RCMOS – Multidisciplinary Scientific Journal of Knowledge.
ISSN: 2675-9128. São Paulo-SP.
Year IV, v.1, n.1, jan./ jul. 2024. | submission: 10/19/2024 | accepted: 10/21/2024 | publication: 10/23/2024

THE APPLICATION OF IN SILICO TOOLS IN THE DEVELOPMENT OF CHEMOTHERAPEUTICS

Marcia Helena Rodrigues Velloso

SUMMARY
This article explores the use of tools*in silico*in the development of chemotherapeutics, highlighting their ability to accelerate the discovery and optimization of new cancer treatments. Through techniques such as *docking*Using molecular chemistry, molecular dynamics, QSAR, and machine learning, researchers can simulate molecular interactions, enabling the identification and improvement of selective kinase inhibitors and other molecules with therapeutic potential. The studies cited demonstrate how these approaches contribute to more effective and personalized treatments, reducing both the costs and time of drug development. Furthermore, the integration of these techniques promises to revolutionize anticancer therapies, moving the field of oncology into an era of precision medicine.
Keywords: Chemotherapeutic agents. Methods*In Silico*.*Docking*Molecular. Molecular Dynamics. QSAR

ABSTRACT
This article explores the use of*in silico*tools in the development of chemotherapeutics, highlighting their ability to accelerate the discovery and optimization of new cancer treatments. Through techniques such as molecular docking, molecular dynamics, QSAR, and machine learning, researchers can simulate molecular interactions, enabling the identification and refinement of selective kinase inhibitors and other molecules with therapeutic potential. The studies cited demonstrate how these approaches contribute to more effective and personalized treatments, reducing both the costs and the time of drug development. Furthermore, the integration of these techniques promises to revolutionize anticancer therapies, moving the field of oncology into an era of precision medicine.

Keywords: Chemotherapeutics.*In Silico*Methods. Molecular Docking. Molecular Dynamics. QSAR.

INTRODUCTION

The techniques*in silico*are widely used in the fields of medicinal chemistry and biotechnology. This approach allows simulating interactions between molecules and their biological targets at the atomic level, providing essential information for the design of new drugs. Among the main techniques used in this area, the following stand out: *docking*molecular, molecular dynamics and quantitative structure-activity relationship (QSAR - *Quantitative Structure-Activity Relationship*).

THE*docking*Molecular chemistry aims to predict how a molecule, such as a potential chemotherapeutic, interacts with its biological target, which may be an enzyme or receptor. This technique provides insights into the binding affinity and mode of action of the compound, and is widely used to investigate the efficacy of potential drugs. Several studies explore the interactions between ligands and proteins in the search for selective inhibitors (Machado, 2023).

In turn, molecular dynamics simulates the interactions between proteins and ligands, capturing their movements under real biological conditions, such as the presence of water and ions, on different time scales. This technique can reveal hidden binding sites that would not be easily identifiable by other methods, increasing the accuracy in the discovery of new drugs (Bukkuru et al., 2016). Meanwhile, QSAR, offers a quantitative methodology for predicting biological and physicochemical properties based on structural parameters, helping to optimize compounds for better therapeutic performance (El Fadili et al., 2024).

Additionally, machine learning excels at analyzing large data sets of molecular properties and biological outcomes, identifying patterns that can guide drug design. Integrating these technologies into oncology research provides a robust approach to developing more effective chemotherapeutics, with faster discovery and optimization processes.

In this way, techniques*in silico*molecular modeling techniques can promote the development of innovative and more targeted treatments to combat cancer. Given their ability to accelerate the process

In order to discover new drugs and improve their efficacy, molecular modeling techniques have become indispensable tools in drug development. Using these techniques, it is possible to predict the interaction of a wide range of candidate compounds with their respective biological targets even before laboratory experiments are performed. This allows for a significant reduction in costs and time, allowing pharmaceutical research to focus efforts on molecules that have already demonstrated promising potential in studies*in silico*(Singh; Bhushan; Singh, 2023), making the clinical and preclinical testing phases more targeted and safe, increasing the chances of success in the development of effective therapies (Ballesta et al., 2016). These advances in molecular modeling, when applied to the development of chemotherapeutics, reinforce its role as an indispensable tool in the process of creating more effective and safer drugs, contributing to the progress of oncology and improving the quality of life of patients.

