

Quantum vs. Classical Approaches: A Comparative Analysis in the Context of Drug Development for Preclinical Applications

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Abstract

Quantum computing is an emerging technology that leverages the principles of quantum mechanics to perform calculations exponentially faster than classical computers for certain applications. In drug discovery and development, quantum algorithms have the potential to accelerate the search for new therapeutics. This review provides a comparative analysis of quantum and classical computational approaches for drug development applications in the preclinical setting. We first give an overview of the principles behind quantum computing and explain how quantum circuits can encode and manipulate quantum information. We then discuss key quantum algorithms that may confer advantages over their classical counterparts for pharmaceutical problems such as molecular docking, molecular dynamics simulations, and machine learning. Current quantum computing hardware restrictions and the applicability of hybrid quantum-classical algorithms are also considered. We analyze early proof-of-concept demonstrations applying quantum methods to drug design problems and discuss the challenges and outlook moving forward. Overall, quantum computing holds promise to expand the scope and scale of computational modeling in drug discovery once the hardware matures, but classical techniques likely still have advantages for certain near-term applications. Further interdisciplinary research is needed to fully leverage the capabilities of quantum computation in the preclinical drug development pipeline.

Indexing terms: quantum computing, drug design, docking, molecular dynamics, machine learning

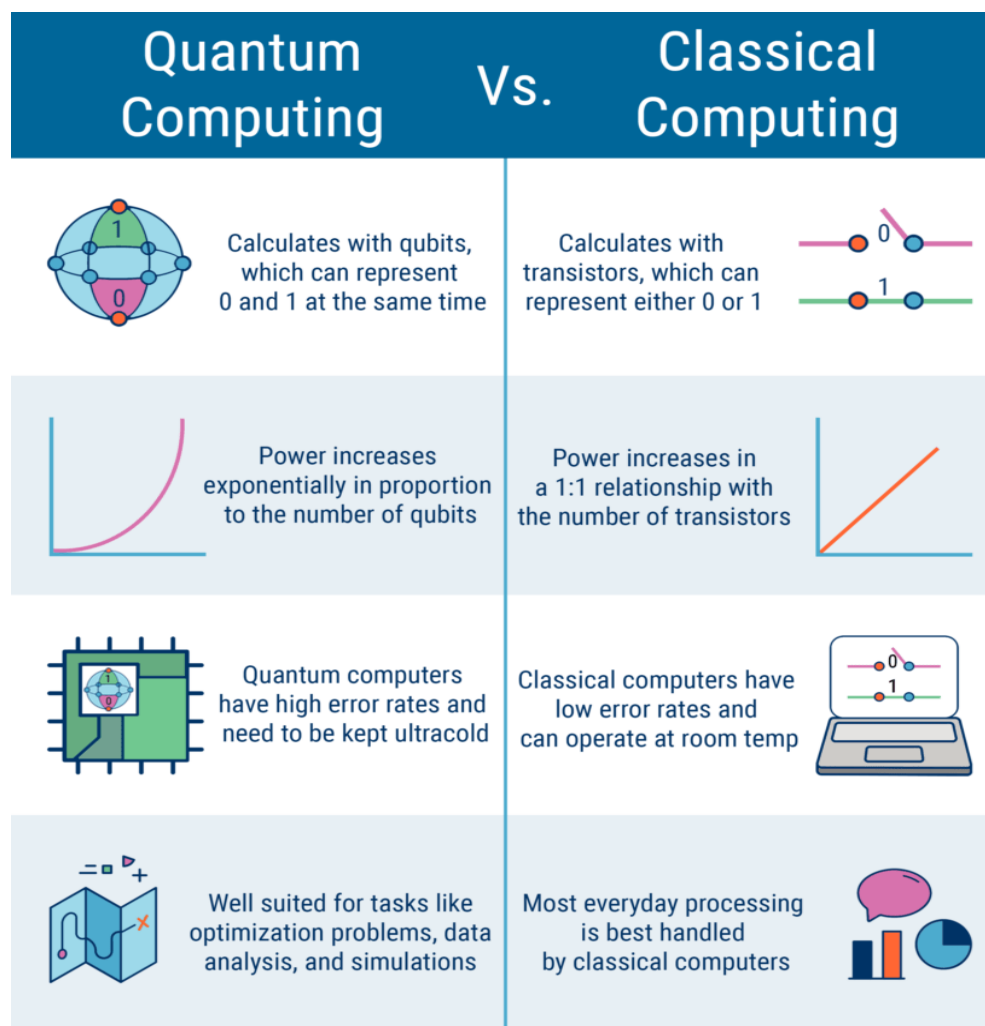
Introduction

The conventional drug development pipeline represents a lengthy and costly journey, spanning approximately 10-15 years from the initial stages of discovery to the eventual market approval. This extensive process demands an investment exceeding \$2 billion for each successfully approved drug [1]. A substantial portion of both time and financial resources is allocated to the preclinical phases, which involve the identification of lead compounds and the optimization of their properties before progressing to clinical trials. This inherently slow and expensive nature of drug development has prompted a keen interest in harnessing advanced computational methods to enhance the efficiency of early-stage drug discovery. In recent years, a paradigm shift has been witnessed in the pharmaceutical industry, as researchers increasingly explore the integration of quantum computing into drug discovery processes. The majority of computational modeling in pharmaceutical research has traditionally relied on classical physics-based simulations executed on conventional digital computers. However, the advent of quantum computing presents a revolutionary alternative, promising to bring about a fundamental transformation in the realm of computation, particularly for crucial applications in pharmaceutical modeling [2].

Quantum computing operates based on the principles of quantum mechanics, utilizing quantum bits or qubits as the fundamental units of information. Unlike classical bits, which can exist in a state of 0 or 1, qubits can exist in multiple states simultaneously, owing to the phenomenon of superposition. This inherent ability to process vast amounts of information concurrently offers a significant advantage over classical computing when applied to complex problem-solving tasks. One of the primary areas where quantum computing holds promise for pharmaceutical research is in the simulation of molecular interactions and drug behavior [3]. Quantum computers excel in solving problems related to the quantum nature of matter, enabling more accurate representations of molecular structures and interactions. Classical simulations often struggle with the intricacies of quantum mechanics, leading to approximations and limitations in the precision of results. Quantum computers, on the other hand, are better equipped to model the complex behavior of molecules, providing researchers with a

