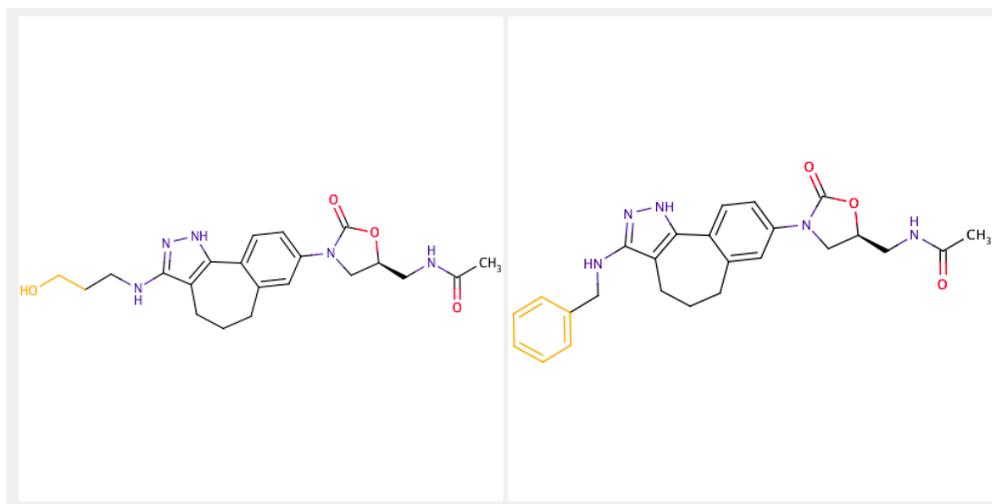
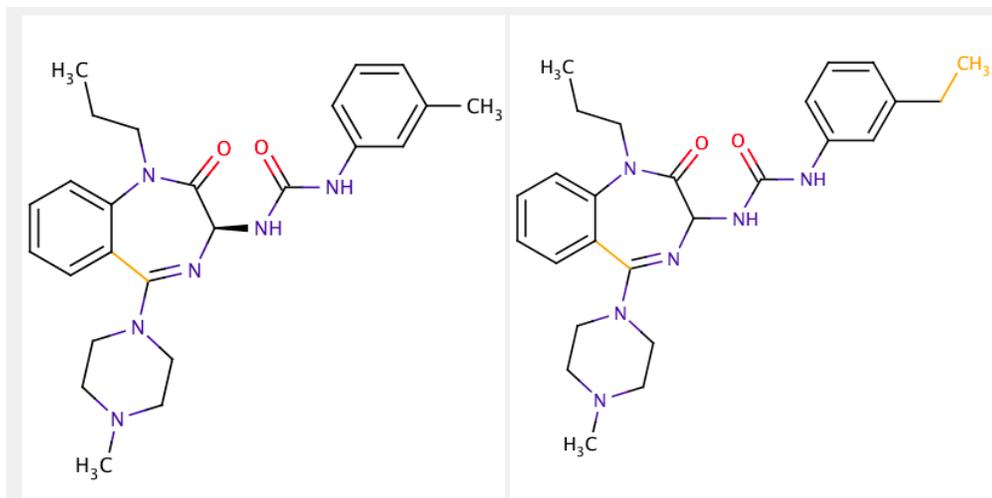


