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Cutting edge and novel approaches of Bioinformatics (OMIC technologies); packed with enhanced AI is a blessing in healthcare

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ABSTRACT

Background: Cellular processes are one of the most complex and sophisticated operations in living biological systems. They are studied piece by piece and with enhanced understanding of synchronization among these pieces, help of advanced AI software's play a key role . For this reason,Bioinformatics is growing and gaining new more improved A.I tools to solve this puzzle of pathologies that we see now a days.

Introduction: OMIC technologies help us to understand cellular processes in a more meaningful way then previously thought. Big and traditional OMIC approaches usually have been consisting of Genomics, Epigenomics, Transcriptomic and Proteomics. These protocols of understanding cellular biological processes through machine learning and AI agents has been tremendously successful in data science, preferential diagnostics and personalized treatment. But very advanced upgrades have been put forward by scientists to develop new cures for human pathologies.

Method: Data gathered and analyzed from Google scholar, PubMed and Science direct.

Result: As scientists dwelled deep into the fascinating world of intra cellular interactions; they have reported and developed something new in Bioinformatics . That is the concept of cutting edge next generation OMICS like epiomics (Epigenomics, epitranscriptomics and epiproteomics), Interactomics (DNA-RNA interactomics, DNA-protein interactomics,RNA-RNA interactomics , RNA -protein interactomics, protein-protein interactomics, protein metabolites interactomics) and Immunomics (immune genomics, immune transcriptomics, immune proteomics and immune metabolomics). All these newly found interactive behaviors and approaches in bioinformatics coupled with advanced AI software's for integrative data analysis pave the way for more development of learned ,therapeutic and targeted personalized medicines.

Conclusion: More improved AI tailored personalized medicines are in the making.

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1. Introduction

If we want to have an understanding of sophisticated processes of biological systems in a better way then it is clear that the way forward is integration. An integration that highlights the inter-associations of complex biomolecules and their operations; also incorporating the multiomics data. As the discoveries of high throughput screening techniques grows big and the presence of multiomics data obtained from large amount of data samples is quite evident ; many useful tools and beneficial methods have been made and put forward(1).A potent tool for to counter sophisticated hinderances in processing, analysis and interpretation of OMICS data is Artificial intelligence. This A.I also helps in incorporation of clinical data and multiomics data. Artificial intelligence has been a key in various scientific fields of biomedical sciences such as protein structure prediction, genome variant interpretation, drug discovery and disease diagnosis(2)

Functionalities of biological functions are determined by an organizational framework of interactions, interactions containing molecules and macromolecules that are an essential part of biochemical and physical protocols in an organized roadmap of environments. Various categories of highly specialized high throughput screening technologies (OMICS) data, permit us to gather data on cellular components of biological domains. All such technologies; for example mass spectrometry,nucleotide sequencing and DNA chips are development in such a way that they interpret large amount of molecular data at the same time. This data of specialized nature includes gene expression, protein abundances and nucleotide sequences. To form a comprehensive picture of complex biological processes, research data based on different layers needs to be integrated and evaluated. Furthermore, main difficulties that originated in this endeavor are; large number of sophistication of biological systems, technological limits as well as low number of samples makes multi-omics analysis a big challenge (3).

2. Methods and materials

To write a narrative review on latest, ,cutting edge and most advance tools, techniques and software’s of A.I in bioinformatics, literature survey was done form 2015-2025 by one author. Truncation techniques and key words were used utilized for the collection of relevant literature from the databases like PubMed, Google scholar, Emerald, National database of Indian National journals, African journals Online(AJOL), Pak Medinet , Bio line International , Biomed central, Directory of open access journals (DOJA).

Thirty four papers of Bioinformatics were downloaded and studied. After proper scrutiny via extracting appropriate information from these articles; well qualified data was assembled, compiled and presented using PRISMA flow diagram(4).The highly efficient PRISMA diagram elaborates the process of articles identification, the inferences of studies abstract after screening, the outcome of full text assessment of eligibility, detailed view of exclusion criteria(5).Each and every study was evaluated for their quality profile including novelty, journal type, statistical tests, methods, significance values and inferences made after in-depth interpretations.

