



# HORTON & ChemTools



---

Farnaz Heidar-Zadeh, Paul Ayers, Toon Verstraelen, Esteban Vohringer, Carlos Cardenas,...

So theory guys have got it made  
in rooms free of pollution.  
Instead of problems with the reflux,  
they have only solutions...  
In other words, experimentalists  
will likely die of cancer  
From working hard, yet fruitlessly,  
till theory gives the answer.

Thomas A. Holme



# HORTON & ChemTools





# HORTON quantum chemistry package

---

Helpful Open-source Research TOol for N-electron systems

- Free & open-source electronic structure code with a strictly modular design.
- Motivated by the difficulty to add new features to the existing quantum chemistry programs.
- Written primarily in Python 3, with C++/Fortran only where necessary for computational performance.
- Computationally efficient enough to be helpful, without compromising code-readability and user-friendliness.
- Well-tested, well-documented, and follows modern “best practices” for software engineering.
- Helpful for prototyping, developing, and exploring new methods!
- [quantumelephant.org](http://quantumelephant.org)

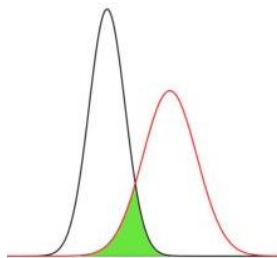
## iodata

```

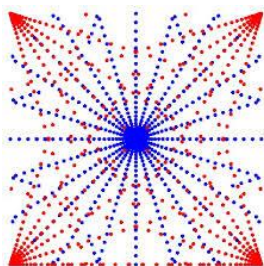
Title Card Required
O 1
N 0.00000000 -0.00000000 -0.11132391
H 0.82002539 -0.47344188 0.25975578
H -0.82002539 -0.47344188 0.25975578
H -0.00000000 0.94688376 0.25975578
X 0.00000000 -0.00000000 -1.11132391

1 3 1.0 4 1.0 2 1.0
2
3
4
    
```

## gbasis



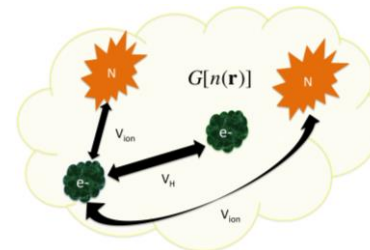
## grid



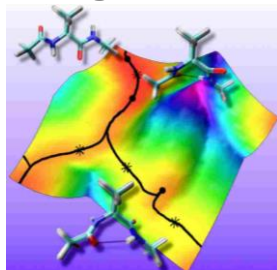
HORTON

MODULES

## meanfield



## gopt



## postscf

$$\begin{aligned}
 0 &= \langle \psi | \hat{H} | \psi \rangle + \langle \psi | \hat{H} | \psi \rangle^* + \langle \psi | \hat{H} | \psi \rangle^* \\
 &+ \langle \psi | \hat{H} | \psi \rangle + \langle \psi | \hat{H} | \psi \rangle + \langle \psi | \hat{H} | \psi \rangle \\
 &+ \langle \psi | \hat{H} | \psi \rangle + \langle \psi | \hat{H} | \psi \rangle
 \end{aligned}$$



# GAIN CHEMICAL INSIGHT FROM COMPUTATIONS





# GAIN CHEMICAL INSIGHT FROM COMPUTATIONS

- ✧ **Free & open-source** Python package for interpreting the results of quantum chemistry calculations!
- ✧ **Easy-to-use core functionality** to compute fundamental descriptors of conceptual quantum chemistry, together with a **flexible set of utilities to easily test your ideas!**
- ✧ Readable, well-documented, well-tested & user-friendly.
- ✧ ChemTools can be used as:
  - Python Library
  - Python Scripts (command line)
- ✧ Release Date: June 2019, Visit: [chemtools.org](https://chemtools.org)
- ✧ Examples and installation instructions (click on “material”)  
[https://wiki.lct.jussieu.fr/workshop/index.php/ChemTools\\_Workshop\\_2019](https://wiki.lct.jussieu.fr/workshop/index.php/ChemTools_Workshop_2019)

# Command-Line Functionality

```
$ chemtools -h
```

```
usage: chemtools [-h] [-v] <Commands> ...
```

ChemTools command-line tools

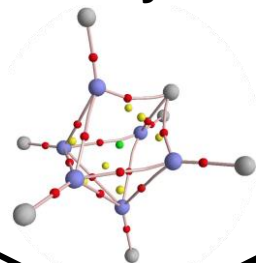
positional arguments:

<Commands>	<Functions>
mot	Molecular Orbital Theory (MOT).
esp	Electrostatic Potential (ESP).
nci	Non-Covalent Interactions (NCI).
elf	Electron Localization Function (ELF).
lol	Localized Orbital Locator (LOL).
gcdft	Global Conceptual DFT.
lcdft	Local Conceptual DFT.
ccdft	Condensed Conceptual DFT.

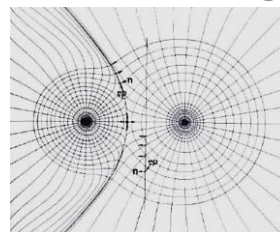
optional arguments:

-h, --help	show this help message and exit
-v, --version	show program's version number and exit

