## An introduction to celib

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Documentation: https://cclib.github.io Source code: https://github.com/cclib/cclib

## 1 Installation

## 2 First steps

## 2.1 Command line using ccget

### Running

```
1 molecule water {
2    0 1
3    0
4    H 1 0.99
5    H 1 0.99 2 106.0
6    }
7    s set {
9        basis sto-3g
10    }
11
12    energy('ccsd(t)')
```

## through Psi4 gives

```
$ ccget --list --verbose water_ccsd\(t\).out
     Attempting to read water ccsd(t).out
     Identified logfile to be in Psi4 format
     cclib can parse the following attributes from

    water_ccsd(t).out:

      atomcoords
       atommasses
       atomnos
       ccenergies
9
       charge
10
       coreelectrons
11
       homos
      metadata
12
13
       moenergies
14
       mosyms
15
      mult
16
       natom
17
       nbasis
18
       nmo
```

```
scfenergies
      scftargets
20
      scfvalues
21
    $ ccget natom atomnos atommasses atomcoords charge mult

→ nbasis nmo homos scftargets scfvalues scfenergies

    Attempting to read water_ccsd(t).out
    natom
    3
    atomnos
    [8 1 1]
    [15.99491462 1.00782503 1.00782503]
    atomcoords
    [[[ 0.
                               -0.06667853]
      Γο
                   -0.79064915 0.52911834]
11
      ΓО.
                    0.79064915 0.52911834]]]
12
    charge
13
    0
14
15
    mult.
16
17
    nbasis
    7
18
19
    nmo
20
    7
21
    homos
    [4]
^{22}
23
    scftargets
    [[1.e-08 1.e-08]]
24
    scfvalues
25
     [array([[-7.47145e+01, 3.03943e-01],
26
           [-2.01407e-01, 5.09857e-02],
27
28
           [-4.62920e-02, 9.16936e-03],
           [-1.69766e-03, 3.56660e-03],
29
           [-4.26333e-04, 3.22652e-04],
30
           [-2.49391e-06, 3.57847e-05],
31
32
           [-2.42460e-08, 1.11355e-06],
           [-2.03499e-11, 5.83644e-10]])]
33
34
    scfenergies
    [-2039.88321508]
35
36
    ccenergies
```

## 2.2 In a Python script (preferred)

[-2041.33710337]

```
from cclib.io import ccread
data = ccread("water_ccsd(t).out")
attrs = ["natom", "atomnos", "atommasses", "atomcoords",

→ "scftargets", "scfvalues", "scfenergies",
for attr in attrs:
   print(attr, type(getattr(data, attr)))
natom <class | int'>
atomnos <class numpy.ndarray'>
atommasses <class | numpy.ndarray'>
atomcoords <class 'numpy.ndarray'>
charge <class | int'>
mult <class "int'>
nbasis <class | int'>
nmo <class | int'>
homos <class 'numpy.ndarray'>
scftargets <class 'numpy.ndarray'>
```

```
11 scfvalues <class list'>
12 scfenergies <class numpy.ndarray'>
13 ccenergies <class numpy.ndarray'>
```

A full list of all available attributes is present in help(cclib.parser.data.ccData).

## 3 Modules

Under cclib, the core modules are

- bridge: Facilities for moving parsed data to other cheminformatic libraries. Currently available are Open Babel, PyQuante 1, and BioPython.
- method: Example analyses and calculations based on data parsed by cclib.
- io: Contains all writers (and some readers) for standard chemical representations.
- parser: Contains parsers for all available programs. Currently, this is ADF, DALTON, GAMESS-US and Firefly, GAMESS-UK, Gaussian, Jaguar, (Open)Molcas, Molpro, MOPAC, NWChem, ORCA, Psi3 and Psi4, Q-Chem, and Turbomole.
- scripts: Contains the command-line scripts ccframe, ccget, ccwrite, and ccframe.

#### 3.1 method

Most methods are classes that take a ccData instance and require a call to .calculate(). The base class is calculationmethod.Method.

- cda.CDA: Charge decomposition analysis, also accessible via the command-line script cda.
- cspa.CSPA: C-squared population analysis,  $\Phi_{\mu i} = \frac{C_{\mu i}^2}{\sum_{\nu} C_{\nu i}^2}.$
- density. Density: Density matrix calculation,  $D_{\mu\nu}^{\rm RHF} = 2\sum_{i}^{{\rm occ\ MO}} C_{\mu i} C_{\nu i}, D_{\sigma\mu\nu}^{\rm UHF} = \sum_{i}^{{\rm occ\ MO}} C_{\mu i}^{\sigma} C_{\nu i}^{\sigma}.$
- electrons. Electrons: Methods pertaining to electrons (just .count() for now).

