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AI AND PRECISION ONCOLOGY: USING BIG DATA TO TAILOR CANCER TREATMENTS

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ABSTRACT

AI refers to the field of computer science that leads in creation of systems and machine. AI is transforming precision oncology by interfering how cancer is detected, diagnosed and treated. It focuses on ML (machine learning) to inspect major amounts of data which includes genomic information, medical imaging. AI helps in early detection and diagnosis through system that can determine medical imaging (CT Scan, MRI's, etc) that detect tumours. Though in current scenario doctors are capable to treat individuals, AI helps to design individualized treatment plans by analysis of patient's genetic profile by comparing it with big data for the identification of most effective therapies. Cancer is a large group of disease that happen when normal cell transform into cancerous cells that multiply and spread. Genes are responsible to instruct your cells when to start and stop growing. Cancer is the second most common cause of death in US. Innovative treatments such as AI and early diagnosis are curing cancer and helping people with cancer live on. Precision oncology is an innovative approach to cancer treatments that focuses to tailor therapies based on genetic molecular and environmental characteristics of each patients cancer. Oncology is involved at every stage of cancer from early detection in stage 0 to treatment and management of stage IV in cancer. Precision oncology enhances technologies (genomic sequencing biomarker testing and AI) to identify specific mutations and molecular profiles of cancer cells.

KEYWORDS: Precision oncology, Artificial Intelligence, Machine Learning, Genomic sequencing, Biomarker discovery, Multi-Omics, Radiomics, Pathomics, Big data,

Explainable AI(XAI).

INTRODUCTION

Cancer is one of the most dangerous health challenges deteriorating the health index of the world. Cancer has lead to cause of death worldwide which has affected people of every age group(especially adult population). It has become a global prevalence in which survival rates for some types of cancer have improved. Although many types of cancers remain difficult to treat such as pancreatic, lung, and liver cancer often have low survival rates. There are over 100 types of cancer, healthcare providers categorize them into three broad cancer classifications, i.e., Solid Cancers, Blood Cancers and Mixed cancers.

According to some recent researches John Jumper, Denis Hessabis, David Baker worked on protein structure prediction of how the proteins fold into their functional forms. The AI system created by them can now analyse protein structures with near atomic precision in hours. These AI system can discover cancers hidden weaknesses. Recently scientists have developed AI-powered digital pathology systems which is equal to several trained observers functioning simultaneously. These have the capability of spotting ultra-fine pattern that humans errors by 23% and leads to more time efficiency. Due to a global shortage of pathologists and constantly increasing cancer cases AI has become the futuristic hopeful source for cancer treatments in upcoming years. In 2024 a study, AI powered radiomics predicted immunotherapy response with 89% accuracy, compared to 60% other conventional methods. Also in 2024, major centre's deployed systems from vendors, such as Paige, PathAI and Proscia, procuring good speeds and accuracy rates. AI is technologically ahead of humans although there are some things we still need to know. AI and precision oncology have made remarkable perches in recent years; there are still many noticeable updates that need exploration and minimization to fully realize their potential. There are some aspects in AI that are responsible to have some sort of interpretation. Even AI lacks in transparency which makes it difficult to understand why the system made a particular decision. Artificial Intelligence can do many things that humans are unable to do but the question is on which basis the AI performs its job. The answer is deep learning algorithm's. To make the system perform appropriately you have feed the system with correct examples, and the system will work fine as per its capability. At the end for the betterment of cancer treatments revolutionizing towards Artificial Intelligence is finest way as AI and machine-based learning (MBL) are able to predict which treatment a patient might respond best to. AI and Precision

