

One central tool for Chemoinformatic

RDKIT UGM 2016

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Firmenich an family 120 year old company



10 year ago, I started as PostDoc

Introduce RDKit 7 years ago in my group



One central tool to do what?

- Read molecules (sdf, smi, canonical smiles,...)
- Flexible descriptors
- Optimized 3D & SCF
- MMFF94 (rdkit, conformers)
- AM1 (mopac, molds)
- PM3/6 (mopac)
- Get Mulliken charges
- Get 3D descriptors:
- Dragon like
- Get Fingerprints:
- Neural networks FP
- Save Data:
- MySQL, ORACLE, files, Matlab,...



Why RDKit?

- Very flexible
- Very supported
- Very Stable
- Very cheap ;-)
- BONUS: Already large toolkit functions
- And...



In progress on my fork

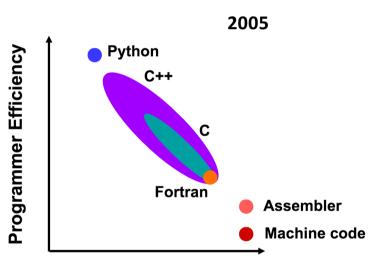
- 3D Descriptors port from Dragon to RDKit:
- 3D autocorrelations (done)
- GETAWAY (done)
- RDF (done)
- Morse (done)
- WHIM (in progress)



Language vs speed coding vs speed processing

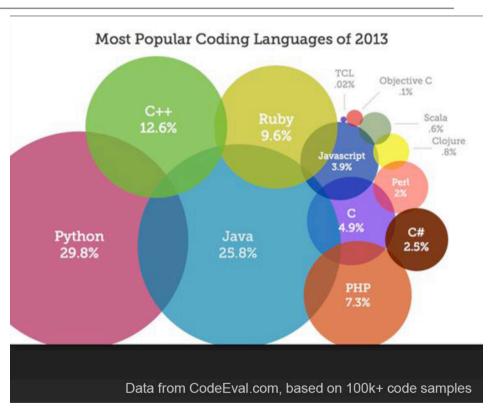
Programmer Efficiency & Performance





Performance

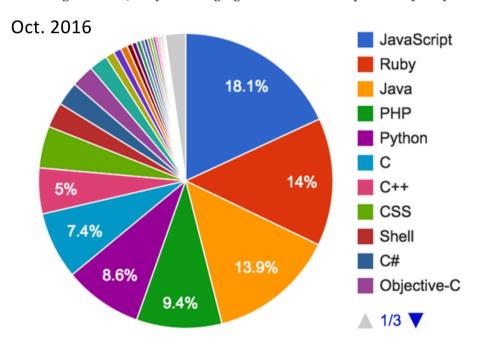
Source: Spectrum of languages Ralf W. Grosse-Kunstleve Computational ...





Future...

According to GitHub, every other language has lost to JavaScript and not just Python.





RDKit.js implementation

Code hosted on friend group at EPFL:

https://github.com/cheminfo/RDKitjs

- In Hibernation:
- Waiting WebAssembly for performance
- http://webassembly.org/stepbystep/
- It's coming ... but





... A more complex challenge

Fast semi empirical for Charges Mulliken distribution and/or 3D geometry conformers

- Initial works on molds opensource package ...
 - Implementing new Atoms not on the original code (P,S,Br,I)
 - Comparing Mopac vs Molds with new Atoms vs RDKit MMFF94 (not stable and slow)
- Go back to basic Indo / cndo / mndo fortran:
 - Open source Fortran available but from divers sources
 - Wrapping fortran in C++ to avoid passing parameters and x,y,z in files

Thanks you!

Thanks you!

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