

The Role of Computer Science based on Industry 5.0 in Bioinformatics

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Abstract: The term "Industry 5.0" was created to address personalized production and the empowerment of humans in manufacturing processes, as Industry 4.0 was unable to meet the increasing need for customization. There are differing opinions about what Industry 5.0 is and what comprises the reconciliation of humans and robots from the term's inception. This provides the driving force behind this paper's identification and analysis of the numerous topics and research trends surrounding Industry 5.0's use of text mining tools and methodologies. The purpose of this paper is to familiarize computer science with the emerging discipline of bioinformatics. The requirement for biologists to make use of and contribute to the interpretation of the enormous volumes of data generated by genomic research—and its more contemporary offshoots, proteomics, and functional genomics—has given rise to this field. The article offers a broad overview of the fundamental ideas in molecular cell biology, defines the types of computer algorithms and methodologies required to comprehend cell behavior, and describes the nature of the data that is now available. There is a lot of overlap regarding the function of computer science despite these distinctions. In addition to comparing different strategies, this research highlights some of the inherent difficulties and explores how computer science has been included in these two undergraduate bioinformatics programs.

Keywords: Computer algorithms, Industry 5.0, bioinformatics, computer scientists, big data

1. Introduction

Due to the introduction of Artificial Intelligence (AI)-based solutions and rapidly expanding digital technologies, the industrial sector is currently undergoing a rapid shift. Increasing productivity while maintaining human involvement in the manufacturing process is an issue addressed by manufacturers worldwide. The increasing importance of robots in the manufacturing process due to the development of upcoming technologies like brain-machine interfaces and artificial intelligence makes this work much more challenging. The upcoming Industrial 5.0 revolution has the potential to tackle these issues. To put it briefly, Industry 5.0 envisions people and robots cooperating instead of competing with one another. The Industry 2.0, Industry 3.0, Industry 4.0, and Industry 1.0 revolutions came before this one. Industry 5.0 acknowledges that the sector can contribute to social goals

beyond job creation and development. It may become an ongoing source of growth by putting worker health first and adjusting production to take into account environmental constraints. Industry 5.0 contributes to the industry-required technological improvement to be a reliable system for those looking for a fulfilling and healthy profession [1]. To generate income beyond job creation and expansion while honoring the limits of the earth, it puts worker welfare first and makes use of emerging technologies. It fulfills workers' evolving skill and training needs while also empowering them. It increases industry competitiveness and draws in top talent.

The domains of biology, computer science (CS), and information technology (IT) are combined in bioinformatics to analyze biological data that has been gathered over at least fifteen years and is still being generated today. Several businesses have begun to mine this data, and it's predicted that the bioinformatics sector may reach \$2 billion in revenue in only five years. The work that bioinformatics conduct in the twenty-first century will have a significant impact on both the biological discovery process and health treatment. To face the demands of this dynamic and quickly evolving discipline, today's bioinformatics graduates must become proficient users of both new and old tools. It's quite evident that the field of bioinformatics is here to stay. Bioinformatics is being marketed as the next "hot" new area at a time when conventional computer science is seeing a decline in enrolment and employment prospects. Computer science educators have a significant role to play in the teaching of future bioinformatics due to the

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fundamental role that computer science plays in this field. Additionally, they may benefit in other ways by their involvement in this emerging field. This is partly

attributable to the rise in financing and job prospects brought about by the high demand for bioinformatics graduates.

