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Artificial intelligence-driven integration of multi-omics and radiomics: A new hope for precision cancer diagnosis and prognosis

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ABSTRACT

Despite advances in cancer diagnosis and treatment, the disease remains a major health challenge. Integrating multi-omics, radiomics, and artificial intelligence has improved detection, prognosis, and treatment monitoring. Molecular multi-omics provides insights into tumor biology, while radiomics extracts imaging features for outcome prediction. Liquid biopsy and circulating tumor DNA aid early detection and personalized therapy. Artificial intelligence-driven models integrate data to identify biomarkers and guide precision oncology. Despite challenges like cost and data integration, future advancements aim to enhance resolution, scalability, and non-invasive diagnostics. This mini-review explores these methodologies, their clinical impact, and their potential in personalized cancer treatment.

Keywords: Artificial intelligence; Liquid biopsy; Machine learning; Multi-omics; Precision oncology; Radiomics

1. Introduction

Although cancer diagnosis and treatment have undergone significant advancements, this disease still presents high morbidity, mortality, and healthcare costs, remaining a major global health challenge. Progress in biochemistry, molecular biology, and associated technologies has driven the emergence of multi-omics, providing new insights into cancer biology. Multi-omics is the integrated analysis of multiple biological data types to comprehensively understand biological systems. This approach aims to provide a more holistic view of cellular processes, disease mechanisms, and how different biological factors interact. By integrating these diverse datasets, multi-omics helps uncover complex relationships between genes, proteins, and other biomolecules, enabling more precise insights into health, disease, and treatment responses. Artificial intelligence (AI) advances have further transformed the analysis of the vast datasets generated by these approaches. Machine learning algorithms, in particular, can uncover complex patterns, identify biomarkers, and deliver predictions for disease progression and treatment response.

Omics research can be classified into molecular and phenotypic/clinical omics, each focusing on different aspects of biological data (Fig. 1). Molecular omics includes fields like genomics, transcriptomics, proteomics, metabolomics, and epigenomics, which analyze molecular components such as DNA, RNA, proteins, metabolites, and epigenetic modifications. Phenotypic/clinical omics deals with data derived from clinical observations and diagnostic tools, including radiomics, pathological omics (pathomics), and hematological omics. Radiomics involves extracting quantitative features from medical imaging, while pathomics integrates molecular variables with digital pathology and histopathological data. Hematological omics refers to comprehensively analyzing the molecular and cellular components of blood cells to understand the complex biology of blood-related diseases, such as leukemias, lymphomas, anemias, and other blood disorders. These categories help structure the integration of various omics data for clinical applications and AI modeling.

This mini-review explores the present and future of cancer diagnosis and prognostics by examining the integration of multi-omics, and AI. By highlighting the synergies among these approaches, we aim to illustrate their potential to advance cancer research, improve diagnostic precision, and optimize patient outcomes. We aim to provide an accessible overview to orient non-specialized readers, including oncologists, molecular biologists, and healthcare professionals. We offer a foundational understanding of these techniques and their transformative possibilities in oncology.

2. Molecular characterization of cancer and the role of liquid biopsy in biomarker discovery

Cancer is a heterogeneous disease driven by complex genetic, epigenetic, and metabolic interactions. Integrating multi-omics data with clinical information provides critical insights into these mechanisms, bridging the gap between genotype and phenotype [1]. Benchmark studies have demonstrated the power of combining omics approaches for understanding tumor biology. For instance, the integration of chromatin immunoprecipitation sequencing (ChIP-seq) and RNA sequencing (RNA-Seq) has been pivotal in elucidating gene regulatory mechanisms and the interaction between genes and proteins. A well-established example is the role of enhancer of zeste homolog 2 (EZH2) in ovarian cancer, where ChIP-seq and RNA-Seq analyses suggested that EZH2 promotes tumor cell proliferation, migration, and invasion by modulating the core steroid biosynthesis gene via H3K27me3 methylation [2]. Similarly, metabolomics and transcriptomics integration has identified sphingosine as a marker distinguishing prostate cancer from benign prostatic hyperplasia. This study also uncovered dysregulation in sphingosine-1-phosphate receptor 2 signaling, highlighting a loss of tumor suppressor function and revealing a key oncogenic pathway with therapeutic potential [3].

