

AI-Based Drug Design: Revolutionizing Drug Discovery through in Silico Analysis

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Abstract

The convergence of artificial intelligence (AI) and drug design has catalyzed a tectonic shift within the pharmaceutical arena, illuminating a new path towards rapid and efficient drug discovery. This review embarks on an odyssey through the transformative landscape of AI-based drug design, delving into its multifaceted applications and profound implications. By harnessing AI's virtuosity, drug discovery processes are imbued with unprecedented speed and precision. Machine learning algorithms harmonize with intricate biological datasets, unraveling patterns and relationships previously enshrouded in complexity. Deep learning models, akin to modern-day alchemists, sculpt molecular structures and decode binding affinities, accelerating the quest for viable drug candidates. The symphony of AI resonates across the stages of drug discovery, from in silico screening to the hallowed realm of de novo drug design. Virtual libraries become a realm of possibility as AI orchestrates the virtual ballet of compound screening, whittling down the ensemble to a chorus of promising candidates. Moreover, AI's creative fervor burgeons in the crucible of de novo design, forging novel molecules with desired properties. The predictive mastery extends to the realm of absorption, distribution, metabolism, excretion, and toxicity (ADMET) modeling, where AI's crystal ball reveals the fate of molecules based on their molecular signatures. The harmonious confluence of AI and drug design unfolds as a symphony of innovation, orchestrating the metamorphosis of drug discovery into an elegant and efficacious masterpiece.

Keywords

AI, Deep Learning, Machine learning, ADMET, Drug design, Biological Data

Introduction

The rapid evolution of artificial intelligence (AI) has brought about a paradigm shift across numerous scientific domains, ushering in a transformative era with profound implications for drug

Submission: 18 August 2023; **Acceptance:** 19 September 2023



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discovery and development (Padhi et al., 2023). The integration of AI-driven methodologies, particularly through in silico analysis, has emerged as a groundbreaking approach to expedite the identification of potential drug candidates and optimize their properties. In this comprehensive review, we delve into recent developments in AI-based drug design and underscore its potential to reshape the pharmaceutical research and innovation landscape.

The conventional drug discovery process is a labyrinthine and resource-intensive journey, often marred by high attrition rates and protracted timelines (Munro et al., 2022). However, the amalgamation of AI and computational biology has birthed unprecedented avenues for streamlining this process, revolutionizing the methodology by which novel therapeutics are identified and designed. By harnessing the computational prowess of AI algorithms, researchers have been empowered to sift through vast datasets, predict intricate molecular interactions, and even generate novel chemical entities tailored for specific attributes. These collective advancements drive an acceleration in the drug discovery pipeline, promising a future of efficiency, innovation, and precision.

The amalgamation of AI and drug design has forged an alliance that leverages machine learning, deep learning, and neural networks to usher in an age of unparalleled innovation (Graham et al., 2022). These technologies excel in unraveling complex biological data, spanning from protein structures to genomic sequences and chemical properties. This achievement's ripples extend far and wide, establishing a foundational cornerstone for rational drug design by equipping researchers with precise insights into molecular interactions.

AI Algorithms in Drug Design

The combination of artificial intelligence (AI) and drug design has sparked an era of innovation. AI algorithms, notably machine learning and deep learning models, have become indispensable tools, revolutionizing the analysis of complex biological data. This synergy has propelled advancements in predicting molecular interactions and reshaping the drug discovery process. These algorithms exhibit remarkable prowess in unraveling intricate biological information, from protein structures to genomic intricacies, offering researchers unparalleled accuracy in identifying potential drug targets and deciphering their interactions (O'Neil et al., 2017., Awad et al., 2018; El-Behery et al., 2021).

Machine learning algorithms, a subset of AI, excel in learning intricate patterns and relationships from data without explicit programming. In drug design, they assimilate massive datasets encompassing information about biological molecules, chemical structures, and experimental outcomes. Through pattern recognition and statistical analysis, they unveil the complex relationships between molecular attributes and their biological activities, enhancing the precision of identifying drug candidates.

