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AND ROLE OF INTERNET OF THINGS (IOT) IN BIOINFORMATICS

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ABSTRACT

During the medieval period, Bio refers only to nature and the environment. In the 17th century, when biology was coined, it relates to the study of humans, animals, living creations, etc. Whereas in the 21st Century, when we're all living in the technological era, the interpretation of biology has been framed as Bioinformatics.

Before moving further, we need to understand Bioinformatics, a branch of technology and biological science, as it has computational science in the biological world. In this chapter, the authors would like to elaborate on recent advances in Bioinformatics in collecting, maintaining, and evaluating large and complex biological data sets. As I've mentioned just now regarding the interpretation of Bioinformatics, cloud computing and IOT (Internet of things) has an essential role in various facets of Bioinformatics which will be discussed in the paper.

So, from the above interpretation, we've got some light on how Bioinformatics performs the rendition with cloud computing and IOT, so it is essential that. Protection in Intellectual Property Rights (IPR) is obtained for research and development. As IPR has various facets, it will help gain investments through assets. Lastly, we would like to conclude our chapter on how IPR has redressed the challenges of cloud computing for Bioinformatics

<u>Keywords</u>: IOT (Internet of Things), Bioinformatics, cloud computing, IPR, Biological databases, Artificial Intelligence, Data mining

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1. INTRODUCTION

Bioinformatics is one of the branches of biology, a combination of information and interpretation of science in technology. It has emerged to sort out the complicated biological data sets through various stages of Genomic structure.

Earlier, when a patient suffers from chromosomal disorders, it takes time to sequence the complicated biological data sets. With the revolution or, in a simple way, technological science advancement, bioinformatics' growth moves on the highest peak. Bioinformatics has two types of databases working simultaneously to figure out information for future benefits as it will help scientists and academic users in their research purpose.

As I've already thrown some light on how Bioinformatics generally works, the authors highlight two emerging points: Cloud Computing and (IOT).

In general, cloud computing is advantageous for Bioinformatics because Bioinformatics analysis requires a quantifiable amount of data. It also involves the study of massive data sets. Standard Bioinformatics techniques require a long time to achieve outcomes and are impossible to decipher due to the data's difficulty. Therefore, cloud computing is a boon for Bioinformatics research. Now another critical tool in information science in the era of technology is IOT, which helps to analyze large quantities of biological data recognizing how it can include molecular biological as well as DNA sequence equations, for this reason, many scholars attempted and competed actively in different tools in this sector. Henceforth IOT is beneficial among all other tools used by the researchers. As of now, the authors throw a light regarding the advancement of the latest techniques, so it is of utmost necessity to look into the scientific-legal protection of those technologies that will address the management of protection and understand all kinds of challenges faced by the users.

The main aim of performing this analytical research is to identify the gaps in understanding the various advancement of Bioinformatics as a tool for helping the researchers in multiple aspects and determining the newest form of technology that researchers are prominently using scientists worldwide. This would allow the readers to understand the current emerging trends about the transcription of biological data. In addition to it, the authors will contemplate the pros and cons

of the current emerging technology, which has significant inception. Secondly, the chapter will deal with the recent IPR protection and its scope to manage all the challenges.

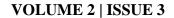
Bioinformatics plays an essential role in pharmaceutical science and biomedical engineering for complicated biological databases in the current information technology era. So, to boost the advancement of Bioinformatics, new trends are developed. Bioinformatics provides financial support in investments, so the authors would like to contribute to significant legal protection, mainly patent protection through Intellectual Property Rights. As Intellectual Property has various facets, all the pros and cons and the People's problems in the current biomedical research advancement will be addressed by Intellectual Property Rights.

