

Exploration on Practical Applications of Artificial Intelligence in the Field of Precision Oncology

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ABSTRACT

Precision oncology is a new model for cancer treatment that will no longer use traditional all-or-nothing methods but rather tailor treatments to specific changes in genes and other factors that cause cancer in different people. As the number of dimensions in biomedical data has been rising, more powerful computing facilities are needed to process such a large amount of data. Systematically explore the applications of artificial intelligence in the field of precision oncology in this paper. Research has been conducted on the use of deep learning and machine learning algorithms for automatic detection and morphological classification of tumours and tissues in oncological medical images and digital pathology. Expand on the above and determine whether artificial intelligence can be employed to analyze large-scale multi-omics data and extract predictive genetic information. A prediction model will also be constructed to anticipate the actual impact and adverse effects on the public of new drugs and so on. Ultimately, this study has shown that artificial intelligence will be used to power high-precision oncology, and at the same time, some problems in infrastructure and future implementation plans need to be addressed.

KEYWORDS

Artificial Intelligence; Precision Oncology; Medical Imaging; Genomic Analysis; Drug Discovery; Machine Learning.

1. INTRODUCTION

Cancer is still one of the most severe health problems in the world today, and it has developed many differences in genes and traits at different times. Historically, the conventional approach in oncology had been an all-encompassing, rather general and experience-based model of medicine, whereby all patients with the same histopathological diagnosis were given the same treatment plan, such as extensive cytotoxic chemotherapy or uniform radiation therapy. Although this method provided a certain extension in life for some people, it did so inconsistently among all groups. A relatively large number of patients experienced severe and sometimes life-threatening toxicities, and none showed any improvement in objective clinical indicators. Therefore, the uneven distribution demonstrated by the two groups shows that the current model is not suitable for all people.

Precision oncology is one such reform. Precision oncology generally refers to the determination of why a particular illness has arisen in one person through exploration of relevant molecular factors and variations in this gene family. Identify the specific molecular reasons and somatic mutations that cause cancer cell proliferation, and then develop targeted inhibitors and immunotherapies to block only the biological mechanisms of the tumour without damaging adjacent healthy tissues. Precision oncology has, however, been implemented at the same time as a significant increase in all sorts of biomedical data. Now, in contemporary clinical practice, a large amount of data is continuously being

generated by high-resolution medical images, digitized histological slides, extensive electronic health records, and complex next-generation sequencing results.

The amount of data is now too large to be handled by human doctors. The patterns to be identified in a large amount of high-dimensional genomic arrays or small-scale morphological variations in gigapixel pathology slides are too subtle and spread out for human vision and analysis to accomplish at this scale and with such precision. Therefore, the full development of precision oncology depends on the application of high-end computational science. General-purpose analysis tools for complicated problems in life science are called artificial intelligence, and they include many forms of machine-learning and deep-neural-network models. Rapidly ingest, integrate and interpret diverse data streams, and thus bridge the original gap between the acquisition of raw biological data and practical clinical application through artificial intelligence.

This paper will systematically investigate how artificial intelligence is currently being applied in the field of precision oncology. Section 2 introduces the changes in oncology medical imaging and digital pathology under deep learning. Section 3 introduces machine learning methods for genomic analysis and discovers new prognostic biomarkers. Section 4 introduces the acceleration of drug discovery pipelines and optimisation of personalised therapy by artificial intelligence. Finally, Section 5 integrates the previous analyses to provide a concluding remark on the current deficiencies and future prospects of algorithmic medicine. Besides the fact that different patients are not the same, there are also many other subclonal cells within a single tumour, so it is very difficult to control these in the long term. As the tumour grows, different types of cells are competing for a limited supply of nutrients and have thus evolved different ways of living; at the same time, these cells have also developed advanced evasive mechanisms against the host's immune system. Targeted therapy can eliminate the main group of cells, but at the same time, resistant cells may be left behind; these resistant cells can then increase in number and cause severe disease recurrence. Therefore, the particular space and time distribution of changes in the tumour microenvironment need to be identified. Human cognition is fundamentally unable to constantly observe and predict the swift, many-sided evolution of these changes at the level of millions of cells. Given the above biological complexity, strong computing resources are now needed to simulate multiple evolutionary routes of diseases and predict whether a specific treatment will fail in advance.

