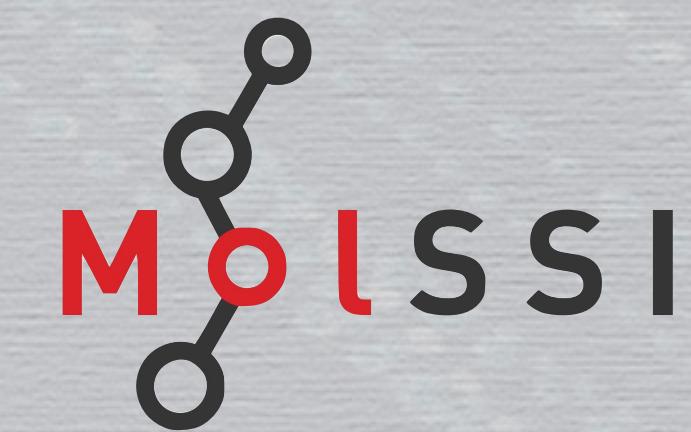


SIMPLIFYING MULTILEVEL QUANTUM CHEMISTRY PROCEDURES THROUGH PSI4 AND QCARCHIVE

LORI A. BURNS

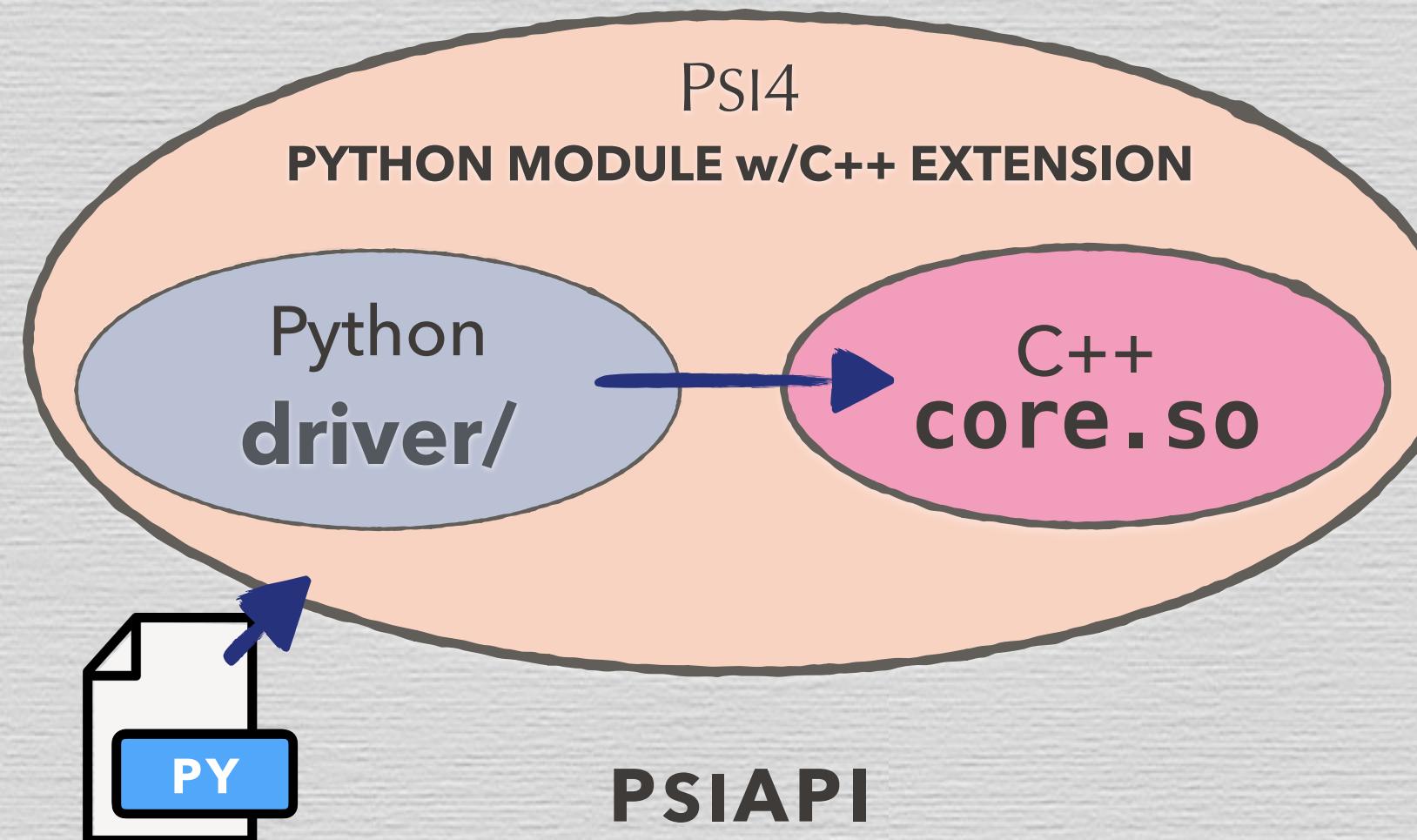
MOLSSI WORKSHOP ON HPC IN COMPUTATIONAL CHEMISTRY & MATERIALS SCIENCE, VIRTUAL

14 DECEMBER 2021



PSI4 ORIENTATION

v1.5 released 2021



```
import psi4

psi4.geometry('''
Ne
Ne 1 3.0
''')

psi4.set_options({
    'freeze_core': 'True'})

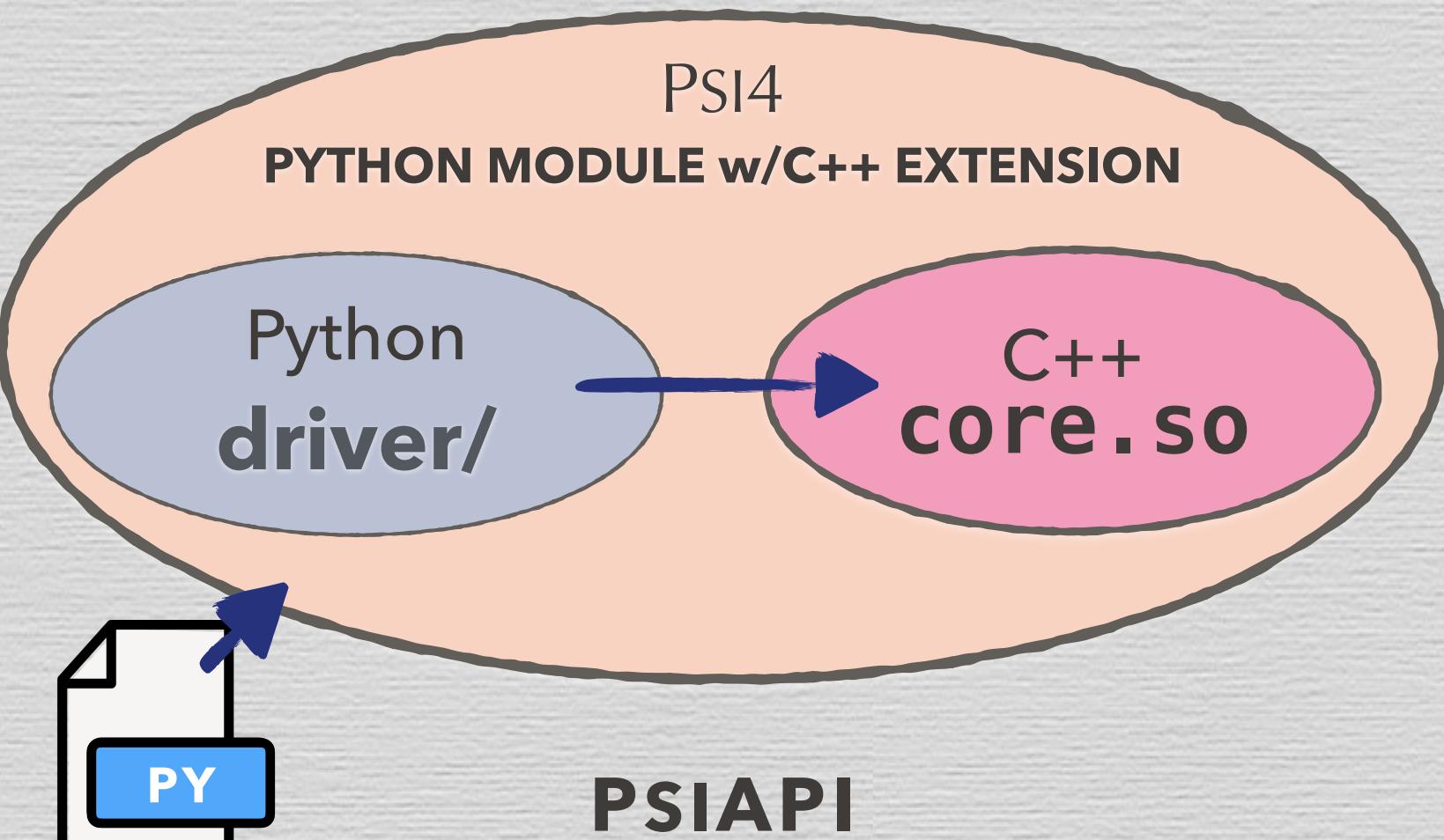
psi4.energy('ccsd(t)/cc-pvtz')
```