Delving deeper into the AI landscape, deep learning, featuring convolutional neural networks (CNNs) and recurrent neural networks (RNNs), tackles intricate tasks like protein structure prediction and ligand-receptor binding affinity estimation (Ghosh et al., 2022). Notable in this domain is DeepMind's AlphaFold, a pioneering deep learning framework that unveils

protein structures with unparalleled accuracy (Senior, 2020; Jumper et al., 2021; Varadi & Velankar, 2023), transcending previous experimental limitations and energizing structure-based drug design.

AI algorithms deftly handle a vast array of biological data, deciphering protein-protein interactions, gene expression patterns, and integrating omics data from genomics, transcriptomics, proteomics, and metabolomics. These insights provide researchers with a comprehensive understanding of disease mechanisms, facilitating the identification of novel therapeutic targets. Furthermore, AI algorithms forecast the binding affinity between drug candidates and target proteins, a pivotal factor in drug efficacy and mitigating potential side effects (Opioids, 2023).

In Silico Screening and Virtual Libraries

In AI-driven drug design, *in silico* screening has emerged as a transformative technique, harnessing AI's computational power to streamline the identification of potential drug candidates. This method involves virtually evaluating vast compound libraries against specific target proteins, offering a more efficient and cost-effective alternative to traditional high-throughput screening (Aggarwal et al., 2023). *In silico* screening's success relies on the synergy between machine learning and deep learning algorithms, trained on comprehensive datasets encompassing molecular structures, chemical properties, and biological activities. These AI models predict new drug candidates, expediting the hit identification process and focusing resources on molecules with the most promising interactions (Gallego et al., 2021).

Furthermore, *in silico* screening aids lead compound optimization by predicting binding affinities and pharmacokinetic properties, guiding researchers in refining lead molecules and reducing the time required for optimization (Baringhaus et al., 2004, Barcelos et al., 2022). One of its major advantages is its ability to reduce the time and costs associated with traditional high-throughput screening. *In silico* screening digitally assesses compounds, making it particularly valuable in the early stages of drug discovery, where timely decision-making is crucial.

In recent years, *in silico* screening has proven its worth, playing a vital role in identifying potential drug candidates for COVID-19 treatment and repurposable drugs for various diseases, such as Ebola (Jin et al., 2020; O'Neil et al., 2020). However, challenges remain, including ensuring model accuracy, addressing training data biases, enhancing interpretability, aligning computational predictions with regulatory frameworks, and integrating *in silico* findings into regulatory processes.

Predictive ADMET Modeling

In drug development, the use of artificial intelligence (AI) to predict a drug's absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties has revolutionized the process (de Araújo et al., 2023). Traditionally, evaluating ADMET has been resource-intensive and relied on extensive experimentation and clinical trials. However, AI now allows us to predict these parameters based on molecular structures, improving drug discovery efficiency. AI models,

particularly those combining machine learning and computational chemistry, can predict ADMET properties from molecular structures. Trained on extensive datasets covering molecular attributes and ADMET outcomes, these models provide quick insights into potential ADMET issues, guiding early decision-making (Webster, 2023). The predictive power of AI enables the strategic allocation of resources, focusing on candidates with favorable profiles and avoiding costly late-phase failures. AI-driven predictive ADMET modeling is an effective early defense against such failures.

AI-driven predictive ADMET modeling streamlines the drug discovery process by quickly analyzing compound structures and providing ADMET forecasts, eliminating the need for extensive experimentation. AI's value is particularly evident in drug repurposing, where it rapidly assesses whether existing drugs have suitable ADMET profiles for new therapeutic uses, facilitating the identification of potential candidates.

Challenges in AI-driven predictive ADMET modeling include refining model accuracy, addressing data biases, improving interpretability, and ensuring the seamless integration of AI-derived ADMET projections into regulatory processes. Overcoming these challenges is crucial for realizing the full potential of predictive ADMET modeling.

Case Studies and Success Stories

The harmonious fusion of artificial intelligence (AI) and drug design has spawned a tapestry of success stories, each a testament to the transformative impact AI wields within the pharmaceutical realm. These triumphs etch an indelible narrative of AI's potential to accelerate drug discovery, optimize therapeutic candidates, and deftly address pressing medical exigencies. Among these resplendent accomplishments, two case studies featuring Atomwise and Exscientia illuminate the efficacy of AI-based drug design, offering a profound symphony of ingenuity and efficacy.