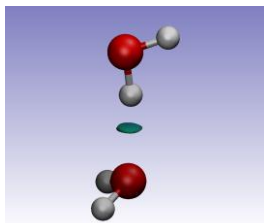
## Topological Analysis



## AIM Partitioning

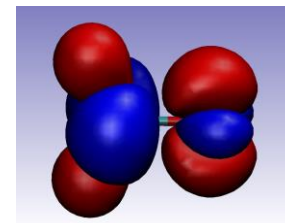


## DFT-Based Descriptors

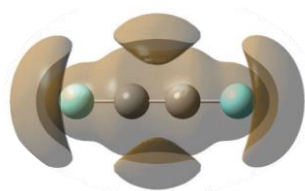


## MODULES

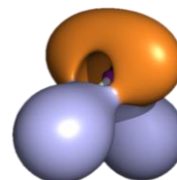
## Conceptual DFT



## Density Matrix Analysis



## Orbital-Based Descriptors



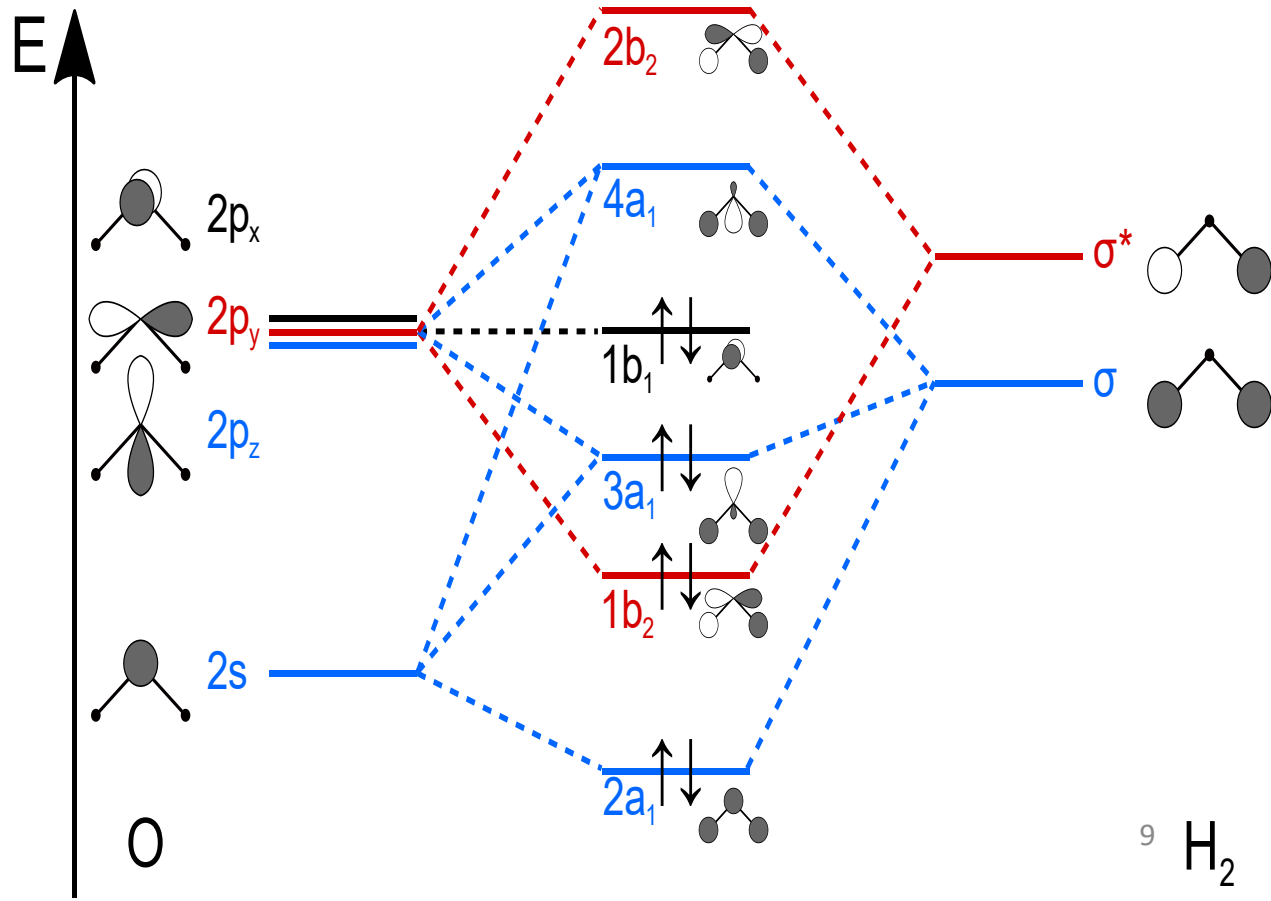




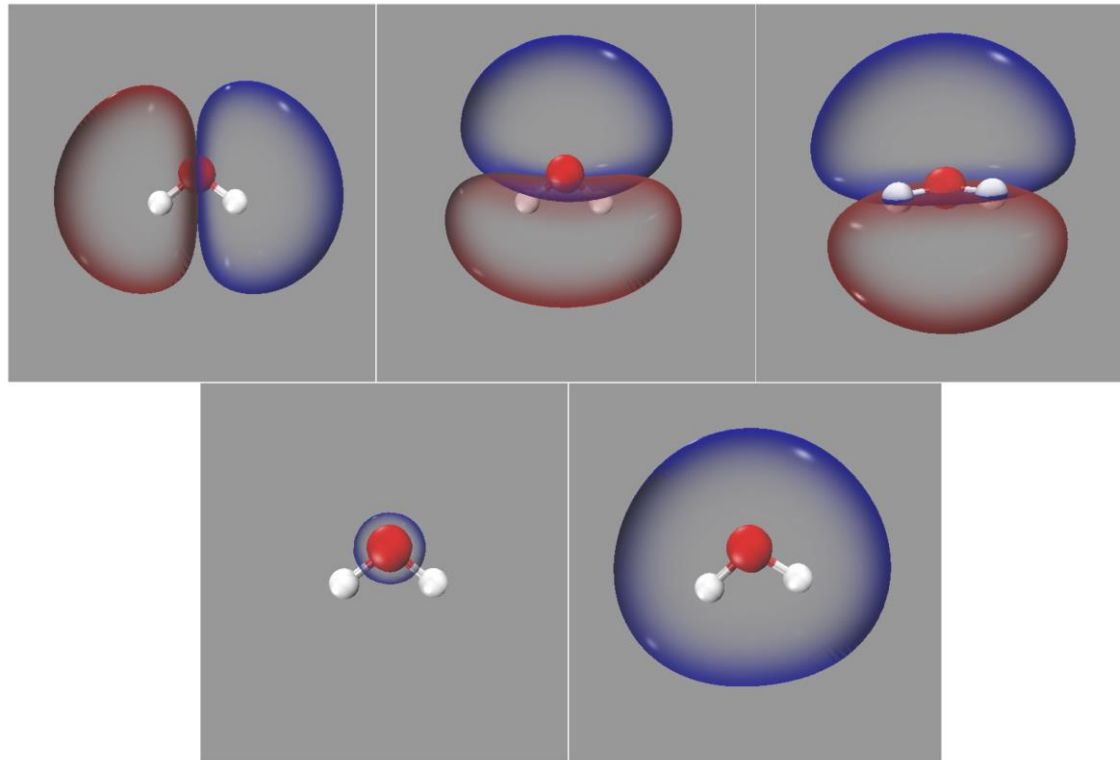
# Included & Planned Features

## Molecular Orbital Theory (MOT) Descriptors and Analysis

- Orbital Energies; Visualize Orbitals
- Draw MO diagram with AO contributions/energies.
- Mulliken, Lowdin, Ruedenberg, Knizia population/bonding analysis.
- Localized Orbitals
- Oxidation states



# Molecular Orbital Theory (MOT)



\$ chemtools **mot** -h

Visualize Molecular Orbitals (MO) using VMD package.

The generated files include:

output.vmd	The VMD script.
output_mo{index}.cube	The MO cube file.

If VMD is setup on your system, you can visualize MO with the command below:

```
$ vmd -e output.vmd
```

Note: The output.vmd script requires output\_mo{index}.cube to plot MO in VMD software (they files should be all in the same directory).

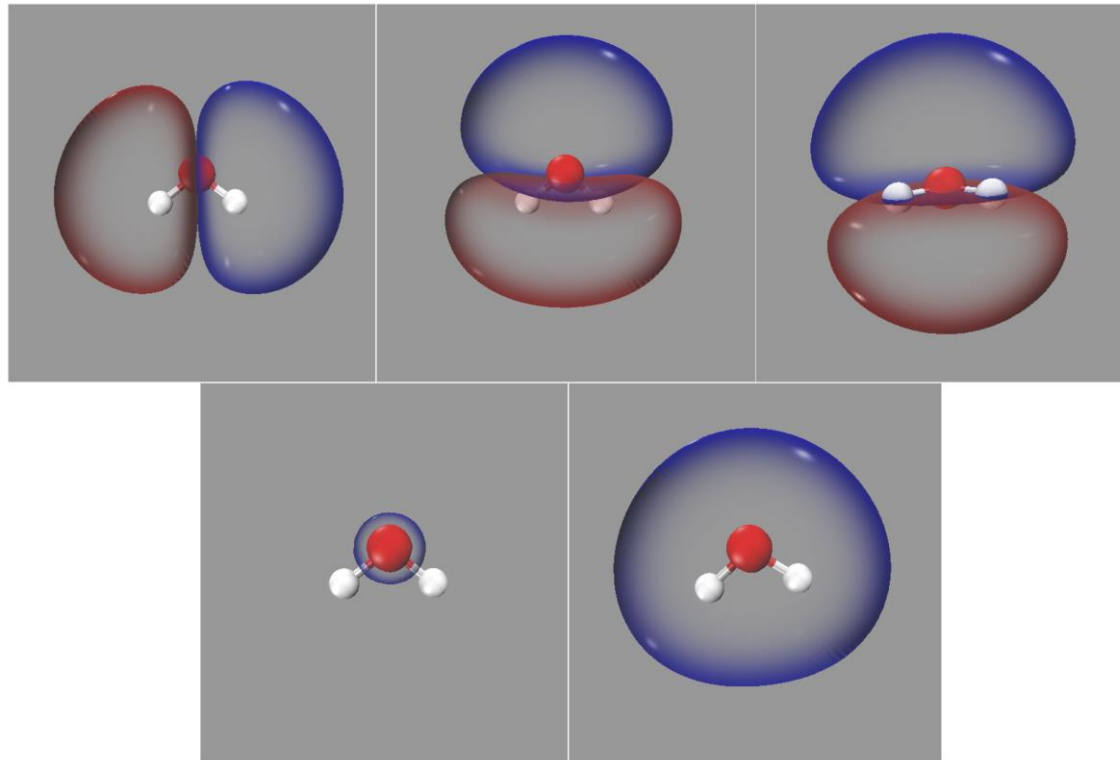
positional arguments:

fname	wave-function file. Supported formats: fchk, mkl, molden.input, wfn.
-------	--

optional arguments:

-h, --help	show this help message and exit
--output OUTPUT	name of generated cube file and vmd script. If None, the output name is derived from fname. [default=None]
--info	print basic information on molecule and wave-function. [default=False]
--spin {a,b}	type of occupied spin orbitals to visualize. [default=a]
--index INDEX	index of spin orbital to visualize represented by comma separated integers. If None, files for generating all occupied molecular orbitals are generated. [default=None]
--cube N	specify the cubic grid used for visualizing MO. This can be either a cube file with .cube extension, or a user-defined cubic grid specified by spacing and extension parameters separated by a comma. For example, 0.2,5.0 which specifies 0.2 a.u. distance between grid points, and 5.0 a.u. extension of cubic grid on each side of the molecule. This cube is used for evaluating MO and visualizing it using VMD program. [default=0.2,5.0]
--isosurface ISOSURFACE	iso-surface value of MO to visualize. [default=0.05]

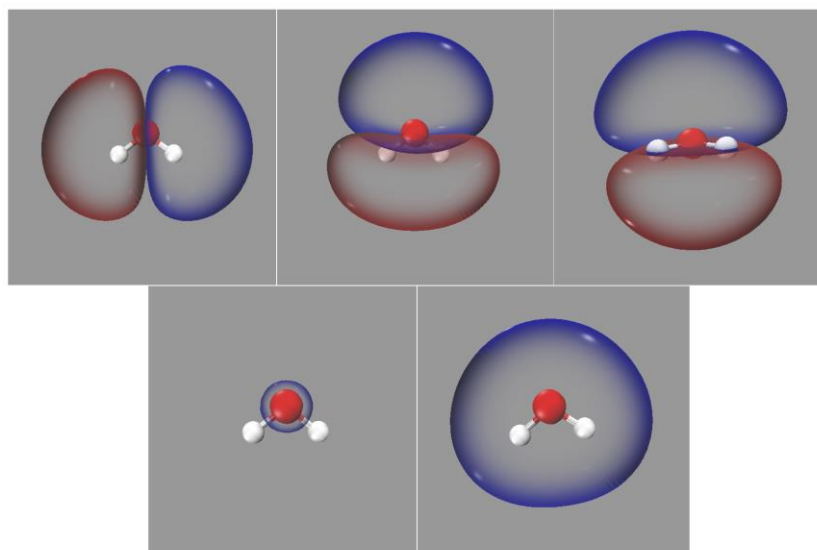
# Molecular Orbital Theory (MOT)



\$ chemtools **mot** -h

\$ chemtools **mot** h2o.fchk

# Molecular Orbital Theory (MOT)



```
from chemtools import MOTBasedTool
```

```
# 1. Build MO Theory model
```

```
mo = MOTBasedTool.from_file('h2o.fchk')
```

```
# 2. Generate cube file(s) and script(s) for visualizing all MO
```

```
# Files generated are h2o_mo{index}.cube & h2o_mo{index}.vmd
```

```
# To visualize the iso-surface, use command: $ vmd -e h2o_mo{index}.vmd
```

```
mo.generate_scripts('h2o', spin='a', index=None, isosurf=0.0045)
```