> **python in.py**

Psi4 ORIENTATION

v1.5 released 2021

- **FULL-FEATURED** (lots of initialisms)
- **SMP** parallelism
- **HYBRID** C++/Python
 - ~70% C++
 - ~30% Python
- **INPUT** by DSL, API, or JSON
- **STRIVE** for easy production-quality user input: **energy()**, **gradient()**, **optimize()**, **hessian()**, **frequency()** are the five driver “user-facing” functions through which 99+% of QC is run in Psi4, so easy to guess command. Minimal entry points
- **SPECIALTIES** include density-fitting & intermolecular interactions

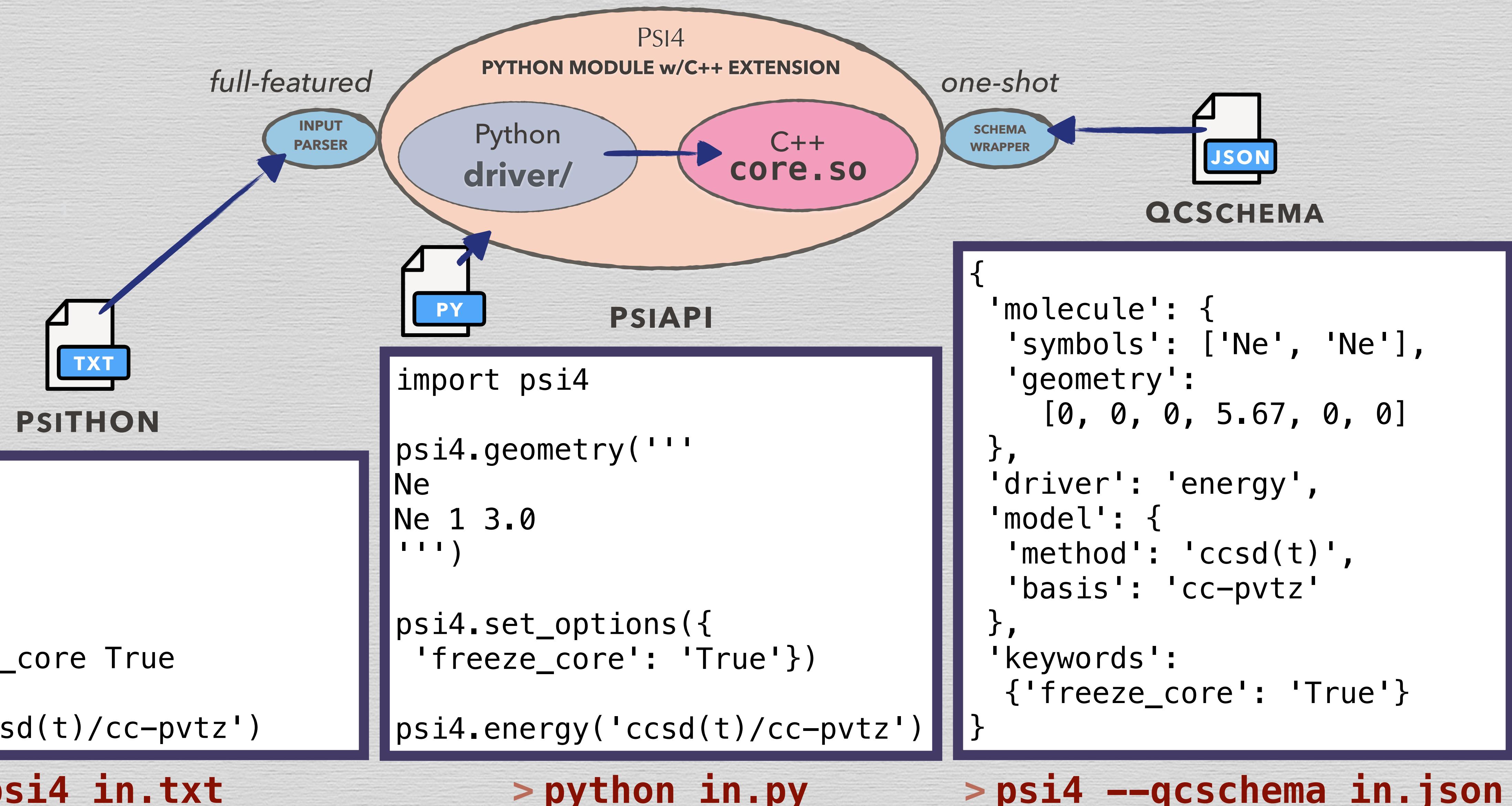


```
import psi4
psi4.geometry('''
Ne
Ne 1 3.0
''')
psi4.set_options({
    'freeze_core': 'True'})
psi4.energy('ccsd(t)/cc-pvtz')
```