Atomwise's AI Platform: Illuminating Pathways in Ebola Treatment

Atomwise's AI platform showcases its agility in identifying existing drugs for repurposing in Ebola treatment. Through AI-driven virtual screening, it probes vast chemical compound repositories, discerning molecules with the potential to inhibit Ebola virus proteins. The AI model predicts binding affinities, aiding researchers in selecting the most promising compounds (O'Neil et al., 2020). This demonstrates AI's prowess in rapidly identifying therapeutic agents, particularly during crises, harmonizing with the rhythm of rapid response.

Exscientia's Ode to Drug Discovery: AI and Obsessive-Compulsive Disorder

Exscientia's AI-driven drug discovery for obsessive-compulsive disorder (OCD) is a paradigm shift. AI acts as a master composer, guiding the creation of potential compounds using its molecular knowledge. This collaboration leads to the discovery of a promising drug candidate (Melo et al., 2022). AI's predictive power accelerates drug discovery and shapes innovative therapies, demonstrating its ability to harmonize data and innovation. These achievements highlight the symphony of AI-based drug design, from rapid response in epidemics to creating

new therapeutic options. AI-driven drug design advances like an opus, combining familiar and novel elements, leading to a future with safer, more potent, and innovative therapies.

Conclusion

The epic saga of AI-based drug design draws to a resounding conclusion, echoing the harmonious symphony of innovation that has reverberated throughout these pages. AI's embrace of complex biological datasets, its alchemical prowess in sculpting molecular structures, and its prophetic revelations in ADMET modeling converge to transform drug discovery into a virtuoso performance of efficiency and efficacy. From the rapid-response cadence of repurposing for epidemics to the sonnet of creating novel therapeutic candidates, AI unfurls a melodic tapestry that shapes a future adorned with safer, more potent, and deeply innovative therapies. The symphony composed by AI's algorithms resonates as a clarion call to a new era of pharmaceutical research, one that harmonizes data and innovation to craft a crescendo of groundbreaking treatments. As the curtains fall on this review, the resounding refrain of AI's symphony lingers—a serenade to the future of drug discovery, where AI's transformative notes echo across laboratories, hospitals, and patient lives alike.

References

- Aggarwal, S., Karmakar, A., Krishnakumar, S., Paul, U., Singh, A., Banerjee, N., Laha, N., Ball, G. R., & Srivastava, S. (2023). Advances in Drug Discovery based on Genomics, Proteomics and Bioinformatics in Malaria. *Current Topics in Medicinal Chemistry*, 23(7), 551-578.
- Awad, A., Trenfield, S. J., Goyanes, A., Gaisford, S., & Basit, A. W. (2018). Reshaping drug development using 3D printing. *Drug discovery today*, 23(8), 1547-1555.
- Barcelos, M. P., Gomes, S. Q., Federico, L. B., Francischini, I. A. G., Hage-Melim, L. I. D. S., Silva, G. M., & de Paula da Silva, C. H. T. (2022). Lead Optimization in Drug Discovery. In *Research Topics in Bioactivity, Environment and Energy: Experimental and Theoretical Tools* (pp. 481-500). Cham: Springer International Publishing.
- Baringhaus, K. H., Matter, H., & Oprea, T. (2004). Efficient strategies for lead optimization by simultaneously addressing affinity, selectivity and pharmacokinetic parameters. *Cheminformatics in drug discovery*, 333-379.
- de Araújo, A. C. J., Freitas, P. R., Araújo, I. M., Siqueira, G. M., de Oliveira Borges, J. A., Alves, D. S., Miranda, G. M., Nascimento, I. J. D. S., de Araújo-Júnior, J. X., da Silva-Júnior, E. F., de Aquino, T. M., Junior, F. J. B. M., Marinho, E. S., Santos, H. S. D., Tintino, S. R., & Coutinho, H. D. M. (2023). Potentiating-antibiotic activity and absorption, distribution, metabolism, excretion and toxicity properties (ADMET) analysis of synthetic thiadiazines against multi-drug resistant (MDR) strains. *Fundamental & Clinical Pharmacology*.
- El-Behery, H., Attia, A. F., El-Fishawy, N., & Torkey, H. (2021). Efficient machine learning model for predicting drug-target interactions with case study for Covid-19. *Computational Biology and Chemistry*, 93, 107536.
- Gallego, V., Naveiro, R., Roca, C., Rios Insua, D., & Campillo, N. E. (2021). AI in drug development: a multidisciplinary perspective. *Molecular Diversity*, 25, 1461-1479.

