

Revolutionizing Drug Discovery; Transformative Role of Machine Learning

Moazzam Siddiq

Independent Researcher, Manchester, United Kingdom.

moazzam.siddiq86@gmail.com

ORCID 0009-0005-0372-3735

Abstract– The use of machine learning in drug discovery is examined in this review article along with any potential advantages, difficulties, and prospective future developments. The article examines the many machine learning models that have been created for these uses and emphasises the value of machine learning in predicting drug characteristics, discovering new therapeutic targets, and creating new drug candidates. The need for high-quality data, increased collaboration and data sharing, as well as ethical and regulatory considerations, are just a few of the obstacles and limitations of employing machine learning in drug discovery that are covered in this article. The study also highlights the necessity of regulatory frameworks that can guarantee the safety and efficacy of novel pharmaceuticals generated using these models, as well as the significance of transparency and accountability in the usage of machine learning algorithms. The discussion of potential future paths and prospects for development in the field of machine learning in drug discovery finishes the essay. Deep learning models, multi-task learning, personalised medicine, and the fusion of machine learning with other technologies like robotics and automation are a few examples of these. In order to speed up the drug discovery process and provide novel, efficient medicines to patients in need, the authors propose tackling the difficulties and limitations of machine learning in drug discovery as well as continuing to investigate these exciting areas of research and development. This review paper offers a thorough summary of the current status of machine learning in drug discovery, stressing its potential advantages and disadvantages as well as outlining the major areas for future research and development that are expected to spur advancement. Researchers, medication developers, and politicians who are curious about how machine learning could change the drug discovery process and enhance patient outcomes will find the paper interesting.

Keywords: Machine Learning, Drug discovery, pharmaceuticals, Robotics, Artificial Intelligence

1.INTRODUCTION

The identification and development of new medications to treat a range of ailments is a complex process called drug discovery [1]. For enhancing human health and lessening the impact of disease, innovative medicine research is crucial [2]. Drug discovery, however, is a time-consuming, expensive process that needs a substantial amount of resources and knowledge [3]. Target identification, lead discovery, lead optimization, preclinical testing, and clinical trials are only a few of the stages in the conventional drug discovery process that are involved. Researchers identify a particular biological target that is linked to a certain disease or condition during the target identification stage [4]. This can be accomplished using a variety of techniques, including high-throughput screening of chemical libraries, proteomics, and genomic analysis. In order to find prospective drug candidates that can bind to the target and change its activity, researchers can screen dozens or even millions of tiny molecules after they have identified a target [5]. Lead discovery is the name of this procedure. The chemical structure of a lead compound can then be improved by researchers in order to increase its efficacy, selectivity, and pharmacokinetic characteristics [6]. Lead optimization is the practise in question. Preclinical testing is done on a lead compound after it has been optimized to determine its safety and effectiveness in animal models [7]. A substance can move on to clinical trials, where it is tested on people to determine its safety, effectiveness, and pharmacokinetic features, if preclinical studies indicate encouraging results [8]. Drug discovery has come a long way over the past few decades, yet there are still many obstacles and restrictions to overcome [9]. One of the biggest obstacles is the biological systems' extreme complexity, which makes it challenging to predict how a medicine will act in vivo. The high failure rate of drug candidates in clinical trials, which might be brought on by subpar pharmacokinetics, toxicity, or ineffectiveness, is another issue. Researchers are using cutting-edge tools and strategies like machine learning and artificial intelligence to tackle these problems. A subset of artificial intelligence called "machine learning" uses algorithms to find patterns and connections in data. Machine learning can be used in drug discovery to analyse massive volumes of data and find prospective new drug candidates that might be successful in treating particular conditions [10]. The role of machine learning in drug development and the many methods that are employed to apply machine learning in this field will be covered in the sections that follow [11]. We will also talk about potential future paths and prospects for study in this field, as well as some of the difficulties and restrictions associated with employing machine learning in drug discovery. In order to increase the effectiveness and success rates of drug development, new technologies and methods are continually being created in the field of drug discovery [12]. One such technology that has the potential to revolutionize drug development is machine learning, which enables researchers to quickly and accurately find new drug candidates by analyzing massive volumes of data [13].

The ability of machine learning to analyse complicated data sets and find patterns and associations that would be challenging to spot using conventional approaches is one of the major benefits of machine learning in drug discovery [14]. For instance, machine learning algorithms can examine extensive genomics data to find gene expression patterns or genetic variants linked to particular diseases or situations [15]. The development of fresh treatment approaches can then be done using this knowledge to determine possible medication targets. High-throughput screening data can be analyzed using machine learning to find substances that have a good chance of attaching to particular targets and modifying their activity. By drastically cutting down on the time and resources needed for lead discovery and optimization, this strategy enables scientists to concentrate on the most promising therapeutic prospects [16].

The advancement of personalized medicine is yet another area where machine learning has the potential to revolutionize drug discovery [17]. Machine learning algorithms can pinpoint patient subgroups that are most likely to respond to a certain medication or treatment plan by analysing large-scale patient data sets [18]. This may make it possible to create therapies that are more individualized, successful, and suited to the needs of each patient [19]. Nevertheless, there are a number of difficulties and restrictions with applying machine learning in drug discovery. The absence of high-quality data, which is necessary for training machine learning algorithms, is one of the key problems [20]. Data in drug development may be insufficient or of low quality, which may reduce the efficacy of machine learning techniques [21]. The need for interpretable models, which may aid researchers in comprehending how machine learning algorithms make predictions and spotting any biases or inaccuracies in the data, is another obstacle [22]. This is crucial in the drug discovery process since poor forecasts might have serious repercussions [23].

