European journal of volunteering and community-based projects Vol.1, No 4; 2021
ISSN: 2724-0592 E-ISSN: 2724-1947
Published by Odv Casa Arcobaleno

Computational mapping and the efficient impacts of Deep learning approaches-DL in the modern computational systematic biology

Muhammad Mazhar Fareed

Faculty of Life Sciences, Department of Bioinformatics and Biotechnology, Government College University Faisalabad, Pakistan

Abstract: Deep learning (DL) has shown unstable improvement in its application to bioinformatics and has displayed thrillingly promising capacity to mine the complex relationship disguised in immense degree natural and biomedical data. A number of comprehensive reviews have been disseminated on such applications, running from evident level studies with future viewpoints to those primarily filling in as educational activities. These reviews have given a sensational preface to and rule for employments of DL in bioinformatics, covering various kinds of Simulated/Machine intelligence (ML) issues, diverse DL constructions, and extents of natural/biomedical issues. Regardless, by far most of these overviews have focused in on past research, while recurring pattern designs in the principled DL field and viewpoints on their future new developments moreover, logical new applications to science and biomedicine are as yet inadequate. We will focus in on present day DL, the constant examples and future headings of the principled DL field, and conjecture new and huge applications in bioinformatics.

Key words: Deep learning, bioinformatics, machine intelligence, biomedicine

Doi: 10.5281/zenodo.5816289

1.Introduction

Machine learning also called ML has been the principle supporter of the new resurgence of man-made brainpower. The most fundamental piece in current ML innovation is DL. DL is established on counterfeit neural organizations (ANNs), which have been hypothetically demonstrated to be fit for approximating any nonlinear capacity inside any predefined precision and have been generally used to tackle different computational assignments. In any case, they have been reprimanded for being dark boxes. deep learning method is very efficient, where experts used to take decades of time to determine the toxicity of a specific structure, but with a deep learning model it is possible to determine toxicity in a very less amount of time (depends on complexity could be hours or days). Deep learning models are able to represent abstract concepts of the input in the multilevel distributed hierarchy. It enables multitask learning for all toxic effects just in one compact neural network, which makes it highly informative (Alshahrani et al., 2017; Altae-Tran, Ramsundar, Pappu, & Pande, 2017). This absence of interpretability has restricted their applications, especially at the point when their presentation didn't stand out among other more interpretable ML techniques, like direct relapse, strategic relapse, support vector machines, and choice trees. During the previous decade, three significant advances in science and innovation have prompted the revival of ANNs, especially by means of DL. To begin with, uncommon amounts of information have been produced in current life, generally imaging and normal language information and The network is forced to efficiently represent the training data, making it more effective at generating data similar to the training data. If we had a large corpus of training images (such as the ImageNet dataset), we could build a generative neural network that outputs images (as opposed to classifications) (Anand & Huang, 2018). The intricate nature of data induction from such information has presented incredible difficulties to other ML strategies however has been taken care of well by ANNs. Additionally, high-throughput natural information, for example, cutting edge sequencing, metabolomic information, proteome information, and electron tiny underlying information, has raised similarly testing computational issues. Second, computational force has been expanding quickly with reasonable expenses, including the improvement of new registering gadgets, for example, designs handling units and field programmable entryway clusters. Such gadgets give ideal equipment stages to profoundly resemble models. Third, a scope of proposed improvement calculations has made profound ANNs stand apart as an ideal method for enormous and complex information investigations and data disclosure contrasted with contending methods in the enormous information time. Here are likewise a few issues in the bioinformatics field as follows, which should be handled. To start with, the interpretability of model is fundamental to researcher to see how model takes care of the natural issue, for example anticipating DNA–protein restricting. Second, the clinical anticipate precision of computational model identified with the medical services or illness conclusion is 98%–close to 100% and it is difficult to arrive at that high exactness (Bocicor, Czibula, & Czibula, 2011; Doersch, 2016). In addition, two major forward leaps have immensely expanded the relevance of ANN strategies: convolutional neural networks (CNNs) for imaging information and repetitive neural organizations (RNNs) for regular language information, which will be presented in the Beneficial material with other notable structures. We reviewed the writing and arranged the quantity of distributions in log-scale for 14 generally examined natural subjects showing up along with 'RNN', 'CNN', or 'profound getting the hang of' as indicated by PubMed, True to form, 'picture' is the most regularly moved toward theme by DL, and 'infection' and 'imaging' follow intently. CNN are significantly more often utilized in bioinformatics than RNNs on the grounds that CNNs can