2. ARTIFICIAL INTELLIGENCE IN ONCOLOGICAL MEDICAL IMAGING AND PATHOLOGY

Non-invasive imaging techniques are used for cancer screening, stage classification and post-treatment evaluation in this paper. The experienced radiologist used to view the manually scanned MRI and CT images on paper. At the same time, artificial intelligence has begun to help perform the diagnosis more easily. Convolutional neural networks have shown outstanding results in automatic image segmentation, feature extraction and morphological classification [7]. Deep learning models are good at finding small changes in the structure of the lung, such as minor nodules or very small microcalcifications that people might miss because they are too small or obscured by other parts of the lung. For example, in foreign studies of artificial intelligence systems for breast cancer screening, it has been found that algorithmic models can reduce both the rate of false-positive and false-negative diagnoses significantly, and their accuracy is comparable to or even exceeds that of expert human radiologists in some cases [10].

Radiomics is another type of AI development in recent years that has been added to traditional radiology. Radiomics is a high-throughput method for extracting thousands of quantitative computational features, such as spatial heterogeneity, texture gray-level co-occurrence matrices and shape-based indicators, from standard medical images [7]. The above sub-visual mathematical characteristics are used as reliable surrogate imaging biomarkers. Radiomics can be used to train a good machine learning model that can predict which genes or mutations are linked to poor or good

outcomes in a patient with cancer. Algorithmic phenotyping is non-invasive; thus, frequent and painful surgical biopsies can be avoided, and continuous observation of changes in tumours and resistance development under treatment may be carried out.

At the same time, artificial intelligence is also transforming digital pathology. Digitisation of glass histopathology slides into high-resolution, gigapixel whole-slide images has created a large dataset suitable for deep learning. Traditionally, pathologists manually examined microscopic images to observe modifications in the speed of cell division, nuclei and tissues, etc., for cancer diagnosis. Now, deep neural networks can automatically identify the areas of interest for diagnosis, quantify tumor-infiltrating lymphocytes, and assess the degree of malignancy accurately [8]. Research has shown that at the level of algorithm models, different types of skin lesions and malignant melanoma can be diagnosed accurately directly from clinical pictures [4]. Standardise the grading of pathology and reduce differences among observers to provide the highly accurate and consistent support needed for the application of precision oncology. Several advanced computational methods have been employed by the developers to achieve the high accuracy mentioned above, such as automatic image segmentation, spatial image registration, and generative data augmentation. Locate and determine the size of the tumour precisely; at the same time, isolate it from the nearby healthy tissue in the organ to minimise damage to this organ from radiation therapy. Spatial image registration can be used to align multi-modal scans of functional Positron Emission Tomography (PET) and structural Magnetic Resonance Imaging (MRI), and a combined high-dimensional clinical model can be constructed. Given that a large number of perfectly labelled medical images are hard to obtain, generative adversarial networks are often used by researchers to create synthetic training data. The generative model generates high-fidelity synthetic medical images that are statistically distributed; thus, it can enhance the robustness and generalisation ability of the primary diagnostic network to new clinical circumstances at the hospital.

3. GENOMIC ANALYSIS AND BIOMARKER DISCOVERY

At the root of cancer is damage to the genome; therefore, many somatic mutations, chromosomal disorders and other epigenetic changes have occurred in the cell. With the introduction of high-throughput next-generation sequencing technologies, whole-genome and transcriptome sequencing of patients can now be performed rapidly and affordably. The top problems in precision oncology are how to distinguish the few harmful 'driver' mutations that drive cancer from the numerous harmless 'passenger' mutations also present in the sequencing data. Machine learning models are good at handling the large number of variables and noise in biological data [5].

The first applications of machine learning in oncology focused on classifying cancer types and predicting a person's survival from basic microarray gene expression data [1]. With the development of data acquisition technologies, the listed algorithms have gradually incorporated large-scale multi-omics datasets including genomics, proteomics and metabolomics. Principal component analysis and deep autoencoders are now commonly used unsupervised machine learning methods for dimensionality reduction to discover latent biological clusters and unmapped molecular pathways involved in cancer. Through the above analysis of large-scale data, artificial intelligence is now able to discover new and very specific biomarkers that can serve as targets for precise drug treatment [2].

Deep learning networks are now being applied more and more frequently to predict the functional consequences of uncharacterized genetic variations. Algorithms can be employed to build a model of the regulatory grammar for the genome, predict the effect of particular single-nucleotide polymorphisms (SNPs) on protein folding and signalling pathways, and study general cellular homeostasis [5]. Anticipating this will provide support for the research on the progress of rare or less frequently occurring cancers with limited study. With the continuous development of computing power and an in-depth understanding of life in all areas of nature, scientists have begun to uncover the reasons for cancer and made new advances in research on its development [6].

