SAFAN-ISP: small molecule in-silico profiling with experimental reliability

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Motivation

The interactions between small molecules and proteins constitute one of the most important parts of interconnected biological networks and are of vital importance for characterizing the expression and function of proteins related to discovering drug candidates for clinical diagnosis.

Pharmaceutical companies are interested in shortening the time and reducing the cost of drug development and SAFAN-ISP can predict effectiveness and potential toxicity of compounds with the same precision of the current experimental protocol, at a fraction of the cost and in a much shorter time.

Methods

Typically, the screening is currently done in a physical lab (in vitro) using protein microarrays, that are powerful tools to examine small molecule and drug substrates and allow the simultaneous specificity assay of a molecule against a large collection of human proteins. However, microarrays still require physical lab work and are relatively slow and expensive to operate. SAFAN-ISP, is a highly effective new fragment-based technology for small molecule profiling, yielding computational (in silico) information comparable to those obtained from protein microarrays. It can be considered a ligand based method relying on the idea that similar structure leads to similar properties, and predict the properties of a molecule by studying the properties of similar molecules, having publicly available ligand target information. The use of fragments (molecules of low complexity) implies a better sampling of the chemical space.

Results

SAFAN-ISP concurrently predict a compound's ability to interact with 3000 protein targets belonging to 12 different classes, yielding binding constant as output. The method also quantitatively correlates predictions to the experiments. Examples of SAFAN-ISP validation will be described.