> **python in.py**

LANGUAGE INTERACTION IN Psi4

feeding and gross anatomy

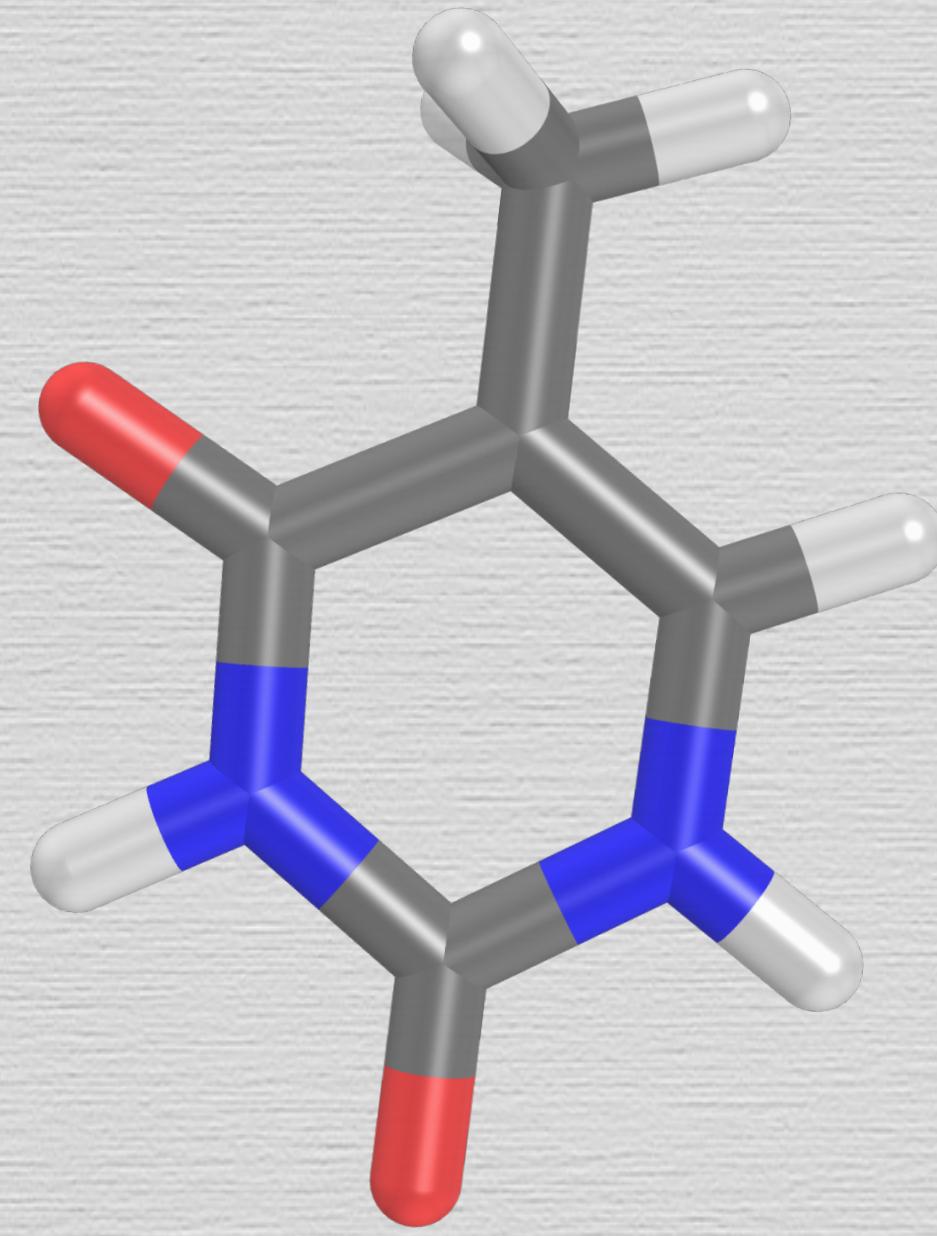
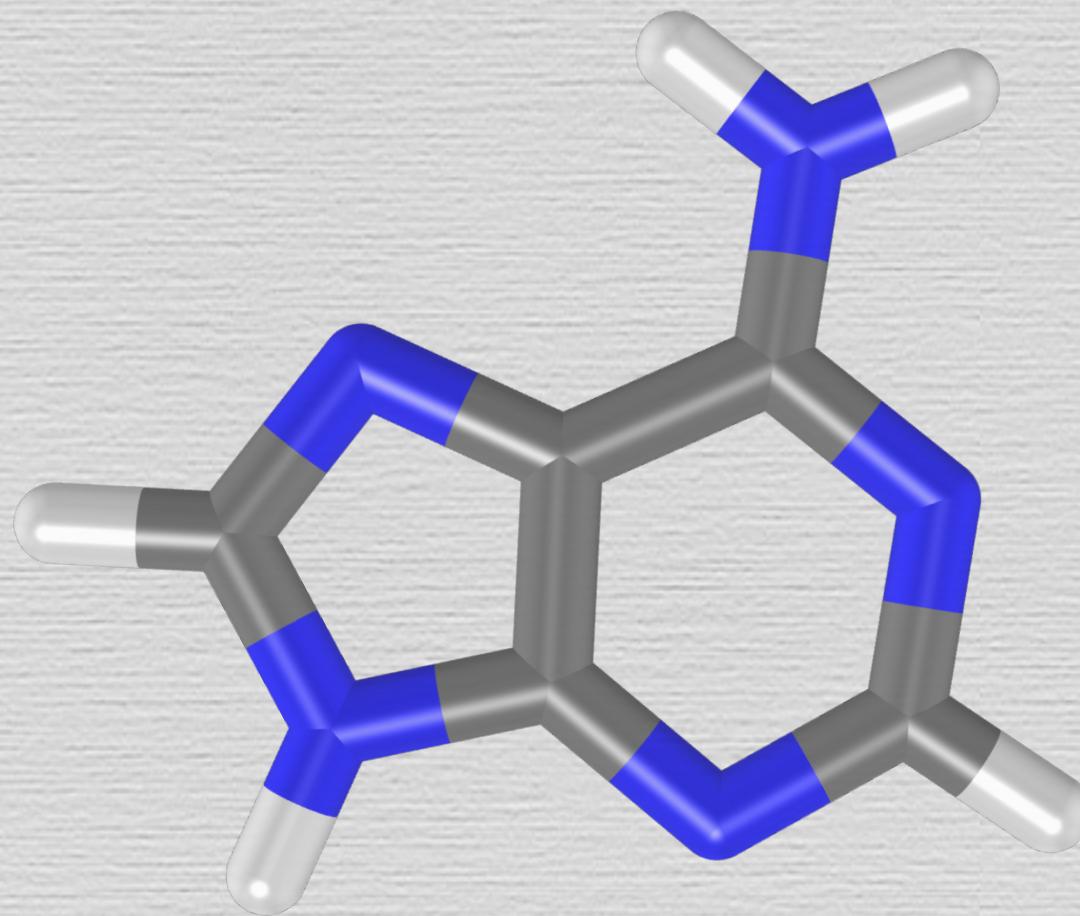


