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ROLE OF COMPUTATIONAL CHEMISTRY DRUG IN DISCOVERY

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ABSTRACT

Computational methods are changing how we discover and develop new drugs. Tools like molecular modeling and machine learning have become much more advanced and widely used. To really make an impact in this fast-moving field, it's important for researchers to understand how these methods work. This review takes a closer look at the main computational techniques used in drug discovery. It explains how they work, where they are used, and how they might improve in the future. The goal is to help researchers better understand these tools so they can contribute to the growing world of computational drug discovery.

KEYWORDS: *Drug Discovery; Drug Development; Computational Methods; Molecular Docking; Molecular Simulation*

1 INTRODUCTION

Traditional methods of drug discovery can be grouped based on whether we know the structures of the target (like a protein) and the ligand (the drug). These standard approaches generally fall into four main categories (as shown in Figure 1):

1. Library design
2. Structure-based design
3. Ligand-based design
4. De Novo design

Besides these traditional types, there are also some newer approaches, like quantum mechanical simulations and cheminformatics, which can be seen as new and emerging categories in drug discovery. (1)Traditional drug discovery methods are usually grouped based on whether we have information about the target (like a protein) and the ligand (the potential drug). Each method has its own benefits and limitations. One common method is Structure-Based Drug Discovery (SBDD). This approach uses the 3D structure of the target protein to design small molecules that can fit into specific areas of the protein and change how it works. To help find promising drug candidates, scientists often use tools like virtual screening and molecular dynamics simulations during this process.(2)

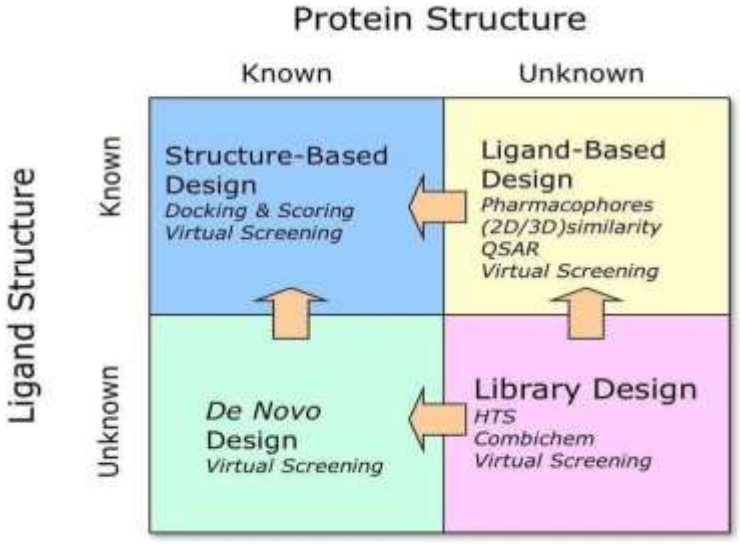

Figure 1: Overview of Conventional Approaches for Drug Discovery

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1.1 Library Design for Drug Screening

Library design is one of the most important—and also one of the most time-consuming—steps in drug discovery (see Figures 1 and 2). This is because, at the beginning of the process, we usually don't yet know the target or the potential drug (ligand).Since the number of possible drug targets (like proteins) is much smaller than the number of possible drug molecules, it makes sense to first focus on building a target-based library. This means creating a collection of chemical compounds that are specifically designed to work on a certain protein or group of proteins.The idea behind using this kind of focused library is that it increases the chances of finding useful compounds (called "hits") more quickly, and with fewer chemicals. These focused libraries often give better results compared to more diverse libraries. Also, when hits are found in a focused library, they usually show clear relationships between their chemical structure and how they act, which makes it easier to study and improve them later (3).

Target-focused libraries usually start with a single core structure (also called a scaffold) that has two or three places where different chemical groups can be attached. By adding different side chains or substituents at these positions, scientists can create a wide variety of new molecules.If you tried every possible combination, even just two or three attachment points could lead to very large number of compounds. But instead of making all of them, researchers usually choose a smaller group—typically between 100 and 500 compounds—to actually make and test.These selected compounds are chosen carefully to test the main design idea while also making sure the molecules still follow important drug-like properties. This approach helps in exploring the chemical space in a smart and efficient way (4).