Despite these difficulties, there are a number of potential methods for applying machine learning to the search for new drugs [24]. For instance, high-dimensional genomics data are analyzed using deep learning algorithms, a form of machine learning algorithm that can analyse complex data sets and find new drug targets. Other methods include reinforcement learning, which involves optimizing the drug development process by training algorithms, and transfer learning, which involves training machine learning algorithms on data from related domains. While machine learning has the potential to completely change the drug development process by allowing researchers too quickly and accurately find novel drug ideas by analyzing massive amounts of data [25]. While employing machine learning for drug discovery has several drawbacks and limits, there are also a number of potential strategies that are being developed to get over these obstacles. Machine learning is predicted to play an increasingly significant part in the creation of novel and efficient treatments for a variety of diseases and disorders as the science of drug discovery continues to advance [26].

THE ROLE OF MACHINE LEARNING IN ANALYZING VAST AMOUNTS OF DATA FOR DRUG DISCOVERY:

In order to find new medication candidates, massive and complex data sets must be analyzed. Researchers can quickly and accurately analyze these enormous volumes of data with the aid of machine learning (ML) [27]. In biological and chemical data, machine learning algorithms can find patterns and associations that can be exploited to create novel medications. A wide variety of data sets, including as genetic information, protein structures, and chemical compounds, can be analysed using machine learning (ML). Researchers can get a more thorough understanding of the molecular mechanisms behind disease and therapeutic activity by combining data from many source [28]. The capability of machine learning to analyze vast and complicated data sets rapidly and accurately is one of the main benefits of ML in drug discovery. This enables scientists to choose the best medicine candidates after doing further study. ML can be used to prioritize compounds for additional testing by predicting the toxicity of possible therapeutic candidates. The capacity of machine learning to analyze data in real-time is another benefit for drug research. Researchers can swiftly find new patterns and associations that can be exploited to generate novel medications by utilizing ML algorithms to analyze streaming data [29].

However, there are a number of difficulties and restrictions with using ML in drug development. For instance, in order to produce reliable predictions, ML models need high-quality data. Additionally, interpretable models that can shed light on the molecular mechanisms behind pharmacological action are required [30]. The possibility of bias and mistake in the data presents another difficulty and may reduce the precision of ML predictions.

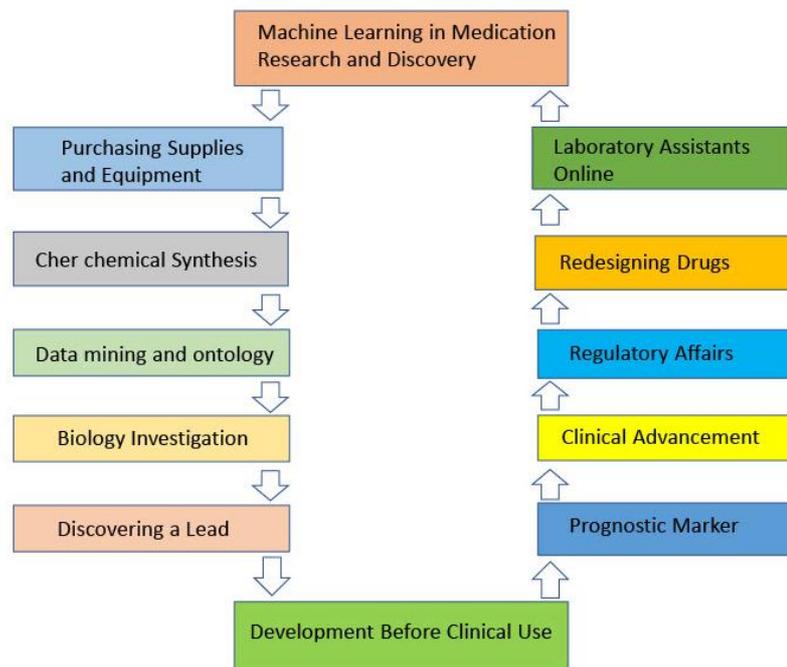


Figure 1: Understanding Drug Discovery by machine learning through Flow Chat

Here **Figure 1** is discussing the method of drug discovery by the use of machine learning. The use of ML in drug discovery is growing in popularity despite these difficulties. Researchers are creating new methods and algorithms to get beyond these restrictions and maximize the potential of ML for drug discovery [31]. Researchers can quickly and reliably analyse enormous volumes of data with the use of machine learning, which enables them to create novel medications that can enhance human health [32]. The two primary categories of ML algorithms are supervised learning and unsupervised learning [32]. In supervised learning, each data point is connected to a particular result or label, and the ML system is trained on a labelled dataset. In order to forecast the behavior of new, unlabeled data, the algorithm learns to identify patterns in the data [33]. The efficacy of possible medication candidates can be predicted using supervised learning in the drug discovery process. Researchers can use an ML model to predict the efficacy of novel, untested substances by training it on a dataset of known medications and their efficacy data [34]. On the other hand, unsupervised learning entails training an ML system on an unlabeled dataset. Without labelled data, the algorithm learns to spot patterns and connections in the data. Unsupervised learning can be used to find new drug development targets as well as to find patterns in very vast and complicated datasets. Designing new medications is a significant use of machine learning in the drug development process [35]. New drugs with particular features, such as increased efficacy, decreased toxicity, or better pharmacokinetics, can be created using ML algorithms. In comparison to conventional trial-and-error procedures, researchers can save time and resources by utilizing ML to create new medications [36]. Drug dosages and treatment plans can potentially be optimized using machine learning (ML). ML algorithms can determine the ideal dosage and timing for a given treatment by examining patient data and drug response data, lowering the risk of adverse effects and increasing patient outcomes [37]. While the world of drug development is being revolutionized by the application of ML in drug discovery, ML algorithms are capable of identifying possible medication candidates and creating novel pharmaceuticals with specified features by swiftly and accurately analyzing enormous amounts of data. Even though there are still difficulties and restrictions with the use of ML in drug discovery, scientists are creating new algorithms and strategies that can get around these problems and enhance people's health [38].