Quality Standards of Literature Analysis: Highly recognized and reliable method of literature analysis; GRADE (Grading of recommendation assessment ,development and evaluation)assessment criteria was utilized for evaluation literature regarding its quality. GRADE is a specific and transparent set of protocols for efficient decision making for excellent literature evaluation(6)

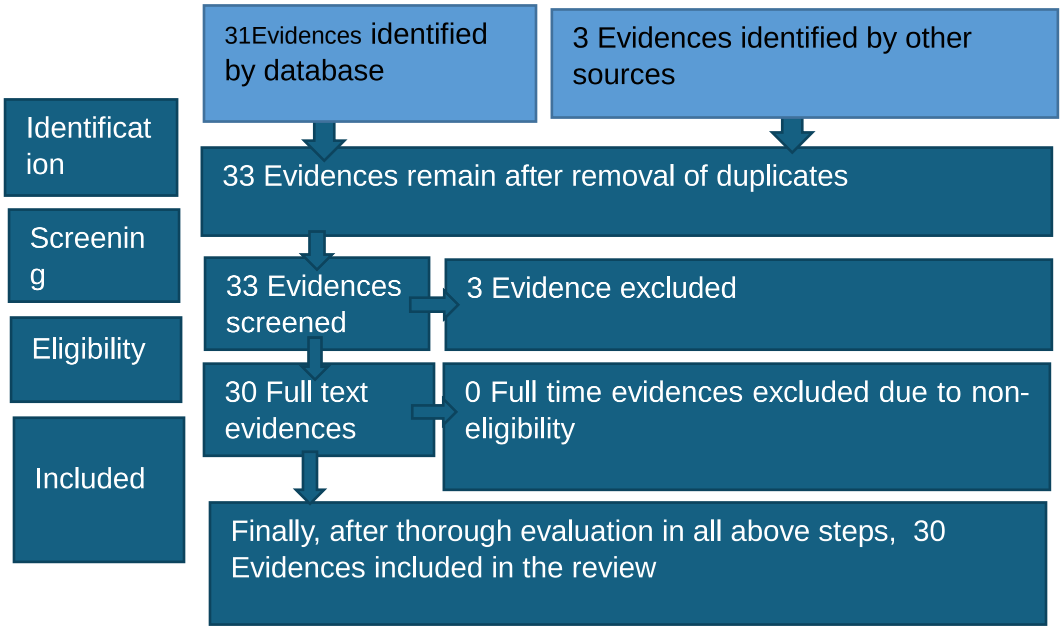

Figure 1:PRISMA diagram

3. Findings

Table 1: Highlighting the significant prospects of Epiomics via use of Advanced A.I software's in Healthcare:

OMICS domain	Concepts of A.I used in each tool	Advance A.I software And tools	Study year	Significant impact of each respective tool	Outcome of evidence	Quality of evidence
Epigenomics	Lasergene genomics utilizes SeqMan NGen for automated project setup and sequence assembly(7)	**Lasergene genomics**	2017	Single nucleotide polymorphism markers were targeted using laser gene software. Results suggest strong ,targeted and precise role of lasergene genomics.	In this study, there were many different genetic markers highlighted in various meat lines paving the way for more development of animal selection strategies(8)	Medium
	QIAGEN CLC Genomics workbench uses A.I like QiaSeq	**QIAGEN CLC Genomics workbench**	2023	Bacterial genome resequencing was the objective of this study	Future roadmap study	Low

	Panel analysis assistant for data analysis(9) and Explainable A.I for (XAI), increasing various workflows(10) and augmented molecular intelligence for enhanced quality knowledge base(10)			using QIAGEN CLC Genomics workbench ; further enhancing its role in drug discovery(11).		
	Geneious uses advance analytics and intuitive visualizations for broader anti-body molecules(12)	**Geneious**	2021	Genious help in the formation of new primers according to this study via interpretation and alignment of DNA SEQUENCES in different templates.	This study reports that Alignment of different templates of DNA sequences was done by highly important Genious bioinformatic software(13).	Low
	Geneyx leverages A.I concepts like prognostic prediction , risk prediction, diagnostic yield(14)	**Geneyx**	2023	Geneyx analysis software can be used for many multiple annotation and phenotype based prioritization for subjected genes.	In this study, genetic testing using geneyx software has an outcome of 45.5%cases(15).	medium
	Nvidia Clara for Genomics uses medical imagery to make deep learning models and medical workflows(16)	**Nvidia Clara for Genomics**	2023	Accelerating genomic workflows was the intended target of this study.	GPUs can be a good factor to efficiently enhance genomic workflows excelling the field of personalized medicine and bio-surveillance(17).	High

