Review Article

# The Role of Artificial Intelligence in Epigenome Editing, Predictive Modeling, Disease Prognosis and Personalized Medicine

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## Abstract

The recent development in Artificial Intelligence (AI) in epigenetics and genome editing is very impressive. AI has been found to be an effective tool to revolutionize the health care industry. AI can be used to develop predictive models to identify diseases such as cancer. Another noteworthy feature of AI is to predict the most effective treatment for the patients. Predictive models for treatment response can also be achieved by AI. By using medical history and genetics, AI can accurately predict the treatment options for each patients allowing doctors to tailor treatment plans. AI is an effective tool to personalize the medicine recommendation for improving health and preventing diseases. Overall, AI has the potential in genome editing, disease prognosis, predictive modeling and personalized medicine to the particular diseases so that it revolutionizes the health care.

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## Introduction

An innovative field in molecular biology, epigenetic editing focuses on modifying the epigenetic landscape of DNA, histones, and more, leaving the underlying genetic code untouched in the process. This approach allows scientists to control gene expression in a precise manner [1,2].

CRISPR-based technologies have emerged as particularly prominent in this field, enabling targeted epigenetic modifications that can significantly influence cellular function and gene activity, especially when paired with Artificial Intelligence (AI) technology [3,4]. This method can help drive significant advancements in biomedicine and thus in understanding and addressing a wide range of medical conditions [2,4]. Monitoring disease progression is essential for effective treatment planning, particularly in chronic and progressive conditions such as cancer and neurodegenerative diseases. Tracking disease progression helps in adjusting therapeutic strategies to slow the progression based on real-time data. AI tools for progression tracking include machine learning models, predictive analytics, and deep learning algorithms [5]. These tools can process large amounts of patient data, including genetic, epigenetic, and clinical data, to identify trends and predict future disease outcomes [6]. These real-world examples demonstrate how AI-enhanced progression tracking is transforming patient care, allowing for more precise and proactive treatment adjustments, ultimately improving patient outcomes and quality of life.

Personalized medicine, or precision medicine, involves the examination of genetics, environment, lifestyle, risk factors, etc. to create a medical plan, intervention, or diagnosis tailored toward each individual. The importance of precision medicine lies in the shift toward prevention and prediction rather than reaction-based treatment. As personalized medicine continues to expand as a field, the use of epigenetics and AI as diagnostic tools is becoming increasingly common. AI capabilities in this field range from computational and virtual functions, such as deep-learning-based health records and management systems, to cyber- physical functions, such as robots used to assist during surgeries [7]. Furthermore, the use of AI is especially significant in regards to epigenetics, the study of how heritable gene activity is controlled without the modification of the DNA sequence [8]. Due to the plasticity of the human genome, which refers to the ability of a genotype to be expressed as a variety of different phenotypes, epigenetics is vital to the advancement of personalized medicine, as this field allows for the subtle nuances of each specific genome to be observed during the course of treatment [9].

## CRISPR-Based Epigenetic Editing and AI Epigenetics and the General Editing Process

Epigenetics studies how gene expression can change across generations without altering the DNA sequence itself [10]. Key mechanisms include DNA methylation, histone modifications, and non-coding RNA interactions [11-13]. In DNA methylation, a methyl group is added to cytosine within CpG

dinucleotides, which can repress transcription by either blocking transcription factors or attracting proteins that compact the chromatin, limiting access for transcription to occur [14].

Histone modifications typically activate transcription by reducing the positive charge on histones. This weakens their interaction with DNA, allowing the transcription machinery to access the genetic material more easily [15]. However, histone methylation can either activate or repress transcription, depending on which amino acids are modified and how many methyl groups are added [16,17]. Non-coding RNAs, such as microRNAs and long non-coding RNAs, play regulatory roles as well. These RNAs can guide chromatin-modifying complexes to specific genome locations or pair with mRNA to block its translation or promote degradation [2].