effectively catch nearby elements, addressing essential issues, for example, recognizing what's more, applying preserved arrangement themes (Fei-Fei, Fergus, & Perona, 2006). The challeneges of deep learning in biological domains today are; in the point of Deep learning then, at that point, refine that preparation, utilizing as not many as a few hundred organic pictures like the ones they wish to consider. One more test with profound learning is that PCs are both unintelligent and languid, When it comes to profound learning, in addition to any information will do. The strategy frequently requires monstrous, very much commented on informational indexes. Imaging information gives a characteristic fit, however in this way, as well, do genomic information. Profound learning apparatuses could likewise assist specialists with delineating illness types, comprehending sickness subpopulations, finding new therapies and matching them with suitable patients for clinical testing and therapy. Finkbeiner, for example, is important for a consortium called Answer ALS, a work to consolidate a scope of information genomics, transcriptomics, epigenomics, proteomics, imaging, and even pluripotent undifferentiated organism science from 1,000 individuals with the neurodegenerative infection amyotrophic horizontal sclerosis (additionally called engine neuron illness). "Interestingly, we'll have an informational collection where we can apply profound learning and see whether profound learning can uncover a connection between the things we can quantify in a dish around a cell, and what's befalling that patient," he says. For all its guarantee, profound learning presents critical difficulties, scientists caution. Likewise, with any computational-science procedure, the outcomes that emerge from calculations are just pretty much as great as the information that go in. Overfitting a model to its preparation information is likewise a worry. Furthermore, for profound learning, the rules for information amount and quality are regularly more thorough than some test scientists may anticipate. Deep learning calculations have required amazingly huge informational indexes that are all around clarified so the calculations can figure out how to recognize includes and classify designs. Bigger, unmistakably named informational indexes with a large number of information focus addressing diverse test and physiological conditions give specialists the most adaptability for preparing a calculation. Finkbeiner noticed that calculation preparing in his work works on essentially after around 15,000 models. Those top-notch 'ground truth' information can be incredibly difficult to find, says Carpenter. To go around this test, specialists have been chipping away at ways of preparing more with less information. Advances in the fundamental calculations are permitting the neural organizations to utilize information substantially more proficiently, Carpenter says, empowering preparing on a small bunch of pictures for certain applications. Researchers can likewise take advantage of move learning, the capacity of neural. organizations to apply grouping ability procured starting with one information type then onto the next kind. For instance, Finkbeiner's group has fostered a calculation that it at first educated to foresee cell passing based on morphology changes. Albeit the analysts prepared it to concentrate on pictures of rat cells, it accomplished 90% exactness whenever it first was presented to pictures of human cells, improving to almost 100% as it acquired insights (Webb, 2018). The socially impact of the simply about the deep learning-DL a structure that consolidates deep learning with network science for demonstrating social impact and foreseeing human conduct on certifiable exercises, like going to an occasion or visiting an area. has offered the chance to concentrate on the elements of data spread and impact proliferation at a colossal scale. Significant exploration has zeroed in on the social impact peculiarity and its effect on OSNs. Social impact assumes a vital part in forming individuals' conduct and influencing human choices in different areas. we concentrate on the effect of social impact on disconnected elements to concentrate on human genuine conduct. We present Social Influence Deep Learning (SIDL), a structure that consolidates profound learning with network science for displaying social impact and foreseeing human conduct on true exercises, like going to an occasion or visiting an area. We propose various methodologies at different levels of organization networks with the target of confronting two normal difficulties of profound learning: interpretability and adaptability. We approve and assess our methodologies utilizing information from Plancast, an Event-Based Social Network, and Foursquare, a Location-Based Social Network. At long last, we investigate the utilization of various profound learning structures, and we examine the connection between's friendly impact and clients protection introducing results and a few notes of alert with regards to the dangers of sharing touchy information (Luceri, Braun, & Giordano, 2019).

For a portion of its organic picture acknowledgment work, Google Accelerated Science utilizes calculations that were at first prepared on a huge number of shopper pictures mined from the Internet. Scientists then, at that point, refine that preparation, utilizing as not many as a few hundred natural biological pictures like the ones they wish to examine. Here, we center around the continuous patterns also, future headings of present-day DL, point of view on future turns of events and likely new applications to science furthermore, biomedicine. And also mapping-flow of this paper sections are shown in Figure A.

