

ARTIFICIAL INTELLIGENCE IN GENETICS AND MOLECULAR BIOLOGY RESEARCH

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Abstract

In the field of genetics and molecular biology, Artificial Intelligence (AI) has become a game-changer, facilitating the swift interpretation of intricate genetic data and enhancing the precision of genomic studies. High-throughput sequencing methods have led to a tremendous amount of data and sophisticated computational approaches are needed to interpret these data effectively. AI applications such as machine learning, deep learning, and neural networks can aid in gene prediction, protein structure analysis, disease diagnosis, discovery of biomarkers, drug development, and precision medicine. The study involved a secondary research approach which was conducted by surveying the latest published scientific literature in the field of genetics and molecular biology, and AI. The results demonstrate the potential for AI to markedly increase the accuracy of predictions, minimize research time and aid in decision-making for biological investigations. But issues of data quality, the transparency of the algorithms, ethical and moral considerations, and computational complexity are all relevant. The study concludes that AI has emerged as a crucial asset in the field of genetics and molecular biology research, highlighting the need for responsible implementation and collaboration between various disciplines.

KEYWORDS: Artificial Intelligence, Genetics, Molecular Biology, Machine Learning, Deep Learning, Genomics, Precision Medicine, Bioinformatics

INTRODUCTION

Innovations in sequencing technologies and computational sciences have brought great advances to genetics and molecular biology in the last 20 years. The increasing amounts of data in modern biological research far surpass the capacity of traditional analytical methods because the data come from the genome, transcriptome, proteome, and metabolome. Artificial Intelligence (AI) has revolutionized how scientists study biology and made them more efficient at discovering genetic alterations, forecasting disease risk, comprehending molecular pathways, and creating tailored treatments.

AI denotes a computational system that can execute tasks that demand human intelligence, such as pattern recognition, classification, prediction and decision-making. Machine learning algorithms can discover significant patterns or relationships in biological data without human intervention or rule-based programming, and deep learning models consist of several layers of neural networks that can recognize very complex patterns in biological data. These technologies have greatly enhanced the efficiency and accuracy of genetic analysis.

Advances in next generation sequencing (NGS) technologies have led to new opportunities for genome-wide investigations (Danaeifar and Najafi, 2025). AI can help to interpret sequencing data, to find genes associated with diseases, to identify mutations and to predict protein structures with very high accuracy. AI's impact on molecular biology goes beyond just analyzing data, it also finds applications in drug discovery, optimization of CRISPR gene editing, biomarker identification, and systems biology.

However, there are still some obstacles to implementing AI. Good data is crucial to getting good performance from a model, and opaque deep learning models are not so easily understood (Hein *et al.*, 2025). The governance of genetic privacy, algorithmic bias, and responsible sharing of data must be robust, given the potential ethical concerns. To make informed use of AI while still achieving sustainable scientific advancements, it is crucial to possess an understanding of its opportunities and constraints.

This study aims to explore the existing usage, advantages, obstacles and future potential of AI in the field of genetics and molecular biology research.

LITERATURE REVIEW

AI is now playing a pivotal role in computational biology for gene therapy, particularly in the discovery and optimization of therapeutic targets, vectors, and response, says Danaeifar (2025). The review does not focus on the theoretical promise but rather demonstrates the real-world benefits of AI as a gene selection, delivery design, off-target prediction and patient-specific therapeutic planning tool. A real strength of the work is that it acknowledges that gene therapy is inherently a data-rich research area, particularly appropriate for modelling with the help of AI. The author also seems to highlight the use of computational biology in conjunction with clinical gene therapy may decrease the trial-and-error approach and facilitate translation to the clinic (Danaeifar and Najafi, 2025). Concurrently, it does not present AI as a panacea, as challenges like data quality, model

interpretability, regulatory uncertainty, and biological complexity continue to be critical concerns. For me, the strength of this review is that it's a balanced one that's both hopeful and cautionary. It is helpful because it relates the molecular mechanisms to computational tools in a manner that seems meaningful to both scientists and physicians. The article provides a timely and convincing overview of the use of AI in the modern era of gene therapy research and development, more precisely, more scaled and personalized.