- Ghosh, R. (2022). A Faster R-CNN and recurrent neural network based approach of gait recognition with and without carried objects. *Expert Systems with Applications*, 205, 117730.
- Graham, S. S. (2022). *The doctor and the algorithm: Promise, peril, and the future of health AI*. Oxford University Press.
- Jin, Z., Du, X., Xu, Y., Deng, Y., Liu, M., Zhao, Y., Zhang, B., Li, X., Zhang, L., Peng, C., Duan, Y., Yu, J., Wang, L., Yang, K., Liu, F., Jiang, R., Yang, X., You, T., Liu, X., Yang, X., Bai, F., Liu, H., Liu, X., Guddat, L. W., Xu, W., Xiao, G., Qin, C., Shi, Z., Jiang, H., Rao Z., & Yang, H. (2020). Structure of M pro from SARS-CoV-2 and discovery of its inhibitors. *Nature*, 582(7811), 289-293.
- Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., Tunyasuvunakool, K., Bates, R., Židek, A., Potapenko, A., Bridgland, A., Meyer, C., Kohl, S. A. A., Ballard, A. J., Cowie, A., Romera-Paredes, B., Nikolov, S., Jain, R., Adler, J., Back, T., Petersen, S., Reiman, D., Clancy, E., Zielinski, M., Steinegger, M., Pacholska, M., Berghammer, T., Bodenstein, S., Silver, D., Vinyals, O., Senior, A. W., Kavukcuoglu, K., Kohli, P., & Hassabis, D. (2021). Highly accurate protein structure prediction with AlphaFold. *Nature*, 596(7873), 583-589.
- Melo, M. C., Maasch, J. R., & de la Fuente-Nunez, C. (2022). *Machine Learning for Drug Discovery*. American Chemical Society, 55(3): 1947–1999.
- Munro, E., Friel, S., Baker, C., Lynch, A., Walker, K., Williams, J., Cook, E. J., & Chater, A. M. (2022). CCTC final report: care leavers' transitions to adulthood in the context of COVID-19. University of Bedfordshire.
- O'Neil, N. J., Bailey, M. L., & Hieter, P. (2017). Synthetic lethality and cancer. *Nature Reviews Genetics*, 18(10), 613-623.
- O'Neil, N. J., Bailey, M. L., Hieter, P., & Lee, W. (2020). DNA damage does not cause replication fork stalling, fork collapse, or a G2 arrest in yeast. *Molecular Cell*, 80(4), 665-673.
- Opioids, E.R. Admission. (2023). Vital signs and laboratory characteristics as predictors of disposition status in a diverse cohort of hospitalized COVID-19 patients in New Mexico. *Journal of General Internal Medicine*, 38(2), S81-S799.
- Padhi, A., Agarwal, A., Saxena, S. K., & Katoch, C. D. S. (2023). Transforming clinical virology with AI, machine learning and deep learning: a comprehensive review and outlook. *VirusDisease*, 34, 345–355.
- Senior, A. W., Evans, R., Jumper, J., Kirkpatrick, J., Sifre, L., Green, T., Qin, C., Židek, A., Nelson, A. W. R., Bridgland, A., Penedones, H., Petersen, S., Simonyan, K., Crossan, S., Kohli, P., Jones, D. T., Silver, D., Kavukcuoglu, K., Hassabis, D. (2020). Improved protein structure prediction using potentials from deep learning. *Nature*, 577(7792), 706-710.
- Varadi, M., & Velankar, S. (2023). The impact of AlphaFold Protein Structure Database on the fields of life sciences. *Proteomics*, 23(17), 2200128.
- Webster, A. A. (2023). *The Ghost of the Lake City: gaming and the crisis of survival in Mexico City* (PhD diss.).