This article aims to present an overview of the use of approaches*in silico*in the development of chemotherapeutics, highlighting the importance of these techniques in accelerating the process of discovering new drugs and optimizing oncological treatments. Through an analysis of the main methodologies and their applications, we seek to demonstrate how molecular modeling can contribute to innovation and effectiveness in the fight against cancer.

TOOLS*IN SILICO*IN THE DEVELOPMENT OF CHEMOTHERAPEUTICS:

An example of the application of*docking*molecular in the*design*of chemotherapeutics is the identification of protein kinase inhibitors. Kinases play essential roles in activating signaling pathways that promote uncontrolled cell growth in several types of cancer. By using*docking* Using molecular techniques, researchers can predict how inhibitors bind to the active site of these enzymes, blocking their activity. This could lead to the development of highly selective kinase inhibitors that specifically target cancer cells without significantly affecting normal cells, minimizing unwanted side effects. Selectivity in inhibitors reduces systemic toxicity, one of the biggest challenges in cancer treatment, especially in conventional therapies that target both healthy and tumor cells.

A recent study by Kaur et al. (2024) highlighted the application of*docking*molecular approach in the development of potential selective kinase inhibitors derived from oxindole, compounds with high anticancer activity. In this study, the technique was essential to evaluate the binding affinity and predict the interactions between oxindole derivatives and the active sites of several kinases involved in tumor cell proliferation. The results not only indicated a strong binding capacity of these compounds, but also provided valuable information on the optimization of pharmacokinetic properties, such as absorption and bioavailability.

Another recent study related to selective kinase inhibitors was conducted by Alanazi et al. (2023). In this work, selective inhibitors of multiple kinases associated with cancer progression were identified. The compounds designed with this technique showed strong binding affinity to their targets and were evaluated for selectivity. The results demonstrated that these inhibitors were effective in inhibiting kinase activity, in addition to having a lower potential to cause damage to normal cells, reducing the side effects typical of traditional oncological treatments.

The study by Umar et al. (2021) used the technique of*docking*molecular combined with the*design* ligand-based drug screening to identify novel anticancer compounds with specific activity against the V600E-BRAF mutation, a mutation found in several cancers, including melanoma. This mutation abnormally activates the MAP kinase (MAPK) signaling pathway, which promotes uncontrolled cell growth. The*docking*molecular was applied to evaluate the interaction of new compounds with the active site of V600E-BRAF, allowing optimization of binding affinity. The study compared the compounds designed with standard inhibitors, such as vemurafenib, a drug widely used in the treatment of melanoma with the V600E-BRAF mutation. The compounds selected in the study showed a higher binding affinity to vemurafenib, suggesting their potential as more effective inhibitors. The analysis of*docking*molecular also allowed the refinement of the compounds' structures, leading to the creation of molecules that bind more efficiently to the mutant receptor, blocking its activity more specifically and, theoretically, reducing side effects. Furthermore, the results indicated that the designed compounds can interact with critical regions of the V600E-BRAF protein, responsible for its kinase activity, which increases the specificity of the treatment. The use of*docking*molecular in this

context has been shown to be a powerful tool not only for the initial screening of new drug candidates, but also for the optimization of compounds that have already shown promising activity. The study highlighted how the *docking* molecular can accelerate the development of personalized and targeted therapies, with potential application in other types of cancer besides melanoma, where the V600E-BRAF mutation is also present.

Another important use of the technique *docking* molecular is in drug repositioning studies, where known compounds are evaluated against multiple kinase targets in different cancer types, such as lung and prostate cancer. This approach highlights the potential to identify more personalized and effective therapies, especially in settings where patients do not respond adequately to traditional single-target therapies. Drug repositioning allows the exploitation of compounds already known for their efficacy in other clinical settings, reducing the time and costs involved in developing new therapies. An example of this type of study was conducted by Shaikh et al. (2022), in which researchers used the *docking* molecular to identify new uses for existing drugs by targeting multiple kinase targets implicated in lung and prostate cancer. The results showed that some of the compounds analyzed had a strong binding affinity for multiple targets, suggesting their potential as effective multitarget therapies. This type of research holds promise for the development of treatments that can attack multiple molecular pathways simultaneously, increasing the chances of therapeutic success and decreasing the possibility of resistance to treatments.

