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A Survey on Artificial Intelligence in Biomedical Sciences

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Abstract:
The study of "intelligent machines" is Artificial Intelligence (AI), and it has applications in various sectors. Similar to how other general-purpose technologies and novel AI applications in workplace of the future raise significant issues for safety and health, it is predicted that AI will have a globally transformative impact on economic and social structures as more applications are integrated into daily life. With a particular emphasis on applications in health, medicine, pharmacology, toxicology, hematology, drug discovery, multi-omics, bioinformatics, nanotechnology and, biotechnology, this review aims to familiarize readers with the broad areas of AI. It also outlines the most recent developments in the field of AI research for medical applications. As new opportunities and concerns materialize, it is as crucial to recognize and comprehend these threats as it is to realize the AI approach itself. Therefore, mitigating the negative consequences of AI on human safety, health, and well-being will need a comprehension of both its potential and its challenges for the future work.
Key words: *Artificial Intelligence, Computational Methods, Health care, Machine Learning*.

I.INTRODUCTION

The study of algorithms that enable machines to think and carry out tasks like problem-solving, object and word recognition, inference of world states and decision-making is Artificial Intelligence (AI). Though AI is frequently associated with computers or robots, its roots may be found in a variety of disciplines including statistics, psychology, linguistics and philosophy (Hashimoto et al., 2020). Almost every sector of society is being shaped by AI. It acts as the primary force behind developing technologies like Big Data, robots, and IoT, and will continue to do so for the future. AI represents, examines and interprets material that is often thought to be beyond complicated for human intellect alone, using sophisticated mathematical techniques, statistical models and machine learning algorithms. AI techniques like machine learning and natural language processing allow computers to learn for themselves how to find and identify correlations in complicated health care data is now a significant interest in the field of healthcare (Matava et al., 2020).

At present AI is in many aspects of our everyday life, including personal assistants, automated public transit, aircraft and video games. AI has more recently started to be used in medicine to enhance patient care by accelerating procedures and obtaining higher accuracy, paving the way for improved healthcare overall. Machine learning involves evaluating pathology slides, radiological images and patient EMRs (electronic medical records), assisting in patient diagnosis and treatment, and enhancing clinicians' abilities (Mintz and Bodie, 2019). Many sectors are quickly adopting AI as a technology, largely to increase performance, precision and time efficiency as well as to save costs. Although AI has received a lot of media attention, many healthcare professionals still view technology as a "black box", which can lead to unrealistic expectations and unjustified anxieties. In this review, we summarize the technological foundations of AI conceptually and succinctly. Also prospective applications of AI are addressed, including their potential roles in the fields of medicine, health, pharmacology, toxicology, hematology, drug discovery, multi-omics, bioinformatics, nanotechnology and biotechnology.

AI in Drug Discovery

For drug manufacturers and chemical experts, developing new drugs is an essential field of study. Low effectiveness, inaccurate delivery, time requirements and high expenses create a barrier, difficulties that affect drug design and development. Additionally, the drug development process is hampered by complicated big data from genomes, proteomics, micro array data and clinical trials. The development of new drugs is greatly aided by AI and machine learning technologies. In other words, the field has become more advanced due to ANN (Artificial Neural Networks and deep learning algorithms. Peptide combination, structure and ligand-based virtual screening, toxicity estimation, drug inspection and release pharmacophore modeling, (QSAR), drug relocation, poly pharmacology, and physiochemical works are just a few of the drug discovery processes that have incorporated machine learning and deep learning algorithms (Gupta et al., 2021).

Because it saves time and money, AI has emerged as a successful and demanding technology today. In general, time-consuming and exhaustive tasks that can be reduced and made faster with the assistance of AI include classification, sorting of cell, calculating the characteristics of small molecules, producing organic compounds using computer programs, design and develop new compounds, assays, and estimate the 3D structure of target molecules. The initial step in the drug screening process involves classifying and sorting cells using AI-powered image analysis (Zhavoronkov et al., 2020). It takes a lot of effort and time to design and monitor drug-likeness. Recently, a number of online tools have been created to study medication release and verify the responsibility of particular bioactive substances as a carrier. The computational analysis is later validated using bench mark datasets. The most appropriate pharmocophore for such evaluations is one based on chemical characteristics. These models generate huge 3D datasets from internal chemical collections or in silico studies (Rollinger et al., 2008).