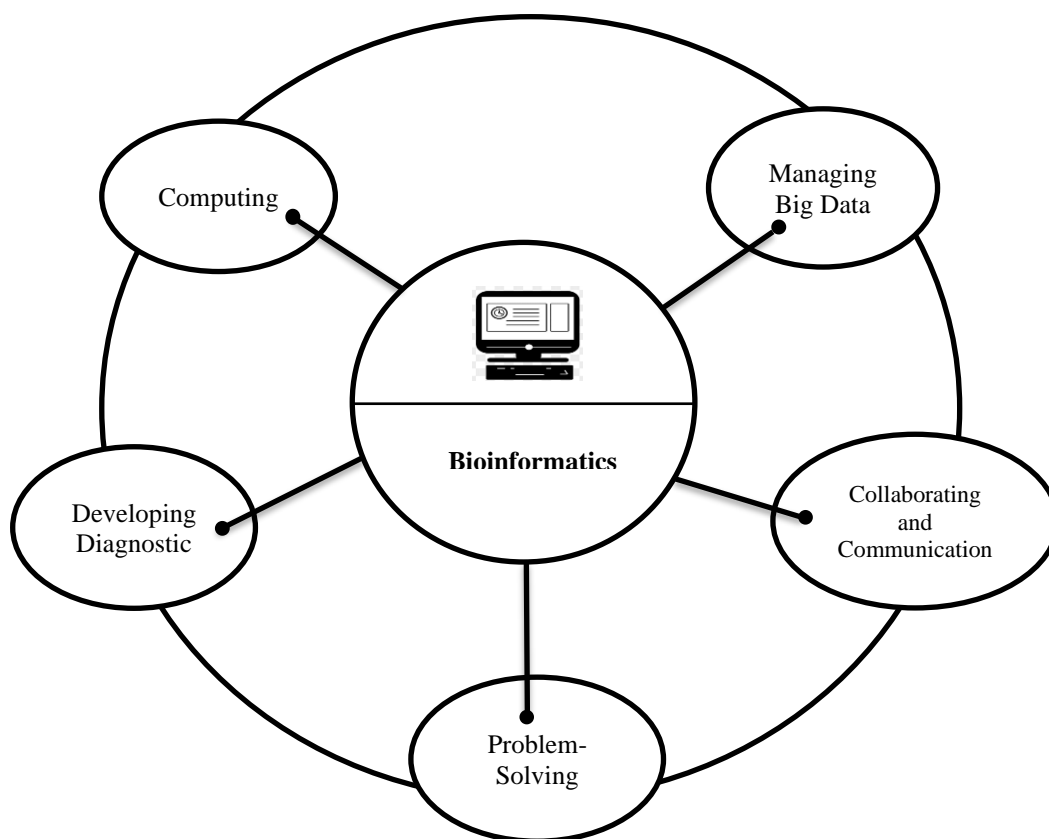


Fig. 1.1. Bioinformatics

Although it is possible to create and deliver new bioinformatics courses, the question of where to put them—a fundamental issue with any interdisciplinary course—arises [2]. The necessary biological knowledge is usually lacking in computer science departments, whereas computational knowledge is lacking in biology departments. Currently, departments of biology, math, computer science, chemistry, and bioinformatics provide these kinds of courses.

The remaining sections of this essay are arranged as follows: Section 2 evaluates the relevant literature. A sneak peek at big data analytics in bioinformatics is given in Section 3. The many big data approaches to data administration and analysis are covered in Section 4. Section 5 brings our article to a close.

2. Literature Review

Dubay, C., et.al [3] Researching biology with computers has a long history. An extensive range of data types were stored and analyzed by early computers: solutions to x-ray crystallographic data for 3D models of biomolecules, pedigree and genetic marker data for linkage analyses, census data for public health analyses (e.g., risk factor identification), and many more. There are now many

branches growing from these roots of genotypes, phenotypes, and systems. One of the fundamental components of bioinformatics is the processing and storage of genotypic data in the form of bio sequences. This is because comparing bio sequences has been a very effective method of determining the biological significance of sequence variants, whether comparing samples or species.

Mathur, M. et.al [4] Identifying every gene and matching it to the protein it encodes, reading the complete genomes of living organisms, and using software and methods to ascertain the structure and functionality of every protein are the implicit objectives of bioinformatics; Comprehensive understanding of the structure and function of proteins, gene expression patterns, and gene sequences to reach the highest level of understanding feasible regarding life. For this reason, bioinformatics must

develop new and improved algorithms for mining data, evaluation, contrasts, and other purposes. Those with programming and math abilities must contribute new ideas and insights.

Payne, P. R., et.al [5] To compare and contrast BMI with other fields, it has proven difficult for BMI to come to a

consensus on and effectively convey a concise description. This is made more difficult in part by the existence of several related or complementary scientific fields, including information technology, math, statistics, cognitive science, social sciences, and several engineering specialties with applications in biomedicine. A person in this field thus has a variety of options when it comes to framing their job and professional identities. A further discussion concerning the distinctions and similarities among the different sub-disciplines of BMI—bioinformatics, translational bioinformatics, clinical research information technology, imaging computer science, medical IT, healthcare informatics, medical information systems, and public health informatics—is currently underway.

Dutta-Moscato, J., et.al [6] Motivated by our high school student academy's triumphant debut in 2011, we decided to create a pipeline of the most exceptional students and inspire them to aspire to professions in informatics. Our goal was to introduce the idea of allowing high school students to participate in research projects and assisting them in planning their college education to best position themselves for careers in informatics. These three individuals turned out to be the group's most heavily cited writers and productive scientists supported by National Institute of Health (NIH) grants.

