clinicians in differentiating between genuine and erroneous illness development. Ultimately, artificial intelligence can assess the benefits and drawbacks of various treatment plans and provide the most optimal course of therapy for patients (5).

NGS technology has led to the accumulation of omics data, including genomes, proteomics, and transcriptomics. Simultaneously, the substantial expansion and extensive accessibility of patients' health data, including electronic medical records, clinical trial information, and medical pictures, have ushered in the era of "big data". The most effective technique of analysis is using AI to analyze data, since ML and DL algorithms may uncover hidden patterns, significant information, and relevant knowledge within the data. The disease-related information is gathered by the extraction of data, which aids in clinical analysis. ML and DL may be used to analyze omics data for many purposes such as creating models, identifying markers for assessment, classification, and outlook, detecting molecular changes in DNA, RNA, and protein, predicting medication effectiveness and treatment response, and developing specific pharmaceuticals (6, 7).

In recent years, a significant amount of research has used DL techniques in the fields of cancer detection, precision medicine, radiation, and cancer research. Furthermore, the American Food and Drug Administration (FDA) has granted permission to many AI algorithms about cancer. In addition, the FDA released a fast-track approval strategy for AI medical algorithms in 2018 (8). In this study, we provide a comprehensive summary of the recent and significant advancements in the use of AI in the field of cancer. In addition, we emphasize the constraints, difficulties, and prospective consequences of using AI technology in cancer treatment. In addition, we discussed the use of AI in the field of omics, followed by its application in pathology and medical imaging. We elaborated on how these applications contribute to the advancement of precision medicine.

A brief introduction to AI in the field of cancer

The identification and cancer screening

Cancer screening has had a role in reducing the death rate of several prevalent malignancies. Notable instances of success include the detection of precancerous abnormalities such as cervical intra-epithelial neoplasia (CIN) for cervical cancer screening and adenomatous polyps for colorectal cancer screening. Treating these abnormalities results in a reduction in the occurrence of invasive cancer. Automation has been employed to enhance the effectiveness of cancer screening due to the need for high throughput technologies and rapid turnaround (9).

Wentzensen et al. created a deep learning classifier to screen for cervical cancer using p16/Ki-67 dual-stained cytology slides. The classifier was trained using biopsy-based gold standards. During independent testing, AI-driven data science (DS) demonstrated equivalent sensitivity and much greater specificity when compared to both Pap smear and manual interpretation of DS. Significantly, AI-DS techniques decreased the number of unnecessary colposcopies by 33% compared to Pap smears (41.9% vs. 60.1%, $P < 0.001$). Furthermore, it demonstrated comparable effectiveness in detecting high-grade CIN, a condition that requires rapid treatment. A prospective randomized controlled trial involving 1,058 patients demonstrated that AI-assisted colonoscopy resulted in significantly higher rates of detecting adenomas and the average number of adenomas per patient compared to conventional colonoscopy (29.1% vs. 20.3%) (10). This improvement was primarily due to the identification of a greater number of small adenomas. It is crucial to note that a mere 1% rise in the adenoma detection rate is linked to a significant 3% decrease in the occurrence of colorectal cancer (11).

There has been considerable interest in using automated methods to identify and classify nodules on low-dose computed tomography (CT) and mammography for screening for lung and breast cancer. Various CNN-based models have shown classification accuracies ranging from 80% to 95%, indicating their significant promise in the field of lung cancer screening. Ardila et al. introduced a deep learning system that utilizes both the present and previous low-dose CT scans of patients to accurately forecast the likelihood of developing lung cancer. The approach achieved exceptional outcomes, with an area under the curve (AUC) of the receiver operating characteristic equal to 0.944. The efficacy of AI mammography in enhancing breast cancer screening has been confirmed in both preclinical and clinical investigations (12). McKinney et al. developed an AI system for detecting breast cancer by using a combination of three convolutional neural network (CNN) models. An improvement in the accuracy of diagnoses was demonstrated when comparing the original choices made during clinical practice with a decrease in both false positives and false negatives. According to a self-directed investigation conducted by six radiologists, the AI system demonstrated an Area Under the Curve (AUC) that was 11.5% greater than the average AUC attained by the six radiologists. Significantly, this AI system can extrapolate from the training data to multicenter data (13).

