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# **Psithon Documentation**

***Release 4.01***

**Psi4 Project**

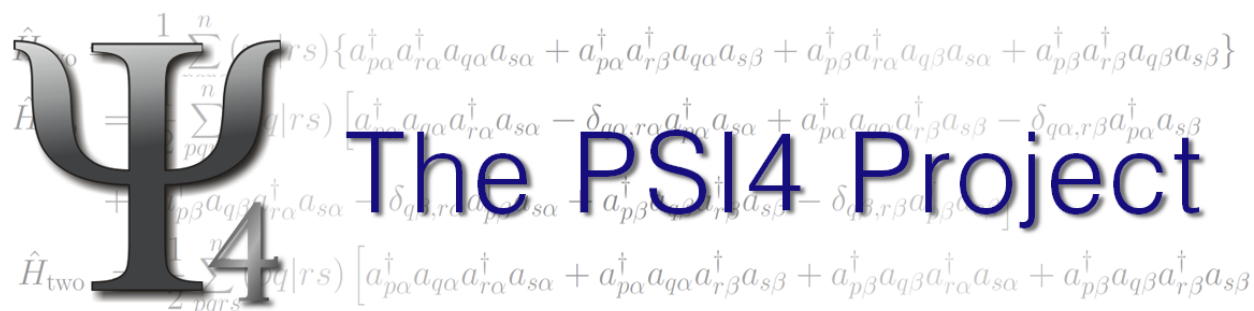
February 27, 2012



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# The PSI4 Project

To allow arbitrarily complex computations to be performed, PSI4 is built upon the Python interpreter, with modifications termed Psithon. Chapter 3 of the User's Manual describes the non-standard Python associated with clean molecule, basis, and option specification in the PSI4 input file. This documentation addresses the pure Python side—what functions allow the efficient compiled code to be run, what functions post-process and interact with that output, and how the ordinary (or ambitious) user can extend PSI4's functionality.

**Warning:** Python naming practices of `file_that_includes_function.function_name()` are followed below. In psi4 input files, it is only necessary to call the function name alone. That is, use `energy('scf')`, not `driver.energy('scf')`.

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**Note:** The options documented below are placed as arguments in the command that calls the Python function, not in the `set globals` block or with any other `set` command.

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**Note:** Psithon keyword names and values are insensitive to case. The few exceptions are documented for the `database()` function, where case structure must match the database file.

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**Note:** Boolean arguments can be specified by `yes`, `on`, `true`, or `1` for affirmative and `no`, `off`, `false`, or `0` for negative, all insensitive to case.

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# ENERGY

`driver.energy(name, **kwargs)`

Function to compute the single-point electronic energy.

**Returns** (*float*) Total electronic energy in Hartrees. SAPT returns interaction energy.

**Psi variables**

**CURRENT ENERGY**

**CURRENT REFERENCE ENERGY**

**CURRENT CORRELATION ENERGY**

name	calls method
scf	Hartree–Fock (HF) or density functional theory (DFT)
mp2	2nd-order Moller-Plesset perturbation theory (MP2)
df-mp2	MP2 with density fitting
dcft	density cumulant functional theory
mcsf	multiconfigurational self consistent field (SCF)
dfcc	coupled cluster with density fitting
mp2c	coupled MP2 (MP2C)
mp2-drpa	random phase approximation?
sapt0	0th-order symmetry adapted perturbation theory (SAPT)
sapt2	2nd-order SAPT, traditional definition
sapt2+	SAPT including all 2nd-order terms
sapt2+(3)	SAPT including perturbative triples
sapt2+3	
sapt0-ct	0th-order SAPT plus charge transfer (CT) calculation
sapt2-ct	SAPT2 plus CT
sapt2+-ct	SAPT2+ plus CT
sapt2+(3)-ct	SAPT2+(3) plus CT
sapt2+3-ct	SAPT2+3 plus CT
cc2	approximate coupled cluster singles and doubles (CC2)
ccsd	coupled cluster singles and doubles (CCSD)
bccd	Brueckner coupled cluster doubles (BCCD)
cc3	approximate coupled cluster singles, doubles, and triples (CC3)
ccsd(t)	CCSD with perturbative triples
bccd(t)	BCCD with perturbative triples
ccenergy	<b>expert</b> full control over ccenergy module
mp <i>n</i>	<i>n</i> th-order Moller–Plesset perturbation theory
zapt <i>n</i>	<i>n</i> th-order z-averaged perturbation theory (ZAPT)
cisd	configuration interaction (CI) singles and doubles (CISD)
Continued on next page	

Table 1.1 – continued from previous page

name	calls method
cisdt	CI singles, doubles, and triples (CISDT)
cisdtq	CI singles, doubles, triples, and quadruples (CISDTQ)
ci $n$	$n$ th-order CI
fci	full configuration interaction (FCI)
detci	<b>expert</b> full control over detci module
cphf	coupled-perturbed Hartree-Fock?
cpks	coupled-perturbed Kohn-Sham?
cis	CI singles (CIS)
tda	Tamm-Dankoff approximation (TDA)
tdhf	time-dependent HF (TDHF)
tddft	time-dependent DFT (TDDFT)
adc	2nd-order algebraic diagrammatic construction (ADC)
eom-cc2	EOM-CC2
eom-ccsd	equation of motion (EOM) CCSD
eom-cc3	EOM-CC3

name	calls method in Kallay's MRCC program
mrccsd	CC through doubles
mrccsdt	CC through triples
mrccsdtq	CC through quadruples
mrccsdtqp	CC through quintuples
mrccsdtqph	CC through sextuples
mrccsd(t)	CC through doubles with perturbative triples
mrccsdt(q)	CC through triples with perturbative quadruples
mrccsdtq(p)	CC through quadruples with perturbative quintuples
mrccsdtqp(h)	CC through quintuples with perturbative sextuples
mrccsd(t)_1	
mrccsdt(q)_1	
mrccsdtq(p)_1	
mrccsdtqp(h)_1	
mrccsd-1a	
mrccsdtq-1a	
mrccsdtqp-1a	
mrccsdtqph-1a	
mrccsd-1b	
mrccsdtq-1b	
mrccsdtqp-1b	
mrccsdtqph-1b	
mrcc2	
mrcc3	
mrcc4	
mrcc5	
mrcc6	
mrccsd-3	
mrccsdtq-3	
mrccsdtqp-3	
mrccsdtqph-3	

## Parameters



- **name** (*string*) – 'scf' || 'df-mp2' || 'ci5' || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the system.

- **bypass\_scf** (*bool*) – 'on' ||  $\Rightarrow$  'off'  $\Leftarrow$

Indicates whether, for *name* values built atop of scf calculations, the scf step is skipped. Suitable when special steps are taken to get the scf to converge in an explicit preceeding scf step.

### Examples

```
>>> # [1] Coupled-cluster singles and doubles calculation with psi code
>>> energy('ccsd')

>>> # [2] Charge-transfer SAPT calculation with scf projection from small into requested basis
>>> energy('sapt0-ct', cast_up=True)

>>> # [3] Arbitrary-order MPn calculation
>>> energy('mp4')
```



# OPTIMIZE

---

**Note:** The derivative level type for `driver.optimize()` and `driver.frequency()` functions can be specified by `energy`, `none`, or 0 for 0th derivative, `gradient`, `first`, or 1 for 1st derivative, and `hessian`, `second`, or 2 for 2nd derivative.

---

`driver.optimize(name, **kwargs)`

Function to perform a geometry optimization.

**Aliases** `opt()`

**Returns** (*float*) Total electronic energy of optimized structure in Hartrees.

**Psi variables**

## CURRENT ENERGY

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**Note:** Analytic gradients area available for all methods in the table below. Optimizations with other methods in the energy table proceed by finite differences.

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**Caution:** Some features are not yet implemented. Buy a developer a coffee.

•Need to check that all methods do return electronic energy. I think gradient got changed at one point.

name	calls method
scf	Hartree–Fock (HF) or density functional theory (DFT)
mp2	2nd-order Moller-Plesset perturbation theory (MP2)
ccsd	coupled cluster singles and doubles (CCSD)
ccsd(t)	CCSD with perturbative triples
eom-ccsd	equation of motion (EOM) CCSD

## Parameters

- **name** (*string*) – 'scf' || 'df-mp2' || 'ci5' || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the database. May be any valid argument to `driver.energy()`.

- **func** (*function*) –  $\Rightarrow$  gradient  $\Leftarrow$  || energy || cbs

Indicates the type of calculation to be performed on the molecule. The default dertype accesses ``gradient`` or 'energy', while 'cbs' performs a multistage finite difference calculation. If a nested series of python functions is intended (see [Function Intercalls](#)), use keyword `opt_func` instead of `func`.

- **mode** (*string*) –  $\Rightarrow$  'continuous'  $\Leftarrow$  || 'sow' || 'reap'

Indicates whether the calculation required to complete the optimization are to be run in one file ('continuous') or are to be farmed out in an embarrassingly parallel fashion ('sow'/'reap'). For the latter, run an initial job with 'sow' and follow instructions in its output file.

- **dertype** (*dertype*) – 'gradient' || 'energy'

Indicates whether analytic (if available) or finite difference optimization is to be performed.

### Examples

```
>>> # [1] Analytic scf optimization
>>> optimize('scf')

>>> # [2] Finite difference mp3 optimization
>>> opt('mp3')

>>> # [3] Forced finite difference ccscd optimization
>>> optimize('ccscd', dertype=1)
```

# RESPONSE

`driver.response(name, **kwargs)`

Function to compute linear response properties.

**Returns** (*float*) Total electronic energy in Hartrees.

**Caution:** Some features are not yet implemented. Buy a developer a coffee.

- Check that energy is actually being returned.
- Check if there're some PSI variables that ought to be set.

name	calls method
cc2	2nd-order approximate CCSD
ccsd	coupled cluster singles and doubles (CCSD)

**Parameters** `name` (*string*) – 'ccsd' || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the system.

## Examples

```
>>> # [1] CCSD-LR properties calculation
>>> response('ccsd')
```



# FREQUENCY

`driver.frequency` (*name*, *\*\*kwargs*)

Function to compute harmonic vibrational frequencies.

