P. Polishchuk[1]

VIRTUAL SCREENING IN DRUG DISCOVERY

[1]Institute of Molecular and Translational Medicine, Faculty of Medicine and Dentistry, Palacký University and University Hospital in Olomouc, Hněvotínská Str., 1333/5, Olomouc, Czech Republic

pavlo.polishchuk@upol.cz

Drug discovery accumulates experimental data very fast. Nowadays, more than 100 million of compounds available in PubChem and other databases which contain information about biological activities and other pharmaceutically important properties of compounds. However, the size of chemical space of drug-like molecules is much larger and is estimated to ~10^{36} compounds. Utilization of accumulated knowledge to navigate in such a vast space is invaluable for drug discovery. This can greatly speed up a whole discovery process and reduce overall costs for research of new therapeutically relevant compounds.

Nowadays, different ligand- and structure-based in silico approaches proved their utility in drug discovery. Most widely used are similarity search, QSAR and pharmacophore modeling, molecular docking which represent molecular structure from different perspectives. All these methods have their own drawbacks and advantages. Application of a single tool for virtual screening can be successful. However, single computational models are not accurate enough to identify hits with high successful rates in all cases. Therefore, using different tools in combination is a more reasonable strategy. Founding an agreement between different models can decrease the number of compounds to be tested and significantly improve hit rates. On the other hand combining a lot of different models may reduce the novelty of identified compounds. Nowadays, in silico screening became already a routine procedure and a lot of examples of successful applications were published recent years.