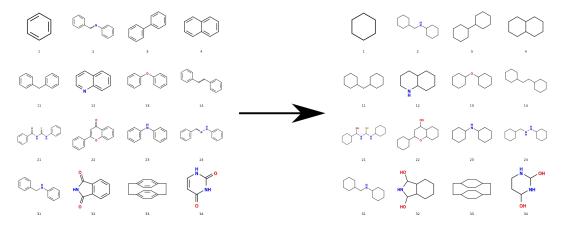
1 Background

The Bemis-Murcko scaffold¹ provided by DataWarrior² retains information about bond order and chirality. Sometimes, however, it suffices to retain only atom connectivity, like an assumption «there are only single bonds». Note, DataWarrior equally offers the export of Bemis-Murcko skeleton, however this simplifies e.g. the scaffold about an imidazole into one of cyclopentane.



2 Typical use

Running from the command line, the script processes one, or multiple SMILES strings listed in an input file (symbolized by text below) to report the processed SMILES strings back to the command line:

python saturate_murcko_scaffolds.py [-h] [-o] text

Instead of an input file, individual SMILES strings equally may be processed; to prevent their misinterpretation by the shell, enclose them by either single, or double quotes. Either approach elected, the result may be redirected into a permanent record with a user defined file name (flag --outfile, or shorter -o). Only modules the standard library of Python 3 provides (e.g., version 3.11.2) are used.

3 Example

For a collection of organic materials, the Bemis-Murcko scaffolds were extracted with DataWarrior (then release 5.0.0 for Linux, January 2019) as listing test_input.smi including higher bond orders (see folder test_data). The effect of the «artificial saturation» is easy to recognize while comparing the scaffold lists (fig. 1) in a difference view of the two .smi files.

¹Bemis, G. W.; Murcko, M. A. The Properties of Known Drugs. 1. Molecular Frameworks. *J. Med. Chem.* **1996**, *39*, 2887–2893 (https://doi.org/10.1021/jm9602928).

²Sander, T.; Freyss, J.; Von Korff, M.; Rufener, C. DataWarrior: An Open-Source Program For Chemistry Aware Data Visualization And Analysis. *J. Chem. Inf. Model.* **2015**, *55*, 460–473 (https://doi.org/10.1021/ci500588j). The

```
C(CC1)CCC10C1CCCCC1
013
       c(cc1)ccc10c1ccccc1
                                                013
                                                014
014
       C(c1ccccc1)=C/c1ccccc1
                                                       C(C1CCCCC1)CC1CCCCC1
                                                015
015
       c1cc2cc3ccccc3cc2cc1
                                                       C1CC2CC3CCCCC3CC2CC1
                                                016
016
       0=C(c1ccccc1)c1ccccc1
                                                       OC(C1CCCCC1)C1CCCCC1
017
       c1c[nH]c2c1cccc2
                                                017
                                                       C1C[NH]C2C1CCCC2
018
       c(cc1)ccc1/N=N/c1ccccc1
                                                018
                                                       C(CC1)CCC1NNC1CCCCC1
                                                019
019
       C(c1ccccc1)=N/N=C/c1ccccc1
                                                       C(C1CCCCC1)NNCC1CCCCC1
020
       C(Cc1ccccc1)c1ccccc1
                                                020
                                                       C(CC1CCCCC1)C1CCCCC1
021
       0=C(c1cccc1)NC(Nc1ccccc1)=S
                                                021
                                                       OC(C1CCCCC1)NC(NC1CCCCC1)S
022
                                                022
       0=C1c(cccc2)c20C(c2cccc2)=C1
                                                       OC1C(CCCC2)C2OC(C2CCCCC2)C1
023
       c(cc1)ccc1Nc1ccccc1
                                                023
                                                       C(CC1)CCC1NC1CCCCC1
024
       C(c1ccccc1)=N/Nc1ccccc1
                                                024
                                                       C(C1CCCCC1)NNC1CCCCC1
025
       0=C(C=CN1[C@@H]20CCC2)NC1=0
                                                025
                                                       OC(CCN1[C@@H]2OCCC2)NC10
026
       c1ccc2c(-c3cccc4ccccc34)cccc2c1
                                                026
                                                       C1CCC2C(-C3CCCC4CCCCC34)CCCC2C1
027
       c1ccc(C(c2cccc2)c2ccccc2)cc1
                                                027
                                                       C1CCC(C(C2CCCC2)C2CCCC2)CC1
028
       c(cc1)cc2c1[nH]c1c2cccc1
                                                028
                                                       C(CC1)CC2C1[NH]C1C2CCCC1
029
       c(cc1)ccc1P(c1ccccc1)c1ccccc1
                                                029
                                                       C(CC1)CCC1P(C1CCCCC1)C1CCCCC1
030
       c1c(-c2cccc2)oc2c1cccc2
                                                030
                                                       C1C(-C2CCCCC2)OC2C1CCCC2
                                                031
                                                       C(C1CCCCC1)NC1CCCCC1
031
       C(c1ccccc1)Nc1ccccc1
032
                                                032
       0=C(c1c2cccc1)NC2=0
                                                       OC(C1C2CCCC1)NC2O
       C(Cc1ccc(CC2)cc1)c1ccc2cc1
                                                       C(CC1CCC(CC2)CC1)C1CCC2CC1
```