# Molecular Orbital Theory (MOT)

```
$ chemtools mot h2o.fchk --info
```

**File: h2o.fchk**

**Atomic number and coordinates:**

<b>8</b>	<b>0.015948</b>	<b>0.017004</b>	<b>0.023858</b>
<b>1</b>	<b>-0.772778</b>	<b>0.561447</b>	<b>1.575012</b>
<b>1</b>	<b>1.298501</b>	<b>1.269512</b>	<b>-0.309113</b>

**Information on alpha & beta electrons:**

<b># electrons</b>	<b>:</b>	<b>5.000</b>	<b>5.000</b>
<b>HOMO index</b>	<b>:</b>	<b>5</b>	<b>5</b>

<b>LUMO+2 index</b>	<b>:</b>	<b>0.100079</b>	<b>0.100079</b>
<b>LUMO+1 energy</b>	<b>:</b>	<b>0.022530</b>	<b>0.022530</b>
<b>LUMO energy</b>	<b>:</b>	<b>-0.024957</b>	<b>-0.024957</b>
<b>HOMO energy</b>	<b>:</b>	<b>-0.323152</b>	<b>-0.323152</b>
<b>HOMO-1 energy</b>	<b>:</b>	<b>-0.399455</b>	<b>-0.399455</b>
<b>HOMO-2 energy</b>	<b>:</b>	<b>-0.539610</b>	<b>-0.539610</b>



# Included & Planned Features

---

## Density-Based Descriptors

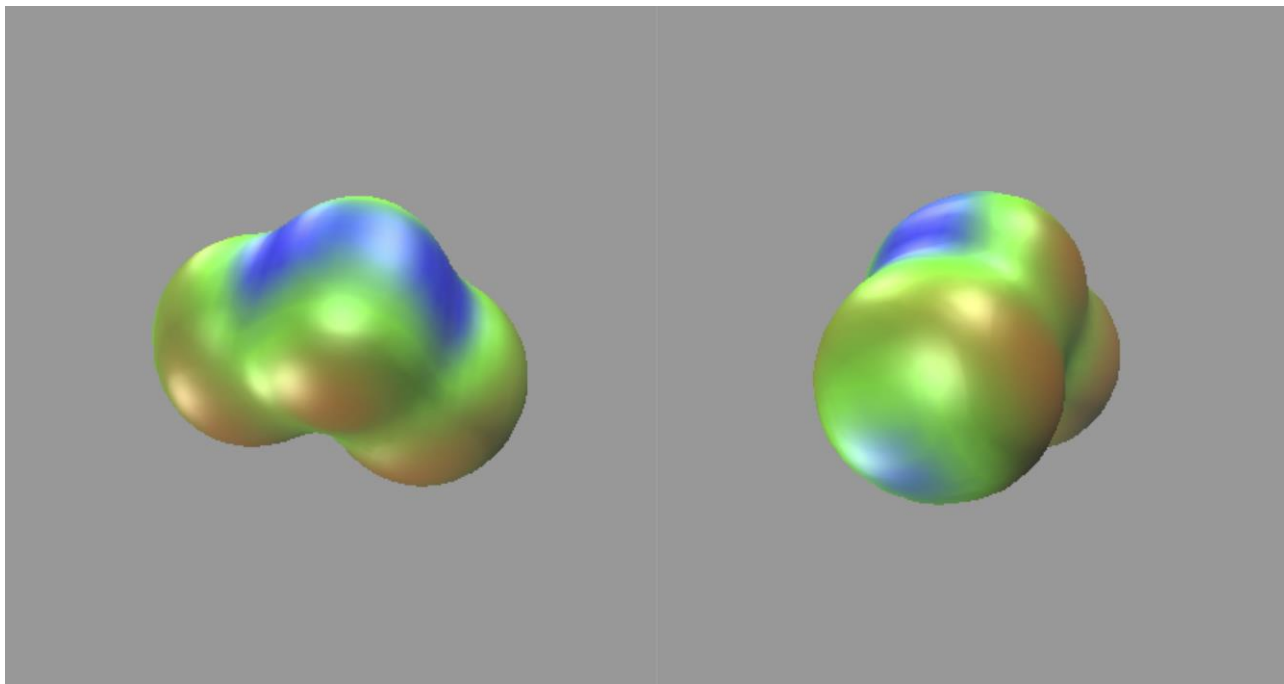
- reduced gradient; Laplacian, arbitrary-order derivatives of electron density and one-electron reduced density-matrix (1DM).
- Information-theoretic descriptors
- Electrostatic potential
- Density-based energy decomposition analysis
- Constrained Quantum Chemistry (and DFT) Analysis

## Electrostatic Potential

- Positive values associated with electrophilic molecular regions
- Negative values associated with nucleophilic molecular regions

$$\Phi(\mathbf{r}) = \sum_{A=1}^{N_{\text{atoms}}} \frac{Z_A}{|\mathbf{r} - \mathbf{R}_A|} - \int \frac{\rho(\mathbf{r}')}{|\mathbf{r} - \mathbf{r}'|} d\mathbf{r}'$$

# Electrostatic Potential (ESP)

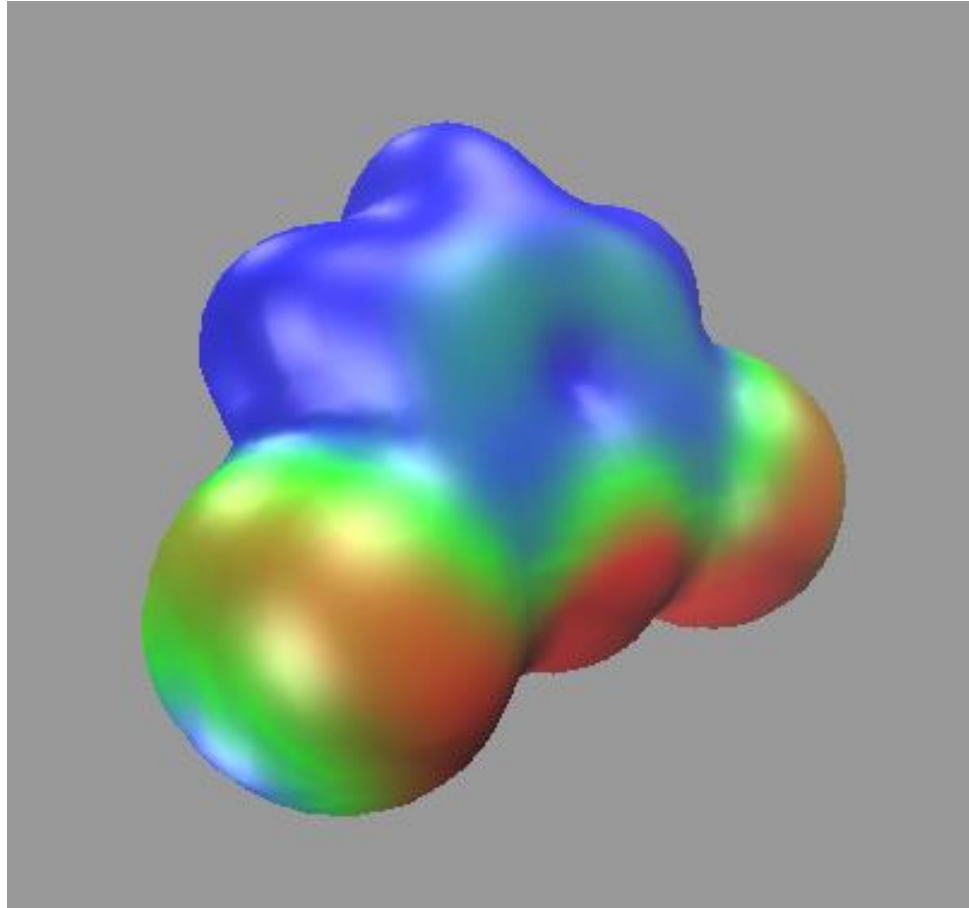
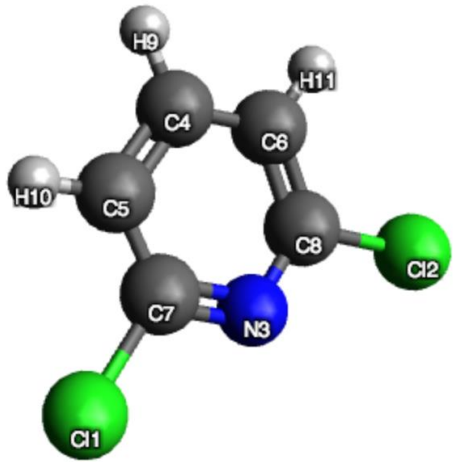


```
$ chemtools esp -h
```

```
$ chemtools esp sc12.fchk --isosurface=0.002
```



# Electrostatic Potential (ESP)



[Python Script & Jupyter Notebooks](#)



# Included & Planned Features

---

## (DFT-based) Descriptors for bonding and nonbonding molecular interactions

- ELF: Electron Localization Function
- LOL: Localized Orbital Locator
- **DORI: Density Overlap Region Indicator**
- Local Kinetic Energy
- **Slater Potential**, Ehrenfest Force, Stress Tensor
- NCI: Non-Covalent Interaction (reduced density gradient)

