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Intellectual Property Protection in Cloud Computing and Role of Internet of Things (IoT) In Bioinformatics

***Aranya Nath[1], Shreeja Shyama Praharaj[2], Antara Paral[3]**

[1]School of Law, KIIT University, Bhubaneswar, India https://orcid.org/0000-0002-1705-2793
[2]School of Law, KIIT University, Bhubaneswar, India https://orcid.org/0000-0002-3690-1658
[3]School of Law, IFIM University, Bangalore, India https://orcid.org/0000-0002-1680-8982

***Abstract**: During Medieval Period it has been observed that Bio refers only about nature and environment. In the 17th century when biology has been coined it refers to study of human, animals, living creations etc. Whereas in 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 about Bioinformatics, it is 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 terms of 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 important role in various facets of Bioinformatics which will discussed in the paper. So from the above interpretation we've got some light that how Bioinformatics perform the interpretation with cloud computing and IOT so it is essential that. Protection in the form of Intellectual Property Rights (IPR) be obtained for such research and development activity. As IPR has various facets so it will help in gaining investments through assets. Lastly, we would like to conclude our chapter that how the challenges of cloud computing has been redressed by IPR for Bioinformatics*

Keywords: IOT (Internet of Things), Bioinformatics, cloud computing, IPR, Biological databases.

1. INTRODUCTION

Background

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

Earlier when a patient suffers from any chromosomal disorders it takes a quite amount of time in order to sequence the complicated biological data sets. Now with the revolution or in a simple way advancement of technological science the growth of the Bioinformatics moves on a highest peak. Bioinformatics have two types of databases which are working simultaneously in order 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 that how Bioinformatics generally works therefore, now the authors would throw some light on two emerging points which are 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. Common Bioinformatics techniques require a long time to achieve outcomes and are impossible to decipher owing to the difficulty of the data involved, therefore cloud computing is a boon for Bioinformatics research. Now another important tool in information science in the era of technology is IOT, which helps to analyse 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 advancement of latest techniques so it is utmost necessary to look into the scientific- legal protection of those technologies which will address the management of protection and to understand all kinds of challenges faced by the users.

Objective

The main aim to perform this analytical research is to identify the gaps pertaining to understanding of various advancement of Bioinformatics as a tool for helping the researchers in various aspects and also to identify the newest form of technology which is being prominently used by researchers, scientists worldwide. This would help the readers to understand the current emerging trends pertaining to 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.

Contribution

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

Structure

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 which are 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 the challenges faced by the cloud computing and IOT has been analyzed by the Intellectual Property thus a legal remedy has been given to the people if any issue occurs with respect to violation of privacy rights

2. EVOLUTION OF BIOINFORMATICS

More than a century ago Bioinformatics was coined by Gregor Mendel, the Austrian monk. The "Father of Genetics" he is considered. He crossed several colours with the same plant flower. He registered systematically the colours of the flowers that he crossed and the colours 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 in order to start Human Genome Project which was the first international research project in earlier 1970 in order to mapped the gene for influenza bacteria specimen.

Now with the origin of network and internet genetic mapping is growing rapidly through the advancement of Java, HTML websites. Now we'll discuss about the origin of biological databases

2.1. Origin of Biological Databases

In 1956, the first protein sequence identified was that of bovine insulin, which had 51 residues. Dayhoff compiled all available sequence data a year later to create the first Bioinformatics database. A biological database is a massive, integrated body of persistent data. A single file with a volume of data, each with the same data set, can be a simple database. 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 which 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, and it includes 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 both 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 as well as 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 important for resolving biological issues [4],[5]