Circulating tumor DNA (ctDNA) analysis represents a major advancement in early cancer detection, treatment monitoring, and guiding personalized therapies through genetic mutation profiling. A landmark study reported that integrating ctDNA with DNA methylation patterns (epigenomics, or the study of changes in gene expression or cellular phenotype caused by mechanisms other than changes in the underlying DNA sequence) further enhances its ability to detect cancers at their earliest stages. Since DNA methylation dysregulation plays a key role in cancer development, progression, and immune suppression, ctDNA methylation analysis is particularly useful, as its patterns closely mirror those of tumor tissues [4]. A case in point is small-cell lung cancer, where ctDNA methylation profiling identified distinct subtypes such as SCLC-I, which was shown to exhibit enhanced responsiveness to immunotherapy and chemotherapy due to specific epigenetic and transcriptomic features [5]. The classification of these subtypes has direct implications for treatment selection and patient outcomes. In ovarian cancer, alterations in cell-free DNA (cfDNA) methylation patterns may serve as promising diagnostic and prognostic indicators, with methods like ColonSecure having superior detection accuracy compared to conventional markers [6,7]. Furthermore, ctDNA methylation has emerged as a highly effective tool in assessing minimal residual disease in solid tumors. Combining circulating free mitochondrial DNA (mtDNA) with ctDNA has also enhanced detection sensitivity [4]. A very recent study reported the creation of a dataset from formalin-fixed paraffin-embedded glioblastomas, enabling for the first time integrative transcriptional and epigenetics studies in a context that considers the degradation and fixation-derived chemical alterations of the most extended archiving format in hospitals [8].

Beyond genetic and epigenetic insights, metabolomics provides a complementary perspective by revealing metabolic alterations that drive tumor progression and identifying novel biomarkers. Large-scale metabolic profiling, using nuclear magnetic resonance or chromatography-coupled mass spectrometry, has played a critical role in uncovering tumor-specific metabolic reprogramming. Seminal studies have shown that glutaminolysis, which converts glutamine to α-ketoglutarate for entry into the tricarboxylic acid cycle, is a key driver of tumor growth. This process fuels macromolecule synthesis and epigenetic modifications, influencing antioxidant defenses and mitochondrial-cytosolic metabolite transport [9]. Clinically, plasma metabolomics has revealed that elevated glutamate concentrations distinguish lung and head and neck cancer patients from healthy individuals with high diagnostic accuracy [10]. Furthermore, high plasma glutamate levels correlate with poor survival in lung cancer patients [11] and predict chemotherapy response in oral squamous cell carcinoma [12]. In addition to glutaminolysis, metabolomic studies have revealed alterations in other pathways across various cancer types, identifying potential biomarkers such as branched-chain amino acids, serine, lauric acid, hypoxanthine, and maltose [13,14].

3. Radiomics and the role of imaging biomarkers

Benchmark studies have demonstrated the predictive power of radiomics in oncology. Computed tomography-based radiomic features can forecast tumor recurrence in non-small cell lung cancer, helping clinicians refine treatment strategies [15]. However, the potential of radiomics extends beyond prediction. When integrated with machine learning, radiomics enables a more precise selection of immunotherapy candidates. For example, a pivotal study found that combining baseline neutrophil-to-lymphocyte ratios (a marker of systemic inflammation) with radiomic features such as surface-to-mass ratio and 2D kurtosis enhanced pembrolizumab response predictions, improving patient stratification and treatment outcomes [16]. Similarly, a non-invasive biomarker was developed using tumoral and peritumoral computed tomography radiomics to differentiate responders to immune checkpoint inhibitors and predict survival outcomes [17].

Emerging radiomic signatures are transforming immunotherapy personalization. The lung cancer immunotherapy radiomics prediction vector, for instance, assesses patient suitability for PD-1/PD-L1 therapy, with delta radiomics providing additional risk stratification post-treatment. A recent study reported that integrating pre- and post-treatment radiomics with clinical data significantly improves progression-free survival predictions [18]. This integration reinforces the crucial role of radiomics in guiding individualized treatment decisions for lung cancer patients receiving immune checkpoint inhibitors, providing reassurance about personalized care in oncology.