In general, these tools consist of a fundamental descriptor,  $\xi(\mathbf{r})$ , which is then transformed onto a convenient interval for visualization. ChemTools provides access to the (raw) fundamental descriptors and a variety of useful mappings:

$$x_a^{(k)}(\xi) = \frac{1}{1 + a\xi^k}$$

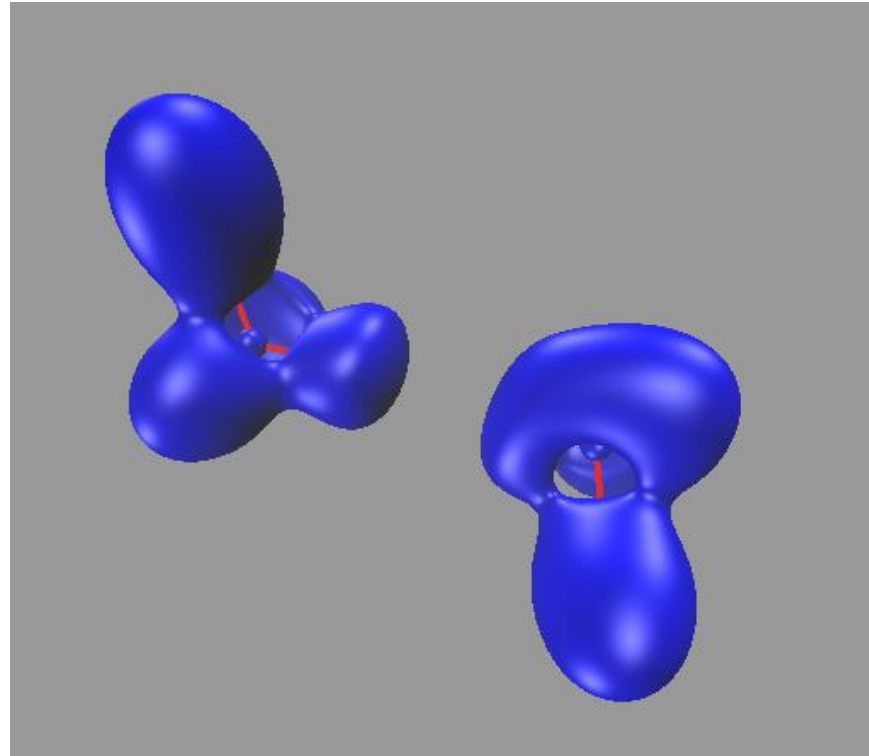
$$\tilde{x}_a^{(k)}(\xi) = 1 - x_a^{(k)}(\xi)$$

$$v_a^{(k)}(\xi) \equiv \frac{1}{2} \left( 1 + \tanh \left( a \left( \xi^{-k} - \xi^k \right) \right) \right)$$

$$\tilde{v}_a^{(k)}(\xi) \equiv \frac{1}{2} \left( 1 + \tanh \left( a \left( \xi^k - \xi^{-k} \right) \right) \right)$$

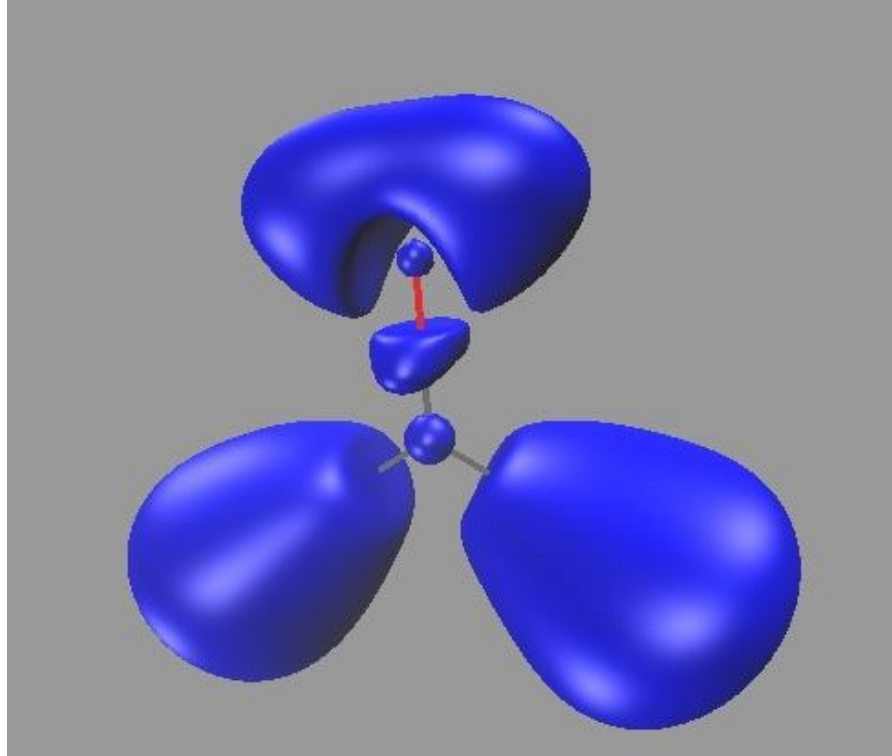
$$w_a(\xi) = \frac{1}{2} \left( 1 + \tanh(a\xi) \right)$$

# Electron Localization Function (ELF)



```
$ chemtools elf -h
```

```
$ chemtools elf h2o_dimer.fchk
```



```
from chemtools import ELF
```

```
# 1. Build ELF model
```

```
elf = ELF.from_file('ch2o_q+0.fchk', trans='rational', trans_k=2, trans_a=1)
```

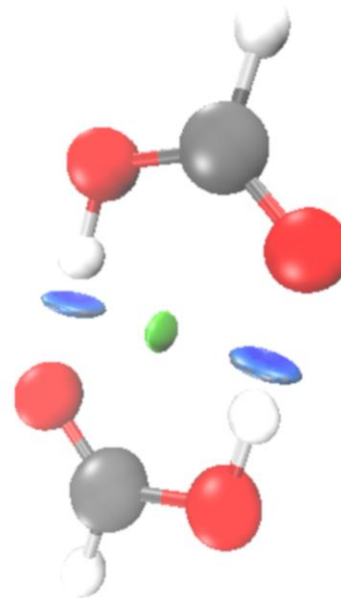
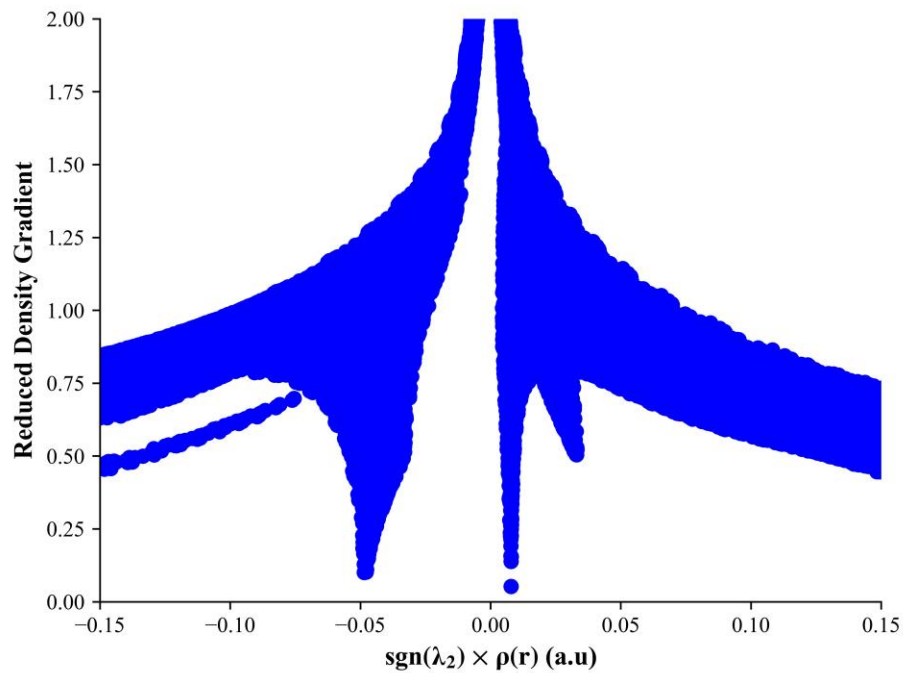
```
# 2. Generate cube file(s) and script for visualizing ELF
```

```
# Files generated are ch2o_q+0-elf.cube & ch2o_q+0.vmd
```

```
# To visualize the iso-surface, use command: $ vmd -e ch2o_q+0.vmd
```

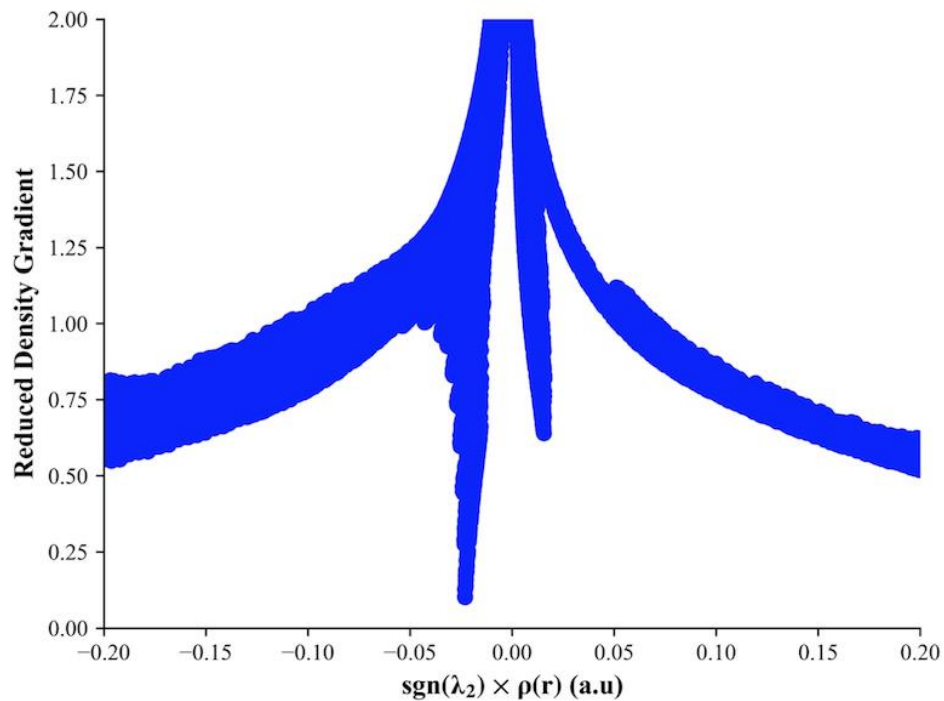
```
elf.generate_scripts('ch2o_q+0', isosurf=0.8)
```

# Non-Covalent Interactions (NCI)



```
$ chemtools nci -h
```

```
$ chemtools nci formic_acid_dimer.fchk
```



```
from chemtools import NCI
```

```
# 1. Build NCI model
```

```
nci = NCI.from_file('h2o_dimer.fchk')
```

```
# 2. Generate plot, cube file(s) and script for visualizing NCI
```

```
# Files generated are h2o_dimer-dens.cube, h2o_dimer-grad.cube, & h2o_dimer.vmd
```

```
# To visualize the iso-surface, use command: $ vmd -e h2o_dimer.vmd
```

```
nci.generate_plot('h2o_dimer')
```

```
nci.generate_scripts('h2o_dimer')
```



# Included & Planned Features

---

## Conceptual DFT Descriptors

- global, (non-)local, & condensed descriptors of arbitrary order
- popular & general (user-defined) energy models (symbolically)
- spin-reactivity indicators
- isomorphic ensemble tools (local hardness, hardness kernel, etc.)
- alchemical energies, responses, and potentials.

