



Open-Source Cheminformatics  
and Machine Learning

# RDKit: The State of the Toolkit

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# Acknowledgements

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## ■ NIBR

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- Paolo Tosco

## ■ knime.com

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- Pavel Velikhov

## ■ Distributions:

- Gianluca Sforna (Fedora)
- Michael Banck (Debian)

# Overview

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- **History**
- Where are we today?
- What next?

# Presentations, tutorials, notes, data, etc.

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[https://github.com/rdkit/UGM\\_2013](https://github.com/rdkit/UGM_2013)

Please do pull requests or just send me materials

# History and milestones

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- 2000-2006: initial development work at Rational Discovery
- 2006: code open sourced and released on sourceforge.net
- 2007: First NIBR contribution (chemical reaction handling); Noel discovers the RDKit (=first rdkit-discuss post?)
- 2008: first POC of Java wrapper; Mac support added; SLN and Mol2 parsers;
- 2009: Morgan fingerprints; switch to cmake; switch to VF2 for SSS
- 2010: PostgreSQL cartridge; First iteration of the KNIME nodes; \$RDBASE/Contrib appears; SaltRemover and FunctionalGroups code
- 2011: New Java wrappers; more functionality moved to C++; InChI support; Avalontools integration
- 2012: First UGM; Speed improvements; MCS implementation; IPython integration; “RDKit Cookbook” appears
- 2013: Move to github; Pandas integration; MMFF support;

# Overview

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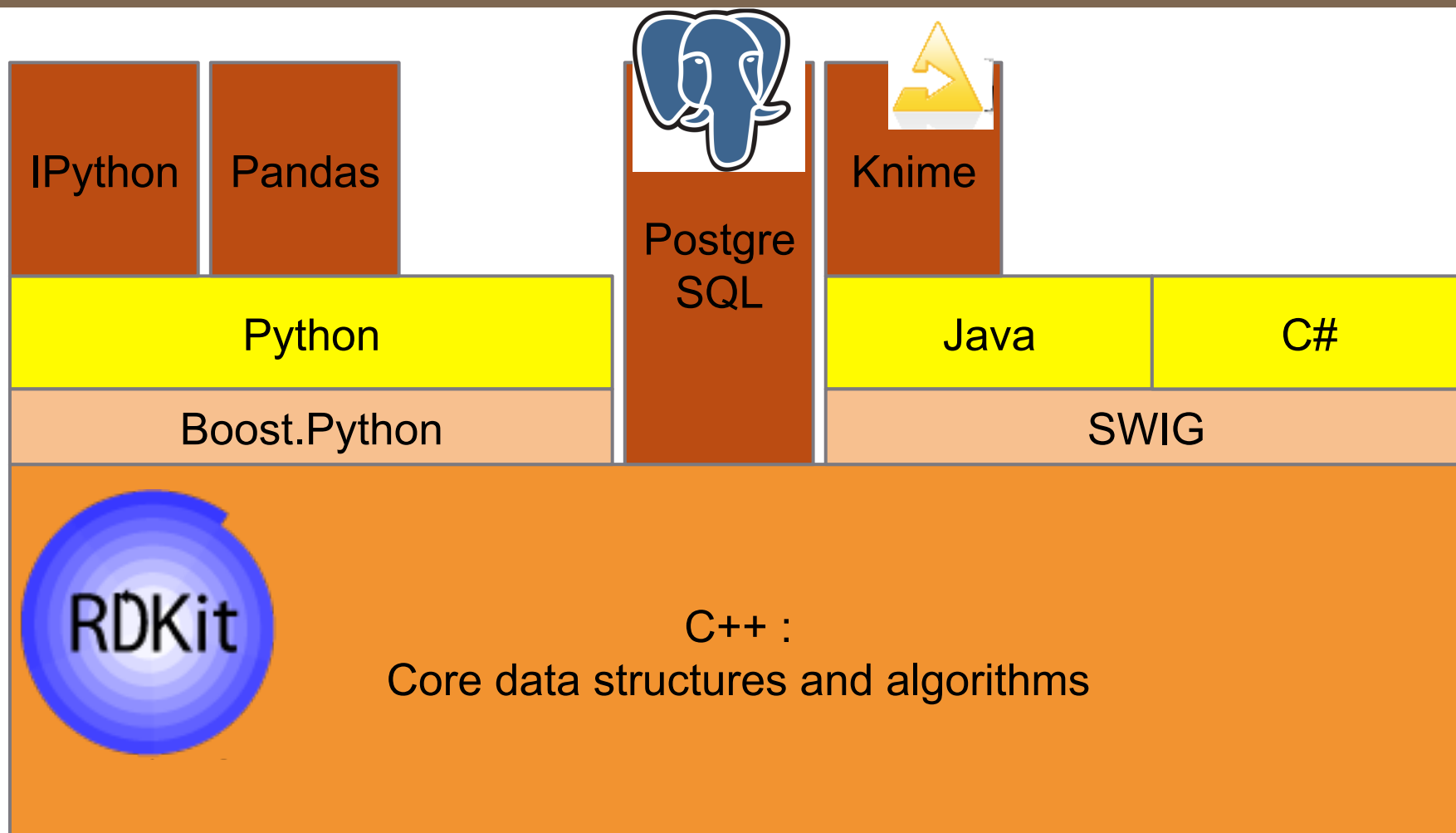
- History
- **Where are we today?**
- What next?