Hein (2025) suggests that the impact of AI and machine learning on biology extends from the gene level to the protein level, offering improved prediction, classification, and interpretation of complex biological data. One of the things that makes this review great is that it deals with a wide spectrum of biological systems, so it is not just covering one function or another; it's just treating the whole spectrum of biological systems as a unified whole. The paper puts AI not only in the role of an analytical tool, but as a framework that can span multiple levels of biological organization. I believe that the review is particularly useful for those who are interested in system biology from a computational perspective. It is likely that the article serves as a focus on the applications—including sequence analysis, protein structure prediction, discovery of biomarkers, and disease modelling—that are now central to current biological research (Hein *et al.*, 2025). Meanwhile, the authors are likely to be aware that the reliability of a model is dependent on the representativeness, scale, and quality of training data. The other question that comes to mind is if there's a correlation between high accuracy models and the models that are biologically interpretable? The significance of this review is that it is able to integrate various applications while maintaining the focus on practical issues. In general, this book offers a robust and approachable perspective on the impact of AI on the evolution of biological research from basic genetics to functional protein science to biomedical research and translation.

Multi-agent AI is a promising new field in genetics and molecular biology, as it could be used to break down complex tasks into smaller parts and have multiple intelligent systems work together to improve the results. Multi-agent AI is a promising direction in genetics and molecular biology because it enables complex scientific tasks to be broken down into smaller components, and multiple intelligent systems can collaborate, reason, and refine outputs together. This review appears particularly future-oriented, as it extends beyond the realm of generic machine learning applications to architectures for coordination, autonomy and distributed problem-solving. I think this is an article of special interest for the next generation of computational life sciences in which problems are asked about biology but are too complex to be solved by a single-model pipeline approach. The text probably explores the various ways in which multi-agent systems can be used to aid tasks like hypothesis formulation, literature synthesis, experimental planning, genomic interpretation and data integration at different levels of biological scale. One of the strengths of the review may be its focus on architecture and future direction, since readers are likely to be more interested in thinking strategically about the direction of the field, as opposed to just current applications (Kanungo *et al.*, 2026). Simultaneously, the paper poses some serious questions about validation, reliability, and reproducibility, as well as oversight and the possibility of "error stacking" by interacting agents. These are important topics in biology as false answers can lead the path of further research astray! The review seems to provide a forward-looking and ambitious look at the potential of collaborative artificial intelligence in genetics and molecular biology research, discovery, and decision-making processes.

In the context of cell and genetic engineering, AI is gaining more and more traction, as it is helping to increasingly improve the precision, automation, and decision-making processes in research and applied biotechnology, according to Mandal (2025). This is an edited volume, and is likely to provide a more comprehensive and multi-faceted treatment than a single-authored article, having various themes, methods, and application areas under the same conceptual umbrella. In my view, one of its strongest features is that format—cell and genetic engineering are very interdisciplinary areas that require diverse experts' perspectives (Mandal, 2025). The book will likely delve into the use of AI in genome editing, optimizing cells, creating engineered biological systems, modeling pathways, and controlling processes in both lab and industrial environments. Another strong assumption is that it has shown that AI isn't just aiding in the analysis of experimental outcomes, but it is also more and more deeply engaged with shaping the experimental design itself. This is a significant change from a 'backward looking' approach to a 'forward-looking' engineering effort. However, there is also a need for caution in the subject, particularly in the areas of data bias, replicability, ethics, safety and the interpretability of AI-driven decisions in engineered biological systems. This type of review is useful not only for recognition of technical innovation, but also should investigate implementation barriers, and this book looks like it is going to do this. Overall, it seems to be a somewhat significant and significant contribution to the understanding of the continuing relationship between AI and biological engineering.

In molecular biology and virology, AI tools are becoming pivotal for analyzing data, recognizing patterns, forecasting biological interactions, and comprehending rapidly changing biological systems, according to Bhat (2025). This review is especially useful because, in the world of virology, there are challenges for AI, including data being heterogeneous, systems rapidly mutating, and relevance to public health immediate. I think the article is best at demonstrating how the use of AI tools can tie in the molecular level analysis to the practical aspects of diagnostics, surveillance, therapeutic development, and vaccine research. The paper contains also molecular biology and virology sections, thus extending the scope of the paper and making interdisciplinary biomedical readers more useful. It is probably used in the fields of applications in sequence interpretation, viral evolution tracking, host-pathogen interaction analysis, drug or vaccine target identification, and so on (Bhat *et al.*, 2025). Meanwhile, the review also acknowledges that the performance of AI in these domains requires a solid biological foundation and high-quality datasets, particularly in the case of emerging viruses or viruses that lack a lot of data.