The chapter has been structured into three parts by the authors; the first part of the chapter will provide a brief introduction regarding Bioinformatics, evolution, function & various mechanisms available currently for the betterment of the researchers and scientists at large. Secondly, the chapter has stated about the Intellectual Property Protection and the evaluation of IP Assets involved in it. Thirdly, intellectual property has analyzed the challenges faced by cloud computing and IOT. Thus, a legal remedy has been given to the people if any issue occurs concerning violation of privacy rights

2. EVOLUTION OF BIOINFORMATICS

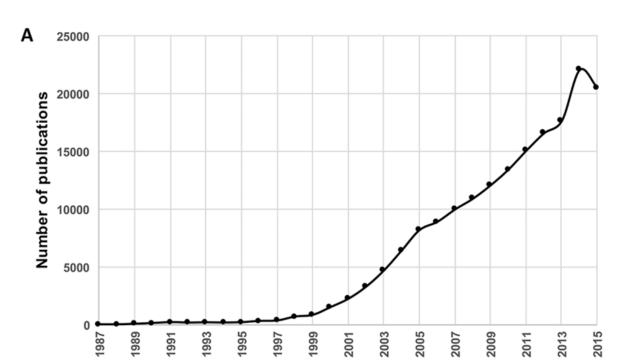
A century ago, Bioinformatics was coined by Gregor Mendel, the Austrian monk. The "Father of Genetics" he is considered. He crossed several colors with the same plant flower. He registered systematically the colors of the flowers that he struck and the colors of the flowers. Mendel showed that the heritage of features could be understood more readily if it was governed by influences passed down between generations. Gregor Mendel already mapped more than 500 genes to start the Human Genome Project, the first international research project in earlier 1970 to map the gene for influenza bacteria specimens.

With the origin of networks and the internet, genetic mapping is increasing through the advancement of Java, HTML websites. Now we'll discuss the advent of biological databases.



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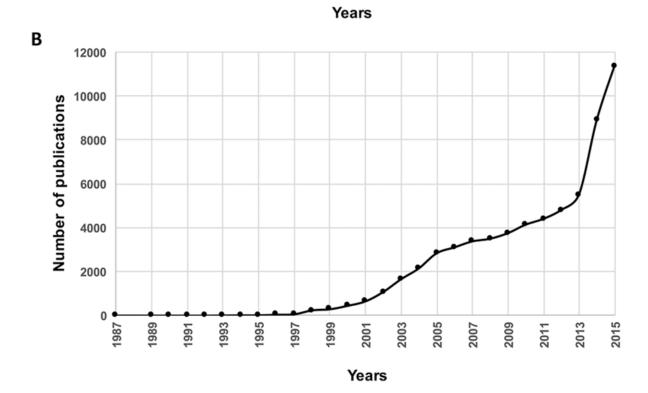


Fig-1 talks about the evolution of Bioinformatics

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2.1. Origin of Biological Databases

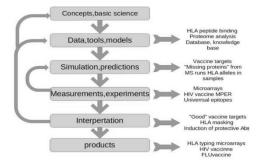
In 1956, the first protein sequence was identified as bovine insulin, with 51 residues. Dayhoff compiled all available sequence data to create the first Bioinformatics database a year later. A biological database is a massive, integrated body of persistent data. A single file with a volume of data can be a simple database, each with the same data set. An example of a nuclear sequence record is the input sequence, with a definition of the molecular type, the scientific name of the originating organism of which the sequence is isolated, and literature citations often identified with the sequence.

We know, then, that Bioinformatics is a new discipline that examines the need to interpret and clarify the vast quantities of data provided during the last decade by Genomic science.[1] This field combines genomics, biotechnology, and information technology, including data processing and transcription, simulation of biological processes, and the advancement of algorithms and statistics. Therefore, Bioinformatics is the toolkit for every biologist using computer science and specialized software for extraction and transcription of DNA Sequences [2]

2.2. Various mechanisms of Bioinformatics

Artificial Intelligence

AI in Bioinformatics encompasses fundamental and clinical studies using biological sequence alignment, protein-protein interaction, and function-structure analysis. This research aids in the creation and discovery of pharmaceuticals and complex structures. As AI is dependent on pattern matching and knowledge-based learning systems in Bioinformatics analysis in response to biological problems. [3] As for the AI analysis of Bioinformatics, patterns fit, and knowledge-based learning mechanisms are essential for resolving biological issues [4],[5]



