A REVIEW ON ARTIFICIAL INTELLIGENCE AND BIOTECHNOLOGY TECHNIQUES APPLIED IN MEDICAL RESEARCH

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Abstract

Biotechnology has to do with the use of biological systems to develop useful products by applying current trend in science, technology and artificial intelligence technique. This article therefore reviews the application of artificial intelligence in current biotechnology techniques applied in advanced medical research. Artificial intelligence and biotechnology techniques applied in medical research covers areas such as therapeutics, molecular diagnosis, drug discovery, personalized medicine, and drug development. Biotechnology techniques applied in advanced medical research include flow cytometry, next generation sequencing, enzyme-linked immunosorbent assay, recombinant deoxyribonucleic acid technology, polymerase chain reaction, and electrophoresis. In conclusion, the integration of artificial intelligence and advanced biotechnology techniques in medical research has benefited humans globally in various healthcare areas namely gene therapy, diagnostics, stem cell therapy, and development of drugs such as vaccine, insulin and antibiotics.

Keywords: Artificial intelligence, biotechnology, medical, research, techniques.

1.0 INTRODUCTION

Biotechnology is the application of biological systems, living organisms, or their derivatives to develop or modify products and processes for specific industrial, medical, agricultural, and environmental applications. It has to do with deliberate and systematic manipulation of biological systems, including living cells and their components, to effectively produce or process valuable products and services aimed at enhancing human life (Saurabh and Divakar, 2018). Biotechnology integrates principles from biology, genetics, biochemistry, pharmacology, physics, chemistry, and engineering to improve medicine, healthcare, agriculture, industrial processes, and environmental management (Glick and Pasternak, 2003). Biotechnology has become a vital component of modern medicine, driving remarkable progress in medicine and healthcare. It has evolved significantly over centuries, transitioning from traditional practices to advanced molecular technologies. Ancient Biotechnology (before 1800s) use techniques such as fermentation of food and beverages [bread, wine, cheese, yogurt] (Trüeb, 2023; Demain and Adrio, 2008; Arnold, 2005); selective breeding in crops and livestock (Mushtaq *et al*., 2025; Husien *et al*., 2024; Gepts, 2004); and traditional medicine derived from plant extracts (Cowan, 1999). Biotechnology techniques applied in medical research include recombinant deoxyribonucleic acid (DNA) technology; polymerase chain reaction (PCR) for DNA amplification; bioinformatics for genetic and protein data analysis; and CRISPR-Cas9 for genome editing (Doudna and Charpentier, 2014). A pivotal technique within this field is gene editing technology, which allows scientists to achieve desired outcomes by altering the genetic composition of organisms. This process can involve creating new traits or modifying existing ones, often through the insertion of genes from one organism into another.

The advent of Artificial Intelligence (AI) continues to transform biotechnology through its ability to manage big data, pattern recognition and predictive analytics to enhance more accurate, more efficient and faster research across the different fields of biotechnology. AI has opened new frontiers in different areas of medical biotechnology research namely drug discovery and development; therapeutics; diagnostics; and personalized medicine. Artificial intelligence algorithms have demonstrated outstanding effectiveness in addressing complex biological problems, including genome sequencing, protein structure prediction, drug development, and tailored medical treatments (Jamialahmadi *et al*., 2024; Holzinger *et al*., 2023). Also, AI and machine learning (ML) models have significantly contributed to the innovative design and development of new biomaterials used in tissue engineering and regenerative medicine, thereby improving healthcare (Varshney *et al*., 2025). Furthermore, AI facilitates medical research by enabling detailed structural characterization of proteins, thereby accelerating drug discovery, enzyme engineering, diagnostics and improving the understanding of disease mechanisms.

There is need to position AI as a central technique applied in advanced medical biotechnology research. This review therefore discusses artificial intelligence and advanced biotechnology techniques applied in medical research, and also the contribution of artificial intelligence technique to medical research.