Radiomics is also gaining traction as a tool for predicting responses to radiotherapy in both primary and metastatic tumors. A meta-analysis highlighted its prognostic value in lung cancer patients undergoing curative radiotherapy [19]. Furthermore, studies suggest that radiomic models can predict outcomes in patients with brain metastases treated with stereotactic ablative radiotherapy [20]. While radiomics research is expanding to multiple cancer types, including breast, prostate, head and neck, and colorectal cancers, lung cancer remains a primary focus due to its clinical relevance and the routine availability of CT imaging. As radiomics-based predictive models continue to evolve, their integration into clinical workflows can optimize treatment selection and enhance personalized oncology.

4. Single-cell multi-omics: A high-resolution approach to cancer biology

Single-cell multi-omics enables the comprehensive integration of diverse molecular data from individual cells. Unlike bulk analyses, which average signals across cell populations, single-cell multi-omics captures cell-to-cell variability, providing insights into cellular heterogeneity, functions, and interactions. By offering a holistic view of cellular states, single-cell multi-omics transforms our understanding of cancer biology, revealing the complexity of tumors and their microenvironments.

The first step in single-cell multi-omics is isolating individual cells using fluorescence-activated cell sorting, microfluidics, or laser capture microdissection [21]. The following steps encompass several methodologies tailored to analyze specific molecular features. For example, single-cell RNA sequencing (scRNA-seq) provides a detailed view of gene expression profiles [22]. Single-cell ATAC-seq (assay for transposase-accessible chromatin using sequencing) reveals chromatin accessibility patterns that reflect regulatory element activity [23]. Emerging technologies now allow for the simultaneous measurement of multiple modalities within the same cell, such as DNA mutations, RNA expression, protein abundance, and chromatin accessibility. Techniques like CITE-seq (cellular indexing of transcriptomes and epitopes by sequencing) and SHARE-seq (single-cell combinatorial indexing for epigenomics and transcriptomics) exemplify this integration, providing comprehensive molecular snapshots that enhance our understanding of tumor cell states and transitions [24].

Single-cell multi-omics has been instrumental in identifying the cellular hierarchies and lineage trajectories within tumors. For instance, single-cell studies have identified rare cancer stem cell populations responsible for tumor initiation, progression, and relapse [25].

Additionally, this approach has revealed the diverse roles of tumor-infiltrating immune cells, including T cells and macrophages, in shaping the tumor microenvironment and modulating responses to therapy [26]. Recent single-cell analyses of glioblastomas have further delineated the crosstalk between stromal cells, immune cells, and extracellular matrix components, leading to the discovery of novel therapeutic targets and biomarkers [27].

5. The role of spatial transcriptomics in understanding tumor architecture

Spatial transcriptomics, an innovative and complementary approach to single-cell multi-omics, focuses on preserving the spatial context of gene expression within tissues. In contrast to single-cell techniques that dissociate cells, spatial transcriptomics maintains the tissue architecture, enabling researchers to analyze gene expression in relation to the physical location of cells. This methodology has revolutionized our understanding of cancer biology by unveiling spatial heterogeneity, cellular niches, and cell-cell interactions within tumor microenvironments.

The process begins with preserving tissue samples using cryopreservation or formalin fixation methods to maintain RNA integrity and spatial information. Next, tissue sections are mounted onto specialized slides containing spatially barcoded probes or oligonucleotides that capture RNA transcripts while retaining their spatial coordinates [28]. Advanced techniques such as Visium Spatial Gene Expression [29] and Slide-seq [30] enable high-resolution gene expression mapping across entire tissue sections. Furthermore, imaging-based methods like MERFISH (multiplexed error-robust fluorescence in situ hybridization) enhance spatial transcriptomics by visualizing the spatial distribution of specific RNA molecules with subcellular precision [31].

Spatial transcriptomics has proven invaluable in deciphering the organization of tumors. It has identified intratumoral heterogeneity by mapping regions with distinct gene expression signatures, often linked to differential therapeutic responses [32]. Additionally, this approach has elucidated the interactions between cancer cells and the surrounding stromal and immune cells, revealing the importance of spatially organized cellular niches in tumor progression [33].

While single-cell multi-omics and spatial transcriptomics offer transformative insights into cancer biology, their methodologies and applications are distinct yet complementary. Single-cell multi-omics provides a high-resolution molecular characterization of individual cells, capturing heterogeneity and functional diversity. In contrast, spatial transcriptomics prioritizes the spatial organization of gene expression, revealing tissue architecture and niche-specific cellular behaviors. By integrating both approaches, researchers can bridge molecular precision with spatial context, driving advancements in cancer diagnostics, biomarker discovery, and targeted therapy development.

