

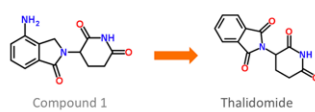
Semantically integrated life science data – The power of workflows for analysis of phenotypic screening data, toxicological read across, and repurposing

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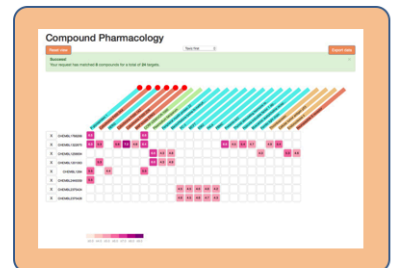
Abstract

The public availability of large, semantically integrated data sources such as the Open PHACTS Discovery Platform allows to run research questions across several data domains in one query. However, submitting complex queries and analyzing the data retrieved still is time consuming and prone to errors. In this context, the use of workflow engines such as KNIME or Pipeline Pilot enables to simultaneously query different domains, such as compounds, targets, pathways, and diseases. Within this contribution, Open PHACTS computational protocols for in silico target validation of cellular phenotypic screens, case studies for the development of ligand-transporter interaction models and their use for predicting complex in vivo toxicity endpoints, as well as workflows for identifying candidates for repurposing will be presented. Finally, we will outline ToxPHACTS, which is based on a KNIME workflow for toxicological read across. .

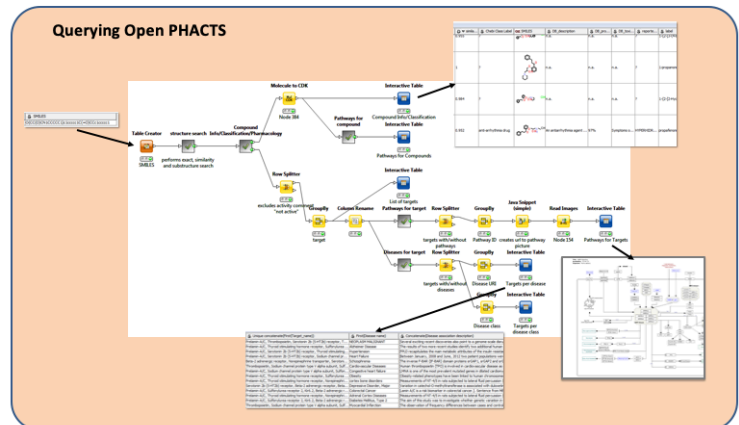
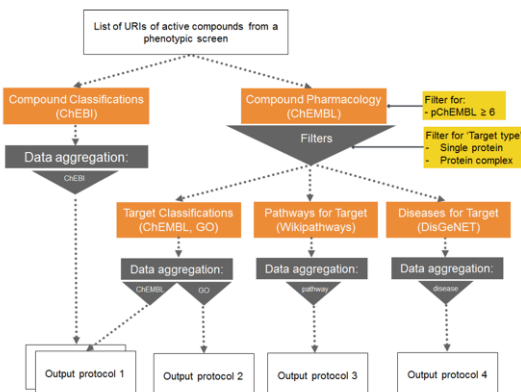
Toxicological Read Across (www.toxphacts.com)



- Compound 1 is queried across the public chemical/pharmacological space
- Thalidomide is one of the compounds found
- Compound 1 is thus de-prioritized in further development due to teratogenic risk



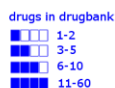
Phenotypic Screening (Digles, MedChemCommun 2016)



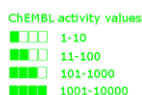
Target profiling (SLC Read Across)

Workflow retrieves compounds from ChEMBL, drugs from DrugBank, and diseases from DisGeNET

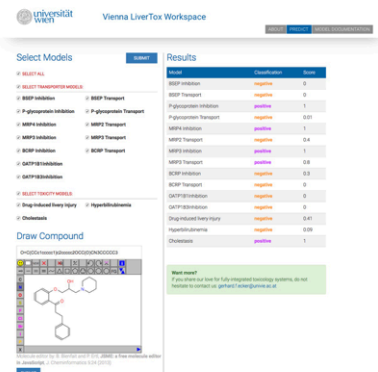
Targets: SERT, DAT, NET, GAT



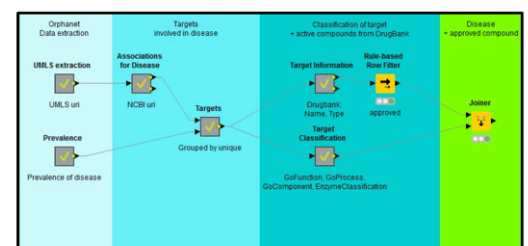
Diseases: Anxiety Disorders, Depressive Disorders, Schizophrenia, Dementia, ...



Transporter Profiling/Tox Pred (livertox.univie.ac.at)



Repurposing



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