2.0 METHODOLOGY

The literature search was carried out via various electronic databases namely ScienceDirect, Google Scholar, PubMed, ResearchGate, MEDLINE and Semantic Scholar. Search terms used include “artificial intelligence”; “biotechnology”; “biotechnology techniques”; “medical research”; “biotechnology techniques applied in medical research”; “drug discovery”. “therapeutics”, “drug development’’, “personalized medicine” and “artificial intelligence applied in medical research”. The search focused on both qualitative and quantitative peer-reviewed journals.

3.0 RESULTS AND DISCUSSION

3.1. *Biotechnology Techniques Applied in Medical Research*

Biotechnology has undergone substantial changes recently with technological and methodological developments being key factors.

The biotechnology techniques applied in medical research for diagnostics, personalized medicine, drug discovery, therapeutics and drug development include recombinant DNA technology, polymerase chain reaction (PCR), enzyme-linked immunosorbent assay, Next Generation Sequencing (NGS), flow cytometry, gene cloning, gene editing technology, stem cell technology, bioinformatics, artificial intelligence, mass spectrometry, electrophoresis, microscopy, spectrophotometry and chromatography.

3.1.1. *Recombinant DNA technology*

Recombinant DNA technology (rDNA) is one of the emerging molecular biology technologies applied in medical research. This technology is increasingly used across various domains. It serves as a fundamental component in enhancing health by creating new drugs and vaccines, along with other pharmaceutical innovations. Additionally, it significantly contributes to the advancement of diagnosis and treatment through improved diagnostic kits, evaluation tools, and novel therapeutic approaches (Ullah *et al*., 2015; Roberts, 2019). Recombinant DNA technology represents a powerful approach that involves altering genetic information outside of an organism to create valuable products with improved traits. This technique effectively employs suitable vectors to facilitate the incorporation of specific DNA segments from various origins, which contain a particular gene sequence. The genetic composition of an organism can be modified by either introducing new genes (regulatory elements) or by recombining existing genes and components to modulate the expression levels of inherent genes (Bazan-Peregrino *et al*., 2013). The method of recombinant DNA technology utilizes restriction endonucleases to enzymatically cut DNA into different fragments of interest. These fragments are subsequently connected using DNA ligase enzymes to incorporate the target gene into the vector. The host organism is introduced to the vector that carries the gene of interest, and the incorporated DNA fragment is replicated throughout the culture to produce clones that contain the specific DNA segment (Venter, 2007). Therapeutics derived from recombinant proteins include insulin for diabetes management, growth hormone for growth-related disorders, vaccines for prevention of diseases, and clotting factors for hemophilia (Walsh and Walsh, 2022; Gomord *et al*., 2005).

3.1.2. *Polymerase chain reaction*

Polymerase Chain Reaction (PCR) is a potent technique for amplifying specific DNA segments. This process is conducted solely in vitro, or biochemically (Gaurav, 2024). A single-stranded DNA template is used in PCR to guide the synthesis of DNA from deoxynucleotide substrates using the enzyme DNA polymerase. DNA polymerase adds nucleotides to the 3~ end of the oligonucleotide when a custom-designed oligonucleotide is annealed to a longer template DNA. Therefore, DNA polymerase can employ a synthetic oligonucleotide as a primer and elongate its 3~ end to create an extended area of double-stranded DNA if it is annealed to a single-stranded template that contains a region complementary to the oligonucleotide (Valones *et al*., 2009). PCR is utilized in forensic laboratories and is particularly helpful because it only needs a very small amount of the original DNA. PCR is utilized in clinical specimen analysis to check for the presence of infectious agents such as HIV, hepatitis, malaria and anthrax. PCR can forecast a patient's response or resistance to treatment and offer insights on their prognosis. PCR is also used to detect tiny changes in certain genes, which are characteristic of many malignancies.