# RDKit: What is it?

- Python (2.x), Java, and C++ toolkit for cheminformatics
  - Core data structures and algorithms in C++
  - Python wrapper generated using Boost.Python
  - Java wrapper generated with SWIG
- Functionality:
  - 2D and 3D molecular operations
  - Descriptor generation for machine learning
  - Molecular database cartridge
  - Supports Mac/Windows/Linux
- History:
  - 2000-2006: Developed and used at Rational Discovery for building predictive models for ADME, Tox, biological activity
  - June 2006: Open-source (BSD license) release of software, Rational Discovery shuts down
  - to present: Open-source development continues, use within Novartis, contributions from Novartis back to open-source version

# The RDKit “ecosystem”



*Exact same algorithms/implementations accessible from many different endpoints*



# What can you do with it?

## *A laundry list*

- Input/Output: SMILES/SMARTS, SDF, TDT, SLN<sup>1</sup>, Corina mol2<sup>1</sup>
- “Cheminformatics”:
  - Substructure searching
  - Canonical SMILES
  - Chirality support (i.e. R/S or E/Z labeling)
  - Chemical transformations (e.g. remove matching substructures)
  - Chemical reactions
  - Molecular serialization (e.g. mol <-> text)
- 2D depiction, including constrained depiction
- 2D->3D conversion/conformational analysis via distance geometry
- UFF/MMFF implementations for cleaning up structures
- Fingerprinting:  
Daylight-like, atom pairs, topological torsions, Morgan algorithm, “MACCS keys”, etc.
- Similarity/diversity picking (including fuzzy similarity)
- 2D pharmacophores<sup>1</sup>
- Gasteiger-Marsili charges
- Hierarchical subgraph/fragment analysis
- RECAP and BRICS implementations
- Multi-molecule maximum common substructure<sup>2</sup>

<sup>1</sup> functional, but not great implementations

<sup>2</sup> Contribution from A. Dalke

# What can you do with it?

## *A laundry list, cntd*

- Feature maps
- Shape-based similarity
- Molecule-molecule alignment
- Shape-based alignment (subshape alignment) <sup>1</sup>
- Integration with PyMOL for 3D visualization
- Database integration
- Molecular descriptor library:
  - Topological ( $\kappa$ 3, Balaban J, etc.)
  - Electrotopological state (Estate)
  - clogP, MR (Wildman and Crippen approach)
  - “MOE like” VSA descriptors
  - Feature-map vectors
- Machine Learning:
  - Clustering (hierarchical)
  - Information theory (Shannon entropy, information gain, etc.)
  - Decision trees, *naïve Bayes*<sup>1</sup>, *kNN*<sup>1</sup>
  - Bagging, random forests
  - Infrastructure (data splitting, shuffling, enrichment plots, serializable models, etc.)
  - Support for standard python packages: pandas, scikit-learn