Analyzing Vast Amounts of Data in Drug Discovery Using Machine Learning

Historically, finding new drugs has been a tedious and expensive process that takes many years to complete [39]. The development of machine learning (ML) has the potential to completely transform the drug discovery process, particularly when it comes to the analysis of enormous volumes of data to find potential new therapeutic candidates. Finding chemical compounds with the potential to be turned into medicines for the treatment of diseases is a key step in the drug discovery process [40]. The goal of this approach is to find compounds that have the requisite biological activity and safety profiles by testing and analyzing a large number of molecules. Drug

development can be expedited and cost-effectively shortened by researchers using machine learning algorithms to analyse massive amounts of data [41].

The capability of employing ML in drug discovery to analyze huge and complicated datasets fast and accurately is one of its main benefits [42]. Machine learning algorithms can find patterns and relationships in enormous amounts of data that might not be immediately obvious using conventional analysis techniques [43]. Researchers may find prospective medication candidates this way that were missed by more conventional screening techniques. Large datasets of chemical compounds and biological data can be used to train machine learning algorithms, which then allows them to predict the attributes of new compounds [44]. For instance, to find the medicinal compounds that have the highest likelihood of being helpful in the treatment of particular diseases, ML algorithms can be trained on vast datasets of known drug compounds [45]. Given that researchers can immediately identify possible medication candidates that are most likely to be successful, this strategy offers the potential to dramatically cut the time and expense of drug development [46].

AI-Based Drug Discovery

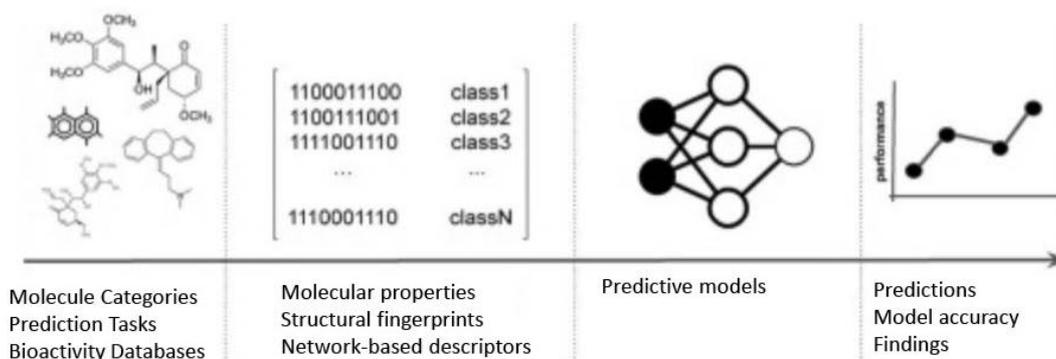


Figure 2: AI based discovery of Drug through

Here **Figure 2** is describing AI based drug discovery process that how we use AI in the field of drug discovery. Predicting the effectiveness and toxicity of new drugs is another way that machine learning may be used to analyze enormous volumes of data in drug research [47]. Large databases of well-known medicinal molecules and the efficacy and toxicity data linked to them can be used to train machine learning algorithms. As a result, scientists can forecast the effectiveness and toxicity of novel chemicals based on those substances' chemical compositions and other characteristics.

The ability of machine learning algorithms to swiftly and precisely analyze enormous amounts of data is a huge benefit in the drug discovery process. This makes it possible for researchers to find prospective medication candidates more rapidly and effectively than using conventional approaches. Additionally, ML algorithms can find links and patterns in the data that conventional techniques of analysis can miss [48].

The use of machine learning in drug discovery is fraught with difficulties. The necessity for a lot of high-quality data poses a problem. For ML algorithms to work well, vast datasets must be trained, and the quality of the data has a big influence on how accurate the predictions are. Additionally, not all organizations may have the specialized knowledge and abilities needed to employ machine learning in drug discovery [49]. Despite these difficulties, the application of machine learning to drug discovery offers a great deal of potential to transform the pharmaceutical industry. The time and expense associated with developing new drugs can be decreased by using machine learning (ML) algorithms to find possible therapeutic candidates more rapidly and effectively than with conventional techniques [50]. In addition to lowering the amount of animal and human trials necessary in the drug development process, the capacity to anticipate the efficacy and toxicity of new compounds using machine learning algorithms can also speed up the process of bringing new medications to market [51]. While machine learning has the potential to revolutionize the drug development process by making it possible to analyze enormous volumes of data in order to find novel therapeutic candidates [52]. Large datasets of biological and chemical molecules can

be analyzed by machine learning (ML) algorithms, which can speed up the process of identifying potential medication candidates [53]. Even though there are difficulties involved, machine learning's potential advantages make it an intriguing area of research for the field of drug development.

Because deep learning algorithms can analyze enormous volumes of data and identify possible drug candidates more quickly and accurately than ever before, their usage in drug discovery has increased recently [54]. This has resulted in the identification of innovative medication candidates with great specificity and efficacy [55]. The use of deep neural networks to predict the biological activity of tiny compounds based on their chemical structures is one of the most promising uses of deep learning in drug discovery.

