e-ISSN: 2582-7405

Transaction on Biomedical Engineering Applications and Healthcare
Vol-3 Issue-1, April 2022

# Differences between Bioinformatics and Computational Biology

**Dr. P Hariharan[1*], Dr. S.V.A.R.Sastry[2]**

[1] Assistant Professor, PSG College of Technology, India
[2] Harcourt Butler Technical University, Kanpur, India
*Corresponding Author Email: phh.bio@psgtech.ac.in

### *Abstract*

*Technology has a great influence on biological science and with the help of biological science and programming bioinformatics and computational biology has the capability of changing the future of Healthcare. Bioinformatics and computational biology are the inclusive and interesting fields of biology. It is evident that both the subjects have some similarities but both have prominent dissimilarities to a great extent. Bioinformatics helps the scientists to organise large biological data apart from that it also facilitates DNA sequencing, structure anticipation and identification of function of proteins and so on. On the other hand, computational biology makes the biological ideology rigorous and experimental and at the same time provides better insight about the respective field. Computational biology allows the researchers to make the procedure of drug discovery more efficiently and seamless. In addition, it allows researchers to develop precise models with the help of 3D modelling to ensure a greater Healthcare system. Computational medicine has the ability to upgrade the overall Healthcare sector through establishing computing models of disease to gain great command over personalised medicine and better and speedy cure of the patients.*

### *Keywords*

*Bioinformatics, Computational Biology, DNA, Healthcare.*

## INTRODUCTION

Bioinformatics follows principles of information science and technology to make the complicated and vast life science data more understanding and usable. On the other hand, computational biology utilises the mathematical and computational or calculative approaches with the aim to address theoretical and exploratory questions in biology. Both aspects are considered as interdisciplinary fields that are capable of development and application of computational methods to assess large biological data like genetic sequences, protein samples, and cell population [1]. All this helps to make better estimation and allows the readers to discover new aspects of biology. Computational biology and bioinformatics are capable of resolving biological and biomedical issues with the help of mathematical and computational techniques. It is noticeable that both are identified by the crucial aspects or elements in modern biology and in biomedical research simultaneously.

Bioinformatics align computer programming, big data, and biology with the aim to allow scientists identify and understand the necessary patterns in biological data. This eventually helps the researchers to study DNA and sequences of genome by organising the large data. In the field of biotechnology, it is widely used as it is capable of boosting the overall field for the sake of better understanding on respective subjects [2]. Whereas, computational biology has the ability to make biological ideology attentive and conclusive and at the same time this provides a road map that holds together individuals' insights. This helps the researchers to sequence the human genome and also helps to create precise models of the essential elements of biology for better understanding and excellence. It is evident that computational biology helps the audience and the researchers to explore various aspects of biology in a broad spectrum.

Computational biology has become an integral part of routine health care and it is estimated that the scope will enhance in the forthcoming years. On the other hand, bioinformatics is primarily used to gain knowledge from biological data by establishing algorithms and software. In the past few years there have been several changes in biology and medicine due to rapid growth in high throughput data gathering in the field of genomics and biomedical imaging. Computational biologists increase and inhabit the confluence of computation and biology in order to transfer all these elements into an integral part of biology and medicine [3]. This field is expanding rapidly not only in academics but also as industry. Bioinformatics consists of research and development or application of computational tools and approaches for making the usages of biological, medical or behavioural data for critical analysis of the subject matter in biology.

This not only helps the researchers to gather biological data but at the same time allows the researchers to successfully and effectively interpret the data. Aim of compositional medicine to advance healthcare by developing computational models of concerned subjects for better understanding and rapid growth [4]. There is a link within artificial intelligence and computational biology as this propels the transformation of big data into useful and less complicated knowledge. With the assistance of analytical programming skills one can interpret large data for better understanding.

## MATERIALS AND METHODS

This research has been conducted with the help of suitable methods and techniques to ensure successful completion of the study. It is critical for the researchers to choose appropriate methods and to seamlessly fulfil the research. The right methods and materials have the ability to ensure that the study is in the right direction and capable of providing sound findings [5]. With the help of qualitative research design the study has been carried out to and this has helped to seamlessly and effectively accomplish the research on time. One of the major advantages of this research design is that it is less complicated and provides the flexibility to conduct entire research. Apart from that, to secure the success of the study, an inductive research approach has been incorporated to critically evaluate all the aspects to develop new theories and represent reliable data. The key features of this approach are that this provides flexibility and this process is comparatively faster than other methods.

