Strategies of Virtual Screening in Medicinal Chemistry

Giovanna Ilaria Passeri, Molecular Discovery Ltd., Pinner, Middlesex, London, United Kingdom
Daniela Trisciuzzi, Dipartimento di Farmacia-Scienze del Farmaco, Università degli Studi di Bari “Aldo Moro”, Bari, Italy
Domenico Alberga, Dipartimento di Farmacia-Scienze del Farmaco, Università degli Studi di Bari “Aldo Moro”, Bari, Italy
Lydia Siragusa, Molecular Discovery Ltd., Pinner, Middlesex, London, United Kingdom
Francesco Leonetti, Dipartimento di Farmacia-Scienze del Farmaco, Università degli Studi di Bari “Aldo Moro”, Bari, Italy
Giuseppe F. Mangiatordi, Dipartimento di Farmacia-Scienze del Farmaco, Università degli Studi di Bari “Aldo Moro”, Bari, Italy
Orazio Nicolotti, University of Bari, Bari, Italy

ABSTRACT

Virtual screening represents an effective computational strategy to rise-up the chances of finding new bioactive compounds by accelerating the time needed to move from an initial intuition to market. Classically, the most pursued approaches rely on ligand- and structure-based studies, the former employed when structural data information about the target is missing while the latter employed when X-ray/NMR solved or homology models are instead available for the target. The authors will focus on the most advanced techniques applied in this area. In particular, they will survey the key concepts of virtual screening by discussing how to properly select chemical libraries, how to make database curation, how to applying and- and structure-based techniques, how to wisely use post-processing methods. Emphasis will be also given to the most meaningful databases used in VS protocols. For the ease of discussion several examples will be presented.

KEYWORDS

Drug Discovery, Ligand- and Structure-based Approaches, Molecular Database, Virtual Screening

1. INTRODUCTION

Virtual screening (VS) is a computational technique developed since early 1990s to meet the needs of pharmaceutical companies to maximize their profit when minimizing time and cost (Lavecchia & Di Giovanni, 2013). It is well known that developing a new drug is a complex process, which can take approximately 12-15 years and huge investments of about $1 billion (Hughes et al., 2011).

In the last decades, pharmaceutical companies have radically changed the approach to the discovery and development of new drugs (Everts et al., 2017; Mangiatordi et al., 2016; Myers & Baker 2001) in the attempt to increase competitiveness and innovativeness. The need to speed-up the entire pipeline of drug discovery and development has given new credit to VS approaches as a viable alternative to the High-Throughput Screening (HTS) (Shoichet, 2004; Klebe, 2006). In this scenario, VS has gained a key role for anticipating the discovery of novel hits by reducing the likelihood of failure and, thus, time and costs (Kar& Roy, 2013).

DOI: 10.4018/IJQSPR.2018010108

Copyright © 2018, IGI Global. Copying or distributing in print or electronic forms without written permission of IGI Global is prohibited.
In addition, VS is effective to investigate ligands promiscuity for unveiling polypharmacological actions for the design of multi-target compounds and/or to detect off-target affinity (Chaudhari et al., 2017). The old paradigm of drug design “one-drug one-target” has been overtaken by the need of having polypharmacological drugs enabling to replace combination therapy with multitarget therapy (Anighoro et al., 2014). VS could be also valuable to draw a preliminary toxicological spectrum and especially about drug efficacy and safety (Chaudhari et al., 2017; Nicolotti et al., 2014). In this respect, main causes of market withdrawal are associated with the occurrence of idiosyncratic adverse liver effects, which are often fatal for people (M. Chen et al., 2011; Fontana et al., 2009). Well known is the case of nimesulide, a non-steroidal anti-inflammatory drug (NSAID) marketed as one of the first selective COX-2 inhibitors and currently banned from several countries in Europe and USA.

Traditionally, VS relies on two main strategies that are ligand-based (LBVS) and structure-based (SBVS) virtual screening approaches (Lionta et al., 2014; Nicolotti et al., 2008). The LBVS strategies are based on the assumption that similar chemical structures should exhibit similar binding properties with respect to a given target (Klabunde, 2007; Koeppen et al., 2011). To carry out LBVS studies, at least one active compound (e.g., agonist for a given target) and a pool of structurally similar compounds are necessary (Koeppen et al., 2011; Rognan, 2017).

On the other side, SBVS approaches are employed when the 3D solved structure, or as alternative a reliable homology model, of a target protein is available. For the sake of clarity, homology models having at least 50% sequence identity compared to the template are suitable for SBVS, being docking studies usually able to globally reproduce the reference interactions with high level of accuracy (Bordgna et al., 2011; Cavasotto & Phatak, 2009; Hillisch et al., 2004; Oshiro et al., 2004).

Generally, a SBVS approach is based on two basic steps: (1) one or more libraries of compounds are screened by biasing the active site of the targets protein (or its model) with a number of different molecular poses; (2) the compound-target affinity is evaluated by means of a scoring function whose value is used for ranking compound. A post-processing phase can be also implemented to refine the selection of the top-ranked compounds for prioritizing experimental tests (i.e., in vitro and/or in vivo assays) (Rognan, 2017). An example of efficient application of SBVS is the identification of molecular scaffolds for developing selective ligands towards human histamine H4 receptor (hH4R). This study was conducted using a library of about 8.7 million 3D-structures screened on a homology model of the hH4R, with 255 compounds selected and successfully tested (Kiss et al., 2008).

Nowadays, various workflow management tools have been developed to facilitate the automated application of VS strategies (GLaaB, 2016). Widely applied are the open-source software KNIME (Beisken et al., 2013; Mazanetz et al., 2012) and the commercial Pipeline pilot (Accelrys http://accelrys.com/). Several other tools have also available including Taverna (Oinn et al., 2004), KDE Bioscience (Lu et al., 2006), Galaxy (Goecks et al., 2010), Kepler (Ludäscher et al., 2006) and SOMA2 (Lehtovuori & Nyrönen, 2006).

Recently, an innovative SBVS approach exploiting the similarity of X-ray solved binding sites has been developed (Siragusa et al., 2015). It is thus demonstrated that VS is also effective to explore the protein cavities whose 3D structures are known on the basis of the shape similarity and irrespective of the primary structures. Several software (e.g., BioGPS (Siragusa et al., 2015), IsoMIF Finder (Chartier et al., 2016), SuMO (Jambon et al., 2003)) able to compare the binding sites of protein structures have been so far developed.

In the first part of this review, we will survey relevant methodological steps of VS protocol (see Figure 1) including the detailed description of the two principal approaches of VS, LBVS and SBVS. In the second part, some case studies are reported in order to illustrate the pros and cons of this simulating technique.
A Quantitative Structure-Property Relationship Study of the Adsorption of Amino Acids on Kaolinite Surfaces
www.igi-global.com/article/a-quantitative-structure-property-relationship-study-of-the-adsorption-of-amino-acids-on-kaolinite-surfaces/204890?camid=4v1a

The History and Development of Quantitative Structure-Activity Relationships (QSARs)
www.igi-global.com/article/the-history-and-development-of-quantitative-structure-activity-relationships-qsars/144688?camid=4v1a