**Aliases** `frequencies()`, `freq()`

**Returns** (*float*) Total electronic energy in Hartrees.

**Caution:** Some features are not yet implemented. Buy a developer a coffee.

- RAK, why are you adding OPTKING options as GLOBALS? And shouldn't they be Py-side not C-side options?
- Put in a dictionary, so IRREPS can be called by symmetry element or 'all'
- Make frequency look analogous to gradient, especially in matching derivative levels. Make dertype actually a dertype type.

## Parameters

- **name** (*string*) – 'scf' || 'df-mp2' || 'ci5' || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the system.

- **dertype** (*dertype*) – ⇒ 'hessian' ⇐ || 'gradient' || 'energy'

Indicates whether analytic (if available- they're not), finite difference of gradients (if available) or finite difference of energies is to be performed.

- **irrep** (*int*) – ⇒ -1 ⇐ || 1 || etc.

Indicates which symmetry block of vibrational frequencies to be computed. 1 represents  $a_1$ , requesting only the totally symmetric modes. -1 indicates a full frequency calculation.

## Examples

```
>>> # [1] <example description>
```

```
>>> <example python command>
```

```
>>> # [2] Frequency calculation for b2 modes through finite difference of gradients
```

```
>>> frequencies('scf', dertype=1, irrep=4)
```





# COUNTERPOISE CORRECT

`wrappers.cp(name[, func, check_bsse])`

The `cp` function computes counterpoise-corrected two-body interaction energies for complexes composed of arbitrary numbers of monomers.

**Aliases** `counterpoise_correct()`, `counterpoise_correction()`

**Returns** (*float*) Counterpoise-corrected interaction energy in kcal/mol

**Psi variables**

**CP-CORRECTED 2-BODY INTERACTION ENERGY**

**UNCP-CORRECTED 2-BODY INTERACTION ENERGY**

**Caution:** Some features are not yet implemented. Buy a developer a coffee.

- No values of `func` besides energy have been tested.
- Table print-out needs improving. Add some PSI variables.

## Parameters

- **name** (*string*) – ‘`scf`’ || ‘`ccsd(t)`’ || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the molecule. May be any valid argument to `driver.energy()`; however, SAPT is not appropriate.

- **func** (*function*) –  $\Rightarrow$  energy  $\Leftarrow$  || `optimize` || `cbs`

Indicates the type of calculation to be performed on the molecule and each of its monomers. The default performs a single-point energy (‘`name`’), while `optimize` performs a geometry optimization on each system, and `cbs` performs a compound single-point energy. If a nested series of python functions is intended (see [Function Intercalls](#)), use keyword `cp_func` instead of `func`.

- **check\_bsse** (*bool*) – ‘`on`’ ||  $\Rightarrow$  ‘`off`’  $\Leftarrow$

Indicates whether to additionally compute un-counterpoise corrected monomers and thus obtain an estimate for the basis set superposition error.

## Examples

```
>>> # [1] counterpoise-corrected mp2 interaction energy
>>> cp('dfmp2')
```



# DATABASE

`wrappers.database` (*name*, *db\_name* [, *func*, *mode*, *cp*, *rlxd*, *symm*, *zpe*, *benchmark*, *tabulate*, *subset* ])

Function to access the molecule objects and reference energies of popular chemical databases.

**Aliases** `db()`

**Returns** (*float*) Mean absolute deviation of the database in kcal/mol

**Psi variables**

`db_name DATABASE MEAN SIGNED DEVIATION`

`db_name DATABASE MEAN ABSOLUTE DEVIATION`

`db_name DATABASE ROOT-MEAN-SQUARE DEVIATION`

---

**Note:** It is very easy to make a database from a collection of xyz files using the script `$PSIDATADIR/databases/ixyz2database.pl`. See [Creating a New Database](#) for details.

---

**Caution:** Some features are not yet implemented. Buy a developer some coffee.

• In sow/reap mode, use only global options (e.g., the local option set by `set scf scf_type df` will not be respected).

## Parameters

- **name** (*string*) – 'scf' || 'sapt0' || 'ccsd(t)' || etc.

First argument, usually unlabeled. Indicates the computational method to be applied to the database. May be any valid argument to `driver.energy()`.

- **db\_name** (*string*) – 'BASIC' || 'S22' || 'HTBH' || etc.

Second argument, usually unlabeled. Indicates the requested database name, matching the name of a python file in `psi4/lib/databases`. Consult that directory for available databases and literature citations.

- **func** (*function*) –  $\Rightarrow$  energy  $\Leftarrow$  || optimize || cbs

Indicates the type of calculation to be performed on each database member. The default performs a single-point energy ('name'), while optimize performs a geometry optimization on each reagent, and cbs performs a compound single-point energy. If a nested series of python functions is intended (see [Function Intercalls](#)), use keyword `db_func` instead of `func`.

- **mode** (*string*) –  $\Rightarrow$  'continuous'  $\Leftarrow$  || 'sow' || 'reap'

Indicates whether the calculations required to complete the database are to be run in one file ('continuous') or are to be farmed out in an embarrassingly parallel fashion

('sow'/'reap'). For the latter, run an initial job with 'sow' and follow instructions in its output file.

- **cp** (*bool*) – 'on'  $\parallel$   $\Rightarrow$  'off'  $\Leftarrow$

Indicates whether counterpoise correction is employed in computing interaction energies. Use this option and NOT the `wrappers.cp()` function for BSSE correction in `database()`. Option available (See [Available Databases](#)) only for databases of bimolecular complexes.

- **rlxd** (*bool*) – 'on'  $\parallel$   $\Rightarrow$  'off'  $\Leftarrow$

Indicates whether correction for deformation energy is employed in computing interaction energies. Option available (See [Available Databases](#)) only for databases of bimolecular complexes with non-frozen monomers, e.g., HBC6.

- **symm** (*bool*) –  $\Rightarrow$  'on'  $\Leftarrow$   $\parallel$  'off'

Indicates whether the native symmetry of the database reagents is employed ('on') or whether it is forced to  $C_1$  symmetry ('off'). Some computational methods (e.g., SAPT) require no symmetry, and this will be set by `database()`.

- **zpe** (*bool*) – 'on'  $\parallel$   $\Rightarrow$  'off'  $\Leftarrow$

Indicates whether zero-point-energy corrections are appended to single-point energy values. Option valid only for certain thermochemical databases. Disabled until Hessians ready.

- **benchmark** (*string*) –  $\Rightarrow$  'default'  $\Leftarrow$   $\parallel$  'S22A'  $\parallel$  etc.

Indicates whether a non-default set of reference energies, if available (See [Available Databases](#)), are employed for the calculation of error statistics.

- **tabulate** (*array of strings*) –  $\Rightarrow$  []  $\Leftarrow$   $\parallel$  ['scf total energy', 'natom']  $\parallel$  etc.

Indicates whether to form tables of variables other than the primary requested energy. Available for any PSI variable.

- **subset** (*string or array of strings*) – Indicates a subset of the full database to run. This is a very flexible option and can be used in three distinct ways, outlined below. Note that two take a string and the last takes an array. See [Available Databases](#) for available values.

- 'small'  $\parallel$  'large'  $\parallel$  'equilibrium' Calls predefined subsets of the requested database, either 'small', a few of the smallest database members, 'large', the largest of the database members, or 'equilibrium', the equilibrium geometries for a database composed of dissociation curves.

- 'BzBz\_S'  $\parallel$  'FaOFFaON'  $\parallel$  'ArNe'  $\parallel$  etc. For databases composed of dissociation curves, individual curves can be called by name. Consult the database python files for available molecular systems. The choices for this keyword are case sensitive and must match the database python file

- [1,2,5]  $\parallel$  ['1','2','5']  $\parallel$  ['BzMe-3.5', 'MeMe-5.0']  $\parallel$  etc. Specify a list of database members to run. Consult the database python files for available molecular systems. The choices for this keyword are case sensitive and must match the database python file

### Examples

```
>>> # [1] Two-stage SCF calculation on short, equilibrium, and long helium dimer
>>> db('scf','RGC10',cast_up='sto-3g',subset=['HeHe-0.85','HeHe-1.0','HeHe-1.5'], tabulate=['scf

>>> # [2] Counterpoise-corrected interaction energies for three complexes in S22
>>> # Error statistics computed wrt an old benchmark, S22A
>>> database('dfmp2','S22',cp=1,subset=[16,17,8],benchmark='S22A')
```

```
>>> # [3] SAPT0 on the neon dimer dissociation curve
>>> db('sapt0', subset='NeNe', cp=0, symm=0, db_name='RGC10')

>>> # [4] Optimize system 1 in database S22, producing tables of scf and mp2 energy
>>> db('mp2', 'S22', db_func=optimize, subset=[1], tabulate=['mp2 total energy', 'current energy'])

>>> # [5] CCSD on the smallest systems of HTBH, a hydrogen-transfer database
>>> database('ccsd', 'HTBH', subset='small', tabulate=['ccsd total energy', 'mp2 total energy'])
```

## 6.1 Output

At the beginning of a database job is printed a listing of the individual system calculations which will be performed. The output snippet below is from the example job [1] above. It shows each reagent required for the subset of database reactions requested. Note that this is an un-counterpoise-corrected example, and the wrapper is smart enough to compute only once the monomer whose energy will be subtracted from each of the three dimers.

```
RGC1-HeHe-0.85-dimer
RGC1-He-mono-unCP
RGC1-HeHe-1.0-dimer
RGC1-HeHe-1.5-dimer
```