Beretta, S., et.al [7] A method for encoding data in a synthetic DNA sequence is presented in the paper Forward Correcting Errors for DNA Data Storage. The forward error correction technique, according to the authors, can handle any kind of error that arises during the modern procedures of DNA synthesis, amplification, and sequencing. This method was also put to the test in an actual experiment where 22 MB of binary data was encoded in a DNA sequence and then deciphered. It uses computational fluid dynamics (CFD) simulations of the airflow through the lungs of humans to analyze the impact of the extra-thoracic lungs on the flow field through the lower airways.

Cannataro, M., et.al [8] Contrarily, computational biology was centered on describing and simulating biological systems and processes, paying close attention to the computational and statistical elements. These two fields are becoming increasingly interconnected as a result of the introduction of advanced technologies. Researchers and developers in the fields of computational biology and bioinformatics must investigate, create, and implement novel computation concepts, methods, tools, and systems to address the increasing complexity of current and upcoming obstacles in life science. It's expected that many of these new methods will make use of sophisticated and

expansive computer techniques, computational methods, technologies, and infrastructure.

Agapito, G., et.al [9] The development, application, and exploration of novel computing concepts, techniques, instruments, and systems are how bioinformatics researchers must address these issues. High-performance architectures and systems, distributed computation, mathematical simulation, algorithm design and engineering, applied genomics, artificial and computational intelligence, and computational methods are likely to be included in the new methodologies. The ETH Zurich hosted the tenth iteration of the Workshop on Biomedical and Bioinformatics Challenges for Computer Science (BBC) from June 12–14, 2017. The purpose of the workshop is to bring together experts in computational biology, bioinformatics, and computer science to showcase their latest research addressing these emerging issues in informatics and healthcare.

Nayak, J., et.al [10] The major objective of this work is to highlight the significance of the Frefy algorithm in biomedical engineering and care. Through cross-disciplinary activities that integrate the engineering sciences through clinical practice and the biological sciences, biomedical engineering promotes knowledge in sciences, medicine, and biology and improves human health. The development or maintenance of health through the prevention, identification, and treatment of disease, trauma, illness, and other conditions affecting the body and mind in humans is known as healthcare. Important medical fields like breast cancer classification, human retinal imaging, breast tumor classification, brain tumor detection, wellness tracking, etc. have made use of the Firefly algorithm.

3. Methods and Materials

3.1 Data Science's Place in Bioinformatics

To answer biological problems, the multidisciplinary field of bioinformatics studies statistics, chemistry, engineering, mathematics, and computer science. Ben Hesper and Paulien Hogeweg created it in 1970. The application and advancement of computing is what generates hypotheses for the biological sciences and offers answers to various issues. The field of biology is constantly growing. By offering resources for managing large datasets, bioinformatics is advancing biology. Bioinformatics involves the storage, retrieval, organization, and analysis of complex data. Because computer science, data, and chemistry are all quite different branches of research, working together to solve problems across these domains is necessary.