APPLICATIONS OF DEEP LEARNING IN DRUG DISCOVERY

Using deep neural networks, quantitative structure-activity relationship (QSAR) modelling uses chemical structure to predict a compound's action against a particular biological target [56]. To create a model that can be used to predict the activity of new compounds, the neural network is trained on a huge dataset of known compounds and their corresponding biological activities [57]. The action of hundreds of tiny compounds across a variety of biological targets has been predicted using this method. In one study, for instance, scientists utilized a deep learning model to forecast the activity of substances against the protein kinase CHK1, a target for cancer treatment [58]. The model was developed by the researchers using a sizable dataset of well-known CHK1 inhibitors, and it was then used to forecast the activity of a group of novel drugs. The model discovered several substances with strong CHK1 inhibitory action, one of which was later found to be efficient in preventing tumor growth in animal models [59]. Generative models are another way that deep learning is being used in the drug development process to create novel molecules with desired attributes. Large datasets of chemicals can be used to train generative models so they can discover the patterns and structures connected to various biological functions [60]. These models can be used to create novel compounds that are anticipated to have the desired activity after being trained. For instance, researchers created novel chemicals that were active against the protein target bromodomain-containing protein 4 (BRD4), a prospective target for the treatment of cancer, using a generative model. The model was trained using a sizable dataset of well-known BRD4 inhibitors, and it was then utilised to produce a collection of novel compounds. After testing these substances in vitro, the researchers discovered that several of them had a lot of action against BRD4. Deep learning can be used to forecast drug toxicity and side effects in addition to finding novel treatment candidates. This may lessen the number of medications that toxicity problems cause to fail in clinical trials. In order to forecast the toxicity of substances based on their chemical structures, for instance, researchers utilized a deep learning model. The program was able to accurately estimate the toxicity of novel compounds after being trained on a sizable dataset of substances with known toxicity profiles.

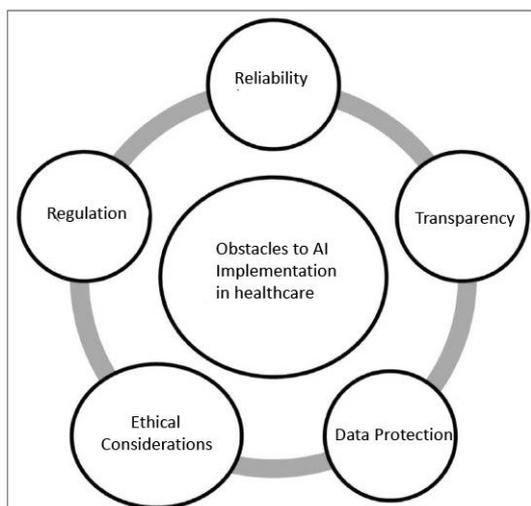


Figure 3: Implication of AI in health care

Figure 3 showing the implication process of AI in health care. These instances highlight deep learning's enormous potential for drug development. Deep learning can speed up the drug development process and assist in bringing new, efficient medicines to patients more rapidly by enabling researchers to analyze huge volumes of data and produce novel compounds with desired properties [61]. Deep learning in drug discovery is not without its

difficulties, though; they will be covered in more detail in the section below. Overall, applying deep learning to drug discovery has the potential to completely change how novel medications are found and developed. Deep learning can speed up the drug development process and assist in bringing new, efficient medicines to patients more rapidly by enabling researchers to analyse huge volumes of data and produce novel compounds with desired properties.

CHALLENGES AND LIMITATIONS OF USING MACHINE LEARNING IN DRUG DISCOVERY

Due to its potential to hasten drug development and enable the identification of innovative drug candidates with higher speed and accuracy than conventional methods, machine learning has attracted a lot of attention in recent years [62]. To fully realize its potential, machine learning must overcome a number of key obstacles and constraints related to the drug discovery process.

The availability and quality of data are two of the main obstacles to applying machine learning in drug discovery. An extensive dataset of compounds with proven activity against certain biological targets is needed to train machine learning models to predict the biological activity of small molecules. However, such information is frequently sparse and of varying quality. As a result, the model's accuracy may suffer and biases may be introduced. Additionally, the data used to train machine learning models is frequently gathered from several sources and can be extremely varied in terms of the quality of the experimentation and the data itself [63]. As a result, there may be difficulties with data pre-processing and normalization, which may affect how accurate the final models are. The interpretability of the models is another difficulty with using machine learning in drug discovery. Machine learning models are frequently referred to as "black boxes" since it can be challenging to comprehend how they make predictions. Finding the underlying biological mechanisms and pathways that underlie the reported activity of small compounds, which is essential for drug discovery, might be difficult as a result. Additionally, machine learning models are frequently extremely complicated and demand a large amount of processing power for both training and inference. Small research teams or those without access to high-performance computing resources may find this to be a significant hindrance. When employing machine learning in drug development, there are not only technological difficulties to be solved, but also ethical and legal issues to be considered. For instance, there are worries about the possibility of discrimination and prejudice ASin machine learning models, which can result in the exclusion of particular patient populations or the creation of medications that are less effective for particular subgroups. Furthermore, using machine learning in drug discovery comes with regulatory obstacles. Because machine learning models present special difficulties that traditional regulatory systems were not intended to address, it may be challenging to have pharmaceuticals produced using these techniques approved [64]. Despite these difficulties and restrictions, machine learning has a lot of potential for use in the drug discovery process. Machine learning has the potential to speed up the drug discovery process and enhance patient outcomes by making it possible to analyze massive datasets and produce fresh drug candidates with desired features. However, it's critical to address the difficulties and restrictions related to using machine learning in drug discovery, as well as to create new strategies and tools, in order to fully realize this promise.