more detailed and realistic understanding of drug actions. The utilization of quantum computing in drug discovery has the potential to expedite the identification of lead compounds and streamline the optimization process. Quantum algorithms can efficiently explore vast chemical spaces, facilitating the rapid screening of potential drug candidates with enhanced accuracy [4]. In their 2023 study, Wong and colleagues introduced an innovative approach employing quantum machine learning and simulation through quantum computing to transform the drug discovery research and development process [5]. The primary objective of their methodology is to reduce the R&D duration to a range of 3-6 months, concurrently minimizing expenses. This is achieved by leveraging machine learning for hit generation and employing quantum simulation to facilitate filtering based on target binding.

Figure 1.



Quantum computers are based on quantum bits (qubits), which can exist in a superposition of 0 and 1 states simultaneously. This enables quantum algorithms to perform parallel calculations on all possible input states at once. The phenomena of quantum entanglement and interference between qubits also allows certain problems like optimization, search, and simulation of quantum systems to be solved faster than any possible classical algorithm. As quantum computing hardware matures over the next 5-10 years, it will become feasible to apply these quantum speedups to large-scale problems in drug discovery.

This review provides a head-to-head comparison between quantum and classical computational methods for pharmaceutical applications in the preclinical setting [6]. We focus on how quantum computing may impact computational drug design techniques like molecular docking, molecular dynamics (MD) simulations, and machine learning. The principles of quantum computation are first introduced, followed by a discussion of relevant quantum algorithms. The challenges and outlook for applying quantum methods to accelerate and expand preclinical drug development are then analyzed.

Overview of Quantum Computing

Quantum computers encode information in quantum bits or qubits. Unlike classical binary bits that exist in definite 0 or 1 states, qubits can exist in a superposition of 0 and 1 at the same time. Mathematically this superposition is represented as a linear combination of basis states:

$$|\psi\rangle = \alpha|0\rangle + \beta|1\rangle$$

Where α and β are complex coefficients that define the probabilities to observe 0 or 1 upon measurement. Multiple qubits can also exhibit entanglement, where the quantum state of each qubit is dependent on the others despite physical separation between qubits. These two unique quantum properties of superposition and entanglement enable quantum parallelism, allowing computations on all possible combinations of qubit states simultaneously.

Quantum algorithms, at the heart of quantum computing, operate by manipulating qubits, the fundamental units of quantum information. These algorithms employ a series of quantum logic gates to process information, and unlike classical bits, qubits can exist in a superposition of both 0 and 1 states simultaneously. This unique property allows quantum computers to perform certain calculations exponentially faster than their classical counterparts for specific problems.

The manipulation of qubits through quantum logic gates is a crucial aspect of quantum algorithm design. Single qubit gates, for instance, are responsible for altering the coefficients α and β , effectively rotating the qubit state in the complex plane. These rotations enable the creation of intricate superpositions, enhancing the quantum computer's computational power [7]. Two-qubit gates, such as the controlled-NOT (CNOT) gate, facilitate conditional operations based on the state of one qubit. This entangling gate, in particular, plays a pivotal role in establishing correlations between qubits, allowing for the execution of complex quantum algorithms. The reversibility of quantum logic gates is a fundamental characteristic, ensuring that the operations can be undone if needed. This reversibility is a direct consequence of the unitary nature of quantum operations, which preserves the normalization of quantum states. As a result, quantum algorithms maintain coherence throughout their execution, exploiting the intricate interplay of quantum superpositions to perform computations efficiently.