PROBING NON-COVALENT INTERACTIONS

a specialty of PSI4

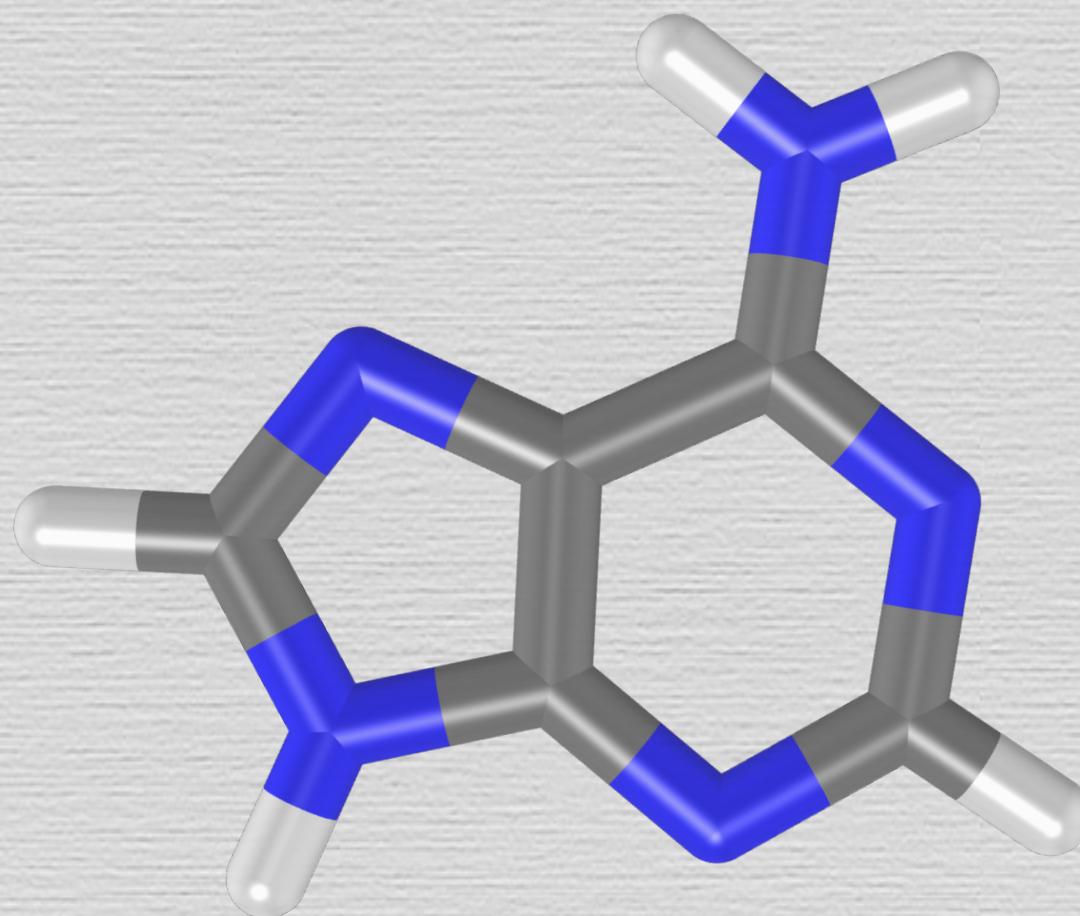
PROBING NON-COVALENT INTERACTIONS

a specialty of PSI4



PROBING NON-COVALENT INTERACTIONS

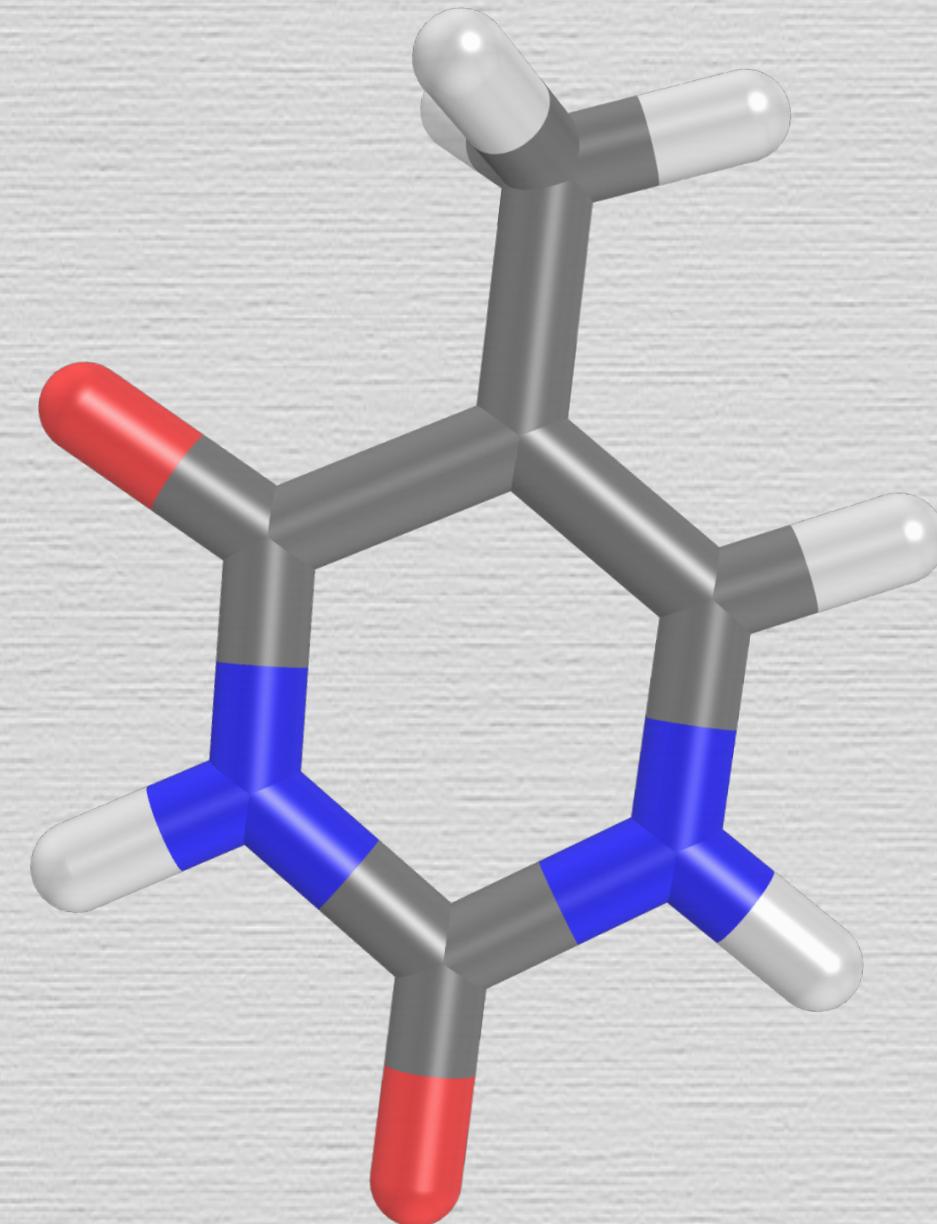
a specialty of PSI4



$$E_A$$



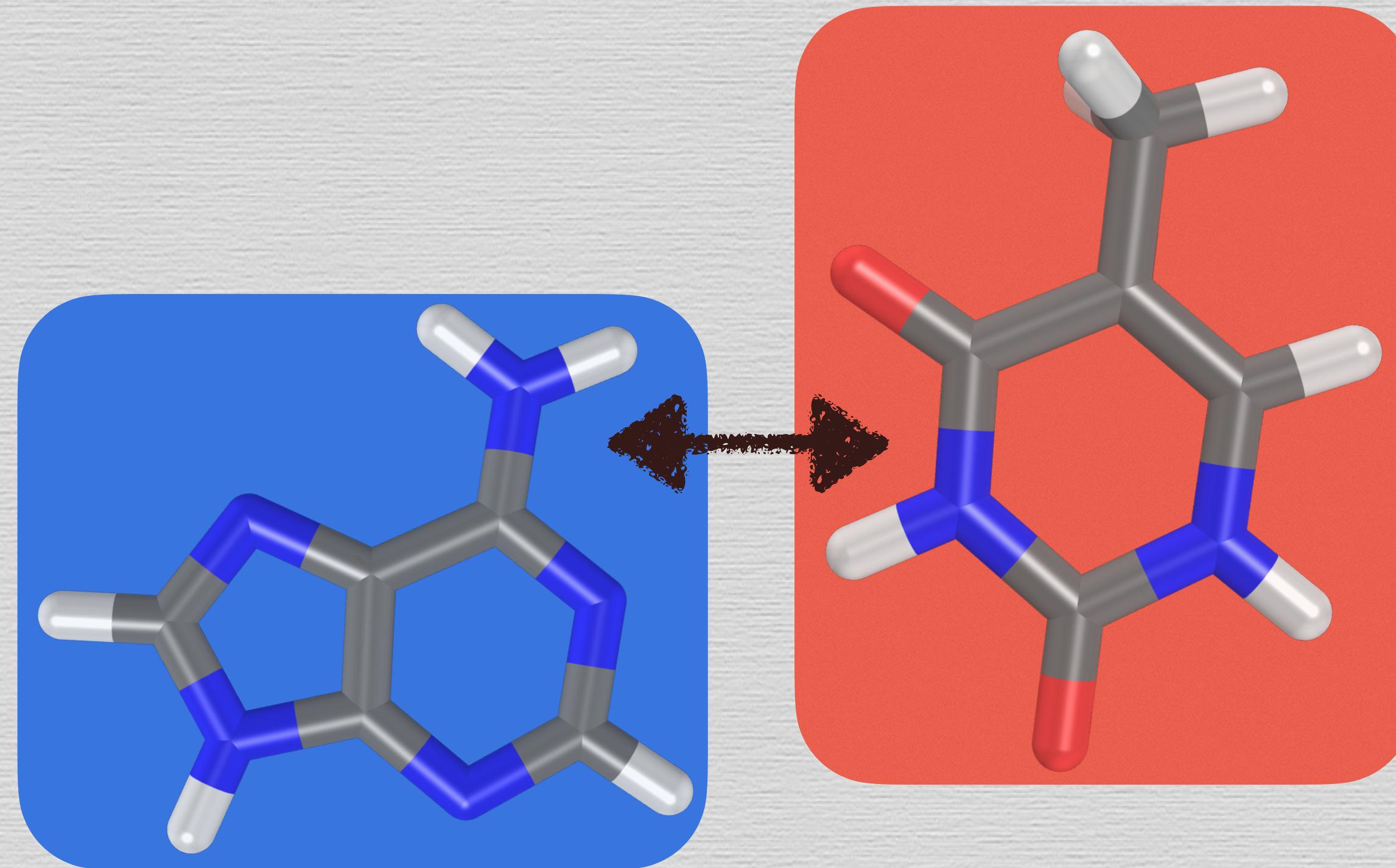
$$E_{AB} = E_A + E_B$$



$$E_B$$

PROBING NON-COVALENT INTERACTIONS

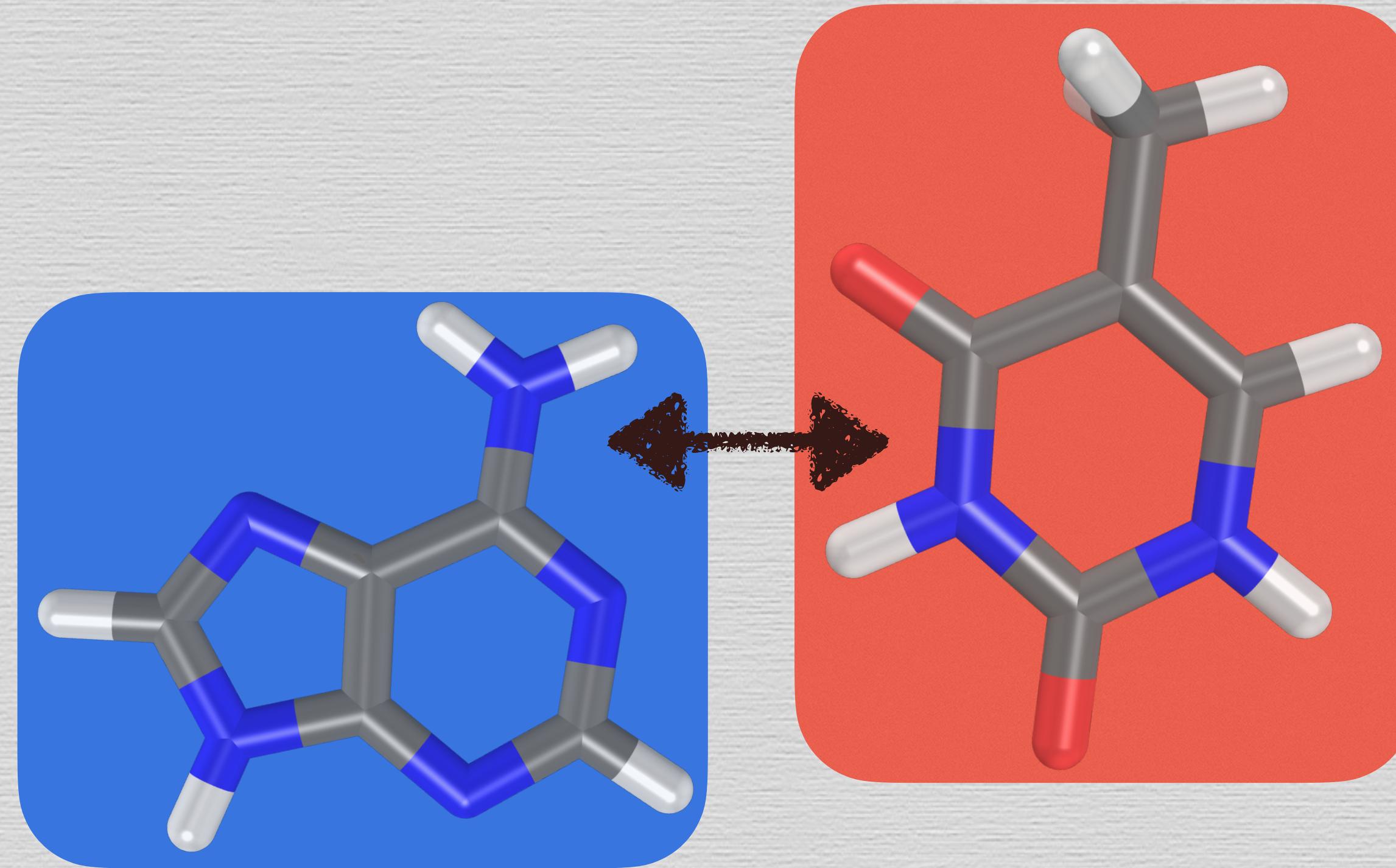
supermolecular approach