- fragments.FragmentAnalysis: Convert a molecule's basis functions from atomic-based to fragment MO-based.
- lpa.LPA: Löwdin population analysis
- mbo.MBO: Mayer's bond orders
- mpa.MPA: Mulliken population analysis  $\Phi_{\mu i} = \sum_{\nu} C_{\mu i} C_{\nu i} S_{\mu \nu}$
- nuclear.Nuclear: Methods pertaining to atomic nuclei (stoichiometry strings, nuclear repulsion energies, rotational constants)
- opa.OPA: Overlap population analysis,  $OP_{AB,i} = 2\sum_{\mu \in A} \sum_{\nu \in B} C_{\mu i} C_{\nu i} S_{\mu \nu}$
- orbitals.Orbitals: Methods containing to orbitals (just .closed\_shell() for now)
- volume: Methods and functions related to volumes (write cube files, form and integrate wavefunctions and electron densities); for more comprehensive functionality, see ORBKIT (https://github.com/orbkit/orbkit), which incorporates cclib.

#### 3.2 io

Accessible via both the command-line scripts (ccget, ccwrite, ccframe)

- Format-specific classes are CJSONReader, CJSONWriter, CML (writer), MOLDEN (writer), WFXWriter, XYZReader, and XYZWriter.
- ccio.ccopen: Guess the identity of a particular 4.2 log file and return an instance of it.
- ccio.ccread: Attempt to open and read computational chemistry data from a file. The most important function in cclib, it calls ccopen then parse(). If the file type can't be determined, fall back to another internal reader or Open Babel
- ccio.ccwrite: Write the parsed data from an outputfile to a standard chemical representation.

The available formats are CJSON (https:// 12 github.com/OpenChemistry/chemicaljson), CML, MOLDEN, AIM Extended Wavefunction (\*.wfx, http://aim.tkgristmill.com/ 14 wfxformat.html), and XYZ. 15

• ccio.ccframe: Returns a pandas.DataFrame of data attributes parsed by from one or more log-files. The command-line version can write CSV, HDF5, JSON, pickle, and XLSX formats.

## 3.3 parser

In addition to all the available parser implementations (which should not be called directly),

- data.ccData: The core data structure returned by parsers that contains attributes corresponding to quantum chemical calculation attributes.
- utils: Common utilities, such as a simple unit convertor and PeriodicTable.

# 4 Examples

# 4.1 Calculate the AO-basis density matrix

```
1 # Need to do this...
2 C = data.mocoeffs[0].T
3 # ...so we can write the correct equation (RHF):
4 # D = 2 \sum_{i=0}^{i=0} CDC_{\mu i} C_{\nu i}
5 D = 2 * np.dot(C[:, :nocc], C[:, :nocc].T)
6 # Compare to the Nethod:
7 from cclib.method import Density
8 m = Density(data)
9 m.calculate()
10 np.testing.assert_allclose(m.density[0], D, rtol=0, \hookrightarrow atol=1.0e-15)
```

# 4.2 Plot geometry optimization convergence

```
energy_changes = [(geovalue[2] *
         \hookrightarrow args.scaling_energy_change) for geovalue in

    data.geovalues]

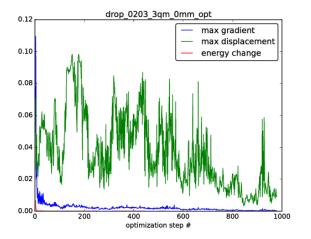
         # If this isn't true, something funny happened during

    the parsing, so fail out.

         assert len(scfenergies) == len(gradients)
16
         steps = range(1, len(scfenergies) + 1)
         # ax.plot(steps, scfenergies, label='SCF energy')
         ax.plot(steps, gradients, label='max gradient')
         ax.plot(steps, displacements, label='max

    displacement')

         ax.plot(steps, energy_changes, label='energy change')
22
23
^{24}
         ax.set title(stub)
         ax.set_xlabel('optimization step #')
     ax.legend(loc='best', fancybox=True)
    fig.savefig(stub + '.pdf', bbox_inches='tight')
```



## 5 Development

Inside of a virtualenv,

```
1 git clone https://github.com/cclib/cclib.git; cd cclib; \hookrightarrow pip install -e .
```

which allows making changes without reinstallation. To run the test suite,

```
pip install -r requirements.txt
bash ./travis/run_travis_tests.sh
```

To build the documentation locally,

```
pip install sphinx sphinx_rtd_theme
cd doc; make; firefox sphinx/_build/html/index.html
```