At the end of the job, the Requested Energy table is printed that gives the total energies for the requested model chemistry for each reagent and each reaction, as well as the stoichiometric weights by which the reagent energies are transformed into the reaction energy. In this case, the dimer is +1 and the monomer is -2, indicating the the interaction energy is computed from dimer less first monomer less second (identical) monomer. Error statistics are computed with respect to the reference energies stored in the database. One of these, the mean absolute deviation, is returned by the wrapper as an ordinary Python variable. (For databases without a stored reference energy, e.g., BASIC, large and meaningless numbers are printed for error.) The other two tables tabulate the PSI variables requested through keyword `tabulate`, in this case the total SCF energy and the number of atoms in each reagent.

```
==> Scf Total Energy <==
```

Reaction	Reaction Value	Reagent 1 Value Wt	Reagent 2 Value Wt
RGC1-HeHe-0.85	0.00011520	-5.71020576 1	-2.85516048 -2
RGC1-HeHe-1.0	0.00000153	-5.71031943 1	-2.85516048 -2
RGC1-HeHe-1.5	-0.00000000	-5.71032096 1	-2.85516048 -2

```
==> Natom <==
```

Reaction	Reaction Value	Reagent 1 Value Wt	Reagent 2 Value Wt
RGC1-HeHe-0.85	0.00000000	2.00000000 1	1.00000000 -2
RGC1-HeHe-1.0	0.00000000	2.00000000 1	1.00000000 -2
RGC1-HeHe-1.5	0.00000000	2.00000000 1	1.00000000 -2

```
==> Requested Energy <==
```

Reaction	Reaction Energy		Error	Reagent 1		Reagent 2	
	Ref	Calc	[kcal/mol]	[H]	Wt	[H]	Wt
RGC1-HeHe-0.85	0.0376	0.0723	0.0347	-5.71020576	1	-2.85516048	-2
RGC1-HeHe-1.0	-0.0219	0.0010	0.0228	-5.71031943	1	-2.85516048	-2
RGC1-HeHe-1.5	-0.0029	-0.0000	0.0029	-5.71032096	1	-2.85516048	-2
Minimal Dev			0.0029				
Maximal Dev			0.0347				
Mean Signed Dev			0.0201				
Mean Absolute Dev			0.0201				
RMS Dev			0.0240				

---

## 6.2 Available Databases

Below are documented for particular databases the availability of the generic database function options **cp**, **rlxd**, **benchmark**, and the string options for **subset**. The full reagent member list, which can also be used in conjunction with **subset**, is not included here for consideration of space and may be found in the database file. The database Python files are very readable and should be consulted for more particular questions.

---

### ACENES

Database of Ed and Rob's favorite linear acene dimers.  
Geometries from nowhere special, and reference energies undefined.

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
    - 'FIRST3' benzene, naphthalene, and anthracene dimers
    - 'FIRST5' benzene - pentacene dimers
    - 'FIRST10' benzene - decacene dimers
- 

### BAKERJCC93

Database of molecules that are challenging to optimize.  
Geometries from Baker J. Comput. Chem. 14 1085 (1993), as reported in Bakken and Helgaker, J. Chem. Phys. 117, 9160 (2002), with a few further corrections.  
No reference energies defined.

- **cp** 'off'

- **rlxd** 'off'
- **subset**
  - 'small'
  - 'large'

---

## BASIC

Database of simple molecules, mostly for testing.  
Geometries from nowhere special, and no reference energies defined.

- **cp** 'off'
- **rlxd** 'off'
- **subset** ['h2o', 'nh3', 'ch4']

---

## BBI

Database (Merz) of protein backbone-backbone interactions.  
Geometries from Kenneth Merz Group, Univ. of Florida.  
Reference interaction energies from Sherrill group, Georgia Tech.

- **cp** 'off' || 'on'
- **rlxd** 'off'

---

## CFLOW

Database of extended conjugated bimolecular systems.  
Geometries and Reference interaction energies from the following articles:

Polyene geometries from Marshall et al. JCTC 6 3681 (2010).  
Polyene reference interaction energies from Sherrill group by ccSD(t\*\*)-f12b/heavy-aug-cc-pvdz.  
Acene geometries (except benzene) from Sherrill group by df-mp2/cc-pvtz c.2011.  
Benzene geometry from NBC10 database and citations therein.  
Acene reference interaction energies (incl. benzene dimer) from Sherrill group by ccSD(t\*\*)-f12b/aug-cc-pvdz.  
Buckybowl (Pulay-labeled) geometries from Sherrill group by PBE1PBE/6-31G\*, following Pulay's instructions in Janowski et al. CPL 512 155 (2011).  
Buckybowl (Pulay-labeled) reference interaction energies from Janowski et al. CPL 512 155 (2011).  
Buckyware (Grimme-labeled) geometries from Grimme PCCP 12 7091 (2010).  
Buckyware (Grimme-labeled) reference interaction energies from Grimme PCCP 12 7091 (2010) by B97-D2/TZVP.  
Collection into CFLOW by Parrish et al. XXX XXX XXXXXX (2012).

- **cp** 'off' || 'on'

- **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
    - 'equilibrium'
    - 'Polyenes' equilibrium for linear polyene dimers for 2 through 16 monomer carbons
    - 'cBzBz' 5-point dissociation curve for benzene dimer
    - 'c2BzBz' 5-point dissociation curve for naphthalene-benzene complex
    - 'c2Bz2Bz' 5-point dissociation curve for naphthalene dimer
    - 'c3Bz2Bz' 5-point dissociation curve for anthracene-naphthalene complex
    - 'c3Bz3Bz' 5-point dissociation curve for anthracene dimer
    - 'c4Bz3Bz' 5-point dissociation curve for tetracene-anthracene complex
    - 'Arenes' equilibrium for benzene dimer through tetracene-anthracene complex linear arenes
    - 'cArenes' 5-point curves around benzene dimer through tetracene-anthracene complex linear arenes
    - 'cPulay' 4-point dissociation curve for bowl-in-bowl corannulene dimer
    - 'Pulay' Pulay bowl-in-bowl corannulene dimer dissociation curve and extra point
    - 'Grimme60' Grimme corannulene dimer, C60 @ buckybowl, and C60 @ buckycatcher
    - 'Grimme70' Grimme C70 @ buckycatcher at three orientations
    - 'Paper' linear polyene dimers, equilibrium arene complexes, Pulay corannulene dimer curve, and Grimme corannulene dimer and C60 complexes
    - 'cPaper' linear polyene dimers, arene complex curves, Pulay corannulene dimer curve, and Grimme corannulene dimer and C60 complexes
- 

## CORE

Database of Pulay corannulene structures. Subsumed into CFLOW.

- **cp** 'off' || 'on'
  - **rlxd** 'off'
- 

## G2

Database of thermodynamic reactions.

WIP

- **cp** 'off'
  - **rlxd** 'off'
- 

## HBC6



Database (Sherrill) of interaction energies for dissociation curves of doubly hydrogen-bonded bimolecular complexes. Geometries from Thanthiriwatte et al. JCTC 7 88 (2011).

Reference interaction energies from Marshall et al. JCP 135 194102 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off' || 'on'
  - **benchmark**
    - 'HBC60' Thanthiriwatte et al. JCTC 7 88 (2011).
    - $\Rightarrow$  'HBC6A'  $\Leftarrow$  Marshall et al. JCP 135 194102 (2011).
    - 'HBC6ARLX' Sherrill group, unpublished.
  - **subset**
    - 'small'
    - 'large'
    - 'equilibrium'
- 

## HSG

Database (Merz) of interaction energies for bimolecular complexes from protein-indinavir reaction site.

Geometries from Faver et al. JCTC 7 790 (2011).

Reference interaction energies from Marshall et al. JCP 135 194102 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **benchmark**
    - 'HSG0' Faver et al. JCTC 7 790 (2011).
    - $\Rightarrow$  'HSGA'  $\Leftarrow$  Marshall et al. JCP 135 194102 (2011).
  - **subset**
    - 'small'
    - 'large'
- 

## HTBH

Database (Truhlar) of hydrogen-transfer barrier height reactions.

Geometries from Truhlar and coworkers at site

[http://t1.chem.umn.edu/misc/database\\_group/database\\_therm\\_bh/raw\\_geom.cgi](http://t1.chem.umn.edu/misc/database_group/database_therm_bh/raw_geom.cgi).

Reference energies from Zhao et al. JPCA, 109 2012-2018 (2005) doi: 10.1021/jp045141s [in supporting information].

- **cp** 'off'

- **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
- 

## JSCH

Database (Hobza) of interaction energies for nucelobase pairs.

Geometries and reference interaction energies from Jurecka et al. PCCP 8 1985 (2006).

Corrections implemented from footnote 92 of Burns et al., JCP 134 084107 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
- 

## NBC10

Database (Sherrill) of interaction energies for dissociation curves of dispersion-bound bimolecular complexes.

Geometries and Reference interaction energies from the following articles:

Benzene Dimers from Sherrill et al. JPCA 113 10146 (2009).

Benzene-Hydrogen Sulfide from Sherrill et al. JPCA 113 10146 (2009).

Benzene-Methane from Sherrill et al. JPCA 113 10146 (2009).

Methane Dimer from Takatani et al. PCCP 9 6106 (2007).

Pyridine Dimers from Hohenstein et al. JPCA 113 878 (2009).

Collection into NBC10 from Burns et al. JCP 134 084107 (2011).

Reference from Marshall et al. JCP 135 194102 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **benchmark**
    - 'NBC100' Burns et al. JCP 134 084107 (2011).
    - $\Rightarrow$  'NBC10A'  $\Leftarrow$  Marshall et al. JCP 135 194102 (2011).
  - **subset**
    - 'small'
    - 'large'
    - 'equilibrium'
    - 'BzBz\_S' dissociation curve for benzene dimer, sandwich
-

- 'BzBz\_T' dissociation curve for benzene dimer, t-shaped
  - 'BzBz\_PD34' dissociation curve for benzene dimer, parallel displaced by 3.4A
  - 'BzH2S' dissociation curve for benzene-H2S
  - 'BzMe' dissociation curve for benzene-methane
  - 'MeMe' dissociation curve for methane dimer
  - 'PyPy\_S2' dissociation curve for pyridine dimer, sandwich
  - 'PyPy\_T3' dissociation curve for pyridine dimer, t-shaped
  - 'BzBz\_PD32' dissociation curve for benzene dimer, parallel displaced by 3.2A
  - 'BzBz\_PD36' dissociation curve for benzene dimer, parallel displaced by 3.6A
- 

## NHTBH

Database (Truhlar) of non-hydrogen-transfer barrier height reactions.