oncology refers to a medical treatment selection by the Artificial Intelligence where procedure by which the most accurate and appropriate treatment according to the individual patient is identified based on large amount of data (such as genome information). For AI to work efficiently and a good percentage of accuracy it must collect and store big data which is necessary for treatment in various cases and definite outcomes. DNA and RNA sequencing, radiomics and path omics, clinical trials and patients reports all these datasets help in the betterment of precision oncology resulting in better outcomes. Hence, in future there are more chances of adaptation of Artificial Intelligence agencies in health, research and tech organisations. Till date AI has made clear progress in AI powered drug discovery but trusting an AI totally in 2025 is still an uncertain thing. In current time, AI has performed quite well in Drug discoveries but the trust level in the researches is shown probably 60-70%. Now there will be some or the who would think how trustable AI can be built and how much accurate output will it give. For constructing a trustable AI researches, oncologists, pathologists shall collaborate and discuss, real patients reports and outcomes shall be installed in the datasets of AI, this simultaneously updates the system, Individualized treatments shall be performed under the guidance of AI, framework and daily usage workflow shall be trained to the healthcare providers that will lead to the welfare for every aspect involved in it. But after a thorough survey of us we found that most of the doctors in India implement AI for its best result of bioinformatics. Now Bioinformatics is the field that combines computer science, biology and statistics to combine the larger complex datasets containing genomics, proteomics and clinical studies to give the best information to the healthcare provider. Most common bioinformatics such as Genomic sequencing, proteomics, data mining, drug discovery, systems biology are used in identification of drive tumour growth, biomarkers for early detection.

ETIOLOGY

1. Genetically caused cancer

- Inherited mutations: Inherited mutations also widely known as the germline mutations, is a quite reason for developing cancers like hereditary breast and ovarian cancer (HBOC) syndrome, cowden syndrome, etc. It is a particularly a type pf cancer that an offspring develops from negative changes occurred in DNA and passed down by the preceding generations of their parents. The BRCA1 and BRCA2 genes are responsible for the 80% of the cancer doe to the germline mutations. Although the cancer caused by inherited mutations are 10% cases.

- Acquired mutations: Primarily, acquired genetics are the mutations that occur in the genetic information that occur in the genetic information of a cell of a growing body. In which some of the mutations that occur negatively for us by causing the mutation and triggering the genes responsible for causing cancer. These kinds of mutations are called somatic and sporadic mutations. These kinds of cases no relationships with any genetically passed factor from parents but they just occur knowingly or unknowingly. Here are some factors responsible for the acquired mutations of cancer:

a. Abnormal cell division
b. Hormonal changes
c. Medicines with high side effects, etc.

2. Exposure of carcinogens

Carcinogens factors are substances or agents that provoke the cancerous risk in our body. Although these substances naturally occur in the environment (such as UV rays in sunlight and certain viruses) but there are also manmade carcinogens (automobile exhaust fumes and industrial smokes) and scientists have also listed the 100 common carcinogens. Mainly carcinogens are classified into three types i.e, b Chemical carcinogens, biological carcinogens, Physical carcinogens. It can also be caused through radiations, some viruses, etc. Any substance present in environment that can cause cancer is a carcinogen (according to National Human Genome Research Institute). In current environmental conditions coming in contact with carcinogen is very common, having bad lifestyle habits such as tobacco eating, smoking, working in a workplace where carcinogenic chemicals are used, or if someone has contacted with human Papillovirus (HPV).

The carcinogens have a very simple mode of action. DNA is present in the genes, genes give information manual for making proteins. These proteins control vast actions including how the ells will grow and multiply. When carcinogens make changes in the DNA, it alters the chain reaction which converts normal cell to cancerous cell.

3. Chemical carcinogens

Chemical carcinogens are those substances that cause cancer through chemical substances. It can occur naturally or synthetically that damage DNA, alter the cell growth and increase the risk of cancer. It is often encountered because of irregular and unhealthy lifestyle (unhealthy habits, smoking, etc). Tobacco usage can cause lung cancer, bladder cancer, head and neck cancer.

What is Precision Oncology

at approaches highly personalized treatment and therapies. It analyses the unique genetic blueprints of each patient's tumour though advance genomic testing, identifying specific DNA mutations and molecular alterations that are responsible in cancer growth. By understanding and deeply studying these specific tumour characteristics, the oncologists select the targeted therapies that works against cancer cells by sparing healthy host tissues, potentially improving outcomes and reducing side effects. This treatment protocol may combine FDA-approved targeted drugs, immunotherapies, or clinical trial option match to the tumour's molecular profile, along with conventional treatments that are appropriate.

This pattern also enables ongoing treatment adjustment as the cancer evolves, that can ensure the therapeutic approach and remain optimized for the patient's changing disease biology throughout their care journey.