Epi-proteomics	Proteome discoverer allows scientists and researchers for deeper mining of proteomic data(18)	**Proteome discoverer**	2021	Proteome discoverer help greatly in protein informatics	This study focuses on how to choose among dozens of processing data and analysis pipelines present for conversion of tandem mass spectrometry files into highly valuable protein informatics(19).	high
	Maxquant uses matching between runs algorithm to enhance the stochastic of proteomics(20)	**Maxquant**	2015	Maxquant software pipeline helps in generating Proteomics Quality Control (PTXQC) for bottom-up LC–MS data.	Maxquant facilitates in highly influential quality control of proteomics via Proteomics Quality Control (PTXQC)(21).	High
	Skyline uses machine learning and deep learning	**Skyline**	2023	Skyline optimizes and predicts LC-MS/MS detection parameters of LPs which is highly influential.	In this study skyline prediction and optimization was also used to determination of the linearity and accuracy of developed analytical assay(22).	Medium
Epitranscriptomics	**DART-seq Uses mapping algorithm ; with candidate alignment processing and seed exploratory protocols(23)**	**DART-seq**	2019	The lifecycle of messenger RNA is influenced by N^6-methyladenosine (m^6A) which is a widespread RNA modification. DART seq has broadened our understanding of these (m^6A).	DART Seq characterizes thousands of m^6A sites in cells from as little as 10 ng of total RNA and can detect m^6A accumulation in cells over time. Additionally, we use long-read DART-seq to gain	High

					insights into m^{6}A distribution along the length of individual transcripts(24).	
	Deep learning (by using convulational and recurrentinal neural networks)(25)	**PAC bio analysis**	2015	PAC bio analysis has the ability to close gaps in standard reference assemblies and identify structural diversities in personal genomes.	This study indicates that PAC bio sequencing by sequencing very diverse repetitive regions and can effectively detect mutations related with different diseases(19)	high

Table 2: Providing updates on importance of Interact omics via use of Advanced A.I software's in Healthcare:

Omics domain	Concepts of A.I used in each tool	Advance A.I software and tools	Study year	Significant impact of each respective tool	Outcome of evidence	Quality of evidence
DNA-RNA interact omics	Alpha fold 3 makes predictions using diffusion network just like AI image generators(26).	**Alpha fold 3**	2024	Alpha fold has key features like that upgraded diffusion based architecture which helps it in predicting joint structure of complexes including small molecules, proteins, ions, nucleic acids and modified residues.	The conclusion of this study states that Alpha fold has much higher accuracy for protein–nucleic acid interactions compared with nucleic-acid-specific predictors as well as far greater accuracy for protein–ligand interactions compared with state-of-the-art	High

					docking tools(27)	
DNA-protein interactomics	STRING uses natural language processing as main AI concept(28)	**STRING**	2015	Major impact of Strings comes from its ability to integration of protein-protein interactions and also their critical assessment which incorporates physical and indirect operational associations.	This paper talks abouts new features added in string v10 and how they are improving the understanding of protein-protein interactions(29)	High
RNA-RNA interactomics	RNA Inter concept of AI called text mining (30).	**RNA Inter**	2020	New features of RNA inter include 1.8-Fold more interaction data and 94 additional species 2. More definite annotations are organized including RNA editing/structure/localization and homology interaction 3.advanced functions using RNA dynamic expression, interaction network and fuzzy batch search 4. Embedded RNA interactome tools Predictor, Deepmind, RIscoper, IntaRNA	From an investigational point of view, to control and regulate the roadmap of cellular RNA ;RNA inter is the one that facilitates in a complete RNA RNA INTERACTOME source(31).	High
	RNAnue Uses AI for improved hybridization potential and statistical importance to enhance prediction cycles	**RNAnue**	2021	Achievement of this tool is the inference of RNA-RNA interactions from (DDD) direct duplex detection.(32)	This study dictates that applying RNAUE to direct duplex detection data studies and it was proven that it performs very good in terms of quality and quantity of predictions(32).	high
	Mario tools uses genetic algorithms via Mario AI	**Mario tools**	2016	Biggest achievement of MARIO (Mapping RNA interactome *in vivo*) is to display RNA-RNA interactions from unperturbed cells solving long standing problem of relying on anchor protein or	This study concluded MARIO successfully inter molecule interactions	high