Geometries and Reaction energies from Truhlar and coworkers at site

[http://t1.chem.umn.edu/misc/database\\_group/database\\_therm\\_bh/non\\_H.htm](http://t1.chem.umn.edu/misc/database_group/database_therm_bh/non_H.htm).

- **cp** 'off'
  - **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
- 

## RGC10

Database (Sherrill) of interaction energies for dissociation curves of rare-gas biatomic complexes.

Geometries and reference interaction energies from Tang et al. JCP 118 4976 (2003).

- **cp** 'off' || 'on'
- **rlxd** 'off'
- **subset**
  - 'small'
  - 'large'
  - 'equilibrium'
  - 'HeHe' 18-point dissociation curve for helium dimer
  - 'HeNe' 18-point dissociation curve for helium-neon complex
  - 'HeAr' 18-point dissociation curve for helium-argon complex
  - 'HeKr' 18-point dissociation curve for helium-krypton complex

- 'NeNe' 18-point dissociation curve for neon dimer
  - 'NeAr' 18-point dissociation curve for neon-argon complex
  - 'NeKr' 18-point dissociation curve for neon-krypton complex
  - 'ArAr' 18-point dissociation curve for argon dimer
  - 'ArKr' 18-point dissociation curve for argon-krypton complex
  - 'KrKr' 18-point dissociation curve for krypton dimer
- 

## S22

Database (Hobza) of interaction energies for bimolecular complexes.

Geometries from Jurecka et al. PCCP 8 1985 (2006).

Reference interaction energies from Marshall et al. JCP 135 194102 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **benchmark**
    - 'S220' Jurecka et al. PCCP 8 1985 (2006).
    - 'S22A' Takatani et al. JCP 132 144104 (2010).
    - $\Rightarrow$  'S22B'  $\Leftarrow$  Marshall et al. JCP 135 194102 (2011).
  - **subset**
    - 'small' water dimer, methane dimer, ethene-ethine
    - 'large' adenine-thymine
    - 'HB' hydrogen-bonded systems
    - 'MX' mixed-influence systems
    - 'DD' dispersion-dominated systems
- 

## S22by5

Database (Hobza) of interaction energies for dissociation curves of bimolecular complexes.

Geometries and reference interaction energies from Grafova et al. JCTC 6 2365 (2010).

Note that the S22by5-N-1.0 members are essentially the same geometries as S22-N (there's trivial round-off error) but the reference interaction energies for S22by5 are of lower quality than those of S22.

- **cp** 'off' || 'on'
- **rlxd** 'off'
- **subset**
  - 'small'
  - 'large'

- 'equilibrium'
  - 'mol11' five-point (0.9, 1.0, 1.2, 1.5, 2.0)  $\times R_{eq}$  dissociation curve for molecule 1
  - ...
  - 'mol22' five-point (0.9, 1.0, 1.2, 1.5, 2.0)  $\times R_{eq}$  dissociation curve for molecule 22
- 

## S66

Database (Hobza) of interaction energies for bimolecular complexes.

Geometries and reference energies from Rezac et al. JCTC 7 2427 (2011).

- **cp** 'off' || 'on'
  - **rlxd** 'off'
  - **subset**
    - 'small'
    - 'large'
    - 'HB' hydrogen-bonded systems
    - 'MX' mixed-influence systems
    - 'DD' dispersion-dominated systems
- 

## SSI

Database (Merz) of interaction energies for protein sidechain-sidechain interactions.

Geometries from Kenneth Merz Group, Univ. of Florida.

Reference interaction energies from <Reference>.

- **cp** 'off' || 'on'
  - **rlxd** 'off'
-



# COMPLETE BASIS SET

```
wrappers.complete_basis_set (name[, scf_basis, scf_scheme, corl_wfn, corl_basis, corl_scheme,
                                delta_wfn, delta_wfn_lesser, delta_basis, delta_scheme, delta2_wfn,
                                delta2_wfn_lesser, delta2_basis, delta2_scheme])
```

Function to define a multistage energy method from combinations of basis set extrapolations and delta corrections and condense the components into a minimum number of calculations.

**Aliases** cbs()

**Returns** (*float*) – Total electronic energy in Hartrees

**Psi variables**

**CBS TOTAL ENERGY**

**CBS REFERENCE ENERGY**

**CBS CORRELATION ENERGY**

**CURRENT ENERGY**

**CURRENT REFERENCE ENERGY**

**CURRENT CORRELATION ENERGY**

**Caution:** Some features are not yet implemented. Buy a developer a coffee.

- Methods beyond basic scf, mp2, ccsd, ccsd(t) not yet hooked in through PSI variables, df-mp2 in particular.
- No scheme defaults for given basis zeta number, so scheme must be specified explicitly.
- No way to tell function to boost fitting basis size for all calculations.
- No way to extrapolate def2 family basis sets
- Need to add more extrapolation schemes

As represented in the equation below, a CBS energy method is defined in four sequential stages (scf, corl, delta, delta2) covering treatment of the reference total energy, the correlation energy, a delta correction to the correlation energy, and a second delta correction. Each is activated by its stage\_wfn keyword and is only allowed if all preceding stages are active.

$$E_{total}^{CBS} = \mathcal{F}_{scf\_scheme} \left( E_{total, SCF}^{scf\_basis} \right) + \mathcal{F}_{corl\_scheme} \left( E_{corl, corl\_wfn}^{corl\_basis} \right) + \delta_{delta\_wfn\_lesser}^{delta\_wfn} + \delta_{delta2\_wfn\_lesser}^{delta2\_wfn}$$

Here,  $\mathcal{F}$  is an energy or energy extrapolation scheme, and the following also hold.

$$\delta_{delta\_wfn\_lesser}^{delta\_wfn} = \mathcal{F}_{delta\_scheme} \left( E_{corl, delta\_wfn}^{delta\_basis} \right) - \mathcal{F}_{delta\_scheme} \left( E_{corl, delta\_wfn\_lesser}^{delta\_basis} \right)$$

$$\delta_{\text{delta2\_wfn\_lesser}}^{\text{delta2\_wfn}} = \mathcal{F}_{\text{delta2\_scheme}} \left( E_{\text{corl, delta2\_wfn}}^{\text{delta2\_basis}} \right) - \mathcal{F}_{\text{delta2\_scheme}} \left( E_{\text{corl, delta2\_wfn\_lesser}}^{\text{delta2\_basis}} \right)$$

A translation of this ungainly equation to example [5] below is as follows. In words, this is a double- and triple-zeta 2-point Helgaker-extrapolated CCSD(T) coupled-cluster correlation correction appended to a triple- and quadruple-zeta 2-point Helgaker-extrapolated MP2 correlation energy appended to a SCF/aug-cc-pVQZ reference energy.

$$E_{\text{total}}^{\text{CBS}} = \mathcal{F}_{\text{highest\_1}} \left( E_{\text{total, SCF}}^{\text{aug-cc-pVQZ}} \right) + \mathcal{F}_{\text{corl\_xtpl\_helgaker\_2}} \left( E_{\text{corl, MP2}}^{\text{aug-cc-pV[TQ]Z}} \right) + \delta_{\text{MP2}}^{\text{CCSD(T)}}$$

$$\delta_{\text{MP2}}^{\text{CCSD(T)}} = \mathcal{F}_{\text{corl\_xtpl\_helgaker\_2}} \left( E_{\text{corl, CCSD(T)}}^{\text{aug-cc-pV[DT]Z}} \right) - \mathcal{F}_{\text{corl\_xtpl\_helgaker\_2}} \left( E_{\text{corl, MP2}}^{\text{aug-cc-pV[DT]Z}} \right)$$

•**Energy Methods** The presence of a `stage_wfn` keyword is the indicator to incorporate (and check for `stage_basis` and `stage_scheme` keywords) and compute that stage in defining the CBS energy.

The `cbs()` function requires, at a minimum, `name='scf'` and `scf_basis` keywords to be specified for reference-step only jobs and `name` and `corl_basis` keywords for correlated jobs.

#### Parameters

- **name** (*string*) – 'scf' || 'ccsd' || etc.

First argument, usually unlabeled. Indicates the computational method for the correlation energy, unless only reference step to be performed, in which case should be 'scf'. Over-ruled if `stage_wfn` keywords supplied.

- **corl\_wfn** (*string*) – 'mp2' || 'ccsd(t)' || etc.

Indicates the energy method for which the correlation energy is to be obtained. Can also be specified with `name` or as the unlabeled first argument to the function.

- **delta\_wfn** (*string*) – 'ccsd' || 'ccsd(t)' || etc.

Indicates the (superior) energy method for which a delta correction to the correlation energy is to be obtained.

- **delta\_wfn\_lesser** (*string*) –  $\Rightarrow$  'mp2'  $\Leftarrow$  || 'ccsd' || etc.

Indicates the inferior energy method for which a delta correction to the correlation energy is to be obtained.

- **delta2\_wfn** (*string*) – 'ccsd' || 'ccsd(t)' || etc.

Indicates the (superior) energy method for which a second delta correction to the correlation energy is to be obtained.

- **delta2\_wfn\_lesser** (*string*) –  $\Rightarrow$  'mp2'  $\Leftarrow$  || 'ccsd(t)' || etc.

Indicates the inferior energy method for which a second delta correction to the correlation energy is to be obtained.

•**Basis Sets** Currently, the basis set set through `set` commands have no influence on a cbs calculation.

#### Parameters



- **scf\_basis** (*string*) –  $\Rightarrow$  corl\_basis  $\Leftarrow$  || 'cc-pV[TQ]Z' || 'jun-cc-pv[tq5]z' || '6-31G\*' || etc.