3.1.3. *Enzyme immunoassays*

The catalytic characteristics of enzymes are used in enzyme immunoassays (EIAs) to identify and measure immune responses. Clinical analyses

employ the heterogeneous enzyme immunoassay method known as enzyme-linked immunosorbent assay [ELISA] (Aydin, 2015, de la Rica and Stevens, 2012). The separation of reactants with and without labels is made easier by ELISA (Engvall, 2010). The most popular method for using the ELISA technique involves adding an aliquot of sample or calibrator containing the antigen (Ag) to be measured to a solid-phase antibody (Ab) and letting it bind. Thereafter followed by washing and introducing an enzyme-labeled antibody which forms a solid-phase Ab-Ag-Ab "sandwich complex." After washing away the unbound antibody, the enzyme substrate is applied. The amount of antigen in the sample determines how much product is produced (Konstantinou 2017, Aydin, 2015). The ELISA method, which involves binding antigen to a solid phase rather than antibody, can also be used to quantify specific antibodies. An enzyme-labeled antibody unique to the analyte antibody is the second reagent (Shah and Maghsoudlou, 2016). Furthermore, ELISA techniques have been widely utilized to identify autoantigens and viral antibodies in serum or whole blood. Additionally, ELISA-type tests with visually interpretable results have been developed using enzyme conjugates in combination with substrates that yield visible products. This assay is highly beneficial for home testing, point-of-care, and screening applications (Konstantinou, 2017).

3.1.4. *Next generation sequencing (NGS)*

Next Generation Sequencing also known as high-through put sequencing is a very powerful DNA sequencing technology which allows rapid sequencing of millions or billions of DNA fragments concurrently (Hensen *et al*., 2012). NGS allows massive parallel sequencing of DNA fragments simultaneously. Next Generation Sequencing has revolutionized genomics, expanded the knowledge on the structure of genome, its functions and dynamics. It has brought about a paradigm shift in genomics research, offering capabilities for analyzing DNA and RNA molecules in a high through put and cost-effective manner. NGS is a transformative technology that has swiftly propelled genomics advancements across diverse fields/domains. NGS allows the rapid sequencing of millions or billions of DNA fragments simultaneously providing a comprehensive insight into genetic variations, genome structure, gene expression profiles and epigenetic modifications. It has expanded the scope of genomic reseal facilitating studies on rare genetic diseases. NGS has revolutionized cancer research in identifying mutations and biomarkers for cancer diagnosis and treatment. It has also helped in infectious diseases research; drug discovery; agriculture and food safety; and played a vital role in personalized medicine by enabling tailored therapies based on individual genetic profiles.

3.1.5. *Flow cytometry*

Flow Cytometry is a technique used for the detection and measurement of the physical and chemical characteristics of a population of cells or particles as they flow in a fluid stream through a laser beam (Picot *et al*., 2012). Flow cytometry works by suspending cells in a fluid stream, passing them one after another through a laser beam and lastly detecting light scatter and fluorescence signals to analyze characteristics. Flow cytometry is used in immune phenotyping to identify and quantify different immune cell populations base on their surface makers. It also used in infectious disease diagnosis, screening for drug efficacy, detecting tumor-markers and toxicity in stern cell research.

3.1.6. *Gene cloning*

Gene cloning is a method that enables researchers to generate numerous copies of a gene or a segment of DNA. It has transformed numerous areas of biology, including genetics, healthcare, agriculture, and biotechnology. The technique entails the extraction and replication of a particular DNA sequence, such as a gene,

from an organism's DNA. The procedure begins with cutting the DNA at designated sites using enzymes known as restriction endonucleases. These enzymes identify and sever the DNA at specific sequences referred to as restriction sites, which typically range from 4 to 8 base pairs in length (Cohen, 2013). After the DNA has been cleaved, it can be incorporated into a vector, a carrier DNA molecule that can replicate separately from the host organism's genome. The primary vectors used are plasmids, which are small circular DNA structures found in bacteria. Plasmids can transport foreign DNA sequences, including genes, and can be shared among different bacterial cells. In order to integrate the DNA fragment into the plasmid, the two molecules are combined with an enzyme known as DNA ligase, which facilitates the formation of covalent bonds between them. The resulting DNA molecule created is referred to as a recombinant DNA molecule. This recombinant DNA molecule can then be inserted into a host cell, such as a bacterial cell, using a method called transformation. Once incorporated into the host cell, the recombinant DNA molecule can replicate alongside the host DNA, leading to the generation of numerous copies of the cloned gene (Yan and Zeng, 2020).