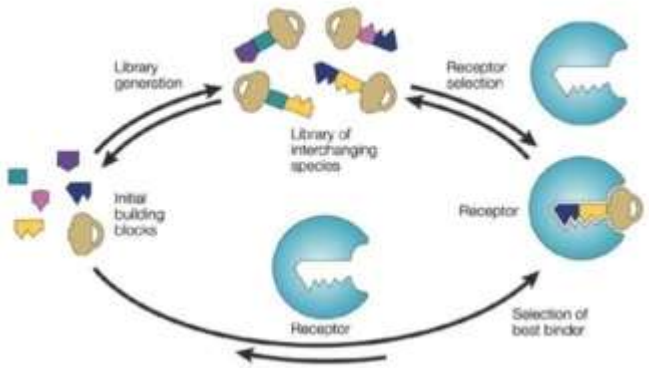

Figure 2: The Schematic Representation of library design

1.2 Structure-Based Drug Discovery (SBDD)

Structure-Based Drug Discovery (SBDD) uses the 3D structure of biological targets, like proteins or DNA, to help design new drugs that bind strongly and specifically to those targets.In simple terms, SBDD is an important modern drug discovery method because it uses detailed knowledge of how a potential drug (ligand) interacts with its target. This helps scientists design small molecules or biologics that fit well and work effectively.By studying the shape and atomic arrangement of the target's binding site, researchers can find key chemical interactions and improve the structure of compounds to increase their binding strength and selectivity.
SBDD includes several techniques such as:
Molecular docking
Virtual screening
Fragment-based design
Molecular dynamics simulations
The main goal of SBDD is to use structural data to speed up the drug discovery process and develop safer and more effective treatments for various diseases (5).

1.3 Ligand-Based Drug Discovery Approaches

Ligand-based drug discovery plays a key role in modern pharmaceutical research. These methods focus on understanding and improving the chemical properties of drug molecules to achieve specific effects in the body.In this approach, scientists study how small molecules (called ligands) interact with biological targets like proteins or DNA. Some common tools and guidelines used in ligand-based design include:
Lipinski's Rule of Five (for drug-likeness)
LogP (for measuring how well a drug dissolves in fat vs. water)
Biopharmaceutics Classification System (BCS)
In-vitro In-vivo Correlation (IVIVC)

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A well-known concept here is the “lock and key” model, which means that similar molecules (keys) often bind to similar targets (locks). This is why molecular similarity is often used to identify potential drug targets.To do this, we need a way to represent molecules in a computer-friendly format. One of the most common methods is SMILES (Simplified Molecular Input Line Entry System), which turns a molecule into a text string using symbols like C, N, O (for atoms) and =, # (for bonds).SMILES is used in various areas like:QSAR (Quantitative Structure-Activity Relationship)
Virtual screening
Toxicity prediction

A good example of a tool used in this area is the MuSSeL algorithm, which compares compounds and can predict values like IC_{50} or K_i, which measure how strongly a drug binds to a target. There are also other methods to compare compounds based on their 2D structures, known as 2D-based similarity kernels, which are used in many research studies. (Figure no 3)

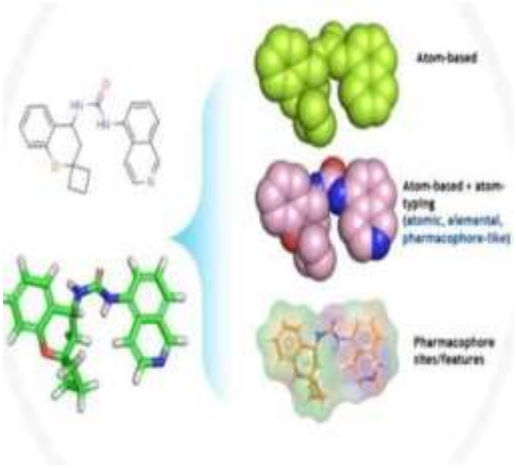

Figure 3: The representation of ligand-based drug discovery approaches

Generally, 2D-based compound similarity kernels, such as SIMCOMP , are preferred to predict drug-target prediction. Here are some examples of 2D-based com- pound similarity techniques to indicate their success. One of the 2D-based compound similarities is Target Hunter, a web-based tool (6)

1.4 De Novo drug

De novo drug design means creating completely new drug molecules from scratch using computer algorithms. The phrase “de novo” literally means “from the beginning,” which reflects the idea that no existing molecule is used as a starting point (7)
These new molecules are designed to meet specific requirements, such as being drug-like, safe, or effective, by using computational growth algorithms that build molecules step by step.
De novo drug design methods are typically grouped into four main types:

1. Structure-based
2. Atom-based
3. Ligand-based4. Fragment-based (See Figure 4)In addition to these, machine learning is opening new possibilities in this field. For example, future directions include using toxic genomics (studying how genes react to toxins) and helping with vaccine development. These are considered the next big steps in de novo drug discovery.