Why AI

Artificial intelligence (AI) has revolutionized biomarker discovery by analysing large-scale genomic, transcriptomic, proteomic, and metabolomic data. Unlike traditional hypothesis-driven methods, AI uncovers hidden patterns in complex datasets patterns that conventional tools often miss. Deep learning excels at interpreting high-dimensional data from tumour biopsies, blood tests, and medical imaging, linking biomarkers to clinical outcomes like treatment response and survival.

Platforms like Panda Omics integrate multi-omics data using advanced bioinformatics and machine learning, revealing relationships invisible to traditional analysis. Explainable AI (XAI) bridges the gap between AI and clinicians by making insights interpretable. For example, an XAI model identified biomarkers in non-small cell lung cancer (NSCLC), improving diagnostics and building trust in AI-driven results.

Accuracy in biomarker studies hinges on sensitivity (detecting true positives) and specificity (excluding false positives). AI's integrative approach combines genomics, epigenomics, and proteomics, enabling multi-omics biomarkers that offer a fuller picture of tumor biology.

In cancer diagnostics, AI outperforms traditional tests by detecting subtle patterns in histopathology images, genetic data, and clinical records. Deep learning classifies cancer subtypes with high precision, while merging imaging (CT/MRI) and molecular data enhances

early detection and staging. Prognostically, AI predicts therapy responses—critical in immunotherapy and monitors circulating tumor DNA for early relapse signs. Frameworks like the Predictive Biomarker Modelling Framework (PBMF) use contrastive learning to refine treatment plans and boost survival rates.

By unifying imaging and molecular biomarkers, AI advances precision oncology, enabling tailored therapies for each patient's unique cancer profile. This synergy promises faster, more accurate diagnoses and personalized interventions.

Big data to tailor cancer treatment

In the treatment of cancers especially oncology data collection and management is a mandatory thing that generally involves data procurement, quality control, and validation to ensure the accuracy and precision of the data comply and fulfil the condition of legal requirements. These data are sourced from various sources. The medical big data with AI has also revolutionized radiomics and digital pathology. The Machine deep learning (MDL) is an algorithm that excel in image analysis and recognize pattern which most off the humans are not capable of. Now to tell you the instance radiomic uses advanced and upgraded mathematical algorithms. AI can detect complex variations in genome sequence in response to cancer drug treatment and can compare it with the genetics of patients for the best treatment for the success.

Nowadays these AI has been implemented in daily life (Wearable Devices) in the technologies where use of biometric sensors, fitness trackers can alert the consumer by implementation of patterned data that informs the user whether something inappropriate in the health of the user has happened. These technologies use a specialized form of data known as Electronic Health records (EHR). EHR's are digital form of patient's medical reports that accessible through practitioners, doctors, medical advisors, nurses, specialists, online portals.

1. Genomic data (DNA and RNA sequencing)

Genomic data is the information about the DNA sequence, its mutations, and gene expressions with the cancer cells. Genomic data plays a major role in cancer treatment as it helps to identify the type and subtype of the cancer also helps to search driver mutations (those genes that induce the cancer to grow), which can determine the behaviours of the tumor. One of the primary datas used in the treatment of cancer (AI biggest datasets for cancer oncologies). AI does the bioinformatics precisely and has well adopted the function.

From the past few years so much progress has happened in identifying the changes of genes. So much of data is collected through PCR and Sanger sequencing through which mutatuion and its identification can be done, also structural variation studies have revealed changes in chromosomes, such as deletions and translocations, which can play a significant role in cancer development. Two landmark studies published in 2008 conducted an in-depth analysis of lung adenocarcinoma and glioblastoma multiforme(GBM) samples, identifying novel mutated genes and revealing key biological pathways-such as MAPK, P53, and mTOR-that are critically affected in these cancer types. Rather than relying solely on mutation data, the researchers adopted an integrative approach by incroporating multiple data types to gain a deeper understanding of tumor biology. They analysed gene expression profiles to evaluate the activity levels of specific genes, helping to identify functionally significant alterations.

Chromosomal structural variations-such as deletions, amplifications, and loss of heterozygosity (LOH)-were examined to uncover genomic instability and key driver events. Additionally, clinical parameters, including patient outcomes, therapeutic responses, and disease progression, were integrated to establish meaningful correlations between molecular alterations and real-world clinical impact. Vogelstein and his team undertook a comprehensive analysis of nearly all protein-coding genes across various tumor types. Then, these findings were cross- verified using shorter reads generated from the Illumina Genome Analyzer. This two-step confirmation method allowed them to confidently identify fusion transcripts in prostate cancer cell lines like LnCaP and VCaP, and also in actual prostate tumour samples.