3.1.7. *Gene editing technology*

Gene editing with CRISPR-Cas9 are novel techniques that help in accurate genomic alterations. CRISPR Cas9 is a powerful gene-editing technology that uses a guide RNA (gRNA) in order to direct the Cas9 enzyme to a specific DNA sequence, where it makes a precise cut in the cells of living organisms (Frangoul *et al*., 2021). This allows Scientist to delete, insert, or modify genes with high efficiency. CRISPR Cas9 has rapidly become a powerful tool in agriculture, medicine and biotechnology. Tools such as CRISPR-Cas9 make it possible to alter genes in organisms or cells, with potential use in the treatment of genetic disorders, cancers, and infectious diseases (Zhang *et al*., 2018; Slaymaker *et al*., 2019). This powerful gene editing technique allows geneticist and medical researchers to add, remove or modify genes. These offers potential treatments for genetic disease like cystic fibrosis, sickle cell anemia and muscular dystrophy. Gene editing technology helps in improving crop traits, studying gene function and developing new models for disease research. This technology has also helped in the development of gene therapies used for the prevention and treatment of genetic illnesses.

3.1.8. *Stem cell technology*

Stem cell technology has advanced and evolved due to the inherent characteristics of stem cells. Stem cells are cells with the ability to self-renew and differentiate into various specialized cell types. These cells play a crucial role in replacing and repairing damaged tissue cells. They also have the potential to develop into a diverse array of specific functional cells that can form tissues like the liver or neurons. The differentiation process necessitates the activation or suppression of specific genes and the involvement of particular molecules or growth factors to trigger this process. Stem cells are categorized according to their potency. For instance, embryonic stem cells, which originate from the inner cell mass (ICM), are considered pluripotent, meaning they can differentiate into all cell type required to construct the human body (Jefferey *et al*., 2006). Another category of stem cells is totipotent cells, which are the initial cells produced from the division of a zygote. Stem cell technology have made it possible to generate stem cells in large quantities and to modify their characteristics for targeted therapeutic use (Trounson and McDonald, 2015; Baghbaderani *et al*., 2018).

3.1.9. *Artificial Intelligence*

Advancements in artificial (AI) tools like machine learning and deep learning contribute to effectiveness and precision across medical research which include genome editing, medical

laboratory automation and workflow optimization. AI addresses key issues in cell culture; and personalized treatments (Bagherpour *et al*., 2025). Also, AI is changing laboratory automation and workflow processes by greatly improving precision, efficiency, and decision-making within laboratory activities. The use of AI-powered robotics, advanced information systems and analytics has improved laboratory operational efficiency (Moses *et al*., 2025). In addition, AI integrated laboratory information management systems (LIMS) provide smart laboratory management, improved data quality, automation of routine tasks, smart data visualization and reporting.

3.1.10. *Bioinformatics*

Bioinformatics is an important aspect of biotechnology technique applied in medical research that makes AI relevant to biotechnology protocols. This technique involves analysis and processing of biological data; conceptualizing biological processes in molecular terms; and utilizing informatics tools from mathematics, computer science, and statistics to comprehend and organize the extensive data related to molecules (Hou *et al*., 2015). There is a corresponding rise in the tools and techniques for data management, visualization, integration, analysis, modeling, and prediction as the volume of data continues to surge at an unprecedented rate. Incorporation of AI in bioinformatics has transformed bioinformatics from using traditional techniques to smarter approaches. The combination of AI models such as machine learning (ML), deep learning (DL), natural language processing (NLP), and advanced predictive modeling is revolutionizing bioinformatics by uncovering hidden patterns, improving accuracy, and accelerating discovery. AI's transformative role in bioinformatics enables advancements in health care and medical research such as drug discovery and diagnostics (Al-Safarini and Baashirah, 2025; Zhang *et al*., 2025). Bioinformatics is also utilized across fundamental areas such as sequence analysis, gene prediction, gene expression analysis, protein and metabolite analysis, database management, and gene annotation.

