

Has Artificial Intelligence Revolutionized Drug Design and Discovery?

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Abstract

Artificial intelligence (AI), particularly machine learning (ML) and deep learning (DL), is reshaping bioinformatics and computational biology by enhancing core techniques such as molecular docking, molecular dynamics (MD) simulations, and drug design. This commentary explores how AI is changing, from specialized, task-focused tools to the broader, long-term dream of artificial general intelligence (AGI). It also examines how these advances are shaping biomedical research and the future of drug discovery. AI-driven tools improve docking accuracy, accelerate MD simulations, and enable generative design of novel compounds, contributing to faster, more cost-effective drug discovery. While breakthroughs such as AlphaFold have transformed protein structure prediction, the broader narrative of an “AI revolution” warrants scrutiny. Despite substantial progress, challenges such as biological complexity, data bias, and regulatory hurdles persist. AI remains a powerful enhancer and a complementary tool, rather than a replacement for experimental methods, and its integration with emerging technologies such as quantum computing may catalyze future transformation in drug discovery.

Keywords: Artificial intelligence; computational biology; Molecular docking; Drug design; Deep Learning.

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Artificial intelligence (AI), particularly machine learning (ML) and deep learning (DL), has emerged as a powerful tool in bioinformatics and computational biology, transforming tasks such as molecular docking, molecular dynamics (MD) simulations, and other essential predictions in drug design and discovery. AI encompasses various subsets, namely, ML, which learns patterns from data, and DL, which uses multi-layer neural

networks. These can power generative AI to create new content, such as molecular structures. Though presently regarded as narrow AI (focused on defined tasks), it is evolving toward artificial general intelligence (AGI), which could enable broader scientific discovery. AGI refers to AI with human-like capabilities in understanding, learning, adapting, and applying knowledge across domains, potentially accelerating progress in fields such as bioinformatics.

While some view AI as a revolution that accelerates biomedical research, others regard it as an overhyped terminology for re-

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finer versions of longstanding computational methods used for many years. This letter examines how AI is contributing to biomedical and drug discovery areas, drawing on recent advances and evaluates whether that progress truly amounts to genuine innovation or is merely a claim.

Computational drug design/ discovery employs multiple approaches, which almost always include molecular docking and MD simulations analyses. Molecular docking, the prediction of ligand-protein binding, has been used for many years. Traditional methods rely on physics-based scoring and exhaustive searches. They tend to be both computationally heavy and often inaccurate when dealing with flexible systems. AI enhances molecular docking by learning from large datasets of known interactions. For instance, DL models such as KarmaDock (1) and DiffDock refine pose predictions and binding affinities, outperforming classical approaches in benchmarks (2). These tools enable rapid virtual screening of vast chemical libraries, integrating generative AI to propose novel ligands. They are highly effective in areas such as drug repositioning, drug discovery, vaccine design, and more. In practice, AI-driven docking has facilitated early-stage screening in different disorders, including oncology and infectious diseases, reducing reliance on resource-intensive wet-lab experiments and potentially lowering development costs (2-4).

The other foundational technique, MD simulations, provides dynamic insights into biomolecular behavior, mainly protein folding and conformational changes. Classical MD is limited by high computational costs, restricting simulations to microseconds on supercomputers. AI addresses this by using ML-accelerated force fields that approximate quantum effects, speeding up simulations by orders of magnitude. Advanced models for predicating protein 3D structures such as AlphaFold3 predict highly accurate static structures and confidence metrics that highlight flexible regions. These outputs serve as valuable starting points for generating conformational ensembles in MD studies, while generative AI aids in predicting stability and allosteric sites (3). This integration can be employed to understand

enzyme mechanisms and membrane interactions, which allows researchers to explore complex biological systems that were previously demanding (2).

In drug design, AI synthesizes data from genomics, proteomics, and chemistry to streamline target identification, lead optimization, and toxicity prediction. Generative models, such as variational autoencoders and diffusion-based architectures, design new molecules from scratch (*de novo* design) optimized for properties including bioavailability and ADMET (absorption, distribution, metabolism, excretion, toxicity). AI also facilitates drug repurposing by mining large databases and supports end-to-end pipelines that combine docking and MD simulations. (2, 5).