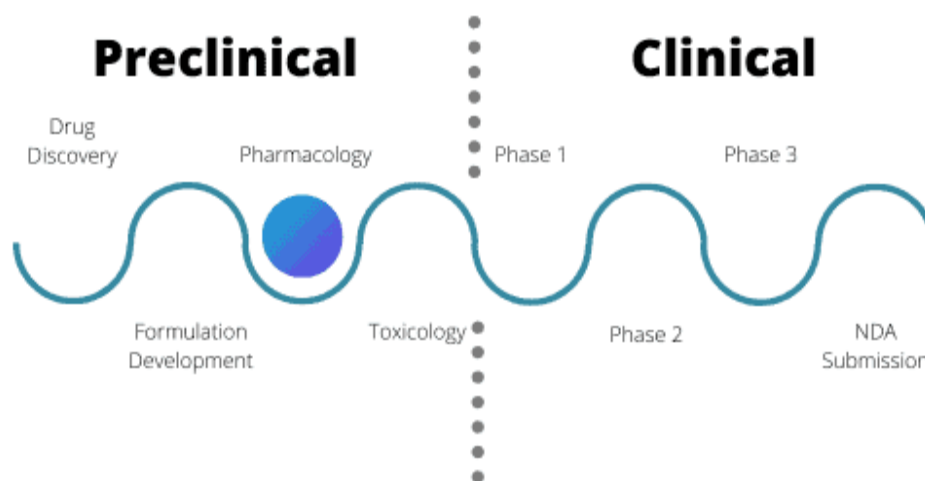
Upon completing the quantum algorithm, the next step involves measuring the qubits. This measurement process collapses the qubits' superposition states to classical 0 or 1 values. However, the outcome is probabilistic, with the probabilities determined by the final superposition state of the qubits. This introduces an inherent randomness into quantum computation. To obtain meaningful results, quantum algorithms are often run multiple times, and the statistics of the measurement outcomes are analyzed. This statistical approach allows researchers to discern patterns and trends in the quantum information processing, contributing to the overall understanding and optimization of quantum algorithms. Repeated runs of the same quantum algorithm build up a distribution of measurement outcomes, providing insights into the quantum system's behavior [8]. Researchers analyze these outcomes to extract meaningful information and validate the correctness of the quantum algorithm. It's important to note that the probabilistic nature of quantum measurements introduces challenges in error correction and fault tolerance, areas actively explored to make quantum computing more robust and reliable for practical applications. Quantum speedups arise from constructive and destructive interference between superposed states during the quantum algorithm. Optimization problems like finding the minimum value of some cost function can achieve quadratic or exponential speedup on a quantum computer compared to the best classical techniques. Other quantum algorithms like Shor's provide exponential speedups for factoring large integers and Grover's algorithm achieves quadratic speedup for searches in unstructured databases. Special-purpose quantum simulators can also efficiently model quantum systems [9].

There are multiple physical implementations of qubits being explored, including superconducting circuits, trapped ions, and photonic systems. Each has tradeoffs between qubit performance factors like coherence time, gate fidelity, connectivity, and scalability. Current noisy intermediate-scale quantum (NISQ) devices contain 50-100 qubits. It is anticipated that fault-tolerant quantum computers with thousands of logical qubits capable of reliably running advanced algorithms will be developed in the next 10-15 years. Hybrid classical-quantum workflows using cloud access to NISQ computers are already being explored for pharmaceutical applications in the near-term.

Quantum Methods for Drug Design

Molecular Docking: Molecular docking, a pivotal computational technique in drug discovery, plays a crucial role in predicting the binding interactions between small molecule drug candidates and target proteins. The process involves modeling the intricate intermolecular relationships and scoring various poses to determine the most favorable binding configuration. The daunting challenge lies in the exhaustive exploration of potential orientations and conformations of the ligand within the binding site. The complexity of this task scales exponentially with the number of rotatable bonds in the ligand, making it computationally intensive, particularly for flexible ligands. Classical docking approaches employ heuristic strategies to navigate and prune the vast search space, yet they encounter scalability issues, especially in handling the flexibility inherent in many drug candidates. However, a notable advancement in this field comes from quantum docking algorithms, such as the Quantum Approximate Optimization Algorithm (QAOA) pioneered by Google AI Quantum. These quantum algorithms leverage the principles of quantum parallelism to expedite the docking process dramatically.

Figure 2.