Finding bioactive ligand is a vital step in choosing a potent medication for a particular target. Currently, scientists are using AI to find bioactive molecules that may be exploited for

particular targets related to a disease. As an example Wu et al., developed WDL-RF by combining DL and RF techniques to assess the bioactivity of G protein-coupled receptors (GPCRs) ligand-targeting mechanisms [53]. Similarly, Cichonska et al., (2018) invented pairwiseMKL, a multiple kernel learning-based technique [12], for figuring out the bioactivity of substances. Additionally, adverse drug responses (ADRs) are unanticipated, deadly side effects brought on by the delivery of drugs. Adverse Drug Responses are a significant barrier in drug development, and in order to make the process more robust and effective, it has become crucial to recognize potential adverse drug responses in the early stages of drug development. Recently, researchers have utilized AI to predict potential ADRs linked to certain medications before they are made available to the general population. For example, Dey et al., (2015) employed a DL based model, which can forecast ADRs connected to medicine and even identify chemical substructures accountable for those adverse drug responses.

AI in medicine

AI, the driving force behind the fourth scientific and technological revolution, offers the chance to attain precision public health and tailored therapy (Xiang et al., 2020). Precision medicine and the growth of artificial intelligence in medicine are frequently linked. The fact that routine tasks take up a significant portion of a physician's daily work is frequently disregarded, but doing so would free up the human workforce's time to concentrate on higher-value tasks that typically call for human qualities like creativity, cognitive insight, meaning, or empathy (Hainc et al., 2017). Planning examinations, identifying pathologies, quantifying them, and manually searching for additional information in medical records and textbooks are just a few of the many tasks involved in the day-to-day work of medical imaging. While these tasks frequently bore and challenge experienced doctors too little intellectually, overwhelm newcomers due to their consistently increasing workloads. Without undermining the potential of "super-diagnostics" and precision medicine, the aims of AI in medicine that appears to be more achievable should not be overlooked since they might free up highly skilled individuals with advanced education from repetitive everyday activities (Nensa et al., 2019).

In instances like rehabilitation, robots can be helpful in assessing how human performance has changed (Simonov and Delconte, 2015). Monitoring the directed distribution of medication to specific organs, tissues, tumors' is another area where AI may be applied to good effect. For instance, it is heartening to read about the recent advancements of nano robots intended to solve delivery issues that occur when therapeutic drug diffusion into a place of interest is problematic. When a therapist tries to treat the tumor's core, which is often less vascularized and anoxic, but most proliferatively active, a difficulty arises. Researchers have tried to use a natural agent with the appropriate qualities in the place of only "intelligent" nanoparticles to overcome the limits of mechanical or radioactive robotics. They are researching a particular form of marine bacteria called Magnetococcus marinus for this purpose since it naturally moves to low-oxygen environments. An external magnetic source provides initial guidance, which is followed by the nanorobots' innate abilities. Covalent

bonds between these nanorobots and nanoliposomes with therapeutic characteristics are possible. According to preliminary data, the gradient of the required medicine into the hypoxic zones has significantly increased (Felfoul et al., 2016).

AI in Pharmaceuticals

For the past ten years, the breakthrough technology that is most predicted to have a transformational impact on pharmaceutical research and development is AI and machine learning. According to DiMasi et al., (2016), the following estimations show that creating a new medicine is a difficult, expensive procedure with a poor success rate: the average cost of research and development (R&D) for each drug is $ 1.3 billion, the median development period for each drug is between 5.9 and 7.2 years for non-oncology drugs and 13.1 years for oncology drugs, and 13.8% of all drug development projects result in approval (Wong et al., 2019). Due to automated nature, predictive skills, and predicted increase in efficiency, AI approaches are appealing to the drug-development business in response to these challenges.

AI encompasses a new and quickly expanding collection of technologies that might alter how pharmaceutical research & development (R&D) is conducted in future and provide prospects that boost R&D productivity (Schuhmacher et al., 2019). The pharmaceutical sector is at an "early mature" stage of using AI in R&D by contrasting top pharmaceutical companies with regard to their internal and external R&D activities [43] (Schuhmacher et al., 2020). While some top manufacturers, including Gilead Sciences and Takeda, have been "Selective AI Explorers" rather than "Digital Pharma Players", others like Astra-Zeneca and Novartis, have used AI more extensively (Schuhmacher et al., 2021).

Machine learning is now the most prevalent AI technology utilized in pharmaceutical R&D with regard to the types of AI techniques being employed. This outcome runs counter to the writers' expertise and experience. Deep learning technologies are anticipated to be the dominant AI technology, as shown for diagnostics (Ardila et al., 2019) or in small-molecule-based drug discovery (Zhavoronkov et al., 2019). Deep learning has also been shown to be superior in the grouping of bio-medical images and in the prediction of biomedical activity and toxicity (Lavecchia, 2019). De Novo drug design, ligand-protein interaction prediction, chemoinformatic analysis, QSAR connections, and selection of cohorts in clinical trials are further areas where deep learning has been used (Chen et al., 2018).

