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The Integration of Laboratory and Radiological Findings for Enhanced Multi-Cancer Early Detection: Implications for Improving Diagnostic Accuracy and Patient Outcomes

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Abstract

Background: Early cancer detection is vital for improving survival rates, as it allows for timely interventions. Traditional screening methods have limitations, including a narrow focus on specific cancer types and low compliance rates. Integrating laboratory and radiology findings presents an opportunity to enhance early detection strategies.

Methods: This review examines the role of integrating laboratory results and radiological imaging in early multi-cancer detection (MCED). A systematic search of relevant literature was conducted across several databases, analyzing studies exploring the effectiveness of combined diagnostic approaches in identifying malignancies at earlier stages.

Results: The findings indicate that combining laboratory and imaging data significantly enhances diagnostic accuracy and the potential for early cancer detection. Multicancer early detection tests utilizing advanced biomarkers, including circulating tumor DNA (ctDNA) and protein markers, alongside radiological assessments, have shown promising results in identifying multiple cancer types. Moreover, artificial intelligence (AI) techniques have facilitated the analysis of complex datasets, further improving screening efficiency and accuracy.

Conclusion: The integration of laboratory and radiology findings in early cancer detection represents a transformative approach to oncology. By leveraging advanced diagnostic technologies and AI, healthcare systems can enhance screening protocols, ultimately leading to improved patient outcomes. Future research should focus on standardizing these integrated approaches and assessing their long-term impact on cancer mortality rates across diverse populations.

Keywords: Multi-cancer early detection, laboratory integration, radiology, artificial intelligence, cancer screening.

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1. Introduction

Historically, the early identification of cancer has centered on methods such as the Pap test, which was established almost a century ago [1]. Early cancer detection is crucial for enhancing patient survival rates, as it facilitates timely intervention, such as the surgical excision of localized solid tumors, thereby preventing the critical metastatic phase where survival rates plummet to below 50%, even with the most

sophisticated systemic therapies [2]. Cancer often advances over many years from its original location to metastasis, providing a possibility for early identification [3]. The COVID-19 pandemic impacted healthcare systems worldwide, resulting in the delay or cancellation of nonessential medical procedures, such as cancer screenings. Recent rises in cancer-related death rates may be partially ascribed to postpones in cancer identification caused by interrupted screening programs [4].

Early cancer identification improves prognosis; nonetheless, this traditional method has significant obstacles. Indeed, a significant percentage (~57%) of cancer-related fatalities in the United States is ascribed to malignancies that now lack efficient screening methods [5]. For decades, early cancer detection has concentrated on identifying specific cancer types. These techniques include low-dose chest computed tomography (CT) for lung cancer, mammography for breast cancer, Pap smear for cervical cancer, and fecal occult blood tests for colorectal cancer [6]. While these screening technologies have markedly improved early cancer diagnosis, the cancer types they assess constitute but a subset of the comprehensive cancer spectrum [7]. Merely 14% of cancer cases in the United States are identified with recommended screening tests, underscoring the inadequacies of conventional screening techniques. The majority of cancer diagnoses are made after the onset of symptoms or during unrelated medical consultations [8]. Furthermore, cancer screening conducted by specific cancer types is cumbersome, necessitating that patients see many healthcare practitioners to complete different screening procedures. These disadvantages lead to reduced compliance with cancer screening using these approaches [9].

The insufficiency of existing cancer screening methodologies may be ascribed to many issues. These include inadequate compliance with screening standards, inequities in access to screening, constraints in current screening technology, and the manifestation of malignancies outside suggested testing intervals [10]. As a result, a considerable number of cancer cases are identified at late stages, making treatment much more difficult. For example, among malignancies with known screening techniques, the percentage of late-stage diagnosis varies from 20.9% for prostate cancer to an alarming 64.7% for lung cancer.

This introduction establishes the basis for examining the potential of multicancer early detection (MCED) techniques, which seek to transform cancer screening by tackling these obstacles. The next sections will explore advancements in MCED methodologies and the crucial role of artificial intelligence (AI) in augmenting the early diagnosis of various malignancies, hence boosting survival rates and treatment efficacy.