The QAOA, based on the principles of quantum mechanics, offers a paradigm shift in computational efficiency. It harnesses the power of superposition and entanglement to explore multiple possibilities simultaneously. In comparison to classical methods, quantum docking algorithms can achieve remarkable speedups, with reported instances of up to 3600 times faster computations. This substantial acceleration stems from the ability of quantum systems to process complex information in parallel, enabling them to explore a vast search space with unprecedented efficiency. The key advantage of quantum docking algorithms lies in their ability to address the scalability issues encountered by classical methods when dealing with flexible ligands. The inherent parallelism in quantum computations allows for the simultaneous evaluation of multiple conformations, significantly reducing the time required to explore potential binding configurations. This not only enhances the speed of the docking process but also opens new avenues for investigating complex biological systems with greater computational accuracy [10].

Despite the promising advancements, it's essential to note that quantum docking algorithms are still in the early stages of development. Challenges such as error correction, noise reduction, and the need for robust quantum hardware pose hurdles to their widespread adoption. However, as quantum computing technology continues to progress, quantum docking holds the potential to revolutionize the field of molecular docking, offering unprecedented computational advantages for drug discovery and molecular design.

QAOA prepares an equal superposition of all ligand poses, then iteratively adjusts superposition phases via a mixing operator and cost Hamiltonian that scores binding affinity [11]. Constructive interference reinforces optimal poses while interfering with suboptimal ones. Measurement reveals the pose with best binding score. Early proof-of-concept used QAOA on Rigetti's quantum computer to dock biotin and tubulin inhibitors. Larger drug-target studies will be possible as quantum hardware improves. Hybrid quantum-classical docking schemes could also have clients submit candidate poses classically which are then scored and optimized by a quantum server.

Molecular Dynamics Simulations: Molecular dynamics (MD) simulations serve as a pivotal tool in the field of computational chemistry, facilitating the exploration of the time-dependent behavior of molecular systems. The fundamental principle underlying MD simulations involves the numerical integration of Newton's equations of motion, allowing for the comprehensive study of conformational changes, binding kinetics, and various thermodynamic properties. Despite their utility, classical MD simulations encounter significant computational challenges when dealing with extended timescales and large system sizes. This predicament arises due to the exponential scaling of computational complexity with the number of particles involved in the simulation. Classical MD simulations are based on classical mechanics and typically involve solving Newton's equations of motion for each particle in the system. While effective for short timescales and smaller systems, the computational demands become formidable as one attempts to model larger and more complex molecular systems over extended periods. The necessity to calculate the interactions between all pairs of atoms in the system contributes to the exponential increase in computational requirements. Consequently, the simulation of long timescales or large molecular systems becomes impractical and often exceeds the capabilities of classical MD approaches [12].

In contrast, quantum molecular dynamics (QMD) algorithms present a promising avenue for overcoming the limitations associated with classical MD simulations. Quantum mechanics governs the behavior of particles at the atomic and subatomic levels, and QMD algorithms leverage quantum principles to simulate molecular systems more efficiently. One key advantage lies in the linear scaling of quantum algorithms, wherein the computational cost grows linearly with the size of the system. This remarkable improvement results from the exploitation of quantum entanglement, a phenomenon that classical simulations cannot fully capture. The inherent nature of quantum systems allows for the simultaneous consideration of multiple particle states through entanglement, providing a more accurate representation of complex molecular interactions. Quantum effects, such as superposition and tunneling, are naturally incorporated into QMD simulations, making them particularly well-suited for modeling phenomena where classical simulations fall short. Consequently, QMD algorithms are capable of addressing the challenges associated with long timescales and large system sizes that classical MD struggles to handle.

The advent of quantum computers has further propelled the development of quantum algorithms for molecular dynamics simulations. Quantum computers leverage quantum bits (qubits) and quantum gates to perform calculations that were previously deemed intractable for classical computers. Quantum MD algorithms capitalize on the parallelism inherent in quantum computing, allowing for the efficient simulation of large and complex molecular systems.

Quantum MD was first theorized in the 1980s, and has been demonstrated recently on small proof-of-concept problems. For example, a photonic quantum processor was used to simulate the dynamics of a two qubit hydrogen molecule over 50 time-steps. Larger implementations will require overcoming decoherence and scaling up the number of qubits substantially. Hybrid classical-quantum frameworks using shallow quantum circuits to generate electron entanglement followed by classical propagation may be more feasible in the near term. Such hybrid quantum MD could potentially enable more accurate simulations of drug binding and reactivity.