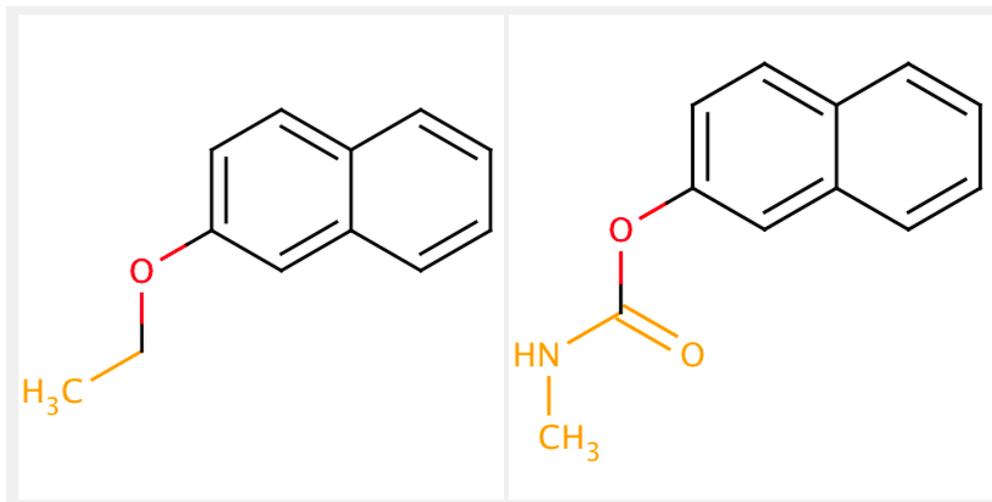
Molecular Matched Pairs

Introduction

A **molecular matched pair** (MMP) is a pair of molecules that have only a minor single-point difference. The typical way is to define a minor difference as a changed molecular fragment with less than 10 atoms.

Exemplary MMPs (differences highlighted in orange):



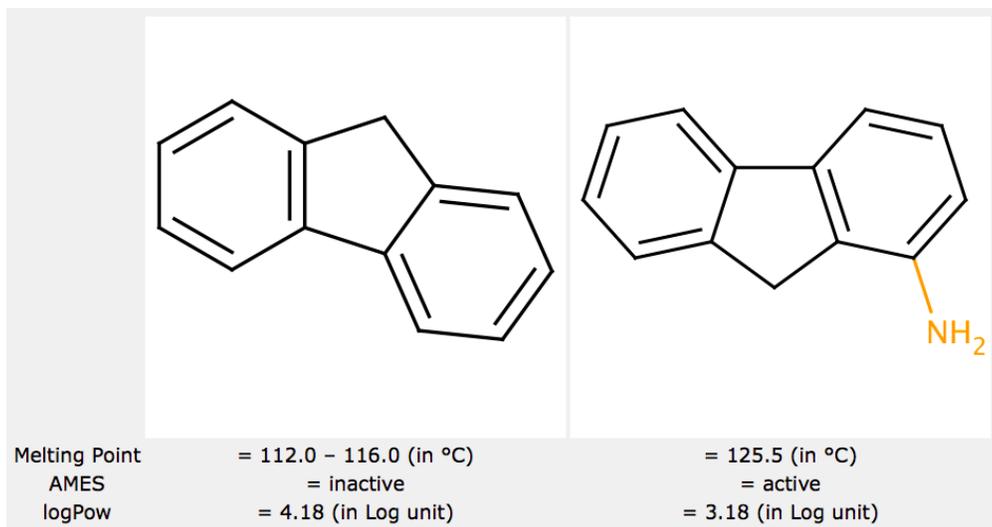


Why MMPs?

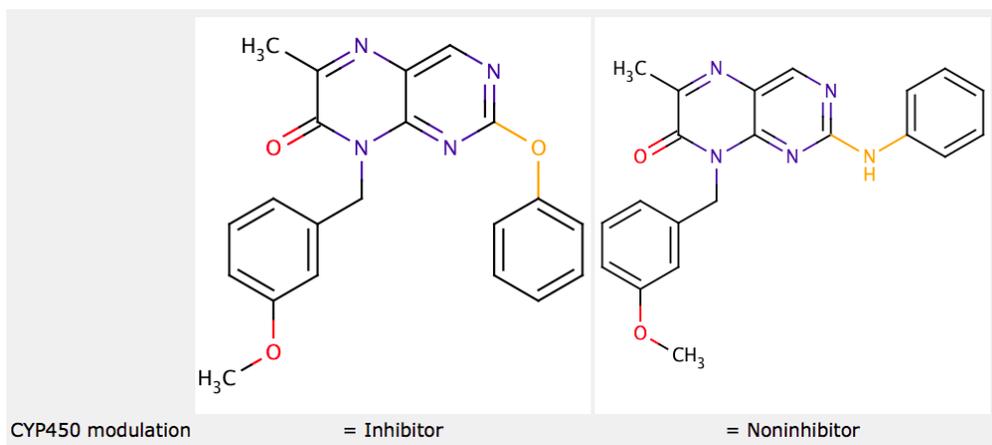
MMPs aid interpreting how particular structural changes affect the chemical and biological properties of a molecule. For example, how addition or replacement of a particular functional group affects the solubility, melting point or toxicity of a molecule?