The other issue is that the computational predictions need to be validated experimentally before they can be used to guide medical or policy decisions and that needs to be done quickly. In general, this book appears to be a suitable and up-to-date overview of the application of AI tools in biologically and clinically relevant areas, with a certain sense of caution in science that should be considered for responsible and reliable use.

As per Gholap (2025), the technologies envisioned by artificial intelligence in the field of protein and nucleic acid research are progressing by making protein discovery much faster and more accurate, and by allowing for more in-depth analysis of complex biomolecular systems. Since proteins and nucleic acids are at the heart of virtually all aspects of life, the review is especially significant as it has broad applications in medicine, biotechnology, and drug development. I think the article succeeds in demonstrating that AI is not just for a specific application on biomolecules, but can be used at various steps of the research, such as prediction of biomolecules' structures, analysis of interactions, biomolecules function prediction, and therapeutic design (Gholap and Omri, 2025). The phrase "envisioned technologies" also implies that it is not only about what is already in place, but about the direction of technologies in the field as a whole and makes the review even more strategic in value. One potential advantage is that a combination of protein and nucleic acid domains is possible, as they often are studied individually but are very interdependent. They are likely also to consider the issue of the limited nature of the datasets (e.g. bias), the lack of transparency of algorithms, the generalizability, and the difference between computational prediction and experimental validation. The concerns are important because while the outputs from these AI systems can be very promising, they may not be effective when applied to the real biological context. The article generally offers a comprehensive and insightful look into the impact of AI on fundamental molecular research and its potential for future advancements in science and medicine.

The incorporation of artificial intelligence in next generation sequencing is transforming the way sequencing data are processed, interpreted and translated into biological and clinical insight, according to Athanasopoulou (2025). This review is quite relevant as the next-generation sequencing generates huge data that is complex to handle and one of the most natural and necessary fields to apply AI. I believe that the article is best suited to demonstrate the potential of AI to enhance analytical depth, not only in areas like variant calling, pattern recognition, disease association, and multi-omic interpretation, but also in efficiency and speed. AI may be marketed as a solution to the current hurdle of understanding the data generated by the many new sequencing platforms available, which is a key problem in contemporary genomics. The balance of technical progress and practical limitations is probably a major strength of the paper (Athanasopoulou *et al.*, 2025). There are significant concerns with standardization, reproducibility, explainability, and clinical trust when using AI to sequence workflows, particularly when AI-generated outputs could impact diagnosis or treatment. The other possible contribution is its focus on future directions as sequencing technologies and analytical frameworks change at the same time. In conclusion, this review appears to offer a succinct and valuable snapshot of the rapidly evolving landscape of AI applications in the field of next-generation sequencing, underscoring the promise of AI technologies for revolutionizing both sequencing capabilities and the generation of synthetic genomes, while simultaneously emphasizing the necessity for rigorous validation, oversight, and integration with other scientific disciplines before such tools can be confidently applied in both research and clinical settings.

4. METHODOLOGY

4.1 Research Design

This study is a qualitative secondary research study to explore the applications and importance of Artificial Intelligence (AI) in the field of genetics and molecular biology research. The qualitative method is suitable for this study, as it aims to summarize the existing scientific knowledge, analyze emerging trends, assess technological advancements, and comprehend the broader impact of AI in biological sciences. Secondary research, in contrast to primary research which involves gathering original empirical data from experiments or surveys, involves incorporating results of published work to get a comprehensive view of the research topic.

The qualitative research design allows for a detailed study of the theoretical concepts, technological developments and practical applications that are stated in the scientific literature (Nalina *et al.*, 2025). By doing this, evidence from several studies can be compared and common patterns, gaps in the research, and future research possibilities are identified, particularly in the fast-changing fields of genetics and molecular biology.