2. The Function of Artificial Intelligence in Multi-Cancer Early Detection

MCED encompasses the identification of various cancer forms. Certain cancer types have similar molecular tendencies, but others do not. To tackle a complex job such as MCED, substantial data is essential to provide enough information for effective discrimination. AI excels in identifying concealed patterns within complex datasets during the analysis of extensive data. Supervised machine-learning algorithms are often the effective AI methodology in the biomedical domain. Due to its exceptional efficacy in categorization and prediction, AI has been extensively used in several biological domains in recent years. The applications include associating genetic data with obesity, using liquid biopsies to predict cancer metastasis, employing clinicopathological data for cancer risk stratification, analyzing genetic data for multi-cancer early detection (MCED), and identifying protein biomarkers for MCED [11-15].

In the domain of MCED, the use of AI has shown efficacy in enhancing diagnostic performance [16]. Utilizing AI has become essential for evaluating MCED data since MCED systems often focus on several analytical tasks. Interpreting intricate patterns made of several components would be challenging without AI methodologies [16]. Although some biomarker specialists excel at deciphering complex data patterns, the interpretation process remains time-consuming and labor-intensive. The use of AI algorithms may substantially improve the MCED tools for liquid biopsy or genetic data analysis due to the vast, complex, and potentially multi-omic nature of the data produced in these procedures. AI enhances multimodal analysis by synthesizing genomic, proteomic, and metabolomic information collected from liquid biopsies, offering a comprehensive perspective for the increased precision of MCED. In the genetic data analysis of MCED, the quantity of analytical objectives is often substantial. AI enhances the study of extensive data by

adeptly identifying complex patterns and correlations, providing critical insights into cancer diagnosis, mutation profiles, and genetic variables. In addition to integrating multi-omic data, AI excels in the seamless amalgamation of mathematical results with clinical information, such as clinicopathological data, hence offering more complete health profiles. Furthermore, AI-powered MCED can assimilate and adapt to new data. The ongoing education of AI will result in perpetual enhancement of MCED. Although the precise patterns of MCED are acquired by AI, the information gained by the AI models may be articulated and compared. In summary, the use of AI in MCED would enhance its accuracy and objectivity. The notion of MCED AI is shown in Figure 1.

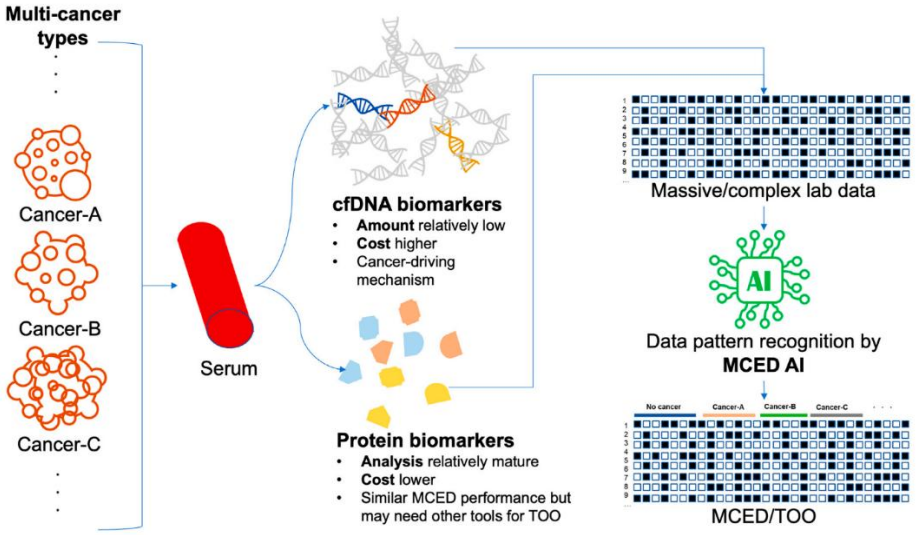

Figure 1. Diagrammatic representation of MCED, serum biomarkers, as well as MCED artificial intelligence.