Epigenome editing allows scientists to modify epigenetic marks at precise genomic sites, regulating gene expression without changing the DNA sequence itself. This method employs engineered DNA-binding proteins, such as CRISPR/Cas9, zinc-finger nucleases, or TALENs, which are fused to catalytic domains that can either add or remove epigenetic modifications [18,19] (Figure 1). The targeting is highly specific, thanks to sequence recognition motifs or RNA molecules like sgRNAs in the CRISPR system, which guide the proteins to the appropriate genomic locations [20].

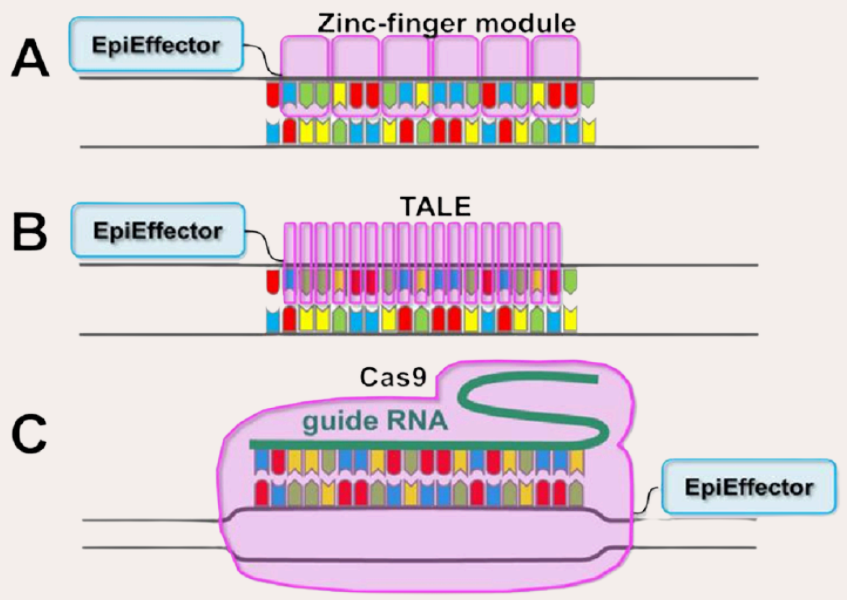


**Figure 1:** Diagram of the DNA recognition domains available for epigenomic-modifying enzymes.

Ueda J, Yamazaki T, Funakoshi H. Toward the Development of Epigenome Editing-Based Therapeutics: Potentials and Challenges. Int J Mol Sci. 2023 Mar 1;24(5):4778. doi: 10.3390/ijms24054778. PMID: 36902207; PMCID: PMC10003136.

The primary approaches to epigenome editing involve altering DNA methylation and histone modifications. For instance, DNA methyltransferases or demethylases can be directed to specific CpG sites to add or remove methyl groups, leading to gene repression or activation. Similarly, histone acetyltransferases

(HATs) or histone deacetylases (HDACs) can be recruited to change histone acetylation levels, affecting chromatin structure and gene accessibility. This targeted approach offers the possibility of long-lasting changes in gene expression, making it a powerful tool for studying gene function, understanding regulatory networks, and developing therapeutic strategies for diseases associated with abnormal epigenetic states [3].

## CRISPR-Based Epigenome Editing Process

The CRISPR-based epigenome editing process begins with the design and synthesis of a specific single guide RNA (sgRNA) that is complementary to the target DNA sequence. This sgRNA directs the dCas9 protein to the precise genomic location where epigenetic modifications are desired. The sgRNA comprises a nucleotide sequence that binds to the target DNA through base pairing and a scaffold region that interacts with the dCas9 protein [21].