A promising field for the early identification of tumours is liquid biopsies, which analyse circulating tumour DNA (ctDNA) or cell-free DNA (cfDNA) collected by a simple blood test. These are especially crucial for cancer forms that presently lack an efficient screening approach. Cohen et al (14). conducted a study where they created CancerSEEK, a method for early detection and prediction of eight forms of cancer using ctDNA. The CancerSEEK method first categorises samples as cancer-positive by using a logistic regression model that analyses 16 gene mutations and the expression levels of 8 plasma proteins. A random forest classifier is used to predict the kind of cancer, with accuracies between 39% and 84%. While liquid biopsies show potential for early cancer diagnosis, their use has been restricted to conventional machine-learning techniques. With the growing use of liquid biopsies to gather data, we expect that DL models will remove the need for human selection and organization of distinguishing characteristics. Additionally, DL models will enable the integration of various kinds of data to improve the early identification of cancer (15).

Diagnosis, categorization, and assessment of cancer

There have been numerous reports on CNN-based deep learning models that can effectively diagnose cancers, classify different types of cancer, and determine the severity of cancer using histopathology (such as whole slide imaging [WSI]), radiology (such as CT and magnetic resonance imaging [MRI]), and endoscopy images (such as esophagogastroduodenoscopy and colonoscopy). These models have been found to achieve accuracies that are at least comparable to those of medical professionals (16). CNN-based DL models have shown remarkable accuracy in detecting malignant tumors from histopathology slides for the identification of cancer. The CAMELYON16 international competition aimed to diagnose breast cancer metastasis in lymph nodes using WSI with hematoxylin-eosin (HE) staining (17). The top-performing CNN algorithm, which was based on the GoogLeNet architecture, achieved an AUC of 0.994. This outperformed the best pathologist, who achieved an AUC of 0.884 and did so in a more time-efficient manner. Deep learning algorithms have also been used to forecast the source of unidentified primary tumors, a very demanding task in cancer diagnostics (18).

DL has repeatedly shown success in diagnosing malignant disorders with the use of CT, MRI, PET-CT scans, and endoscopy (19). In a recent study, Yuan et al. utilized CT scans to create a classifier using a three-dimensional (3D) ResNet algorithm. The purpose was to predict occult peritoneal metastasis in colorectal cancer. The classifier achieved an AUC of 0.922, which was significantly higher than the AUC of 0.791 obtained through routine contrast-enhanced CT diagnosis (20). Ke et al. used MRI data from 4,100 patients diagnosed with nasopharyngeal carcinoma (NPC) to develop and evaluate a self-constrained 3D DenseNet model. The purpose was to accurately differentiate between NPC and benign nasopharyngeal hyperplasia. The model achieved an AUC of 0.95-0.97, indicating high performance (21).

In a multicenter investigation, Luo et al. created a gastrointestinal AI diagnostic system (GRAIDS) for the detection of upper gastrointestinal tumors using a CNN-based model. They then conducted a prospective study comprising six different graded hospitals to evaluate the system. The diagnostic accuracies ranged from 0.915 to 0.977 across the six hospitals. These accuracies were comparable to those of specialist endoscopists and better than those of non-experts. This suggests that community-based hospitals can enhance diagnostic efficacy. Overall, if their effectiveness is validated in multicenter prospective trials, these models might significantly enhance the accuracy of cancer detection, particularly in rural hospitals that have limited access to specialists (22).

In addition to dichotomous diagnosis, DL models are utilised for more complex cancer groupings and grading activities. Coudray et al. created DeepPATH, a model based on the Inception-v3 architecture, to categorise whole slide images (WSI) of lung tissues into three classes: normal, lung adenocarcinoma, and lung squamous cell carcinoma. The model achieved an AUC of 0.97. The CNN was effectively taught to automatically execute the Gleason grading of prostate cancer, achieving a 75% concordance between the algorithm and pathologists. Radiology scans may also be used for cancer grading (23). Zhou et al. devised a deep learning methodology, using SENet and DenseNet, to forecast the grades of liver cancer (low vs high) by analysing MRI images. The reported AUC for this strategy was 0.83. Collectively, these studies demonstrate the encouraging use of artificial intelligence in the classification and assessment of cancer, with comparable results to those of highly skilled professionals (24).