<sup>1</sup> *functional, but not great implementations*

# RDKit: Where is it?

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- Web page: <http://www.rdkit.org>
- github: code repository, bug tracker, downloads
  - <https://github.com/rdkit/rdkit>
- sourceforge: mailing lists, downloads
  - <http://sourceforge.net/projects/rdkit>
- Google code: wiki, downloads
  - <http://code.google.com/p/rdkit/>
- Releases: quarterly
- Licensing: new BSD
- Documentation:
  - HTML/PDF “Getting Started” documentation
  - in-code docs extracted by either doxygen (C++) or epydoc (python)
- Getting help:
  - Check the wiki and “Getting Started” document
  - The rdkit-discuss mailing list

# RDKit: Documentation?

## The documentation:

[The RDKit 2013.06.1 documentation](#) »

[next](#) | [index](#)

### The RDKit Documentation

- [An overview of the RDKit](#)
  - [What is it?](#)
  - [Functionality overview](#)
  - [The Contrib Directory](#)
  - [License](#)
- [Installation](#)
  - [Linux and the Mac](#)
    - [Installation from repositories](#)
      - [Ubuntu 12.04 and later](#)
      - [Fedora, CentOS, and RHEL](#)
      - [MacOS](#)
    - [Building from Source](#)
      - [Prerequisites](#)
      - [Building the RDKit](#)
      - [Testing the build \(optional, but recommended\)](#)
      - [Advanced](#)
      - [Frequently Encountered Problems](#)
  - [Windows](#)



Open-Source Cheminformatics  
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#### Table Of Contents

[An overview of the RDKit](#)  
[Installation](#)  
[Getting Started with the RDKit in Python](#)  
[The RDKit Book](#)  
[RDKit Cookbook](#)  
[The RDKit database cartridge](#)

[Next topic](#)

Built using Python's standard docs tool: Sphinx

# RDKit: Documentation?

## Sample section from introductory docs:

### Reading and Writing Molecules

#### Reading single molecules

The majority of the basic molecular functionality is found in module [rdkit.Chem](#):

```
>>> from rdkit import Chem
```

Individual molecules can be constructed using a variety of approaches:

```
>>> m = Chem.MolFromSmiles('Cc1ccccc1')
>>> m = Chem.MolFromMolFile('data/input.mol')
>>> stringWithMolData=file('data/input.mol','r').read()
>>> m = Chem.MolFromMolBlock(stringWithMolData)
```

All of these functions return a [Mol](#) object on success:

```
>>> m
<rdkit.Chem.rdchem.Mol object at 0x...>
```

#### Molecules

- Working with Molecules
- Substructure Searching
- Fingerprinting and Molecular Similarity
- Descriptor Calculation
- Chemical Reactions
- Chemical Features and Pharmacophores
- Molecular Fragments
- Non-Chemical Functionality
- Getting Help
- Advanced Topics/Warnings
- Miscellaneous Tips and Hints
- List of Available Descriptors
- List of Available Fingerprints
- Feature Definitions Used in the Morgan Fingerprints
- License