Next, the Cas9 protein is modified to be catalytically inactive, creating dCas9. This dCas9 is then fused to an epigenetic modifier such as a DNA methyltransferase (DNMT), a ten-eleven translocation (TET) enzyme, a histone acetyltransferase (HAT), or a histone deacetylase (HDAC), depending on the goal of adding or removing specific epigenetic marks. This fusion allows the precise targeting of epigenetic modifications to specific genomic sites, enabling control over gene expression [2,22]. Once the sgRNA/dCas9 fusion protein complex is constructed, it is introduced into the cells, typically using a plasmid or viral vector [23]. Once inside the cell, the sgRNA guides the dCas9 fusion protein to the target DNA sequence by complementary base pairing. The dCas9 protein binds to the DNA at the target site, positioning the attached epigenetic modifier precisely at the desired location. This precise binding is crucial for ensuring that the epigenetic modifications occur only at the intended sites, minimizing off-target effects [2].

The epigenetic modifier attached to dCas9 then carries out its function at the targeted genomic locus. If the dCas9 is fused to a DNA methyltransferase (DNMT), it will add methyl groups to cytosine residues in CpG dinucleotides, leading to gene repression. Conversely, if it is fused to a TET enzyme, it will oxidize methyl groups, promoting their removal and resulting in gene activation. Similarly, histone acetyltransferases (HATs) will add acetyl groups to histone tails, promoting a more open chromatin state and increased gene expression, while histone deacetylases (HDACs) will remove acetyl groups, leading to chromatin condensation and gene repression [3].

After introducing the sgRNA/dCas9 fusion protein complex and performing the desired epigenetic modification, researchers verify the changes using various techniques. Bisulfite sequencing can detect changes in DNA methylation, while chromatin immunoprecipitation (ChIP) followed by sequencing (ChIP-seq) can analyze histone modifications. These methods confirm that the epigenetic marks were successfully added or removed at the targeted loci, ensuring the accuracy and effectiveness of the epigenome editing process [21,24].

## AI Application in CRISPR-Based Epigenome Editing

Artificial intelligence (AI) is increasingly critical in enhancing the precision and effectiveness of CRISPR-based epigenome editing. By optimizing key aspects such as single guide RNA (sgRNA) design and fusion protein engineering, AI is transforming genome editing into a more efficient and versatile tool for research and therapeutic applications [25,26].

AI's impact on sgRNA design is particularly significant. AI has revolutionized sgRNA design by utilizing machine learning algorithms trained on vast datasets of previously tested sgRNAs. These algorithms can accurately predict the most effective sgRNAs by considering DNA sequence composition, secondary structures that might impede sgRNA binding, and the local epigenetic landscape. This allows for optimized sgRNA design with enhanced specificity and efficiency, especially when targeting complex genomic regions [27].

Proteins, including those used in CRISPR-based epigenome editing, can be designed computationally with the help of AI to optimize their structure and function. For example, EED binders (EBs) are designed to recruit the Polycomb Repressive Complex 2 (PRC2) to targeted genomic regions to induce repressive chromatin states. Deep mutational scanning, combined with machine learning can contribute to leveraging structural and interaction data to predict the most effective configurations of EED binders. By analyzing the binding affinity and specificity of various protein domains, AI can refine these designs to ensure that

EED binders efficiently interact with PRC2 components, such as EED, and achieve precise histone modification. This computational approach allows for the systematic optimization of fusion proteins, enhancing their targeting accuracy and overall effectiveness in epigenetic modifications [4,28].

Furthermore, AI helps mitigate one of CRISPR's primary challenges: the risk of off-target effects. Off-target modifications can occur at sequences similar to the target, potentially causing unintended gene activation or repression. AI models address this by analyzing genomic data to identify potential off-target sites. By refining sgRNA design through AI-driven insights, researchers can significantly reduce the risk of off-target effects, enhancing the safety and reliability of CRISPR-based epigenome editing, particularly in clinical applications [29].

In summary, AI is not just a supportive tool but a transformative force in CRISPR-based epigenome editing. By streamlining sgRNA design, optimizing fusion protein engineering, and minimizing off-target effects, AI is accelerating the development of more precise and effective epigenome editing strategies.