The development of the above genomic models is based on the combination of many large-scale, worldwide patient data. A large-scale, multi-national genomic database has been used to train an AI system that can find small differences in the frequency of genes among different populations. Thus, the model of precision oncology will be more widely applicable to all people in the world and can be adapted to different genetic backgrounds across the globe to provide high-end molecular diagnostic services to a broader population.

4. AI-DRIVEN TREATMENT PERSONALIZATION AND DRUG DISCOVERY

The goal of precise oncology is to tailor treatments according to the particular molecular deficiencies in a person's cancer at the most basic level. Artificial Intelligence is the general-purpose controller of the problem at hand. Machine learning algorithms can be employed to combine a patient's multi-omics data, historical electronic health records, and real-time continuous biometric data to predict an individual's response to treatment prior to the use of any pharmaceutical agents [3]. Predictive models can determine the efficacy of treatment and the risk of serious side effects to avoid harm from ineffective or harmful drugs and find suitable ones more quickly [2].

At present, artificial intelligence is being employed in many parts of the hospital to help doctors' daily work. Traditional oncology drug development is generally slow, very costly and has a high failure rate. Machine learning can help to accelerate the identification of *in silico* drug targets and large-scale virtual high-throughput screening of chemical libraries. Deep neural networks can precisely simulate the mechanics of molecular docking to predict the binding affinity and pharmacokinetic properties of millions of new compounds in a fraction of the time required for physical laboratory experiments [9].

Algorithms can also be used to discover new uses for the same approved drugs in the search for cancer treatment. Map the interaction network of known drugs and new cancer targets to discover alternative therapeutic applications by artificial intelligence, thereby reducing the time and regulatory burden for new drug development. As these computational technologies advance, the ability to design custom-made molecular compounds that address individual genetic mutations quickly will gradually move from the realm of theory to practical application in a clinical setting, and thus, the potential of artificial intelligence in fighting cancer will be realised [11].

The next demand for clinical application is to build a multi-stage validation path. Before an artificial intelligence model is used to guide treatment, it should be tested on retrospective data as well as external hospital cohorts with different demographics and technical features. Therefore, verification can be conducted to check the stability of the algorithm under various conditions of different imaging equipment, sequencing platforms and patient groups. Oncologists should be able to present all the reasons for a prediction, such as mutation status, imaging features, previous treatment history and toxicity risk. A human-in-the-loop model is used to reduce the risk of autonomous operation by AI and retain the computational efficiency of AI. Therefore, in practice, high-precision oncology needs strong models that are also explainable, subject to clinical supervision, and continuously monitored after deployment.

5. CONCLUSION

In recent years, there have been many achievements in the field of artificial intelligence for precision oncology that have changed how research is conducted. As shown in the above analysis, advanced computational algorithms have begun to change the entire process of oncology. Deep learning models for diagnosis of medical images and pathology have achieved high levels of automation and reproducibility in recent years. These systems can find very small structural defects and extract rich radiomic features that are too subtle for the human eye to notice. At the same time, machine learning

can also address the problem of disorder and high dimensionality in genomic data to find new biomarkers and map complex molecular pathways of cancer. Artificial intelligence can also accelerate the relatively slow process of new drug discovery by rapidly conducting in silico experiments on new chemical compounds and precisely matching patients to suitable medicines based on algorithms.

Although there have been many improvements recently, algorithmic medicine has yet to be widely applied in hospitals. The operation of artificial intelligence relies on providing it with a large amount of high-quality data continuously. As a result, many problems have arisen in the field: poor infrastructure for protecting patient data, data silos at institutions, and a lack of standardised interoperability among different electronic health record (EHR) systems. In addition, many advanced deep neural networks are also "black boxes" and thus difficult to interpret. To be widely accepted by doctors in China, artificial intelligence needs to have good explainability and provide clear, biologically plausible reasons for its diagnostic and treatment decisions; therefore, researchers need to strengthen the construction of explainable algorithmic models.

Artificial intelligence will help doctors decide how to treat patients, but it will not operate independently at this time. In the future, high-precision oncology will be realised through the collaboration of cutting-edge computation and warm-hearted human care. Systematically address the current infrastructure deficiencies and maintain high ethical standards to enable the medical community to fully realise the potential of artificial intelligence in delivering personalised, high-efficacy and long-term cancer treatment.

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