Secondary data has also been gathered for the sake of the study and to ensure successful accomplishment of the entire study. In order to secure the success of the study all the data has been gathered from peer-reviewed journals and articles about the differences of bioinformatics and computational biology. In addition, secondary research types have also been followed by looking into the demands of the research and to ensure timely compilation of the research. It has also been taken care of that only secondary data has been collected for the sake of the research success. Apart from that, it has also ensured that no primary data is being used in the study and on the other hand, to maintain the authenticity of the research all the ethical consideration has been followed to secure success of the overall study.

## RESULTS

### Concept of bioinformatics and its advantages

Bioinformatics is considered as a multidisciplinary field that unifies biological information or knowledge with computer programming and big data. It is an integrative area that makes techniques and software tools for understanding large and completed biological data. In the majority of cases this is used to deal with large amounts of data such as genomic sequencing data. This field needs more expertise on programming and technological knowledge to critically explore large and complicated data and interpret it successfully. Some major examples of bioinformatics incorporate assessment of genetics and genomic data, structure of protein cheminformatics comparison of protein to facilitate personalised medicine [6]. Furthermore, in bioinformatics, a genomic browser is like a graphical connection that allows the researchers to exhibit information from a biological database. Genome browsers helps researchers to conceptualise and browse entire genome along with other data that consists of gene prediction, expression regulation, variation and comparative analysis.

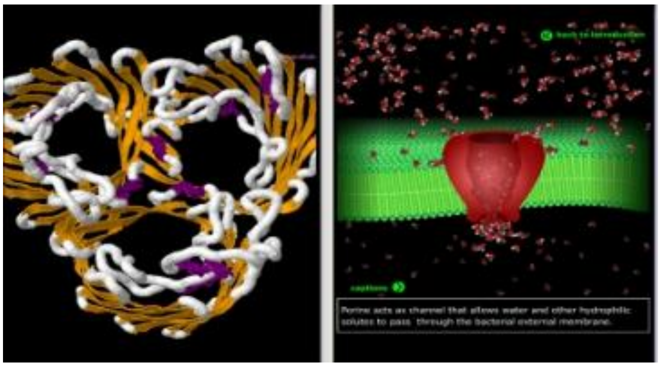

**Figure 1:** Bioinformatics

Some well-known genome browsers are "UCSC genome browser, Ensembl genome browser and NCBI's genome data viewer and so on". All these help scientists to evaluate various aspects of biology in the respective field for a better future. Apart from that, there are some well-known protein browsers that allow scientists to research protein structures and their functions [7]. Uniprot, Swissprot are the names of some protein browsers that are frequently used for research purposes. Bioinformatics is considered as the costly method that helps the researchers to discover new sequences in the genome and identify the function of proteins for upgrading the scope of biology in several markets. This has a great influence on medical science as this helps the researchers to manage large and complicated data in modern biology and medicine [8]. Most essentially, bioinformatics is rapidly used in new drug discovery and development. Molecular methods faces issues to identify new pathogens and that make the process difficult and on the other hand, it often fails to detect unsuspected samples and that eventually makes the process difficult for the researchers.

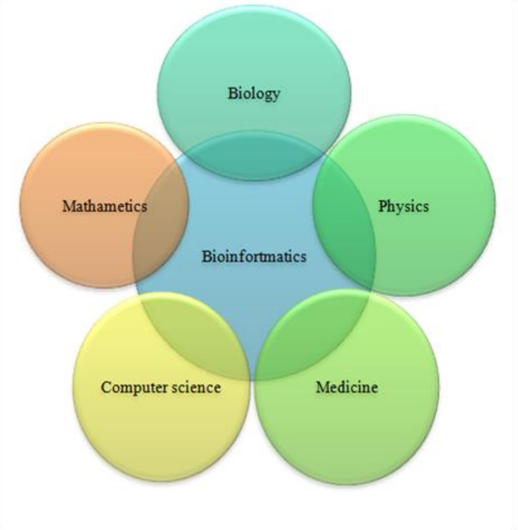

**Figure 2:** Scope of bioinformatics

There is a huge role of technology in bioinformatics and in that scenario AI plays a huge role. Artificial intelligence (AI) is used in bioinformatics for better estimation with the growth and the data at a molecular level. Additionally, this also helps the researchers to anticipate the sequence of DNA and RNA strands and also helps the researchers to classify the various sequences for new discovery.  Apart from that, machine learning algorithms are also frequently used in bioinformatics for estimation, classification of substances, and selection of features [9]. Technology has become an integral part in biological science and this combination has changed the entire game in the industrial biology sectors.  With the assistance of this alignment drug discovery and identification of genomic sequences has become seamless and easier than before and this in turn has facilitated a robust path for the development of science.