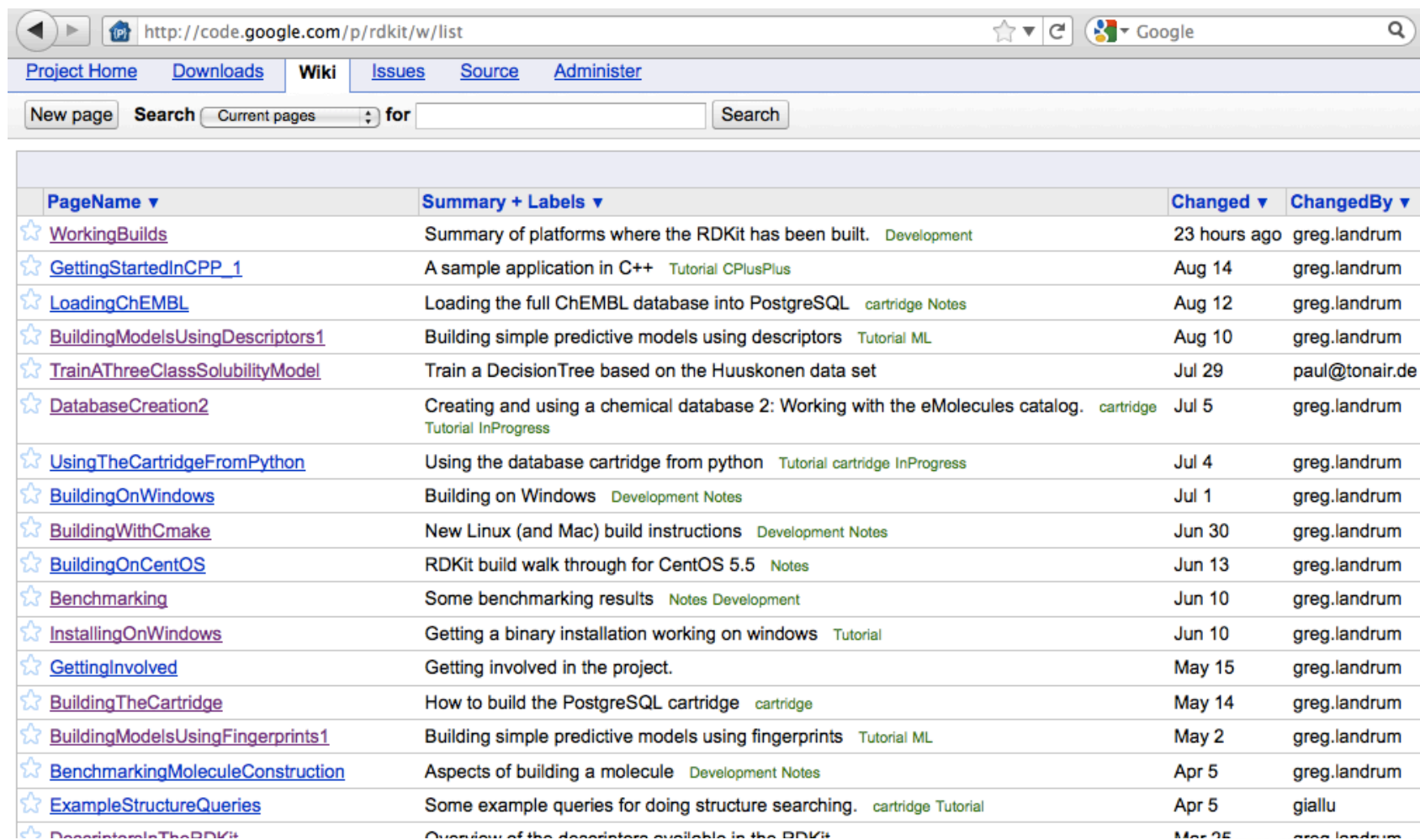
The RDKit Book

[Previous topic](#)

Note: docs that include python code snippets are *tested*.

# RDKit: Documentation?

The wiki: <http://code.google.com/p/rdkit/w/list>



The screenshot shows a web browser window with the address bar displaying <http://code.google.com/p/rdkit/w/list>. The page has a navigation bar with links: Project Home, Downloads, Wiki, Issues, Source, and Administer. Below the navigation bar is a search section with a 'New page' button, a 'Search' button, a text input field containing 'Current pages', and another 'Search' button. The main content is a table listing wiki pages.