## Clinical Applications

Epigenome editing is growing to be an innovative approach in medical research and treatment, providing precise interventions for diseases driven by dysregulated gene expression. Genetic disorders can be potentially treated, where epigenetic causes of such diseases can be addressed with the precise modulation of gene activity [3]. For instance, diseases like Fragile X syndrome which are characterized by the silencing of a critical gene can be managed by reactivating the gene using epigenome editing, creating a therapeutic path to mitigate symptoms [30].

In oncology, epigenome editing is being explored as a powerful tool for both direct and adjunctive cancer therapies. Many cancers are driven by aberrant epigenetic modifications that lead to the activation of oncogenes or the suppression of tumor suppressor genes. By reversing these modifications, epigenome editing can restore normal gene expression patterns, potentially halting the progression of cancer or even reversing malignant phenotypes [31,32]. Regenerative medicine is another area where epigenome editing shows considerable promise. The ability to precisely control the expression of genes involved in cell differentiation and proliferation opens up new possibilities for tissue repair and regeneration. For instance, modulating the expression of specific genes could enhance the regenerative capabilities of stem cells or even reprogram mature cells to adopt new identities, which could be particularly useful in treating neurodegenerative diseases or repairing damaged tissues [33].

As research continues to advance, the applications of epigenome editing in the medical field are expected to expand, offering new hope for conditions that are currently difficult to treat with conventional therapies. This technology's precision and versatility make it a valuable tool for developing personalized treatments, potentially revolutionizing how we approach complex diseases [22].

## Monitoring Disease Progression (Pranathi)

The integration of epigenetics and artificial intelligence (AI) in cancer prognosis involves a multi-step process that uses advanced computational methods to enhance disease prediction and management [34]. First, high-throughput epigenetic data, including DNA methylation profiles, histone modifications, and non-coding RNA expression levels, are collected from cancer patients using techniques like whole-genome bisulfite sequencing and RNA sequencing [35]. This raw data goes through preprocessing to eliminate noise and biases, which ensures reliability. AI algorithms then identify relevant epigenetic features associated with cancer prognosis through methods such as LASSO regression and random forests. These features train predictive models using supervised learning techniques, including neural networks and gradient boosting machines. Model validation, employing cross-validation and metrics like AUC-ROC, ensures predictive accuracy [36]. Once validated, models predict cancer prognosis in new patients based on their epigenetic profiles, with explainable AI techniques elucidating influential markers. Clinically, these AI-driven insights enable physicians to tailor treatments based on individual risk profiles, improving patient outcomes and personalizing cancer care.

Neurodegenerative diseases, such as Alzheimer's and Parkinson's, are characterized by the progressive degeneration of the nervous system, leading to a decline in cognitive, motor, and functional abilities over time. Monitoring disease progression is crucial for optimizing treatment strategies and improving patient outcomes. By leveraging epigenetic changes, which involve modifications in gene expression that do not alter the DNA sequence, researchers can gain insights into the disease's progression and tailor therapeutic

interventions accordingly. Advanced AI tools, including machine learning and deep learning algorithms, play a significant role in tracking these changes by analyzing vast amounts of genetic, epigenetic, and clinical data. For instance, AI models can evaluate medical imaging and patient records to detect patterns of cognitive decline in Alzheimer's patients, enabling more personalized and timely interventions [37]. The integration of AI in clinical practice, such as at institutions like the Mayo Clinic, enhances the ability to monitor and adjust treatment plans based on real-time data, ultimately contributing to more effective management of neurodegenerative diseases (Figure 2).

It is important to use the right type of artificial intelligence model to accurately predict diseases. The following graph illustrates the trade-off between performance and explainability across different machine learning models used for predicting neurodegenerative disease progression, such as Alzheimer's. Deep learning models (e.g., GAN, CNN, RNN) offer high performance but limited explainability, while rule-based models and decision trees provide greater interpretability at the cost of predictive accuracy. Ideal models strive to balance both performance and explainability. Ensembles like XGBoost and Random Forests offer a middle ground, combining high performance with moderate explainability. The perfect balance is necessary to provide accurate predictive modeling.