6. Pathomics and hematological omics: Emerging areas in omics research

Pathomics and hematological omics are emerging disciplines integrating advanced molecular and computational approaches with specialized medical fields, offering deeper insights into cancer and blood disorders beyond traditional omics technologies. Pathomics is an emerging discipline that enhances tissue analysis by integrating computational and omics approaches to extract quantitative, explainable morphological features from histopathology. Traditional histopathology has long been essential for cancer diagnosis but remains limited by qualitative and manual assessments that lack reproducibility and scalability. While genomics, transcriptomics, and proteomics have significantly advanced molecular characterization, they often overlook the spatial organization and structure of tissues. Recent spatial transcriptomics and proteomics methods have begun addressing this gap, yet they still do not fully incorporate detailed morphological insights. Pathomics overcomes these challenges by systematically extracting and analyzing morphological data at a microscopic scale [34], much like radiomics does for imaging modalities such as MRI and CT. This approach enables large-scale, high-throughput quantification of tissue structures, allowing deeper exploration of disease mechanisms, tissue organization, and their relationship with molecular alterations. For example, studies have suggested that KRAS mutations in lung adenocarcinomas are associated with particular histological patterns, such as acinar and solid growth patterns [35]. In addition, pathomics represents a promising area of research for analyzing tumor heterogeneity, potentially identifying cellular subpopulations that exhibit distinct molecular profiles influencing disease progression and drug resistance. However, further studies are needed to establish its full role.

Conversely, hematological omics applies genomics, transcriptomics, proteomics, and metabolomics to blood cancers and other hematologic diseases, refining our understanding of the molecular and genetic mechanisms that drive these conditions. Genomic studies identify key mutations, such as JAK2 in myeloproliferative neoplasms or TP53 in acute myeloid leukemia, which have diagnostic and prognostic significance and inform targeted therapies [36]. Transcriptomics reveals gene expression signatures associated with different leukemia or lymphoma subtypes, while proteomics helps identify biomarkers for early diagnosis, prognosis, and treatment monitoring [37]. Integrating these omics data with digital pathology may enhance precision medicine, offering more accurate classifications, personalized treatment plans, and improved patient outcomes. In clinical practice, these technologies support early disease detection, minimal residual disease monitoring, and relapse prediction, providing valuable tools for optimizing therapeutic strategies.

7. AI-driven multi-omics and radiomics in precision oncology

AI encompasses the development of computational systems capable of performing tasks that typically require human intelligence, such as pattern recognition, decision-making, and problem-solving. These systems rely on algorithms, machine learning models, and neural networks to simulate cognitive functions and enhance their performance through data-driven learning. Several AI tools are particularly suited for integration with multi-omics data. For instance, machine learning includes algorithms like random forests, support vector machines, and gradient boosting models, which are used for feature selection and predictive analytics by identifying patterns in complex datasets. Deep learning involves advanced neural networks such as convolutional neural networks for analyzing medical images in radiomics, recurrent neural networks for processing transcriptomic time-series data, and transformer-based architectures for multi-omics integration. Graph neural networks are designed to integrate heterogeneous omics datasets while capturing complex biological interactions. Additionally, federated learning is a privacy-preserving AI approach that enables multiple institutions to collaboratively train models without sharing raw patient data, thus ensuring data security while improving predictive capabilities [38-40]. These approaches, as outlined, form the basis for integrating AI tools with multi-omics data, driving significant advancements in clinical prediction and personalized treatment strategies.