Definitely, such interpretation is possible only if the experimental data (or predicted values) is available for both molecules in the pair.

For example, in the MMP below, a minor change resulted into molecule being active according to the Ames test:



In the following example, after a minor structural change, a molecule changed its inhibitory activity for the human P450 cytochrome :



MMPs and OCHEM

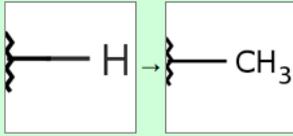
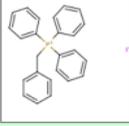
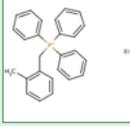
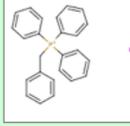
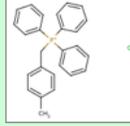
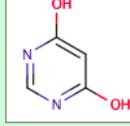
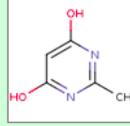
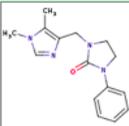
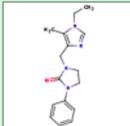
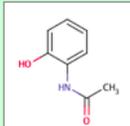
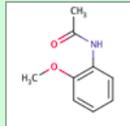
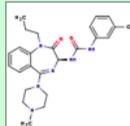
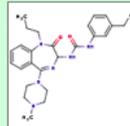
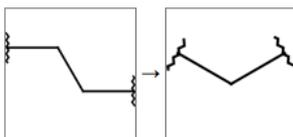
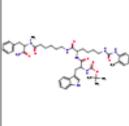
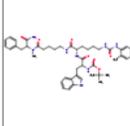
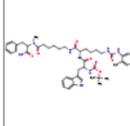
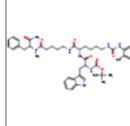
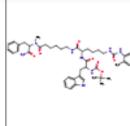
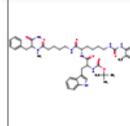
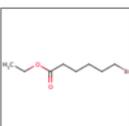
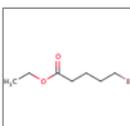
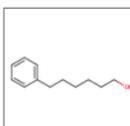
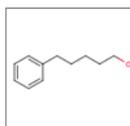
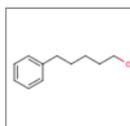
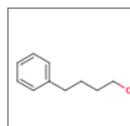
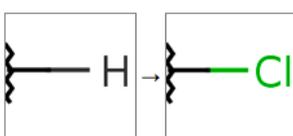
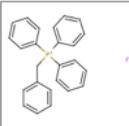
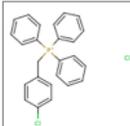
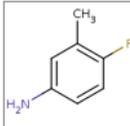
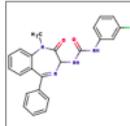
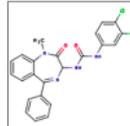
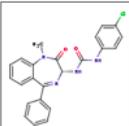
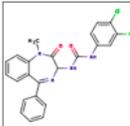
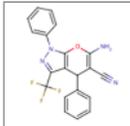
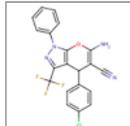
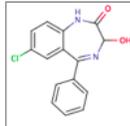
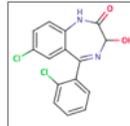
Automatic identification of MMPs

OCHEM has a separate module that allows to identify molecular matched pairs, to group them by molecular transformations and to calculate various statistical information for particular pairs or transformations. OCHEM automatically indexes all the molecules having any experimental data associated with them and identifies the matched pairs.