Figure 1: Difference view of the SMILES strings of a Murcko scaffold *prior* (left hand column) and *after* an «artificial saturation» (right hand column). The processing affects explicit bond order indicators, e.g. double bond (equality sign, e.g., line #14), triple bond bond (number sign #, not shown); or about implicit aromatization (lower case to upper case) for atoms of carbon, nitrogen, oxygen (depicted); or phosphorus, sulfur (not depicted). Stereochemical indicators about double bonds will be removed (e.g., slashes in lines #18 and #19). Descriptors of stereogenic centers (@-signs, e.g., line #25) and charges (not shown) are copied verbatim.

The work can be illustrated by OpenBabel³ with instructions to the command line in the pattern of

```
obabel -ismi test_input.smi -0 test_input_color.svg -xc10 -xr12 -xl --addinindex

to generate a .svg file (vector representation), or

obabel -ismi test_input_sat.smi -0 test_input_sat_color.png -xc10 -xr12 -xl

→ --addinindex -xp 3000
```

to generate a bitmap .png with structure formulae depicted in a grid of 10 columns by 12 rows. It is remarkable how well OpenBabel's displays the molecular structures with advanced motifs. In addition to those shown in the first illustration of this guide, see sub-folder test_data for a more extensive survey (e.g., the scaffold of cyclophane [entry #33], sparteine [#38], or adamantane [#50]).

program, (c) 2002–2023 by Idorsia Pharmaceuticals Ltd., is freely available under http://www.openmolecules.org. For the source code (GPLv3), see https://github.com/thsa/datawarrior.

³www.openbabel.org For the most recent documentation, see https://open-babel.readthedocs.io/en/latest/ ReleaseNotes/ob310.html

4 Known peculiarities

The script provides «saturation» by dropping explicit information related to double and triple bonds which SMILES encode (=, # regarding bond order; / (forward slash), \ (backward slash) regarding (cis)-(trans) relationship around double bonds). While processing double bonds of e.g., ketones to yield secondary alcohols, the script refrains from the assignment of new CIP priorities and a corresponding label. It then depends on the program used for a visualization, if an explicit wedge is used (e.g., OpenBabel), or the absence of information is highlighted (e.g., as question mark in DataWarrior, or the project of CDK depict⁴) as ambiguous. Absolute configuration of stereogenic centers (indicated in SMILES with the @ sign) already assigned in the input however is retained.

For a selection of elements (C, N, O, P, S), the implicit description of aromatic systems (e.g., as c1ccncc1 in pyridine, c1c[nH]cc1 in pyrrol) is recognized. To offer a «saturation», these characters returned as upper case characters to yield e.g., piperidine (C1CCNCC1) and pyrrolidine (C1C[NH]CC1).

The script equally preserves up to one single negative, or single positive charge of these five elements (e.g., [0-]c1cccc1 about the phenolate anion, and C[N+](c1cccc1)(C)C about N,N,N-trimethylbenzenaminium cation). Here, it can be sensible to «sanitize» the results this script provides by other libraries as e.g. RDKit.⁵

The capitalization of the five characters is constrained to prevent non sensible transformations of e.g., an (implicitly) aromatic atom of tin [sn] into the invalid form [SN]. Though the script is going to write tin as [Sn], an adjustment of valence for elements written with two characters is beyond the current scope of the script.

A SMILES string may describe more than one molecule. Thus, the concatenation with "." (period character) as seen for example in descriptions of co-crystals like about 1,4-benzoquinone and hydroquinone, C1=CC(=0)C=CC1=0.c1cc(ccc10)0, is retained. The example is resolved as C1CC(0)CCC10.C1CC(CCC10)0.

5 License

Norwid Behrnd, 2019-23, GPLv3.

⁴https://www.simolecule.com/cdkdepict/depict.html For the mentioned annotation of CIP labels, change No Annotation (second pull down menu from the left) to CIP Stereo Label.

⁵For an overview about the freely available RDKit library, see www.rdkit.org. An introduction into the topic of «molecular sanitization» is provided in the section of this very title in the on-line RDKit Book.