**Key Idea:** Chemical reactivity can be understood by studying how molecules respond to changes in the number of electrons and external potential.

[https://chemtools.org/sci\\_doc\\_conceptual.html](https://chemtools.org/sci_doc_conceptual.html)

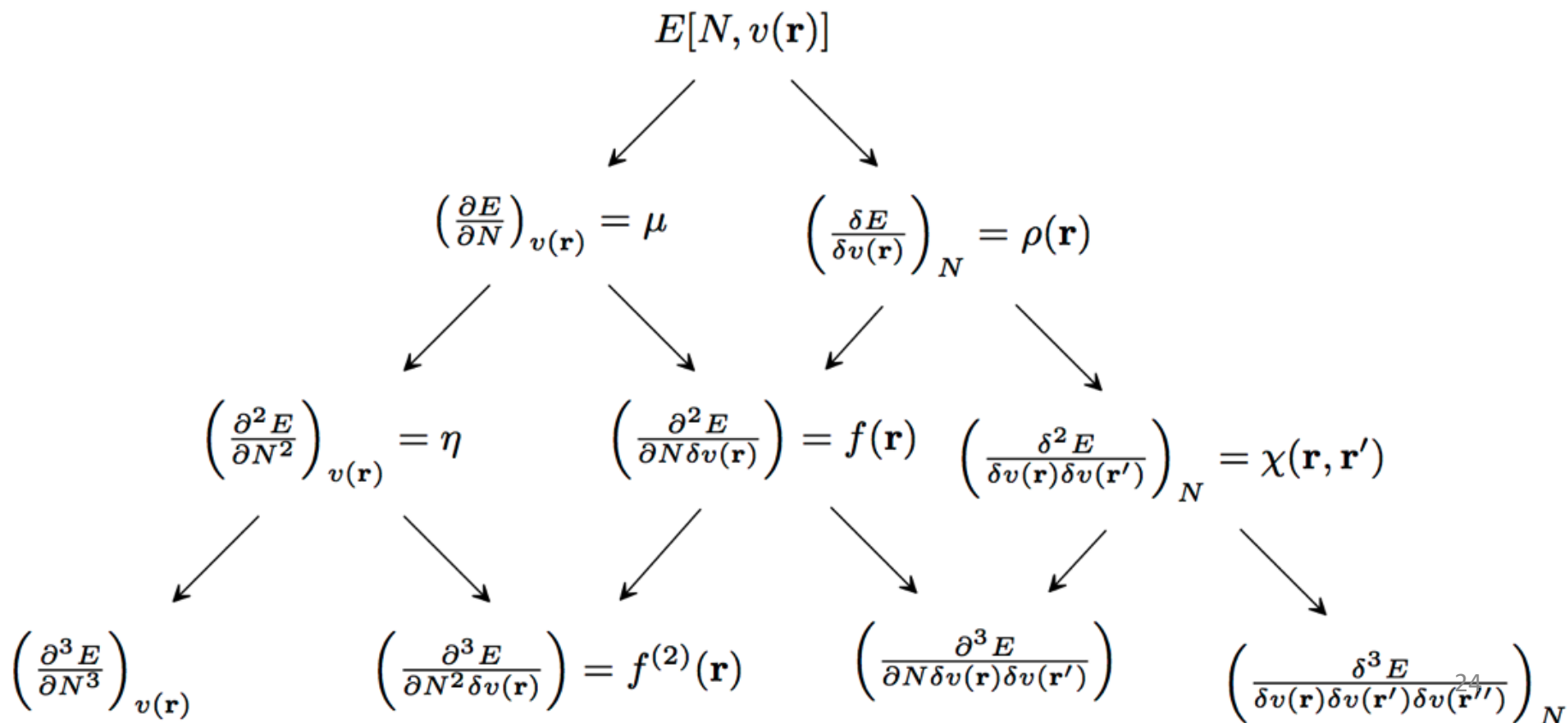
**Key Reactivity Indicators:** Response functions. Understanding how the energy changes as the number of electrons changes requires an energy model and data about the energy for different numbers of electrons.



# Included & Planned Features

## Conceptual DFT Descriptors

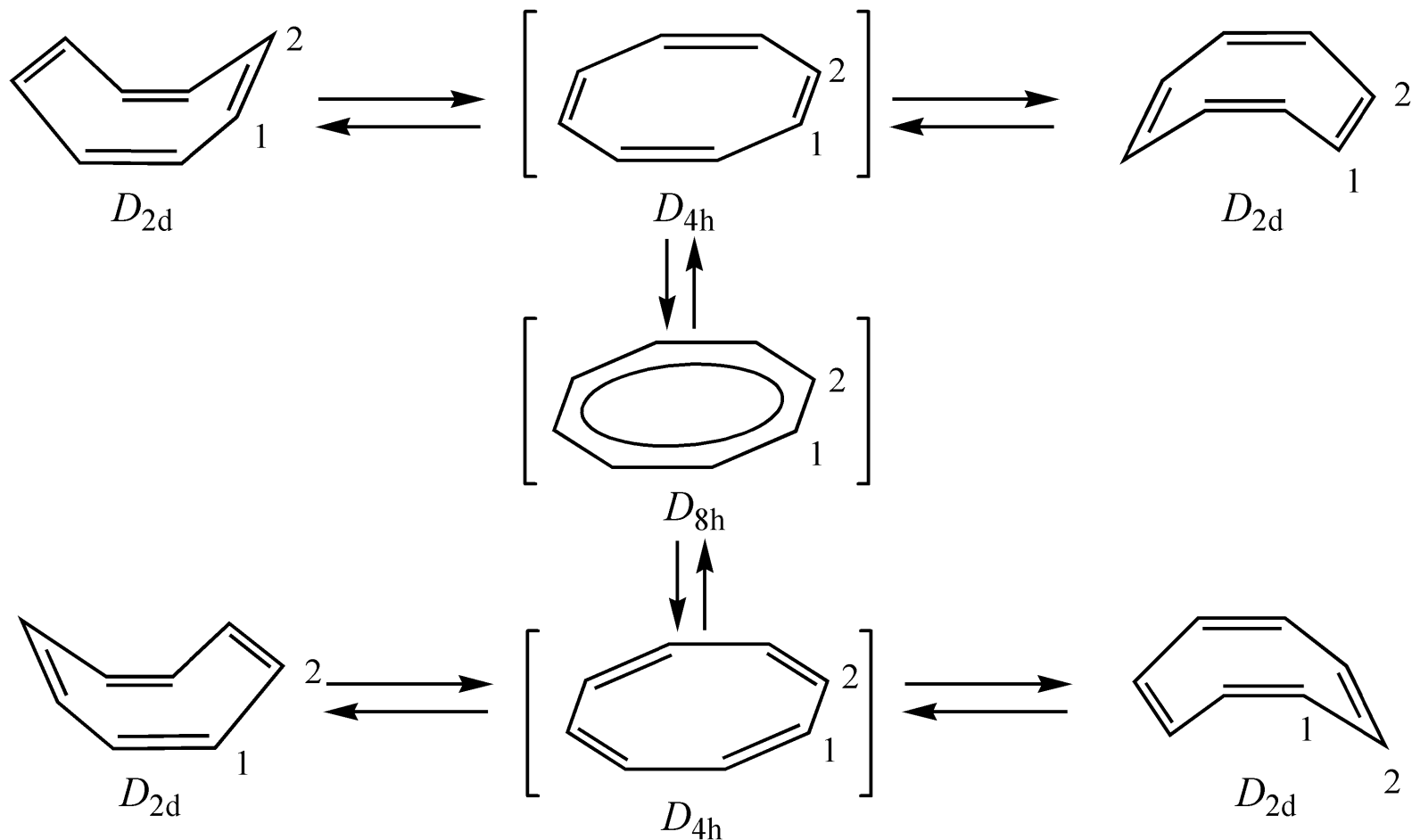
- global, (non-)local, & condensed descriptors of arbitrary order
- popular & general (user-defined) energy models (symbolically)
- alchemical energies, responses, and potentials.





