Abstract

Computational methods have revolutionized the field of drug discovery, playing a vital role in the identification and development of potential therapeutic compounds. Among these methods, virtual screening has emerged as one of the most widely used approaches in the early stages of the drug discovery process. This approach utilizes computational techniques to sift through vast libraries of chemical compounds and predict their potential activity against a target of interest. One of the key tools employed in virtual screening is molecular docking, which allows researchers to simulate the binding interactions between small molecules (ligands) and target proteins (receptors). Scoring functions form a critical component of molecular docking, as they are responsible for evaluating and predicting the binding affinity between ligands and receptors. These scoring functions encompass a range of mathematical algorithms and empirical energy-based models that estimate the strength of the molecular interactions within a complex. By calculating scores based on predicted binding energies, scoring functions enable the ranking of compounds according to their potential to bind and interact with the target protein. This ranking process is crucial in identifying hit compounds that have the potential to be further developed into effective drugs. However, the accuracy of scoring functions is influenced by the inherent complexity of molecular recognition processes. Due to the computational limitations in accurately modeling all aspects of these processes, scoring functions rely on approximations to make predictions within a reasonable timeframe. These approximations introduce unavoidable inaccuracies, leading to a compromise between computational efficiency and predictive accuracy. Consequently, the performance of scoring functions is adversely affected, hindering their ability to effectively prioritize compounds and predict their actual binding affinities. To shed light on the foundations and limitations of current scoring functions, extensive studies and comparative analyses have been conducted. These investigations aim to evaluate the performance of different scoring functions in various scenarios, identify their strengths and weaknesses, and highlight strategies for overcoming the associated limitations. By comparing the results of these studies, researchers can gain insights into the relative performance of different scoring functions and make informed decisions about their implementation.

Furthermore, addressing the inaccuracies and limitations of scoring functions requires the development of innovative strategies and approaches. Researchers have proposed various strategies to improve the performance of scoring functions, such as incorporating more detailed and accurate representation of molecular interactions, refining the energy models used in scoring functions, and integrating machine learning and artificial intelligence techniques into the scoring process. These advancements have the potential to enhance the accuracy and reliability of scoring functions, empowering researchers to make better-informed decisions when selecting potential drug candidates.

When it comes to selecting a scoring scheme for structure-based virtual screening, several factors need to be considered. These include the nature of the target.

Keywords
scoring functions, virtual screening, molecular docking, structure-based drug discovery, scoring performance, drug Discovery

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