Integrating AI with multi-omics has led to significant advances in clinical prediction, enabling more accurate cancer diagnosis, prognosis, and treatment personalization. Table 1 summarizes key omics approaches, their biological focus, clinical applications, benchmark studies, and representative databases that have contributed to the field. Genomics analyzes genetic alterations, including mutations, single nucleotide polymorphisms, and copy number variations, which can drive tumorigenesis. AI models trained on large genomic datasets such as The Cancer Genome Atlas and OncoKB improve cancer risk prediction and molecular classification. Transcriptomics focuses on gene expression patterns to identify biomarkers for cancer subtypes and therapeutic response, leveraging databases like METABRIC and GTEx for AI-driven predictive analytics and precision medicine applications. Epigenomics examines DNA methylation and histone modifications that regulate gene expression, with studies from The Cancer Epigenome Atlas demonstrating the potential of AI-based models in early cancer detection and classification. Proteomics, supported by initiatives like the Clinical Proteomic Tumor Analysis Consortium, has benefited from AI-assisted analyses that identify novel prognostic and therapeutic targets through protein expression mapping. Moreover, AI models trained on metabolomics databases predict tumor behavior and therapy response, aiding personalized treatment strategies. AI-driven radiomic models successfully applied in lung and brain cancer imaging using datasets like The Cancer Imaging Archive. Integrating multiple omics layers with AI enhances predictive power, and deep learning models such as DeepMO are designed to merge genomic, transcriptomic, proteomic, and metabolomic data for improved disease stratification and treatment optimization. These benchmark studies have established the foundation for AI-driven omics integration in clinical practice, demonstrating that researchers can develop robust, clinically applicable prediction systems by leveraging large-scale datasets and advanced computational models. For a deeper understanding of these advancements and their clinical implications, readers are encouraged to explore references [41-43], which provide comprehensive insights into AI-driven multi-omics integration in cancer research.

AI algorithms, particularly deep learning models, have emerged as transformative tools in precision oncology, integrating multi-omics and radiomics to uncover complex patterns associated with cancer biology, prognosis, and treatment response (Fig. 2). For instance, a study by Chen et al. [44] showed the potential of AI in combining genomic data with radiomic features to predict overall survival in non-small cell lung cancer. The study developed a fusion model that effectively stratified patients into low- and high-risk groups with high efficacy. In another example, researchers applied AI to integrate radiology, pathology, and genomic features to predict response to PD-L1 blockade in non-small cell lung cancer patients. This multimodal model achieved a global accuracy that outperforms unimodal measures, including tumor mutational burden and PD-L1 immunohistochemistry scores.

In breast cancer, AI-driven multi-omics models have been employed to integrate transcriptomics, proteomics, and histopathological imaging data. For example, a recent study developed a convolutional neural network to analyze histopathology slides alongside transcriptomic data. The model stratified patients into risk categories with distinct survival outcomes and treatment susceptibilities and, although the obtained accuracy was modest, was higher than histopathology alone [45]. In ovarian cancer, several studies have leveraged AI to integrate clinical data, serum markers, imaging, genomics, and transcriptomics, concluding that multi-omics approaches consistently outperform single-data-type models and highlighting the potential of imaging for longitudinal tracking of tumor heterogeneity both spatially and temporally [46].

Furthermore, multi-omics-driven AI has been demonstrated to be instrumental in understanding drug resistance. A notable case is the development of PERCEPTION

(PERsonalized Single-Cell Expression-Based Planning for Treatments In ONcology), a precision oncology computational pipeline using publicly available matched bulk and single-cell expression profiles from large-scale cell-line drug screens. This approach successfully predicted responses to targeted therapies in cultured and patient-tumor-derived primary cells in two clinical trials for multiple myeloma and breast cancer and in patients with lung cancer treated with tyrosine kinase inhibitors [47].

8 Challenges and future directions

AI-driven multi-omics analysis presents a transformative opportunity to enhance precision medicine by integrating diverse biological data; however, its implementation faces several real-world challenges. One significant issue is data heterogeneity and standardization, as omics datasets originate from different platforms, protocols, and populations, leading to inconsistencies that complicate AI model training and validation. Computational and infrastructure limitations also pose obstacles, as processing and analyzing large-scale multi-omics data require significant computational power and storage, which may not be accessible to all research institutions or clinical settings [48]. Another critical challenge is the interpretability of AI models. Many of these models function as "black boxes," making it difficult for clinicians to understand their decision-making processes and integrate predictions into clinical practice [49]. Without clear explanations of how AI algorithms derive conclusions, medical professionals may struggle to trust or apply these insights effectively.