Table 1. Comparison of Quantum and Classical Computing

Quantum Computing	Classical Computing
Based on quantum bits (qubits) that leverage superposition and entanglement for parallelism	Based on classical bits with discrete 0 or 1 states
Exponentially faster for certain problems like optimization, simulation, factoring	Efficient general-purpose computing for most tasks
Limited by small qubit numbers, noise, and decoherence in NISQ devices	Mature, large-scale digital computers commercially available
Requires quantum algorithms and programming techniques	Conventional software programming languages and techniques
Emerging hardware with rapid pace of progress	Mature hardware progressing at Moore's Law rate
Potential to simulate quantum systems, intractable classically	Approximations required when modeling quantum effects

Promising quantum speedups predicted for pharmaceutical problems once scaled	Known scalability and performance for computational chemistry and machine learning
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Machine Learning: Machine learning (ML) has become an integral tool in the realm of computational drug discovery, playing a pivotal role in the development of predictive models, virtual screening techniques, and the optimization of molecular properties. The application of ML in this domain has significantly expedited the drug discovery process, enabling researchers to sift through vast datasets, identify potential drug candidates, and optimize molecular structures with greater efficiency. However, the evolution of quantum machine learning (QML) introduces a paradigm shift in computational approaches, holding the promise of unparalleled speedups and enhanced capabilities in processing quantum data. Quantum machine learning leverages the principles of quantum mechanics to encode both machine learning models and data into qubits, the fundamental units of quantum information [13]. This quantum encoding enables the execution of quantum computations for various stages of the ML pipeline, including training and inference. Quantum circuit learning, a notable facet of QML, closely mimics classical neural networks but employs trainable qubit rotation gates in lieu of classical neurons. These gates introduce quantum parallelism and entanglement, offering a unique avenue for enhancing the computational capacity of ML models [14]. Within the realm of quantum machine learning, several algorithms have emerged, each designed to address specific challenges in the field. The HHL (Harrow-Hassidim-Lloyd) algorithm, for instance, specializes in solving linear systems of equations—an essential task in many scientific and engineering applications. Quantum support vector machines (QSVM) have been proposed as an alternative to classical support vector machines, harnessing the power of quantum parallelism for efficient classification tasks. Additionally, quantum Boltzmann machines, inspired by classical counterparts, aim to model complex probabilistic relationships in quantum systems. The integration of quantum computing with machine learning is not without its challenges. Quantum computers are susceptible to errors, and the delicate nature of quantum states requires sophisticated error correction techniques. Furthermore, the practical implementation of quantum machine learning algorithms demands a concerted effort in developing scalable quantum hardware and optimizing quantum software for real-world applications. Despite these challenges, the potential benefits of quantum machine learning in drug discovery and other scientific domains are undeniable.

Early applications of quantum ML to drug discovery show potential for speeding up molecular property predictions. Quantinuum's quantum algorithm toolkit was used with quantum circuit learning to rapidly predict logP values for drug-likeness. Rigetti Forest has demonstrated hybrid classical-quantum ML workflows for predicting pharmaceutical solubility and performing generative modeling of molecular structures [15]. As quantum ML hardware and algorithms mature, broader pharmaceutical use cases in virtual screening, property optimization, and de novo molecular design are anticipated. However, modeling large molecular datasets may face qubit limitations in the near term.

Table 2. Comparison of Quantum and Classical Performance

Application	Quantum Advantage	Classical Scalability
Molecular Docking	Exponential speedup possible for pose search and scoring	Heuristics enable application to large protein/ligand systems
Molecular Dynamics	Linear scaling possible with full quantum simulation	Approximations allow classical MD up to millions of atoms
Machine Learning	Potential for faster training and quantum feature learning	Train/predict on large molecular datasets and conventional features
Quantum Chemistry	Accurate electronic structure and properties	Approximate methods for large systems
Optimization	Quadratic to exponential speedup over classical techniques	Heuristics work well for many pharmaceutical optimizations

Hybrid Quantum-Classical Computing: The potential of quantum computing looms large, promising revolutionary advancements in problem-solving and computational efficiency. However, the current landscape of Noisy Intermediate-Scale Quantum

(NISQ) devices is marked by inherent limitations that impede their seamless integration into practical applications. A primary constraint is the existence of a small number of qubits, the fundamental units of quantum information. These qubits are susceptible to noise and errors, posing significant challenges to the reliability and stability of quantum computations. Decoherence, another critical issue plaguing NISQ devices, arises from the sensitivity of quantum states to their external environment. Quantum systems are highly susceptible to decoherence, leading to the loss of quantum information and compromising the accuracy of computations. Managing and mitigating decoherence represent formidable obstacles on the path to realizing the full potential of quantum computing [16]. Additionally, the connectivity of qubits within existing quantum processors is restricted, limiting the range of feasible computations [17]. Quantum algorithms, often intricate and demanding, frequently require extensive connectivity and interactions among qubits. The current constraints on connectivity hinder the implementation of various algorithms that could otherwise exploit the true power of quantum parallelism.