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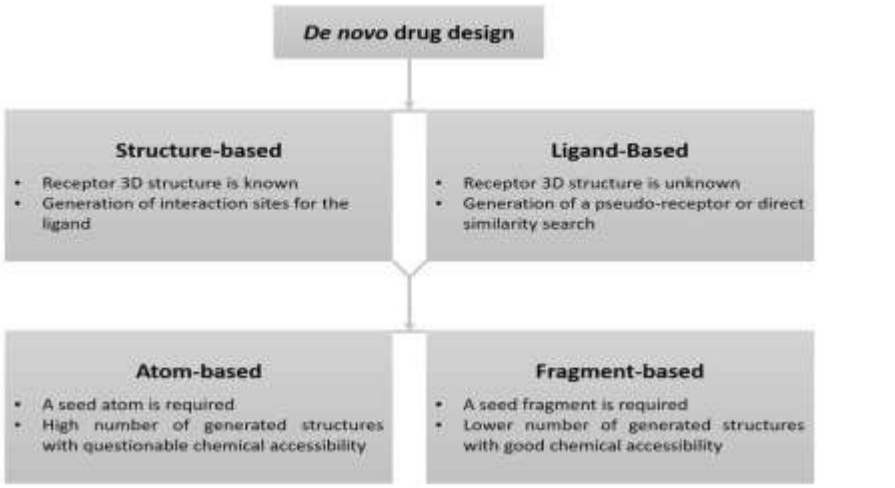

Figure 4 : Classification of De novo drug design methods

De novo drug design has several key advantages. It allows scientists to: Explore a wider variety of chemical structures Create completely new compounds that can be patented Develop new and improved treatments Save time and money by using efficient computer-based methods However, one major challenge is that some of the molecules designed using this method may be very difficult or even impossible to actually make in the lab. This issue is known as synthetic inaccessibility (8)

This section gives background information to help explain key terms and improve understanding of the research. The supporting literature review is divided into three parts:

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2. Quantum mechanical simulations used in drug discovery
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3. Cheminformatics approaches that support the drug discovery professoriates approaches that support the drug discovery process.

1.5Quantum Mechanical Simulations

Quantum mechanics focuses on how electrons and atomic nuclei behave, without depending on traditional ideas like chemical bonds. It uses the Schrödinger equation to help understand matter at the atomic level (9).Solving this equation shows how electrons are arranged in space and what their energy levels are. This helps scientists understand molecular structure, chemical bonding, and interactions between molecules (10).However, the Schrödinger equation can only be exactly solved for the hydrogen atom, which is the simplest atom. For all other atoms, scientists use approximations to estimate the results (see Figure 5).