Regulatory and ethical considerations further complicate AI integration in clinical settings [50]. AI-driven clinical tools must navigate complex regulatory frameworks while addressing concerns about data privacy, patient consent, and algorithmic bias. Bias in AI models is particularly concerning, as it can lead to disparities in healthcare outcomes. If trained on non-representative datasets, AI algorithms may produce less accurate predictions for underrepresented populations, reinforcing healthcare inequities. Moreover, identifying risk factors through AI-driven analyses raises ethical dilemmas regarding potential discrimination in healthcare access, insurance policies, and employment opportunities. Individuals classified as high-risk for specific diseases could face unintended consequences, such as increased insurance premiums or differential treatment by employers. These concerns necessitate the development of fairness-aware AI models, transparent validation processes, and regulatory safeguards to prevent the misuse of genomic and clinical data.

Addressing these challenges requires strategic solutions, including improved data-sharing initiatives, federated learning approaches, and enhanced model interpretability techniques. Federated learning, which allows multiple institutions to collaboratively train AI models without sharing raw patient data, offers a privacy-preserving solution to data accessibility issues. Additionally, advances in explainable AI aim to improve model transparency, enabling clinicians to interpret predictions and integrate them more confidently into decision-making. By prioritizing these approaches, the integration of AI with multi-omics can progress toward more equitable, reliable, and clinically actionable applications, ensuring that its benefits are widely distributed while mitigating risks associated with bias and discrimination.

CRediT authorship contribution statement

Jordi Camps: Conceptualization, Formal analysis, Visualization, Writing – original draft, Writing – review & editing. **Andrea Jiménez-Franco:** Visualization, Writing – original draft, Writing – review & editing. **Raquel García-Pablo:** Visualization, Writing – original draft, Writing – review & editing. **Jorge Joven:** Writing – original draft, Writing – review & editing. **Meritxell Arenas:** Writing – original draft, Writing – review & editing.

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Declaration of competing interest

There are no conflicts of interest to disclose; all authors have read the journal's authorship statement. The manuscript has been reviewed and approved by all named authors.

Data availability

There are no original data associated with this article.

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used CHAT GPT 4.0 (developed by OpenAI) to improve the grammar, syntax, and clarity of the text and GRAMMARLY (from Grammarly Inc.) for orthographic corrections. After using these tools, the authors reviewed and edited the content as needed and took full responsibility for the content of the published article. The content, ideas, and scientific conclusions presented in this manuscript are solely the authors' work and have not been generated by AI. The AI tools were utilized exclusively to enhance the readability and presentation of the text.

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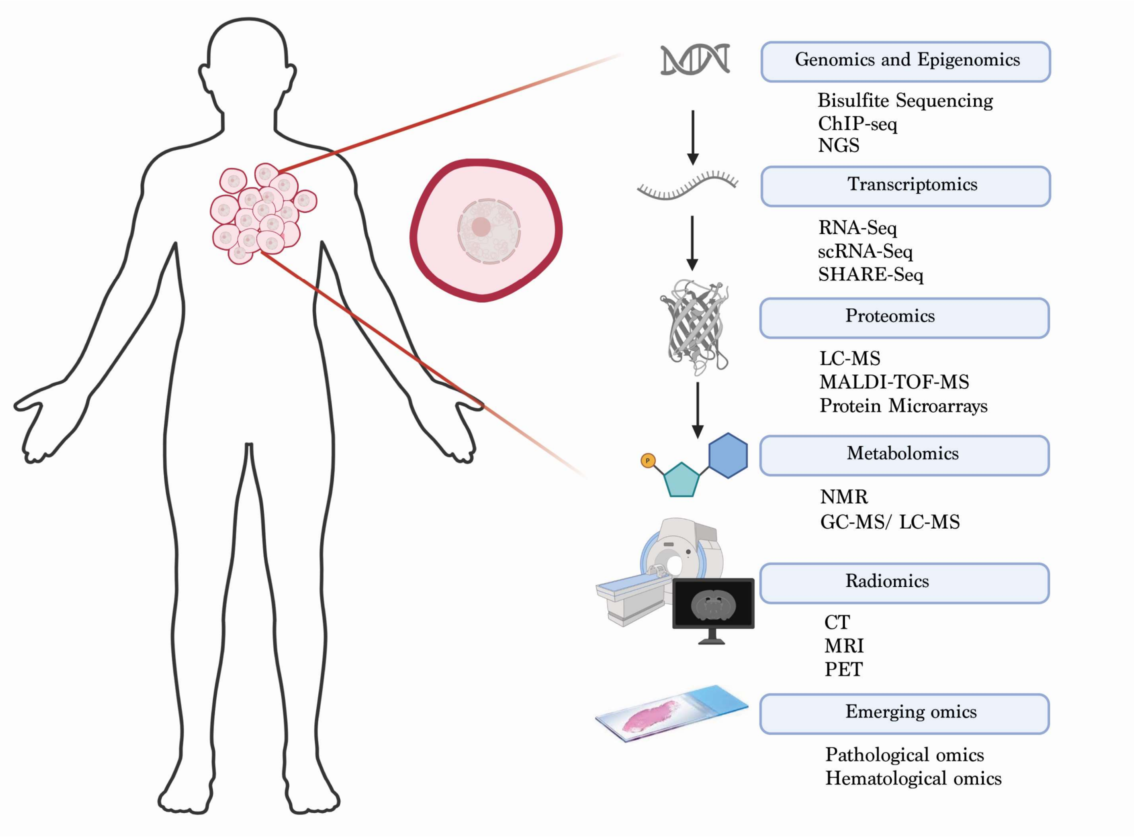
Figure legends