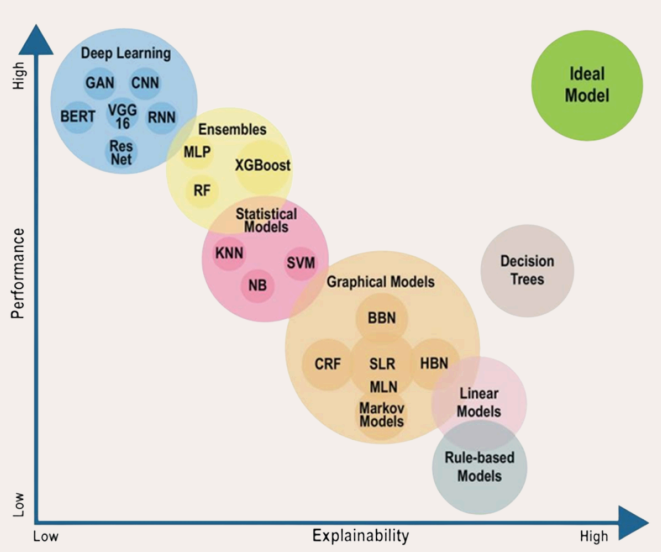


**Figure 2:** Performance vs. Explainability in AI Models for Neurodegenerative Disease Prediction.

Jain S, Singh P (2023) A framework for AI-based diagnostic and prognostic prediction in neurodegenerative diseases. Journal of Neurology and Neurorehabilitation Research 15(3): 249-261. https://doi.org/10.1038/s41598-023-40192-7.

Cardiovascular diseases (CVDs), including conditions such as coronary artery disease, hypertension, and heart failure, are a leading cause of morbidity and mortality worldwide. Effective management of CVDs requires continuous monitoring of disease progression to adapt treatment strategies and improve patient outcomes. The integration of epigenetics into cardiovascular research offers insights into how genetic expression changes contribute to disease development and progression, independent of DNA sequence alterations. AI tools, including predictive analytics and machine learning models, are increasingly employed to analyze extensive datasets from medical records, imaging studies, and genetic information. These AI systems can identify patterns and predict cardiovascular events, such as heart attacks or stroke, by evaluating risk factors and disease markers. For example, AI-driven algorithms can assess patient data to predict the likelihood of adverse cardiac events, allowing for timely intervention and personalized treatment plans [38]. Institutions like the Cleveland Clinic use AI to enhance cardiovascular care by analyzing patient histories and diagnostic data, leading to more precise and effective management strategies. The application of AI in cardiovascular health not only helps in monitoring disease progression but also in optimizing therapeutic approaches to improve patient quality of life and outcomes.

In breast cancer prognosis, predictive modeling using AI and epigenetics has shown promising applications in improving early detection, personalized treatment, and overall survival outcomes. AI models, particularly those utilizing machine learning techniques, can analyze epigenetic markers such as DNA methylation and histone modifications, which are crucial in breast cancer development and progression [39]. By integrating these epigenetic patterns with clinical data, AI algorithms can identify specific biomarkers linked to different breast cancer subtypes. For example, studies have shown that certain methylation signatures are highly associated with more aggressive forms of breast cancer, like triple-negative breast cancer, which lack targeted therapies. By incorporating these epigenetic signatures into AI models, researchers can more accurately predict disease prognosis and identify patients who may benefit from specific interventions.