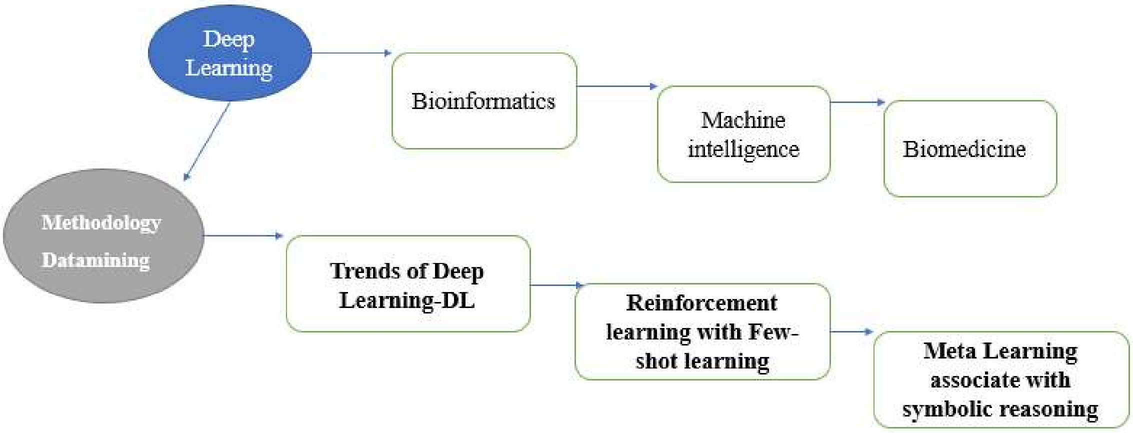

Figure A: The overall map of this research under the domains of Deep Learning approaches with biological systems

2.Methodology

2.1 Data Mining

These all data of mining and biological data are extracted from different resources and different reviews about the current situations, challenges, future perspectives in the domains of deep learning and computational biology like Pubmed, DeepLearn, MIT-DL and many others biological resources are taken to the final perspectives about the impact of deep learning or machine learning-ML in computational biology and systematic metanalytic bioresources systems (http://introtodeeplearning.com/) (Antun, Renna, Poon, Adcock, & Hansen, 2020; Hinton, 2018).

3.Trends of Deep Learning-DL

Consideration instruments, which were first proposed to direct machine-based interpretation assignments can ease the issues confronted by RNNs when applied to bioinformatics issues, consequently growing their space of uses in bioinformatics. The self-consideration layer can decipher the unique portrayal of an info arrangement (for example one-hot encoding for RNA, DNA, or protein arrangements) into one more portrayal of the arrangement (Finn, Abbeel, & Levine, 2017). For each position in the arrangement, the different situations in the information arrangement attempt to all the more likely describe that position for catching the semantic importance of the arrangement and collaborations between diverse consecutive positions.

Consideration instruments might possibly be utilized in a wide scope of bio-sequence investigation issues, like RNA grouping investigation and forecast protein structure and work expectation from amino corrosive arrangements, and IDs of enhancer–advertiser collaborations (EPIs). For model, EPIs show incredible importance to human advancement since they are basic to the guideline of quality articulation and are firmly identified with the event of human sicknesses. In any case, exploratory strategies to recognize EPIs require a lot of time, labor, and cash. EPIVAN was intended to anticipate long-range EPIs utilizing just genomic arrangements through DL strategies and considerations systems (Hamilton, Bajaj, Zitnik, Jurafsky, & Leskovec, 2018; Hong, Zeng, Wei, & Liu, 2020). This strategy has been tried on six cell lines, and the region under the beneficiary working attributes (AUROC) and region under the accuracy review bend (AUPR) upsides of EPIVAN are higher than those without the consideration instrument, which demonstrates that the consideration component is more worried about cell line-explicit includes and can all the more likely catch the concealed data according to the points of view of successions The surprising adaptability and versatility of gathering techniques and profound learning models have prompted the multiplication of their application in bioinformatics research. Generally, these two AI strategies have to a great extent been treated as autonomous philosophies in bioinformatics applications. AI in bioinformatics helps in this part to arrange protein structures, i.e., essential, optional, and tertiary constructions. Practical genomics: In this part, analysts try to portray quality capacities and collaborations. AI in science can assist with ordering transformations and protein subcellular confinement. What's more, profound learning has been fused into bioinformatic calculations. Profound learning applications have been utilized for administrative genomics and cell imaging. Different applications incorporate clinical picture order, genomic grouping examination, just as protein structure arrangement and forecast (Hornik, 1991), and the major classification of machine learning are shown in Figure 01 (Gao, Calhoun, & Sui, 2018).