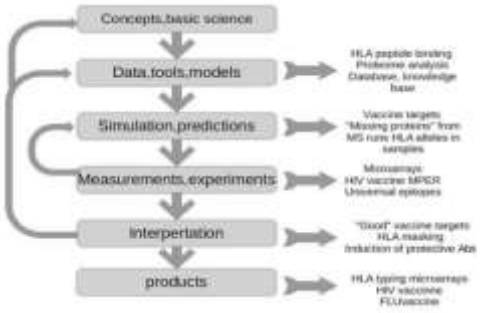

Figure 1 here depicts the application of AI in Bioinformatics

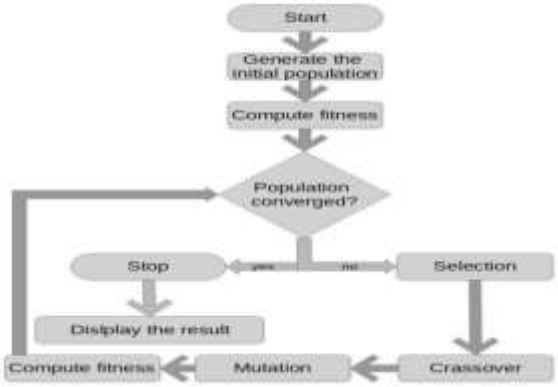

Figure 2 depicts flowchart of genetic algorithm for Bioinformatics

Data Mining

Data mining is called the retrieval or "mining" of data from huge amounts of data. Data Mining is an analysis of new and interesting patterns and interactions in huge 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 the discovery of genes, the recognition of protein function domains, motif function detection, protein function inference, cancer prediction, forecasting, disease optimization care, and the network of protein and gene interactions.[8]

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 the interpretation of biological databases.It is much more advantageous because the tools used over here are of valuable and mathematical in nature. Some of the valuable tools are discussed below

1. Computational evolution is a series of techniques known as algorithms of evolution. 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 optimisation problems. A large number of workers with very basic and low intelligence are either cooperating or competing to form a new type of swarm or collective intelligence. One of the swarm intelligence algorithms is the ant-colony optimization algorithm, which is simulated by ants 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. On the basis of the discoveries of the neuro scientist, a number of 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 found in this phase of research by means of 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.

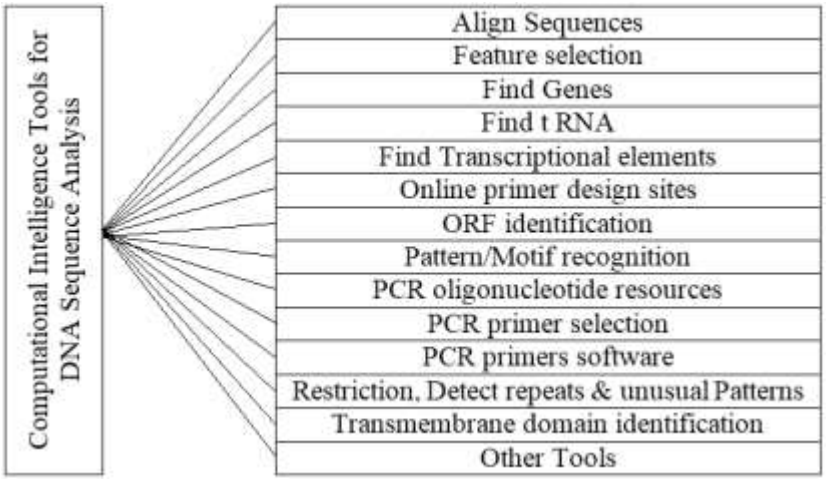

Figure 3- Computational Intelligence for DNA Sequence analysis

1. Second Phase

This process is aimed at evaluating the value of parameters by using the entropy analysis of Shannon.[12] Therefore a survey and special matrices have been prepared for each of the Bioinformatics experts to produce the best results.

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

The above expression helps in obtaining the weight of the variable of biological databases.