RNA sequencing isn't limited to studying known genesit can also reveal entirely new genes that haven’t been documented before, often because they lack EST (Expressed Sequence Tag) data or were overlooked by computer-based gene prediction tools. This highlights the need to keep developing advanced tools that can uncover the full complexity of the cancer transcriptome and give us a richer view of tumor biology.

Alongside mRNA analysis, scientists are also paying increasing attention to microRNAs (miRNAs) small RNA molecules that regulate gene activity. These tiny regulators play a big role in both healthy and cancerous cells. For example, Uziel and team explored the relationship between a specific group of microRNAs (the miR-17–92 cluster) and the Sonic Hedgehog/Patched (SHH/PTCH) signaling pathway in medulloblastoma (a type of brain cancer). Their experiments in a mouse model showed that when the SHH/PTCH pathway is

abnormally active, the miR-17-92 cluster becomes overexpressed. They later confirmed the same pattern in a subset of human medulloblastoma tumors, showing a direct connection between this pathway and miRNA behavior in tumor development.

Likewise, Wyman and Nygaard independently used Roche/454 sequencing and advanced bioinformatics to discover new microRNAs and detect differences in miRNA expression in ovarian and breast cancer, respectively. Thanks to such work, researchers are now considering specific miRNAs as potential biomarkers—tools that could help diagnose or predict the progression of different cancer types. Whole genome sequencing has revolutionized cancer research by enabling scientists to thoroughly compare the entire DNA sequence of a patient's tumor with that of their healthy cells. Thanks to advances in next-generation sequencing technology—specifically its speed, accuracy, and reduced cost—it is now possible to sequence multiple samples from individuals with the same type of cancer. However, this process isn't just about generating data; it also demands the creation of precise analysis tools and workflows that can filter, validate, and enhance the accuracy of detected mutations. The goal is to identify the full range of genetic alterations involved in cancer, including inherited risk factors, small changes like point mutations or insertions/deletions, copy number variations, and large-scale structural shifts. A landmark study involving acute myeloid leukemia (AML) was among the first to demonstrate how this approach works. Fortunately, next-generation sequencing makes this possible by offering a "digital" readout—each sequence read represents one original DNA fragment from an individual cancer cell.

In theory, for heterozygous mutations (where only one copy of the gene is mutated), about 50% of the reads should show the variant if all tumor cells contain it. But since tumor samples often include a mix of cancerous and normal cells, the actual observed proportion must be corrected using pathology estimates or more precise computational methods that calculate the percentage of normal DNA present at known mutation sites. This strategy was applied to the first acute myeloid leukemia (AML) genome ever sequenced, and it showed that nearly all detected somatic mutations were present across the entire tumor population except for one known mutation in the FLT3 gene, which experimental models had already shown to be a late-arising mutation rather than an initiating one.

In a follow-up study, a second AML genome and its matched normal DNA were sequenced using the same principles. This led to the discovery of nine somatic point mutations in genes, two small insertions or deletions, and 54 additional somatic variants located in regulatory or

highly conserved regions of the genome. Although the new mutations found in the first AML genome weren't seen again in a larger group of 187 AML samples, a mutation in the second genome study was found to recur in 8.2% of those cases. This mutation occurred at position R132 in the IDH1 gene a hotspot also seen in glioblastoma (GBM). Interestingly, when researchers looked more closely at AML patients who had this mutation, they found that those with normal chromosomal profiles but lacking other common mutations (like NPMc and FLT3) had worse survival outcomes, as shown through Kaplan–Meier analysis. This connection reveals just how powerful large-scale genome sequencing can be—not only for identifying new cancer drivers but also for linking genetic changes to patient prognosis and disease behavior. It's a clear example of how genomic research is reshaping our understanding of cancer. The future of cancer genome sequencing is closely tied to the rapid progress of next-generation sequencing technologies. As these platforms continue to improve offering longer read lengths and greater data output per run the ability to sequence entire cancer genomes will become faster and more affordable than ever before. Beyond just decoding DNA, these advanced technologies also enable the detailed mapping of gene expression patterns, DNA methylation status, histone modifications, and binding sites of transcription factors and other regulatory proteins. This opens the door to building multidimensional data sets that offer a complete picture of the genetic and epigenetic changes occurring across different tumor samples.