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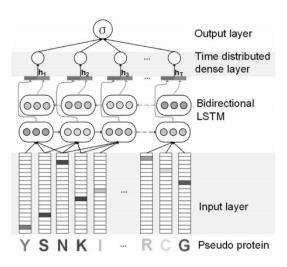
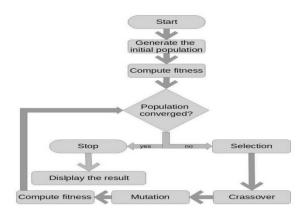


Figure 2 here depicts the application of AI in Bioinformatics



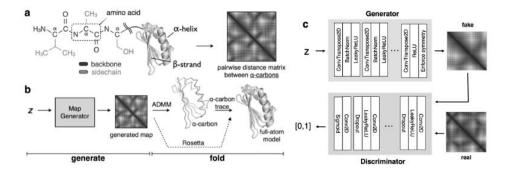


Figure 3 depicts a flowchart of genetic algorithm for Bioinformatics

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Data Mining

Data mining is called the retrieval or "mining" of data from vast amounts of data. Data Mining analyses new and interesting patterns and interactions in enormous quantities of data. Data Mining is an investigation. [6] It is defined as "the mechanism of selecting vast quantities of information stored in warehouses for meaningful new relationships, models, and developments." Information Discovery of databases is also called Database mining [7]. Data mining strategies include discovering genes, recognizing protein function domains, motif function detection, protein function inference, cancer prediction, forecasting, disease optimization care, and the network of protein and gene interactions.[8]

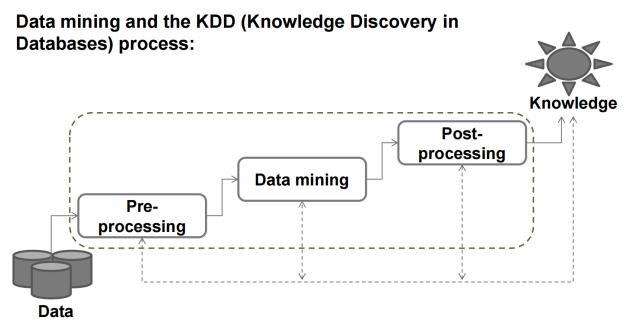


Figure 4 represent the application of knowledge Data Mining

Internet of Things (IOT)

The internet of things is one of the most enhanced economic revolutions in the twenty-first century. As a result of significant developments on the internet, objects or input databases are becoming much more recognized, which aids in interpreting biological databases. It is much more advantageous because the tools used here are valuable and mathematical. Some of the valuable tools are discussed below

- 1. Computational evolution is a series of techniques known as evolutionary algorithms. The most common algorithms are evolutionary algorithms based on evolution theory and genetics. This algorithm has accelerated the evolutionary process over millions of years. Evolutionary algorithms solve statistical strategy and optimization problems [9]
- 2. Swarm intelligence and approaches in this area suggest another approach to solve optimization problems. Many fundamental and low intelligence workers cooperate or form a new swarm or collective intelligence. One of the swarm intelligence algorithms is the ant-colony optimization algorithm, which ants simulate in mutual presence.[10]
- 3. Artificial Neural Networks are also among the most effective CI algorithms (ANN). Almost all scientists agree that the human brain is the most well-known and complex organ in the universe. Based on the discoveries of the neuroscientist, several knowledge and classification models have been presented by mathematicians and artificial intelligence technicians. Neural networks could be the perfect way to learn machinery. [11]

2.3. Research Techniques for Internet of Things

1. Early Phase

Both DNA sequence analysis computing resources in Bioinformatics are found in this research phase through library studies, literary examination, and all current research in this field. They were then put in a loop shape with a suitable arrangement, the principal elements of the loop being a total of 14 parameters. In conclusion, Bioinformatics experts verified the components and sub-components collected.

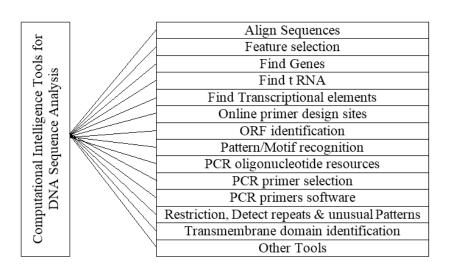


Figure 5- Computational Intelligence for DNA Sequence analysis

1. Second Phase

This process aims to evaluate the value of parameters by using the entropy analysis of Shannon.[12] Therefore, each Bioinformatics expert has prepared a survey and special matrices to produce the best results.

$$\mathbf{D} = \left\| a_{ij} = \frac{w_i}{w_j} \right\|$$

The above expression helps obtain the weight of the variable of biological databases.