2. Third Phase

Finally in this phase data structure for Computation of IOT in DNA analysis are evaluated for 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 organization with Bioinformatics, information science, policymakers, and decision makers. In the future, the Internet of Things is crucial in a number of areas.The growing demand for both technologies is driven by many forces and a growing number of companies, governments, engineers, scientists and technologists are beginning to implement both. If the potential benefits and opportunities of IoT are combined, they can be discovered on both the device and the server levels.AI methods in combination with IoT are finally possible to analyse people's behaviour by using Analog transmission, motor sensors or face detection technology, and to change lighting and room temperatures. The aim of the research is to collect new findings about new artificial intelligence methods for data processing and storage from the cloud-based Internet of Things. Bioinformatics now uses computational information based on Internet of Things to archive, search, display, analyse 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 internet, is viewed as a parasite on computers and their various fields as hosts in terms of research.In terms of research, 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 data 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 analyse such massive amounts of data in a smooth and comfortable manner. [15] Accepting the challenge, the IT sector responded with the option of operating in a simulated world with no real resources. As it is considered in online platform so the term cloud computing evolved over here. [16]

Previously, the term "cloud" [17] was used as a metaphor for 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 used 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 use for personal purposes only authorized persons of the enterprises are able to access the databases.[19]
2. Public Cloud: It is operated by third parties which are easily accessible with certain security measures.[20]
3. Hybrid Cloud : It is the combination of the both the clouds which are discussed above which states that some parts of the information are of public use and the rest part are restricted for public only the concerned persons are able to 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 in order 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 fragments are looked for to classify the organism. This is a computing component that requires heavy computing and high machine capital. A technique used for metagenomical studies is Meta Genome Rapid Annotation with the aid of subsystem technology (MGRAST).[21] In a sample of only 10 KB of Metagenomics data, which was used for analysis in cloud systems, dedicated servers and local environments to calculate the calculation necessary for a blow. [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 to analyze or solve the 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 generate data very rapidly and promise to grow exponentially in the future. Unfortunately, since the data formats created by tools are in their own informal metadata format, neurological data is not shared. CARMEN [23]

4. RNA Analysis

Myrna is a pipeline that complements the RNA sequence analysis of current ERANGE, Cufflinks platform for measuring differential gene expression. It can be used in cloud computing with Hadoop, Map Reduce or on a single-tone screen. It took about four hours and twenty minutes with 1 master and 10 nodes to measure differential gene expression of 1, 1 billion RNA [24] sequencing. It was concluded, however, that the use of the Amazon Elastic Compound Cloud 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

In order to evaluate a human re-sequencing experiment and note down the whole genome, [25] even a single traditional machine took weeks. This mixture evaluated vast collections of DNA sequences with virtual data sets, which retained a minimum accuracy

rate, [26],[27] of 98, 9 per cent. The system of input files was spread in a south-western cloud over many nodes. No comprehensive software engineering was also needed for parallel calculations. The same topic of analysis is solved in a particular order for the 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 variant of blast to increase sequence searching speed. Database segmentation was implemented using Mpi, and Mpi blast divides the databases into small bits on pooled storage so that each worker node can execute blast scan using a database segmentation piece. As a result, Mpi blast reveals that a single worker needs 22.4 hours to complete the task, while 128 employees complete the search in 8 minutes. In the simulation, the Beowulf cluster was used to take advantage of a low-cost and powerful Linux cluster.

3) INTELLECTUAL PROPERTY AND BIOINFORMATICS

Now in this paper, the authors would like to depict intellectual property law, as one of the legislative framework, intellectual property holders' rights and liabilities with special reference to patentee and the rights that intellectual property provides. We will also discuss the scope and significance of Bioinformatics, various components of Bioinformatics and with 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 to be a 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 the isolation of DNA sequences does not imply that it is part of Bioinformatics. Bioinformatics does not provide the separation of complex DNA sequences or the human genome. Bioinformatics is defined as the use of computer technology, such as software and programmes, 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] which doesn't discuss whether there is space for IP security in the isolation of DNA sequences; rather, 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 huge, well-organized, stable infrastructure, which reflects information technology, and data collection software. Biological databases of four forms exist: principal, secondary, composite and integrated.