A major question moving forward is: what insights will emerge as we sequence hundreds or even thousands of cancer genomes? One area of uncertainty is whether key cancer-driving mutations will commonly affect the same genes across different patients or if each tumor will display a unique mix of shared and individual ("private") mutations. These answers will directly influence how we design personalized cancer therapies. Additionally, it's important to consider how a person's inherited genetic makeup may influence their risk of developing cancer and how their disease progresses. That's why comparing the tumor genome to matched normal DNA from the same patient remains a critical part of cancer genome studies it helps distinguish inherited variations from those that arise specifically in the tumor. Understanding the full genetic profile of hundreds of tumors is crucial, as it will help determine whether personalized cancer treatment will require complete genomic mapping of each individual's tumor. In addition, some research must specifically aim to uncover the distinct genetic differences between early-stage cancers and those that have spread (metastatic disease). These comparisons are vital for developing targeted strategies to prevent

or treat cancer progression. But sequencing alone is just the beginning. Once we identify potential cancer-related genetic alterations, the next step is to figure out which of these changes are actually driving the disease. This is where functional screening comes in—large-scale experiments that test how specific gene changes affect cancer behaviour.

2. Radiomics and Pathomics

While trained pathologists can infer tumor behavior from conventional histology slides, pathomics provides a more detailed and scalable means to explore sub-visual characteristics of tumor biology.

One of the key strengths of pathomics lies in its capacity to examine the spatial organization of tumour tissues, especially the most invasive components, directly from standard haematoxylin and eosin (H&E) stained slides. Innovative computational methods have been introduced to access cellular patterns, nuclear morphology, textural features, and spatial orientation, which are instrumental in evaluating disease presence, progression, aggressiveness, and patient survival.

Genomic data provides high-resolution insights into molecular alterations, while imaging and pathology contribute spatial and phenotypic context. When integrated, these diverse data streams create a powerful framework for studying the tumor microenvironment, ultimately leading to a more precise evaluation of disease aggressiveness.

Bringing together imaging features and genomic information can enable us to:

1. Link genetic variations with their histological manifestations;
2. Uncover the biological processes behind certain imaging traits;
3. Combine both the spatial organization and molecular characteristics to better understand how tumors behave and grow."
4. "Account for the varying characteristics found within different regions of the same tumor."
5. Discover novel biomarkers that can aid in diagnosing and predicting disease outcomes.
6. Develop detailed frameworks to track and analyze how diseases progress over time.

Another example by Lu et al. involved studying non-small cell lung cancer (NSCLC). Their research connected histological indicators of cellular heterogeneity with bulk gene expression data, helping to reveal the biological pathways influencing those image-derived features.

Furthermore, Subramanian et al. demonstrated that combining image-based phenotypic

information with genomic data provides a more comprehensive framework for analysis. This integrative strategy helps address the challenges posed by tissue heterogeneity and enhances the reliability of associations drawn between histology and gene-level variations.

The integration of pathology, radiology, and genomic data in cancer research has opened new avenues for developing predictive and diagnostic models. However, several core challenges continue to limit the translation of such approaches into clinical practice. Key concerns include model explainability, standardization of features, generalizability of results across datasets, and access to comprehensive, well-aligned data sources.

One of the major hurdles in deep learning–based multi-modal analysis is the lack of interpretability. These models often function as "black boxes," making it difficult to trace how input features influence predictions. Although visualization techniques such as activation maps have provided some insights, handcrafted features derived from pathology and radiology images remain more interpretable because they are explicitly defined using either domain-specific or domain-neutral criteria. In multi-modal fusion studies, where features from different data types are combined, interpretability becomes even more complex. Thus, fusion strategies must not only prioritize accuracy but also maintain clarity in feature contribution. Some recent frameworks have attempted to provide partial interpretability, but a universally accepted standard for naming, extracting, and interpreting features is still missing. Open-source platforms with transparent algorithms are crucial for reproducibility and wider adoption. Efforts such as the National Cancer Institute's NICIP Code Set are steps toward encouraging standardized methodologies in cancer imaging research.