2. Third Phase

Finally, in this phase, the data structure for the Computation of IOT in DNA analysis is evaluated for the DNA replication and analysis process. [13]

2.4 Role of Internet of Things in Bioinformatics

The IOT is a term coined recently to describe objects that connect and transmit information over the internet. Smart IOT systems produce a large amount of data, known as "big data," which cannot process traditional data processing algorithms and applications. Scientists of Health, [14] IOT-based sensor information concerns all government and business organizations with Bioinformatics, information science, policymakers, and decision-makers. The Internet of Things

will be crucial in several areas in the future. Many forces drive the growing demand for both technologies, and an increasing number of companies, governments, engineers, scientists, and technologists are beginning to implement both. Suppose the potential benefits and opportunities of IOT are combined. In that case, they can be discovered on both the device and the server levels. AI methods combined with IOT are finally possible to analyze people's behavior by using Analog transmission, motor sensors, face detection technology, and change lighting and room temperatures. The research aims to collect new findings of new artificial intelligence methods for data processing and storage from the cloud-based Internet of Things. Bioinformatics now uses computational information based on the Internet of Things to archive, search, display, analyze and interpret biological information. The development of new computer intelligence results from the growth of Bioinformatics and increasing demand for actuarial, computer sciences, and programming.

2.5 Cloud Computing

Bioinformatics, a scientific sector that applies the biological environment to data, computing devices, and the internet, is viewed as a parasite on computers and their various fields as hosts in terms of research. In terms of analysis, Bioinformatics, a branch of science that applies data, computer, and computational science to biological environments, is viewed as a parasite on computers and their various fields. The information was overcome by pyrosequencing, nanometre, and non-optical Ion chips of the second and third generation generations, which collect pettabytes of data every day, casting doubt on the ability to analyze such massive amounts of data smoothly and comfortably. [15] Accepting the challenge, the IT sector responded with the option of operating in a simulated world with no natural resources. As it is considered in online platforms, cloud computing evolved over here. [16]

Previously, the term "cloud" [17] was used to metaphor mobile devices and the internet. However, it is now a changing concept that alters both the scenario and its definition. Forrester defines cloud computing as a pool of abstract, highly flexible, and controlled computing resources to host customer applications and bill usage. In a broader sense, it includes stakeholders who offer metered services.

Now before moving towards the application of cloud computing in Bioinformatics, the authors would like to explain the different kinds of clouds available in the client' services are [18]

- 1. Private Cloud: It is used for personal purposes only authorized persons of the enterprises can access the databases.[19]
- 2. Public Cloud: It is operated by third parties easily accessible with specific security measures.[20]
- 3. Hybrid Cloud: It combines both the clouds discussed above, which states that some parts of the information are of public use and the rest are restricted for the public. Only the concerned persons can access the databases.

2.6 Application of Cloud in Bioinformatics

1. Metagenomics

Metagenomics is a genome analytical technique. The data is scanned for all Genomic data to find the best fit. The Bioinformatics method BLAST is used for the quest. The data are subdivided into smaller fragments, and their counterparts and similar pieces are looked for to classify the organism. This is a computing component that requires heavy computing and high machine capital. Meta Genome Rapid Annotation with subsystem technology (MGRAST) is used for metagenomic studies.[21] A sample of only 10 KB of Metagenomics data is used to analyze cloud systems, dedicated servers, and local environments to calculate the necessary calculation. [22]

2. Cloud Computing and formation of Clusters

Cloud computing providers have accommodated High-Performance Computing (HPC) in the cloud with highly scalable computing resources. Map Reduce/Hadoop is useful for analyzing or solving problems in clusters of commodity machines. HPC is not as fast as traditional HPC or Grid from top research institutions.