# Global Conceptual DFT

(cyclooctatetraene Jahn-Teller distortion)

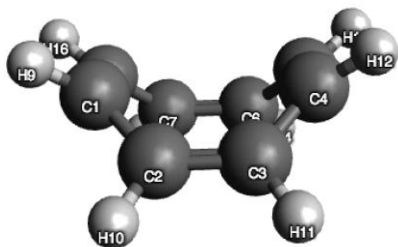


# Global Conceptual DFT

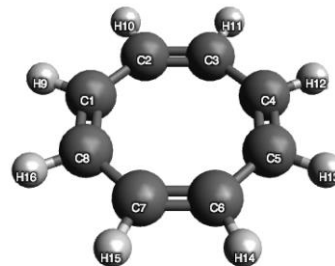
(Frontier Molecular Orbital Approach)

```
$ chemtools gcdft quadratic cyclooctatetraene_planer_q+0.fchk  
$ chemtools gcdft quadratic cyclooctatetraene_boat_q+0.fchk
```

chemical_hardness	0.155428
chemical_potential	-0.140308
ea	0.062594
electrofugality	0.281352
electron_affinity	0.062594
electronegativity	0.140308
electrophilicity	0.063329
eta	0.155428
ionization_potential	0.218022
ip	0.218022
mu	-0.140308
n0	56.000000
n_max	56.902721
nucleofugality	0.000735
softness	6.433845



chemical_hardness	0.085737
chemical_potential	-0.152984
ea	0.110116
electrofugality	0.332341
electron_affinity	0.110116
electronegativity	0.152984
electrophilicity	0.136489
eta	0.085737
ionization_potential	0.195852
ip	0.195852
mu	-0.152984
n0	56.000000
n_max	57.784350
nucleofugality	-0.026373
softness	11.663633

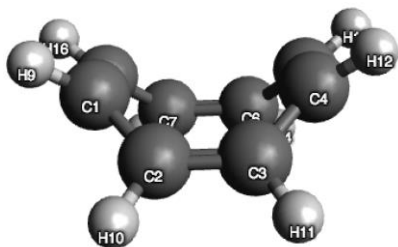


# Global Conceptual DFT

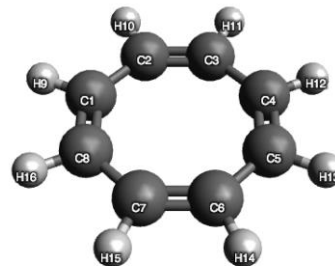
(Finite Difference Approach)

```
$ chemtools gcdft quadratic cyclooctatetraene_planer_q*.fchk  
$ chemtools gcdft quadratic cyclooctatetraene_boat_q*.fchk
```

chemical_hardness	0.294339
chemical_potential	-0.142420
ea	-0.004749
electrofugality	0.324046
electron_affinity	-0.004749
electronegativity	0.142420
electrophilicity	0.034456
eta	0.294339
ionization_potential	0.289590
ip	0.289590
mu	-0.142420
n0	56.000000
n_max	56.483864
nucleofugality	0.039205
softness	3.397441



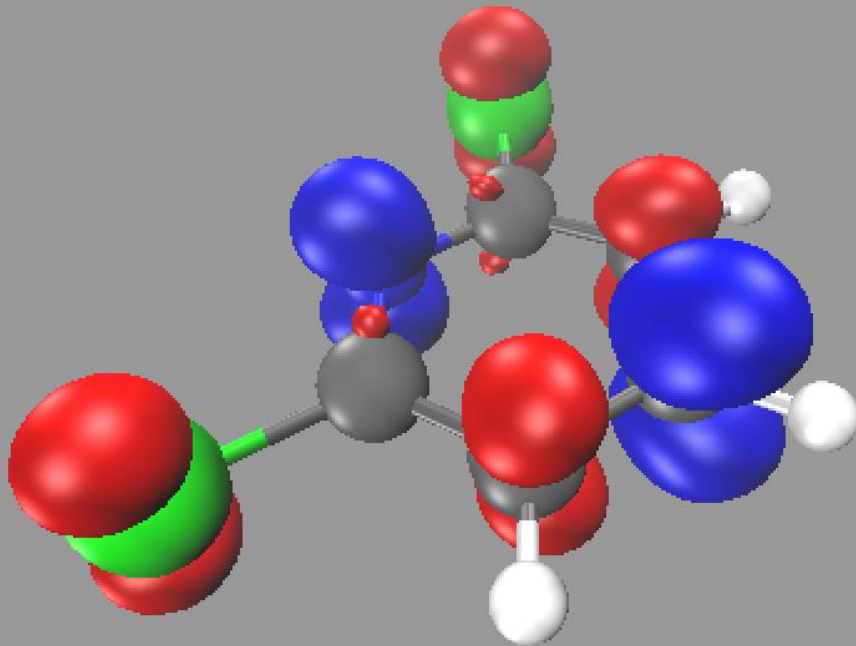
chemical_hardness	0.223606
chemical_potential	-0.154832
ea	0.043029
electrofugality	0.320240
electron_affinity	0.043029
electronegativity	0.154832
electrophilicity	0.053605
eta	0.223606
ionization_potential	0.266635
ip	0.266635
mu	-0.154832
n0	56.000000
n_max	56.692431
nucleofugality	0.010576
softness	4.472143



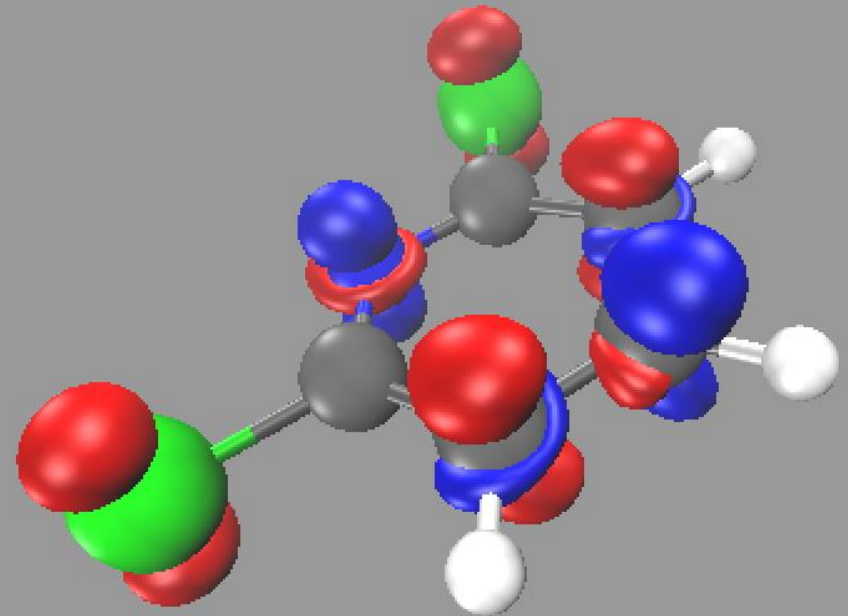
# Local Conceptual DFT

(Dual Descriptor)

```
$ chemtools lcdft quadratic dual dichloropyridine_q+0.fchk  
$ chemtools lcdft quadratic dual dichloropyridine_q*.fchk
```

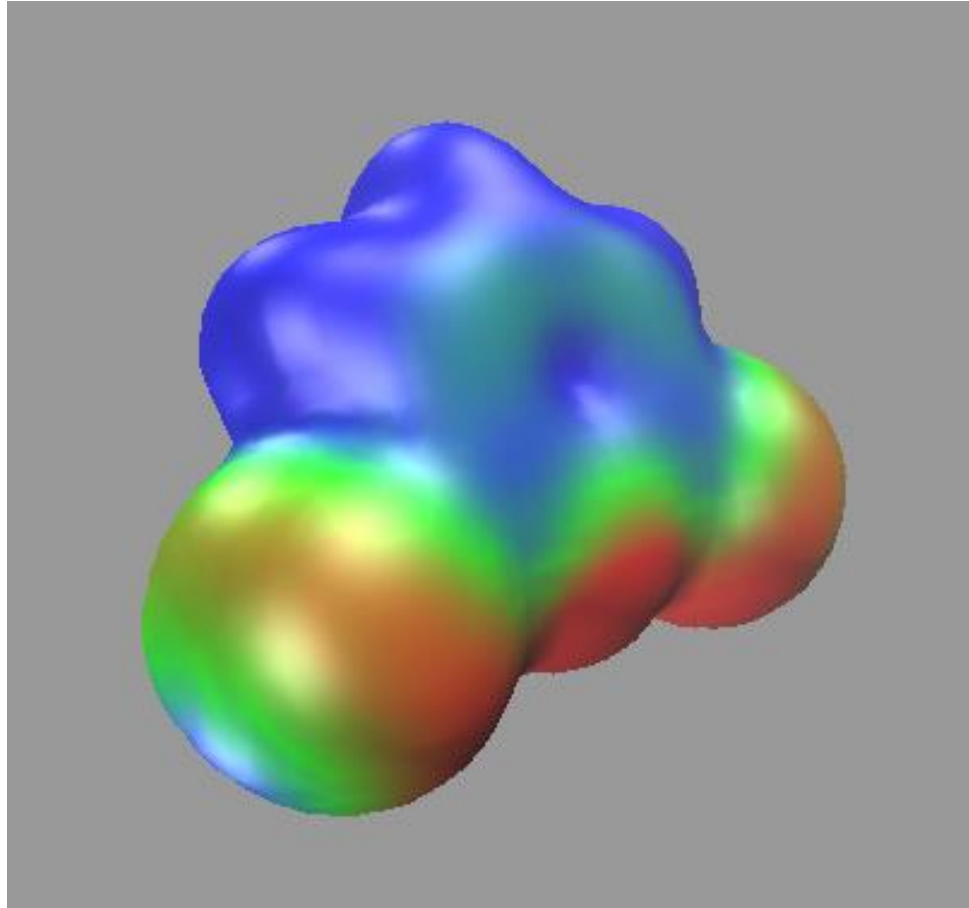
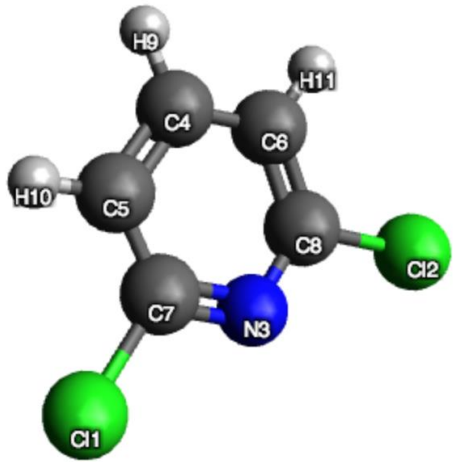