AI in Toxicology

The Frank R. Lautenberg Chemical safety for the 21st Century Act, passed in 2016, is the first piece of US legislation to promote chemical safety assessments by adopting cutting-edge testing methods that minimize the use of vertebrate animals in testing. The development of computational toxicology and AI strategies for applying cutting-edge testing techniques is crucial to this objective. Currently available chemical, in vitro, and in vivo data for toxicity modeling uses have been described using the words volume, velocity, and variety. The diversity of publicly accessible data pools, like PubChem, also poses considerable computational issues, as indicated by a number of academics (Ciallella and Zhu, 2019). To find substances that potentially cause chemical toxicity, conventional empirical testing

approaches, both in vivo and in vitro, are typically expensive and time-consuming (Luechtefeld et al., 2018). A viable alternative for assessing chemical toxicity is computational modeling. QSAR models for different toxicity end points are examples of existing computational methods for risk assessment that may be used to prioritize potentially dangerous compounds for experimental testing and swiftly forecast huge numbers of novel compounds (Ciallella and Zhu, 2019).

The growth of data-directed technology and the creation of computational tools to address the problems of four V's (volume, variety, velocity and veracity) give the new potential for present model enhancement and innovative model advancement, not with-standing the difficulties brought on by big data in analytical toxicology modeling. Examples of early data mining technologies that connect different public data origins to target compounds are Chem2BioRDF [9] (Chen et al., 2020) and HTS Navigator [18] (Fourches et al., 2014). Additionally, certain data distributing gateways have useful data mining instruments available, such as rpubchem90 and ToxCast pipeline (tcpl) [17] (Filer et al., 2016) which are designed to make parsing and gathering information from the ToxCast database and PubChem repositories respectively, simpler and more efficient. There are new ways to automatically extract data from REACH and PubChem databases and recently created online tools REACHacross [29] (Luechtefeld et al., 2018) and the Chemical In Vitro, In Vivo Profiling site (CIIPro) [40] (Russo et al., 2016). Additionally there are online resources that may be used to speed up the creation and dissemination of structured toxicity data and QSAR models such as Chembench [6] (Capuzzi et al., 2017) and the Chemistry at Harvard Macromolecular Mechanics web-user interface (CHARM-Ming) [51] (Weidlich et al., 2015).

Computational models are becoming suitable for huge chemical space examination, various biological data expansion, and complicate operation research as big data warehouses continue to increase quickly and latest approaches that cope with enormous data sets are being created. This ground-breaking movement will enable not only the prediction of novel chemicals but also the visualization of the toxicity mechanisms of probable toxins. Regulatory agencies urgently need to integrate analytical models into process oriented chemical risk estimations, this expanding big toxicity data prospects and improvements in modeling approach expansion leads to taking care the wealth of toxicity data available together establish a new way that is optimum for doing so (Ciallella and Zhu, 2019).

AI in Multi-Omics

Modern high-throughput omic measuring technologies have made it necessary for biomedical investigations to adopt an integrated (combined) strategy in order to make the most of this data and learn more about biological systems. Using machine learning-based prediction algorithms it is possible to decipher the complicated operation of systems biology by combining information from diverse omics sources such as metabolomics, proteomics, and genetics. In order to combine and analyze the diverse omics data and find new biomarkers, machine learning algorithms provide fresh approaches. These biomarkers may aid in the delivery of precision medicine, precise illness prognosis, and patient stratification (Reel et al., 2021).

The core tenet of molecular biology governs how genetic information in living things is conveyed in the cells from DNA to mRNA to protein. This information flow, which has made it easier to comprehend how biological information is processed, is frequently compared to a computer system. Transcriptomics investigates the genes that are actively expressed and evaluate the transcribed genetic material to offer insight into what's occurring at the biological level (Milward et al., 2016). In the form of protein pathways and their networks, proteomics aids in defining the data flow occurring inside the cell and the structure (Wu et al., 2014). Although they are not included in the core dogma analysis (Cobb, 2017), metabolomics, lipidomics, and glycomics nonetheless offer a wealth of knowledge about metabolites, lipids, and glycans [5] (Barh et al., 2011). These compounds have thought to be effective markers of a cell's activity since they are the intermediary outcomes of a cell's information flow. According to Reel et al., metagenomics is used for the arrangement of genetic data from ambient materials not having the need to isolate specific species, similar to single-genome investigations.

The field of precision and computational medicine, on the other hand, has seen a rise in publications by depending on "multi-omics integration" and "multi-omics & machine learning" during the past five years. Although deep learning is quite popular in fields that are linked to multi-omics research, such as clinical natural language processing and medical imaging, interest in this field has lagged (Wu et al., 2020; Tan et al., 2020). Model-based supervised learning has also used deep learning techniques [36] (Poirion et al., 2020). The MOLI (Multi-Omics Late Integration) technique [45] (Sharifi-Noghabi et al., 2019) employed definite encoding sub-networks to get attributes from physical mutation, CNA, and gene expression information separately and afterwards integrated them to predict the outcome to a particular medication. A DL-based auto-encoding method has been put out by Lee et al., (2020) for combining four omics to produce a survival prediction model. In addition, the HIDFNForest framework (Xu et al., 2019) was created that employs a stacked autoencoder to train leading descriptions from 3 omic datasets. These depictions are later combined to forecast the organization of cancer subtypes. Similarly, to this, Chaudhary et al., employed SVM and autoencoders to predict the survival in subgroups with hepatocellular carcinoma.