	simulator(33)			RNA and frequently required pertubations at molecular level.	in thousands that also provides in vivo data on RNA structures(34).	
	Encori uses algorithms for predicting binding sites(35)	**Encori/ Star base**	2021	Encori helped in Identification of a potentially novel LncRNA-miRNA-mRNA competing endogenous RNA network in pulmonary arterial hypertension via integrated bioinformatic analysis (lead by Encori)	This study indicates that pan co-expression cancer analysis and the valuable stepwise reverse prediction by ENCORI helped marked new hypothesis for molecular understanding in PAH (Pulmonary arterial hypertension)(36).	Medium
RNA-protein interactomics	ZHMolGraph uses large language models and graph neural networks to predict RNA protein interactions (37)	**ZHMolGraph**	2025	Precise computational targeting of RNA PROTEIN INTERACTION has been a major obstacle specially when dealing with unknown proteins and RNA. ZHMol Graph, provides a robust and improved method for integration of neural networks and also use non-supervised large language models that predict RNA protein interaction.	This extremely novel study dictates that ZHMolGraph was highly successful in predicting unbound RNA-protein complexes and SARSCov2 RPI (38)	high
Protein-protein interactomics	PIONEER Deep learning as AI concept	**PIONEER (protein-protein interaction interface prediction)**	2024	It basically works on the prediction capability for protein binding partner specific interfaces ; not only of all known protein interactions for humans but of seven different common model organisms to develop a robust structurally potent protein interactomes.	This study indicates that PIONEER works on identification of functional consequences of disease-associated alleles(39).	High

Protein metabolites interactomics	MIDAS uses AI to help in achieving biophysical principle of equilibrium dialysis ; ultimately assisting to understand protein metabolite regulatory network(40)	**MIDAS (mass spectrometry integrated with equilibrium dialysis for the discovery of allostery systematically**	2023	MIDAS addresses the poorly defined and understood linkage of Protein-metabolite interaction	This study reports that there are more evidences today indicating metabolites are not only the valuable substrates for metabolic functions but also have a great operational influence through their interacting protein molecules(40).	High

Table 3: Evaluating critical aspects of Immunomics via use of Advanced A.I software's in Healthcare:

Omics domain	Concepts of A.I used in each tool	Advance A.I software and tools	Study year	Significant impact of	Outcome of evidence	Quality of evidence
Immune genomics	**SC Repertoire Uses machine learning**	**SC Repertoire**	2020	It processes data derived from 10x Genomics Chromium Immune Profiling for both T-cell receptor (TCR) .	This study validates that Sc repertoire collaborates with multiple R packages for single cell expression(41)	Medium
	Immune lens Deep learning	**Immune lens**	2025	Immune lens ; it basically estimates the T-cell and B-cell	This study validates that by applying Immune lens the 100000 genome	High

				estimates, processing and sequencing data at depths of 5x coverage.	project, identification of highly sensitive genes enriched with somatic nature mutations in highly sophisticated T-cell tumors(42).	
Immune transcriptomics	**scAtlasVAE** uses AI concept of deep learning in integration of singles cell sequence data in large scales(43)	**scAtlasVAE**	2024	Sc Atlas VAE helps in creating human $CD8^+$ T cell atlas. It also helps in building computational framework and single cell referencing.	This study validates that scAtlas VAE accommodates the automatic annotation of $CD8^+$ T cell subtypes in single-cell RNA sequencing datasets (43)	High
	TISCH 2 **Machine learning and dee p learning**	**TISCH 2**	2023	This tools facilitates in appropriate characterization of gene expression analysis (covering microenvironment of tumors) in different cancer types.	This study indicates that TISCH2 helps with several new functions for better use of large scale scRNA seq datasets by its users. It also provide excellent cell-cell communications (44)	High
Immune proteomics	A.I cell (artificial immune cell) Uses AIS algorithm for clonal selection principle, affinity maturation principle and immune network theory(45)	**A.I cell (artificial immune cell)**	2022	A.I-cell ;A computational model that is able to predict immunological activities of nucleic acid nanoparticles NANP.	This study validates that the AI-CELL can and will facilitate in addressing public health obstacles that are attached to safety criteria's of NANPs (46)	High

	Deep visual proteomics uses AI to classify distinctive cell states for novel proteins(47)	**Deep visual proteomics**	2022	This landmark technology incorporates A.I enhanced image analyses of cellular phenotypes	This research indicates that deep visual proteomics can help in molecular profiling of clinical samples(48)	High
Immune metabolomics	IMA (Immunometabolic Atlas) uses AI to infer immune responses related with particular metabolites (49)	**IMA (Immunometabolic Atlas)**	2022	Capabilities of IMA includes deriving the metabolite immune process associations which is required to use protein metabolite network analysis algorithm which works on the principle of relating immune system associated annotated protein into the gene ontology and subsequently the metabolites	In this landmark study, IMA based metabolite-immune system relations using a strategy consisting of text mining ,which identifies substantial overlap, and also demonstrates a significant chemical space of immunology related metabolites that should be confirmed experimentally. Whereas, it was noted that the IMA facilitates the interpretation and design of immunometabolomics studies (49)	Medium