- 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 huge volume of data collected from experiments. Mostly the state money maintains these databases. Many of the main databases are publicly available and are also opening accessible to everyone.[35]

- Secondary Databases

Secondary databases are extracted from the information available in main databases from the biological archive. Protein databases like CATH, OMIM, SCOP and 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 primary information.

Trademark and Trade secret Protection for Bioinformatics

The secondary databases are also covered by trade Secret Law. [37] Because the developer does whatever it can to prevent entry to the database, it can be protected by commercial secrets. In today's world, though, it is a difficult job to maintain the database private. Marking legislation will include only the contents of the archive. The database creators will also be covered under copyright

legislation. They can forbid copying or downloading of material by third parties under contract law. The only protection form for non-original databases is contract law. In contract law, the creator of the database has the ability to avoid a conflict of confidence and violation.

At the moment, the most often used contracts for database security are Shrink wrap and Click wrap. The shrink wrap licence is the licence written in the wrapping procedure used in CD databases. When using the products, it complies with all product requirements. Click wrap licence 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 bio molecules can be patented as compositions, it is not patentable to use the composition information, i.e. the abstract biological sequence itself. In order to register as patentable subject-matter, a biological 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. The patent protection for DNA, RNA and protein sequence therefore is restricted not to the abstract biological sequence of details which characterize the structure, but to biological and physical compositions. As a consequence, only the composition itself, rather than the specifics within the molecule, cannot be prohibited by a patentee.

- Patent Protection for Biological Sequences

A compilation of biological sequences is a biology library and biological collections, if bio-sequences are not patentable. In order to be patentable, they need to be applicable 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] In the State Street case the information could be processed, while information as 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 easily 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 protecting other databases. The EU, on its way to protect 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 is so different that certain databases will be protected at the same time in each country, and EU law cannot cover all databases at once. The US will only secure certain databases and a limited amount of bigger databases can be protected within the European Union. In the US, the Berne Convention on Intellectual Property Rights examined whether databases can be covered under copyright or copyright.

3.4 Challenges of cloud computing in Bioinformatics

Cloud Computing

With respect to Management, Technological, Legal there are certain 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 serious 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 massive distributed cloud networks. [45] Two core advantages in cloud computing are low cost and computing power accessible upon request. Many cloud vendors commit computer capital in order to retain consumers due to the heavy competition. Certain cloud users can also need to upload or download huge volumes of cloud

data. Errors are more complex to detect and remedy in these very massive distributed cloud infrastructures. The migration of data and services to an internal IT environment is difficult for cloud users to do so. 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 have more than one legal place simultaneously 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 means that cloud users are at greater risk of communicating confidential data to unwanted parties (such as health records). The privacy risk in this sort of setting involves the lack of separation systems for the distribution, storage, routing and even integrity of various building partners.

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 violation of the trademark and whether the privilege is to be 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 is shall be 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 use of a sign and the defence of a trademark must be internationally agreed. The European Court of Justice says the courts have to conform their orders to the cyberspace world. There has been no agreement on the conditions on which trademark rights could be violated by the international law fraternity. The courts should note, according to the European Court of Justice that the long-term authority which 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, as well as to close friends and family circles, to make copies of songs, movie files for private use.

Trade Secret/ Confidentiality

In cloud storage, private and sensitive data privacy is a major 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. In certain nations, the lack of data protection in the clouds is of interest. 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 which is used by the scientist and the researchers for meeting up the primary need in pharmaceutical and biomedical engineering. So with the recent advancement in the field of information technology with respect to internet of things, cloud computing in the arena of computational intelligence has meet 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 the field of Bioinformatics and Internet of things especially the Patent and Trademark are of main importance other IPR legislation are also involved which helps in analyzing the privacy protection for Bioinformatics.