AI in Haematology

Massive amount of data has been produced as a result of digitizing the medical records and the implementation of genetic approaches in clinical practice. The goal of machine learning is to computationally extract useful information from complicated data structures. Machine learning is increasingly being used in haematological settings (Shouval et al., 2021). Among the many activities that machine learning may help with, include limiting a differential diagnosis, assisting in therapy selection, providing risk forecasts, lowering the incidence of medical mistakes, and increasing efficiency (RajKomar et al., 2019). Diagnostics, image analysis, and predictive modeling are the key areas. Shouval et al., (2017) created a model for the prediction of 100-day mortality following allogenic HSCT and internal and externally verified it in a registry study from the European Society of Blood and Marrow transplantation that included patients with acute leukemia. To improve upon the prior benchmark for

outcome prediction, an interpretable boosted decision tree model was employed for model building. To forecast acute graft-versus-host disease, Arai et al., (2019) employed a similar strategy. Agius et al., (2020) used an elegant ensemble technique to predict the need for therapy and infections in chronic lymphocytic leukemia by combining many separate machine learning algorithms. On the basis of imaging data and gene expression, other organizations have concentrated on developing techniques for predicting therapy response (Milgrom et al., 2019; Herold et al., 2018). Overall, there is little question that in the near future, the use of recommendation systems in diagnostic and therapeutic decision-making as well as mistake avoidance will increase.

AI in Bioinformatics

In order to tackle biological issues, frequently at the molecular level, bioinformatics uses methods from computer science, artificial intelligence, informatics, applied mathematics, statistics, chemistry and biochemistry. Alignment of sequence, gene discovery, genome assembly, protein structure alignment and prediction, gene expression prediction, protein-protein interaction prediction, and evolution modeling are some of the major research initiatives in this area. Consequently, another way to define bioinformatics is the use of computer techniques to create biological discoveries (Hassanien et al., 2013). In the relatively recent subject of bioinformatics, characteristics of bio-molecules, in particular, DNA, RNA, and proteins on a genomic and proteomic scale are computationally analyzed and predicted. In the discipline of bioinformatics, machine learning models are becoming more and more crucial for the creation of innovation techniques, summarization, and high-throughput analysis. A number of works that provide an overview of particular sub-areas of protein bioinformatics have been published. These works summarize developments in the fields related to protein structure and function prediction, structural bioinformatics, and peptide analysis (Andrews, 2020).

AI in Nanotechnology

Nano, biological and information sciences are becoming more important to the advancement of modern science and technology. The thought that the fusion of nanotechnology, AI, and biology will ignite another practical and scientific revolution is lingering for more than a decade. Nevertheless, work is still being done to complete the anticipated integration of diverse research. While AI has largely drawn inspiration from biological principles to construct the most successful paradigms, are neural networks or evolutionary algorithms, nanotechnology integrates the understanding of physics, chemistry and engineering. A new era of communication and information technologies which have a significant influence on our society can be produced by bridging the gap between present nanosciences and AI. These technologies may also provide the means for the eventual fusion of technology and biology (Sacha and Varona, 2013).

In reality, by filling the space between nanotechnology and AI might enable the fusion of technology and biology that results in more efficient brain-machine communication. Simulating the system under investigation is one of the major issues that researchers have

identified while working at nanoscale. Real optical pictures cannot be produced at the nanoscale, which is how macroscopic and nanoscopic images vary from one another. These sizes of images need interpretation, and numerical models are occasionally the best option. There are several tools and programs available right now that can faithfully mimic various systems with atomic effects (Zhang et al., 2021).

Naturally, AI is advantageous for nano computing, in which computing is done via microscopic mechanics, in the future. Nano-computing devices may perform a function in a variety of ways, ranging from computational techniques to physical actions. Machine learning techniques may be used to create unique information representations for a variety of functions because many of these devices depend on complex physical systems to enable complex computational methods. Since both the development and success of AI and nanotechnology are on an upward slope, it appears that these two curves have grown closer to one another until we can distinguish a gap between them. This suggests that they are the ideal spouse and companions for each of these businesses since their strengths complement one another. The integration of AI with nanoscience/nanotechnology in today's technology seems to be a virtual certainty (Farahnaz and Bahman, 2020).