Although the technique of *docking* molecular modeling is valuable for drug development, it has some limitations because in most experiments the protein is kept rigid. To obtain the conformational variations that occur during interaction with ligands, it is necessary to go beyond the *docking* molecular, using complementary techniques, such as molecular dynamics simulations which, unlike *docking*, allows to simulate the dynamic behavior of both proteins and ligands over time, under real biological conditions, such as the presence of water and ions. This is essential to accurately predict binding poses and the stability of these interactions over time, being particularly useful in understanding protein conformational variations, identifying allosteric sites and guiding the development of selective inhibitors.

An example of the application of molecular dynamics techniques in the design of chemotherapy drugs is the study by Malla et al. (2022), who used the technique to investigate the interaction of natural compounds, such as rutin and MG-132, with the p53 protein, a tumor suppressor frequently mutated in cancer cells. By simulating these interactions in real time, the researchers were able to identify promising inhibitors, such as rutin, that demonstrated not only high binding affinity but also prolonged stability in the simulations.

Molecular dynamics was also applied in the study by Spill et al. (2023), which investigated the interaction between p53 and XIAP (apoptosis inhibitor protein). The study explored how p53 conformation changes in response to treatment with chemotherapy drugs such as doxorubicin and how these changes impact its ability to induce apoptosis in cancer cells. Molecular dynamics was used to study the influence of different concentrations of p53 and XIAP on cell fate, promoting programmed cell death or allowing resistance to treatment. This type of simulation is extremely valuable for understanding response variability between patients and can be applied to optimize chemotherapy dosage, seeking the ideal balance between efficacy and toxicity.

In addition to molecular dynamics approaches, other innovative techniques such as QSAR and machine learning are gaining prominence in the development of chemotherapeutics, providing new perspectives for oncology research. QSAR and machine learning have proven to be valuable tools in *design* and development of chemotherapeutics. QSAR uses mathematical models to correlate chemical structure with biological activity, while machine learning analyses use algorithms that analyze large molecular data sets to identify patterns and predict outcomes that guide the design of new drugs.

In the study by Asaad et al. (2024), a machine learning-based QSAR model was applied to screen small molecules against the IDH1 mutation in glioblastoma multiforme, an aggressive type of cancer. The results showed that the model predicted new compounds with high accuracy, demonstrating the effectiveness of the combination of QSAR and machine learning in accelerating drug discovery.

Another relevant application was presented by Karampuri and Perugu (2024), who developed QSAR models for breast cancer treatment. Using deep learning algorithms, such as *Deep*

Neural Networks(Using DNNs, or neural networks, the researchers were able to create QSAR models with impressive accuracy (R^2 = 0.94), allowing them to predict the efficacy of drug combinations against specific breast cancer cell lines. Not only did these models show impressive accuracy, but they also raised questions about the generalizability of the results to different cell lines. This consideration is essential to ensure that the predictions are applicable in diverse clinical settings.

While QSAR and machine learning offer significant advances in*design*of drugs, challenges such as the need for large quality data sets and model interpretation still persist. Future work could focus on integrating experimental data with computational models to improve prediction accuracy.

In short, the approaches*in silico*, including molecular dynamics, QSAR and machine learning, are revolutionizing the development of chemotherapy drugs. These techniques not only accelerate the discovery of new compounds, but also promote more personalized and effective treatments, with the potential to transform clinical practice in oncology.

FINAL CONSIDERATIONS

The tools*in silico*, are indispensable in modern chemotherapy development, providing valuable insights that transcend the capabilities of traditional experimental methods. The application of these technologies not only accelerates the development of new treatments but also paves the way for personalized therapies, tailored to individual patient needs and significantly increasing success rates in cancer treatment. Looking ahead, it is essential that research continues to integrate these tools with large-scale clinical and genetic data to better predict treatment efficacy and minimize drug resistance. In addition, continued collaboration between computer scientists, chemists, pharmacists and oncologists will be essential to transforming insights*in silico*in effective and safe anticancer therapies, marking a new chapter in the fight against cancer.

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