When employing machine learning in drug discovery, there are a number of additional aspects to take into account in addition to the difficulties and restrictions mentioned above. The necessity of cooperation amongst various stakeholders in the medication development process is one of these elements. Researchers, doctors, and industry partners must collaborate and exchange knowledge in order to produce high-quality data and create accurate models. The requirement for machine learning model validation and testing is another element that needs to be taken into account. The activity of tiny molecules can be predicted by machine learning models with great accuracy, but it is crucial to evaluate these predictions in experiments. This is crucial when developing new pharmaceuticals because before a drug can be licensed for use in humans, its safety and effectiveness must be thoroughly assessed. Additionally, there is a requirement for enhanced accountability and openness in the application of machine learning to drug discovery. Developing techniques for deciphering the conclusions produced by machine learning models and spotting biases or limitations in the data or models employed is crucial as these models grow more complicated and challenging to interpret. The long-term effects of applying machine learning to drug discovery must be carefully considered [65]. Even though these techniques can hasten the development of new drugs and enhance patient outcomes, they also raise moral and cultural concerns regarding the use of technology in healthcare and the possibility that they might worsen already-existing disparities in access to care. The difficulties and restrictions related to using machine learning for drug discovery underline the necessity of continued study and advancement in this area. It is conceivable to realize the full potential of machine learning

in drug discovery and to improve patient outcomes in a safe and efficient manner by tackling these issues and creating new techniques and tools to get beyond these restrictions.

FUTURE DIRECTIONS AND OPPORTUNITIES FOR ADVANCEMENT IN THE FIELD

There are numerous intriguing potential directions and opportunities for advancement in the fast developing field of machine learning in drug discovery. We will go through some of the major areas of research and development that are anticipated to propel advancement in the upcoming years in this post [66]. The creation of deep learning models is among the most promising machine learning research topics for drug discovery. Artificial neural networks are used in deep learning, a sort of machine learning, to learn from data. These models have the ability to greatly increase prediction accuracy while minimizing the requirement for massive volumes of labelled data. The creation of models for multi-task learning is another field of study [67]. A kind of machine learning called multi-task learning allows for the simultaneous learning of several related tasks using a single model. This strategy enables the prediction of numerous properties of a chemical using a single model, potentially increasing the efficiency and accuracy of drug discovery.

In addition to these technical developments, the application of machine learning to drug discovery presents prospects for innovation. For instance, the application of machine learning in the creation of personalized medicine is gaining popularity. An approach to healthcare known as "personalized medicine" aims to cater each patient's care to their unique needs. The identification of patient-specific biomarkers and the prediction of individualized treatment outcomes are both possible thanks to machine learning, which has the potential to greatly enhance patient outcomes. The creation of new forms of data for machine learning models is another area of innovation. For instance, the utilization of imaging data for drug discovery is becoming more and more popular. Imaging information, such as that obtained from MRI and CT scans, can provide thorough details about the composition and operation of tissues and organs, which may be used to forecast the behavior of tiny molecules. The application of machine learning to the development of fresh medication candidates is also gaining popularity [68]. In this method, referred to as generative modeling, new molecules with desired features are created using machine learning. By enabling the quick development and testing of numerous novel drug candidates, generative modelling has the potential to drastically cut down on the time and cost involved in drug discovery. Finally, there is a lot of room for machine learning to be used with other technologies, such automation and robotics, to speed up the drug development process even further. Machine learning might, for instance, be applied to high-throughput screening technologies' massive volumes of data analysis and experiment design optimization. Machine learning for drug development has a lot of potential for innovation and advancement, but there are also obstacles that must be overcome if this technology is to reach its full potential. The requirement for more high-quality data is one of the main difficulties. The amount of data needed for drug development may be greatly reduced with machine learning, but accurate model training still requires high-quality data.

Greater cooperation and data sharing across various players in the drug development process is a challenge as well. Researchers, doctors, and industry partners must collaborate and exchange knowledge in order to produce high-quality data and create accurate models [69]. Additionally, there is a need for increased accountability and openness in the application of machine learning to drug discovery. Developing techniques for deciphering the conclusions produced by machine learning models and spotting biases or limitations in the data or models employed is crucial as these models grow more complicated and challenging to interpret.

When utilizing machine learning in drug development, ethical and legal issues must be taken into account. For instance, there are worries about the possibility of discrimination and prejudice in machine learning models, which can result in the exclusion of particular patient populations or the creation of medications that are less effective for particular subgroups. There are numerous interesting potential for innovation and advancement in the fast developing field of machine learning for drug discovery [70]. However, it is crucial to solve the difficulties and constraints connected with this strategy in order to fully realise its potential. Machine learning has the ability to dramatically enhance the drug discovery process and provide innovative, efficient medicines to patients in need by tackling these issues and cooperating to produce accurate and transparent models.

CONCLUSION

In summary, the use of machine learning in drug development is a fascinating and quickly developing topic that has enormous potential for expediting the discovery of novel drugs and providing patients with cutting-edge treatments. It has been demonstrated that machine learning models are useful for developing new drug candidates, finding novel therapeutic targets, and forecasting pharmacological attributes. The use of deep learning models, multi-task learning, personalized medicine, and the incorporation of machine learning with other technologies like robotics and automation are just a few of the promising areas of research and development that are likely to propel advancement in the upcoming years. To fully realise the potential of machine learning in drug discovery, there are other issues and constraints that must be resolved. These consist of the requirement for more high-quality data, increased collaboration and data sharing, accountability and transparency in the application of machine learning models, as well as ethical and legal considerations. The potential for additional advancement in the field of machine learning in drug discovery is substantial. We can use the power of machine learning to speed the drug discovery process and create more efficient medicines for patients in need if we solve these issues and collaborate.