Frontier Molecular Orbital Approach



Finite Difference Approach

# Electrostatic Potential (ESP)



[Python Script & Jupyter Notebooks](#)

# Local Conceptual DFT

## (Dual Descriptor)

```
from chemtools import LocalConceptualDFT, UniformGrid, print_vmd_script_isosurface

# 1. Make cubic grid for plotting dual descriptor.
#   The cubic grid points are spaced by 0.2 a.u. & extending 5.0 a.u. on each side.

fname = 'dichloropyridine26_q+0'
cube = UniformGrid.from_file(fname + '.fchk', spacing=0.2, extension=5.0)

# 2. Build quadratic energy model for Formaldehyde using FMO approach.

tool = LocalConceptualDFT.from_file(fname + '.fchk', model='quadratic', points=cube.points)

# 3. Dump dual descriptor evaluated on cubic grid.

cube.generate_cube(fname + '_dual.cube', tool.dual_descriptor)

# 4. Generate VMD scripts to plot dual-descriptor iso-surface.
#   To visualize the iso-surface, use command: $ vmd -e coh2_dual_fmo.vmd

print_vmd_script_isosurface(fname + '.vmd', fname + '_dual.cube', isosurf=0.005,
                           scalemin=-0.005, scalemax=0.005, colorscheme=[0, 1], negative=True)
```



# Included & Planned Features

---

## Atoms-in-Molecules Partitioning

- Hirshfeld-family of partitioning (Hirshfeld, Hirshfeld-I, Minimal-Basis-Iterative-Stockholder (MBIS), Additive-Variational-Hirshfeld (AVH), etc.)
- QTAIM: Quantum Theory of Atoms-in-Molecules
- Quantum Chemical Topology. (Partition with respect to arbitrary scalar/vector field.)
- Orbital-based population analysis (Mulliken/Löwdin/Ruedenberg/Knizia)

$$\rho_A^{\text{Hirshfeld}}(\mathbf{r}) = \frac{\rho_A^0(\mathbf{r})}{\sum_{B=1}^{N_{\text{atoms}}} \rho_B^0(\mathbf{r})} \rho_{\text{mol}}(\mathbf{r})$$

$$= \arg \min_{\rho_{\text{mol}}(\mathbf{r}) = \sum_A \rho_A(\mathbf{r})} \sum_A \int \rho_A(\mathbf{r}) \ln \left( \frac{\rho_A(\mathbf{r})}{\rho_A^0(\mathbf{r})} \right) d\mathbf{r}$$

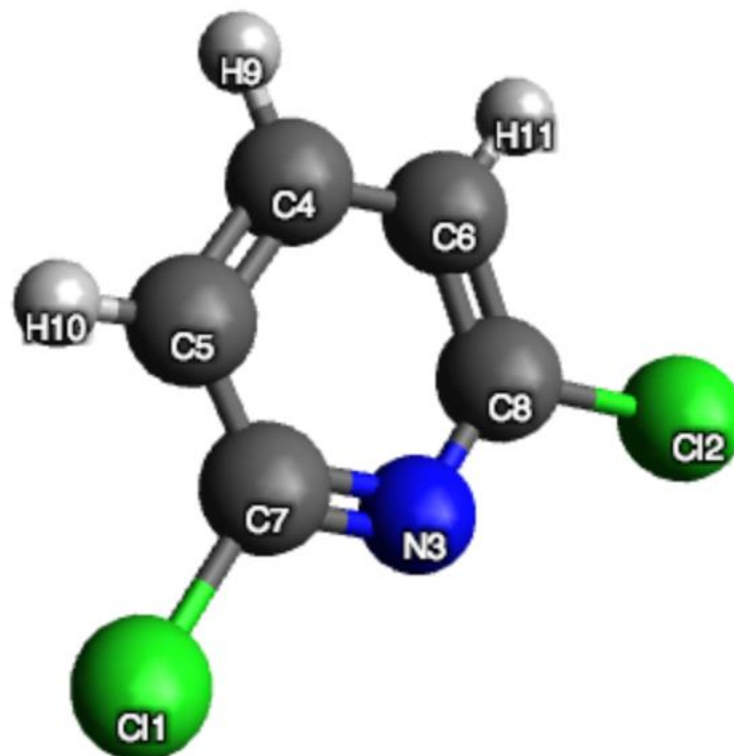
# Condensed Conceptual DFT

(Condensed Dual Descriptor)

```
$ chemtools ccdft quadratic dual dichloropyridine_q*.fchk  
--scheme mbis --approach RMF
```

Atomic contribution of dual\_descriptor for scheme=MBIS & approach RMF:

0	17	-0.128441
1	17	-0.128449
2	7	0.047067
3	6	0.474485
4	6	-0.413597
5	6	-0.413582
6	6	0.089405
7	6	0.089391
8	1	0.360509
9	1	0.011791
10	1	0.011793







# Included & Planned Features

---

## Density-Matrix Analysis

- Bonding indicators (SEDI, Multi-center indices)
- Effective Oxidation State (EOS)
- Intracule and Extracule
- Density Matrix, Fukui Matrix, Dual Descriptor Matrix, etc.
- Local Ionization Energy and Local Electron Affinity
- Maximum Probability Domains

**Conceptual Density-Matrix Functional Theory extends Conceptual Density Functional Theory to the 1-electron reduced density matrix.**

$$\frac{\partial^k \delta E}{\partial N^k \delta v(\mathbf{r})} = \left( \frac{\partial^k \rho(\mathbf{r})}{\partial N^k} \right)_{v(\mathbf{r})} \rightarrow \frac{\partial^k \delta E}{\partial N^k \delta h(\mathbf{r}, \mathbf{r}')} = \left( \frac{\partial^k \gamma(\mathbf{r}, \mathbf{r}')}{\partial N^k} \right)_{h(\mathbf{r}, \mathbf{r}')}$$

$$\frac{\partial^k \delta E}{\partial \mu^k \delta v(\mathbf{r})} = \left( \frac{\partial^k \rho(\mathbf{r})}{\partial \mu^k} \right)_{v(\mathbf{r})} \rightarrow \frac{\partial^k \delta E}{\partial \mu^k \delta h(\mathbf{r}, \mathbf{r}')} = \left( \frac{\partial^k \gamma(\mathbf{r}, \mathbf{r}')}{\partial \mu^k} \right)_{h(\mathbf{r}, \mathbf{r}')}$$

The effects of electron correlation of the electron density are often small, but correlation has a qualitative influence the 1DM and its derivatives.



# Included & Planned Features

---

## Density-Matrix Analysis

- Bonding indicators (SEDI, Multi-center indices)
- Effective Oxidation State (EOS)
- Intracule and Extracule
- Fukui Density Matrix, Dual Density Matrix, etc.
- Local Ionization Energy and Local Electron Affinity
- Maximum Probability Domains

The intracule and extracule show the position and extent of electron pairs

$$I_{\sigma\sigma'}(\mathbf{u}) = \iint \rho_2^{\sigma\sigma'}(\mathbf{r}_1, \mathbf{r}_2) \delta(\mathbf{r}_1 - \mathbf{r}_2 - \mathbf{u}) d\mathbf{r}_1 d\mathbf{r}_2$$

$$E_{\sigma\sigma'}(\mathbf{R}) = \iint \rho_2^{\sigma\sigma'}(\mathbf{r}_1, \mathbf{r}_2) \delta\left(\frac{1}{2}(\mathbf{r}_1 + \mathbf{r}_2) - \mathbf{R}\right) d\mathbf{r}_1 d\mathbf{r}_2$$



# Included & Planned Features

---

## Density-Matrix Analysis

- Bonding indicators (SEDI, Multi-center indices)
- Effective Oxidation State (EOS)
- Intracule and Extracule
- Density Matrix, Fukui Matrix, Dual Descriptor Matrix, etc.
- Local Ionization Energy and Local Electron Affinity
- Maximum Probability Domains

Politzer's Average Local Ionization Energy is the ionization energy, per electron, at a given point in space.

$$\text{ALIE}(\mathbf{r}) = \frac{\int \dots \int \left( \Psi^{(N)}(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) \right)^* \left( \hat{H}^{(N)} - \hat{H}^{(N-1)} \right) \Psi^{(N)}(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) d\mathbf{r}_2 \dots d\mathbf{r}_N}{\int \dots \int \left( \Psi^{(N)}(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) \right)^* \Psi^{(N)}(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N) d\mathbf{r}_2 \dots d\mathbf{r}_N}$$
$$= \frac{\sum_{i=1}^{N_{\text{orbitals}}} n_i \varepsilon_i |\phi_i(\mathbf{r})|^2}{\sum_{i=1}^{N_{\text{orbitals}}} n_i |\phi_i(\mathbf{r})|^2}$$