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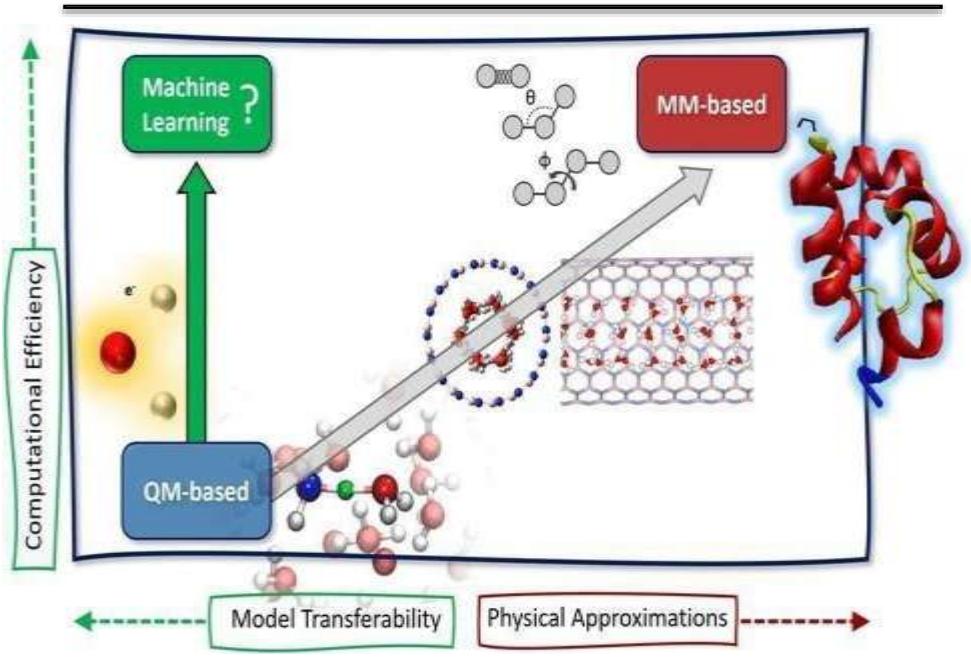

Figure 5: Based on the description of the system

Quantum mechanics (QM) methods show great potential, but they face challenges such as limited computing power, missing atomic-level details on proteins, and weak handling of entropy. Still, QM has strong abilities to predict binding free energy. By combining QM with machine learning, we can overcome these problems and discover new possibilities for drug design.

1.6 Cheminformatics Approaches for Drug Discovery

Cheminformatics uses computer-based and data-driven tools to solve chemical problems and support the discovery of new drugs. By combining information from chemistry, biology, and pharmacology, cheminformatics helps manage and analyze large sets of data efficiently (11). This field plays an important role in speeding up the identification of drug candidates, improving their chemical properties, and predicting how they might behave in the body (12).

Some key benefits of cheminformatics include the ability to quickly search large chemical databases, reduce the cost and time of laboratory experiments, and improve the accuracy of identifying drug targets and optimizing lead compounds. These advantages make the overall drug discovery process more efficient and increase the chances of developing successful and innovative treatments.(13)

Three common cheminformatics approaches in drug discovery are:

1. Machine learning-based methods.
2. Graph-based methods.
3. Network model approaches.

1.6.1 Machine learning-based methods in Cheminformatics

Machine learning techniques in cheminformatics have changed how drugs are developed. These advanced algorithms help analyze complex chemical and biological data . By finding patterns and relationships in large datasets, machine learning can predict how potential drug compounds will behave, helping scientists discover and improve new medicines faster. The main advantage of machine learning is its ability to handle huge amounts of information, uncover hidden trends, and make more accurate predictions than traditional methods. Some of its key benefits include: Better analysis of large chemical libraries, Ability to model and understand complicated biological systems, Reduction in both the cost and time required for drug development (14).

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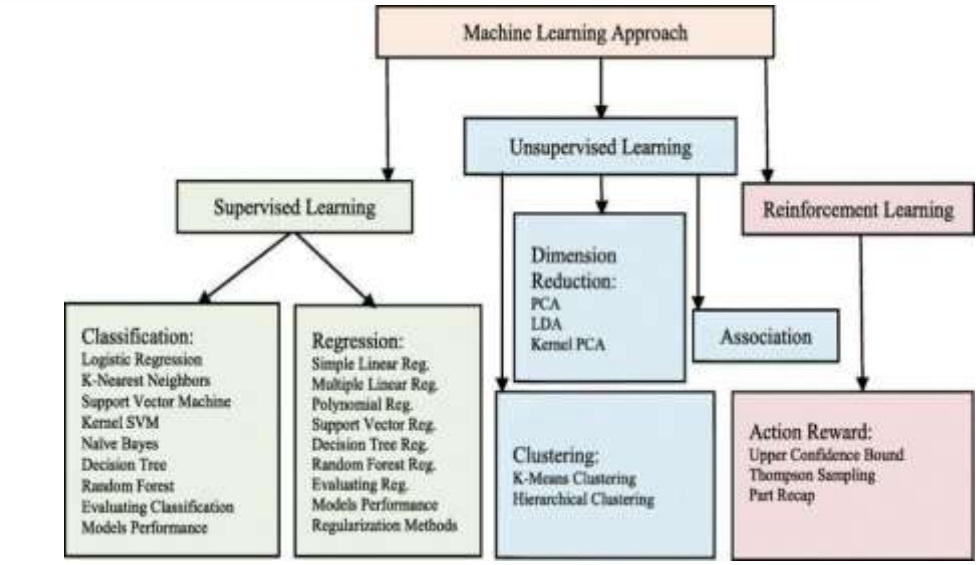

Figure 6 : Various machine learning techniques applied in the field of drug discovery are shown in this diagram.