Components of bioinformatics can be divided into three parts such as creation of databases, development of algorithms and statistics and assessment of data and interpretation of findings. All components are crucial for ensuring a successful process and effective data presentation. Creation of database processes includes organising, storage and management of biological data sets that are accessible to scientists in order to know the existing information and gain new information [10]. The second component is the development process that includes the establishment or development of instruments and resources with the aim to identify the interrelation within the substance of large data. This process is more like the detection of finding the relation of protein sequence of a sample with existing protein sequence. The assessment of data is more like a combination process of component one and two and this is related to the successful compilation of the research.

### An overview of computational biology and its utilisation

Computational biology is considered as a polymathic field that uses computer science, statics and mathematics with the aim to solve problems or issues of biology. In other words, computational biology utilises computational approaches and mathematics to resolve experimental and theoretical problems of biological science. Additionally, this includes “the establishment of algorithms, theoretical models and computational simulation and mathematical models also” [11].  With the assistance of this phenomenon researchers can effectively possess better understanding in the field of biology. Computational biology is solely dependent on computers and there are great impacts of advanced technologies such as machine learning.  Computational biology covers various parts of biology that are usually not covered in big data. In present days, one of the most used applications of computational biology is computer-based mathematical modelling to identify and understand disease patterns for better and speedy cure.  This is more frequently used in the medicine industry with the aim to upgrade healthcare and prevent diseases effectively.

With assistance of computational models of disease, customising these models by incorporating data of the patients and applying the models for improvement and better and fast diagnosis of the disease. The role of a computational biologist is to look into the betterment and improvement of the resources and tools to help both the biomedical researchers and common people to recognise and interpret the genome sequence data. Artificial intelligence has great influence on computational biology as this technology helps the researchers to transfer large data into a less complicated knowledge that is accessible for everyone. In Addition, AI also helps scientists to discover new drugs to make treatment faster than before [12]. Incorporation of technology such as machine learning and AI allows the researchers to ensure that the chances of error are less and this in turn increases the chances of success to a great extent. This helps the researchers to gather data organise and evaluate data at unpredictable scales and at the same time it also helps researchers to establish comprehensive predictive models that bridge several subfields.

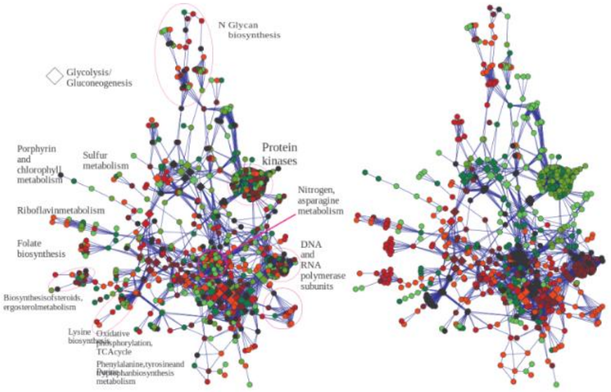

**Figure 3:** Computational biology

Computational biology has the capability of allowing the researchers to recognise the pattern and also facilitates better and speedy mitigation of issues in biology. This helps scientists to develop a graph for genome mapping and also helps to discover fragments of DNA on chromosomes. It performs peptide sequencing methods for the identification of certain types of DNA and clustering algorithms for the assessment of gene expression [13]. All these processes eventually help in better understanding of biological substances and lead to better and upgraded medical treatment. Technology and biology have changed the traditional usage and implication of biology in terms of resolving issues of biology and facilitating a better future.

### Relation between bioinformatics and computational biology and their differences

It is clear that there is a thin line within bioinformatics and computational biology but despite the differences there are some similarities. Most prominent similarity of bioinformatics and computational biology is that both are essential and incorporative fields in biological science and both of the areas need the assistance of computer science, mathematics and statistics [14]. Both the elements are capable of strengthening life science and ensure a better future of the respective field. By looking at the market trend it is noticeable that both the areas are rapidly expanding in academics and industries. On the other hand, it is also visible that both the elements complement each other and possess a great influence on each other. The only difference is that bioinformatics requires more programming compared to computational biology.