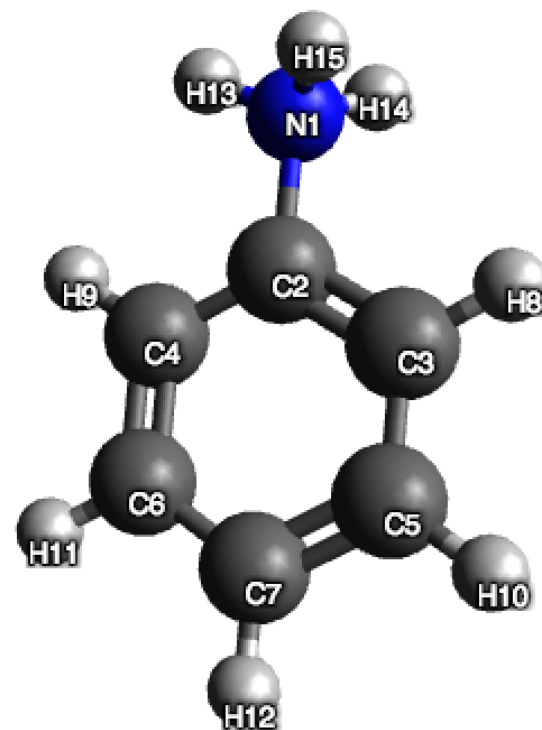
# Density-Matrix Tools & Local Conceptual DFT

(Fukui Function vs. Local Ionization Potential)

```
$ chemtools mot aniline_protonated_q+1.fchk --info
```

Information on alpha & beta electrons:

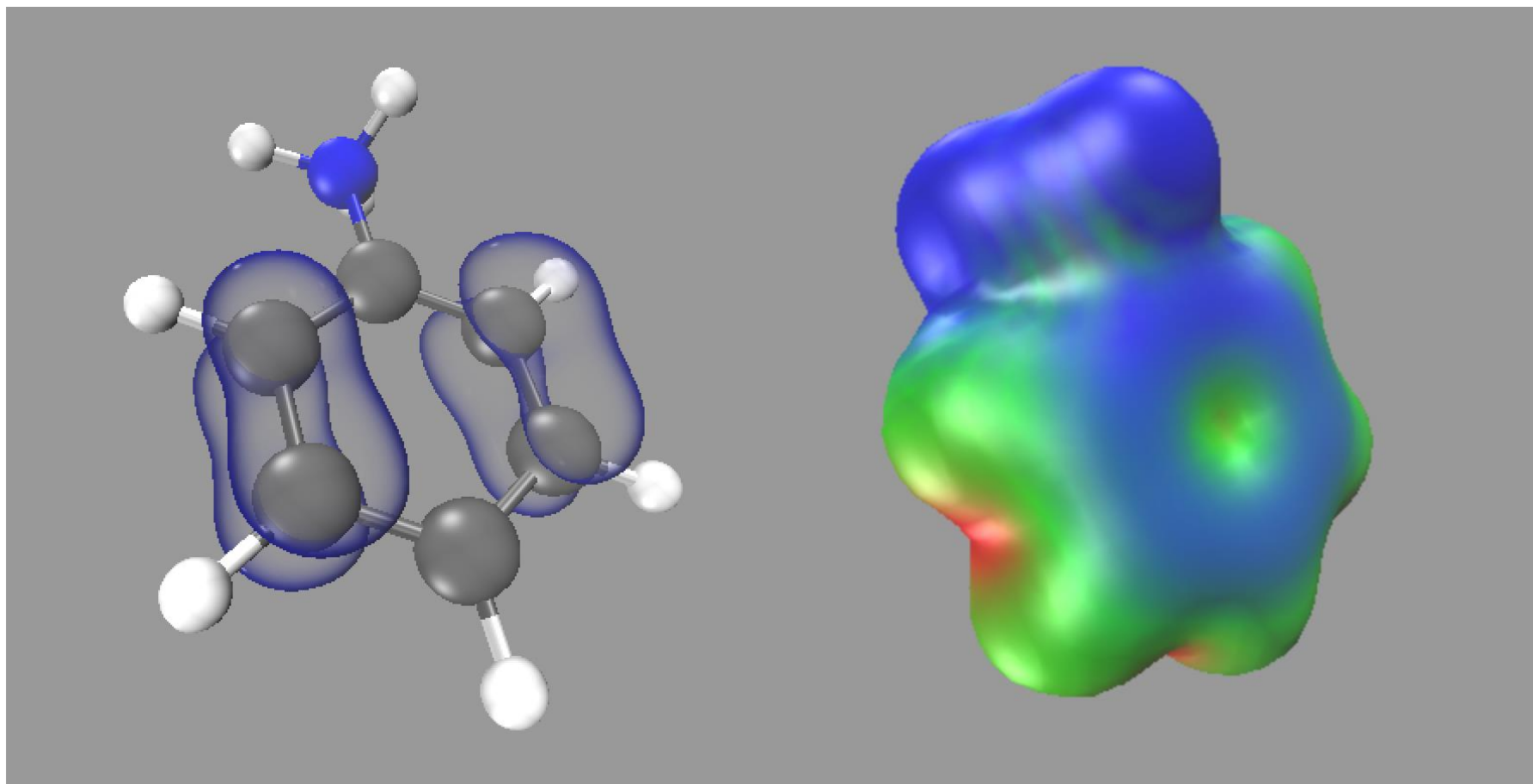
# electrons	: 25.000	25.000
HOMO index	: 25	25
LUMO+2 index	: -0.183982	-0.183982
LUMO+1 energy	: -0.191697	-0.191697
LUMO energy	: -0.196214	-0.196214
HOMO energy	: -0.425635	-0.425635
HOMO-1 energy	: -0.429398	-0.429398
HOMO-2 energy	: -0.517611	-0.517611



# Density-Matrix Tools & Local Conceptual DFT

(Fukui Function vs. Local Ionization Potential)

```
$ chemtools lcdft linear ff_minus aniline_protonated_q+1.fchk  
$ chemtools lip aniline_protonated_q+1.fchk
```





# Included & Planned Features

---

## Topological Analysis

- Find critical points and basins of scalars
- High-accuracy integration over basins

Take an arbitrary scalar or vector field, locate and classify critical points

$$\nabla p(\mathbf{r}_{\text{cp}}) = \mathbf{0}$$

and topological basins,  $\Omega$ ,

$$\nabla p(\mathbf{r} \in \partial\Omega) \cdot \mathbf{n}_{\partial\Omega} = 0$$

Properties at the critical points elucidate molecular interactions.

Integration of descriptors over topological basins allows one to compute energetic and other contributions from distinct chemical features.

We are using new algorithms for finding critical points, for topological partitioning, and for high-accuracy integration over topological regions.

# Topological Analysis

(Finding critical points of scalar fields)

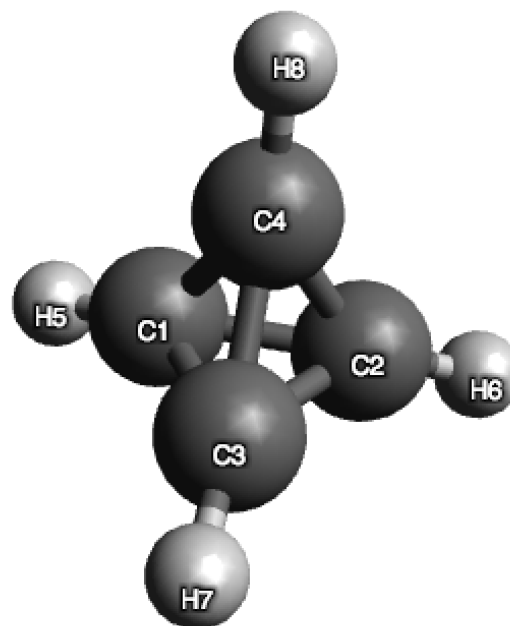
```
from chemtools import Molecule, UniformGrid, TopologicalTool
```

```
mol = Molecule.from_file('c4h4.fchk')
```

```
cub = UniformGrid.from_molecule(mol, spacing=0.25, extension=0.1, rotate=False)
```

```
top = TopologicalTool.from_molecule(mol, points=cub.points)
```

**# NA = 8**  
**# BCP = 10**  
**# RCP = 4**  
**# CCP = 1**



# Topological Analysis

(Finding critical points of scalar fields)

```
from chemtools import Molecule, UniformGrid, TopologicalTool
```

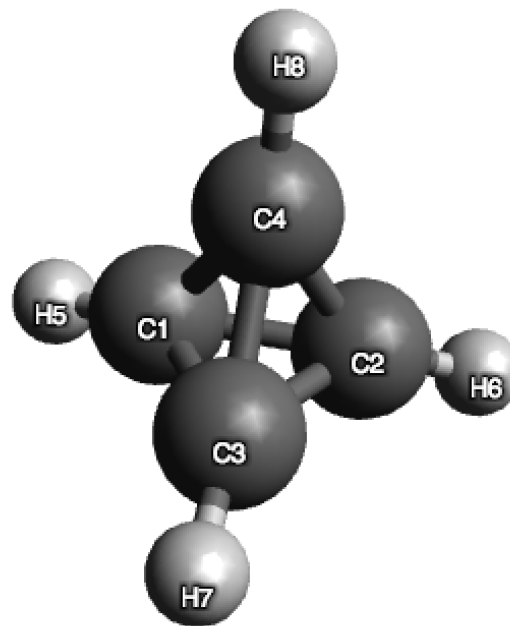
```
mol = Molecule.from_file('c4h4.fchk')
```

```
cub = UniformGrid.from_molecule(mol, spacing=0.25, extension=0.1, rotate=False)
```

```
top = TopologicalTool.from_molecule(mol, points=cub.points)
```

## Evaluate Ellipticity on BCP:

0	0.000002
1	0.000001
2	0.012131
3	0.012131
4	0.012131
5	0.012130
6	0.012131
7	0.000001
8	0.012131
9	0.000001







**Xiaotian (Derrick) Yang**



**Alireza Tehrani**



**Stijn Fias**



**Farnaz Heidar-Zadeh**



**Michael Richer**



**Taewon (David) Kim**



**Esteban  
Vohringer-Martinez**