Fig. 1. Methodologies currently used across various omics fields. In genomics and epigenomics, key techniques include bisulphite sequencing, chromatin immunoprecipitation sequencing (ChIP-seq), and next-generation sequencing (NGS). In transcriptomics, they include RNA sequencing (RNA-Seq), single-cell RNA sequencing (scRNA-Seq), and single-cell combinatorial indexing for epigenomics and transcriptomics (SHARE-Seq). Proteomics methods involve liquid chromatography-mass spectrometry (LC-MS), matrix-assisted laser desorption ionization-time-of-flight mass spectrometry (MALDI-TOF-MS), and protein microarrays. Metabolomics employs nuclear magnetic resonance (NMR) and gas or liquid chromatography coupled to mass spectrometry (GC-MS or LC-MS). Radiomics leverages imaging modalities such as computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography (PET). Emerging areas in omics research include the comprehensive analysis of histopathological and hematological features. Created with BioRender.com.

Fig. 2. Approaches to integrating multi-omics data. Integration methods are based on analyzing correlations across omics layers, constructing molecular networks at various biological levels, and applying machine learning techniques. The ultimate objectives of these approaches are to identify disease biomarkers, elucidate phenotypic spectra and underlying mechanisms, and discover therapeutic targets. Created with BioRender.com.


Genomics and Epigenomics
Bisulfite Sequencing
ChIP-seq
NGS
Transcriptomics
RNA-Seq
scRNA-Seq
SHARE-Seq
Proteomics
LC-MS
MALDI-TOF-MS
Protein Microarrays
Metabolomics
P
NMR
GC-MS/ LC-MS
Radiomics
CT
MRI
PET
Emerging omics
Pathological omics
Hematological omics