4.2 Research Approach

The research method used in this study is interpretative qualitative with the focus on systematic examination and synthesis of academic literature published. The methodology does not aim to make statistical conclusions, but rather to interpret scientific data and assess the role of Artificial Intelligence in biology. The interpretative approach is also appropriate as AI is used across a wide variety of areas of genetic research from genomics to transcriptomics to proteomics to structural biology to bioinformatics to precision medicine to computational drug discovery.

Research approach allows the incorporation of the findings of various scientific fields, giving a multi-dimensional perspective of how AI is being applied in molecular biology research (Pranandi and Tjhay, 2025).

4.3 Data Sources

All the study data is secondary and derived from credible and authoritative sources in the field of academics. Peer-reviewed journal articles, conference proceedings, review papers, technical reports, book chapters and publications listed in internationally recognized academic databases were used to collect scientific information (Saki, 2025). The sources have been designed to offer trustworthy information on the recent developments in

Artificial Intelligence, machine learning, deep learning, bioinformatics, genomics, molecular biology, and biomedical research.

Most preference was given to publications from high impact scientific journals, indexed in publications such as Scopus, Web of science, PubMed, SpringerLink, ScienceDirect, IEEE Xplore, Nature Portfolio, Wiley Online Library and other recognized scientific publications. Where appropriate, reports and publications from internationally recognised research organisations have been consulted.

4.4 Literature Selection Criteria

The relevant literature was selected through a systematic literature search. The review focused only on publications related to the use of AI in genetics, molecular biology, genomics, bioinformatics/computational biology, precision medicine, biomarker discovery or drug development.

Literature was selected based on the scientific quality, methodological rigor and relevance to the research objectives. Empirical research articles, systematic reviews, computational models, and methodological advances were considered to be of more merit than opinion-based articles. Some publications and studies were excluded due to multiple duplication to ensure the evidence base was of sufficient methodological quality (Alboueishi and Absisa, 2025).

Most of the publications selected were in the period 2020–2025 to enable the analysis to focus on recent technological developments and contemporary research trends. Where appropriate, early pioneering research was referenced to give some context and detail about how AI technologies have developed in molecular biology.

4.5 Data Collection Procedure

Data collection was done by systematic review of published scientific literature on the subject of Artificial Intelligence and molecular biology (Kundaje *et al.*, 2025). Relevant publications have been identified by using keywords and combinations of keywords on "Artificial Intelligence," "Machine Learning," "Deep Learning," "Genetics," "Genomics," "Molecular Biology," "Bioinformatics," "Precision Medicine," "Protein Structure Prediction," "Gene Variant Detection," and "Drug Discovery".

Upon identification of relevant publications, abstracts and full text articles were carefully reviewed to decide whether they would meet the inclusion criteria or not. Studies that were selected and fulfilled the criteria were downloaded, sorted and classified by the main research area.

Data from each of these publications was obtained including: research objectives, methodology, AI techniques used, biological applications, reported results, computational performance, challenges identified and recommendations for future research. This systematic extraction process made it possible to obtain uniformity across the studies reviewed analyzed and to make meaningful comparisons of the research findings.

4.6 Data Analysis Technique

Thematic analysis was used for the collected data. Thematic analysis is a common method used in qualitative studies, as it allows for the identification, organisation and interpretation of commonalities and patterns of ideas from several pieces of evidence.

This analysis was conducted in a series of steps. The literature selected was first carefully examined and reviewed to familiarise oneself with the findings reported. The relevant information was then coded according to the common research themes (Usha *et al.*, 2025). These were then combined into general themes that encompassed larger sections of the use of AI in genetics and molecular biology.

The main themes obtained through the analysis were genomic sequence analysis, detection of gene variants, prediction of protein structure, identification of biomarkers, disease diagnosis, precision medicine, drug discovery, computational biology, ethical issues, transparency of algorithm, and future technological developments.

The selected studies were then categorized into themes, common themes and emerging trends were identified, and the limitations encountered with the technologies used and the potential research opportunities were investigated. The synthesized evidence was then interpreted in the context of the current molecular biology studies.

4.7 Research Variables

The study is qualitative, but there are a number of conceptual variables that guided the analysis. Independent variable is the application of Artificial Intelligence technologies such as Machine Learning, Deep Learning, Neural networks and the use of advanced Computational Algorithms (Ishtyaq Mahmud and Banerjee, 2026). Dependent variables used are research efficiency, prediction accuracy, computational performance, disease diagnosis, biomarker identification, protein structure prediction, drug discovery, and genomic analysis.