Moreover, predictive models are now being designed to not only assess overall risk but also predict treatment response. Epigenetic modifications influence the expression of genes involved in drug resistance, and AI can help identify these changes early on, allowing clinicians to personalize treatment plans. For instance, epigenetic-based AI models have been developed to predict the likelihood of response to chemotherapy in breast cancer patients, leading to more tailored treatment strategies and better management of adverse effects [40]. This approach enhances decision-making and improves patient outcomes by shifting from a one-size-fits-all strategy to a more individualized approach based on precise epigenetic risk factors.

AI-driven models utilizing epigenetic data have made significant advancements in risk assessment and disease prediction. A key application is in predicting heart failure risk using DNA methylation profiles combined with clinical features. This study developed a model that integrates machine learning algorithms like LASSO and XGBoost for feature selection, followed by training with deep neural networks [41]. The model achieved high accuracy in predicting heart failure by analyzing both low-order and high-order feature interactions within epigenetic data, showcasing the potential of combining genomic and clinical data for early detection.

In cancer research, AI models integrating epigenetic factors have also proven transformative. For example, a UCLA study focused on analyzing the gene expression patterns of 720 epigenetic factors across 24 cancer types. The researchers discovered that clustering tumors based on these patterns allowed for more accurate predictions of patient outcomes, particularly in cancers such as adrenocortical carcinoma, kidney renal clear cell carcinoma, and lung adenocarcinoma [42]. The AI models outperformed traditional methods like cancer stage and grade by categorizing patients into high-risk and low-risk groups based on epigenetic markers. This breakthrough could guide personalized therapies by targeting specific chromatin regulators and other epigenetic factors linked to disease progression.

Methodologically, these models employ a blend of machine learning techniques and deep learning frameworks. Factorization-machine-based neural networks, for instance, are used to learn complex interactions between epigenetic features and clinical data. In the heart failure study, the Deep FM algorithm, incorporating DNA methylation data and electronic health records (EHRs), demonstrated enhanced predictive capability through optimized parameter settings and rigorous model validation techniques [43]. Similarly, in cancer prediction, clustering epigenetic factors allowed for the development of robust AI models that could generalize across multiple tumor types, leading to improved patient stratification and prognosis. Overall, these advancements underscore how AI and epigenetics are driving a shift toward precision medicine. By integrating complex epigenetic data with cutting-edge algorithms, these models enable more nuanced risk assessments, providing clinicians with powerful tools to tailor prevention and treatment strategies based on an individual's unique epigenetic profile.

The integration of epigenetics and artificial intelligence (AI) in disease progression tracking marks a significant advancement in personalized medicine. By analyzing vast amounts of genetic, epigenetic, and clinical data, AI tools provide real-time insights into the course of various diseases, enabling more precise and individualized treatment strategies. The application of these technologies in clinical settings, such as oncology, neurodegenerative diseases, and cardiovascular care, has already demonstrated improved patient outcomes through tailored interventions. As AI continues to evolve, its role in enhancing disease monitoring and management will only become more prominent, driving further innovation in healthcare.

Ultimately, the synergy between AI and epigenetics offers a promising pathway towards more effective and personalized treatment approaches, improving both the quality and longevity of patients' lives

## Personalized Medicine: Applications and Techniques (Pranaya)

Due to its versatility, personalized medicine applies to many aspects of healthcare. Still, it is especially so in disease detection and management, which uses genetic analyses to predict patient predisposition toward developing certain conditions or disease susceptibility. For example, in recent years, an increasing amount of research has been done on the genetic and biological factors that contribute to the formation of chronic diseases, which may include

obesity, cardiovascular disease, type 2 diabetes, autoimmune diseases, etc. Certain genetic loci, paired with may increase an individual's predisposition to being affected by many chronic diseases. However, due to the genetic diversity of many populations, data collected from one group may not apply to another [44]. Personalized medicine has also been used in oncology to treat cancer, which includes genetic testing to find specific information about an individual's cancer to create a treatment plan that delivers the correct medicine to the patient in the correct dose and at the correct time. For example, for patients with late-stage non-small cell lung cancer, conventional treatments are often ineffective. Thus, personalized medicine has been used for genetic testing to understand the nature of the cancer and to develop an appropriate medicine.

