Abstract

Back-screening is an activity where Drug Design can significantly help to improve the outcome of High Throughput Screening (HTS). Indeed, using hits obtained from HTS, back-screening allows selecting new compound lists in larger databases with the help of ligand-based methods. Then with these new compounds, the purpose is to use the close analogs in order to build a SAR model and/or find new hits from new chemical series.

The main idea in the following study, is to compare several fingerprints employed in ligand-based similarity search methods. The criterion of comparison is based on the effectiveness to retrieve actives for known targets. We used a public dataset, DUD\textsuperscript{1}, which is composed of 40 target proteins with associated ligands. We chose to focus our study in a lead hopping context. In order to discard too similar compounds, a cut-off based on Daylight fingerprint has been applied.

Afterwards, two different approaches were then carried out. First, we considered only the ligand for each protein. Then we tried to retrieve the associated actives among the decoys. The provided results enable to show the different chemical information felt by each descriptor. In the second approach, we selected several actives for a specific target, and we tried to retrieve the other ones.