A noteworthy challenge in the quantum computing landscape is the realization of fault-tolerant logical qubits. While fault-tolerant quantum computing is an aspirational goal, it remains elusive in the current NISQ era. The fragility of quantum states to errors and environmental influences necessitates the development of error-correction mechanisms and fault-tolerant architectures, prerequisites for unleashing the full potential of quantum computing in practical scenarios. Amidst these challenges, a pragmatic approach to quantum computing emerges through the paradigm of hybrid classical-quantum workflows [18]. This approach acknowledges the current limitations of quantum processors and seeks to leverage their strengths in tandem with classical systems. By partitioning computational tasks and delegating specialized subtasks such as optimization or integration to the quantum processor, while retaining classical systems for overall coordination, a synergistic collaboration between classical and quantum computing can be established [19].

This hybrid approach allows organizations and researchers to extract value from near-term quantum capabilities without being hindered by the constraints of existing quantum hardware. Classical computers, with their robustness and maturity, serve as orchestrators, managing the overall workflow and handling tasks that are currently beyond the reach of NISQ devices. Meanwhile, the quantum processor contributes its unique strengths in tackling specific computational challenges that align with its capabilities [20].

For pharmaceutical applications, strategies like using classical machine learning to reduce the search space followed by quantum search for optimizations show promise. Early-stage molecular screening could run classically, then quantum molecular dynamics used for lead optimization. Hybrid algorithms utilizing shallow circuits with fewer gates may be more robust to noise on NISQ hardware [21]. Vendors like Amazon Braket, Rigetti, D-Wave, and IBM Q offer hybrid cloud platforms combining quantum and classical resources. As quantum volume increases over time, more computation can shift to the quantum processor in a modular fashion.

Table 3. Outlook for Quantum Applications in Drug Development

Stage of Drug Development	Potential Quantum Applications	Timeframe
Target Identification and Validation	Quantum machine learning for genomic analysis	Long-term
Lead Generation	Virtual screening with quantum ML and docking	Mid-term
Lead Optimization	Quantum molecular dynamics and property predictions	Near-term
Preclinical Development	Quantum protein-ligand binding and reactivity modeling	Mid-term
Clinical Trials	Quantum ML for clinical data analysis	Long-term
FDA Review and Approval	-	No impact
Post-Market Surveillance	Quantum ML on pharmacovigilance data	Long-term

Challenges and Outlook

Quantum computing represents a promising avenue for revolutionizing computational methodologies in the field of drug discovery. The potential quantum advantages it offers could significantly augment existing approaches, potentially accelerating the drug development process and improving the understanding of complex biological systems. Nevertheless, the realization of these benefits is impeded by formidable challenges that need to be addressed comprehensively. At present, the field of quantum computing faces significant limitations, primarily embodied by the constraints of Noisy Intermediate-Scale Quantum (NISQ) devices. These devices, characterized by a limited number of qubits, susceptibility to noise, and stability issues, hinder the widespread application of quantum computing in pharmaceutical research [22]. The current state of NISQ devices confines their utility to proof-of-concept demonstrations rather than practical, large-scale applications essential for drug discovery.

One of the foremost impediments in the path towards harnessing quantum computing for pharmaceutical development lies in the restriction of qubit number. The current NISQ devices are constrained by the relatively small number of qubits they can reliably handle [23]. To unlock the full potential of quantum computing in drug discovery, substantial advancements in qubit count are imperative. Researchers and engineers are actively working on developing scalable quantum processors that can accommodate a more significant number of qubits while maintaining the required coherence. Noise, an inherent challenge in quantum systems, poses another significant barrier. Quantum bits, or qubits, are susceptible to environmental disturbances and fluctuations, leading to errors in calculations. Enhancing the stability of qubits and minimizing the impact of noise is crucial for achieving accurate and reliable quantum computations in drug discovery [24]. Developing error-correction techniques and error-mitigation strategies is pivotal to overcome the inherent noise issues in quantum systems. Moreover, the coherence time of quantum bits, which represents the duration over which a qubit can maintain its quantum state, is a critical factor. Current NISQ devices exhibit limited coherence times, restricting the window of time available for quantum computations. Progress in extending coherence times is essential to enable more complex calculations and analyses required for drug discovery applications.

Connectivity is yet another challenge that needs to be addressed for quantum computing to realize its potential in pharmaceutical development. The ability of qubits to efficiently communicate and share information across the quantum processor is vital for solving complex problems [25]. Improving connectivity within quantum processors will enhance the efficiency of quantum algorithms, making them more applicable to the intricate tasks involved in drug discovery. Furthermore, the implementation of robust quantum error correction is imperative to mitigate the impact of errors induced by environmental factors and imperfections in quantum hardware. Developing effective error-correction codes and error-mitigation techniques is a crucial aspect of advancing quantum computing for drug discovery beyond proof-of-concept stages [26].