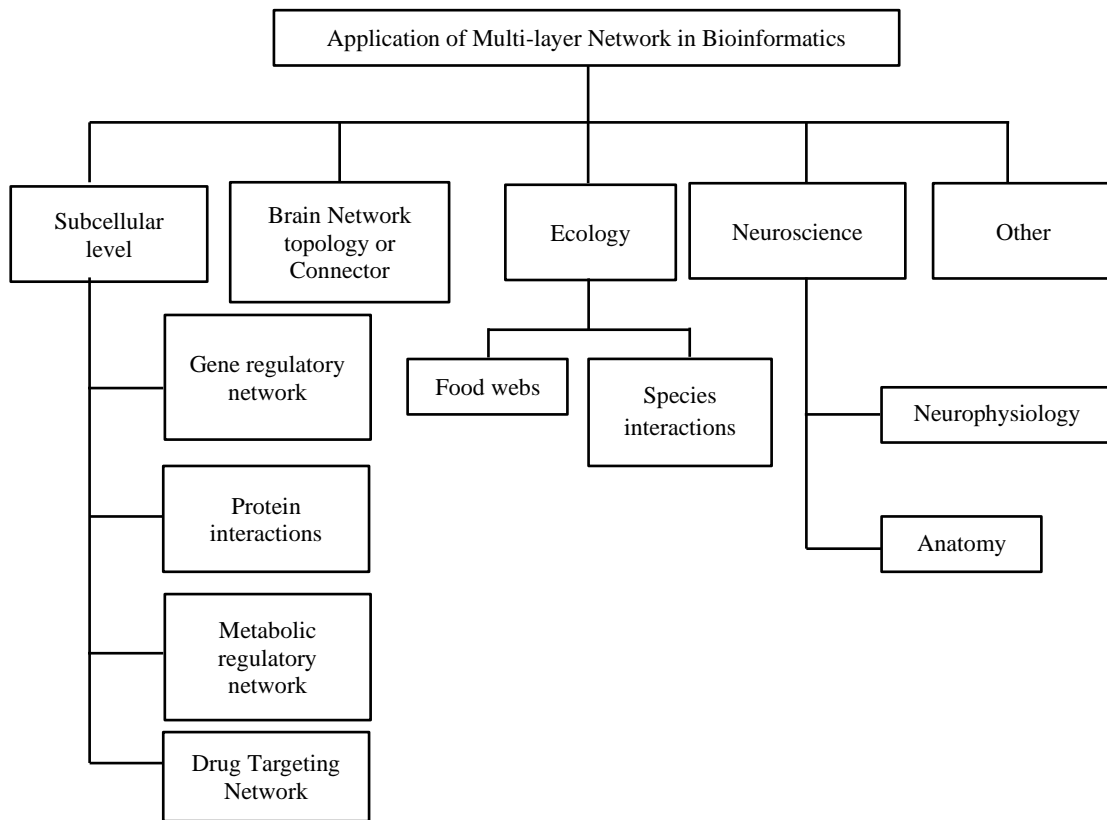


Fig. 3.1. Bioinformatics Application Area Framework using Multilayer Network Design

Bioinformatics has vast applications in many domains, including agriculture, medicine, and other fields. Among these is to determine whether a chemical complex contains any drugs that employ a unique structure. It is preferable to prevent a disease by diagnosing it early rather than treating it after it has already happened [11]. This can be done easily using bioinformatics. If the original solution to a given issue cannot be found, it can direct the search for a substitute. They may offer novel pairings of chemical substances with alternative applications. To increase the

iron and other nutrients of rice and other millet, several genes have recently been added to these crops. It is simple to identify the pattern of protein structure. Gene therapy can effectively employ it. There are several applications for this idea in biotechnology. This approach is an efficient way to boost crops. In bioinformatics, the definition and approach of multilayer network models vary depending on the particular study question.

Different systems can be applied to different levels of organisms, and such systems typically undergo dynamic changes over time.

As a result, depending on the particular biological system, bioinformatics-related networks typically have different representations. We divide the study subjects in this review into several groups based on the various biological system

levels. In bioinformatics, multilayer networks fall into five main kinds, as seen in Figure 3.1.

3.2 Classification of Biomedical Data

Potential methods and some statistical tools to manage them will be required as the volume and complexity of biological data increase. Data on biology collected in different formats is called bioinformatics data, the kinds of information that various databases are capable of holding. Gene, protein, nucleic acid, and other bioinformatics data sequences are all included in the informatics data set. They identify different patterns in the data and get accurate information for certain cell types. This picture was taken while the data was being gathered.

3.2.1. Information on Genomic Profiles

One novel technique for studying gene expression is RNA sequencing from Next Generation Sequencing (NGS). In numerous investigations, RNA sequencing is superior to microarray. Alternative splicing analysis, gene regulation research, differential expression analysis, and other applications can all benefit from its use. NCBI-GEO and NCBI-Sequence Read Archive are two of the publicly accessible repositories.

3.2.2. Transcriptomics Profile Information

One novel technique for studying gene expression is RNA-Sequencing from Next Generation Sequencing (NGS). In

numerous investigations, RNA sequencing has been shown to be superior to microarray. Alternative splicing analysis, gene regulation research, differential expression analysis, and other applications can all benefit from its use. NCBI-GEO and NCBI-Sequence Read Archive are two of the publicly accessible repositories.

3.2.3. Proteomics Profile Information

Proteomics is the investigation of all the proteins that a cell produces. The proteome is an ever-evolving and dynamic group of proteins. The collection of proteins produced in different organs is influenced by gene expression. Proteomics uses high throughput technology to analyze the three-dimensional structure and functionality of proteins. Software-based methods can also be employed to predict the three-dimensional structure of the protein. Protein expression can be investigated using protein microarrays. Protein-protein interactions can be ascertained by producing protein network maps. The three types of proteomics are structure, function, and translation.

3.3 Current bioinformatics goals

Currently, bioinformatics helps biologists collect and analyze genomic data to study protein function. Helping pharmaceutical company researchers conduct in-depth analyses of protein architectures to facilitate medication design is another crucial function. In bioinformatics, common tasks include:

- Determining the structure and purpose of a protein based on its amino acid sequence.
- Identifying every gene and protein present in a particular genome,
- Locating potential attachment sites for medicinal compounds within the structure of proteins.