4. Discussion

Impact of Epiomics: (Summary of Table -1)

In Table 1 , we have tried to explain the highly novel field of epi-omics which comprises of epigenomics, epi-proteomics and epi-transcriptomics . The Concepts are quite new and are still being studied extensively by researchers of genomics as they deal with the environmental influences on complex processes of genomics, proteomics and transcriptomics. The highly valuable tools that are included in this table focuses solving issues like investigating single nucleotide polymorphism markers, bacterial genome resequencing, manufacturing of new polymers and alignment of DNA sequencing in multiple templates ,RNA modification process understanding and prediction of LC-MS/MS detection parameters of LPs which is highly influential (reference table 1).

Significance of OMICS technologies:

The system of personalized medicine applies novel protocols of molecular diagnostics ; this is done to elevate the efficacy of curing of patients and to check whether patients are prone to pathologies. For this, the development, research and implementation of modern protocols and techno logics in fields of biophysics and biomedicine are an extremely significant goal for in theses types of innovated domains of knowledge. For example, Pharmacogenomics have proven to be highly efficient in predicting the realms of metabolomics in diabetes patients. So, OMICs technologies are truly the backbone of personalized medicine evaluations; both substantially and practically(50)

Novel and cutting edge aspects of OMICS:

One of the most major reason for mortality and morbidity globally is heart attack. Conventional approaches of biomarkers to counter this phenomenon like NT-ProBNP and BNP are good but insufficient to imitate the sophistication of heart failure; specifically phenotypes with the likes of heart failure with preserved ejection fraction (HFPeF).Current developments in multi-omic technology and most cutting edge markers such as galectin-3, microRNAs (miRNAs), cell free DNA (cfDNA) have great potential for heart failure managing and evolutionary transformation. Through utilization of multi-omics technologies , involving metabolomics and lipidomics; clinicians can unravel new mechanisms, refining of hierarchical system of HF phenotypes and developmental goals of personalized therapeutic strategies to specific patient profiles can be achieved drastically. Also, technological advancements of metabolomics and proteomics; main heart failure pathways such as inflammation, fibrosis and mitochondrial dysfunction which promotes early diagnostics and therapeutic targeting(51).

Impact of Bioinformatics tools for better Healthcare:

Tools of epiomics have so many advancements which help them to perform highly valuable data mining tasks to make human life better by helping in curing diseases, these data include; insights of single nucleotide polymorphism, genomic resequencing , formation of primers , protein informatics, Identifying structural diversities in personal genomes (TABLE 1).

In interact omics; advanced software's and tools reported were known to provide key aspects to excel domains of clinical pharmacy and diagnostics. These include; prediction of complex structures of nucleic acids, control and regulation of cellular RNA, precise computational targeting of RNA protein interactions and identification of functional sequence of disease associated alleles (Table 2).

Software's of immunomics have been very useful to propagate the significance of personalized medicine and role of A.I in multi-omic integrative analysis by following; helping in single cell expression, observing cell-cell communication and also microenvironment of tumors as well as molecular profiling of clinical samples(Table 3).

Futuristic approaches of A.I in Personalized Medicine:

The compilation of precision medicine and artificial intelligence can take health care into a new era of revolution. Protocols of precision medicine helps the needy patients who are very less responsive to therapies or have many specific healthcare requirements. Artificial intelligence has to offer key complex computational and inferential insights , which allows system based framework to use logic and improve by learning and all this helps in informed clinical decision making via best possible intelligence sources. Recent literature (table 1, 2 and 3) recommends that translational research that deals with this convergence will pave the way for solving most harsh challenges of precision medicine , exclusively those of non-genomic and no-genomic determinants, this adding with data from patients clinical history, lifestyle and symptoms will enhance the domains of prognostication and personalized diagnosis(52).

5. Conclusion

Bioinformatics plays a key role in Personalization of medicine. It has comprehensive OMICS tools and technologies to understand processes of life with great detail. New and improved advancements of A.I based software's and data mining tools are allowing us to be more specific in precise and accurate targeting of diseases. Reversing progression of pathologies can become the futuristic approach in cure and health science using advanced A.I. Many of the above mentioned software's and tools are very novel and provide new paths in advancing fields and core concepts of A.I in bioinformatics like machine learning, data mining, text mining , neural networks , prediction algorithms and visualizations. This is very beneficial for the betterment of human society in terms of personalized and tailored healthcare .

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