Indicates the sequence of basis sets employed for the reference energy. If any correlation method is specified, scf\_basis can default to corl\_basis.

- **corl\_basis** (*string*) – 'cc-pV[TQ]Z' || 'jun-cc-pv[tq5]z' || '6-31G\*' || etc.

Indicates the sequence of basis sets employed for the correlation energy.

- **delta\_basis** (*string*) – 'cc-pV[TQ]Z' || 'jun-cc-pv[tq5]z' || '6-31G\*' || etc.

Indicates the sequence of basis sets employed for the delta correction to the correlation energy.

- **delta2\_basis** (*string*) – 'cc-pV[TQ]Z' || 'jun-cc-pv[tq5]z' || '6-31G\*' || etc.

Indicates the sequence of basis sets employed for the second delta correction to the correlation energy.

• **Schemes** Transformations of the energy through basis set extrapolation for each stage of the CBS definition. A complaint is generated if number of basis sets in stage\_basis does not exactly satisfy requirements of stage\_scheme. An exception is the default, 'highest\_1', which uses the best basis set available. See [Extrapolation Schemes](#) for all available schemes.

#### Parameters

- **scf\_scheme** (*function*) –  $\Rightarrow$  highest\_1  $\Leftarrow$  || scf\_xtpl\_helgaker\_3 || etc.

Indicates the basis set extrapolation scheme to be applied to the reference energy.

- **corl\_scheme** (*function*) –  $\Rightarrow$  highest\_1  $\Leftarrow$  || corl\_xtpl\_helgaker\_2 || etc.

Indicates the basis set extrapolation scheme to be applied to the correlation energy.

- **delta\_scheme** (*function*) –  $\Rightarrow$  highest\_1  $\Leftarrow$  || corl\_xtpl\_helgaker\_2 || etc.

Indicates the basis set extrapolation scheme to be applied to the delta correction to the correlation energy.

- **delta2\_scheme** (*function*) –  $\Rightarrow$  highest\_1  $\Leftarrow$  || corl\_xtpl\_helgaker\_2 || etc.

Indicates the basis set extrapolation scheme to be applied to the second delta correction to the correlation energy.

#### Examples

```
>>> # [1] replicates with cbs() the simple model chemistry scf/cc-pVDZ: set basis cc-pVDZ energy
>>> cbs('scf', scf_basis='cc-pVDZ')

>>> # [2] replicates with cbs() the simple model chemistry mp2/jun-cc-pVDZ: set basis jun-cc-pVDZ
>>> cbs('mp2', corl_basis='jun-cc-pVDZ')

>>> # [3] DTQ-zeta extrapolated scf reference energy
>>> cbs('scf', scf_basis='cc-pV[DTQ]Z', scf_scheme=scf_xtpl_helgaker_3)

>>> # [4] DT-zeta extrapolated mp2 correlation energy atop a T-zeta reference
>>> cbs('mp2', corl_basis='cc-pv[dt]z', corl_scheme=corl_xtpl_helgaker_2)

>>> # [5] a DT-zeta extrapolated coupled-cluster correction atop a TQ-zeta extrapolated mp2 corr
>>> cbs('mp2', corl_basis='aug-cc-pv[tq]z', corl_scheme=corl_xtpl_helgaker_2, delta_wfn='ccsd(t)')
```

```
>>> # [6] a D-zeta ccSD(t) correction atop a DT-zeta extrapolated ccSD cluster correction atop a
>>> cbs('mp2', corl_basis='aug-cc-pv[tq]z', corl_scheme=corl_xtpl_helgaker_2, delta_wfn='ccSD',

>>> # [7] cbs() coupled with database()
>>> database('mp2', 'BASIC', subset=['h2o','nh3'], symm='on', func=cbs, corl_basis='cc-pV[tq]z',
```

## 7.1 Output

At the beginning of a `cbs()` job is printed a listing of the individual energy calculations which will be performed. The output snippet below is from the example job [2] above. It shows first each model chemistry needed to compute the aggregate model chemistry requested through `cbs()`. Then, since, for example, an `energy('ccSD(t)')` yields CCSD(T), CCSD, MP2, and SCF energy values, the wrapper condenses this task list into the second list of minimum number of calculations which will actually be run.

Naive listing of computations required.

scf / aug-cc-pvqz	for SCF TOTAL ENERGY
mp2 / aug-cc-pvtz	for MP2 CORRELATION ENERGY
mp2 / aug-cc-pvqz	for MP2 CORRELATION ENERGY
ccSD(t) / aug-cc-pvdz	for CCSD(T) CORRELATION ENERGY
ccSD(t) / aug-cc-pvtz	for CCSD(T) CORRELATION ENERGY
mp2 / aug-cc-pvdz	for MP2 CORRELATION ENERGY
mp2 / aug-cc-pvtz	for MP2 CORRELATION ENERGY

Enlightened listing of computations required.

mp2 / aug-cc-pvqz	for MP2 CORRELATION ENERGY
ccSD(t) / aug-cc-pvdz	for CCSD(T) CORRELATION ENERGY
ccSD(t) / aug-cc-pvtz	for CCSD(T) CORRELATION ENERGY

At the end of a `cbs()` job is printed a summary section like the one below. First, in the components section, are listed the results for each model chemistry available, whether required for the `cbs` job (\*) or not. Next, in the stages section, are listed the results for each extrapolation. The energies of this section must be dotted with the weightings in column `Wt` to get the total `cbs` energy. Finally, in the CBS section, are listed the results for each stage of the `cbs` procedure. The stage energies of this section sum outright to the total `cbs` energy.

==> Components <==

Method / Basis	Rqd	Energy [H]	Variable
scf / aug-cc-pvqz	*	-1.11916375	SCF TOTAL ENERGY
mp2 / aug-cc-pvqz	*	-0.03407997	MP2 CORRELATION ENERGY
scf / aug-cc-pvdz		-1.11662884	SCF TOTAL ENERGY
mp2 / aug-cc-pvdz	*	-0.02881480	MP2 CORRELATION ENERGY
ccSD(t) / aug-cc-pvdz	*	-0.03893812	CCSD(T) CORRELATION ENERGY
ccSD / aug-cc-pvdz		-0.03893812	CCSD CORRELATION ENERGY
scf / aug-cc-pvtz		-1.11881134	SCF TOTAL ENERGY
mp2 / aug-cc-pvtz	*	-0.03288936	MP2 CORRELATION ENERGY
ccSD(t) / aug-cc-pvtz	*	-0.04201004	CCSD(T) CORRELATION ENERGY
ccSD / aug-cc-pvtz		-0.04201004	CCSD CORRELATION ENERGY

==> Stages <==

Stage	Method / Basis	Wt	Energy [H]	Scheme
-------	----------------	----	------------	--------

scf	scf / aug-cc-pvqz	1	-1.11916375	highest_1
corl	mp2 / aug-cc-pv[tq]z	1	-0.03494879	corl_xtpl_helgaker_2
delta	ccsd(t) / aug-cc-pv[dt]z	1	-0.04330347	corl_xtpl_helgaker_2
delta	mp2 / aug-cc-pv[dt]z	-1	-0.03460497	corl_xtpl_helgaker_2

==> CBS <==

Stage	Method / Basis	Energy [H]	Scheme
scf	scf / aug-cc-pvqz	-1.11916375	highest_1
corl	mp2 / aug-cc-pv[tq]z	-0.03494879	corl_xtpl_helgaker_2
delta	ccsd(t) - mp2 / aug-cc-pv[dt]z	-0.00869851	corl_xtpl_helgaker_2
total	CBS	-1.16281105	

## 7.2 Extrapolation Schemes

`wrappers.highest_1(**largs)`

Scheme for total or correlation energies with a single basis or the highest zeta-level among an array of bases.

Used by `wrappers.complete_basis_set()`.

$$E_{total}^X = E_{total}^X$$

`wrappers.scf_xtpl_helgaker_2(**largs)`

Extrapolation scheme for reference energies with two adjacent zeta-level bases. Used by

`wrappers.complete_basis_set()`.

$$E_{total}^X = E_{total}^{\infty} + \beta e^{-\alpha X}, \alpha = 1.63$$

`wrappers.scf_xtpl_helgaker_3(**largs)`

Extrapolation scheme for reference energies with three adjacent zeta-level bases. Used by

`wrappers.complete_basis_set()`.

$$E_{total}^X = E_{total}^{\infty} + \beta e^{-\alpha X}$$

`wrappers.corl_xtpl_helgaker_2(**largs)`

Extrapolation scheme for correlation energies with two adjacent zeta-level bases. Used by

`wrappers.complete_basis_set()`.

$$E_{corl}^X = E_{corl}^{\infty} + \beta X^{-3}$$



# FRACTIONAL OCCUPATION

```
frac.frac_nuke (mol, **kwargs)  
frac.frac_traverse (mol, **kwargs)  
frac.ip_fitting (mol, omega_l, omega_r, **kwargs)
```



# BEGINNER PSITHON PROGRAMMING

---

**Note:** No recompile of the PSI program is necessary for changes made to files in \$PSIDATADIR, including those described below.

---

## 9.1 Defining a Method Alias

Since quantum chemical methods in PSI4 are accessed through Python functions, and most important quantities are available as PSI variables, it is straightforward to create aliases to commonly run calculations or to define hybrid methods. The \$PSIDATADIR/python/aliases.py file is intended for editing by the user for this purpose.