Computational biology and bioinformatics both possess a great influence in medical biology and medicine and allow scientists to discover new drugs. In addition, AI also has a great role in both bioinformatics and computational biology and this makes the process of drug discovery fast and that eventually results in accurate and effective treatment within time. In the case of bioinformatics the personnel requires concrete skill and knowledge over technology and programming. Whereas compilation biologists do not need to possess extensive knowledge and skills related to programming and technology [15]. Application of bioinformatics is a vast area and this includes gene therapy, anticipation of protein sequence, identification of antibiotics resistance, development of personalised medicine and so on. Whereas the application of computational biology is mainly the functional prediction that involves artificial intelligence data mining, cellular biology and utilisation of advanced mathematics for better understanding of models and development of new drugs.

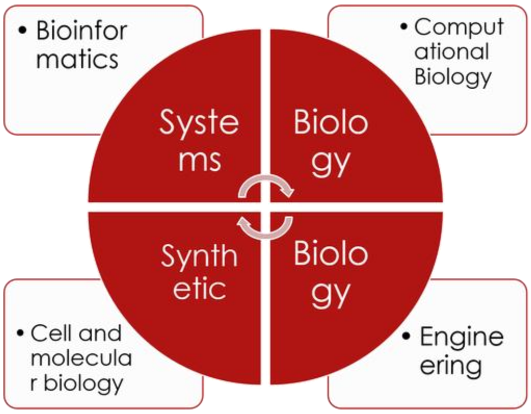

**Figure 4:** Relationship of computational biology and bioinformatics

The researchers are helped by computational biology to decode the human genome for better understanding and also help the scientists to create precise models of human organs to facilitate better diagnosis. This also helps in the development of medicine with the aim to upgrade the Healthcare system with the help of technology and biological science. Both the fields are effective and help scientists to ensure a bright future. It is essential for the scientists to look into the betterment of the Healthcare sector to encourage fast recovery with the assistance of the fast and effective identification of issues and speedy implementation of right treatment [16]. On the other hand, it is also evident that in present days the demands of medicines are increasing immensely. With the help of bioinformatics and computational biology research can provide best services and can fulfil the needs of the patient by providing the best as effective solution to the problem.

Both the subjects help the researchers to gain concrete knowledge related to biological data with the help of development of algorithms and software. In both the cases technology plays a critical role and helps pharma companies to develop new drugs that have the above to cure certain problems. Further, bioinformatics helps the researchers to recognise the target of the drug and validation and also helps in the development of biomarkers and toxic genomic. In addition, this also helps in the pharmacogenomics tools in order to maximise the therapeutic advantages of the drugs [17. Apart from that, computational biology allows the researchers to make the time period of drug discovery fast and effective. In this scenario, CADD is used in most of the cases and this helps the researchers to organise the entire process by filtering the large components into comparatively smaller sets and that eventually used to test the components seamlessly and successfully.

## Bioinformatics and computational tools for sequencing analysis of next-generation in clinical genetics

Clinical genetics has a great influence on healthcare sectors and this is capable of providing better cure of several rare diseases. This also has a great influence on preservation of genes, and allows the researchers to discover better opportunities to facilitate greater and faster response to treatment. Next generation sequencing has the ability to transform the game in clinical genetics for sake of better understanding of sequence of genes. It is essential for the researchers to focus on the assessment of the gene to boost the development of drugs and to ensure better treatment of the patients in a comparatively less time span [18]. Genetics is considered as one of the most critical and an important part of medical practice and it has the strength to change the traditional way of treatment to a great extent. Researchers are using bioinformatics with the aim to identify genes, discover their functions and generate gene-based strategies for upgradation of treatment.

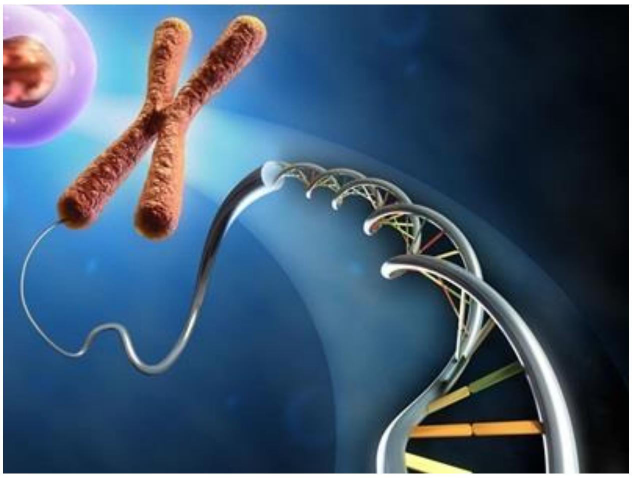

**Figure 5:** Genomic DNA

This eventually allows the researchers to boost up the diagnosis process and ensure that the treatment of the disease is fast and seamless. This eventually facilitates more accurate diagnosis and helps the healthcare specialists to provide best services to the patients that include fast identification of disease and fast and effective treatment. With the help of