Nonetheless, the diagnostic efficacy of using AI in MCED remains inconsistent across several investigations. Numerous factors may account for the uneven outcomes. A notable element is the diversity in research designs. Most relevant research employs information from case-control research for the instruction and validation of AI models [15,17]. Only a limited number of research laboratories use information from cancer screenings for the creation and evaluation of associated AI models [18]. Utilizing actual cancer screening data is crucial as it is the only means to coordinate the practical implementation of these models. AI models are reliant on data and are significantly affected by the characteristics of the training data. Should the information utilized in training the model diverge from that of the intended-use situations, the application of AI algorithms to real-world medicine would be somewhat constrained. Analytical variance across distinct ethnic groups is an additional issue that must be taken into account. The clinical sector can effectively use the potential and benefits of AI in cancer screening only when the aspects influencing AI, such as input analytical information and simulation training/validation, are well-tuned and standardized.

3. Pathway of Initial Cancer Detection Techniques

In recent years, substantial advancements have occurred in cancer screening, particularly in early detection methods. Various single-cancer screening modalities, including low-dose chest CT, mammography, Pap smear, and colonoscopy, are being used for certain malignancies. The advancement of MCED has been propelled by the acknowledgment of the constraints associated with conventional single-screening methods [19]. Unlike multimodal single-cancer screening approaches, MCED tests consolidate the incidence of many cancer types within a certain population [20]. This method offers a comprehensive assessment while maintaining a comparatively low false-positive rate [20]. Furthermore, the inconsistency in adherence to existing screening procedures has hindered cancer identification, hence prompting the creation of noninvasive multicancer screening techniques to mitigate cancer-related morbidity and death [21].

Historically, the investigation of whole-body imaging as well as endoscopic methodologies has been seen as a pathway to attaining comprehensive cancer screening [19]. Nonetheless, enduring challenges, including elevated rates of false-positives and possible repercussions from receiving radiation or invasive tests, need resolution [22-24]. Recently, a groundbreaking advancement has arisen in the manner of liquid biopsies, which examine cancer-associated biomarkers found in bodily fluids [24]. This advancement has added a revolutionary aspect to the domain, providing a less intrusive and more accessible method for early cancer diagnosis. Furthermore, AI has been used to scrutinize extensive datasets, including medical imaging and genomic information, to discern patterns and abnormalities suggestive of cancer [24]. The integration of AI into the diagnosis procedure enhances the precision and efficacy of cancer detection. In the present clinical process, MCEDs may act as a prelude to more precise cancer diagnosis. MCEDs should be seen as predictive of risk rather than diagnostic, which fundamentally modifies the acceptable degree of specificity.

Imaging modalities, including computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography (PET), possess promise in multi-cancer early detection (MCED) by offering noninvasive approaches to detect cancers in asymptomatic individuals. Nonetheless, these approaches include limits and problems. Imaging is perpetually restricted to the smallest size of a lesion that is detectable, even by artificial intelligence, on a scan. False positives arise when imaging misclassifies benign abnormalities as worrisome, resulting in superfluous testing, treatments, and psychological distress for the patient [25]. Previous research on whole-body MRI indicated that aberrant results were anticipated in around 95% of screened individuals; around 30% would need additional examinations, however, less than 2% would be classified as questionable for malignant tumors [22]. Furthermore, there exists a carcinogenic risk linked to receiving radiation from these tests [26]. Annual CT scans from ages 45 to 75 may elevate the risk of cancer death by 1.9%, equating to around 1 in 50 individuals [23].

Endoscopic procedures provide direct observation and biopsies of worrisome lesions. The advancement of innovative endoscopic technologies, including narrow-band imaging (NBI) and confocal laser endomicroscopy (CLE), has improved the capacity to identify lesions in the gastrointestinal system and other organs [27]. Nonetheless, these invasive treatments are not cost-effective and may pose hazards including hemorrhage and intestinal perforation. The observed post-colonoscopy perforation incidence is under 0.1%, although it is a considerable worry owing to its classification as a serious complication linked to elevated death rates [28].