Anticipating genetic alterations in cancer

Deep learning algorithms have also been used to analyze histopathology photos to identify and describe the genetic and epigenetic variations present. A Convolutional Neural Network (CNN) was trained to predict six distinct genetic mutations in lung cancer using Haematoxylin and Eosin (HE) stained WSI (23). The performance of the model was evaluated on a separate testing cohort, yielding AUC values ranging from 0.733 to 0.856. The use of WSI allowed the CNN model, namely Inception-V3, to accurately detect prevalent genetic alterations in liver cancer, achieving AUC values greater than 0.71. WSI has facilitated the development of DL techniques that can forecast various genetic alterations, including whole-genome duplications, chromosomal arm gains and losses, localized enhancements and eliminations and gene changes, across different types of cancer (25). DL models have been utilized for predicting mutational footprints, including microsatellite instability (MSI) status and tumor mutational burden (TMB) status. These footprints are crucial indicators for determining the effectiveness of checkpoint immunotherapy (25). In a recent study, Yamashita et al. used the MobileNetV2 architecture to develop a transfer learning model called MSINet. They trained and evaluated this model to identify the MSI status in HE-stained WSI in a sample of 100 primary tumors from colorectal cancer patients. The researchers obtained an impressive AUC of 0.93 for the model (26).

Cao et al. used many examples of learning-based deep learning to classify the MSI condition in a colorectal cancer population using WSI. They successfully reached an AUC of 0.85 (27). Wang et al. conducted a study to categorise TMB status using WSI. They evaluated eight different DL models and found that GoogLeNet performed the best for stomach tumors with an AUC of 0.75, while VGG-19 was the top performer for colon cancer with an AUC of 0.82. The findings suggest that characteristics extracted from histopathology pictures may serve as predictors of genetic mutations in situations when it is not feasible to get tumor samples for mutation screening. Significantly, it might be more economical than direct sequencing (28).

Artificial intelligence big data helps PM manage malignancies

Big data technology primarily encompasses the processes of data analysis, data mining, and data exchange. The potential impact of this technology on cancer diagnosis, treatment, prevention, and prognosis is groundbreaking. However, the process of converting data into useful information for the benefit of patients is now experiencing a significant slowdown. One of the main causes for this is the substantial delay in data analysis compared to data creation (29). Almost every element of tumor research has been impacted by the changes brought about by “big data”. For instance, the technology may use data from NGS to identify frequently mutated genes, aberrant gene expression, and biomarkers in tumors. This enables precise diagnosis and prediction of prognosis, as well as the identification of the underlying cause of a disease. Additionally, it facilitates the development of targeted medications for effective therapy (30).

The equipment can evaluate both visible and invisible aspects in medical pictures, and extract and refine these characteristics to get data about evaluation, therapy, and prediction. Furthermore, the technology can examine patients' demographic and medical data, together with result data, to forecast the elements that influence the prognosis of cancer patients (31). Furthermore, AI is employed to examine, extract, and manipulate tumor-related information, construct a healthcare provider platform using a substantial amount of tumor-related data, effectively address the challenge of complex medical therapy for patients, and minimize the wasteful utilization of medical resources. The potential of big data reanalysis has not been fully exploited so far, but we cannot disregard its significance. It can analyze the data inside a pre-existing database and provide novel insights. For instance, Borziak et al. identified the dedifferentiation indicators of liver cancer by using data from pre-existing datasets.

Big data innovation is primarily employed in particular domains, including omics, pathological imaging, and medical imaging (32). Nevertheless, it fails to integrate data from many domains for data analysis, mining, and sharing, resulting in incomplete utilization of data and failure to fulfil the requirements of physicians and patients. Combining omics and non-omics information may help solve the obstacles associated with diagnosing, treating, and monitoring cancer. AI is valuable for analyzing complex and diverse high-dimensional data sets, particularly in the fields of multi-omics, intergroup methods, and data integration. This enables the identification of cancer molecular mechanisms and the discovery of new diagnostic and prognostic indicators, leading to more precise treatment for cancer (33).