3.1.11. *Mass spectrometry*

Mass spectrometry (MS) is an analytical technique that separates ionized particles such as atoms, molecules and clusters by using differences in the ratios of their changes to their masses (mass/charge; m/z) (Sparkman *et al*., 2020) and it can be used to determine the molecular weight of the particles. Mass spectrometry works by ionizing chemical compounds to general ions, separating the ions based on that mass-to-charge ration (m/z) and lastly detecting the ions and displaying the results as a mass spectrum. Steps in Mass Spectrometry involves introducing gaseous, liquid, or solid sample into the MS instrument, then bombarding the sample with energy to form ions through election impact (EI) Electrospray Ionization (ESI) or Matrix-Assisted Lase-Desorption Ionization (MALDI).The ions are accelerated by an electric field into the mass analyzer, and ions separate based on their mass-to-charge ratio with lighter ions travelling faster than heavier ones. A detector records the ions and their intensities, producing a mass spectrum (a graph of m/z verses abundance). MS is used is in the study of proteins/protein development, forensic analysis, environmental testing and identifying unknown compounds.

3.1.12. *Electrophoresis*

Electrophoresis is a key technique utilized in biochemistry, molecular biology, forensics, genetics, and biomedical research, enabling researchers to segregate macromolecules like DNA, ribonucleic acid (RNA) and proteins according to their size, shape, and electrical charge. This method has been instrumental in various major scientific advancements in the 21st century. Electrophoresis is based on the idea that charged particles will move within an

electric field by placing these particles in a conductive medium (usually a liquid or gel) and applying an electric current (Arora *et al*., 2020). The particles then travel towards the electrode that has an opposite charge (Basile et al., 2021). The velocity of these particles is influenced by a range of factors, including their charge, size, shape, the intensity of the electric field, and the characteristics of the medium they are traversing. In general, smaller particles tend to move more quickly than larger particles, while those with a stronger charge travel faster than those with a weaker charge (Wu *et al*., 2019). Electrophoresis assists in analyzing DNA and RNA fragments, which aids in identifying gene mutations linked to genetic disorders. It plays a fundamental role in the Human Genome Project, which mapped all the genes within the human genome. In the fields of biochemistry and molecular biology, electrophoresis is utilized to study the structure and function of proteins. This method can indicate the presence or absence of specific proteins, assisting in the diagnosis of various illnesses. In forensic science, DNA electrophoresis is crucial, as it is used to compare DNA samples from crime scenes with those of suspects or to establish biological relationships in paternity tests. Electrophoresis is also employed to assess the purity of drugs and to separate and identify various compounds within a mixture (Campbell *et al*., 2018, Ghashghaei *et al*., 2018).

3.1.13. *Microscopy*

Microscopy is vital in biotechnology, enabling scientists to visualize and examine cellular structures and processes across different scales. It provides essential insights into various aspects of research and development, whether it's observing tiny microorganisms or exploring intricate cellular interactions (Reigoto *et al*., 2021). Microscopy remains a fundamental component of research even with the growing reliance on sophisticated genomic and proteomic methods. The illumination of the sample using light is arguably the most crucial component of microscopy (Wang *et al*., 2022). The illumination source can be either white light or ultraviolet light. Visualization of the specimen is impossible without proper lighting. It is important to understand that all microscopic methods depend on controlling light (or electrons in the case of electron microscopy) to enhance the resolution of a specimen. Microscopy aids in recognizing various components within a sample, including microorganisms that exhibit different shapes and structures. Microscopy is also employed to evaluate cell viability by staining cells and distinguishing between those that are alive and those that are dead.