Development of Liquid Biopsy Methodologies

Liquid biopsy has been developed as a groundbreaking method for multi-cancer early detection (MCED). This novel technique using phlebotomy significantly reduces the potential risks linked to more intrusive screening procedures. Liquid biopsy is an examination of disease-associated indicators present in human fluids, including various analytes including circulating tumor DNA (ctDNA), circulating tumor RNA (ctRNA), circulating tumor cells (CTCs), proteins, as well as metabolites [24].

In the last ten years, next-generation sequencing (NGS)-based techniques have rapidly advanced and been embraced in cancer research [29]. These approaches enabled us to detect tumor-specific genetic abnormalities in circulation [29]. Two principal avenues for tumor DNA that may be noninvasively evaluated in the circulatory system are ctDNA and CTCs [30]. Circulating tumor DNA (ctDNA) comprises diminutive nucleic acid fragments released by necrotic or apoptotic neoplastic cells [31]. Conversely, CTCs signify intact and often alive cells, perhaps arising from aggressive cellular invasion or the passive detachment of tumor cell aggregates [30]. Genomic biomarkers can provide a more comprehensive 'summary' of tumor diversity within an individual and facilitate the early detection of cancer. Numerous commercial medicines, including GRAIL, have shown remarkable efficacy in detecting various cancer forms and determining their origin in asymptomatic individuals [32].

Conversely, serum protein tumor indicators such as AFP, CEA, CA-19.9, PSA, CA-125, and others have been used for decades to assist in the diagnosis and management of many malignancies [33]. Nevertheless, owing to their very poor specificity and sensitivity for initial cancer diagnosis, the majority of international recommendations advocate their use mainly for monitoring cancer recurrence or evaluating therapeutic

response, rather than as screening instruments for early detection. A possible technique to mitigate this constraint is the integration of several serum indicators into clinical biomarker panels [33,34]. Prior studies have shown that using AI algorithms to train serum marker panels results in useful tools for cancer detection [16]. These AI algorithms frequently demonstrate elevated precision, generalizability, and affordability, positioning them as viable options for enhancing early cancer diagnosis [6,35].

Although imaging or endoscopic instruments may be precise and provide supplementary therapies in addition to diagnosis, some limitations, such as being labor-intensive, needing high technical skill, and the potential for consequences, continue to hinder the widespread use of these tools for MCED. In contrast, liquid biopsy methodologies provide potential solutions to the previously noted limitations in achieving screening objectives. This section will provide many serum indicators to facilitate multi-cancer early detection (MCED) utilizing liquid biopsy methods, illustrating different kinds of cancer.

Serum Biomarkers as Essential Indicators

Cancer cells and other cell types within the tumor microenvironment secrete soluble chemicals recognized as serum tumor markers using noninvasive diagnostic procedures. These molecules optimally identify diseases at an early stage, forecast responses, and assist in therapy monitoring. In breast cancer, various serum markers include the soluble form of the MUC-1 protein (CA15-3), carcinoembryonic antigen (CEA), circulating cytokeratins such as tissue polypeptide-specific antigen (TPS), cytokeratin 19 fragment (CYFRA 21-1), tissue polypeptide antigen (TPA), and the proteolytically cleaved ectodomain of the human epidermal growth factor receptor 2 (s-HER2). These indicators are mostly used in follow-up but are not employed in the screening of breast cancer [36].

Protein tumor indicators have not been completely used in clinical practice for diagnostic and prognostic purposes. Consequently, the transition from specific protein biomarker evaluation to protein panels or proteomes facilitates a thorough prognostic assessment for predicting disease start and development [37,38]. The protein panel evaluation far surpasses the single-biomarker assessment in enabling targeted intervention or directing therapy, particularly in cases of drug resistance. Challenges persist in the shift from individual biomarkers to proteomic sheets, including both process development and technological aspects. Recent improvements in proteomic methods have enhanced the capability to analyze numerous proteins concurrently in blood, urine, cerebrospinal fluid, or other biological samples.