AI aids cancer PM in omics

The vast volume of data resources produced by NGS may provide crucial insights into tumors. Integrating AI with the available data will aid in elucidating the causes and development of tumors, as well as facilitating precise diagnosis, risk assessment, and study of different subtypes of the illness (33, 34). In addition, AI can identify novel therapeutic targets, assess the effectiveness and resistance of anticancer medications, create new targeted drugs, enhance cancer immunotherapy, monitor tumor recurrence and progression, uncover new biomarkers, and forecast the prognosis and survival analysis of patients with tumors. AI facilitates precision medicine for cancer patients, effectively bridging the gap between omics data and clinical practice. Due to the high-dimensional and complex nature of the data produced by NGS, cancer detection techniques using NGS often need comprehensive coverage of higher-dimensional and deeper-seated data. This is done to increase the chances of identifying a small number of mutations in tumor cells and to raise the sensitivity and accuracy of AI algorithms (35).

AI supports tumor PM in genomics

Genomics, a field that utilizes nucleotide sequences for data processing, has increasingly integrated with clinical practice in recent years. The substantial aggregation of data has enhanced the comprehension of cancer susceptibility and has empowered us to progressively predict discernible therapeutic outcomes for tumor sufferers (36). Utilizing spatial and single-cell genomics may help rebuild the process of carcinogenesis, leading to a more thorough knowledge of tumors, clarifying the ambiguous etiology in humans, and enabling the development of targeted therapies based on this mechanism. The integration of machine learning (ML) with genomics data may facilitate the identification of cancer subtypes, the identification of novel markers and therapeutic targets, and the enhanced comprehension of cancer-causing genes (37, 38). This, in turn, enables the provision of personalized therapy for patients. Wang et al. created a complex deep network model that combines image-genomics data to detect different forms of lung cancer. This model also uses attention weights to assist biomedical specialists in identifying prospective therapy targets (39). Furthermore, Vanderbilt et al. devised and verified a novel method to detect DNA viruses from matched normal or tumor NGS samples and investigate the association between viruses and tumor types without the need for further sequencing. Information on these viruses may be used for the diagnosis and treatment of people with tumors. Their investigation demonstrated the role of DNA viruses in the development of tumors (40). Sudhakar et al. used cancer genomics data to construct a pan-cancer model to predict and discover novel driver genes. Identifying driving genes is crucial for comprehending the process of carcinogenesis and developing treatment methods since it has significant biological and therapeutic implications (41).

AI helps PM for cancers in transcriptomics

Transcriptomics is a potent method for assessing all the transcripts generated during metabolism. Transcriptomics has enhanced our understanding of malignancy by providing insights into its incidence, development, tumor microenvironment, and immune-oncology (42). It enables the direct measurement of gene expression levels and analysis of the activation of relevant biochemical pathways. Transcriptomics serves as a connection between genomics and proteomics, primarily using quantitative reverse-transcription-polymerase chain reactions, microarrays, and NGS (43). RNA sequencing is widely regarded as the premier method for high-throughput gene expression assessment due to its superior accuracy in quantifying gene expression (43). Data extraction or advanced mathematical techniques, such as ML or DL, are used to extract features that aid in cancer evaluation as well as initial diagnosis. These methods also help identify new or previously unknown cancer markers and possible targets for therapy. Additionally, they assist in prioritising drugs and predicting cancer drug sensitivity and prognosis (43). Warnat-Herresthal et al. showed that machine learning-based transcriptomics may aid in the identification of acute myeloid leukaemia (44). Furthermore, Ben Azzouz et al. used a machine learning methodology using transcriptomics data to determine the subtypes of triple-negative breast cancer. This strategy was implemented to address the challenge of heterogeneity in the management of the illness. ML-based transcriptomics have been utilized to identify predictive biomarkers for prostate cancer, diagnose colorectal cancer, and predict the immune reaction (45).