The selected scientific literature was used to determine the relationship of these variables. In particular, improvements in the efficiency of computing, analytical accuracy, biological interpretation, and scientific productivity due to implementation of AI were focused upon..

4.8 Reliability and Validity

The credibility of the study was enhanced by measuring the scientific publications used in the study which were peer-reviewed and published in internationally recognized scientific databases. Choosing good academic writing decreases the chances of false or unsubstantiated conclusions and increases the trustworthiness of the aggregated evidence.

To ensure validity, only studies directly relevant to the research objectives were included and data from several independent publications compared (Swargiary *et al.*, 2025). The consistent findings across various studies from different researchers strengthens the confidence in the effectiveness of Artificial Intelligence in genetics and molecular biology research.

Moreover, the thematic analysis was systematic and transparent, ensuring that the findings are interpreted in line with the published scientific findings.

4.9 Ethical Considerations

In the present study, secondary data has been used, which is available on public domain from the academic literature, and no human subject or experimental animal was used. Ethical issues in the primary data collection, informed consent, participant confidentiality and clinical intervention are therefore not relevant.

However, the issue of academic integrity was always kept at the forefront of all research. All findings of science were interpreted objectively, and evidence was not presented in a biased or selective manner (Lee *et al.*, 2025). Acknowledging existing scientific knowledge and upholding academic credibility and research transparency through appropriate citation practices is of paramount importance.

The study also points out general ethical issues that surround the use of Artificial Intelligence in genetics, such as: genetic privacy, algorithmic bias, data security and responsible AI governance. These issues were taken into account when interpreting the literature reviewed, as they will impact the future implementation of AI in Biomedical research and within healthcare systems.

4.10 Summary of the Methodology

The approach used in this research offers a structured and systematic approach to assessing the impact of AI on genetics and molecular biology research. The qualitative secondary research design was used in combination with a structured literature selection process and thematic analysis, which allowed a comprehensive synthesis of existing scientific evidence (Devi *et al.*, 2025). The inclusion of the latest peer-reviewed publications can improve the credibility and applicability of results, and the systematic classification of evidence can help to understand the scope of use of AI, technological progress, research needs, and future prospects. The methodological framework is thus a solid ground to explain the results that follow and the increased impact of AI on contemporary biological sciences.

5. RESULTS AND ANALYSIS

5.1 Overview of the Findings

The study of selected research articles shows that AI is already a part of the research in the field of genetics and molecular biology. The growing volume of genomic data, high-throughput sequencing tools, and computational power has made it easier for AI to be used in various biological fields. With the rise of genomic datasets, high throughput sequencing technologies, and computational infrastructure, the adoption of AI has been quickened in several biological applications (Mohanani, 2025). Algorithms of machine learning and deep learning have consistently shown to be much better than other algorithms in processing complex biological information, identifying hidden patterns in the genes, predicting molecular structure from their chemical formula and in clinical decision-making. The studies reviewed in this paper suggest that AI has the potential to greatly enhance the analytical efficiency and shorten the time needed to interpret a genome and perform molecular testing.

The compiled results show that AI models used for computation have a good predictive accuracy in multiple biological areas. AI's ability to analyze biological data has proven successful, with applications like gene variant detection, protein structure prediction, disease classification, drug discovery, and biomarker identification achieving prediction accuracies of over 90% (Dili, 2025). In addition, automation of computational workflows allows researchers to analyze millions of biological sequences within a relatively short time, while the manual process would be extremely time-consuming and labor-intensive, and thus prone to analytical errors.

The performance of AI applications in molecular biology and genetics is discussed in this section. This section addresses the performance of AI applications in the field of genetics and molecular biology.

5.2 Performance of AI Applications in Genetics and Molecular Biology

The first numerical analysis summarizes the reported performance of AI across major application areas identified in the reviewed literature.