Most proposed quantum algorithms also require thousands of logical qubits to show unambiguous speedup over classical techniques for large-scale problems in drug discovery. Hybrid quantum-classical computing and algorithmic improvements like error mitigation will stretch NISQ capabilities in the near term. Libraries for interfacing with NISQ computers are still maturing. Domain expertise in quantum programming to develop practical applications is lacking. Close collaboration between quantum physicists, chemists, and computer scientists will be crucial to design optimized hybrid quantum-classical algorithms and software stacks tailored for pharmaceutical challenges. Investment into research and development partnerships between drug companies, hardware vendors, and quantum software startups will drive progress. Application chemists and modelers will need new skills to productively employ quantum computing.

Once the hardware and software matures over the next 5-10 years, quantum advantages could enable accurate simulations of drug molecules and targets that are intractable classically. Protein-ligand docking and molecular dynamics simulations may be performed on unprecedented scales to drive precision drug discovery. Machine learning models could be trained on extensive molecular data far faster to optimize leads. We anticipate quantum approaches will first make inroads for molecular problems dependent on representing quantum effects and electronic structure accurately. Impact should then broaden across areas like genomics and clinical trial data as quantum scalability improves [27]. The next decade will be a critical period to build up the

software, workflows, and personnel infrastructure to eventually utilize the profound power of quantum computation for pharmaceutical innovation [28]. Companies that invest early in quantum computing may achieve dramatic competitive advantages once the technology matures. With prudent strategy and execution, the pharmaceutical industry is poised to become one of the greatest beneficiaries from the quantum computing revolution [29].

References

- [1] W. Zhang, Y. Lv, J. Yang, Y. Chen, Y. He, and J. Huang, "Study design characteristics and pharmacological mechanisms in International Clinical Trials Registry Platform: Registered clinical trials on antiviral drugs for COVID-19," *Drug Des. Devel. Ther.*, vol. 14, pp. 3803–3813, Sep. 2020.
- [2] J. Song, C. Duan, W. Cai, W. Wu, H. Lv, and J. Xu, "Comparison of GnRH-a prolonged protocol and short GnRH-a long protocol in patients with thin endometrium for assisted reproduction: A retrospective cohort study," *Drug Des. Devel. Ther.*, vol. 14, pp. 3673–3682, Sep. 2020.
- [3] S. Xu *et al.*, "Integrating Unified Medical Language System and kleinberg's burst detection algorithm into research topics of medications for post-traumatic stress disorder," *Drug Des. Devel. Ther.*, vol. 14, pp. 3899–3913, Sep. 2020.
- [4] R. Luo, X. Sun, F. Shen, B. Hong, and Z. Wang, "Effects of high-dose rosuvastatin on ventricular remodelling and cardiac function in ST-segment elevation myocardial infarction," *Drug Des. Devel. Ther.*, vol. 14, pp. 3891–3898, Sep. 2020.
- [5] Y. K. Wong, Y. Zhou, Y. S. Liang, H. Qiu, Y. X. Wu, and B. He, "Implementation of The Future of Drug Discovery: QuantumBased Machine Learning Simulation (QMLS)," *arXiv preprint arXiv:2308.08561*, 2023.
- [6] T. M. Belete, "Recent progress in the development of new antimalarial drugs with novel targets," *Drug Des. Devel. Ther.*, vol. 14, pp. 3875–3889, Sep. 2020.
- [7] O. A. von Lilienfeld, K.-R. Müller, and A. Tkatchenko, "Exploring chemical compound space with quantum-based machine learning," *Nat. Rev. Chem.*, vol. 4, no. 7, pp. 347–358, Jul. 2020.
- [8] Y. K. Wong, Y. Zhou, Y. S. Liang, H. Qiu, Y. X. Wu, and B. He, "The New Answer to Drug Discovery: Quantum Machine Learning in Preclinical Drug Development," in *2023 IEEE 4th International Conference on Pattern Recognition and Machine Learning (PRML)*, 2023, pp. 557–564.
- [9] C. Gorgulla, A. Jayaraj, K. Fackeldey, and H. Arthanari, "Emerging frontiers in virtual drug discovery: From quantum mechanical methods to deep learning approaches," *Curr. Opin. Chem. Biol.*, vol. 69, no. 102156, p. 102156, Aug. 2022.
- [10] Y.-Q. Tan, H.-W. Chen, and J. Li, "Astragaloside IV: An effective drug for the treatment of cardiovascular diseases," *Drug Des. Devel. Ther.*, vol. 14, pp. 3731–3746, Sep. 2020.
- [11] T. Morawietz and N. Artrith, "Machine learning-accelerated quantum mechanics-based atomistic simulations for industrial applications," *J. Comput. Aided Mol. Des.*, vol. 35, no. 4, pp. 557–586, Apr. 2021.
- [12] Z. Zhao, A. Pozas-Kerstjens, P. Rebentrost, and P. Wittek, "Bayesian deep learning on a quantum computer," *Quantum Mach. Intell.*, vol. 1, no. 1–2, pp. 41–51, May 2019.
- [13] D. T. Lennon *et al.*, "Efficiently measuring a quantum device using machine learning," *Npj Quantum Inf.*, vol. 5, no. 1, Sep. 2019.
- [14] K. Batra *et al.*, "Quantum machine learning algorithms for drug discovery applications," *J. Chem. Inf. Model.*, vol. 61, no. 6, pp. 2641–2647, Jun. 2021.
- [15] A. Nassar and M. Kamal, "Machine Learning and Big Data Analytics for Cybersecurity Threat Detection: A Holistic Review of Techniques and Case Studies," *Intelligence and Machine Learning ...*, 2021.
- [16] G. Garau Estarellas, G. L. Giorgi, M. C. Soriano, and R. Zambrini, "Machine learning applied to quantum synchronization-assisted probing," *Adv. Quantum Technol.*, vol. 2, no. 7–8, p. 1800085, Aug. 2019.
- [17] Y. Cao, J. Romero, and A. Aspuru-Guzik, "Potential of quantum computing for drug discovery," *IBM J. Res. Dev.*, vol. 62, no. 6, p. 6:1-6:20, Nov. 2018.
- [18] T. Kong, N. Backes, U. Kalwa, C. Legner, G. J. Phillips, and S. Pandey, "Adhesive tape microfluidics with an autofocusing module that incorporates