3.1.14. *Spectrophotometry*

Spectrophotometry is a method that employs light absorption to quantitatively assess substances. It evaluates the extent to which a chemical substance absorbs or transmits light at specific wavelengths. This assessment can be utilized to ascertain the concentration of the substance in a solution. Spectrophotometry finds extensive applications across various scientific disciplines, including chemistry, biology, medicine, and different fields of science and engineering. Any application involving substances or materials can utilize this technique for both quantitative and qualitative analysis. In biochemistry, for instance, it is utilized to investigate enzyme-catalyzed reactions. In medical contexts, it is employed to analyze blood or tissues for diagnostic purposes.

Additionally, there are various types of spectrophotometry, such as atomic absorption spectrophotometry and atomic emission spectrophotometry, which are used for routine analyses in hospitals, the petrochemical industry, the food industry, water quality control labs (both for purity monitoring and purification), and in chemical and biological plants (Alvarado-Lorenzo *et al*., 2024; Gore, 2000).

3.1.15. *Chromatography*

Chromatography is a biophysical technique that enables the separation, identification, and purification of the components of a mixture for qualitative and quantitative analysis (Klein *et al*., 1989). Chromatographic techniques use variations in size, charge, binding affinities, and other characteristics to separate materials. Chromatography is a method used for separating components from complex mixtures and is a potent separation tool utilized in all fields of science. Chromatography has evolved significantly throughout time, leading to increased speed, adaptability, and sensitivity. These developments have expanded its use in a variety of fields, including forensics, environmental monitoring, food safety, and pharmaceuticals (Gajos, 2024). Differential partitioning between a stationary phase and a mobile phase is the basis for chromatography. Through the stationary phase, which is usually a solid or a liquid supported on a solid, the mixture is carried by the mobile phase, which can be either a liquid or a gas. Depending on their affinities, the mixture's constituents split as it moves through the stationary phase because of their varied interactions with the stationary material. The special relationships that exist between the mixture's molecules and the stationary phase are what drive the separation process. These interactions can be driven by numerous forces, including van der Waals forces, hydrogen bonding, ionic contacts, and hydrophobic effects. The specific nature of these interactions defines the retention time of each component, which is the time it takes for a given chemical to transit through the system. When determining and measuring the mixture's constituent parts, this retention period is a crucial factor. The versatility of chromatography is one of its most intriguing features. Scientists can fine-tune the separation process to target a particular type of molecule by changing the characteristics of the stationary and mobile phases (Coskun, 2016). Chromatography techniques include gas chromatography, liquid chromatography, ion exchange chromatography, gel-permeation (molecular sieve) chromatography, chromatography, affinity chromatography, paper chromatography, thin-layer chromatography, dye-ligand chromatography, hydrophobic interaction chromatography, pseudo affinity chromatography (Debnath, 2025; Coskun, 2016).

3.2. Artificial Intelligence (AI) Applied in Medical Research

Artificial intelligence in medical research enhances the processing, analysis, and interpretation of enormous and complex biological datasets effectively. It has also contributed immensely to medical research in different areas namely drug discovery and development; therapeutics; diagnostics; and personalized medicine (Figure. 1).