Typically, to do these tasks, one must look at similar sequences or proteins whose structures and genes have been identified [12]. A shared ancestry is suggested when two sequences or structures exhibit homology. Given the possibility of their extinction, homology should be well-indicated by sequence or structural similarities. It's crucial to remember that sequence resemblance does not necessarily translate into structural similarity. In actuality, it is known that two largely different amino acid sequences can fold into comparable three-dimensional structures.

Nonetheless, the core of bioinformatics is the search for similarities. Upon receiving a sequence, either nucleotides or amino acids, one typically searches databases containing all known proteins and genomes for similarities. Many patterns with varying degrees of similarity are typically

found during the search. The user bears the responsibility of choosing those that could potentially be homologous.

3.4 Efficient bioinformatics and cooperative computer systems

Funding organizations have had to adjust due to the surge in bioinformatics research and the exponential growth in data. Similar to most other scientific investigations, bioinformatics research necessitates resources. Naturally, the computer is the most frequently used tool for bioinformatics projects. While a basic desktop computer may suffice in certain scenarios and based on the necessary computations, many bioinformatics projects will call for infrastructures that are considerably more imposing, costly, and require specialized knowledge. There are now numerous government-sponsored high-performance computing organizations, including:

- Compute Canada is responsible for overseeing the establishment and availability of computer services to scientists in Canada.
- The High-Performance Computing Programme in New York State.
- The High-Performance Computing European Technology Platform.
- Nationwide Centre for High-Performance Computing in China.

Furthermore, community computing's rise has completely changed the way that people can engage in bioinformatics. A collaborative platform called BOINC serves as an example of this, enabling users to make their personal computers available for distributed computations for various projects. BOINC accepts computing tasks from experts, and science enthusiasts and/or non-experts can volunteer by contributing their computer capabilities to jobs that BOINC has received. Through BOINC [13], several life science-related projects are currently accessible, including those for protein-ligand docking, malaria models, and folding protein molecules.

3.5 Big data applications in bioinformatics

The various big data analytics ecosystems were covered in the previous section. Understanding how these tools are used in various bioinformatics disciplines is also crucial. Utilizing big data analytics, the ultra-large-scale bioinformatics datasets need to be carefully managed, kept, and analyzed. Figure 3.2 illustrates a broad paradigm for big data insights in bioinformatics. One of the numerous potential frameworks for big data analytics that have been presented is this one [14]. Using big data analytics as its main focus, this section highlights the various bioinformatics areas.