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

ANNOTED BIBLIOGRAPHY

[1] Avery, o. T., McLeod, c. M., & McCarty, m. (1944). Studies on the chemical nature of the substance inducing transformation of pneumococcal types: Induction of transformation by a desoxyribonucleic acid fraction isolated from pneumococcus type iii. *The journal of experimental medicine*, *79*(2), 137–158. https://doi.org/10.1084/jem.79.2.137

[2] Shameer, K., Badgeley, M. A., Miotto, R., Glicksberg, B. S., Morgan, J. W., & Dudley, J. T. (2017). Translational bioinformatics in the era of real-time biomedical, health care and wellness data streams. *Briefings in Bioinformatics*, *18*(1), 105–124. https://doi.org/10.1093/bib/bbv118

[3] *Agrawal—Fast Algorithms for Mining Association Rules.pdf*. (n.d.). Retrieved May 2, 2021, from http://www.vldb.org/conf/1994/P487.PDF

[4] Altman, R. B. (2001). Challenges for intelligent systems in biology. *IEEE Intelligent Systems*, *16*(6), 14–18. https://doi.org/10.1109/5254.972065

[5] Narayanan, A., Wu, X., & Yang, Z. R. (2002). Mining viral protease data to extract cleavage knowledge. *Bioinformatics (Oxford, England)*, *18 Suppl 1*, S5-13. https://doi.org/10.1093/bioinformatics/18.suppl_1.s5

[6] Raza, K. (n.d.). *APPLICATION OF DATA MINING IN BIOINFORMATICS*. *1*(2), 5.

[7] *Principles of Data Mining | The MIT Press*. (n.d.). Retrieved May 2, 2021, from https://mitpress.mit.edu/books/principles-data-mining

[8] *The-Morgan-Kaufmann-Series-in-Data-Management-Systems-Jiawei-Han-Micheline-Kamber-Jian-Pei-Data-Mining.-Concepts-and-Techniques-3rd-Edition-Morgan-Kaufmann-2011.pdf*. (n.d.). Retrieved May 2, 2021, from http://myweb.sabanciuniv.edu/rdehkharghani/files/2016/02/The-Morgan-Kaufmann-Series-in-Data-Management-Systems-Jiawei-Han-Micheline-Kamber-Jian-Pei-Data-Mining.-Concepts-and-Techniques-3rd-Edition-Morgan-Kaufmann-2011.pdf

[9] Sastry, K., Goldberg, D. E., & Kendall, G. (2014). Genetic Algorithms. In E. K. Burke & G. Kendall (Eds.), *Search Methodologies: Introductory Tutorials in Optimization and Decision Support Techniques* (pp. 93–117). Springer US. https://doi.org/10.1007/978-1-4614-6940-7_4

[10] Alam, S., Dobbie, G., Koh, Y. S., Riddle, P., & Ur Rehman, S. (2014). Research on particle swarm optimization based clustering: A systematic review of literature and techniques. *Swarm and Evolutionary Computation*, *17*, 1–13. https://doi.org/10.1016/j.swevo.2014.02.001

[11] *Principles of Artificial Neural Networks | Advanced Series in Circuits and Systems*. (n.d.). Retrieved May 2, 2021, from https://www.worldscientific.com/worldscibooks/10.1142/8868

[12] Shannon, C. E. (2001). A mathematical theory of communication. *ACM SIGMOBILE Mobile Computing and Communications Review*, *5*(1), 3–55. https://doi.org/10.1145/584091.584093

[13] *Ross—2010—Fuzzy logic with engineering applications.pdf*. (n.d.). Retrieved May 2, 2021, fromhttp://iauctb.ac.ir/Files/%D9%88%D8%A8%20%D8%B3%D8%A7%DB%8C%D8%AA%20%D8%A7%D8%B3%D8%A7%D8%AA%DB%8C%D8%AF/fuzzy%20logic%20with%20engineering%20application-3rdEdition.pdf