REFERENCES

1. Utsha Sinha, Abhinav Singh, Deepak Kumar Sharma, Machine Learning in the Medical Industry, Handbook of Research on Emerging Trends and Applications of Machine Learning, 10.4018/978-1-5225-9643-1.ch019, (403-424), (2020).
2. Susanne Uusitalo, Jarno Tuominen, Valtteri Arstila, Mapping out the philosophical questions of AI and clinical practice in diagnosing and treating mental disorders, Journal of Evaluation in Clinical Practice, 10.1111/jep.13485, 27, 3, (478-484), (2020).
3. Rashid, M. T., Zhang, D. Y., & Wang, D. (2019, December). Socialcar: A task allocation framework for social media driven vehicular network sensing systems. In *2019 15th International Conference on Mobile Ad-Hoc and Sensor Networks (MSN)* (pp. 125-130). IEEE.
4. Shams, A. T., & Akter, S. (2022). Eco-Centric Versus Anthropocentric Approach in Literary Pedagogy: Inclusion of Non-Human Narratives as Teaching Social Justice.
5. Ozlem Erdas-Cicek, Ali Osman Atac, A. Selen Gurkan-Alp, Erdem Buyukbingol, Ferda Nur Alpaslan, Three-Dimensional Analysis of Binding Sites for Predicting Binding Affinities in Drug Design, Journal of Chemical Information and Modeling, 10.1021/acs.jcim.9b00206, 59, 11, (4654-4662), (2019).
6. Sebastian Raschka, Automated discovery of GPCR bioactive ligands, Current Opinion in Structural Biology, 10.1016/j.sbi.2019.02.011, 55, (17-24), (2019).
7. Javier Pérez-Sianes, Horacio Pérez-Sánchez, Fernando Díaz, Virtual Screening Meets Deep Learning, Current Computer-Aided Drug Design, 10.2174/1573409914666181018141602, 15, 1, (6-28), (2018).
8. Rashid, M. T., Zhang, D. Y., & Wang, D. (2020). DASC: Towards a road Damage-Aware Social-media-driven Car sensing framework for disaster response applications. *Pervasive and Mobile Computing*, 67, 101207.
9. Isidro Cortés-Ciriano, Nicholas C. Firth, Andreas Bender, Oliver Watson, Discovering Highly Potent Molecules from an Initial Set of Inactives Using Iterative Screening, Journal of Chemical Information and Modeling, 10.1021/acs.jcim.8b00376, 58, 9, (2000-2014), (2018).
10. Dries Harnie, Mathijs Saey, Alexander E. Vapirev, Jörg Kurt Wegner, Andrey Gedich, Marvin Steijaert, Hugo Ceulemans, Roel Wuyts, Wolfgang De Meuter, Scaling machine learning for target prediction in drug discovery using Apache Spark, Future Generation Computer Systems, 10.1016/j.future.2016.04.023, 67, (409-417), (2017).
11. Akhter, A., & Shams, A. T. (2022). Identity Economics in Emily Brontë's Wuthering Heights: An Empathetic Inquiry into Psychoanalysis. *SCHOLARS: Journal of Arts & Humanities*, 4(2), 74-80.
12. Hongming Chen, Udo Bauer, Ola Engkvist, Merged Multiple Ligands, Drug Selectivity, 10.1002/9783527674381.ch9, (247-274), (2017).
13. Rashid, M. T., Chowdhury, P., & Rhaman, M. K. (2015, December). Espionage: A voice guided surveillance robot with DTMF control and web based control. In *2015 18th International Conference on Computer and Information Technology (ICCIT)* (pp. 419-422). IEEE.
14. Fenglei Li, Qiaoyu Hu, Xianglei Zhang, Renhong Sun, Zhuanghua Liu, Sanan Wu, Siyuan Tian, Xinyue Ma, Zhizhuo Dai, Xiaobao Yang, Shenghua Gao, Fang Bai, DeepPROTACs is a deep learning-based targeted degradation predictor for PROTACs, Nature Communications, 10.1038/s41467-022-34807-3, 13, 1, (2022).
15. Muhammad Waqar Ashraf, Artificial Intelligence for Drug Development, Advances in Artificial Intelligence, Computation, and Data Science, 10.1007/978-3-030-69951-2_5, (127-132), (2021).
16. Ling Hao, Tyler Greer, David Page, Yatao Shi, Chad M. Vezina, Jill A. Macoska, Paul C. Marker, Dale E. Bjorling, Wade Bushman, William A. Ricke, Lingjun Li, In-Depth Characterization and Validation of Human Urine Metabolomes Reveal Novel Metabolic Signatures of Lower Urinary Tract Symptoms, Scientific Reports, 10.1038/srep30869, 6, 1, (2016).
17. Zhang, Y., Zong, R., Shang, L., Rashid, M. T., & Wang, D. (2021, June). Superclass: A deep duo-task learning approach to improving qos in image-driven smart urban sensing applications. In *2021 IEEE/ACM 29th International Symposium on Quality of Service (IWQOS)* (pp. 1-6). IEEE.