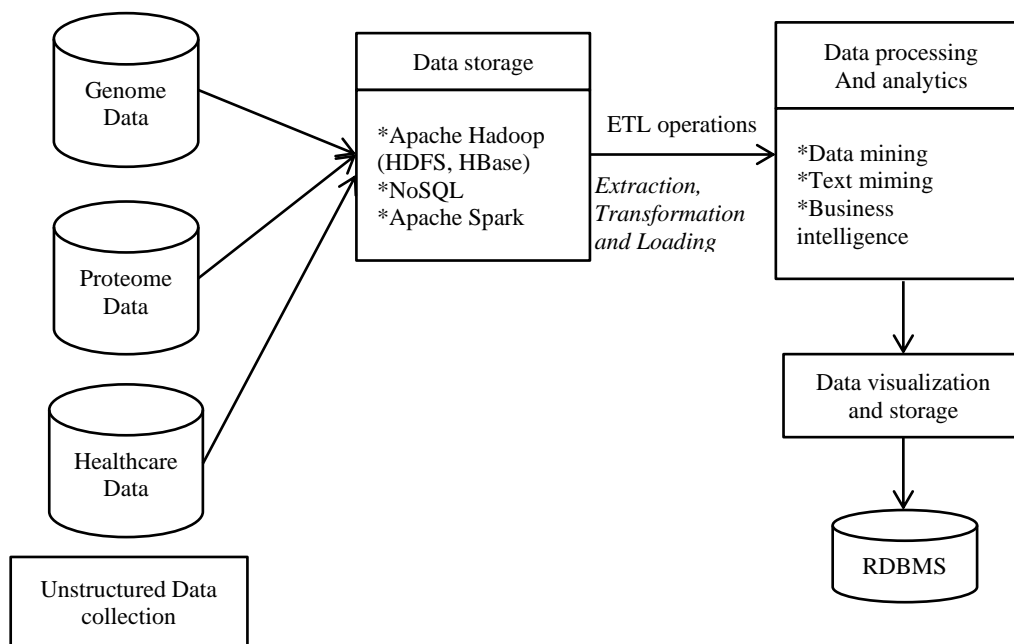


Fig. 3.2. The Bioinformatics Workflow For Big Data Analytics

3.6 Large-scale data in bioinformatics

Bioinformatics is generating enormous amounts of data every day, propelling the field into a new era of "big data." Research on omics provides one such instance. Recent developments in genome sequencing have been made possible by the completion of the Human Genome Project (HGP) in the early 2000s. Several projects were started following HGP's accomplishment. Large-scale genome sequencing was initiated with the 1000 Genomes project, which produced over 100 gigabytes of enormous genetic data (Siva, 2008). The large-scale genome sequencing initiative known as the Genome 10K Project came after it. Additionally, starting in 2014, the new Genome 100K initiative aims to sequence the genomes of 30,000 patients per year, to sequence 100,000 genomes by 2017. A typical laptop's hard drive might hold up to 200 GB of raw data, which is the amount of data from a single genome. It is anticipated that the 100K Genome project will produce 100 times as much data as the 1000 Genome project.

With these advancements, the amount and complexity of genomic data have grown dramatically. The genomes have been extensively sequenced using methods like high throughput screening (HTS), next-generation sequencing (NGS), and genome-wide association studies (GWAS). These developments in technology have made it possible to sequence genomes quickly and cheaply. Human genome sequencing cost \$1000 in 2012, but in 2014, it was less than \$1000—less than the price of an X-ray report. Health informatics produces enormous amounts of biological data in a manner comparable to that of omics research. Large

and intricate data are produced from a patient's clinical report. Numerous clinical and medical applications rely heavily on such massive amounts of data.

They are employed in community health management, clinical monitoring, clinical decision-making, early disease detection, and the identification of healthcare fraud. Storing such large electronic health records (EHRs) on a conventional computer is a challenging task.

The accumulation of "big" data in bioinformatics throughout time has given researchers a wealth of opportunities to extract knowledge from unprocessed data. One emerging approach to address the variety and complexity of bioinformatics applications is to model complicated bioinformatics applications as collections of web services positioned atop processes. To handle such data, several procedures utilizing multi-stage models and analytics on distributed networks have been developed recently. We go over a few of the well-known procedures developed for bioinformatics purposes. Galaxy is an open-source, web-based bioinformatics platform with a large amount of data. It provides integrated visualization tools and access to several bioinformatics datasets. Taverna is an object model with multiple threads that is intended for use in scientific applications. In this case, local method calls signify data transmission between machines, while processors themselves represent objects. On the other hand, Tavaxy is a bioinformatics workflow that relies on pattern recognition. It unifies the current Taverna and Galaxy platforms into a unified setting that supports cloud apps.