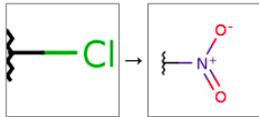
The pairs identification process is running in background and can take some time (hours to days) for new molecules.

Matched pairs and transformations

Each matched molecular pair is related to a particular molecular transformation. For example, replacement of a functional group with another group is a transformation. OCHEM groups all pairs by transformations allows to see them in the transformations browser, as show in the screenshot below.

 <p>[transformation profile]</p>	158375 matched pairs [view all]					
	 M108628	 M69669	 M108628	 M746289	 M24863	 M108543
	 M1000303369	 M1000303376	 M74	 M2585	 M1000288941	 M1000289089
	Click the molecule to enlarge it					
 <p>[transformation profile]</p>	48547 matched pairs [view all]					
	 M1000218901	 M1000218906	 M1000218901	 M1000218906	 M1000218901	 M1000218906
	 M2354	 M122	 M2525	 M2182	 M2182	 M6093
 <p>[transformation profile]</p>	47333 matched pairs [view all]					
	 M108628	 M69670	 M66395	 M108627	 M1000289022	 M1000288950
	 M1000289104	 M1000288950	 M2340	 M6149	 M65	 M1992

Each transformation has its profile page that contains different details: SMIRKS of the transformation, all the molecular pairs related to this transformation and, if applicable, affected properties and activities:



Transformation ID: TR3651397
 SMIRKS: *Cl -> [O-][N+](*)=O

Affected properties

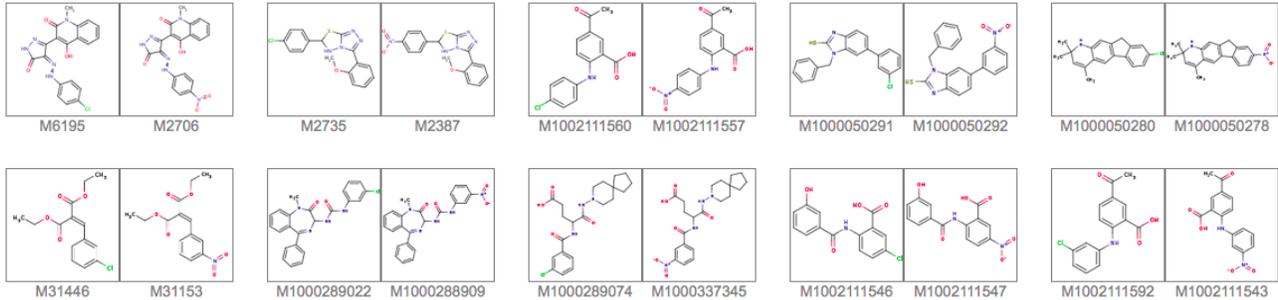
- ↑ Boiling Point $\Delta_{\text{pair}} = 53.0 \pm 22.0$
- ↓ logPow $\Delta_{\text{pair}} = -0.67 \pm 0.32$
- ↑ AMES $\uparrow 40 \text{ pairs}, \downarrow 3 \text{ pairs}, 21 \text{ negative and } 51 \text{ positive molecules unaffected}$

Molecular pairs matching this transformation.

Minimal similarity:

1 - 100 of 5150

100 items on page 1 of 52 > >>

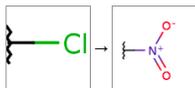


Transformations annotation

Transformations can affect particular properties. For example, alter toxicity, lipophilicity, melting point and so on. OCHEM can automatically identify and annotate transformations that affect various molecular properties in a statistically significant manner.

Such annotations is shown on the transformations profile.

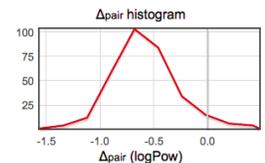
For each affected property, it is possible to see a basic statistical info, a histogram of the pair deltas and all the pairs used to calculate statistics for this transformation.