AI in Biotechnology

Over the past 50 years, rapid advancements in information technology and biotechnology have happened side by side at a rate unmatched in any other industry. The expanding advancements in information applied sciences, which are uncommon outside the computer industry, are both a cause and effect of Moore's law. The field of biotechnology is excluded, where advances in sequencing and other high-throughput instruments have exceeded Moore's law in terms of exponential growth (Oliveira, 2019). High-dimensional data like photographs or videos may be processed at a pace that is much faster than which is achievable by utilizing humans to analyse the data as machine learning technology, most notably with the advent of deep learning algorithms [50] (Webb, 2018). To accomplish supervised machine learning, a wide range of methods can be utilized, including SVM, deep neural networks, and regression and decision trees. Since these methods got insrtucted to categorize examples into one of a limited number of classes, they are sometimes referred to as "classifiers" (LeCun et al., 2015).

Drug development, drug recycling, and drug safety studies can all benefit from the knowledge that can be obtained through mining EHRs (Electronic Health Records). EHRs will rank among the most important tools that hospitals and other healthcare organizations can maintain and research with the support of the biotechnology field and academic community gave the present emphasis on fact-based medicine. EHRs may exploit both structured and unstructured data, with the second one needing the use of natural language processing tools that are only recently become mature. The capacity of businesses to combine patient genetic data with HER data, which will become increasingly prevalent, will be crucial to the development of pharmacogenomics in the future. Machine learning may be used in genome analysis, including GWAS (Genome-Wide Association Study), to not only estimate genotype-phenotype but also to pinpoint the connections between genetic traits and the

reaction to certain therapies. A growing number of people are increasingly interested in learning more about their own genomes and the potential effect that certain traits may have on their lifestyle due to the sharp decline in the cost of genotyping and sequencing. Numerous organizations, like 23andme and Veritas Genetics, aim to gather, aim to gather genetic information from millions of people, use it to further understanding, and encourage the creation of novel products (Oliveira, 2019).

II.LIMITATIONS

There are few limitations in our review; for instance, we only included peer-reviewed English language journal papers. It is conceivable that some pertinent papers were published in conferences, seminars, and news reports or were written in other languages. This may help to explain why some countries are over-represented in the evaluated publications, as was already mentioned. Furthermore, we excluded publications that were released prior to 2010, as AI has just recently begun to make headway in the clinical field. Another issue is the possibility that some AI applications have been used in therapeutic settings without any publicly available papers. For instance, more than 20 healthcare facilities, including the University of Iowa Health Care, have installed IDx-DR, the first FDA-approved AI system (Carfagno, 2019).

III.CONCLUSION

In conclusion, AI covers a wide range of recent technological developments that continue to have an influence on our day-to-day lives. Big data analysis is now feasible because of the development of AI, which helps decision-making by supplying accurate information. According to the literature described here, there is a lot of interest in creating AI tools to help clinical processes as more high-quality data is produced. As a result, in the future, it is anticipated that the AI-based comprehensive system would assist cutting-edge research and development while establishing high-quality human life. We came to the conclusion that AI has made significant strides in recent years and will soon play a crucial role in everyday life and healthcare in general. However, in order to transition from theory to clinical practice, a comprehensive, meticulous, and rigorous evaluation is required in the healthcare industry.

IV.REFERENCES

1. Agius R, Brieghel C, Andersen MA, Pearson AT, Ledergerber B, Cozzi-Lepri A, et al., Machine learning can identify newly diagnosed patients with CLL at high risk of infection. Nat Commun. 2020; 11:363.
2. Andrews J.L (2020). Maintaining Privacy in Artificial Intelligence-driven Bioinformatics: An Inquiry into the Suitability of Australia's Laws. Journal of law and medicine, 28(1), 179-196.
3. Arai Y, Kondo T, Fuse K, Shibasaki Y, Masuko M, Sugita J, et al., Using a machine learning algorithm to predict acute graft-versus-host disease following allogeneic transplantation. Blood Advances. 2019; 3:3626-34.
4. Ardila D, Atilla P. Kiraly, Sujeeth Bharadwaj, Bokyung Choi, Joshua J. Reicher, Lily Peng et al., (2019). End-to-End lung cancer screening with three-dimensional deep

learning on low-dose chest computed tomography. Nature medicine, 25(6), 954-961. https://doi.org/10.1038/s41591-019-0447-x.