The technical challenges in tumor marker assessment involve discrepancies across laboratories and variations within batches. The combinations of these variations to create a panel provide poor robustness and repeatability. Thus, the establishment of a reliable panel assay throughout time and among labs allows for the assessment of mistakes and batch variability via a singular analytical parameter assessed by a single technique. Moreover, data are compared using absolute quantitative methodologies instead of relative quantitative methods. Absolute quantification necessitates independence from affinity reagents, which are instead governed by mass spectrometry-based proteomics [39]. The US FDA has sanctioned 15 protein biomarker tests in serum and/or plasma. Among the 15 FDA-approved biomarkers of proteins for cancer, 9 are suitable for serum and 6 for serum/plasma. Despite the similarity in protein composition between plasma and serum, the expression or recovery of certain proteins differ significantly. The concentration of free PSA varies between serum and plasma [40]. The Human Proteome Organization advocates for the use of plasma in proteomics research [41].

Panel testing for proteome analysis has come to be a useful tool in cancer diagnoses; specifically, tumor proteomics is medically viable. The enzyme-linked immunosorbent test, immunohistochemistry, and flow cytometry are dependable, sensitive, and extensively used in the medical diagnosis, prediction, and therapy monitoring of cancer [42]. Alternative methodologies, including mass spectrometry, protein arrays, as well as microfluidics, are widely used and are under development for clinical application [43-45]. The extensive data generated by panel testing has been enhanced by proteomic workflows for targeted protein panel analysis, utilizing highly standardized sample preparation protocols, data-independent acquisition techniques, increased sensitivity, and accelerated mass spectrometers integrated with micro- and analytical

flow rate chromatography. Absolute quantification has enhanced statistical analysis, and comparability among studies and laboratories, and streamlined the certification of analytical procedures [46].

In 2009, OVA1 received approval for the assessment of ovarian cancers in conjunction with the quantification of five blood proteins: apolipoprotein A1, β-2 microglobulin, CA-125, transferrin, and transthyretin [47]. In 2011, ROMA was sanctioned for the prognostication of ovarian cancer in conjunction with two proteins—human epididymis protein 4 and CA-125 [48]. A total of 1261 proteins implicated in oncogenesis, tumor formation, proliferation, differentiation, apoptosis, the cell cycle, and signaling were discovered for the early detection of cancer. The USFDA has approved 9 protein biomarkers as "tumor-associated antigens" in a total of 1261 proteins. Despite the lack of approval for these protein biomarkers in MCED, their use has been implemented for over a decade in many Asian areas, including China, Taiwan, and the Republic of Korea. This strategy is popular because of its ease, allowing for the screening of several cancer types using a simple blood analysis. This encompasses several cancer forms for which no optimal screening approach exists [18]. Moreover, the expense of protein tumor marker testing is very little; the price of a single marker test may be approximately USD 10 or less, making it economically viable for extensive use. The diagnostic performance of protein biomarker panels yields around 40% sensibility and 90% accuracy [33]. In areas with readily available follow-up diagnostic methods (e.g., endoscopy, CT, and MRI), this is an efficient and competitive strategy.

In the post-Human Genome Project period, the cost of gene detection and genomics has consistently decreased, making genetic testing accessible and providing potential biomarkers, such as protein biomarkers, for multi-cancer early detection (MCED). Furthermore, genetic indicators enable the identification of cancer-driving pathways. The subsequent section will cover the evaluation of genes as biomarkers for MCED [49,50].

Cell-free DNA (cfDNA) are noninvasive biomarkers identified in serum, plasma, urine, and cerebrospinal fluid (CSF), and are increasingly preferred for cancer detection, exceeding the invasive and limited biopsy sample method [51]. It illustrates tumor heterogeneity by a thorough depiction, enabling several measurements from a single blood sample and including distinct tumor clones and locales. All cells emit cfDNA that may be derived via necrosis or apoptosis. Circulating free DNA (cfDNA) discloses mutations, methylation patterns, and variations in copy numbers potentially associated with cancer [52]. Consequently, its molecular profiling may play a significant role in noninvasive cancer care due to the emergence of ultrasensitive technologies (e.g., NGS, BEAMing, and droplet digital PCR). It has developed into a significant surrogate marker for tumor detection, staging, prognosis, localization, and the discovery of acquired treatment resistance mechanisms [53].