AI supports cancer PM in proteomics

Proteomics offers extensive and precise data on proteins in organs, bloodstream, and cell specimens. Proteomics and machine learning-based profile evaluation may provide protein expression profiles that are more precise and responsive in identifying protein biomarkers compared to conventional single-omics approaches (46). These molecules can diagnose cancer, forecast prognosis, uncover crucial signalling pathways involved in disease processes, identify novel targets for therapy, assess the effectiveness and toxicity of pharmacological treatments, and predict therapeutic responses, recurrence, and metastasis. Henry et al. have introduced a technique for medication ranking that uses machine learning to forecast drug response based on proteomics data. This approach prioritises pharmaceuticals to choose the most appropriate one for each patient. Furthermore, Federica et al. developed a more explicit and easily understandable Decision Support System (DSS) to aid in the diagnosis of high-grade serous ovarian cancer. Hence, the use of AI-driven proteomics is likely to have a significant impact on the precise identification and management of tumors in the next years (47, 48).

In addition to the aforementioned commonly used omics data, additional types of omics data such as metabolomics, immunomics, and microbiome data are also employed. For example, using AI to dispose of metabolomics data might aid in diagnosing and evaluating therapy response, discovering novel biomarkers, and determining patient tolerance and cancer status (whether it is invasive or non-invasive). Furthermore, the AI model using immunomics data can predict the urgent immunological features of individuals with cancer (49-52).

Drug design in cancer via ML

The process of drug creation is both expensive and time-consuming, sometimes spanning a duration of up to 15 years. The creation of the pipeline starts with the first phase 0, which involves basic studies or identifying drugs. Phase I, phase II, and Phase III are clinical studies, while Phase IV involves pharmacovigilance research. Phase I is investigating the relationship between dosage, toxicity, and short-term adverse effects (53). In contrast, phase II and Phase III are dedicated to evaluating the effectiveness of the medicine by comparing it to established treatments for the specific condition under research. The purpose of Phase IV is to closely observe and assess any enduring adverse effects of the medication. The primary obstacle encountered in the medication development process is the substantial rate of failure and subsequent financial detriment throughout the concluding phases of development (53).

Thanks to the recent progress in AI technologies and machine learning approaches, we can now accelerate creation and decrease the chances of error. Machine learning models, including support vector machines, random forests, Bayes' theorem, and others, are used at every step of drug discovery to make precise predictions and gain valuable insights. Scientists working in the area of cancer treatment development are increasingly using the Bayesian method as a strategy (54). Bayesian approaches provide a seamless solution for addressing case fatality, survival analysis, dropouts from clinical studies, and difficult computing challenges. In the age of vast information, the Bayesian statistical technique is more appropriate for merging the existing data with prior knowledge and generating posterior probability for both the efficacy and safety of medicine (54).

Bayesian statistics may be used at several stages of the research process, including planning, trial actions, analysis, post-marketing surveillance, and meta-analysis. A novel technique called Bayesian Analysis to identify Drug Interaction Targets (BANDIT) has been created. BANDIT utilizes an integrated big data approach to predict drug targets, validate them for clinical development, and explore medication repurposing. This machine-learning algorithm discovered a new substance that inhibits microtubules and is effective against breast cancer cells that are resistant to all existing officially licensed medications targeting microtubules. The Bayesian adaptive design may also be used in phase I oncology trials, which are carried out in a limited patient population to ascertain the maximum tolerable dosage (MTD) of the therapeutic compound (55).

A multicenter and non-randomized Bayesian adaptive design research was done to evaluate the security and to identify the suggested dosage of the combination therapy of the γ-secretase inhibitor MK-0752 and gemcitabine for individuals with pancreatic ductal adenocarcinoma. The research accomplished these objectives. Yan et al. introduced a Bayesian keyboard decision approach that utilises the posterior distribution of the toxicity probability to accurately determine the genuine MTD. Oncology medication development often includes a proof-of-concept study (PoC) conducted towards the conclusion of the phase I or phase II trial (56). PoC research is conducted to gather preliminary evidence of the therapeutic effectiveness by using a limited number of patients. By using a Bayesian framework, decision-making in PoC may be enhanced since it allows for the direct estimate of data on the desired outcome. The Bayesian design can reduce the length of a cancer clinical trial by combining the phase II/III studies into a single validation trial. A new adaptive shrinking approach called ComPAS was recently created utilising Bayesian model selection and hierarchical methodologies. This technique enables the removal of unsuccessful medications and the incorporation of novel combinations into existing clinical pipelines, using accumulated trial data in an adaptable and seamless manner (56).