$$E_{AB} = E_A + E_B$$

PROBING NON-COVALENT INTERACTIONS

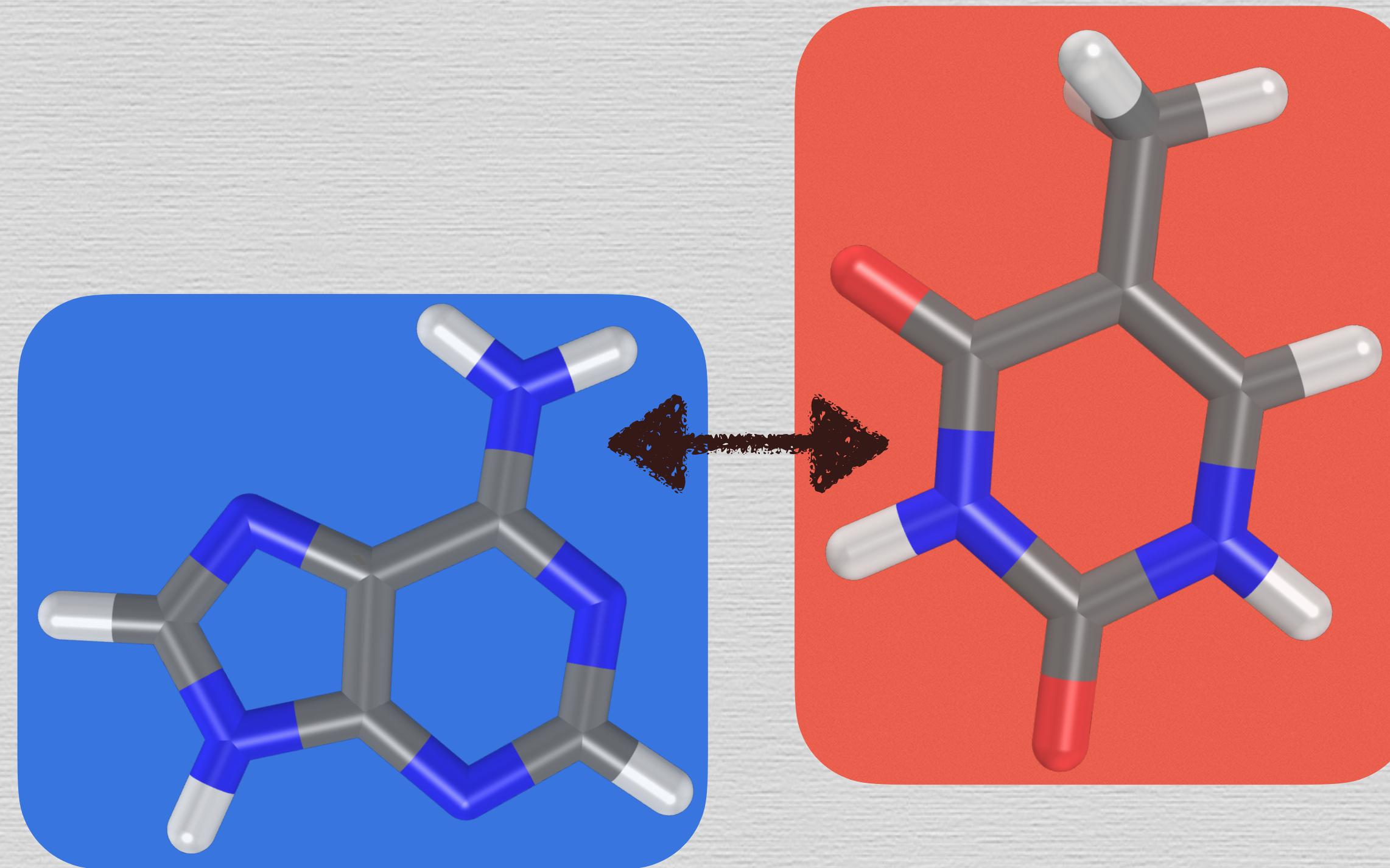
supermolecular approach



$$E_{AB} = E_A + E_B + \Delta E_{AB}$$

PROBING NON-COVALENT INTERACTIONS

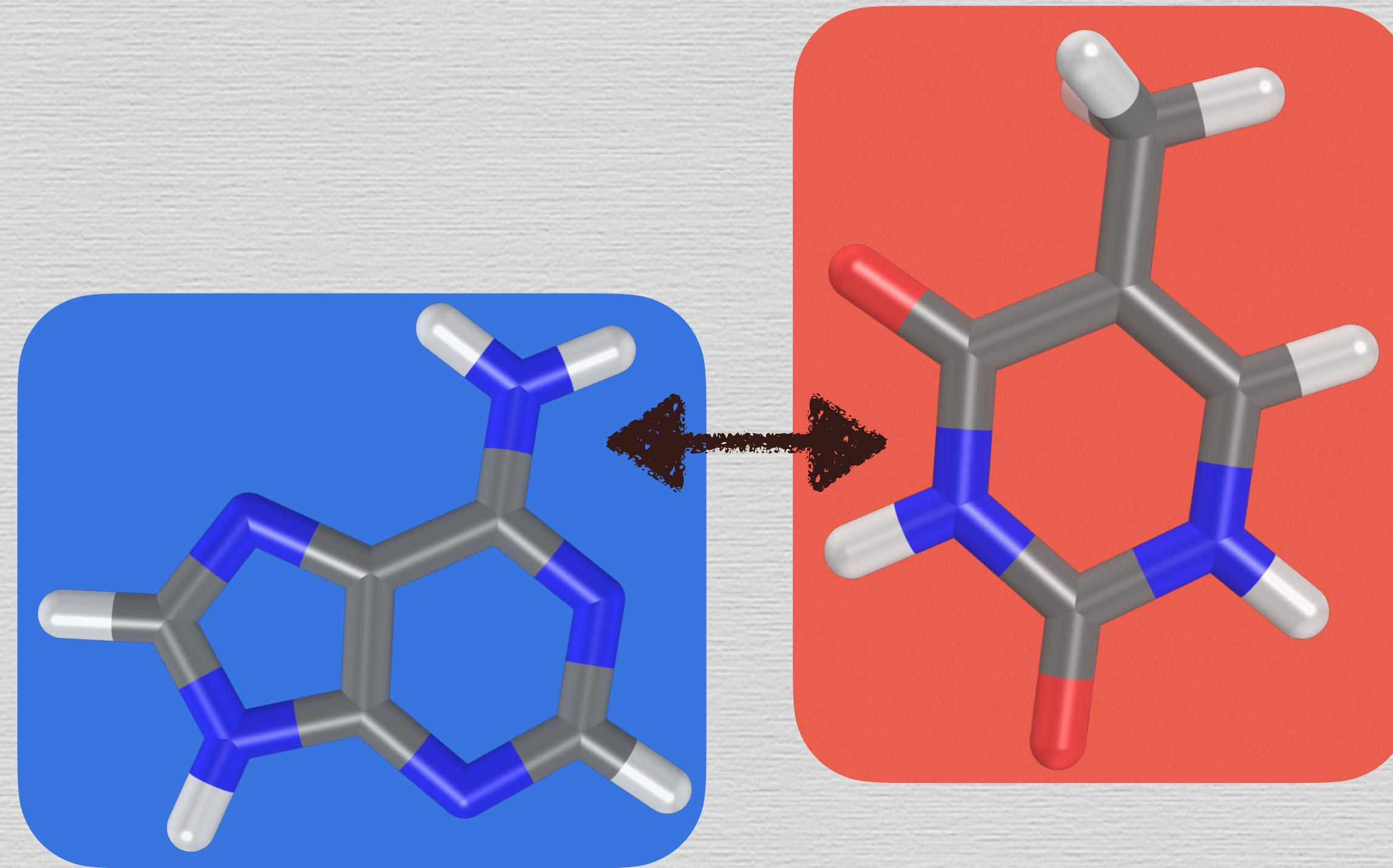
supermolecular approach



$$E_{AB} = E_A + E_B + IE_{AB}$$

PROBING NON-COVALENT INTERACTIONS

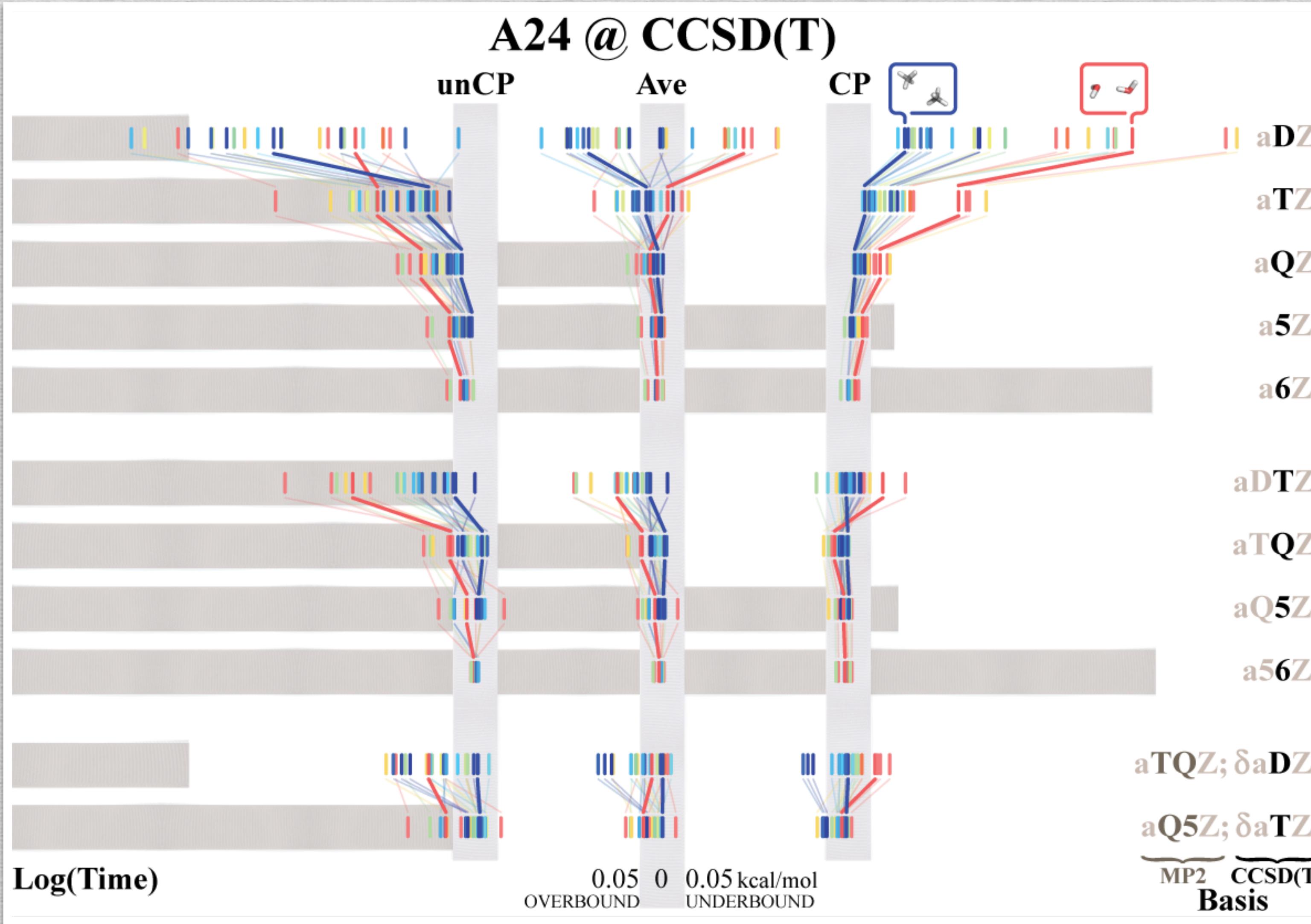
supermolecular approach



$$IE_{AB} = E_{AB} - E_A - E_B$$