As an example, the MP2.5 method is the average of MP2 and MP3. The latter is available through the arbitrary order MPn code and returns all lower energies along with it in PSI variables. The following is basic code that will compute and return the MP2.5 energy.

```
def run_mp2_5(name, **kwargs):

    energy('mp3', **kwargs)
    e_scf = PsiMod.get_variable('SCF TOTAL ENERGY')
    ce_mp2 = PsiMod.get_variable('MP2 CORRELATION ENERGY')
    ce_mp3 = PsiMod.get_variable('MP3 CORRELATION ENERGY')

    ce_mp25 = 0.5 * (ce_mp2 + ce_mp3)
    e_mp25 = e_scf + ce_mp25

    print "MP2.5 total energy:                %16.8f\n" % (e_mp25)
    print "MP2.5 correlation energy:          %16.8f\n" % (ce_mp25)

    return e_mp25
```

Compare the above to the method that resides in aliases.py. The rationale for the changes is indicated in the comments below.

```
def run_mp2_5(name, **kwargs):
    lowname = name.lower() # handy variable with name keyword in lowercase
    kwargs = kwargs_lower(kwargs) # removes case sensitivity in keyword names

    # Run detci calculation and collect conventional quantities
    energy('mp3', **kwargs)
    e_scf = PsiMod.get_variable('SCF TOTAL ENERGY')
    ce_mp2 = PsiMod.get_variable('MP2 CORRELATION ENERGY')
    ce_mp3 = PsiMod.get_variable('MP3 CORRELATION ENERGY')
```

```
e_mp2 = e_scf + ce_mp2  # reform mp2 and mp3 total energies for printing
e_mp3 = e_scf + ce_mp3

# Compute quantities particular to MP2.5
ce_mp25 = 0.5 * (ce_mp2 + ce_mp3)
e_mp25 = e_scf + ce_mp25
PsiMod.set_variable('MP2.5 CORRELATION ENERGY', ce_mp25)  # add new method's important results
PsiMod.set_variable('MP2.5 TOTAL ENERGY', e_mp25)          # to PSI variable repository
PsiMod.set_variable('CURRENT CORRELATION ENERGY', ce_mp25)
PsiMod.set_variable('CURRENT ENERGY', e_mp25)             # geometry optimizer tracks this variable, permit
                                                           # MP2.5 finite difference optimizations

# build string of title banner and print results
banners = ''
banners += """PsiMod.print_out('\n')\n"""
banners += """banner(' MP2.5 ')\n"""
banners += """PsiMod.print_out('\n')\n\n"""
exec banners

tables = ''
tables += """   SCF total energy:                %16.8f\n""" % (e_scf)
tables += """   MP2 total energy:                %16.8f\n""" % (e_mp2)
tables += """   MP2.5 total energy:              %16.8f\n""" % (e_mp25)
tables += """   MP3 total energy:                %16.8f\n\n""" % (e_mp3)
tables += """   MP2 correlation energy:          %16.8f\n""" % (ce_mp2)
tables += """   MP2.5 correlation energy:        %16.8f\n""" % (ce_mp25)
tables += """   MP3 correlation energy:          %16.8f\n""" % (ce_mp3)
PsiMod.print_out(tables)  # prints nice header and table of all involved quantities to output fi

return e_mp25
```

One final step is necessary. At the end of the `aliases.py` file, add the following line.

```
procedures['energy']['mp2.5'] = run_mp2_5
```

This permits the newly defined MP2.5 method to be called in the input file with the following command.

```
energy('mp2.5')
```

## 9.2 Creating a New Database

A necessary consideration in constructing a database is the distinction between reagents and reactions. A reagent is a single molecular system (may be a dimer) whose geometry you are possession of and whose electronic energy may be of interest. A reaction is a combination of one or more reagent energies whose value you are interested in and a reference value for which you may or may not be in possession of. A few examples follow. In a database of interaction energies, the reagents are dimers and their component monomers (usually derived from the dimer geometry), and the reactions are the dimer less monomers energies. In a database of barrier heights, the reagents are reactants, products, and transition-state structures, and the reactions are the transition-states less minimum-energy structures. Possibly you may have a collection of structures to simply be acted upon in parallel, in which case the structures are both the reagents and the reactions. The role of the `database.py` file is to collect arrays and dictionaries that define the geometries of reagents (GEOS), their combination into reactions (RXNM & ACTV), available reference values for reactions (BIND), and brief comments for reagents and reactions (TAGL). The journey from reagent geometries to functional `database.py` file is largely automated, in a process described below.

- **Prepare geometry files** Assemble xyz files for all intended reagent systems in a directory. Follow the rules below for best results. The filename for each xyz file should be the name of the system. lowercase or MixedCase is preferable (according to Sherrill lab convention). Avoid dashes and dots in the name as



python won't allow them. If you're determined to have dashes and dots, they must be replaced by other characters in the `process_input` line, then translated back in the GEOS section; see `NBC10.py` for an example.

- The first line for each xyz file should be the number of atoms in the system.
  - The second line for each xyz file can be blank (interpreted as no comment), anything (interpreted as a comment), or two integers and anything (interpreted as charge, multiplicity, and remainder as comment).
  - The third and subsequent lines have four fields: the element symbol and the three cartesian coordinates in angstroms. The atom lines should not contain any dummy atoms (what's the use in cartesian form). For dimer systems, an algorithm is used to apportion the atoms into two fragments; thus the atoms need not be arranged with all fragmentA atoms before all fragmentB atoms. The algorithm will fail for very closely arranged fragments. For dimers, any charge and multiplicity from the second line will be applied to fragmentA (python); charge and multiplicity may need to be redistributed later in the editing step.
- Run script `ixyz2database.pl`

Move into the directory where all your xyz files are located. Run the script in place, probably as `$PSIDATADIR/databases/ixyz2database.pl`. It will ask a number of questions about your intended database and generate a python file named for your database. Uppercase is preferable for database names (according to Sherrill lab convention). Note your choice for the route variable for the next step.
  - Edit file `database.py`
    - All routes. Optionally, rearrange the order of reactions in `HRXN` as this will define the order for the database.
    - All routes. Optionally, add sources for geometries and any reference data to commented lines above the `dbse` variable.
    - All routes. Optionally, the comment lines of `TAGL` may be edited in plain text.
    - All routes. Optionally, fill in reference values (in kcal/mol) into `BIND`.
    - All routes. Optionally, define alternate sets of reference values in the array `BIND_ALTREF` in the `database.py` file to be called in a `psi4` input file as `benchmark='ALTREF'`. See `S22.py` as an example.
    - All routes. Optionally, fill in the least computationally expensive 2-3 reactions into `HRXN_SM` and the most expensive into `HRXN_LG`.
    - All routes. Optionally, define subsets of reactions in the array `SUBSETARRAY = ['reaction', 'reaction']` in the `database.py` file to be called in a `psi4` input file as `subset='SUBSETARRAY'`. See `NBC10.py` as an example.
    - All routes. Necessarily (if charge and multiplicity not read in through `line2 = cgm` and nor all neutral singlets), assign correct charge and multiplicity to all reagents.
    - Route 3. Necessarily (if any charge and multiplicity specified for the whole reagent is not intended for fragmentA with neutral singlet fragmentB), apportion charge and multiplicity properly between fragmentA and fragmentB. This is not likely necessary if all subsystems are neutral singlets.
    - Route 2. Necessarily, define the reagents that contribute to each reaction by filling in the empty single-quotes in `ACTV`. Add or delete lines as necessary if for each reaction more or fewer than three reagents contribute. See `NHTBH.py` as an example.
    - Route 2. Necessarily, define the mathematical contribution of reagents to reactions by adding a number (most often +1 or -1) for each reagent to the `RXNM` of each reaction. See `NHTBH.py` as an example.
    - All routes. Necessarily, copy your new database into `$PSIDATADIR/databases`.



# FUNCTION INTERCALLS

For many of the PSI4 Python functions described above, it makes scientific sense that they could be called in combination. For instance, one could optimize all the reagents in a database or compute a counterpoise-corrected interaction energy with an extrapolated method. The table below outlines permitted intercalls between functions, showing that `db(opt(cbs(energy())))` is allowed, while `db(cp(energy()))` is not. This table is not yet validated for calls with `cp()`.

Caller	Callee				
	cp	db	opt	cbs	energy
cp		—	Y	Y	Y
db	—		Y	Y	Y
opt	—	—		Y	Y
cbs	—	—	—		Y
energy	—	—	—	—	

- The command `db(opt(cbs(energy())))` is actually expressed as `db(..., db_func=opt, opt_func=cbs)`. The perhaps expected final argument of `cbs_func=energy` is not necessary since `energy()` is always the function called by default. Also, the outermost internal function call (`db_func` above) can be called as just `func`. Several examples of intercalls between Python functions can be found in sample input *pywrap\_all*.
- All keyword arguments are passed along to each function traversed in the Python driver, so there should be no concern for separating them, grouping them, or designating them for a particular function when undertaking a nested calculation. Where the same keyword is used by multiple functions, prefixes are added, e.g., **db\_mode** and **opt\_mode**.
- Function intercalls should not be used in sow/reap mode.



# EMBARRASSING PARALLELISM

what functions; no intercalls; no local set; special section in parameter list



# PSITHON PROGRAMMING BEST PRACTICES

- Thy python functions shall always have final argument `**kwargs`, that they may take in and pass on keywords meant for other functions. Yea, even the `run_mscf()`, and `run_ccsd()` -type functions that have no use for `kwargs`. The exceptions are python functions that are only helpers called by a driver function.
- Python functions should read the `kwargs` dictionary and (possibly) add to it. Functions should not pop or remove keywords from `kwargs`, even those keywords meaningful only to itself. This will ensure that the complete `kwargs` is available for pickling and sow/reap procedures. The exception is the `molecule` argument, which is read by the first function that gets ahold of it. This first function activates the molecule and pops it out of `kwargs`, effectively setting molecule for all subsequent functions. The code below should suffice.

```
# Make sure the molecule the user provided is the active one
if 'molecule' in kwargs:
    activate(kwargs['molecule'])
    del kwargs['molecule']
molecule = PsiMod.get_active_molecule()
molecule.update_geometry()
```

- Preferably, the python function signature (for functions intended to be called in input files) is `function(name, **kwargs)`. For functions that have other positional keywords, please bundle them into `kwargs` at earliest convenience (see `wrappers.database()` argument `db_name` for example).
- After the docstring, the first two lines of your function should be the ones below. The first provides a case insensitive handle to the name argument value. The second converts all the `kwargs` dictionary keys to lowercase versions of themselves, so that input files can be case insensitive.

```
lowername = name.lower()
kwargs = kwargs_lower(kwargs)
```