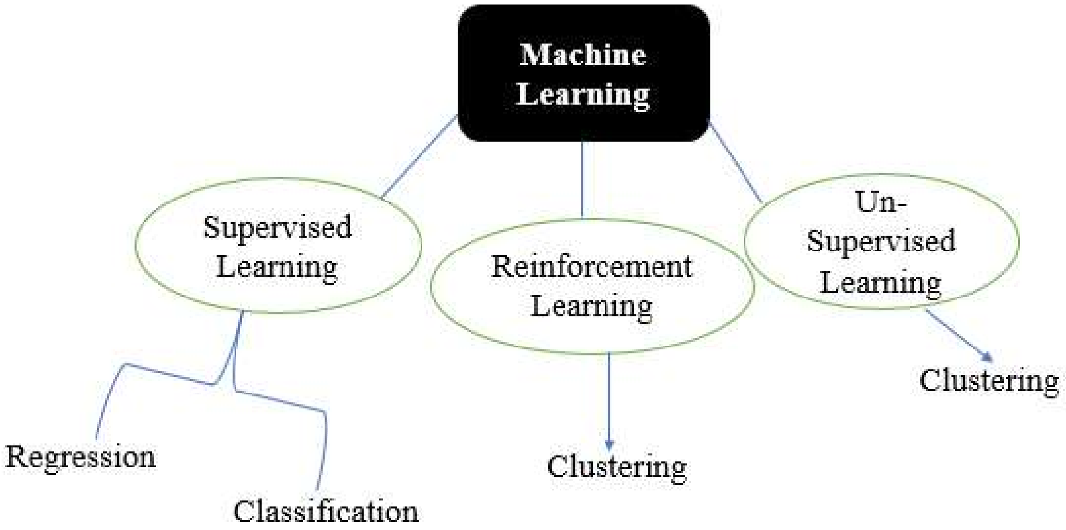

Figure 01: Classification of Machine learning

4.Reinforcement learning with Few-shot learning

Reinforcement learning also called RL, as considered what moves to make, given the present status of the fractional answer for expand the combined award. After each activity, the state can change. Perceptions about the arrangement of change-of-state become directing data for future activities. This kind of support learning has as of late been joined into the DL worldview, alluded to as profound support learning (Hou et al., 2019). Note that a key recognizing highlight is that clients don't need to predefine every one of the states, and a model can be prepared in a start to finish way, which has turned into an undeniably dynamic examination field with various calculations being created. Support learning can be applied in aggregate cell relocation, DNA section get together furthermore, portraying cell development. DNA part gathering is a strategy that expects to recreate the first DNA arrangement from an enormous number of pieces by deciding the request in which the parts must be gathered back into the first DNA particle, furthermore, it is additionally a NP-hard enhancement issue. proposed another support learning-based model for taking care of this issue (Y.-J. Hu, Lin, Lin, Lin, & You, 2014; Z. Hu, Ma, Liu, Hovy, & Xing, 2016). Support learning in this issue was formed as preparing the specialist to discover a way during collecting pieces from the underlying to a last arrangement state, boosting the exhibition measure, one of the wellness capacities, which totals the cross-over scores over every single nearby part. This support learning model shows less computational intricacy and pointless outside management in the learning process contrasted and the hereditary calculation and directed methodology, separately, the despite the fact that there is a lot of information in the bioinformatics field, information shortage actually happens in science and biomedicine (Imrie, Bradley, van der Schaar, & Deane, 2020). For instance, under the enzyme/catalyst commission (EC) grouping, just one catalyst has a place with the class of phosphonate dehydrogenase (EC 1.20.1.1). For this situation, standard DL calculations can't work since one necessity various information for each class to prepare a generalizable DL model. Hardly any shot learning, as its name shows, is intended to deal with these cases. On a fundamental level, scarcely any shot learning trains a ML model with a tiny amount of information. In outrageous cases, there is just one preparing test for one class, alluded to as a single shot learning. Also characterized is zero-shot realizing when a class has no preparation test. Utilizing not many shot learning calculations, a model can be prepared with sensible execution on some troublesome issues by using as it were the current restricted information. Hardly any shot learning is appropriate for some issues in bioinformatics that have restricted information, for example, protein work expectation and medication revelation. For example, the medication revelation issue is to enhance the competitor particle that can adjust fundamental pathways to accomplish restorative action by finding simple atoms with expanded drug action. Because of the limit of little organic information, it is trying to shape exact expectations for novel mixtures (Ingraham, Garg, Barzilay, & Jaakkola, 2019). As we looked, a single shot learning has been utilized to altogether bring down the amount of information required and accomplishes exact forecasts in drug disclosure, the strategy proposed in this work joins iterative refinement long momentary memory (LSTM) and chart CNNs and can work on the learning of significant distance measurements over little particles. Iterative refinement LSTMs can sum up to new trial tests related yet not indistinguishable from tests in the preparation assortment, and chart convolutional networks are helpful for changing little atoms into nonstop vectoral portrayals. The consequences of applying a single shot model to various examine assortments show solid execution contrasted with other strategies, like irregular timberland and diagram CNNs. Thusly, this a single shot technique is equipped for moving data between related however unmistakable learning errands (Joslin et al., 2018). And the reinforcement learning algorithm are shown in Figure 02 (Gullapalli, 1990).