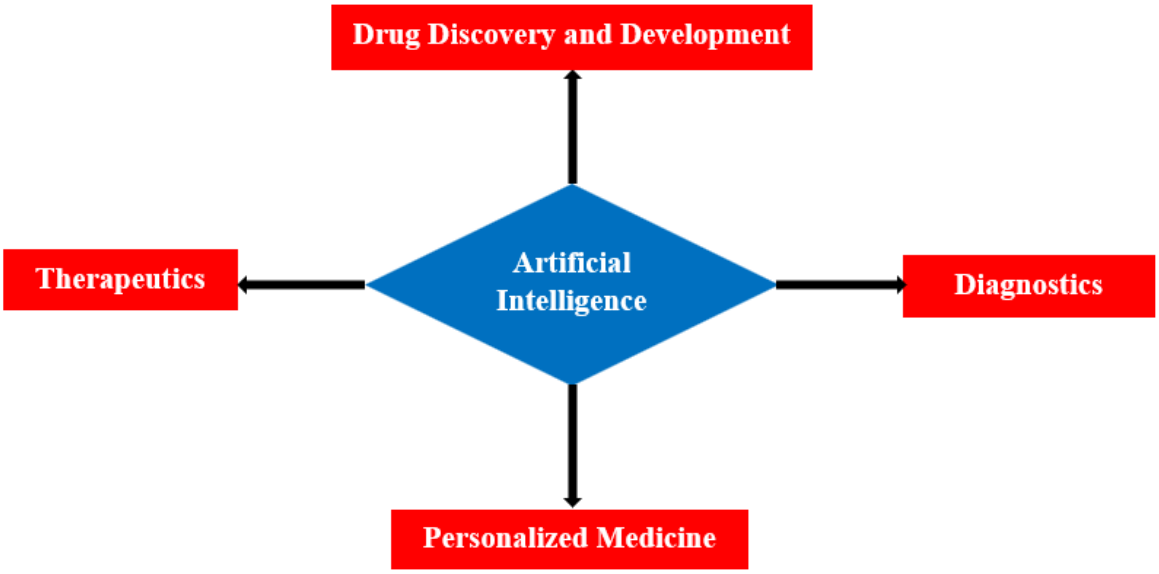

Figure 1: Artificial intelligence applied in medical research

3.2.1. *Drug discovery and development*

The absence of advanced technologies in traditional drug discovery hinders the drug development process, rendering it lengthy, costly with frequent failures. Through the integration of AI-based methodologies, these challenges can be mitigated. Artificial intelligence is restructuring drug discovery and development by leveraging its capacity to process large-scale, complex biological information, discover innovative molecules, and enhance efficiency across all stages of the drug development pipeline (Paul *et al*., 2020). Likewise, machine learning techniques are applied to identify potential drug targets, determine the 3D structures of these targets, locate binding sites, conduct ligand-based similarity assessments, and create novel ligands with specific desired characteristics. In drug discovery and development, AI aid in developing scoring functions for molecular docking, constructing Quantitative Structure-Activity Relationship (QSAR) models to predict biological activities, and forecasting the pharmacokinetics, toxicity and pharmacodynamic profiles of candidate molecules (Mannan *et al*., 2025). Other applications include, drug optimization and design, preclinical and clinical development, drug repurposing, automation and integration, drug screening, de novo drig design (Jiménez-Luna *et al*., 2021; Kant *et al*., 2025). Furthermore, AI plays a key role in poly-pharmacology by integrating and interpreting data from extensive databases such as ZINC, PubChem, and DrugBank, which contain comprehensive information on molecular pathways, binding affinities, and chemical characteristics. The integration and interpretation of these data, AI algorithms uncover intricate relationships within biological systems (Abbas *et al*., 2024). Platforms like DeepDDI exemplify AI's capabilities by predicting drug-drug interactions and suggesting alternative therapeutic applications while minimizing adverse effects (Chaudhari *et al*., 2020).

