
pyrrole Documentation

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WARNING: this project has been retired. Please migrate to [geem-lab/overreact](#).

A Python package for solving chemical problems with computational modeling.

Usage example

As a usage example, let's calculate the energy barrier involved in [nitrogen inversion in ammonia](#).

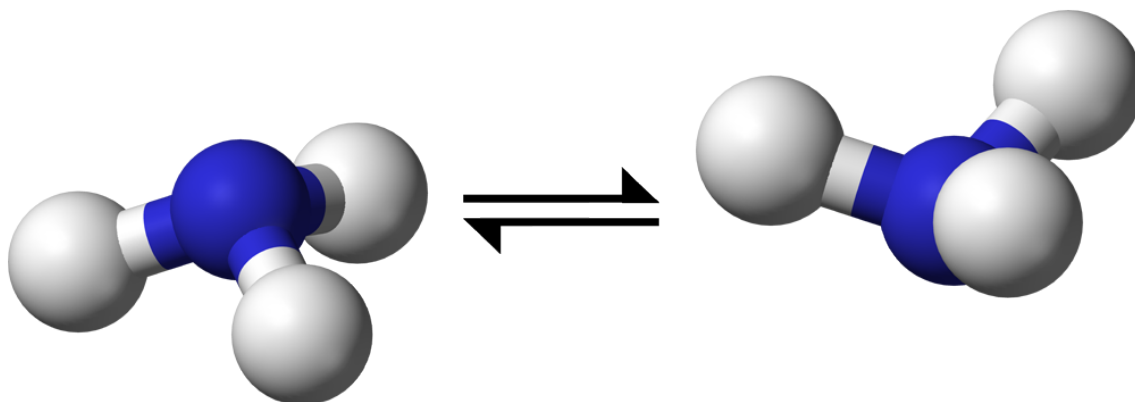


Fig. 1: When ammonia turns “inside out”, it passes through a planar transition state ([image in public domain](#)).

We do this in three simple steps (only eight lines of code):

1. Get the data

We first obtain the raw data, which will later be fed to our chemical model. Below we read computational chemistry logfiles of both ground and transition states¹.

```
>>> from pyrrole.atoms import read_cclib, create_data
>>> gs = read_cclib("data/ammonia/ammonia.out", name="NH3(g) ")
```

(continues on next page)

¹ Optimizations and frequency calculations of both ammonia and the planar transition state were performed at PBEh-3c using the ORCA electronic structure package (version 4.0.1.2). Logfiles can be found in the [project's repository](#).

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```
>>> ts = read_cclib("data/ammonia/invers.out", name="NH3(g) #")
>>> data = create_data(gs, ts)
```

Pyrrole uses `cclib` for reading logfiles, which is compatible with all major computational chemistry packages. You could also want to read tabular data from a file (or even from the web) using `pandas`.

2. Specify the model

We now describe our model. This is accomplished through chemical equations:

```
>>> from pyrrole import ChemicalEquation
>>> equation = ChemicalEquation("NH3(g) -> NH3(g) #", data)
```

While model above consists of a single `ChemicalEquation`, you could create complex models with multiple chemical equations with `ChemicalSystem` objects. You might want to store your complex models in text files too.

3. Obtain the results

Simply let pyrrole calculate the energy barrier:

```
>>> results = equation.to_series()
>>> results["freeenergy"] * 2625.4996382852164 # Hartree to kJ/mol
19.30952589472923
```

(As a side note, the reference value is 21.162 kJ/mol².)

Interested? [Have another example](#).

² *Chem. Phys. Lett.*, **2003**, 370 (3), pp 360-365 DOI: 10.1016/S0009-2614(03)00107-6.

CHAPTER 2

Installation

You can get the library directly from [PyPI](#):

```
$ pip install pyrrole
```


3.1 Getting started

In simple terms, the basic usage of pyrrole can be outlined in three steps:

1. Create a `data` object (this is actually a `pandas.DataFrame`).
2. Create a `ChemicalSystem` object.
3. Manipulate a `ChemicalSystem` object.

In order to understand each of them, let's walk through core API concepts as we tackle one everyday use case: the calculation of solvation free energy of acetic acid in water.

3.1.1 Solubility of acetic acid

Let's say that, after optimization and frequency calculations of `acetic acid` were done (both in vacuo and using an implicit solvation method¹), we wanted to calculate the `solvation energy` of acetic acid in water. This simple model perfectly exemplifies the usage of pyrrole, starting with the creation of a `data` object.

The data object

The `data` object consists of a `pandas.DataFrame` whose records represent chemical species. For our specific problem, we read logfiles (using the `read_cclib` function, which parses logfiles with the `cclib` library) and store them in the required tabular form (using `create_data`):

