Cheminformatics for Natural Products with the CDK

Maria Sorokina, Aziz M. Yirik, Jonas Schaub, Christoph Steinbeck

Friedrich-Schiller University Jena, Germany





About us











Dr. Maria Sorokina

Research interests:
NP cheminformatics, databases,
enzyme promiscuity and metabolic
networks



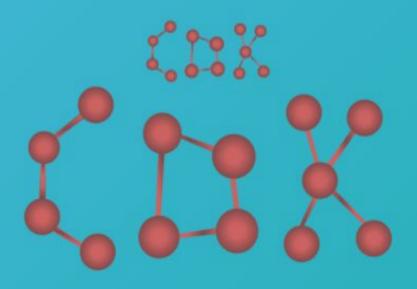
Mehmet Aziz Yirik

Research Interests: Chemical Graphs, Graph Isomorphism, Graph Generation



Jonas Schaub

Research interests: NP and carbohydrate cheminformatics, molecular fragmentation algorithms



Chemistry Development Kit

Open Source modular Java libraries for Cheminformatics

Java - a modern object-oriented language

- Java was created in 1995 for Sun Microsystems
- It is a **platform independent** language following the logic "Write Once, Run Everywhere"



Simple



Object-Oriented

Secure

































CDK: Chemistry Development Kit

The Chemistry Development Kit (CDK) is a collection of modular Java libraries for processing chemical information (Cheminformatics). The modules are free and open-source and are easy to integrate with other open-source or in-house projects.



Egon L. Willighagen¹*, John W. Mayfield², Jonathan Alvarsson³, Arvid Berg³, Lars Carlsson⁴, Nina Jeliazkova⁵, Stefan Kuhn⁶, Tomáš Pluskal⁷, Miquel Rojas-Chertó⁸, Ola Spjuth³, Gilleain Torrance⁹, Chris T. Evelo¹, Rajarshi Guha¹⁰, and Christoph Steinbeck¹¹



> 100 Contributors

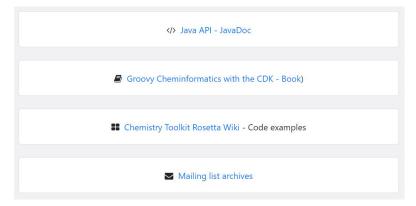
Key people: Christoph Steinbeck, Egon Willighagen, Dan Gezelter, Rajarshi Guha, John Mayfield

Get Started with CDK!



- check the general documentation (Java API): it's very detailed http://cdk.github.io/cdk/latest/docs/api/index.html
- join the CDK mailing list <u>https://sourceforge.net/projects/cdk/lists/cdk-user</u>
- download the latest release JAR from GitHub
- OR use Maven or Gradle dependencies, which will automatically fetch the CDK modules

<dependency>
 <groupId>org.openscience.cdk</groupId>
 <artifactId>cdk-bundle</artifactId>
 <version>2.3</version>
</dependency>



CDK in action

Webservices:

- CDK Depict: https://www.simolecule.com/cdkdepict/depict.html
- NP-likeness score, Sugar Removal Utility, NP databases: https://naturalproducts.net/

Workflows:

- MetFrag: https://msbi.ipb-halle.de/MetFrag/
- CDK KNIME nodes https://doi.org/10.1186/1471-2105-14-257

Stand-alone tools:

- CDK Descriptor GUI: http://www.rguha.net/code/java/cdkdesc.html
- Scaffold Hunter: Visual analysis of large and complex data sets http://scaffoldhunter.sourceforge.net

And many many more....

naturalproducts.net Resources



NaPLeS - Natural Product Likeness Score calculator





About

Natural product-likeness of a molecule, i.e. similarity of this molecule to the structure space covered by natural products, is a useful criterion in screening compound libraries and in designing new lead compounds. This NP-likeness score has been trained on 315 91 natural products (NP) from <u>various public databases</u>, on a manually curated NP dataset used for the publication of the previous standalone NP-likeness scorer [1] and on 488 642 randomly selected synthetic molecules (SMI) from the Zilko database.