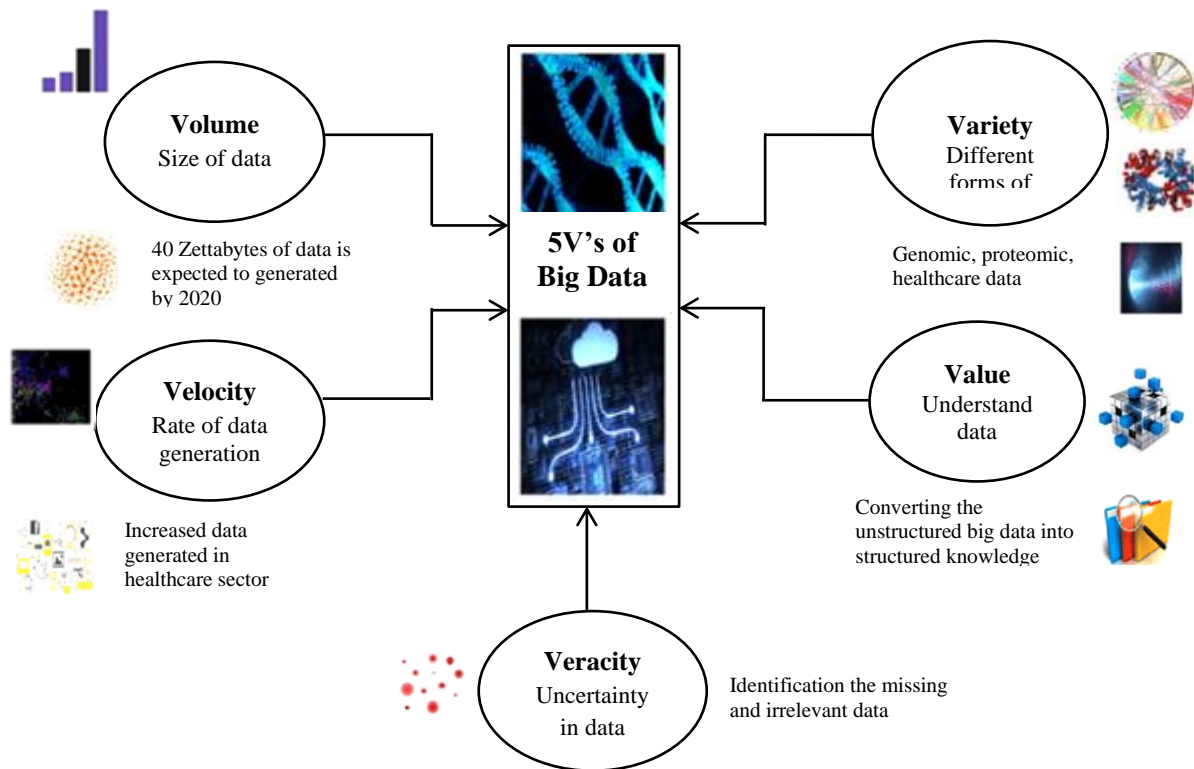


Fig. 3.3 Big data attributes in bioinformatics

Another workflow designed for scientific automation management is called Pegasus. Over the past 12 years, scientists in a variety of fields, including bioinformatics, have employed the approach. It seems that this process may produce consistent results across a variety of computer architectures. Figure 3.3 illustrates the features of big data in bioinformatics.

4. Implementations and Experimental Results

The computer algorithms' ability to identify gene sequences is measured by the sensitivity of gene sequence alignment. Table 1's 10 gene sequences underwent a sensitivity comparison using the dynamic programming approach and ACA-GA. The comparison's average result was derived from the 10 comparisons.

Table 1. Findings regarding sensitivity in gene sequence alignment

No	Sequence of primates	Number of sequences	Length	Algorithm A	Algorithm B
1	Lemur	3	600	335	268
2	Gorilla	3	1451	390	468

3	Loris	3	1101	568	568
4	Tarsier	3	1291	521	541
5	Prosimii	3	1101	503	521
6	Lemuridae	3	1679	671	641
7	Macaque	3	1088	490	522
8	Lagothrix	3	1891	699	699
9	Baboon	3	2257	703	668
10	Hominidae	–	1081	–	–

Table 1 displays the sensitivity findings for the gene sequence alignment for the ACA-GA (B algorithm) and dynamic programming approach (A algorithm). The third group and the eighth group are the two sets of data that are identical to both the dynamic programming algorithm and ACA-GA. Within ACA-GA [15], four data groups—the second, fourth, fifth, and seventh groups—have sensitivity levels higher than those of the dynamic programming technique.

Therefore, when it comes to the total sensitivity of the aforementioned 10 gene sequences, ACA-GA is more sensitive than the dynamic programming technique.

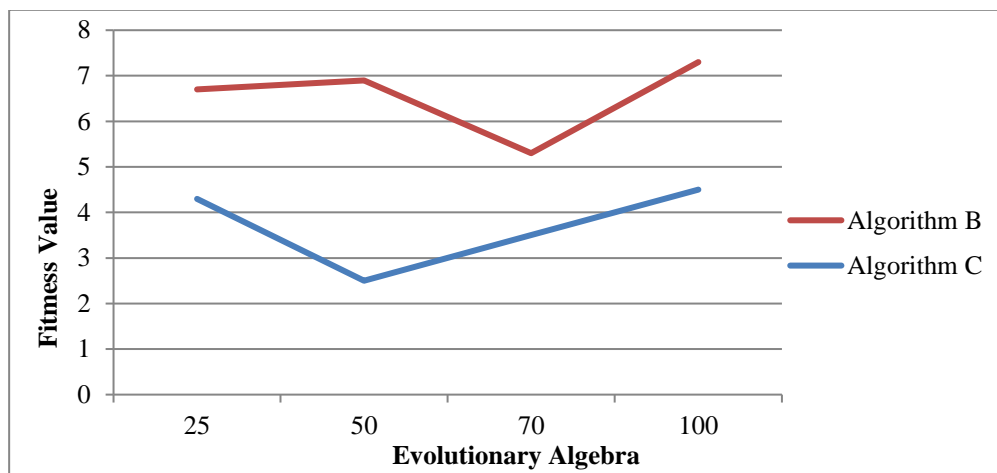


Fig. 4.1. Results of Gene Sequence Convergence Speed Comparison

The identical initial population is employed, and experiments are conducted using the classic GA (C algorithm) and ACA-GA to examine their convergence speed, to make the experimental findings comparable. To evaluate the convergence speeds of the two methods, the experiment will choose two groups of gene sequences: the first group and the second group. By modifying the parameter in the formula, ACA-GA may determine the ideal gene sequence alignment because of the features of ACA optimization [16]. Figure 4.1 compares the effects of the traditional GA and ACA-GA on the rate at which the gene sequence converges.