5. Barh D, Blum K, Madigan, M.A. (Eds.), 2011. OMICS: Biomedical Perspectives and Applications, 1 edition. CRC Press, Boca Raton.
6. Capuzzi SJ, Kim ISJ, Lam WI, Thornton TE, Muratov EN, Pozefsky D, and Tropsha A (2017) Chembench: A Publicly Accessible, Integrated Cheminformatics Portal. J. Chem. Inf. Model 57(2), 105-108.
7. Carfagno J. IDx-DR, the first FDA-Approved AI system, is Growing Rapidly Internet. DocWireNews. 2019. [2021-04-05]. https://docwirenews.com/docwire-pick/future-of-medicine-picks/idx-dr-the-first-fda-approved-ai-system-is-growing-rapidly/
8. Chaudhary K, Poirion O.B, Lu L, Garmire L.X, 2017. Deep Learning based multiomics integration robustly predicts survival in liver cancer. Clin. Cancer Res. Off. J. Am. Assoc. Cancer Res. Doi. https://doi.org/10.1158/1078-0432.CCR-17-0853.
9. Chen B, Dong X, Jiao D, Wang H, Zhu Q, Ding Y, and Wild D92010) Chem2Bio2RDF: A Semantic Framework for Linking and Data Mining Chemogenomic and Systems Clinical Biology Data. BMC Bioinf 11, 255.
10. Chen H, Engkvist O, Wang Y, Olivecrona M, Blaschke T. (2018). The rise of deep learning in drug discovery. Drug discovery today, 23(6), 1241-1250. https://doi.org/10.1016/j.drudis.2018.01.039.
11. Ciallella H.L, and Zhu H. (2019). Advance Computational Toxicology in the Big Data Era by Artificial Intelligence: Data-Driven and Mechanism-Driven Modelling for Chemical Toxicity. Chemical research in toxicology, 32(4), 536-547. https://doi.org/10.1021/acs.chemrestox.8b00393.
12. CichonskaA, Pahikkala T, SzedmakS, et al., Learning with multiple pairwise kernels for drug bioactivity prediction. Bioinformatics. 2018; 34:i509-i518.
13. Cobb M, 2017. 60 years ago, Francis Crick changed the logic of biology. PLoS Biol. 15, e2003243 https://doi.org/10.1371/journal.pbio.2003243.
14. DiMasi JA, Grabowski HG, Hansen RW. Innovation in the pharmaceutical industry: new estimates of R&D costs. J Health Econ. 2016; 47:20-33.
15. Farahnaz Behgounia, Bahman Zohuri. Artificial Intelligence Integration with Nanotechnology. Op Acc J Bio Sci & Res 6(3)-2020.
16. Felfoul O, Mohammadi M, Taherkhani S, de Lanauze D, Zhong Xu Y, Loghin D, Essa S, Jancik S, Houle D, Lafleur m, Gaboury L, Tabrizian M, Kaou N, Atkin M, Vuong T, Batist G, Beauchemin N, Radzioch D, & Martel S. (2016). Magneto-aerotactic bacteria deliver drug-containing nanoliposomes to tumour hypoxic regions. Nature nanotechnology, 11(11), 941-947. https://doi.org/10.1038/nnano.2016.137.
17. Filer DL, KOthiya P, Woodrow Setzer R, Judson RS, and Martin MT (2016) Tcpl: The ToxCast Pipeline for High-Throughput Screening Data. Bioinformatics 33(4), 618-620.
18. Fourches D, Sassano MF, Roth BL, and Tropsha A (2014) HTS Navigator: Freely Accessible Chemoinformatics Software for Analyzing High-Throughput Screening Data. Bioinformatics 30(4), 588-589.