DNA sequencing researchers can ensure better and fast identification of the problem and this in turn allows the researchers to make the process more effective and seamless. In this present day, gene sequencing has a great influence on the Healthcare sector. This process is cost effective and this has changed the game in the diagnosis treatment sectors [19]. The future of gene sequence is considered to be bright as this has the ability to make the identification of the disease process fast and that is able to increase the potential of the tools that tell the researchers that kind of genetic information that is carting by that particular gene in the specific DNA system.

**Figure 6:** DNA sequencing

In order to perform next generation sequencing the researchers need to isolate nucleic acid and then the individuals prepare the library, clone gamification and sequencing and assessment of gained data. Gene sequencing determines entire genetic makeup with a specific organism or cell type. This method is used to change the places of the genome. There are various types of gene sequencing: fragment analysis, NGS, Sanger sequencing that leads in application of advanced scientific understanding [20]. In these types NGS type of gene sequencing is the good choice in healthcare services. This type is vital as this analyses a large panel of genes with detecting rare variants, diagnostic and discovery.

## DISCUSSION

Bioinformatics and computational biology are integral parts of biological science and both the elements are capable of transforming the entire process of gene sequencing. From the assessment of all the aspects it is clear that both the elements possess some similarities and dissimilarities and that make both the subjects different from each other. The major visible change within these two elements is that bioinformatics requires intensive and concrete technological and programming knowledge to achieve success in the process. Computational biologists do not require many technical and programming skills to accomplish all the activities and achieve success in the process. Computational biology helps in the process of drug design and on the other hand, bioinformatics allows the researchers in the identification of target drugs and identification of gene sequence. Both the elements are the combination of biological science and technology and possess a great impact on the Healthcare system

Both the elements share some similarities and also have several differences and that makes these two subjects more inclusive. Bioinformatics is the area that brings biological science and programming for the upgradation of the field. On the other hand, computational biology is the field that comprises statistics, computer science and mathematics to resolve the problems of biology. Both the subjects allow the researchers to strengthen genetics and utilise this for upliftment of the healthcare system. Apart from that, this helps researchers to gather and manage large biological data to solve existing problems. Despite the advantages, there are several differences within these two areas, and the most evident difference is that in the case of bioinformatics scientists need to possess great skills in programming and technological knowledge to ensure successful accomplishment of the entire process. On the other hand, in the field of computational biology, scientists do not need to possess extensive knowledge and skills regarding programming.

Bioinformatics acts as the tool that even helps the researchers to decode the human genome, and this helps to solve critical problems of biology and at the same time this also aids the researchers to develop personalised medicine. On the other hand, in modern biology and medicine, bioinformatics allows researchers to manage big data to boost the future of the Healthcare system. With the help of bioinformatics; scientists ultimately strengthening the genetic sequencing process to identify the cause of disease and the appropriate way to resolve the issues. By incorporating tools of bioinformatics professionals can effectively analyse molecular sequence and genomics information or data and also can identify protein sequence and its functions to make the drug discovery and identification of target organs seamless and fast. There are several software that helps the researchers to effectively carry out the activities and achieve their goal. In both the subject's technology such as AI and machine learning and technology has a great influence on the effectiveness of the process.

## CONCLUSION

Bioinformatics and computational biology are the essential and incorporative fields in life science and both the sectors have some unique features that help the researchers to upgrade the entire field. It is evident that both the field completed each other to a great extent but despite the similarities both the subjects are different from each other. Bioinformatics helps the researchers to manage large biological data and also assist to interpret findings. Computational biology helps the researchers to make the genomic mapping process seamless and this also helps in the drug discovery process to a great extent. The primary goal of computational biology is to anticipate protein structure from amino acid sequence and this eventually facilitates a greater path for identification of disease and drug discovery.