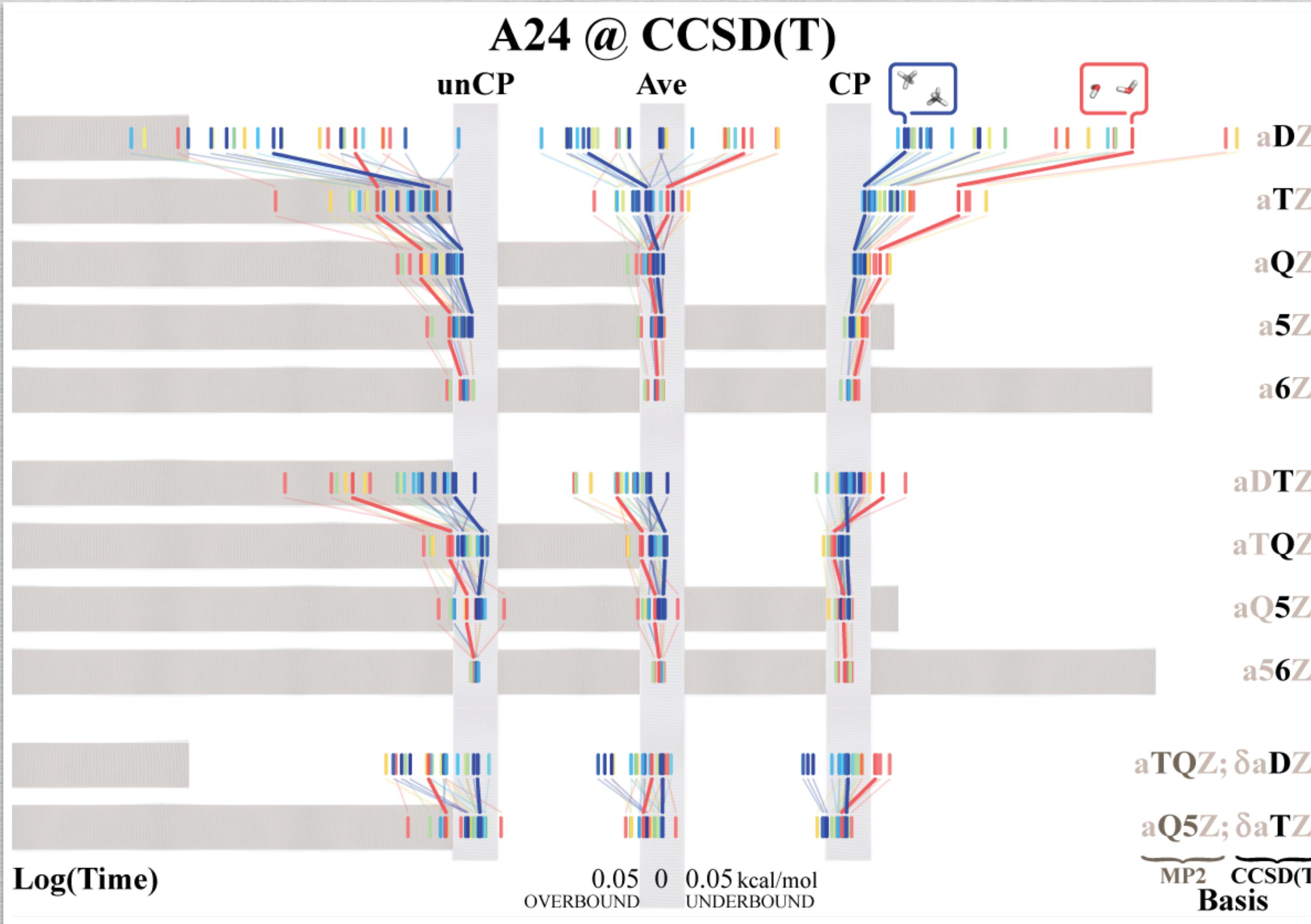
COMPOSITE METHODS APPROXIMATIONS

complete basis set (CBS) approximations, delta corrections, focal point methods



COMPOSITE METHODS APPROXIMATIONS

complete basis set (CBS) approximations, delta corrections, focal point methods



```
psi4.energy("ccsd(t)/cc-pvdz")
```

```
psi4.energy("ccsd(t)/cc-pvtz")
```

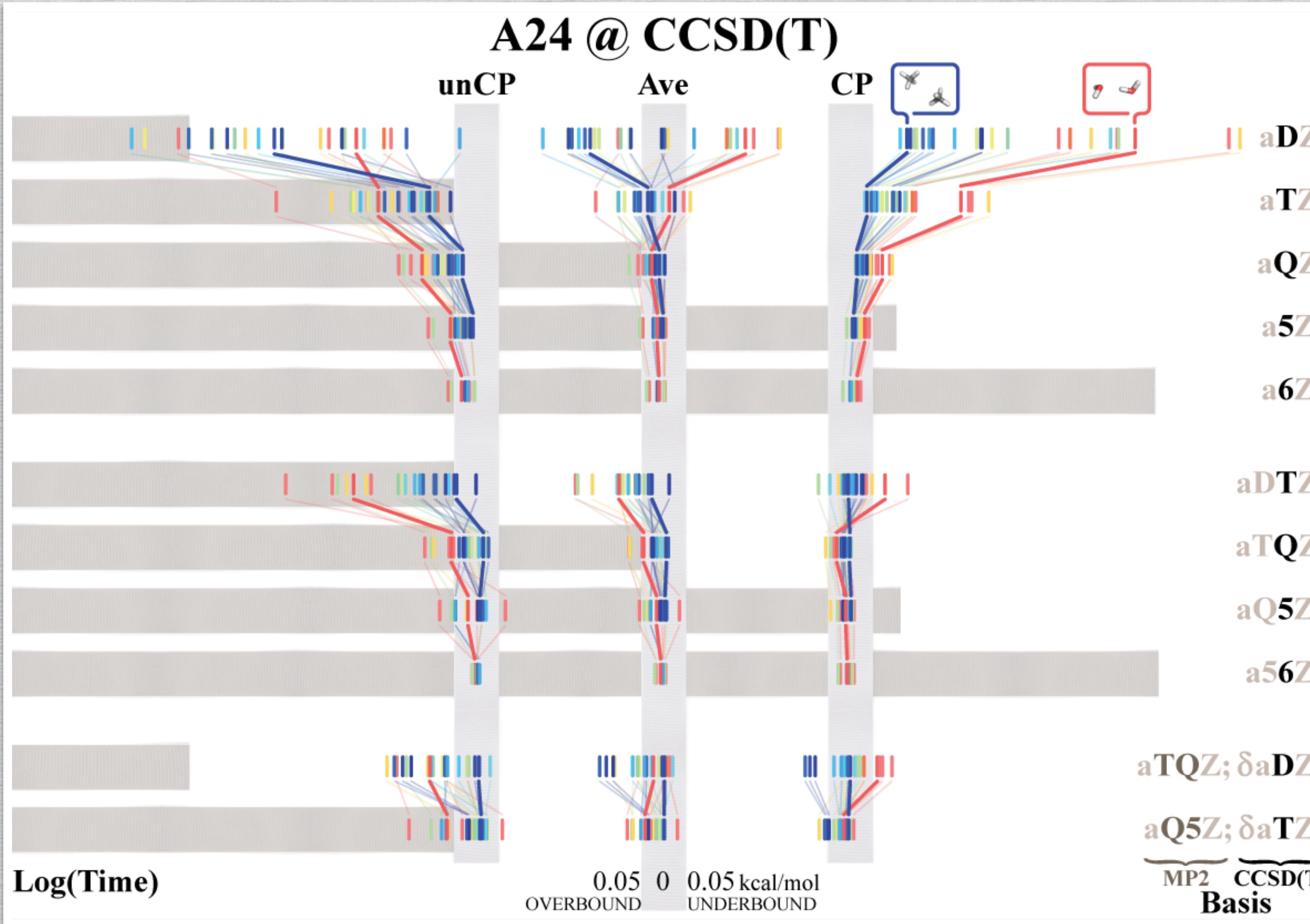
$$\text{AB}\xi : E_{\text{total}}^{\text{post-HF/TQ}\xi} = E_{\text{total}}^{\text{HF/Q}\xi} + \frac{\ell_{\max}^{\text{pow}}}{\ell_{\max}^{\text{pow}} - (\ell_{\max} - 1)^{\text{pow}}} E_{\text{corr}}^{\text{post-HF/T}\xi} - \frac{(\ell_{\max} - 1)^{\text{pow}}}{\ell_{\max}^{\text{pow}} - (\ell_{\max} - 1)^{\text{pow}}} E_{\text{corr}}^{\text{post-HF/T}\xi}. \quad (7)$$

```
psi4.energy("ccsd(t)/cc-pv[dt]z")
```

```
psi4.energy("ccsd(t)/cc-pv[tq]z")
```