- CRISPR interference: applications to long-term bacterial antibiotic studies,” *ACS sensors*, vol. 4, no. 10, pp. 2638–2645, 2019.
- [19] F. Bouchama and M. Kamal, “Enhancing Cyber Threat Detection through Machine Learning-Based Behavioral Modeling of Network Traffic Patterns,” *IJBIBDA*, vol. 4, no. 9, pp. 1–9, Sep. 2021.
- [20] A. Suresh, R. Kishorekumar, M. S. Kumar, and K. Elaiyaraja, “Assessing transmission excellence and flow detection based on Machine Learning,” *Opt. Quantum Electron.*, vol. 54, no. 8, Aug. 2022.
- [21] M. Zinner, F. Dahlhausen, P. Boehme, J. Ehlers, L. Bieske, and L. Fehring, “Quantum computing’s potential for drug discovery: Early stage industry dynamics,” *Drug Discov. Today*, vol. 26, no. 7, pp. 1680–1688, Jul. 2021.
- [22] D. Li, F. Xu, J. Zhao, and W. Zhang, “An algorithm for synthesis of quantum reversible logic circuits based on decomposition,” *Int. J. Mach. Learn. Comput.*, pp. 10–13, Feb. 2014.
- [23] L. Lamata, M. Sanz, and E. Solano, “Quantum machine learning and bioinspired quantum technologies,” *Adv. Quantum Technol.*, vol. 2, no. 7–8, p. 1900075, Aug. 2019.
- [24] F. Kong, College of Computer and Information Science, Southwest University, Chongqing 400715, China, H. Lai, and H. Xiong, “Quantum hierarchical clustering algorithm based on the nearest cluster centroids distance,” *Int. J. Mach. Learn. Comput.*, vol. 7, no. 5, pp. 100–104, Oct. 2017.
- [25] A. Zlokapa, A. Mott, J. Job, J.-R. Vlimant, D. Lidar, and M. Spiropulu, “Quantum adiabatic machine learning with zooming,” *arXiv [quant-ph]*, 13-Aug-2019.
- [26] S.-X. Zhang, C.-Y. Hsieh, S. Zhang, and H. Yao, “Neural predictor based quantum architecture search,” *Mach. Learn. Sci. Technol.*, vol. 2, no. 4, p. 045027, Dec. 2021.
- [27] N. Pirnay, A. Pappa, and J.-P. Seifert, “Learning classical readout quantum PUFs based on single-qubit gates,” *Quantum Mach. Intell.*, vol. 4, no. 2, Dec. 2022.
- [28] J. A. Carr, R. Lycke, A. Parashar, and S. Pandey, “Unidirectional, electro-tactic-response valve for *Caenorhabditis elegans* in microfluidic devices,” *Applied Physics Letters*, vol. 98, no. 14, 2011.
- [29] Z. Njus *et al.*, “Flexible and disposable paper-and plastic-based gel micropads for nematode handling, imaging, and chemical testing,” *APL bioengineering*, vol. 1, no. 1, 2017.