Transformation ID: TR3651397
 SMIRKS: *Cl -> [O-][N+](*)=O

Affected properties

- ↑ Boiling Point $\Delta_{\text{pair}} = 53.0 \pm 22.0$
- ↓ logPow $\Delta_{\text{pair}} = -0.67 \pm 0.32$
- ↑ AMES $\uparrow 40 \text{ pairs}, \downarrow 3 \text{ pairs}, 21 \text{ negative and } 51 \text{ positive molecules unaffected}$

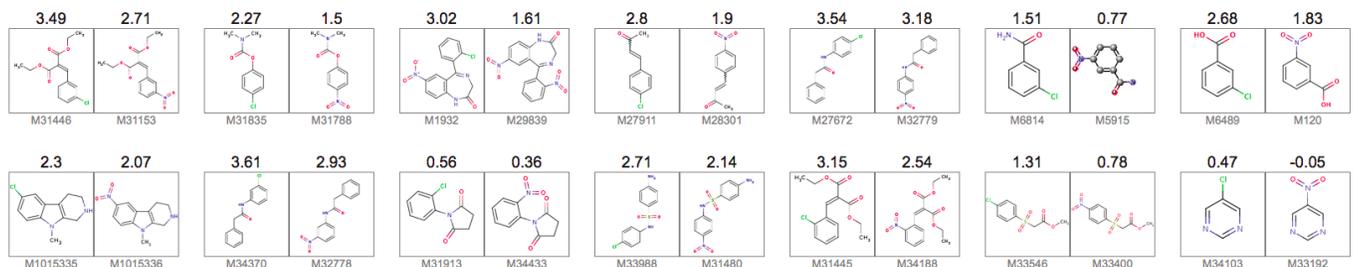


Molecular pairs matching this transformation.

Minimal similarity:

1 - 100 of 322

100 items on page 1 of 4 > >>



To select the transformations that affect the desired properties or activities, there is a transformation optimiser utility.

The following screenshot shows the transformations that affect the inhibition growth concentration (log[IC50]) but

do not affect lipophilicity:



MatchedPairs: Transformations optimiser

This utility allows to select the transformations that affect the desired properties of interest.

Affected properties

Melting Point	<input type="checkbox"/> Decrease (444)	<input type="checkbox"/> No effect	<input type="checkbox"/> Increase (965)
logPow	<input type="checkbox"/> Decrease (443)	<input checked="" type="checkbox"/> No effect	<input type="checkbox"/> Increase (502)
logS	<input type="checkbox"/> Decrease (9)	<input type="checkbox"/> No effect	<input type="checkbox"/> Increase (1)
CYP450 modulation	<input type="checkbox"/> Decrease (22)	<input type="checkbox"/> No effect	<input type="checkbox"/> Increase (17)
log(IC50-1)	<input checked="" type="checkbox"/> Decrease (19)	<input type="checkbox"/> No effect	<input checked="" type="checkbox"/> Increase (66)
Boiling Point	<input type="checkbox"/> Decrease (360)	<input type="checkbox"/> No effect	<input type="checkbox"/> Increase (701)
AMES	<input type="checkbox"/> Decrease (3)	<input type="checkbox"/> No effect	<input type="checkbox"/> Increase (41)

Inverse the desired effect

1 - 24 of 24

 [transformation profile]	 [transformation profile]	 [transformation profile]
 [transformation profile]	 [transformation profile]	 [transformation profile]
 [transformation profile]	 [transformation profile]	 [transformation profile]
 [transformation profile]	 [transformation profile]	 [transformation profile]