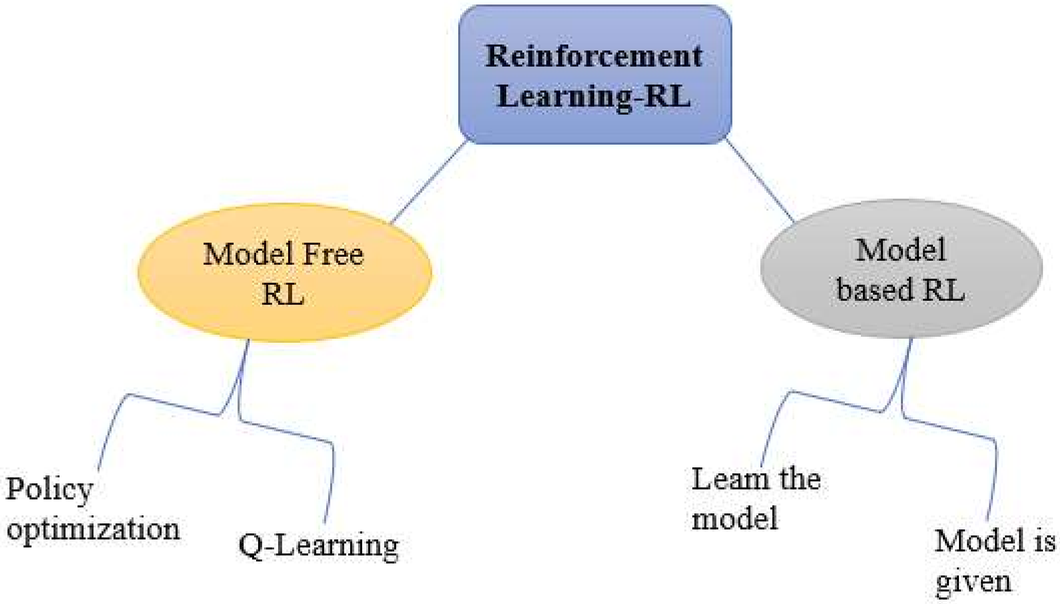

Figure 02: The Reinforcement Learning RL algorithms

5.Meta Learning associate with symbolic reasoning

Meta learning also known as ‘learn-to-learn’, which can rapidly gain proficiency with another undertaking with a couple of preparing tests dependent on models prepared for related undertakings. A decent meta learning model ought to sum up to another undertaking regardless of whether the undertaking has never been experienced during the preparation time. The key thought is that when preparing a model is done, the model should be presented to a new task during the testing stage, a few steps of adjusting are performed, and then, at that point, the model's exhibition on the new errand is checked. In a nutshell, meta learning yields a ML model that can adapt rapidly. For example, the capacity of a counter acting agent to react to an antigen relies upon the counter acting agent's particular acknowledgment of an epitope. In this way, meta learning can be utilized in B-cell conformational epitope forecast in ceaselessly advancing infections, which is valuable for immunizations plan (Killoran, Lee, Delong, Duvenaud, & Frey, 2017; Y. Li et al., 2019). The proposed meta learning approach depends on stacked and course speculations. In the progressive engineering, the meta student of each level will include the meta highlights yielded from a low level and yield the meta elements to progressive levels until the high level which will yield the last grouping result, and the many other healthcare perspectives in DL are observed and under consideration like in virological sciences (Calandra & Favareto, 2020). Low connection among these meta students shows that these students genuinely have correlative prescient capacities, what's more, the removal investigation demonstrates that these students differentially cooperated also, added to the last meta model. Subsequently, the meta student can