Notable real-world impacts include AI-enabled pipelines that have dramatically shortened early discovery timelines. During the COVID-19 pandemic, AI platforms (e.g., BenevolentAI) rapidly identified and prioritized baricitinib for repurposing, shortening design cycles, and helping improve preclinical and clinical success rates (5). Moreover, AI tools contributed to the design, optimization, and data analysis in the rapid development of Moderna and Pfizer's COVID-19 mRNA vaccines (6). Exscientia, in collaboration with Sumitomo Dainippon Pharma, designed a novel small-molecule candidate (DSP-1181) for obsessive-compulsive disorder in less than 12 months (from screening to preclinical candidate), compared to typical timelines of 4–5 years (7). Similarly, Insilico Medicine advanced a preclinical candidate (rentosertib) for idiopathic pulmonary fibrosis from target discovery to IND-enabling studies in under 30 months, at a fraction of conventional costs. Its phase 2a trial results were published in 2025 (8).

With advancements in AI algorithms, its role will expand in the future. In biological sciences, AI is expected to have an even greater influence on drug design and discovery for biologicals than for small molecules (9). The genuine impact of AI is already visible in some areas. Breakthroughs such as AlphaFold have undeniably transformed protein structure prediction, enabling downstream efficiencies in docking, MD, and design (3). Substantial

investments since the mid-2010s have yielded tangible progress, for instance, novel antibiotics and targeted therapies. Despite these advances, the narrative of an "AI revolution" needs scrutiny. As of early 2026, several AI-assisted discovery pipelines produced candidates now in trial (e.g., Insilico's rentosertib), but none have full approval yet. Critics argue that AI often rebrands existing techniques. The overuse of the term AI in scientific papers and publications is probably prompted by its fame in our everyday lives and community, also fueled by the media and venture capital (10-11). AI models in docking and MD simulations are not without significant limitations and occasional performance failures. DL-based docking methods, while often superior in speed, can produce physically implausible poses, fail to recover critical molecular interactions even when RMSD is acceptable, and exhibit poor generalization to novel protein pockets. Benchmarks such as PoseBusters have revealed that several leading DL docking tools (e.g., DiffDock, TankBind) do not consistently outperform classical methods in physical plausibility or generalization. Similarly, ML-accelerated force fields, though enabling longer timescales, can introduce instabilities or inaccuracies in approximating quantum effects, particularly for complex systems (12). These issues underscore that AI remains complementary to, rather than a full replacement for, traditional physics-based approaches and experimental validation.

Regulatory implications also represent a key hurdle for the broader adoption of AI-driven pipelines. The US FDA issued draft guidance ('Considerations for the Use

of Artificial Intelligence to Support Regulatory Decision-Making for Drug and Biological Products', Jan. 2025) outlining a risk-based framework for assessing AI model credibility in submissions supporting safety, effectiveness, or quality decisions. The European Medicines Agency (EMA) has published a Reflection Paper on AI (finalized 2024), emphasizing human-centric approaches and early regulatory engagement. Unresolved issues, particularly model interpretability (the 'black-box' nature of many DL systems), can complicate submissions, as regulators require transparent rationales for AI-generated data or predictions. This may prolong review timelines until standardized explainability metrics and validation protocols are established, though ongoing qualification procedures (e.g., EMA's first AI methodology qualification in March 2025 for an AI tool in liver disease trials) signal progress toward precedents (12-15). Regulatory acceptance of AI outputs is still limited to supportive evidence, not primary proof of safety/efficacy.

To conclude, AI has transformed specific niches in bioinformatics and drug discovery, enhancing efficiency and innovation. AI has accelerated early-stage discovery but has not yet delivered approved drugs. Its current role is best described as augmentative, with potential for a paradigm shift when combined with quantum computing and improved regulatory frameworks in near future.

Conflict of Interest

The authors declare that they have no conflict of interest.

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