Crizotinib, which inhibits the c-ros oncogene 1 and ALK, is used for the 5% of patients who are receptive toward this anti-cancer drug. Also, for cancer treatment, next-generation sequencing (NGS), a parallel sequencing technology used to determine the order of nucleotides in a genome or targeted area of DNA, has been seen to lead to viable data for the treatment of cancerous tumors [45]. Another application of personalized medicine lies in the management of diet-related diseases. Using the precision approach healthcare providers and nutritionists are able to create a customized diet that aids the individual in managing their diet-related conditions. For example, a study using a precision nutrition approach created a personalized diet based on biochemical, anthropometric, dietary, and physical factors to predict blood glucose response, demonstrating the viability and importance of personalized medicine in this area of study [44].

## Current Innovations and Areas for Development in Personalized Medicine

Regarding the future of personalized medicine, one key innovation by the FDA is the evaluation of the safety and effectiveness of bacteriophage cocktails by using animal models to treat bacterial infections that are thought to be antibacterial resistant. Other innovations include the development of pharmacogenetic tests, which provide healthcare professionals with information about a patient's genetic makeup and how that may affect their response to treatments [46]. However, personalized medicine is not always effective. The incredibly specific nature of the field causes limited accessibility, as not all facilities are equipped to create and implement personalized treatment plans. Additionally, personalized medicine poses some ethical concerns as the heavy reliance on genetic data and personal information raises concerns about data privacy and misuse. Also, due to this usage of genetics and data, personalized medicine can be time-consuming and expensive. As personalized medicine is becoming more popular, however, scientists and healthcare providers are working to improve shortcomings in the field.

## AI and Epigenetics in Personalized Medicine

Epigenetics is immensely useful in personalized medicine. Because every individual's epigenome is different, the analysis and usage of epigenetics in precision medicine can offer the patient a more efficient and accurate treatment plan and healthcare experience. As for the application of epigenetics in personalized medicine, epigenetic disease associations are key to providing clues for disease etiology and function as diagnostic biomarkers. Epigenetics are also used in drug production, as some disease-associated epigenetic states can be counteracted with pharmacological treatments, often called 'epidrugs'. As an extension, epigenetic biomarkers are able to be used to predict drug response [47]. More than biomarkers, however, epigenetics in personalized medicine has had the most number of applications in oncology (Figure 3).