```
>>> from pyrrole.atoms import read_cclib, create_data
>>> gas = read_cclib("data/acetate/acetic_acid.out", name="AcOH(g) ")
>>> aquo = read_cclib("data/acetate/acetic_acid@water.out", name="AcOH(aq) ")
>>> data = create_data(gas, aquo)
```

¹ Calculations were done at PBEh-3c/SMD (water) using the ORCA electronic structure package (version 4.0.1.2). Logfiles can be found in the project's repository.

Each row of data above contains information found in a single logfile:

```
>>> columns = ["enthalpy", "entropy", "freeenergy"]
>>> data[columns] # doctest: +NORMALIZE_WHITESPACE
           enthalpy  entropy  freeenergy
name
AcOH(g)   -228.533374  0.031135 -228.564509
AcOH(aq)  -228.544332  0.030936 -228.575268
```

The energy values above are in [Hartree](#), which is the convention in the cclib project. Learn more about data objects in [Using data objects](#).

The ChemicalSystem object

We are now in position to define our chemical system with `ChemicalSystem`. Our model consists of a single equilibrium between gas phase and aqueous acetic acid:

```
>>> from pyrrole import ChemicalSystem
>>> system = ChemicalSystem("AcOH(g) <=> AcOH(aq)", data)
>>> system
ChemicalSystem(["AcOH(g) <=> AcOH(aq)"])
```

Usage of ChemicalSystem

`ChemicalSystem` objects can be manipulated in a variety of ways. For instance, they can be converted to `pandas.DataFrame` (with the `ChemicalSystem.to_dataframe` method):

```
>>> reactions = system.to_dataframe()
>>> reactions[columns] # doctest: +NORMALIZE_WHITESPACE
           enthalpy  entropy  freeenergy
chemical_equation
AcOH(g) <=> AcOH(aq) -0.010958 -0.000198  -0.010759
```

Again, energy values are given in Hartree. Conversion factors can be used for handling other units (with the help of the `scipy.constants` module):

```
>>> from scipy.constants import kilo, N_A, physical_constants
>>> hartree, _, _ = physical_constants["Hartree energy"]
>>> factor = hartree * N_A / kilo # Hartree to kJ/mol
>>> factor
2625.4996382852164
```

The calculated factor can be used to convert a whole table if so desired:

```
>>> reactions[columns] * factor # doctest: +NORMALIZE_WHITESPACE
           enthalpy  entropy  freeenergy
chemical_equation
AcOH(g) <=> AcOH(aq) -28.76991 -0.521109  -28.248775
```

(By the way, the reported experimental value for the solvation free energy of acetic acid in water is -28.0 kJ/mol².)

Now we're ready to start [Using data objects](#).

² *J. Phys. Chem. B*, **2009**, *113* (18), pp 6378-6396 DOI: 10.1021/jp810292n (supporting information).

3.2 Using data objects

Any `pandas.DataFrame` indexed by names of chemical species is a valid data object in pyrrole¹:

```
>>> import pandas as pd
>>> data = pd.DataFrame(
...     [{ 'name': 'CO3-2(aq)', 'freeenergy': -527.8},
...       { 'name': 'HCO3-(aq)', 'freeenergy': -586.85},
...       { 'name': 'H2CO3(aq)', 'freeenergy': -623.1},
...       { 'name': 'OH-(aq)', 'freeenergy': -157.2},
...       { 'name': 'H2O(l)', 'freeenergy': -237.14}])
>>> data = data.set_index('name')
>>> data # doctest: +NORMALIZE_WHITESPACE
           freeenergy
name
CO3-2(aq)      -527.80
HCO3-(aq)      -586.85
H2CO3(aq)      -623.10
OH-(aq)        -157.20
H2O(l)         -237.14
```

The `pandas` library, a dependency of pyrrole, can be used to create data objects. Below are examples of creating data objects from different sources.

3.2.1 Reading local files

Pandas can read data sets in various formats, such as comma-separated values (CSV), Google BigQuery, Hierarchical Data Format (HDF), JavaScript Object Notation (JSON), Microsoft Excel, and many other supported format types:

```
>>> data = pd.read_hdf("data/acetate/data.h5")
>>> data[['jobfilename', 'freeenergy', 'enthalpy']]
           jobfilename  freeenergy  enthalpy
0  data/acetate/acetate.out -228.000450 -227.969431
1  data/acetate/acetate@water.out -228.120113 -228.089465
2  data/acetate/acetic_acid.out -228.564509 -228.533374
3  data/acetate/acetic_acid@water.out -228.575268 -228.544332
```

Pyrrole requires indices to represent names of chemical species, which is, like above, not always the case. Setting meaningful indices can be accomplished by feeding a custom function to `data.apply`:

```
>>> def update(series):
...     """Compute a new column 'name' and add it to row."""
...     series['name'] = (series['jobfilename']
...                       .replace('data/acetate/', '')
...                       .replace('.out', ''))
...     series['name'] = (series['name']
...                       .replace('acetate', 'AcO-')
...                       .replace('acetic_acid', 'AcOH'))
...     series['name'] = series['name'].replace('@water', '(aq)')
...     if '(aq)' not in series['name']:
...         series['name'] += "(g)"
...     return series
```

The function above should be applied to the `data` object, which can then be reindexed:

¹ Obtained from standard Gibbs free energy of formation.