PageName ▼	Summary + Labels ▼	Changed ▼	ChangedBy ▼
<a href="#">WorkingBuilds</a>	Summary of platforms where the RDKit has been built. <span>Development</span>	23 hours ago	greg.landrum
<a href="#">GettingStartedInCPP_1</a>	A sample application in C++ <span>Tutorial CPlusPlus</span>	Aug 14	greg.landrum
<a href="#">LoadingChEMBL</a>	Loading the full ChEMBL database into PostgreSQL <span>cartridge Notes</span>	Aug 12	greg.landrum
<a href="#">BuildingModelsUsingDescriptors1</a>	Building simple predictive models using descriptors <span>Tutorial ML</span>	Aug 10	greg.landrum
<a href="#">TrainAThreeClassSolubilityModel</a>	Train a DecisionTree based on the Huuskonen data set	Jul 29	paul@tonair.de
<a href="#">DatabaseCreation2</a>	Creating and using a chemical database 2: Working with the eMolecules catalog. <span>cartridge Tutorial InProgress</span>	Jul 5	greg.landrum
<a href="#">UsingTheCartridgeFromPython</a>	Using the database cartridge from python <span>Tutorial cartridge InProgress</span>	Jul 4	greg.landrum
<a href="#">BuildingOnWindows</a>	Building on Windows <span>Development Notes</span>	Jul 1	greg.landrum
<a href="#">BuildingWithCmake</a>	New Linux (and Mac) build instructions <span>Development Notes</span>	Jun 30	greg.landrum
<a href="#">BuildingOnCentOS</a>	RDKit build walk through for CentOS 5.5 <span>Notes</span>	Jun 13	greg.landrum
<a href="#">Benchmarking</a>	Some benchmarking results <span>Notes Development</span>	Jun 10	greg.landrum
<a href="#">InstallingOnWindows</a>	Getting a binary installation working on windows <span>Tutorial</span>	Jun 10	greg.landrum
<a href="#">GettingInvolved</a>	Getting involved in the project.	May 15	greg.landrum
<a href="#">BuildingTheCartridge</a>	How to build the PostgreSQL cartridge <span>cartridge</span>	May 14	greg.landrum
<a href="#">BuildingModelsUsingFingerprints1</a>	Building simple predictive models using fingerprints <span>Tutorial ML</span>	May 2	greg.landrum
<a href="#">BenchmarkingMoleculeConstruction</a>	Aspects of building a molecule <span>Development Notes</span>	Apr 5	greg.landrum
<a href="#">ExampleStructureQueries</a>	Some example queries for doing structure searching. <span>cartridge Tutorial</span>	Apr 5	giallu
<a href="#">DescribingTheRDKit</a>	Overview of the descriptors available in the RDKit	Mar 25	greg.landrum

## RDKit: Documentation?

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The documents that come out of the tutorials here are going to be another good source of information

# RDKit: Who is using it?

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- Hard to say with any certainty
- ~500 downloads of each new version
- Active contributors to the mailing list from:
  - Big pharma
  - Small pharma/biotech
  - Software/Services
  - Academia
- Starting to see contributions coming from the community (wiki pages, code patches, changes to the build system, etc.) as well as active use in other systems.
- Community contributions for packaging:
  - rpms/debs for Fedora/Debian linux
  - homebrew recipe for MacOS



# Sustainability of the RDKit

*... thinking about the bus problem*

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- This clearly isn't just a hobby project any more
- Used internally in NIBR in multiple production systems
- Contributions coming in from outside
- I'm no longer the only one answering questions on the mailing list

# Switch to notebook

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# Overview

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- History
- Where are we today?
- **What next?**

# What's next?

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- We'll decide some of that here in the round-table session and discussions
- Obvious candidates:
  - Further performance improvements
  - Improved documentation
  - Move more code into C++ (allows access from Knime and the cartridge)
  - Better packaging

# Presentations, tutorials, notes, data, etc.

[https://github.com/rdkit/UGM\\_2013](https://github.com/rdkit/UGM_2013)

Please do pull requests or just send me materials