1 - 24 of 24

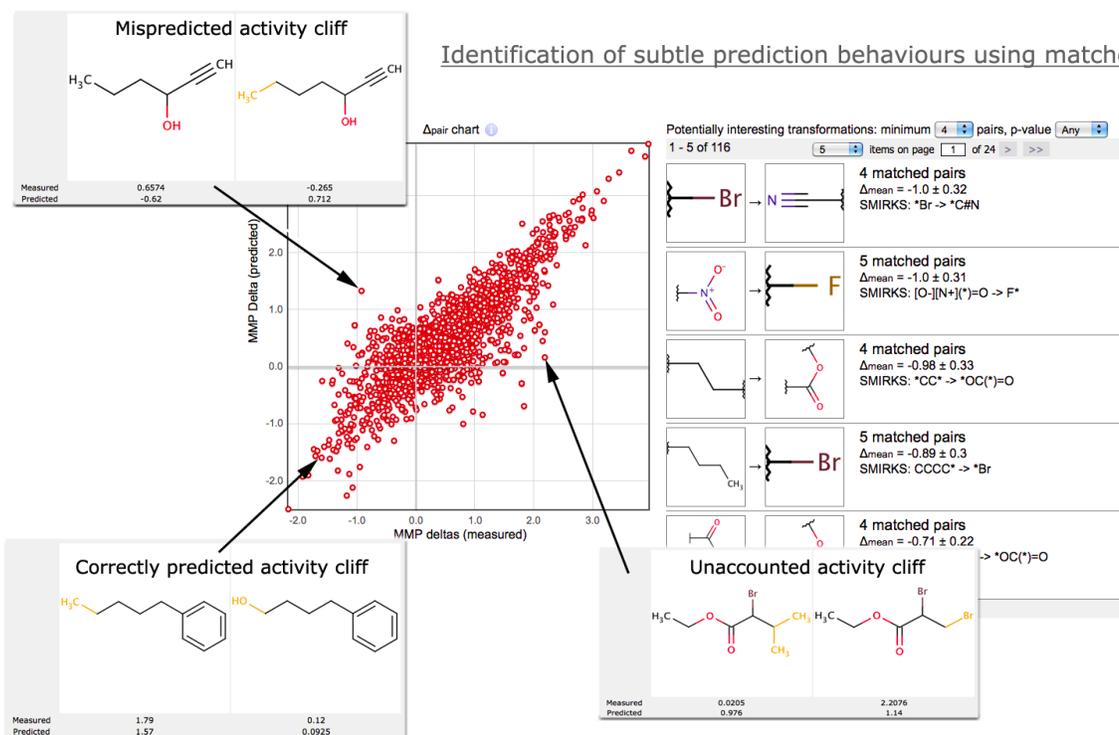
MMP-based interpretation of QSAR models

MMPs can be used to identify subtle prediction behaviours, e.g., model reaction to activity cliffs. The delta-pair chart shows the *actual* and *predicted* effects of molecular transformations.

Significant molecular transformations. The list on the right shows the "interesting" molecular transformations that have a statistically significant effect on the property of interest. From the screenshot below, it can be seen that replacement of Bromine to Nitrile group (1st transformation in the list) reduces toxicity of compounds.

We will call such transformations "*significant*".