- Case sensitivity for `kwargs` dictionary values still needs to be handled. The first line below shows how to convert argument values to lowercase for matching. When not matching a whole value such that regular expressions are needed, the second line below performs a case insensitive match.

```
if (kwargs['db_mode'].lower() == 'continuous'):
if re.match(r'^sapt', name, flags=re.IGNORECASE):
```

- Match boolean keywords (`db_cp` in the example below) with expressions like the following, which allow case insensitive `yes/true/on/1/no/false/off/0` user input. If your argument's value is a derivative level, similarly, use `input.der0th`, `input.der1st`, and `input.der2nd`.

```
if input.yes.match(str(db_cp)):
elif input.no.match(str(db_cp)):
```

- For keywords that might be used in other functions as well as your own, prepend the argument name with a short representation of your function name. For example, there are keywords `cp_func`, `db_func`, and `opt_func` to request what python function, if not `energy()`, is called by `cp()`, `database()`, and `optimize()`.
- Upon checking in a new python file, edit the file `psi4/doc/userman/source/index.rst` and follow the instructions therein that your file may be autodocumented here.
- Write docstrings! For a major function intended for use in input files, start with the skeleton docstring in `psi4/lib/python/example_docstring` and replace anything that looks like `<this>`. For a behind-the-scenes function or if you don't want the bother of dealing with `reStructuredText`, just write an ordinary docstring. It will get slurped into the documentation in plain text.
- Your python function should follow [PEP8](#) conventions (without the line-length restriction). I'm aiming for files to pass the line below, unless for good reason. The second line is for database Python files.

```
>>> pep8.py -r --ignore=E501 pythonfile.py
>>> pep8.py -r --ignore=E501,E221,E222,E241,E201,E202 databasefile.py
```

- Your python function should not prevent any test case (make tests, NOT make longtests) from passing. A test case(s) should be written and checked in for any major python function, so that others do not break your code. If most of your work was on the python (as opposed to c++) side, the test case prefix `pywrap_` is suggested.
- Be sure to set any new PSI variables through lines like those below. Especially if the function returns an energy, set the 'current energy' variable. This last is needed to communicate with the optimizer.

```
PsiMod.set_variable('MP2.5 CORRELATION ENERGY', ce_mp25)
PsiMod.set_variable('MP2.5 TOTAL ENERGY', e_mp25)
PsiMod.set_variable('CURRENT ENERGY', e_mp25)
```

- Once your python function is fairly stable on its own, it's potential for interoperability with `energy()/opt()/cp()/db()/cbs()/etc.` should be evaluated. If it makes physical sense that it should work, you should strive to make that interoperability a reality. Some steps:

- If any interoperability is possible, define an argument `xx_func`, where `xx` is a short name for your function. Add near the top of your function code like the below (less the final two lines). The net result of this code is that if the user specifies no `*_func` arguments, then `energy()` gets called. If the user defines `xx_func`, then its value gets called. If the user defines `func`, then its value gets reassigned to `xx_func`, `func` itself is deleted, and `xx_func()` gets called. Whatever is getting called is stored in `func` within the function.

```
# Establish function to call
if not ('xx_func' in kwargs):
    if ('func' in kwargs):
        kwargs['xx_func'] = kwargs['func']
        del kwargs['func']
    else:
        kwargs['xx_func'] = energy
func = kwargs['xx_func']
if not func:
    raise ValidationError('Function \'%s\' does not exist to be called by wrapper counterpoise')
if (func is db):
    raise ValidationError('Wrapper xx is unhappy to be calling function \'%s\'' % (func.__name__))
```

- If specific interoperabilities are known, code them in. For example, if `xx` shouldn't call `db`, add the last two lines above to the `xx` function. If `db` shouldn't call `xx`, add the following two lines below to the `db` function.

```
if (func is xx):
    raise ValidationError('Wrapper database is unhappy to be calling function \'%s\'' % (func.__name__))
```



- Create a multipart test case that runs some intercalls between your function and others (akin to `pywrap_all`). In trials, permute the order of calls a few times to expose any calls that don't clean up after themselves and need further attention.
- When all is validated, add your findings to the great interoperability table in the documentation.



# PSIMOD METHODS



# MOLECULE METHODS



# EXPERT

## 15.1 aliases

Module with functions that call upon those in modules `proc`, `driver`, and `wrappers`.

Place in this file quickly defined procedures such as

- aliases for complex methods
- simple modifications to existing methods

`aliases.run_mp2_5(name, **kwargs)`

Function that computes MP2.5 energy from results of a DETCI MP3 calculation.

```
>>> energy('mp2.5')
```

`aliases.run_plugin_ccsd_serial(name, **kwargs)`

Function encoding sequence of PSI module and plugin calls so that Eugene DePrince's `ccsd_serial` plugin can be called via `driver.energy()`.

```
>>> energy('plugin_ccsd_serial')
```

`aliases.run_plugin_omega(name, **kwargs)`

Function encoding sequence of PSI module and plugin calls, as well as typical options, to access Rob Parrish's `omega` plugin.

```
>>> energy('plugin_omega')
```

`aliases.sherrillgroup_gold_standard(name='mp2', **kwargs)`

Function to call the quantum chemical method known as 'Gold Standard' in the Sherrill group. Uses `wrappers.complete_basis_set()` to evaluate the following expression. Two-point extrapolation of the correlation energy performed according to `wrappers.corl_xtpl_helgaker_2()`.

$$E_{total}^{Au\_std} = E_{total, SCF}^{aug-cc-pVQZ} + E_{corl, MP2}^{aug-cc-pV[TQ]Z} + \delta_{MP2}^{CCSD(T)}|_{aug-cc-pVTZ}$$

```
>>> energy('sherrillgroup_gold_standard')
```

## 15.2 driver

Module with a *procedures* dictionary specifying available quantum chemical methods and functions driving the main quantum chemical functionality, namely single-point energies, geometry optimizations, response properties, and vibrational frequency calculations.

`driver.gradient` (*name*, *\*\*kwargs*)

Function complementary to `optimize()`. Carries out one gradient pass, deciding analytic or finite difference.

`driver.hessian` (*name*, *\*\*kwargs*)

Function to compute force constants. Presently identical to `frequency()`.

`driver.parse_arbitrary_order` (*name*)

Function to parse name string into a method family like CI or MRCC and specific level information like 4 for CISDTQ or MRCCSDTQ.

## 15.3 input

Module import

`input.process_input` (*raw\_input*, *print\_level=1*)

## 15.4 molutil

Module with utility functions that act on molecule objects.

`molutil.activate` (*mol*)

Function to set molecule object *mol* as the current active molecule.

`molutil.dynamic_variable_bind` (*cls*)

Function to bind PsiMod.Molecule class.

`molutil.extract_cluster_indexing` (*mol*, *cluster\_size=0*)

Function to returns a LIST of all subclusters of the molecule *mol* of real size *cluster\_size*. If *cluster\_size* = 0, returns all possible combinations of cluster size.

`molutil.extract_clusters` (*mol*, *ghost=True*, *cluster\_size=0*)

Function to return all subclusters of the molecule *mol* of real size *cluster\_size* and all other atoms ghosted if *ghost* equals true, all other atoms discarded if *ghost* is false. If *cluster\_size* = 0, returns all possible combinations of cluster size.

`molutil.geometry` (*geom*, *name='default'*)

Function to create a molecule object of name *name* from the geometry in string *geom*.

`molutil.new_get_attr` (*self*, *name*)

Function to redefine `get_attr` method of molecule class.

`molutil.new_set_attr` (*self*, *name*, *value*)

Function to redefine `set_attr` method of molecule class.



## 15.5 physconst

## 15.6 proc

Module with functions that encode the sequence of PSI module calls for each of the *name* values of the `energy()`, `optimize()`, `response()`, and `frequency()` function.

`proc.run_adc(name, **kwargs)`

Function encoding sequence of PSI module calls for an algebraic diagrammatic construction calculation.

**Caution:** Get rid of active molecule lines- should be handled in energy.

`proc.run_bccd(name, **kwargs)`

Function encoding sequence of PSI module calls for a Brueckner CCD calculation.

`proc.run_bccd_t(name, **kwargs)`

Function encoding sequence of PSI module calls for a Brueckner CCD(T) calculation.

`proc.run_cc_gradient(name, **kwargs)`

Function encoding sequence of PSI module calls for a CCSD and CCSD(T) gradient calculation.

`proc.run_cc_response(name, **kwargs)`

Function encoding sequence of PSI module calls for a CC2 and CCSD calculation.

`proc.run_ccenergy(name, **kwargs)`

Function encoding sequence of PSI module calls for a CCSD, CC2, and CC3 calculation.

`proc.run_dcft(name, **kwargs)`

Function encoding sequence of PSI module calls for a density cumulant functional theory calculation.

`proc.run_detci(name, **kwargs)`

Function encoding sequence of PSI module calls for a configuration interaction calculation, namely FCI, CIn, MPn, and ZAPTn.

`proc.run_dfcc(name, **kwargs)`

Function encoding sequence of PSI module calls for a density-fitted coupled-cluster calculation.

`proc.run_dfmp2(name, **kwargs)`

Function encoding sequence of PSI module calls for a density-fitted MP2 calculation.

**Caution:** Get rid of madness-era restart file

`proc.run_eom_cc(name, **kwargs)`

Function encoding sequence of PSI module calls for an EOM-CC calculation, namely EOM-CC2, EOM-CCSD, and EOM-CC3.

`proc.run_eom_cc_gradient(name, **kwargs)`

Function encoding sequence of PSI module calls for an EOM-CCSD gradient calculation.

`proc.run_libfock(name, **kwargs)`

Function encoding sequence of PSI module calls for a calculation through libfock, namely RCPHF, RCIS, RTDHF, RTDA, and RTDDFT.

`proc.run_mscf(name, **kwargs)`

Function encoding sequence of PSI module calls for a multiconfigurational self-consistent-field calculation.