Sugar moleties are removed from the molecules for the training and for the computation of the NP-likeness score as in [2]

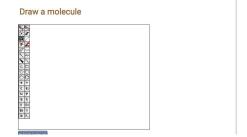
The stereochemistry is removed from the training set and from the user-submitted molecules.

Four ways to use the NP-likeness scorer

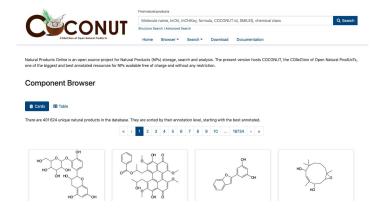
- . Upload a molecular file in one of the accepted formats (MOL, SDF or smiles). Maximum 1000 molecules per
- file.

 Paste a SMILES string of a molecule
- Draw a molecule
 Visualise the distribution of the NP-likeness score across natural products of public databases and taxonomy
- (bacteria, fungi and plants)

Upload a file







MetFrag

MetFrag is a freely available software for the annotation of high precision tandem mass spectra of metabolites which is a first and critical step for the identification of a molecule's structure. Candidate molecules of different databases are fragmented in silico and matched against mass to charge values. A score calculated using the fragment peak matches gives hints to the quality of the candidate spectrum assignment.



Link: https://ipb-halle.github.io/MetFrag/



MetFrag

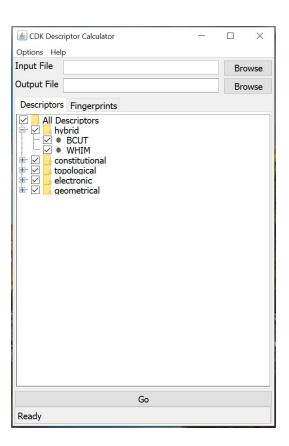
In silico fragmentation for computer assisted identification of metabolite mass spectra

→ Database Settings	
Database: KEGG ▼	Parent Ion: [M+H]+ ▼ Calculate
Neutral Mass: 253.966126 Search ppm: 5	
Formula:	
Identifiers:	
Retrieve Candidates	Download Candidates
Candidate Filter & Score Settings	
▼ Fragmentation Settings & Processing	
Mzppm: 5 Mzabs: 0.001	MS/MS Peak list 90.97445 681 106.94476 274 110.02750 110 115.98965 95
Mode: [M+H]+	117.98540 384 124.93547 613 124.99015 146 125.99793 207
Tree depth:	133.95592 777
Group candidates	Show Spectrum
Process Candidates	Download Parameters

CDK Descriptor Calculator

- Calculate multiple fingerprints and molecular descriptors easily
- Developed by one of the CDK developers, Rajarshi Guha

Link: http://www.rguha.net/code/java/cdkdesc.html





CDK hands-on!

CDK examples in GitHub: https://github.com/mSorok/CDK_secondary_metabolites_in_plants_2021

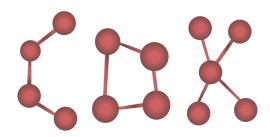
- a. Basics
- b. AtomContainer manipulation:
 - i. <u>Molecular descriptors calculation</u>
 - ii. <u>Fingerprints</u>

CDK in the world: other cheminformatic libraries

A very nice article on Open Source Cheminformatic Toolkits:

https://www.macinchem.org/scientificsoftware/toolkits.php

- **RDKit**: Python, great and active community, lots of functionalities. Try it out: http://www.rdkit.org
- OpenBabel: chemical file formats manipulation (http://openbabel.org/wiki/Main_Page)
- OpenChemLib: JavaScript, multiple tools, especially adapted for web. Try it out: https://www.npmjs.com/package/openchemlib
- and many more....!









Question time

Acknowledgements



