Subject: Suggestion: tautomer-check
Posted by nbehrnd on Wed, 06 May 2020 13:40:09 GMT
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DataWarrior's model to assign Druglikeness depends on the encoded structure a tautomer is represented. With Ambit-Tautomer, Kochev et al. published an open source tool (Java based), to predict tautormers and to rank their likelyhood. If wanted, their executable may be run without the larger Ambit framework, just by

java -jar ambit-tautomers-2.0.0-SNAPSHOT.jar

Thus, I would like to suggest DataWarrior could implement a function to check if the structures to consider could reasonably yield a tautomer worth to probe equally. This equally could be complementary to your recently published reference tautomer.dwar.

Out of curiosity, I drew a pyridone, a pyrazole, and a thalomide with ACD ChemSketch in two tautomeric forms, exported the SMILES strings (as defined by ACD ChemSketch) into a .smi file:

With openbabel, it was converted into a .sdf accessible for DataWarrior by

obabel -ismi tautomers.smi -osd -O tautomers.sdf

successfully read and used to compute the Druglikeness. At least as the examples about «hydroxypyridine» and the enol form of the thalomide differ in the results examined.

To ease replication of the findings, the relevant files are provided below.

Publication about Ambit-Tautomer: https://doi.org/10.1002/minf.201200133
github-entry about Ambit-Tautomer:
https://github.com/ideaconsult/apps-ambit/tree/master/tautom ers-example

## File Attachments

1) tautomers.gif, downloaded 467 times
2) tautomers.smi, downloaded 269 times
3) tautomers.sdf, downloaded 267 times
4) tautomers.dwar, downloaded 283 times
5) tautomer_DW.png, downloaded 554 times

Subject: Re: Suggestion: tautomer-check
Posted by thomas on Mon, 11 May 2020 18:59:48 GMT
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This is, of course, and important issue. Having the right tautomer to start with is crucial for any reliable prediction.
The intention behind the work on the published tautomer database is to allow others and ourselves to work on algorithms
to predict the most prominent tautomer. If we had such an algorithm with a reasonable performance at hand, we could use
it as input before training any prediction model. It also would allow to normalize pKa databases to improve or develop
algorithms to more reliably predict pKa-values, which is also in big demand. We have it in the pipeline, but it will
take time...