The convergence speed of ACA-GA is much higher than GA in the first set of gene sequences in Figure 4.1,

specifically when evolutionary times range from 25 to 125. In the second group, the convergence is completed by ACA-GA after 140 evolutionary algebras, whereas the typical GA requires 200 iterations to attain the completion. For gene sequence alignment, the convergence rate for ACA-GA is hence quicker than that of conventional GA.

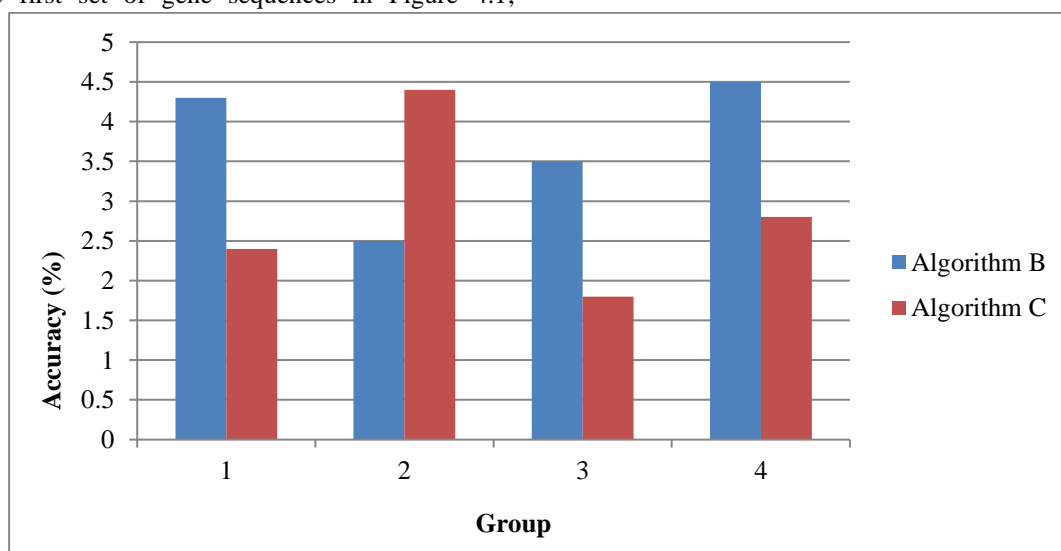


Fig. 4.2. Shows the Precision of the Gene Sequence Alignment

The findings of the ACA-GA and traditional GA gene sequence alignment accuracy are displayed in Figure 4.2. In Figure 4, ACA-GA aligns these nine groupings of gene sequences more accurately than GA. The typical algorithm's average accuracy is 94.6%, whereas the average accuracy of ACA-GA is 97.2%. Hence, in terms of

gene sequence matching accuracy, ACA-GA outperforms regular GA.

5. Conclusions

Our bioinformatics program aims to provide a broad variety of abilities that are matched to taxonomy of the field, with a particular emphasis on fostering cross-cultural

engagement between participants in CSE and biomedical research. We think that this curriculum contributes to closing the "gap" that exists between these domains, which hinders the development of bioinformatics applications that will be useful to industry and biomedical researchers in the post-genomic period.

As demonstrated by the experimental results, ACA-GA converges to gene sequence alignments substantially faster than GA. The two algorithms' respective averages for gene alignment accuracy are 97.2% and 94.6%. ACA-GA and the dynamic programming algorithm perform gene sequence comparisons and analyses. The results show that while the accuracy is similar, ACA-GA is more sensitive to gene sequence alignment than the dynamic programming approach. In-depth summaries of several new studies and large data analysis methods for bioinformatics are given in this overview. Future big data analytics applications must concentrate on creating sophisticated integrated technologies that can analyze large amounts of biological data quickly, cheaply, and securely to advance bioinformatics research. Shortly, bioinformatics and analytics combined can provide a new wave of job possibilities in the information technology and pharmaceutical industries' research and development sectors.

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