3. Neuroscience

The experimental data generated and used to explain the meaning transmitted are the cornerstone of every scientific work. Technological advances create data very rapidly and promise to grow

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exponentially in the future. Unfortunately, since the data formats created by tools are in their informal metadata format, neurological data is not shared. CARMEN [23]

4. RNA Analysis

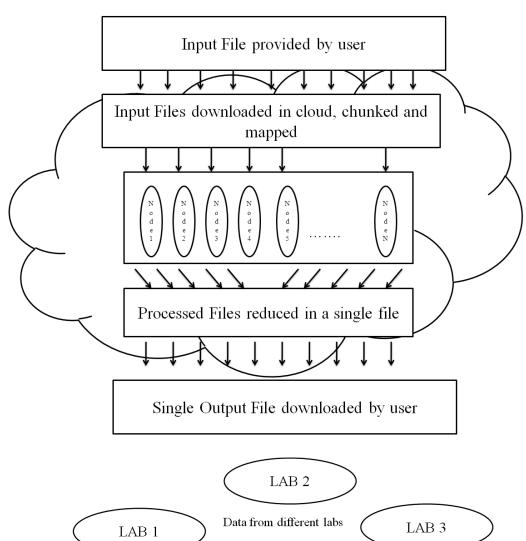
Myrna is a pipeline that complements the RNA sequence analysis of the current ERANGE, Cufflink's platform for measuring differential gene expression. It can be used in cloud computing with Hadoop, Map Reduce, or single-tone screens. It took about four hours and twenty minutes with one master and ten nodes to measure differential gene expression of 1, 1 billion RNA [24] sequencing. However, it was concluded that the Amazon Elastic Compound Cloud was used to study massive data (1, 1 milliard sequences read) within 2 hours with a cost of \$66.

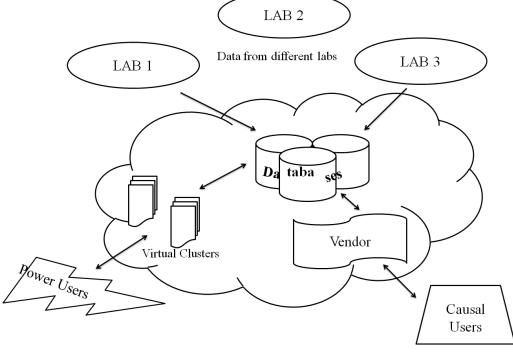
5. Analysis of Genome and detection of SNP

Even a single traditional machine took weeks to evaluate a human re-sequencing experiment and note down the whole genome [25]. This mixture evaluated vast collections of DNA sequences with virtual data sets, which retained a minimum accuracy rate, [26],[27] of 98, 9 percent. The system of input files was spread in a southwestern cloud over many nodes. No comprehensive software engineering was also needed for parallel calculations. The same analysis topic is solved in a particular order for a similar analysis.[28] the approach has been considered more time-consuming and laborious in the wet laboratory.

6. Mpi BLAST

In 2003, Mpi blast was implemented as a parallelization blast to increase sequence searching speed. Using Mpi, database segmentation was implemented, and Mpi blast divides the databases into tiny bits on pooled storage. Each worker node can execute a blast scan using a database segmentation piece. As a result, the Mpi blast reveals that a single worker needs 22.4 hours to complete the task, while 128 employees complete the search in 8 minutes. The Beowulf cluster was used to take advantage of a low-cost and powerful Linux cluster in the simulation.





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3) INTELLECTUAL PROPERTY AND BIOINFORMATICS

In this paper, the authors would like to depict intellectual property law as one of the legislative frameworks, intellectual property holders' rights, and liabilities with particular reference to the patentee and the rights that intellectual property provides. We will also discuss the scope and significance of Bioinformatics, various Bioinformatics components, and the relation of IPR. [29]