1.6.2Graph-Based Methods in Cheminformatics

In cheminformatics, graph-based methods use graphs to represent the structure and interactions of molecules (15). In this approach, atoms are shown as nodes and bonds as edges, which helps describe both the structure and relationships within a molecule. This method is especially useful in drug discovery because it can handle complex molecular structures more effectively than traditional techniques. Using graph theory and algorithms, scientists can: Analyze molecular fingerprints, Predict how a compound might act in the body, Improve lead compounds (16).As a result, graph-based methods play an important role in computational chemistry and help speed up the discovery of new drug candidates.

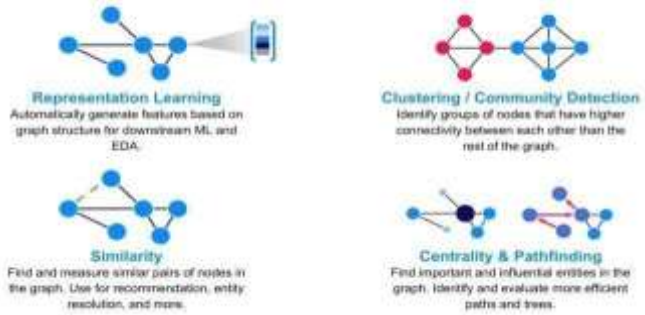

Figure 7: This figure illustrates how graph-based methods are used in drug discovery.

1.3.3 Network-based Models in Cheminformatics

Network-based cheminformatics models use the principles of network science to represent molecules, their interactions, and biological data as networks or graphs . These models help scientists study and understand the complex relationships within chemical and biological systems in a structured way. They are especially useful in areas like network pharmacology, understanding how drugs interact with their targets, and analyzing how molecules function. One of their strengths is the ability to combine different types of data—such as chemical structures, biological pathways, and protein-protein interactions—into a single, unified system (17).

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2 FUTURE DIRECTION

Developing advanced artificial intelligence (AI) and machine learning (ML) algorithms can greatly improve the accuracy and efficiency of structure-based drug discovery. When these models are combined with detailed protein structure data, they can more accurately predict protein-ligand interactions, helping researchers find promising drug candidates faster.These AI models can also predict how changes in protein structure affect molecular interactions, improving the overall accuracy of current computational methods. Another exciting direction is the use of deep learning, especially geometric deep learning (18), which helps analyze complex ligand-binding data and build powerful prediction models. Deep learning improves virtual screening by finding new binding patterns and enhancing chemical libraries with better compounds. This can lead to the discovery of drugs that are more effective and have fewer side effects.However, one limitation is that deep learning models can be difficult to interpret, meaning it's harder to understand how they make decisions .Still, deep learning has strong potential to boost the performance of existing computational tools. Lastly, hybrid methods—which combine different techniques—look promising. They can improve performance without losing the ability to interpret the results (19).

Will quickly provide higher performance and dominate computational drug discovery and development methods.

CONCLUSION

The use of advanced computer technologies has completely transformed how drugs are discovered and developed. Tools like molecular modelling, structure-based and ligand-based approaches, and de novo drug design have made it much easier to identify and design new medicines. As these methods continue to improve and become more integrated, they will help drive even more breakthroughs in the future of drug discovery.

This review explains the key ideas and applications of various computational methods, giving a complete overview of how they support drug discovery. Future progress in this field will benefit from high-resolution structural data, powerful algorithms, and emerging technologies like artificial intelligence. However, these methods are complex and constantly evolving, so they require advanced knowledge and continuous learning to keep up with new advancements.

To move forward and unlock new opportunities, it's essential to:

Develop more accurate prediction models,

Combine different types of biological data, and

Improve computational workflows. By staying updated with these advancements and applying the insights shared in this review, researchers can help speed up the discovery of new and effective treatments that address important medical needs .

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