18. Harsh Chauhan, Jonathan Bernick, Dev Prasad, Vijay Masand, The Role of Artificial Neural Networks on Target Validation in Drug Discovery and Development, *Artificial Neural Network for Drug Design, Delivery and Disposition*, 10.1016/B978-0-12-801559-9.00002-8, (15-27), (2016).
19. Sergio Ruiz-Carmona, Xavier Barril, Docking-undocking combination applied to the D3R Grand Challenge 2015, *Journal of Computer-Aided Molecular Design*, 10.1007/s10822-016-9979-z, 30, 9, (805-815), (2016).
20. Dries Harnie, Alexander E. Vapirev, Jorg Kurt Wegner, Andrey Gedich, Marvin Steijaert, Roel Wuyts, Wolfgang De Meuter, undefined, 2015 15th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing, 10.1109/CCGrid.2015.50, (871-879), (2015).
21. Antonino Marvuglia, Mikhail Kanevski, Enrico Benetto, Machine learning for toxicity characterization of organic chemical emissions using USEtox database: Learning the structure of the input space, *Environment International*, 10.1016/j.envint.2015.05.011, 83, (72-85), (2015).
22. Rashid, M. T., Zhang, D., & Wang, D. (2020, July). A Computational Model-Driven Hybrid Social Media and Drone-Based Wildfire Monitoring Framework. In *IEEE INFOCOM 2020-IEEE Conference on Computer Communications Workshops (INFOCOM WKSHPS)* (pp. 1362-1363). IEEE.
23. Robert Wolfgang Rumpf, Samuel L. Wolock, William C. Ray, StickWRLD as an Interactive Visual Pre-Filter for Canceromics-Centric Expression Quantitative Trait Locus Data, *Cancer Informatics*, 10.4137/CIN.S14024, 13s3, (CIN.S14024), (2014).
24. Bin Chen, Huijun Wang, Ying Ding, David Wild, Semantic Breakthrough in Drug Discovery, *Synthesis Lectures on the Semantic Web: Theory and Technology*, 10.2200/S00600ED1V01Y201409WEB009, 4, 2, (1-142), (2014).
25. Donald Petrey, Barry Honig, Structural Bioinformatics of the Interactome, *Annual Review of Biophysics*, 10.1146/annurev-biophys-051013-022726, 43, 1, (193-210), (2014).
26. Agarwal S, Dugar D, Sengupta S. 2010. Ranking chemical structures for drug discovery: A new machine learning approach. *J Chem Info Model* 50:716–731.
27. Arodz T, Yuen DA, Dudek AZ. 2006. Ensemble of linear models for predicting drug properties. *J Chem Info Model* 46:416–423.
28. Chowdhury, M. S. S., Nawal, M. F., Rashid, T., & Rhaman, K. (2015, December). Terminal analysis of the operations of a Rescue Robot constructed for assisting secondary disaster situations. In *2015 IEEE Region 10 Humanitarian Technology Conference (R10-HTC)* (pp. 1-5). IEEE.
29. Chen B, Harrison RF, Papadatos G, Willett P, Wood DJ, Lewell QX, Greenidge P, Stiefl N. 2007. Evaluation of machine learning methods for ligand based virtual screening. *J Comput-Aided MolDes* 21:53–62.
30. Deshpande M, Kuramochi M, Wale N, Karypis G. 2005. Frequent substructure based approaches for classifying chemical compounds. *IEEE TKDE* 17:1036–1050.
31. Rashid, M. T., & Wang, D. (2021, October). Unravel: An anomalistic crowd investigation framework using social airborne sensing. In *2021 IEEE International Performance, Computing, and Communications Conference (IPCCC)* (pp. 1-10). IEEE.
32. Devore J, Peck R. 2004. *Statistics: the exploration and analysis of data*, 5th ed. Belmont, CA: Duxbury Press.
33. Dix DJ, Houck KA, Martin MT, Richard AM, Woodrow Setzer R, Kavlock RJ. 2007. The toxcast program for prioritizing toxicity testing of environmental chemicals. *Toxicol Sci* 95:5–12.
34. Eom JH, Zhang BT. 2004. Pubminer: Machine learning based text mining system for biomedical information mining.
35. Feldman HJ, Snyder KA, Ticoll A, Pintilie G, Hogue CWV. 2006. A complete small molecule dataset from the protein data bank. *FEBS Lett* 580:1649–1165.
36. Geppert H, Horvath T, Gartner T, Wrobel S, Baorath J. 2008. Support vector machine based ranking significantly improves the effectiveness of similarity searching using 2d fingerprints and multiple reference compounds. *J Chem Info Model* 48:742–746.
37. Guo J, Chen H, Sun Z, Lin Y. 2004. A novel method for protein secondary structure prediction using dual layer svm and profiles. *Proteins* 54:738–743.
38. Helma C, Cramer T, Kramer S, Raedt LD. 2004. Data mining and machine learning techniques for the identification of mutagenicity inducing substructures and structure activity relationships of noncongeneric compounds. *J Chem Info Comp Sci* 44:1402–1411.
39. Rashid, M. T., Zhang, D., & Wang, D. (2019, August). Edgestore: Towards an edge-based distributed storage system for emergency response. In *2019 IEEE 21st International Conference on High Performance Computing and Communications; IEEE 17th International Conference on Smart City; IEEE 5th International Conference on Data Science and Systems (HPCC/SmartCity/DSS)* (pp. 2543-2550). IEEE.
40. Hert J, Willet P, Wilton D. 2006. New methods for ligand based virtual screening: use of data fusion and machine learning to enhance the effectiveness of similarity searching. *J Chem Info Model* 46:462–470.
41. Hopkins AL. 2008. Network pharmacology: the next paradigm in drug discovery. *Nat Chem Biol* 4:682–690.
42. Hopkins AL. 2009. Drug discovery: predicting promiscuity. *Nature* 462:167–168.
43. Jacob L, Vert JP. 2007. Kernel methods for in silico chemogenomics. In: *Proceedings of the NIPS Workshop on Machine Learning in Computational Biology*; Vancouver, Canada: Curran Associates,
44. Jenkins JL, Bender A, Davies JW. 2006. In silico target fishing: Predicting biological targets from chemical structure. *Drug Discov Today* 3:413–421.
45. Jensen D, Neville J. 2002. Data mining in social networks. In: *National Academy of Sciences Symposium on Dynamic Social Network Modeling and Analysis*; November 7–9, 2002. Washington, DC: The National Academies of Sciences.