[14] *Future Generation Computer Systems*. (n.d.). Retrieved May 18, 2021, from https://www.journals.elsevier.com/future-generation-computer-systems/call-for-papers/artificial-intelligence-for-cloud-based-internet-of-things-i

[15] *40-h-anwar_al-zaid_-cloud_computing_an_overview.pdf*. (n.d.). Retrieved May 2, 2021, from https://www.ijarcce.com/upload/2013/september/40-h-anwar_al-zaid_-cloud_computing_an_overview.pdf

[16] Gutiérrez, V., Galache, J. A., Sánchez, L., Muñoz, L., Hernández-Muñoz, J. M., Fernandes, J., & Presser, M. (2013). SmartSantander: Internet of Things Research and Innovation through Citizen Participation. In A. Galis & A. Gavras (Eds.), *The Future Internet* (pp. 173–186). Springer. https://doi.org/10.1007/978-3-642-38082-2_15

[17] Frankenfield, J. (n.d.). *How Cloud Computing Works*. Investopedia. Retrieved May 2, 2021, from https://www.investopedia.com/terms/c/cloud-computing.asp

[18] Thakur, R., & Bandopadhyay, R. (2013). *Role of cloud computing in bioinformatics research for handling the huge biological data* (pp. 321–329)

[19] *What is a Private Cloud and What are its Advantages?* (n.d.). SearchCloudComputing. Retrieved May 2, 2021, from https://searchcloudcomputing.techtarget.com/definition/private-cloud

[20] *What is a Public Cloud—Definition | Microsoft Azure*. (n.d.). Retrieved May 2, 2021, from https://azure.microsoft.com/en-in/overview/what-is-a-public-cloud/

[21] Meyer, F., Bagchi, S., Chaterji, S., Gerlach, W., Grama, A., Harrison, T., Paczian, T., Trimble, W. L., & Wilke, A. (2019). MG-RAST version 4—Lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. *Briefings in Bioinformatics*, *20*(4), 1151–1159. https://doi.org/10.1093/bib/bbx105

[22] Qiu, J., Ekanayake, J., Gunarathne, T., Choi, J. Y., Bae, S.-H., Li, H., Zhang, B., Wu, T.-L., Ruan, Y., Ekanayake, S., Hughes, A., & Fox, G. (2010). Hybrid cloud and cluster computing paradigms for life science applications. *BMC Bioinformatics*, *11*(12), S3. https://doi.org/10.1186/1471-2105-11-S12-S3

[23] Watson, P., Lord, P., Gibson, F., Periorellis, P., & Pitsilis, G. (2008). Cloud Computing for e-Science with CARMEN. *Proceedings of the 2nd Iberian Grid Infrastructure (IBERGRID)*. https://eprint.ncl.ac.uk/159845

[24] Langmead, B., Hansen, K. D., & Leek, J. T. (2010). Cloud-scale RNA-sequencing differential expression analysis with Myrna. *Genome Biology*, *11*(8), R83. https://doi.org/10.1186/gb-2010-11-8-r83