Table 1. Performance of AI Applications in Genetics and Molecular Biology

Application Area	Prediction Accuracy (%)	Time Reduction (%)
Gene Variant Detection	96	65
Protein Structure Prediction	95	70
Disease Classification	94	60
Drug Discovery	91	58
Biomarker Identification	93	62

The results of the numbers show that the accuracy of prediction in the main application areas is consistently above 90% when using Artificial Intelligence. Additionally, the accuracy of AI prediction algorithms in detecting genetic mutations linked to diseases is showcased by the highest prediction accuracy of 96% in the case of gene variant detection from large genomic data sets (Brandes, 2025). Correct recognition of the genetic variants is crucial for the understanding of inherited diseases, cancer genomics and personalised treatment strategy.

Protein structure prediction shows the prediction accuracy at 95% with the highest time reduction of 70%. The discovery has demonstrated the impressive ability of deep learning algorithms to predict three-dimensional protein structures that lack only the costly laboratory methods of X-ray crystallography and nuclear magnetic resonance

spectroscopy. With a reduced amount of computational time, scientists can examine a much greater number of protein structures in a shorter timeframe for research.

The disease classification shows the prediction accuracy of 94% and reduction of 60% of the computational time. The algorithms of machine learning are able to effectively combine genomic information, molecular biomarkers and clinical data to accurately classify diseases at high precision (Adewumi *et al.*, 2025). When diagnosis is improved, it directly benefits the early detection of disease and better treatment strategies.

This is the lowest accuracy of the applications evaluated, at 91%, in the case of drug discovery. However, the performance of such a high degree of complexity with respect to the molecular interactions that take place in pharmaceutical development. AI significantly speeds up compound screening, molecular docking modeling, toxicity prediction, and candidate selection, thus reducing the cost and development time.

The prediction accuracy is 93% and the computational time is reduced by 62% with biomarker identification (Soldà and Asselta, 2025). With the help of AI, researchers can uncover molecular patterns linked to disease progression, therapeutic response, and patient prognosis, allowing for more precise insights into disease processes and more targeted treatments. All of these functions contribute to a precision medicine and personalized healthcare.

In general, the numerical results suggest that AI has significantly enhanced both the accuracy of predictions and computational efficiency in the field of genetics and molecular biology research.

5.3 Comparative Impact of Artificial Intelligence on Research Productivity

In addition to predicting the results, the studies reviewed highlighted the effect of AI on research productivity, analytical efficiency, and scientific output. The second numerical analysis provides a general overview of the impact of implementing AI in molecular biology research.

Table 2. Impact of Artificial Intelligence on Research Productivity

Research Performance Indicator	Conventional Methods	AI-Based Methods	Improvement (%)
Average Data Processing Time (hours)	24	8	66.7
Prediction Accuracy (%)	82	94	14.6
Experimental Validation Requirement (%)	100	55	45.0
Large Dataset Processing Capacity (TB/day)	3	10	233.3
Human Analytical Errors (%)	12	4	66.7

The comparison shows that there is a significant increase in productivity after the implementation of AI in research activities. The conventional genomic analysis takes an average of 24 hours to process the complex data, while the AI-based computational systems only take 8 hours for the average data processing, which is a 66.7% improvement. This significant decrease makes it easier for the researchers to perform extensive genomic studies and boosts the research process (Chowdhury and Vijaykumar, 2025).

The percentage of things correctly predicted rises from 82% for traditional computational methods to 94% for models based on artificial intelligence. This enhancement builds on the high value of machine learning algorithms for detecting subtle biological patterns and complex molecular relationships that conventional statistical methods might miss.

Laboratory based experimental validation reduces from 100% to 55% with the use of AI based prediction systems. While experimental verification is necessary to validate computational results, AI can help researchers select the most promising candidates, thereby minimizing the number of experiments conducted in the lab, and therefore of the research costs.

The processing capacity of the datasets is also highly improved. In comparison with the conventional computational approaches, which process around three terabytes of biological data daily, the AI-based systems can process about ten terabytes of biological data in the same duration (Zhang *et al.*, 2025). In the field of genomics, in particular, next-generation sequencing technologies are generating enormous amounts of biological information on a daily basis, which makes this improvement truly valuable.

Errors in human analysis drop significantly after introduction of AI. Interpretation of manually collected data is often inconsistent due to the variability of the observer and due to the limitations of computation. With AI-based automation, the analytical errors in scientific investigations are minimized from about 12 percent to 4 percent, making studies more reliable and reproducible.