`proc.run_mp2(name, **kwargs)`

Function encoding sequence of PSI module calls for a MP2 calculation.

`proc.run_mp2_gradient (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a MP2 gradient calculation.

`proc.run_mp2c (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a coupled MP2 calculation.

`proc.run_mp2drpa (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a MP2-DRPA calculation.

`proc.run_mrcc (name, **kwargs)`  
 Function that prepares environment and input files for a calculation calling Kallay's MRCC code.

`proc.run_psimrcc (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a PSIMRCC computation using a reference from the MC-SCF module

`proc.run_psimrcc_scf (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a PSIMRCC computation using a reference from the SCF module

`proc.run_sapt (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a SAPT calculation of any level.

`proc.run_sapt_ct (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a charge-transfer SAPT calculation of any level.

`proc.run_scf (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a self-consistent-field theory (HF & DFT) calculation.

`proc.run_scf_gradient (name, **kwargs)`  
 Function encoding sequence of PSI module calls for a SCF gradient calculation.

`proc.scf_helper (name, **kwargs)`  
 Function serving as helper to SCF, choosing whether to cast up or just run SCF with a standard guess. This preserves previous SCF options set by other procedures (e.g., SAPT output file types for SCF).

## 15.7 procutil

Module with utility functions used by several Python functions.

`procutil.format_kwargs_for_input (filename, lmode=1, **kwargs)`  
 Function to pickle to file *filename* the options dictionary *kwargs*. Mode *lmode* =2 pickles appropriate settings for reap mode. Used to capture Python options information for distributed (sow/reap) input files.

`procutil.format_molecule_for_input (mol)`  
 Function to return a string of the output of `input.process_input()` applied to the XYZ format of molecule *mol*. Used to capture molecule information for distributed (sow/reap) input files.

`procutil.format_options_for_input ()`  
 Function to return a string of commands to replicate the current state of user-modified options. Used to capture C++ options information for distributed (sow/reap) input files.

**Caution:** Some features are not yet implemented. Buy a developer a coffee.

- Does not cover local (as opposed to global) options.
- Does not work with array-type options.

`procutil.get_psifile (fileno, pidspace='83189')`  
 Function to return the full path and filename for psi file *fileno* (e.g., psi.32) in current namespace *pidspace*.

`procutil.kwargs_lower(kwargs)`

Function to rebuild and return *kwargs* dictionary with all keys made lowercase. Should be called by every function that could be called directly by the user.

## 15.8 psiexceptions

Module with non-generic exceptions classes.

**exception** `psiexceptions.PsiException`

Error class for Psi.

**exception** `psiexceptions.ValidationError(msg)`

Error called for problems with the input file. Prints error message *msg* to standard output stream and output file.

## 15.9 pubchem

Queries the PubChem database using a compound name (i.e. 1,3,5-hexatriene) to obtain a molecule string that can be passed to Molecule.

```
results = getPubChemObj("1,3,5-hexatriene")
```

Results is an array of results from PubChem matches to your query.

```
for entry in results:
    entry["CID"]          => PubChem compound identifier
    entry["IUPAC"]        => IUPAC name for the resulting compound
    entry["PubChemObj"]   => instance of PubChemObj for this compound

    entry["PubChemObj"].getMoleculeString() => returns a string compatible
                                                with PSI4's Molecule creation
```

**class** `pubchem.PubChemObj(cid, mf, iupac)`

**getCartesian()**

Function to return a string of the atom symbol and XYZ coordinates of the PubChem object.

**getMoleculeString()**

Function to obtain a molecule string through getCartesian() or fail.

**getSDF()**

Function to return the SDF (structure-data file) of the PubChem object.

**getXYZFile()**

Function to obtain preferentially a molecule string through getCartesian() or a query string otherwise.

**name()**

Function to return the IUPAC name of the PubChem object.

`pubchem.getPubChemResults(name)`

Function to query the PubChem database for molecules matching the input string. Builds a PubChem object if found.

## 15.10 qmmm

Module with classes to integrate MM charges into a QM calculation.

**class** `qmmm.Diffuse` (*molecule, basisname, ribasisname*)

**fitGeneral** ()

Function to perform a general fit of diffuse charges to wavefunction density.

**fitScf** ()

Function to run scf and fit a system of diffuse charges to resulting density.

**populateExtern** (*extern*)

**class** `qmmm.QMMM`

**addChargeAngstrom** (*Q, x, y, z*)

Function to add a point charge of magnitude *Q* at position (*x, y, z*) Angstroms.

**addChargeBohr** (*Q, x, y, z*)

Function to add a point charge of magnitude *Q* at position (*x, y, z*) Bohr.

**addDiffuse** (*diffuse*)

Function to add a diffuse charge field *diffuse*.

**populateExtern** ()

Function to define a charge field external to the molecule through point and diffuse charges.

## 15.11 text

Module with utility classes and functions related to data tables and text.

**class** `text.Table` (*rows=()*, *row\_label\_width=10*, *row\_label\_precision=4*, *cols=()*, *width=16*, *precision=10*)

Class defining a flexible Table object for storing data.

**absolute\_to\_relative** (*Factor=627.5095*)

Function to shift the data of each column of the Table object such that the lowest value is zero. A scaling factor of *Factor* is applied.

**copy** ()

Function to return a copy of the Table object.

**format\_label** ()

Function to pad the width of Table object labels.

**format\_values** (*values*)

Function to pad the width of Table object data cells.

**save** (*file*)

Function to save string of the Table object to *file*.

**scale** (*Factor=627.5095*)

Function to apply a scaling factor *Factor* to the data of the Table object.

`text.banner` (*text, type=1, width=35*)

Function to print *text* to output file in a banner of minimum width *width* and minimum three-line height for *type* = 1 or one-line height for *type* = 2.

`text.print_stderr` (*stuff*)

Function to print *stuff* to standard error stream.

`text.print_stdout(stuff)`  
 Function to print *stuff* to standard output stream.

## 15.12 util

Module with utility functions for use in input files.

`util.compare_integers(expected, computed, label)`  
 Function to compare two integers. Prints `util.success()` when value *computed* matches value *expected*. Performs a system exit on failure. Used in input files in the test suite.

`util.compare_matrices(expected, computed, digits, label)`  
 Function to compare two matrices. Prints `util.success()` when elements of matrix *computed* match elements of matrix *expected* to number of *digits*. Performs a system exit on failure to match symmetry structure, dimensions, or element values. Used in input files in the test suite.

`util.compare_strings(expected, computed, label)`  
 Function to compare two strings. Prints `util.success()` when string *computed* exactly matches string *expected*. Performs a system exit on failure. Used in input files in the test suite.

`util.compare_values(expected, computed, digits, label)`  
 Function to compare two values. Prints `util.success()` when value *computed* matches value *expected* to number of *digits*. Performs a system exit on failure. Used in input files in the test suite.

`util.compare_vectors(expected, computed, digits, label)`  
 Function to compare two vectors. Prints `util.success()` when elements of vector *computed* match elements of vector *expected* to number of *digits*. Performs a system exit on failure to match symmetry structure, dimension, or element values. Used in input files in the test suite.

`util.get_memory()`  
 Function to return the total memory allocation.

`util.get_num_threads()`  
 Function to return the number of threads to parallelize across.

`util.set_memory(bytes)`  
 Function to reset the total memory allocation.

`util.set_num_threads(nthread)`  
 Function to reset the number of threads to parallelize across.

`util.success(label)`  
 Function to print a '*label*...PASSED' line to screen. Used by `util.compare_values()` family when functions pass.

## 15.13 wrappers

Module with functions that call the four main `driver` functions: `driver.energy`, `driver.optimize`, `driver.response`, and `driver.frequency`.

`wrappers.call_function_in_1st_argument(funcarg, **larg)`  
 Function to make primary function call to `energy()`, `opt()`, etc. with options dictionary *larg*. Useful when *funcarg* to call is stored in variable.

`wrappers.drop_duplicates(seq)`  
 Function that given an array *seq*, returns an array without any duplicate entries. There is no guarantee of which duplicate entry is dropped.

`wrappers.n_body` (*name*, *\*\*kwargs*)

`wrappers.reconstitute_bracketed_basis` (*needarray*)

Function to reform a bracketed basis set string from a sequential series of basis sets (e.g, form ‘cc-pv[q5]z’ from array [cc-pvqz, cc-pv5z]). The basis set array is extracted from the *f\_basis* field of a *NEED* dictionary in `wrappers.complete_basis_set()`. Result is used to print a nicely formatted basis set string in the results table.

`wrappers.split_menial` (*menial*)

Function used by `wrappers.complete_basis_set()` to separate *menial* ‘scftot’ into [scf, tot] and ‘mp2corl’ into [mp2, corl].

`wrappers.tblhead` (*tbl\_maxrgt*, *tbl\_delimit*, *ttype*)

Function that prints the header for the changable-width results tables in `db()`. *tbl\_maxrgt* is the number of reagent columns the table must plan for. *tbl\_delimit* is a string of dashes of the correct length to set off the table. *ttype* is 1 for tables comparing the computed values to the reference or 2 for simple tabulation and sum of the computed values.

`wrappers.validate_bracketed_basis` (*basisstring*)

Function to transform and validate basis sets for `cbs()`. A basis set with no paired square brackets is passed through with zeta level 0 (e.g., ‘6-31+G(d,p)’ is returned as [6-31+G(d,p)] and [0]). A basis set with square brackets is checked for sensible sequence and Dunning-ness and returned as separate basis sets (e.g., ‘cc-pV[Q5]Z’ is returned as [cc-pVQZ, cc-pV5Z] and [4, 5]). Note that this function has no communication with the basis set library to check if the basis actually exists. Used by `wrappers.complete_basis_set()`.

`wrappers.validate_scheme_args` (*functionname*, *\*\*largs*)

Function called by each extrapolation scheme in `wrappers.complete_basis_set()`. Checks that all the input arguments are present and suitable so that the scheme function can focus on defining the extrapolation.

# INDICES AND TABLES

- *genindex*
- *modindex*
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