The sensitivity for detecting tumor-derived cfDNA is quantified by the mutant allele fraction (MAF), defined as the ratio of mutant alleles to wild-type alleles in a sample. The detection limits for MAF in quantitative PCR vary from 10% to 20% [54]. Nonetheless, changes in PCR methodologies, such as allele-specific amplification, allele-specific nonextendable primer blocker PCR, and peptide nucleic acid-locked nucleic acid PCR clamp, enhance sensitivity [55,56]. Numerous genome-wide sequencing techniques have been created over the last decade. The techniques included plasma-Seq, Parallel Assessment of RNA Ends sequencing, and altered rapid aneuploidy screening test-sequencing for cfDNA identification at 5–10% MAF [57-59]. Targeted sequencing methodologies include exome sequencing, Cancer Customized Assessment by Deep Sequencing (CAPP-Seq), and electronic sequencing [60-62]. Targeted sequencing methods have great protection, while whole-genome sequencing (WGS) methods demonstrate poor coverage. Targeted methods identify mutations at low concentrations of ctDNA, whereas whole genome sequencing evaluates copy number alterations in ctDNA. The digital PCR (dPCR) approach, including microfluidic-based ddPCR and BEAMing, achieves a reduced minor allele frequency (MAF) measured with exceptional sensitivity. The multiplexing possibilities are limited since the primers or probes are designed to target certain mutations or loci [63].

For the objective of MCED, cfDNA identifies a tumor in an asymptomatic phase with a diameter of 5 mm. The proportion of tumor-derived cfDNA to normal cfDNA of less than 1–100,000 copies indicate a tumor

size of 5 mm in diameter [64]. In blood, 1 mL of plasma contains around 3000 whole-genome equivalents, resulting in a total of 9,000,000 copies in 3 L of plasma. Within the whole cfDNA population, just one cancer genome is produced from a tumor with a diameter of 1 mm, hence diminishing the likelihood of isolating a tumor-derived cfDNA segment from a 10 mL blood sample, which is very low. Consequently, these approaches identify malignancies above 1 cm in diameter (0.5 cm^3) [64]. Unlike protein-based approaches, tumor-derived cfDNA consists of DNA fragments liberated from necrotic cancer cells, with restricted DNA copy numbers present inside a cell. Consequently, there exists a detection threshold and a possible limitation on the timing of early detection. Consequently, the identification of a cancer-associated MAF suggests the presence of cancer. Protein biomarkers are secreted in significant quantities by cancer cells, facilitating early detection; however, they lack specificity since they may also be released by normal cells [65,66].

The expense of cfDNA testing has markedly decreased in recent years, however, it remains more than five times the cost of protein biomarker arrays [5]. A significant issue is its limited half-life, which may range from a few minutes to hours [67,68]. A short half-life would lead to an unstable cfDNA concentration in the sample. Moreover, specimen preservation is a hurdle, since cfDNA may deteriorate within hours of in vitro storage. Conversely, protein indicators possess a half-life that extends over many days or even weeks [69,70]. The inherent difficulties may explain why the efficacy of cfDNA screening in MCED is not as encouraging as previously expected. Research indicates that the integration of cfDNA with protein biomarker testing does not enhance cancer effectiveness compared to the use of protein biomarkers alone [71]. Additional optimization is necessary for the use of cfDNA screening in MCED.

4. Obstacles and Prospects

The deployment of Medical Computer-Assisted Drug Delivery (MCED) AI algorithms in healthcare facilities encounters several obstacles, such as data quality and quantity, comprehension, explanation, and integration. The efficacy and applicability of MCED AI models are contingent upon the quality and amount of data, which are influenced by its properties. The intrinsic variability of datasets from diverse medical institutions and labs is a significant difficulty, resulting in discrepancies in analytical observations, biomarker assessments, and computational complications. Regional or national diversity significantly influences data collecting, since disparities in medical coverage compensation systems and medical cultures across various areas or nations might affect outcomes.

Obtaining training data that accurately reflects real-world conditions is crucial for the successful use of an MCED AI model in cancer screening. Nonetheless, the acquisition of such data sets presents considerable difficulties owing to the limited availability of cancer cases concerning healthy instances. Gathering a significant volume of instances is essential, and blockchain technology may mitigate this issue by offering incentives for patients to provide their data and establishing a cyclical compensation system for the AI model's profitability while safeguarding individual privacy.