3.1 Scope of IPR in Bioinformatics

The scope of IP protection for Bioinformatics [30] can be divided into two main components: Bioinformatics resources in the form of databases and raw data compilations, and Bioinformatics tools in the form of specific software that aids in data retrieval and analysis. Any researchers consider DNA sequencing or separation of DNA sequences part of Bioinformatics.[31] The scholar, on the other hand, disagrees with this latter classification. Since it is a research project that offers raw data, it is essential to use Bioinformatics techniques to solve the problem. The sole use of computer-based technologies in isolating DNA sequences does not imply that it is part of Bioinformatics. Bioinformatics does not separate complex DNA sequences or the human genome. Bioinformatics is defined as computer technology, such as software and programs, for data compilation and cataloguing. In reality, it is a branch of molecular biology science. It is, after all, a branch of computational biology[32] that doesn't discuss whether there is space for IP security in the isolation of DNA sequences; instead, it assesses the different protection of innovation in the context of biomedical databases; and data-mining computer platforms and applications.[33]

3.2 BIOINFORMATICS DATABASE IP SECURITY

A biological database is a vast, well-organized, stable infrastructure reflecting information technology and data collection software. Biological databases of four forms exist principal, secondary, composite, and integrated.

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Primary Databases

Primary databases include raw nucleic acid sequences (DNA and RNA), [34] protein sequences, and biochemical reactions. They are constantly revised and provide a massive volume of data collected from experiments. Mostly the state money maintains these databases. Many of the central databases are publicly available and accessible to everyone.[35]

Secondary Databases

Secondary databases are extracted from the information available in central databases from the biological archive. Protein databases like CATH, OMIM, SCOP, PROSITE, and Swiss-Prot. Protein databases. [36] Any secondary databases are not widely publicly accessible.

Composite Databases

Composite Databases include information from various other primary sources like NCBI, which contains all the prior reports.

Trademark and Trade secret Protection for Bioinformatics

Trade Secret Law also covers the secondary databases. [37] Because the developer does whatever it can to prevent entry to the database, it can be protected by commercial secrets. However, it is difficult to maintain the database private in today's world. Marking legislation will include only the contents of the archive. The database creators will also be covered under copyright legislation. They can forbid the copying or download of material by third parties under contract law. The only protection form for non-original databases is contract law. The database's creator can avoid a conflict of confidence and violation of contract law.

Currently, the most often used contracts for database security are Shrink-wrap and Clickwrap. The shrink-wrap license is written in the wrapping procedure used in CD databases. When using the products, it complies with all product requirements. Clickwrap license is for internet users, on the other hand. When customers want to view the material of the database, they need to electronically enter the "agreement" indicating their commitment to the agreement.

Patent Protection for Bioinformatics

➤ Patent Protection for DNA RNA and other Bioinformatics tools

Although biomolecules can be patented as compositions, it is not patentable to use the composition information, i.e., the abstract biological sequence itself. To register as patentable subject matter, a natural sequence must, according to Diamond vs. Diehr [38], [39], be defined as a process, device, and apparatus. A definition and an abstract idea are not patentable in and of itself. Therefore, the patent protection for DNA, RNA, and protein sequence is restricted not to the abstract biological sequence of details that characterize the structure but to biological and physical compositions. Consequently, only the design itself, rather than the specifics within the molecule, cannot be prohibited by a patentee.

Patent Protection for Biological Sequences

If bio-sequences are not patentable, a compilation of biological sequences is a biology library and biological collections. To be patentable, they need to apply to a statutory issue. The process by which the database was developed does not, even though the database itself is not a patentable issue. [40] The information could be processed in the State Street case, while a completed product was not patentable. Second, copyright is restricted instead of to the database itself to the process of constructing a database. That will reduce the patent's validity, so a manufacturer who wants to infringe on the copyrighted invention may quickly produce the product in a non-infringing way. [41]

3.3 BIOLOGICAL DATABASES PROTECTION IN INDIA

At the moment, many countries' laws protecting databases are the same as those watching other databases. The EU, on its way to protecting Bioinformatics databases, [42] follows the sui generis path. Copyright regulation is used to shield them in most other jurisdictions. Excluded from cooperation with non-EU states, the EU can be affected. This is the case in the EU and the USA. The Database Directive's goal was to protect databases and create a special right for the first time. State law and the right to use the database or to have their registered office, principal office, or place of operation. The laws in the United States and the EU are so different that specific databases will be protected at the same time in each country, and EU law cannot cover

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all databases at once. The US will only secure particular databases, and a limited amount of more enormous databases can be protected within the European Union. The Berne Convention on Intellectual Property Rights examined whether databases can be covered under copyright or copyright in the US.