46. Rashid, M. T., Abir, I. K., Shourove, N. S., Muntaha, R., & Rhaman, M. K. (2016, May). Intelligent intrusion prevention system for households based on system-on-chip computer. In *2016 IEEE Canadian Conference on Electrical and Computer Engineering (CCECE)* (pp. 1-5). IEEE.
47. Joachims T. 1998. Text categorization with support vector machines: Learning with many relevant features. In: Proc. of the European Conference on Machine Learning. Chemnitz, Germany: Springer. p 137–142.
48. Karypis G. 2006. Yasspp: better kernels and coding schemes lead to improvements in protein secondary structure prediction. *Proteins* 64:575–586.
49. Kola I, Landis J. 2004. Can the pharmaceutical industry reduce attrition rates? *Nature Rev Drug Discov* 3:711–716.
50. Yasar, M. S., & Rashid, M. (2015). Implementation of dynamic traffic light controllers using artificial neural networks to diminish traffic ordeals. In *IEEE European Modelling Symposium*.
51. Kosala R. 2000. Web mining research: a survey. *SIGKDD Explor* 2:1–15.
52. Kubinyi H. 2006. Chemogenomics in drug discovery. *Ernst ScheringRes Found Workshop* 58:1–19.
53. Lanckriet GR, Deng M, Cristianini N, Jordan MJ, Noble WS. 2004. Kernel based data fusion and its application to protein function prediction in yeast. *Proceedings, January 6–10, 2004, Hawaii. World Scientific: Pac Symp Biocomput.* p 300–311.
54. Menchetti S, Costa F, Frasconi P. 2005. Weighted decomposition kernels. *Proceedings of the 22nd International Conference in Machine Learning; August 7–11, 2005; Bonn, Germany. New York: ACM* 119:585–592.
55. Michielan L, Stephanie F, Terfloth L, Hristozov D, Cacciari B, Klotz K, Spalluto G, Gasteiger J, Moro S. 2009. Exploring potency Mitchell TM. 1997.
56. Muegge I, Oloff S. 2006. Advances in virtual screening. *Drug Discov Today* 3:405–411. Palmer DS, O’Boyle NM, Glen RC, Mitchell JBO. 2007. Random forest models to predict aqueous solubility. *J Chem Info Model* 47:150–158.
57. Paolini GV, Shapland RH, Van Hoorn WP, Mason JS, Hopkins AL. 2006. Global mapping of pharmacological space. *Nature Biotechnology* 24:805–815.
58. Ralaivola L, Swamidass SJ, Saigo H, Baldi P. 2005. Graph kernels for chemical informatics. *Neural Netwk* 18:1093–1110.
59. Rangwala H, Karypis G. 2006. Building multiclass classifiers for remote homology detection and fold recognition. *BMC Bioinformatics* 7:455.
60. Rangwala H, Karypis G. 2007. frmsdpred: predicting local rmsd between structural fragments using sequence information. *Comput Syst Bioinform Conf* 6:311–322.
61. Rangwala H, Karypis G. 2008. frmsdalign: frmsdalign: Protein sequence alignment using predicted local structure information. In: *Proceedings of the 6th Asia Pacific Bioinformatics Conference; January 17–19, 2008. London: Imperial College.*
62. Rangwala H, Kauffman C, Karypis G. 2007. A generalized framework for protein sequence annotation. In: *Proceedings of the NIPS Workshop on Machine Learning in Computational Biology; December 10, 2008. Vancouver, Canada: Curran Associates.*
63. Raymond JW, Cardiner EJ, Willet P. 2002. Heuristic for similarity searching of chemical graphs using a maximum common edge subgraph algorithm. *J Chem Info Comp Sci* 42:305–316.
64. Rognan D. 2007. Chemogenomic approaches to rational drug design. *Br J Pharmacol* 152:38–52.
65. Root DE, Kelley BP, Stockwell BR. 2002. Global analysis of large scale chemical and biological experiments. *Curr Opin Drug Discov Dev* 5:355–360.
66. Russ AP, Lampel S. 2005. The druggable genome: an update. *Drug Discov Today* 10:1607–1610.
67. Sakiyama Y. 2009. The use of machine learning and nonlinear statistical tools for adme prediction. *Expert Opin Drug Metab Toxicol* 5:149–169.
68. Salim N, Holliday JD, Willett P. 2003. Combination of fingerprint based similarity coefficients using data fusion. *J Chem Info Comput Sci* 43:435–442.
69. Schreiber SL. 1998. Chemical genetics resulting from a passion for synthetic organic chemistry. *Bioorg Med Chem* 6:1127–1152.
70. Schroeter TS, Schwaighofer A, Mika S, Laak AT, Suelzle D, Ganzer U, Heinrich N, Muller KR. 2007. Estimating the domain of applicability for machine learning qsar models: a study on aqueous solubility of drug discovery molecules. *J Comput-Aided* 21:485–498.