While the Bayesian technique has shown to be efficient in all stages of drug development in cancer, it is also accompanied by many obstacles. Applying the Bayesian technique necessitates making decisions on prior knowledge, trial-derived information, and the mathematical model to be used, right from the outset of the design phase. Modifications in the initial data and the accuracy of the information during a subsequent phase might potentially impact the scientific integrity of the study findings (57). There is a proposal to establish the appropriate statistical analysis method for cancer clinical trials at an earlier stage. The Bayesian adaptive design may be affected by operational biases, hence it is crucial to ensure the secrecy of the data. Recent progress in machine learning techniques and increased computer performance have enabled the execution of computations for intricate Bayesian models. Moreover, the use of machine learning techniques and statistical instruments in drug development pipelines has the potential to reduce the expenses and duration of drug development, while also advancing the progress of precision medicine for cancer therapy (57).

Challenges

AI technology's significance has gained global recognition, leading numerous nations to actively promote AI research as a part of their national policies. Given its immense potential, there are elevated anticipations for AI technology, and AI technology will probably be progressively integrated into the area of cancer in the next years. Although AI technology has immense promise, there are still certain obstacles that must be addressed. Thus, we have outlined the primary obstacles that must be consistently addressed.

Overfitting

Overfitting refers to a situation in machine learning where a model becomes too specialised to the training data and performs poorly on new, unseen data. In the context of machine learning and deep learning approaches, overfitting occurs when the training error is low, but the generalization error (the mistake in predicting unknown data) is high. Especially in the medical area, where there is a limited quantity of training data, it is always important to carefully assess the ability of the developed model to apply its knowledge to new situations. Validation is crucial when seeking to clinically integrate medical devices with AI. It is necessary to meticulously check the overall performance of these devices via clinical studies, surpassing the level of scrutiny applied to traditional medical equipment.

Black box problem

Due to the intricate nature of the analysis process involved in machine learning and deep learning approaches, a black box issue emerges wherein people are unable to comprehend the analysis process of the generated findings. The inclusion of an opaque component in the system poses challenges for both the designer and user in accurately anticipating the system's behaviour throughout the design and use stages, hence impeding the system's safety. The General Data Protection Regulation (GDPR), implemented in May 2018, mandates transparency of AI under Article 22 in Europe. Therefore, it is imperative to solve the problem of black box to comply with GDPR. Three primary methodologies are often used to enhance the interpretability of ML and DL (58).

Discrepancies across facilities, particularly in healthcare imaging

Medical imaging analysis is susceptible to variations in facility characteristics, such as the use of different manufacturers and models of devices, variations in protocols, and differences in operators. Several studies, including our own, have observed that the accuracy of predicting data from one facility using a trainer built on data from another facility is significantly diminished. This issue is often referred to as the domain shift problem, and it is a crucial matter that must be addressed to advance the field of medical AI (58).

Conclusion

Artificial intelligence has shown encouraging outcomes in several domains of oncology, such as tumor screening, identification, diagnosis, therapy, and prognosis forecasting. As AI advances and computer performance improves, along with the rapid growth of data, new learning methods like hybrid learning will continue to emerge. These methods will enhance the overall performance of models by enabling efficient data analysis and accurate prediction. The newest machine learning and deep learning model, capable of analyzing diverse datasets, will enhance the potential of project management. To summarize, AI-supported precision medicine may aid in the early detection, diagnosis, and treatment of cancer. Additionally, it can assist in determining the most effective treatment plan, thereby enhancing patient prognosis and treatment outcomes.

Authors' Contribution

Yasam Vojgani and Mohadeseh Sadeghinia were involved in the conceptualization, design and writing of the manuscript draft. The authors read and confirmed the final manuscript.

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