[25] Rust, A. G., Mongin, E., Birney, E., Rust, A. G., Mongin, E., & Birney, E. (n.d.). *Genome annotation techniques:*
[26] Schatz, M. C., Langmead, B., & Salzberg, S. L. (2010). Cloud Computing and the DNA Data Race. *Nature Biotechnology*, *28*(7), 691–693. https://doi.org/10.1038/nbt0710-691
[27] Schadt, E. E., Linderman, M. D., Sorenson, J., Lee, L., & Nolan, G. P. (2010). Computational solutions to large-scale data management and analysis. *Nature Reviews. Genetics*, *11*(9), 647–657. https://doi.org/10.1038/nrg2857
[28] Thakur, R. S., Bandopadhyay, R., Chaudhary, B., & Chatterjee, S. (2012). Now and Next-Generation Sequencing Techniques: Future of Sequence Analysis Using Cloud Computing. *Frontiers in Genetics*, *3*. https://doi.org/10.3389/fgene.2012.00280
[29] Madhani, P. M. (2011). *Indian Bioinformatics: Growth Opportunities and Challenges* (SSRN Scholarly Paper ID 1967317). Social Science Research Network. https://papers.ssrn.com/abstract=1967317
[30] *Gopalan—2009—Bioinformatics Scope of Intellectual Property Pro.pdf*. (n.d.). Retrieved May 2, 2021, from http://docs.manupatra.in/newsline/articles/Upload/4277A947-FC79-4F6D-B213-82A67D76754B.pdf
[31] *Bioinformatics and Intellectual Property Protection*. (n.d.). Retrieved May 2, 2021, from https://lawcat.berkeley.edu/record/1118214?ln=en
[32] University, C. M. (n.d.). *What is Computational Biology? - Computational Biology Department - School of Computer Science - Carnegie Mellon University*. Retrieved May 2, 2021, from http://cbd.cmu.edu/about-us/what-is-computational-biology.html
[33] INSIGHTS. (2016, March 21). Intellectual Property Rights and India. *INSIGHTSIAS*. https://www.insightsonindia.com/2016/03/21/intellectual-property-rights-india/
[34] Chang, J., & Zhu, X. (2010). Bioinformatics Databases: Intellectual Property Protection Strategy. *Undefined*. /paper/Bioinformatics-Databases%3A-Intellectual-Property-Chang-Zhu/aeb9ee2dfd8794f2fd82b85abbf66b4154af90dd
[35] McBride, M. S. (2002). Bioinformatics and Intellectual Property Protection. *Berkeley Technology Law Journal*, *17*(4), 1331.
[36] *Human Genome Project Information*. (n.d.). Retrieved May 2, 2021, from https://web.ornl.gov/sci/techresources/Human_Genome/
[37] *Bioinformatics And Intellectual Property Rights*. (2014, August 13). Academike. https://www.lawctopus.com/academike/bioinformatics-intellectual-property-rights/
[38] *Diamond v. Chakrabarty | Case Brief for Law Students*. (n.d.). Retrieved January 2, 2021, from https://www.casebriefs.com/blog/law/intellectual-property-law/intellectual-property-keyed-to-merges/patent-law-intellectual-property-keyed-to-merges/diamond-v-chakrabarty/
[39] *Diamond v. Diehr, 450 U.S. 175 (1981)*. (n.d.). Justia Law. Retrieved May 2, 2021, from https://supreme.justia.com/cases/federal/us/450/175/
[40] *Intellectual Property: Companies Rush to Patent DNA | Science*. (n.d.). Retrieved May 2, 2021, from https://science.sciencemag.org/content/275/5301/780.summary
[41] *Intellectual Property Issues in Bioinformatics | Manualzz*. (n.d.). Manualzz.Com. Retrieved May 2, 2021, from https://manualzz.com/doc/31769238/intellectual-property-issues-in-bioinformatics
[42] Singh, K. (2015). *Intellectual Property Protection in Bioinformatics and Open Bio Development*. *163*, 25–45.
[43] Everett, C. (2009). Cloud computing – A question of trust. *Computer Fraud & Security*, *2009*, 5–7. https://doi.org/10.1016/S1361-3723(09)70071-5
[44] Jansen, W., & Grance, T. (n.d.). *Guidelines on Security and Privacy in Public Cloud Computing*. 80.
[45] Schweitzer, E. J. (2012). Reconciliation of the cloud computing model with US federal electronic health record regulations. *Journal of the American Medical Informatics Association: JAMIA*, *19*(2), 161–165. https://doi.org/10.1136/amiajnl-2011-000162
[46] Sen, J. (n.d.). *Security and Privacy Issues in Cloud Computing*. 42.
[47] *Grojil_volume-2_issue-2.pdf*. (n.d.). Retrieved May 2, 2021, from https://grojil.files.wordpress.com/2015/04/grojil_volume-2_issue-2.pdf