It is essential for the researchers to ensure the procedure of identification of genetic patterns in large biological data. This in turn helps the personals to uplift the field of biotechnology. On the other hand, bioinformatics allows the researchers to accomplish sequencing the human genome to explore and unlock the hidden information related to several critical diseases. Technology and programming help the researchers to make the Healthcare system more robust and ensure speedy recovery with the assistance of personalised medicine and make the process of gene therapy strong. Apart from that, bioinformatics also has the ability to reduce the cost of research remarkably by decreasing by exploring all the possible ways. This facility is the optimum condition for the assessment of large biological data in the laboratory.

## REFERENCES

[1] Kusch, Nina, Lisa Turnhoff, and Andreas Schuppert. "Computational Biology: Modeling from Molecule to Disease and Personalized Medicine." *Handbook of Biomarkers and Precision Medicine*. Chapman and Hall/CRC, 2019. 245-252.

[2] Tangyu, Muzi, et al. "Fermentation of plant-based milk alternatives for improved flavour and nutritional value." *Applied microbiology and biotechnology* 103 (2019): 9263-9275.

[3] Tsaramirsis, Georgios, et al. "A modern approach towards an industry 4.0 model: From driving technologies to management." *Journal of Sensors* 2022 (2022).

[4] Elmore, Lynne W., et al. "Blueprint for cancer research: Critical gaps and opportunities." *CA: A Cancer Journal for Clinicians* 71.2 (2021): 107-139.

[5] Sherafat, Behnam, et al. "Automated methods for activity recognition of construction workers and equipment: State-of-the-art review." *Journal of Construction Engineering and Management* 146.6 (2020): 03120002.

[6] Kumar, Rishav, Meenakshi Gupta, and Maryam Sarwat. "Bioinformatics in Drug Design and Delivery." *Computer Aided Pharmaceutics and Drug Delivery: An Application Guide for Students and Researchers of Pharmaceutical Sciences*. Singapore: Springer Nature Singapore, 2022. 641-664.

[7] Du, Zongyang, et al. "The trRosetta server for fast and accurate protein structure prediction." *Nature protocols* 16.12 (2021): 5634-5651.

[8] Silverman, Edwin K., et al. "Molecular networks in Network Medicine: Development and applications." *Wiley Interdisciplinary Reviews: Systems Biology and Medicine* 12.6 (2020): e1489.

[9] Rifaioglu, Ahmet Sureyya, et al. "Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases." *Briefings in bioinformatics* 20.5 (2019): 1878-1912.

[10] Oliveira, Arlindo L. "Biotechnology, big data and artificial intelligence." *Biotechnology journal* 14.8 (2019): 1800613.

[11] Dr. S, “What is the Difference Between Bioinformatics and Computational Biology”, *Difference Between. Com*, 23rd January 2023 https://www.differencebetween.com/what-is-the-difference-between-bioinformatics-and-computational-biology/

[12] Secinaro, Silvana, et al. "The role of artificial intelligence in healthcare: a structured literature review." *BMC medical informatics and decision making* 21 (2021): 1-23.

[13] Kim, Taiyun, et al. "Impact of similarity metrics on single-cell RNA-seq data clustering." *Briefings in bioinformatics* 20.6 (2019): 2316-2326.

[14] Mitra, Debasis, et al. "Evolution of Bioinformatics and its impact on modern bio-science in the twenty-first century: special attention to pharmacology, plant science and drug discovery." *Computational Toxicology* (2022): 100248.

[15] Perrotta, Carlo, and Neil Selwyn. "Deep learning goes to school: Toward a relational understanding of AI in education." *Learning, Media and Technology* 45.3 (2020): 251-269.

[16] Tagde, Priti, et al. "Blockchain and artificial intelligence technology in e-Health." *Environmental Science and Pollution Research* 28 (2021): 52810-52831.

[17] Malsagova, Kristina A., et al. "Pharmacogenetic testing: a tool for personalized drug therapy optimization." *Pharmaceutics* 12.12 (2020): 1240.

[18] Strianese, Oriana, et al. "Precision and personalized medicine: how genomic approach improves the management of cardiovascular and neurodegenerative disease." *Genes* 11.7 (2020): 747.

[19] Lee, DonHee, and Seong No Yoon. "Application of artificial intelligence-based technologies in the healthcare industry: Opportunities and challenges." *International Journal of Environmental Research and Public Health* 18.1 (2021): 271.

[20] Pervez, Muhammad Tariq, et al. "A Comprehensive Review of Performance of Next-Generation Sequencing Platforms." *BioMed Research International* 2022 (2022).