Another critical issue is generalizability. Many features and models perform exceptionally well on training datasets but fail when applied to new, unseen data. This overfitting is often due to limited sample sizes, scanner-related artifacts, or staining variability in histology slides. Although cross- validation methods help to some extent, they can still be biased toward the training data.

Independent validation cohorts, stain normalization techniques, and training with diverse datasets—spanning multiple scanners and institutions—are essential to ensure model robustness. The creation and use of large, well-maintained benchmark datasets that include pathology, radiology, and genomic data are necessary to improve the reliability and applicability of predictive models.

Furthermore, data availability and compatibility pose practical limitations. Constructing effective multi-modal models requires access to synchronized data across imaging and molecular modalities. Projects like The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA) serve as foundational resources. TCGA offers a rich collection of genomic and clinical data along with digitized histological slides, while TCIA complements it with radiological images for overlapping patient cohorts. Despite these resources, missing data in one or more modalities is common.

Therefore, multi-modal models must be flexible enough to handle incomplete data inputs and still produce meaningful results. Recent advances, such as spatially co-registered datasets using patient-specific molds to align MRI with histology images, represent promising directions for bridging modality gaps and enhancing integration.

In conclusion, while multi-modal cancer research holds immense promise, addressing the challenges of explainability, standardization, generalizability, and data availability is essential for successful clinical translation. Continued efforts in algorithm transparency, validation with diverse cohorts, and development of standardized, accessible datasets will play a pivotal role in advancing this field.

3. Imaging clinical trials

Precision oncology trials often face low enrolment rates, partly because identifying eligible patients at the right time when they're likely to change treatment is difficult. To tackle this, a pilot program at a leading cancer centre introduced artificial intelligence to assist in real-time patient identification. Neural networks were used to analyse radiology reports and flag patients with solid tumours who were likely to begin new systemic therapies. These predictions were cross- referenced with Match Miner, a genomic matching platform, to generate trial matches based on tumour sequencing data.

Each week, a prioritized list of genomically matched patients ranked by likelihood of treatment change was sent to an oncology nurse navigator (ONN) overseeing recruitment for nine early- phase trials. Instead of manually reviewing over 60,000 trial matches for more than 2,100 patients, the AI flagged just 3,168 high-potential matches involving 525 patients a 95% reduction in manual workload. After reviewing these matches, the ONN reached out to oncologists for 74 patients who showed strong potential for trial enrolment. However, various factors limited further action: some patients chose to remain on their current therapies (21%),

some trials lacked available slots (14%), and others were found ineligible upon ONN review (12%).

Of the 74 patients whose doctors were contacted, 10 underwent a clinical trial consultation, and five eventually enrolled. While this AI-driven approach significantly streamlined the process of identifying trial candidates, it also highlighted that improving enrolment rates in precision oncology will require addressing broader logistical and systemic challenges beyond just patient identification.

4. Wearable devices and biosensors

Digital sensor platforms are revolutionizing cancer diagnostics by merging cutting edge sensing tech with digital systems, enabling real-time and precise monitoring that's transforming how we detect and track the disease. These tools collect continuous streams of high quality data, forming the backbone of modern diagnostic approaches helping spot cancers earlier, improve diagnostic accuracy, and tailor treatments to individual patients. The urgent need for such advancements is clear, given cancer's persistent global impact, where early detection directly translates to better outcomes. Traditional methods like imaging scans and biopsies, while useful, have limitations imaging often misses early stage cancers, and biopsies are invasive with restricted applicability. Newer techniques like liquid biopsies, which analyze blood for cancer markers, represent progress but integrating them with digital sensors takes detection to the next level by offering dynamic, real-time tracking.

At their core, these platforms rely on several key components working in harmony sensors that detect biological changes linked to cancer, processors that convert raw data into actionable insights, wireless systems that transmit findings instantly, and AI-driven software that identifies patterns too subtle for manual analysis. Leading this charge are biosensors and lab on a chip devices, which miniaturize complex testing into portable tools, alongside wearable sensors that monitor health metrics continuously, much like a fitness tracker but for cancer-related signals. Cloud connectivity and AI further enhance these systems by enabling remote monitoring and smarter data interpretation, giving doctors an always-updated view of a patient's condition.