Identification of subtle prediction behaviours using matched pairs

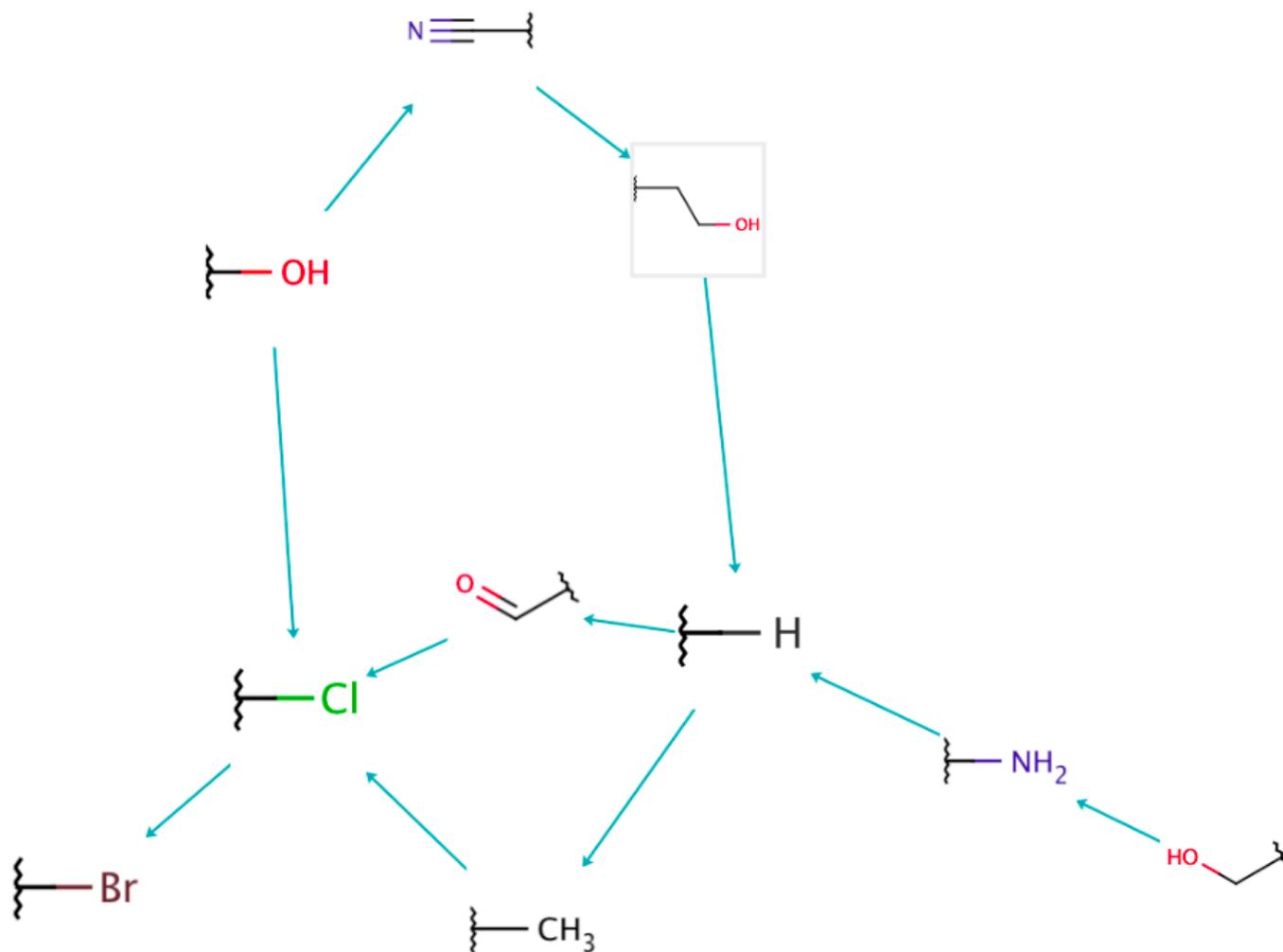


Molecular Fragments Graph

Each molecular transformation is a replacement of one molecular fragment to another one. That is, a transformation is a relation between two molecular fragments.

Based on the "significant" transformations, it is possible to create a directed graph of molecular fragments. Each node in this graph is a fragment, each edge is a significant transformation. Such graphs can display a number of transformations and allow for a better interpretation.

The following graph display a part of the transformations related to Aquatic toxicity. Arrows point the direction of increasing toxicity. For example, it can be seen that the presence of Bromine is potentially more toxic than the presence of Chlorine.



References

The article with description of a use of MMPs to analyze models has been published in [Prediction-driven matched molecular pairs to interpret QSARs and aid the molecular optimization process](#). Sushko Y, Novotarskyi S, Körner R, Vogt J, Abdelaziz A, Tetko IV. *J Cheminform.* 2014 Dec 11;6(1):48. doi: 10.1186/s13321-014-0048-0.