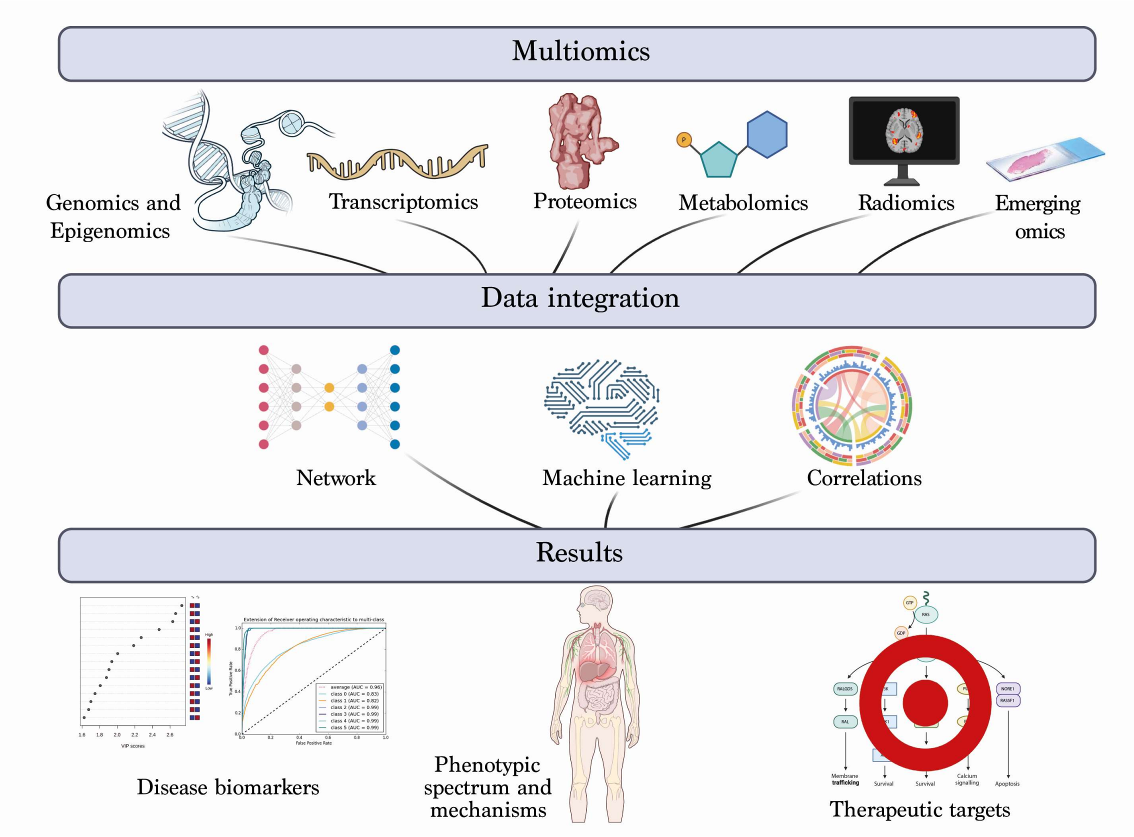

Multiomics
Genomics and Epigenomics
Transcriptomics
Proteomics
P
Metabolomics
Radiomics
Emerging omics
Data integration
Network
Machine learning
Correlations
Results
1.6
1.8
2.0
2.2
2.4
2.6
VIP scores
High
Low
Extension of Receiver operating characteristic to multi-class
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
average (AUC = 0.96)
class 0 (AUC = 0.83)
class 1 (AUC = 0.82)
class 2 (AUC = 0.99)
class 3 (AUC = 0.99)
class 4 (AUC = 0.99)
class 5 (AUC = 0.99)
Disease biomarkers
Phenotypic spectrum and mechanisms
GTP
RAS
GDP
RALGDS
RAL
NORE1
RASSF1
Membrane trafficking
Survival
Survival
Calcium signalling
Apoptosis
Therapeutic targets

Table 1

Categorization of omics approaches and their integration with clinical prediction models

Omics approach	Biological focus	Integration with clinical prediction	Key benchmark studies and databases
Genomics	Mutations, SNP, CNV	AI-driven genomic risk prediction for cancer susceptibility	TCGA https://www.cancer.gov/ccg/research/genome-sequencing/tcga OncoKB https://www.oncokb.org/
Transcriptomics	Gene expression profiles	Biomarker discovery for prognosis and treatment response	RNA-seq studies in METABRIC https://ega-archive.org/studies/EGAS00000000083 GTEx https://www.gtexportal.org/home/
Epigenomics	DNA methylation, histone modifications	Early cancer detection and classification	TCEA https://fcgportal.org
Proteomics	Protein expression and interactions	Identifying prognostic and therapeutic targets	CPTAC https://proteomics.cancer.gov/programs/cptac
Metabolomics	Metabolic pathway alterations	Predicting tumor progression and drug response	Metabolomic studies in precision oncology https://www.cancer.gov/research/infrastructure/bioinformatics
Radiomics	Imaging feature extraction	AI-based tumor characterization and response prediction	TCIA https://www.cancerimagingarchive.net/
Multi-Omics integration	Combined analysis across omics layers	Personalized medicine and treatment optimization	Pan-Cancer Atlas https://gdc.cancer.gov/about-data/publications/pancanatlas DeepMO

AI: Artificial intelligence; CPTAC: Clinical Proteomic Tumor Analysis Consortium; CNV: Copy number variation; DeepMO: Deep Learning in Multi-Omics; GTEx: Genotype-Tissue Expression project; SNP: Single nucleotide polymorphisms; OncoKB: Memorial Sloan Kettering Precision Oncology Knowledge Base; TCEA: The Cancer Epigenome Atlas; TCGA: The Cancer Genome Atlas; TCIA: The Cancer Imaging Archive.