investigate the reciprocal prescient qualities in various expectation instruments what's more, incorporate these devices to outflank the single best-performing model through meta learning. Emblematic thinking engaged DL It is essential that as of not long ago, DL still can't seem to incorporate emblematic thinking or rationale as a feature of its toolbox, subsequently having discarded the fundamental data given by rationale reason and the related clarify capacity. In ongoing years, ML analysts have fostered various techniques to join representative dissuading DL. For model, SATNet utilizes a differentiable satisfiability solver to connect DL and rationale thinking; NLM takes advantage of the force of both DL and rationale programming, using it to perform inductive learning and rationale thinking productively. In the bioinformatics field, representative thinking is applied and assessed on organized natural information, which can be utilized for information incorporation, recovery, and combined inquiries in the information chart (Y. Li et al., 2018; Z. Li, Nguyen, Xu, & Shang, 2017). This strategy consolidates representative strategies, specifically, information portrayal utilizing representative rationale and mechanized thinking, with neural organizations that encode for related data inside information charts (Secinaro, Calandra, Secinaro, Muthurangu, & Biancone, 2021), and these embeddings can be applied to anticipate the edges in the information chart, such as medication target relations. The exhibition joining representative strategies beats customary methodologies (Park, Min, Choi, & Yoon, 2017; Socher et al., 2013; Zou, Tian, Gao, & Li, 2019), and the deep learning pipelines networking in biological and computational sciences are shown in Figure 03 (M. Li et al., 2021).

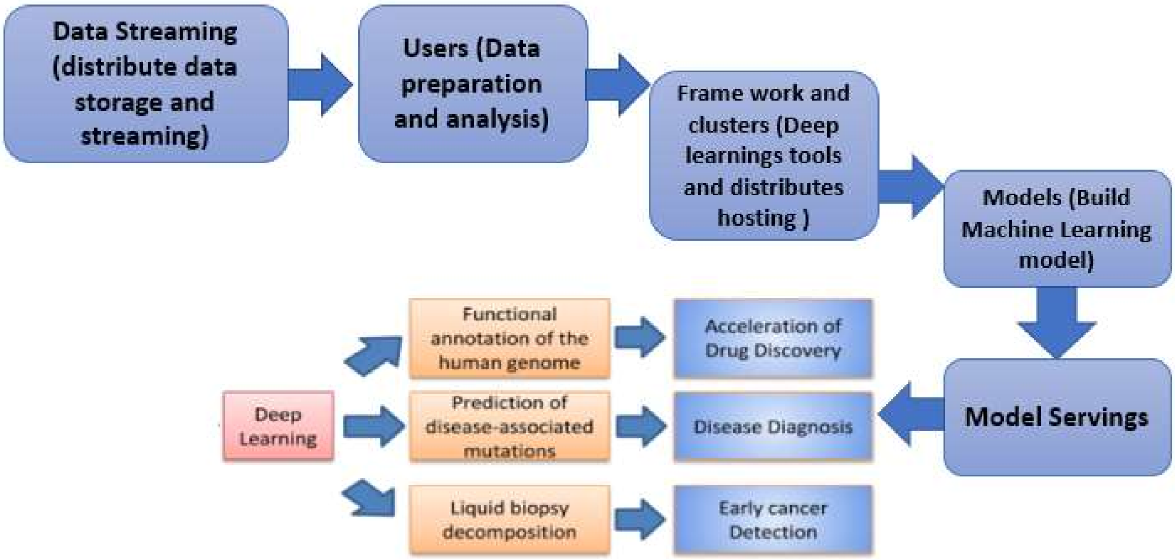

Figure 03: The Deep Learning pipeline and obstacles of computational biology network

6.Conclusion:

DL is a moderately new field analysed to customary ML, and the use of DL in bioinformatics is an even more current field. Nonetheless, the last decade has seen the quick advancement of DL with thrillingly encouraging ability to mine complex connections concealed in largescale natural and biomedical information. The future challeneges in the domains of deep learning; In the section on deep learning, information procurement instruments permitted life researchers to gain multimodal information from various organic application areas. Sorted in three expansive sorts (for example pictures, signals, and successions), this information is tremendous in sum and complex in nature. Mining such a tremendous measure of information for design acknowledgment is a major test and requires refined information concentrated AI strategies. Counterfeit neural organization-based learning frameworks are notable for their example acknowledgment abilities, and recently their profound structures known as profound learning (DL)- have been effectively applied to tackle numerous perplexing example acknowledgment issues. To examine how DL-particularly its various designs have contributed and been used in the mining of natural information relating to those three kinds, a meta-investigation has been performed and the subsequent assets have been fundamentally breaking down. Zeroing in on the utilization of DL to examine designs in information from assorted organic spaces, this work explores diverse DL structures' applications to this information. This is trailed by an investigation of accessible open-access information sources relating to the three information types alongside well-known open-source DL devices appropriate to this information. Additionally, near examinations of these apparatuses from subjective, quantitative, and benchmarking points of view are given. At last, some open examination challenges in utilizing DL to mine organic information are laid out and various conceivable future viewpoints are placed forward. Recent innovative headways in information securing instruments permitted life researchers to gain multimodal information from various natural application areas. Classified in three-wide sorts (for example pictures, signals, and groupings), this information is colossal in sum and complex in nature. Mining such a tremendous measure of information for design acknowledgment is a major test and requires refined information concentrated AI strategies. Counterfeit neural organization-based learning frameworks are notable for their example acknowledgment abilities, and recently their profound models known as profound learning (DL) have been effectively applied to tackle numerous mind-boggling design acknowledgment issues. To examine how DL-particularly its various structures has contributed and been used in the mining of natural information relating to those three kinds, a meta-investigation has been performed and the subsequent assets have been fundamentally dissected. Zeroing in on the utilization of DL to examine designs in information from assorted natural spaces, this work explores diverse DL structures' applications to this information. This is trailed by an investigation of accessible open-access information sources relating to the three information types alongside well-known open-source DL instruments relevant to this information. Additionally, similar examinations of these apparatuses from subjective, quantitative, and benchmarking points of view are given. At long last, some open exploration challenges in utilizing DL to mine organic information are illustrated and various conceivable future points of view are advanced. In this article, we assessed some chose present day and principled DL approaches, some of which have as of late been applied to bioinformatics, while others have not yet been applied. This viewpoint might reveal new insight for a significant length of time utilizations of present-day DL strategies in bioinformatics.

References:

Alshahrani, M., Khan, M. A., Maddouri, O., Kinjo, A. R., Queralt-Rosinach, N., & Hoehndorf, R. (2017). Neuro-symbolic representation learning on biological knowledge graphs. *Bioinformatics, 33*(17), 2723-2730.

Altae-Tran, H., Ramsundar, B., Pappu, A. S., & Pande, V. (2017). Low data drug discovery with one-shot learning. *ACS central science, 3*(4), 283-293.

Anand, N., & Huang, P. (2018). Generative modeling for protein structures.

Antun, V., Renna, F., Poon, C., Adcock, B., & Hansen, A. C. (2020). On instabilities of deep learning in image reconstruction and the potential costs of AI. *Proceedings of the National Academy of Sciences, 117*(48), 30088-30095.

Bocicor, M.-I., Czibula, G., & Czibula, I.-G. (2011). *A reinforcement learning approach for solving the fragment assembly problem.* Paper presented at the 2011 13th International Symposium on Symbolic and Numeric Algorithms for Scientific Computing.

Calandra, D., & Favareto, M. (2020). Artificial Intelligence to fight COVID-19 outbreak impact: an overview. *European Journal of Social Impact and Circular Economy, 1*(3), 84-104.

Doersch, C. (2016). Tutorial on variational autoencoders. *arXiv preprint arXiv:1606.05908*.

Fei-Fei, L., Fergus, R., & Perona, P. (2006). One-shot learning of object categories. *IEEE transactions on pattern analysis and machine intelligence, 28*(4), 594-611.

Finn, C., Abbeel, P., & Levine, S. (2017). *Model-agnostic meta-learning for fast adaptation of deep networks.* Paper presented at the International Conference on Machine Learning.

Gao, S., Calhoun, V. D., & Sui, J. (2018). Machine learning in major depression: From classification to treatment outcome prediction. *CNS neuroscience & therapeutics, 24*(11), 1037-1052.