```
>>> data = data.apply(update, axis='columns').set_index('name')
>>> data[['jobfilename', 'freeenergy', 'enthalpy']] # doctest: +NORMALIZE_WHITESPACE
               jobfilename  freeenergy  enthalpy
name
AcO- (g)          data/acetate/acetate.out -228.000450 -227.969431
AcO- (aq)         data/acetate/acetate@water.out -228.120113 -228.089465
AcOH (g)          data/acetate/acetic_acid.out -228.564509 -228.533374
AcOH (aq)         data/acetate/acetic_acid@water.out -228.575268 -228.544332
```

The data object is now ready to be used:

```
>>> from pyrrole import ChemicalSystem
>>> system = ChemicalSystem(['AcO- (g) <=> AcO- (aq)',
...                         'AcOH (g) <=> AcOH (aq)'],
...                         data['freeenergy'])
>>> system.to_dataframe() # doctest: +NORMALIZE_WHITESPACE
               freeenergy
chemical_equation
AcO- (g) <=> AcO- (aq)    -0.119663
AcOH (g) <=> AcOH (aq)    -0.010759
```

In *Getting started*, we showed how to use `create_data` to produce a data object by reading output files from computational chemistry programs. Reading lots of logfiles is slow, which is why storing the data in a file translates to faster retrievals later. This can be accomplished with `ccframe`, a command-line tool that is part of `cclib` (a dependency of `pyrrole`). In fact, the file `data.h5` used in the example above was produced using `ccframe`:

```
$ ccframe -O data/acetate/data.h5 data/acetate*out \
          data/acetic_acid*out
```

Learn more about `ccframe` in both its help page (`$ ccframe -h`) and [documentation](#).

3.2.2 Reading the web

There's a lot of freely available data on the internet. For instance, [NIST](#) offers [enthalpies of formation at 0K](#) (in kJ/mol). Luckily, `pandas` supports [reading HTML tables](#) directly:

```
>>> url = "https://cccbdb.nist.gov/hf0k.asp"
>>> data = pd.read_html(url, header=0)[3] # fourth table in page
>>> data = data.set_index("Species")
>>> data = data[["Name", "Hfg 0K", "DOI"]]
>>> data.head() # doctest: +NORMALIZE_WHITESPACE
               Name  Hfg 0K          DOI
Species
D           Deuterium atom    219.8         NaN
H           Hydrogen atom    216.0  10.1002/bbpc.19900940121
H+        Hydrogen atom cation  1528.1         NaN
D2         Deuterium diatomic     0.0         NaN
H2         Hydrogen diatomic     0.0  10.1002/bbpc.19900940121
```

This data allows us to calculate the [bond-dissociation enthalpy](#) of the hydrogen molecule at 0K, for instance:

```
>>> from pyrrole import ChemicalEquation
>>> equation = ChemicalEquation("H2 -> 2 H", data)
>>> equation.to_series()
Hfg 0K    432.0
Name: H2 -> 2 H, dtype: float64
```

That's 432 kJ/mol, or 103.3 kcal/mol.

It's time to take a deeper look at *Systems and equations*.

3.3 Systems and equations

3.3.1 The ChemicalSystem object revisited

In *Getting started*, we saw the basics of chemical systems.

Drawing.

Internally, a ChemicalSystem object consists of individual ChemicalEquation objects, which can be manipulated on their own.

3.3.2 The ChemicalEquation object

Single chemical equations in pyrrole are handled by ChemicalEquation objects. A special mini-language is used to define chemical equations in a way that makes it easy to simply copy and paste from the web. For instance, the following metal displacement was obtained from a [Wikipedia entry](#):

```
>>> from pyrrole import ChemicalEquation
>>> half_zinc = ChemicalEquation('Zn(s) -> Zn+2(aq) + 2 e-')
>>> half_copper = ChemicalEquation('Cu+2(aq) + 2 e- <- Cu(s)')
```

ChemicalEquation objects can be manipulated just like vectors, i.e., summed and multiplied by scalar values:

```
>>> half_zinc - half_copper
ChemicalEquation('Cu+2(aq) + Zn(s) -> Cu(s) + Zn+2(aq)')
```

Stoichiometry coefficients can be obtained individually:

```
>>> half_zinc.coefficient['e-']
2.0
```

There's no need to use chemical formulae for chemical species. Any mix of printable characters can be used:

```
>>> ChemicalEquation('cis-A <=> trans-A')
ChemicalEquation('cis-A <=> trans-A')
```


CHAPTER 4

Indices and tables

- `genindex`
- `modindex`
- `search`