The primary problem in deploying an MCED AI algorithm in clinical settings is the interpretation and communication of the outcomes produced by the AI models. Establishing a trusting connection between clinical doctors and AI models is a crucial initial phase for the development of MCED AIs. Clinical parameters such as age or sex are crucial inputs for medical diagnosis, and adding additional clinical aspects to MCED AI models together with serum biomarkers will provide medical practitioners with a more complete answer. Alongside delivering a rational and explicable MCDE AI approach, MCED AI models must also provide medically relevant information to effectively assimilate into existing clinical processes.

5. Conclusions

AI systems based on serum biomarkers show potential in multi-cancer early detection (MCED) and are advancing rapidly. The analytical objectives involve cfDNA, protein biomarkers, or their amalgamation. When blood biomarkers exhibit significant predictive qualities, several machine learning algorithms may provide effective diagnostic performance. The essential factor in developing a reliable MCED AI is the use of authentic mimetic data instead of a case-control approach for validation and training, ensuring a robust

application in real-world contexts. Similar to other medical goods, MCED AIs characterized by high understanding, comprehensibility, and actionability will assimilate more effectively into clinical workflows and enhance patient outcomes in early cancer detection.

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تكامل النتائج المخبرية والإشعاعية لتعزيز الكشف المبكر عن الأورام المتعددة: الآثار المترتبة على تحسين دقة التشخيص ونتائج المرضى

الملخص

الخلفية :يُعد الكشف المبكر عن السرطان أمرًا ضروريًا لتحسين معدلات البقاء على قيد الحياة، حيث يسمح بالتدخلات العلاجية في الوقت المناسب. ومع ذلك، فإن طرق الفحص التقليدية تعاني من بعض القيود، مثل التركيز الضيق على أنواع معينة من السرطان وانخفاض معدلات الامتثال. يتيح تكامل النتائج المخبرية والتصوير الإشعاعي فرصة لتعزيز استراتيجيات الكشف المبكر.

الطرق :يستعرض هذا البحث دور دمج نتائج المختبرات مع التصوير الإشعاعي في الكشف المبكر عن الأورام المتعددة .(MCED) تم إجراء بحث منهجي في العديد من قواعد البيانات لتحليل الدراسات التي تستكشف فعالية النهج التشخيصية المدمجة في تحديد أنواع السرطان المختلفة في مراحلها المبكرة.

النتائج :تشير النتائج إلى أن الجمع بين البيانات المخبرية والتصويرية يعزز بشكل كبير دقة التشخيص وإمكانية الاكتشاف المبكر للسرطان. لقد أظهرت اختبارات الكشف المبكر عن الأورام المتعددة، التي تعتمد على المؤشرات الحيوية المتقدمة، مثل الحمض النووي المنتشر للخلايا السرطانية (ctDNA)والبروتينات المرتبطة بالسرطان، إلى جانب التقييمات الإشعاعية، نتائج واعدة في تحديد أنواع متعددة من السرطان. علاوة على ذلك، ساهمت تقنيات الذكاء الاصطناعي في تحليل مجموعات البيانات المعقدة، مما أدى إلى تحسين كفاءة الفحص ودقته.

الاستنتاج :يمثل تكامل النتائج المخبرية والتصوير الإشعاعي في الكشف المبكر عن السرطان نهجًا تحوليًا في علم الأورام. من خلال الاستفادة من التقنيات التشخيصية المتقدمة والذكاء الاصطناعي، يمكن لأنظمة الرعاية الصحية تحسين بروتوكولات الفحص، مما يؤدي في النهاية إلى تحسين نتائج المرضى. ينبغي أن تركز الأبحاث المستقبلية على توحيد هذه الأساليب المدمجة وتقييم تأثيرها طويل الأجل على معدلات وفيات السرطان عبر الفئات السكانية المختلفة.

الكلمات المفتاحية :الكشف المبكر عن الأورام المتعددة، تكامل المختبرات، التصوير الإشعاعي، الذكاء الاصطناعي، فحص السرطان.