Gullapalli, V. (1990). A stochastic reinforcement learning algorithm for learning real-valued functions. *Neural networks, 3*(6), 671-692.

Hamilton, W. L., Bajaj, P., Zitnik, M., Jurafsky, D., & Leskovec, J. (2018). Embedding logical queries on knowledge graphs. *arXiv preprint arXiv:1806.01445*.

Hinton, G. (2018). Deep learning—a technology with the potential to transform health care. *Jama, 320*(11), 1101-1102.

Hong, Z., Zeng, X., Wei, L., & Liu, X. (2020). Identifying enhancer–promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. *Bioinformatics, 36*(4), 1037-1043.

Hornik, K. (1991). Approximation capabilities of multilayer feedforward networks. *Neural networks, 4*(2), 251-257.

Hou, H., Gan, T., Yang, Y., Zhu, X., Liu, S., Guo, W., & Hao, J. (2019). Using deep reinforcement learning to speed up collective cell migration. *BMC bioinformatics, 20*(18), 1-10.

Hu, Y.-J., Lin, S.-C., Lin, Y.-L., Lin, K.-H., & You, S.-N. (2014). A meta-learning approach for B-cell conformational epitope prediction. *BMC bioinformatics, 15*(1), 1-15.

Hu, Z., Ma, X., Liu, Z., Hovy, E., & Xing, E. (2016). Harnessing deep neural networks with logic rules. *arXiv preprint arXiv:1603.06318*.

Imrie, F., Bradley, A. R., van der Schaar, M., & Deane, C. M. (2020). Deep generative models for 3D linker design. *Journal of chemical information and modeling, 60*(4), 1983-1995.

Ingraham, J., Garg, V. K., Barzilay, R., & Jaakkola, T. (2019). Generative models for graph-based protein design.

Joslin, J., Gilligan, J., Anderson, P., Garcia, C., Sharif, O., Hampton, J., . . . Jiang, S. (2018). A fully automated high-throughput flow cytometry screening system enabling phenotypic drug discovery. *SLAS Discovery: Advancing Life Sciences R&D, 23*(7), 697-707.

Killoran, N., Lee, L. J., Delong, A., Duvenaud, D., & Frey, B. J. (2017). Generating and designing DNA with deep generative models. *arXiv preprint arXiv:1712.06148*.

Li, M., Zhou, J., Hu, J., Fan, W., Zhang, Y., Gu, Y., & Karypis, G. (2021). Dgl-lifesci: An open-source toolkit for deep learning on graphs in life science. *ACS omega*.

Li, Y., Huang, C., Ding, L., Li, Z., Pan, Y., & Gao, X. (2019). Deep learning in bioinformatics: Introduction, application, and perspective in the big data era. *Methods, 166*, 4-21.

Li, Y., Wang, S., Umarov, R., Xie, B., Fan, M., Li, L., & Gao, X. (2018). DEEPre: sequence-based enzyme EC number prediction by deep learning. *Bioinformatics, 34*(5), 760-769.

Li, Z., Nguyen, S. P., Xu, D., & Shang, Y. (2017). *Protein loop modeling using deep generative adversarial network.* Paper presented at the 2017 IEEE 29th International Conference on Tools with Artificial Intelligence (ICTAI).

Luceri, L., Braun, T., & Giordano, S. (2019). Analyzing and inferring human real-life behavior through online social networks with social influence deep learning. *Applied network science, 4*(1), 1-25.

Park, S., Min, S., Choi, H.-S., & Yoon, S. (2017). *Deep recurrent neural network-based identification of precursor micrornas.* Paper presented at the Proceedings of the 31st International Conference on Neural Information Processing Systems.

Secinaro, S., Calandra, D., Secinaro, A., Muthurangu, V., & Biancone, P. (2021). The role of artificial intelligence in healthcare: a structured literature review. *BMC Medical Informatics and Decision Making, 21*(1), 1-23.

Socher, R., Ganjoo, M., Sridhar, H., Bastani, O., Manning, C. D., & Ng, A. Y. (2013). Zero-shot learning through cross-modal transfer. *arXiv preprint arXiv:1301.3666*.

Webb, S. (2018). Deep learning for biology. *Nature, 554*(7690), 555-558.

Zou, Z., Tian, S., Gao, X., & Li, Y. (2019). mldeepre: Multi-functional enzyme function prediction with hierarchical multi-label deep learning. *Frontiers in genetics, 9*, 714.