19. Gal O, Auslander N, Fan Y, Meerzaman D. Predicting complete remission of acute myeloid leukemia: machine learning applied to gene expression. Cancer Inform. 2019; 18:1176935119835544.
20. Gupta R, Srivastava D, Sahu M, Tiwari S, Ambasta R.K, & Kumar P. (2021). Artificial intelligence to deep learning: machine intelligence approach for drug discovery. Molecular diversity, 25(3), 1315-1360. https://doi.org/10.1007/s11030-021-10217-3.
21. Hainc N, Federau C, Stieltjes B, Blatow M, Bink A, Stippich C. The bright, artificial intelligence-augmented future of neuro imaging reading. Front Neurol. 2017;8:489.
22. Hashimoto D.A, Witkowski E, Gao L, Meireles O, & Rosman G. (2020). Artificial Intelligence in Anesthesiology: Current Techniques, Clinical Applications, and Limitations. Anesthesiology, 132(2), 379-394. https://doi.org/10.1097/ALN.0000000000002960.
23. Hassanien AE, Al-Shammari ET & Ghali NI. (2013). Computational intelligence techniques in bioinformatics. Computational biology and chemistry, 47, 37-47. https://doi.org/10.1016/j.compbiolchem.2013.04.007.
24. Herold T, Jurinovic V, Batcha AMN, Bamopoulos SA, Rothenberg-Thurley M, Ksienzyk B, et al., A 29-gene and cytogenetic score for the prediction of resistance to induction treatment in acute myeloid leukemia. Haematologica. 2018; 103:456-65.
25. Lavecchia A.(2019). Deep learning in drug discovery: opportunities, challenges and future prospects. Drug discovery today, 24(10), 2017-2032. https://doi.org/10.1016/j.drudis.2019.07.006.
26. LeCun Y, Benigo Y, & Hinton G. (2015). Deep learning Nature, 521(7553), 436-444. https://doi.org/10.1038/nature14539.
27. Lee T-Y, Huang K-Y, Chuang C-H, Lee C-Y, Chang T-H, 2020. Incorporating deep learning and multi-omics auto-encoding for analysis of lung adenocarcinoma prognostication. Comput.Bio.Chem.87, https://doi.org/10.1016/j.compbiolchem.2020.107277.
28. Liu X, Gao Y, Peng J, Wang Y, Zhou N, Xing J, Luo X, Jiang H, & Zheng M. (2015). Tarped: a web application for predicting therapeutic and side effect targets of chemical compounds. Bioinformatics (Oxford, England), 31(12), 2049-2051. https://doi.org/10.1093/bioinformatics/btv099.
29. Luechtefeld T, Rowlands C, and Hartung T (2018) Big-Data and Machine Learning to Revamp Computational Toxicology and Its Use in Risk Assessment. Toxicol. Res. (Cambridge, U. K.) 7, 732-744.
30. Matava C, Pankiv E, Ahumada L, Weingarten B, & Simpao A. (2020). Artificial intelligence, machine learning and the paediatric airway. Paediatric anaesthesia, 30(3), 264-268. https://doi.org/10.1111/pan.13792.
31. Milgrom SA, Elhalawani H, Lee J, Wang Q, Mohamed ASR, Dabaja BS, et al., A PET radiomics model to predict refractory mediastinal Hodgkin lymphoma. Sci Rep. 2019; 9:1322.
32. Milward E.A, Shahandeh A, Heidari M, Johnstone D.M, Daneshi N, Hondermarck H, 2016. Transcriptomics, in: Encyclopedia of Cell Biology. Academic Press, Waltham, pp.160-165. https://doi.org/10.1016/B978-0-12-394447-4.40029-5.

33. Mintz Y, & Brodie R. (2019). Introduction to artificial intelligence in medicine. Minimally invasive therapy & allied technologies: MITAT: official journal of the Society for Minimally Invasive Therapy, 28(2), 73-81. https://doi.org/10.1080/13645706.2019.1575882
34. Nensa, Felix; Demircioglu, Aydin; Rischpler, Christoph (2019). Artificial Intelligence in Nuclear Medicine. Journal of Nuclear Medicine, 60(Supplement 2), 29S-37S.doi:10.2967/jnumed.118.220590.
35. Oliveira A.L. (2019). Biotechnology, Big Data and Artificial Intelligence. Biotechnology journal, 14(8), e1800613. https://doi.org/10.1002/biot.201800613.
36. Poirion O.B, Zheng Jing, Chaudhary K, Huang S, Garmire L.X, 2020. Multi-omics-based pan-cancer prognosis prediction using an ensemble of deep-learning and machine learning models. medRxiv 19010082. https://doi.org/10.1101/19010082.
37. Rajkomar A, Dean J, Kohane I. Machine learning in medicine. N Engl J Med. 2019; 380:1347-58.
38. Reel PS, Reel S, Pearson E, Trucco E, & Jefferson E. (2021). Using machine learning approaches for multi-omics data analysis: A review. Biotechnology advances, 49, 107739. https://doi.org/10.1016/j.biotechadv.2021.107739.
39. Rollinger JM, Stuppner H, & Langer T. (2008). Virtual screening for the discovery of bioactive natural products. Progress in drug research. 65, 211-249. https://doi.org/10.1007/978-3-7643-8117-26.
40. Russo DP, Kim MT, Wang W, Pinolini D, Shende S, Strickland J, Hartung T, and Zhu H (2016) CIIPro: A New Read-across Portal to Fill Data Gaps Using Public Large-Scale Chemical and Biological Data. Bioinformatics 33(3), 464-466.
41. Sacha G.M, & Varona P. (2013). Artificial intelligence in nanotechnology. Nanotechnology, 24(45), 452002. https://doi.org/10.1088/0957-4484/24/45/452002
42. Schuhmacher A, Gassmann O, Kuss M, & Hinder M. (2019). The Art of Virtualizing Pharma R&D. Drug discovery today, 24(11), 2105-2107. https://doi.org/10.1016/j.drudis.2019.07.004
43. Schuhmacher A, Gatto A, Hinder M, Kuss M, & Gassmann O. (2020). The upside of being a digital pharma player. Drug discovery today, 25(9), 1569-1574. https://doi.org/10.1016/j.drudis.2020.06.002.
44. Schuhmacher A, Gatto A, Kuss M, Gassmann O, & Hinder M. (2021). Big Techs and startups in pharmaceutical R&D - A 2020 perspective on artificial intelligence. Drug discovery today, 26(10), 2226-2231. https://doi.org/10.1016/j.drudis.2021.04.028.
45. Sharifi-Noghabi H, Zolotareva O, Collins C.C, Ester M, 2019. MOLI: Multi-Omics Late Integration with deep neural networks for drug response prediction. Bioinformatics 35, i501-i509. https://doi.org/10.1093/bioinformatics/btz318.
46. Shouval R, Bonifazi F, Fein J, Boschini C, Oldani E, Labopin M, et al., Validation of the acute leukemia-EBMT score for prediction of mortality following allogeneic stem cell transplantation in a multi-center GITMO cohort. Am J Hematol. 2017; 92:429-34.
47. Shouval R, Fein J.A, Savani B, Mohty M, & Nagler A. (2021). Machine learning and artificial intelligence in haematology. British journal of haematology, 192(2), 239-250. https://doi.org/10.1111/bjh.16915.