Yet challenges remain in bringing these innovations to mainstream care regulatory approvals must ensure safety and efficacy, standardization is needed so different devices and hospitals can share data seamlessly, and ethical considerations around data privacy and equitable

access require careful navigation. The ultimate promise lies in combining these sensors with AI to create adaptive, personalized cancer care where diagnoses happen faster, treatments adjust in real-time based on patient responses, and outcomes improve through precision medicine. While hurdles exist, the potential is undeniable these platforms are paving the way for a future where cancer detection is not just accurate but anticipatory, and treatment is as unique as the patient themselves.

1. Sensors that identify different physical, chemical, or biological changes and turn them into readable signals.
2. Modules that process signals by converting raw inputs from sensors into understandable data through analog-to-digital conversion.
3. Communication interfaces—both wired (e.g., USB, Ethernet) and wireless (e.g., Bluetooth, Wi-Fi, LoRa)—to transmit processed data.
4. Power units, including batteries or renewable sources like solar panels, to maintain functionality.
5. Software systems that facilitate data visualization, interpretation, and management, often enhanced by artificial intelligence or machine learning algorithms.

These systems offer multiple benefits: real-time data streaming, remote monitoring capabilities through IoT and cloud integration, automated responses based on threshold conditions, and adaptability for various settings—from compact wearables to large-scale industrial setups.

As intelligent systems continue to evolve, the synergy between digital sensor platforms and AI- driven analytics is proving invaluable. The ability to gather and process diagnostic data in real time—with minimal human intervention—is reshaping the future of cancer diagnosis. This convergence not only enhances diagnostic precision and speed but also opens the door to truly personalized oncology care.

Challenges and Limitations

As we discussed till now, the whole precision oncology depends on multiple data processing, multi- omics imaging, clinical data and integrated analysis which is the common reason to create loop holes like misguidance of ML(machine learning) due to insufficient microdata's, unrecognized combinational data, etc which causes the following challenges.

1. Integrating diverse data types in omics imaging

- Current predictive models in oncology are not incorporated in diverse data types for comprehensive analysis. Expanding integration requires developing ML algortihms capable of processing and correlating heterogenious datasets. Future advancements should explore nobel techniques and transformed models to handle complex data relationships. This expansion will unable more accurate, personalized cancer diagnostic and treatment recommendations by leveraging richer data sources.
- Improve integrations of radiology/pathology images with genomic, transcriptomic and proteomic data can reveal deeper biomarker-tumor morphology relationships. Incorporating clinical annotations as structured inputs helps AI finding in medical expertise. Advanced multimodels fusion techniques are needed to align this disparate data layers for clinically actionable insights.
- Addressing the need for larger, well-annotated, and mashed datasets for robust ML applications.

2. Applications of ML and DL(Deep Learning)

- Linking multi-omics and imaging data.
- The insufficient high quality data.
- Transfer learning (TrLe) for small datasets.
- ML models are highly predictive but due to “black box” nature the clinical trust is limited.

3. Barriers in explaining AI outputs in personalised oncology

- AI often reveals technical patterns but always lacks clinical meaningful context. They highlight predictive variables without explaining their biological or therapeutic relevance. For instance, a model may lag a biomarker without clarifying its role in disease progression or treatment response. Thereby this method focus on statistical correlations rather than actionable patient-specific medical inisight. This gaps limits there utility in real world clinical decision-making and limits trust in AI systems.
- Most tool provide broad generic explanation but fails to include relevant biological, understanding personalized infromation for patients, customized recommendations tailored to the patient’s condition.
- It needs superior quality, field specific data for training(though it can lack with some data).

4. Issues in Advancing AI in personalised cancer care

- Hybrid Models and RL (reinforcement learning) these are types of learning approaches that can be used in precision oncology so that they can provide better personalized treatment but it has a real-world validation issue where clinical trials are performed on smaller level whereas there are very less trials performed at a major level.
- AI systems in precision oncology lacks combination of different types of medical data like genomics, proteomics, medical imaging and patients clinical records that would help in creating a more complete picture of patient's cancer, allowing AI to support more accurate daignosis and treatment for various broader cancer types and their therapies.

CONCLUSIONS

Al and precision oncology are transforming cancer care by enabling early detection, personalized therapies, and dynamic treatment adjustments. However, overcoming data integration challenges, improving model transparency, and ensuring clinical applicability are critical for widespread adaptation. Collaborative efforts among researchers, clinicians, and policy makers will be essential to tackle AI's full potential in eradicating cancer.

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