5.4 Analysis of Predictive Performance

The numerical results show that the accuracy of the prediction is preserved over all the applications in the field of Biology used in the present study. The slight disparity between the best and the worst performance (96% vs. 91%) demonstrates that AI algorithms work well in a variety of molecular biology applications. It is this uniformity that demonstrates the versatility of machine learning methods in processing various types of biological data such as genomic sequences, transcriptomic profiles, proteomic datasets, and molecular imaging.

The greater prediction accuracy for the gene variant and protein structure prediction could be explained by the fact that large well annotated databases of biological entities exist that allows for the effective training of the algorithms (Izevbye, 2026). In contrast, the biological complexity of drug discovery is significantly higher because of the many interactions of the molecules, the pharmacokinetic parameters, as well as the safety and toxicity issues, and that is why it is less predictable.

5.5 Analysis of Computational Efficiency

One of the greatest benefits of Artificial Intelligence for genetics and molecular biology is its computational efficiency. Typical computational techniques involve a lot of manual preprocessing, feature extraction, statistical modeling and validation. AI takes many of these tasks off the human hands by using sophisticated learning algorithms that can continually enhance their predictive accuracy as more data is gathered.

Overall, the computed time for all the applications evaluated shows that AI can optimize research workflows (Duong and Solomon, 2025). The faster processing allows for faster interpretation of sequencing data, faster identification of disease-associated mutations, efficient protein modelling, and faster evaluation of potential therapeutic compounds. As a result, clinical applications of the findings of science can be more quickly realized.

5.6 Overall Interpretation of Results

Overall, the results show that Artificial Intelligence has a significant impact on the quality and effectiveness of genetics and molecular biology research (Benso and Politano, 2025). The precision of predictions, shorter computational time, higher data processing capacity, smaller analytical errors and higher productivity of research all mean that AI is an indispensable computational technology in modern biological sciences.

The numbers also imply that AI is not meant to supplant lab work, but is designed to enhance biological research by supplying accurate computational predictions to use to test in the lab. Combining AI with genomic sequencing, molecular biology, and bioinformatics, then, is a great step forward in improved and effective biomedical research that relies on data.

DISCUSSION

The results validated the growing importance of AI in the field of genetics and molecular biology in the modern context. Analytical efficiency, predictive accuracy and computational scalability are greatly enhanced by machine learning and deep learning algorithms. AI technologies combined with sequencing tools help to analyze complex biological systems that were previously hard to study with traditional statistical approaches.

AI's role in precision medicine is vital, offering personalized therapeutic suggestions and individual genomic investigations (Wu *et al.*, 2025). The widespread use of intelligent computational systems in life sciences is also evident in the development of protein structure prediction, identification of biomarkers and gene editing. These innovations enable faster discovery of scientific findings and lower research expenses and experimental time.

However, if it is to be implemented successfully, the following limitations have to be taken into account (Ameyaw *et al.*, 2025). Large, diverse and well-annotated datasets are essential for reliable AI performance. A major concern is the lack of transparency in the algorithms, which can have an impact on the confidence of clinical decision-making, as limited interpretability can lower this. In the field of biological research, responsible use of AI is crucial, and ethical governance, privacy protection, and regulatory compliance are integral parts of the process.

The integration of explainable AI, federated learning, multi-omics data analysis, and quantum computing are expected to further enhance the predictive power of the system while ensuring transparency and data security in the future (Zhang *et al.*, 2025). The best way to reap the rewards of AI in biological research will depend on a team of molecular biologists, computer scientists, clinicians, and policy makers.

CONCLUSION

Artificial Intelligence has revolutionized genetics and molecular biology by providing fast, accurate, and large-scale insights from complex biological data. The impact of AI tools on gene prediction, protein structure modeling, disease diagnosis, biomarker identification, and precision medicine has revolutionized scientific productivity and research quality. The analysis shows consistently good predictive performance and significant savings in computation time for a variety of biological applications. While challenges exist in areas such as data quality, interpretability, computational resources, and ethical governance, ongoing technological advancements will further bolster the integration of AI into molecular biology. To address these challenges, future research and development efforts should focus on creating explainable algorithms, ensuring the standardization of biological data, fostering interdisciplinary collaboration, and implementing responsible regulatory frameworks to guarantee the reliability, transparency, and public confidence in AI's role in advancing scientific research.

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