48. Simonov M, Delconte G. Humanoid assessing rehabilitative exercises. Methods Inf Med.2015; 54 (2):114-21.
49. Tan X, Yu Y, Duan K, Zhang J, Sun P, Sun H, 2020. Current advances and limitations of deep learning in anticancer drug sensitivity prediction [WWW Document] Curr. Top. Med. Chem. 20(21), 1858-1867. https://doi.org/10.2174/1568026662007101013 07.
50. Webb S. (2018). Deep learning for biology. Nature, 554(7693), 555-557. https://doi.org/10.1038/d41586-018-02174-z.
51. Weidlich IE, Pevzner Y, Miller BT, Filippov IV, Woodcock HL, and Brooks BR (2015) Development and Implementation of (Q)SAR Modeling within the CHARMMing Web-User Interface. J. Comput. Chem 36(1), 62-67.
52. Wong CH, Siah KW, LO AW. Estimation of clinical trial success rates and related parameters. Biostatistics. 2019; 20(2): 273-286.
53. Wu J, Zhang Q, Wu W, et al., WDL-RF: predicting bioactivities of ligand molecules acting with G protein-coupled receptors by combining weighted deep learning and random forest. Bioinformatics. 2018; 34:2271-2282.
54. Wu S, Roberts K, Datta S, Du J, Ji Z, Si Y, Soni S, Wang Q, Wei Q, Xiang Y, Zhao B, Xu H, 2020. Deep learning in clinical natural language processing: a methodical review. J. Am.Med. Inform. Assoc. 27, 457-470. https://doi.org/10.1093/jamia/ocz200.
55. Wu X, Hasan M.A, Chen J.Y, 2014. Pathway and network analysis in proteomics. J. Theor. Biol. 0, 44-52. https://doi.org/10/1016/j.jtbi.2014.05.031.
56. Xiang Y, Zhao L, Liu Z, Wu X, Chen J, Long E, Lin D, Zhu Y, Chen C, Lin Z, & Lin H. (2020). Implementation of artificial intelligence in medicine: Status analysis and development suggestions. Artificial intelligence in medicine, 102, 101780. https://doi.org/10.1016/j.artmed.2019.101780
57. Xu J, Wu P, Chen Y, Meng Q, Hussain Dawood, & Hassan Dawood, 2019. A hierarchical integration deep flexible neural forest framework for cancer subtype classification by integrating multi-omics data. BMC Bioinformat. 20, 527. https://doi.org/10.1186/s12859-019-3116-7.
58. Zhang P, Guo Z, Ullah S, Melagraki G, Afantitis A, & Lynch I. (2021). Nanotechnology and artificial intelligence to enable sustainable and precision agriculture. Nature plants, 7(7), 864-876. https://doi.org/10.1038/s41477-021-00946-6.
59. Zhavoronkov A, Ivanenkov Y.A, Aliper A, Veselov M.S, Aladinskiy V.A, Aladinskaya A.V, Terentiev V.A, Polykovskiy D.A, Kuznetsov M.D, Asadulaev A, Volkov Y, Zholus A, Shayakhmetov R.R, Zhebrak A, Minaeva L.I, Zagribelnyy B.A, Lee L.H, Soll R, Madge D, Xing L, Aspuru-Guzik A. (2019). Deep learning enables rapid identification of potent DDR1 kinase inhibitors. Nature biotechnology, 37(9), 1038-1040. https://doi.org/10.1038/s41587-019-0224-x.
60. Zhavoronkov A, Vanhaelen Q, & Oprea T.I. (2020). Will Artificial Intelligence for Drug Discovery Impact Clinical Pharmacology? Clinical pharmacology and therapeutics, 107(4), 780-785. https://doi.org/10.1002/cpt.1795.