3.2.2. *Therapeutics*

AI is applied in therapeutics by improving genomics and gene editing techniques. AI improves advanced genomics and gene editing by providing tools and methods for designing, optimizing, and evaluating genomics and gene editing research. AI enhances precision,

efficiency, and safety of gene editing technologies such as clustered regularly interspaced short palindromic repeat (CRISPR)-based genome editing (CRISPR/Cas9) and other cutting-edge editing technologies thereby unlocking possibilities for better insights into genes and enhancing medical treatments (Pandey *et al*., 2025). In genome editing, AI improves efficiency of CRISPR-Cas9 by enhancing guide RNA design, forecasting the results of gene edits, and minimizing unintended genetic modifications (Mirchandani *et al*., 2025). Furthermore, the integration of AI in therapeutics plays a transformative role as it proffers innovations in biomedicine, personalized medicine and genetics. In personalized medicine, AI combined with genome editing and precision medicine facilitates the development of customized therapies designed to match an individual's distinct genetic makeup. It also allows for the detection of mutations, genetic variations, and biomarkers associated with diseases such as cancer, diabetes (Dixit *et al*., 2023). Several AI models have been used to enhance genomics and gene editing applications. These include Deep CRISPR, DeepCas9, SeqCrispr, DeepHF, and DeepSgRNA (Chuai *et al*., 2018; Xue *et al*., 2019; Liu *et al*., 2019; Wang and Zhang 2019; Shrawgi and Sisodia, 2019).

3.2.3. *Diagnostics*

AI technique is applied in diagnostics for protein structure and function prediction. In protein structure and function prediction, artificial intelligence utilizes sophisticated machine learning, deep learning, and generative modeling techniques to accurately infer the 3-D structures of proteins based on their amino acid sequences. The application of AI in this area tackles a long-standing challenge in diagnostics, as the specific 3D arrangement of a protein is crucial for determining its function and how it interacts with other molecules. Artificial intelligence is significantly advancing the field of protein structure and function prediction through several key contributions these include highly accurate prediction of protein structures directly from amino acid sequences (Anil *et al*., 2025), functional annotation by predicting protein subcellular localization, and protein design and engineering using generative AI models (Zhang and Zeng, 2025).

3.2.4. *Personalized medicine*

The use of AI systems in personalized medicine and diagnostics is being deployed in the development of treatment plans tailored towards individualized treatment plans. In addition, machine learning, deep learning, and generative modeling are used to process extensive and intricate datasets including genetic information, clinical records, medical images, and multi-omics data to customize therapies and enhance the precision of diagnoses (Fabiyi *et al*., 2025). AI and ML are being used to improve disease detection and diagnosis compared to traditional methods because of its capacity to analyze and interpret complex medical images efor instance X-rays, MRIs, CT scans and other complex patient data. AI and ML are also crucial in identifying and predicting the efficacy of new therapeutics, in addition to aiding the design and optimization of clinical trials (Al-Antari, 2023). Additionally, in personalized medicine, artificial intelligence and machine learning combine genetic data, lifestyle information, and medical history to develop individualized treatment plans that align with each patient's distinct molecular and clinical characteristics especially in diseases like cancer (Alum and Ugwu, 2025). AI diagnostics have gradually become an integral component of modern healthcare as it greatly improves the precision, speed, and effectiveness of disease detection and management. Advanced AI methods, including machine learning and deep learning techniques, improve diagnostic accuracy, enable early disease detection, process diverse data types such as bio-signals, genetic information, and

patient medical histories, which contributes to better decision-making and boosts efficiency and workflow management (Al-Antari, 2023).

Despite the advances in AI technology, limitations such as the high expenses involved, the risk of unintended or imprecise genetic modifications, challenges in efficiently delivering CRISPR components, the need to enhance editing accuracy, and ensuring safety in clinical settings still exist (Dixit *et al*., 2023).

4.0 CONCLUSION

The integration of AI in biotechnology techniques applied in medical research has helped immensely in drug discovery and development; diagnostics; therapeutics and personalized medicine. AI has significantly transformed the approach to biotechnology techniques applied in medical research. AI and medical biotechnology techniques offers solutions that not only improve quality of life but also address pressing healthcare issues globally. Application of biotechnology techniques in medical research has helped in stem cell therapy, personalized medicine, immunotherapy, and development of drugs such as insulin, antibiotics and vaccines.
It is recommended that integration of artificial intelligence in all the techniques applied in medical research may help in the creation of novel solutions to chronic diseases and complex health problems.

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