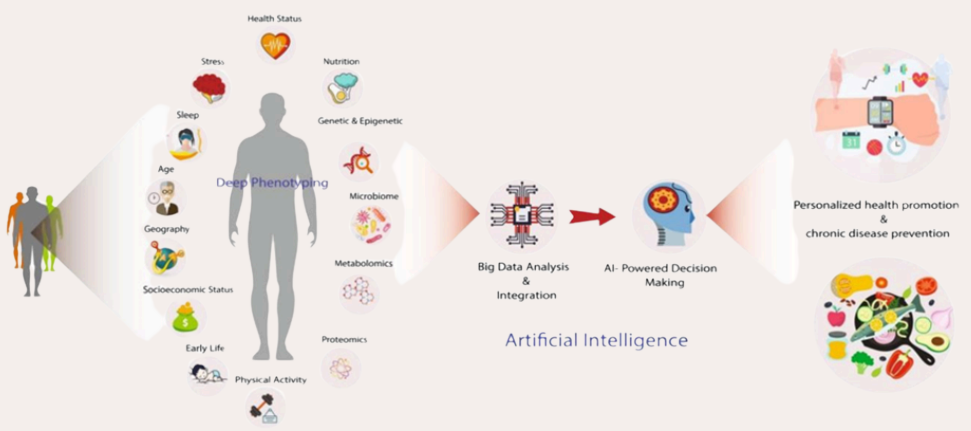


**Figure 2:** Flow Chart Depicting the Relationship Between Personalized Medicine and AI.

## Deep Learning in Personalized Medicine

One of the main aspects that allowed personalized medicine to advance as far as it has so far is AI. The specific form of AI that extracts patterns from data has been especially advantageous in furthering the field of personalized medicine. A key subset of AI, deep learning, is efficient in analyzing datasets and detecting patterns that can identify genetic variations [48]. Deep learning, more simply put, is a way of processing data done by computers that imitates the human brain by recognizing complex patterns in images, texts, sounds, etc. Thus, deep learning has been used in the diagnosis, monitoring, and treatment of many diseases. Furthermore, deep learning has greatly improved medical imaging as it provides the means for more accurate and efficient data analysis, accelerating the precision medicine approach to treatment. Deep learning is also applicable to pharmacogenomics. Researchers can predict a patient's response to a drug by analyzing their epigenome, which increases the efficiency of personalized medicine regarding treatment outcomes (Figure 3).

## Types of Deep Learning

Many forms of deep learning accomplish different goals in the personalized healthcare field. One of those, convolution neural networks, recognize patterns in medical images that can indicate a disease, based on what the system is told to 'look' for [48]. Additionally, related methods can be used to analyze changes in images over time. Another form of deep learning, artificial neural networks (ANN), a simpler version of a neural network, mimic the information processing nodes in biological systems but are static, not dynamic like an organism's biological brain [8]. Another type of ANN, recurrent neural networks (RNN), use sequential data to assist with tasks such as clinical trial participant selection, as they can be 'trained' to check if patients meet a certain amount of criteria. Of the many types of deep learning methods tested for this purpose, RNNs performed the best. Deep neural networks have a greater amount of layers than other neural networks that perform mathematical translation to convert raw data to useful information. This method has been used in tracking patient no-shows and providing possible explanations for the absence, such as weather information for the day of the appointment.

Generative adversarial networks generate photos, videos, and audios. In healthcare, they are often used to generate artificial MRI images to train deep learning models. Though there are many types of deep learning, the

aforementioned methods are predominantly used in healthcare to provide a personalized and efficient experience for the patient and provider.

## Applications of Deep Learning in Personalized Medicine

Deep learning is immensely impactful in the advancement of personalized medicine. At Stanford University, researchers developed a deep learning algorithm to analyze genomic data to aid a risk prediction model for the development of cardiovascular diseases. At the University of California San Francisco, deep learning models are being used with brain MRI data to predict the progression of Alzheimer's. Many EWASs have recognized differently methylated DNA and new genes associated with Alzheimer's. In a recent study, a deep neural network was used to predict Alzheimer's by integrating DNA methylation and gene expression. This integration greatly improves prediction accuracy [49]. Deep learning is also being included in clinical workflows to strengthen personalized medicine. In a study analyzing the connection between deep learning and cancer epigenetics, it was seen that many deep learning models can be applied to diagnose cancer epigenetics and diseases, predict methylation states, discover epigenetic biomarkers, etc. [50].

## Conclusion

Epigenome editing provides a precise method to control gene expression without changing the underlying DNA, offering new hope for treating diseases like cancer, genetic disorders, and neurodegenerative conditions. By using CRISPR technology with epigenetic modifiers, it allows targeted activation of genes and correction of abnormal epigenetic changes. As research moves forward, this approach could transform personalized medicine and improve therapies, especially in areas like oncology and regenerative medicine. The integration of epigenetics and AI has revolutionized disease progression tracking in conditions like cancer and neurodegenerative diseases. By combining thorough epigenetic data with AI models, clinicians can more accurately predict patient outcomes and personalize treatments. As AI technology continues to advance, its application in tracking disease progression will lead to even greater precision in personalized medicine, enhancing both patient outcomes and quality of life. The application of AI in the field of epigenetics essentially increases the efficiency of personalized healthcare providers, as various algorithms and methods can be applied to visualize and analyze an epigenome.

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