3.4 Challenges of cloud computing in Bioinformatics

Cloud Computing

Concerning Management, Technological, Legal there are specific challenges are there

> The Aspect of Management

The key issues include lack of confidence in users' data protection and privacy, loss of governance, and unsure enforcement by providers. [43] Often, an arrangement at the service level could not include an undertaking to permit customers to inspect their records. Loss in data management may have a severe effect on the approach of a cloud customer. [44]

Technological

Various technological problems in cloud computing usage include resource depletion, performance unpredictability, data lock-in, data transmission bottlenecks, and vulnerabilities within massively distributed cloud networks. [45] Cloud computing's two core advantages are low cost and computing power accessible upon request. Many cloud vendors commit computer capital to retain consumers due to the heavy competition. Certain cloud users can also upload or download vast volumes of cloud data. Errors are more complex to detect and remedy in these massively distributed cloud infrastructures. The migration of data and services to an internal IT environment is challenging for cloud users. The cloud is the company's future; now, it is the cloud.

Legal

Various legal concerns such as contract law, intellectual freedom, computer jurisdiction, and confidentiality are raised when using cloud storage. [46] Cloud data can simultaneously have more than one legal place with varying legal implications. Poor reporting of violations is also a

critical matter of privacy.[47] Cloud computing is a multi-level power, storage, and network shared resource environment. Centralized computing and pooled storage capacity mean that cloud users are at greater risk of communicating confidential data to unwanted parties (such as health records). The privacy risk in this setting involves the lack of separation systems for various building partners' distribution, storage, routing, and even integrity.

3.5. Role of IPR in meeting up the challenges of cloud computing in Bioinformatics

Trademark

The protection of trademarks is challenging since it is uncertain what constitutes a Trademark violation and whether the privilege is protected in the cloud. International acceptance is increasing that marking rights can extend to the Internet and that such security should not be weaker or more stringent than outside the Internet. The international consensus shall proceed.

IP issues

Clouds, such as eBay and Amazon, which allow the sale of certain assets, are more likely to infringe on trademarks. The conditions to establish the relation between the use of a sign and the defense of a trademark must be internationally agreed upon. The European Court of Justice says the courts have to conform their orders to the cyberspace world. There has been no agreement on the international law fraternity's conditions could violate trademark rights. According to the European Court of Justice, the courts should note that the long-term authority they exercise does not interfere with the sovereignty of another nation.

Copyright

What is an infringement in one country may not be so in another? When seeking to describe the complex cloud world in terms of copyright, the courts ought to be careful. In the cloud arena, the extent of copyright is in doubt. There is no specific liability for the copyright-protected content provided by intermediaries. Some countries encourage people and close friends and family circles to make copies of songs and movie files for private use.

Trade Secret/Confidentiality

In cloud storage, personal and sensitive data privacy is a significant concern. A take-it-or-leave-it deal may be used for cloud computing services (standard form contracts) If the "reasonably secure" requirements of trade secrets are held in the cloud is yet to be determined. The lack of data protection in the shadows is of interest in certain nations. Cloud downtime can be potentially catastrophic for businesses that rely on these clouds for their daily transactions. The only good advice is not to hold classified items in the cloud to safeguard trade secrets.

4. CONCLUSION

As an innovator in the light of Bioinformatics, researchers are well-positioned in the interpretation of science in the form of technology as Bioinformatics is the tool used by the scientist and the researchers for meeting up the primary need in pharmaceutical and biomedical engineering. So, with the recent advancement in information technology concerning the internet of things, cloud computing in computational intelligence has met up the updated scientific knowledge for the research interactions in the research professionals.

Now, as an IP enthusiast in the field of scientific application, the authors have concluded in the chapter that Intellectual Property (IP) has various facets in a lot of Bioinformatics and Internet of things especially the Patent and Trademark are of paramount importance other IPR legislation are also involved which helps in analyzing the privacy protection for Bioinformatics.

So, it is crucial which shall be looked over by the researchers and various other scientific organizations to embellish a revolution.

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