COMPOSITE METHODS APPROXIMATIONS

complete basis set (CBS) approximations, delta corrections, focal point methods



```
psi4.energy("ccsd(t)/cc-pvdz")
```

```
psi4.energy("ccsd(t)/cc-pvtz")
```

$$AB\xi : E_{\text{total}}^{\text{post-HF/TQ}\xi} = E_{\text{total}}^{\text{HF/Q}\xi} + \frac{\ell_{\max}^{\text{pow}}}{\ell_{\max}^{\text{pow}} - (\ell_{\max} - 1)^{\text{pow}}} E_{\text{corr}}^{\text{post-HF/Q}\xi} - \frac{(\ell_{\max} - 1)^{\text{pow}}}{\ell_{\max}^{\text{pow}} - (\ell_{\max} - 1)^{\text{pow}}} E_{\text{corr}}^{\text{post-HF/T}\xi}. \quad (7)$$

```
psi4.energy("ccsd(t)/cc-pv[dt]z")
```

```
psi4.energy("ccsd(t)/cc-pv[tq]z")
```

```
psi4.energy("mp2/cc-pv[tq]z + D:ccsd(t)/cc-pvdz")
```

$$[A\xi; \delta; B\xi] : E_{\text{total}}^{\text{post-MP2/[Q5}\xi;\delta;\text{T}\xi]} = E_{\text{total}}^{\text{MP2/Q5}\xi} + \delta_{\text{MP2/T}\xi}^{\text{post-MP2/T}\xi}, \quad (8)$$

$$= E_{\text{total}}^{\text{HF/S}\xi} + E_{\text{corr}}^{\text{MP2/Q5}\xi} + E_{\text{corr}}^{\text{post-MP2/T}\xi} - E_{\text{corr}}^{\text{MP2/T}\xi}, \quad (9)$$

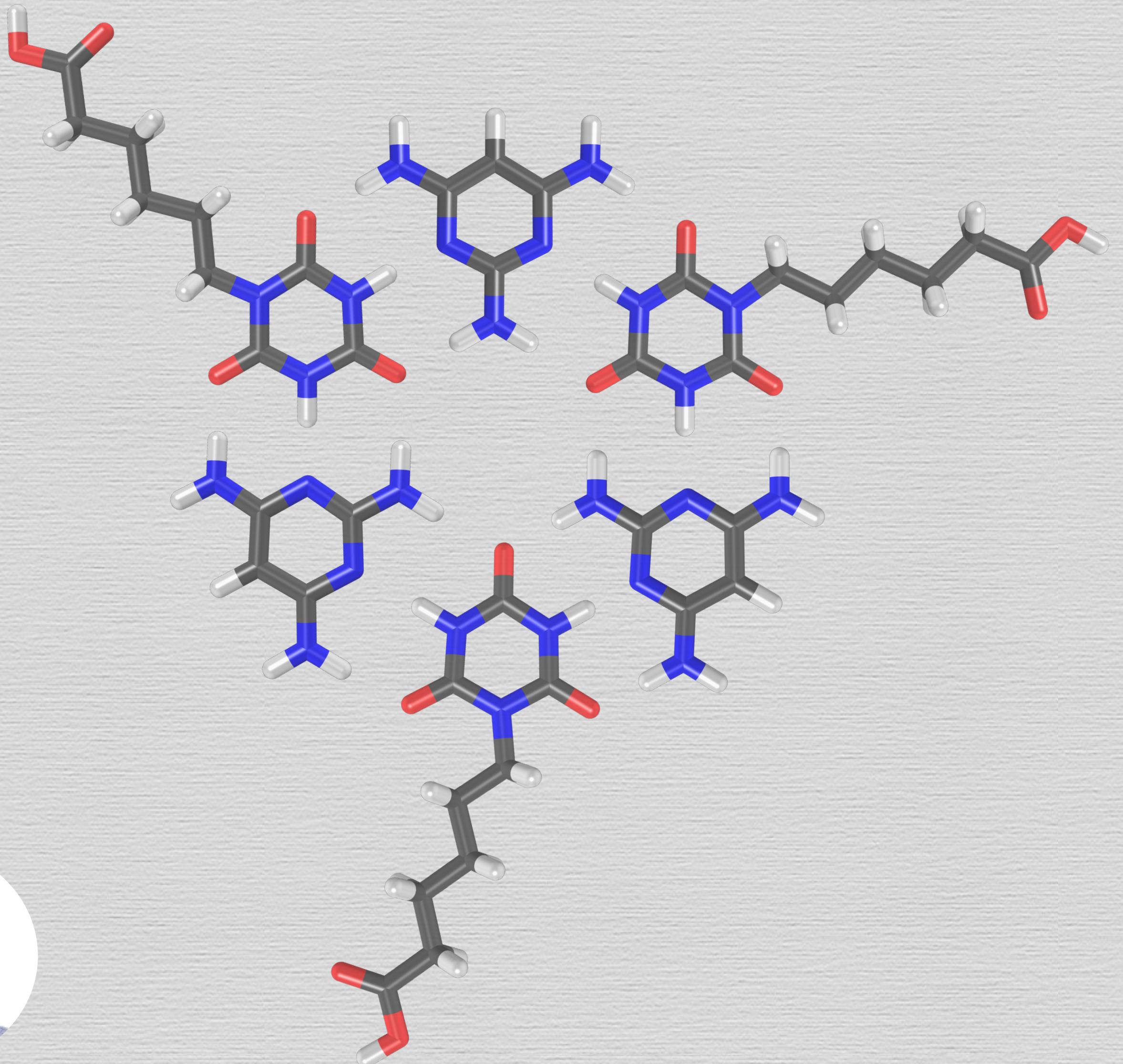
MANY-BODY EXPANSION (MBE)

and basis-set superposition error (BSSE) corrections



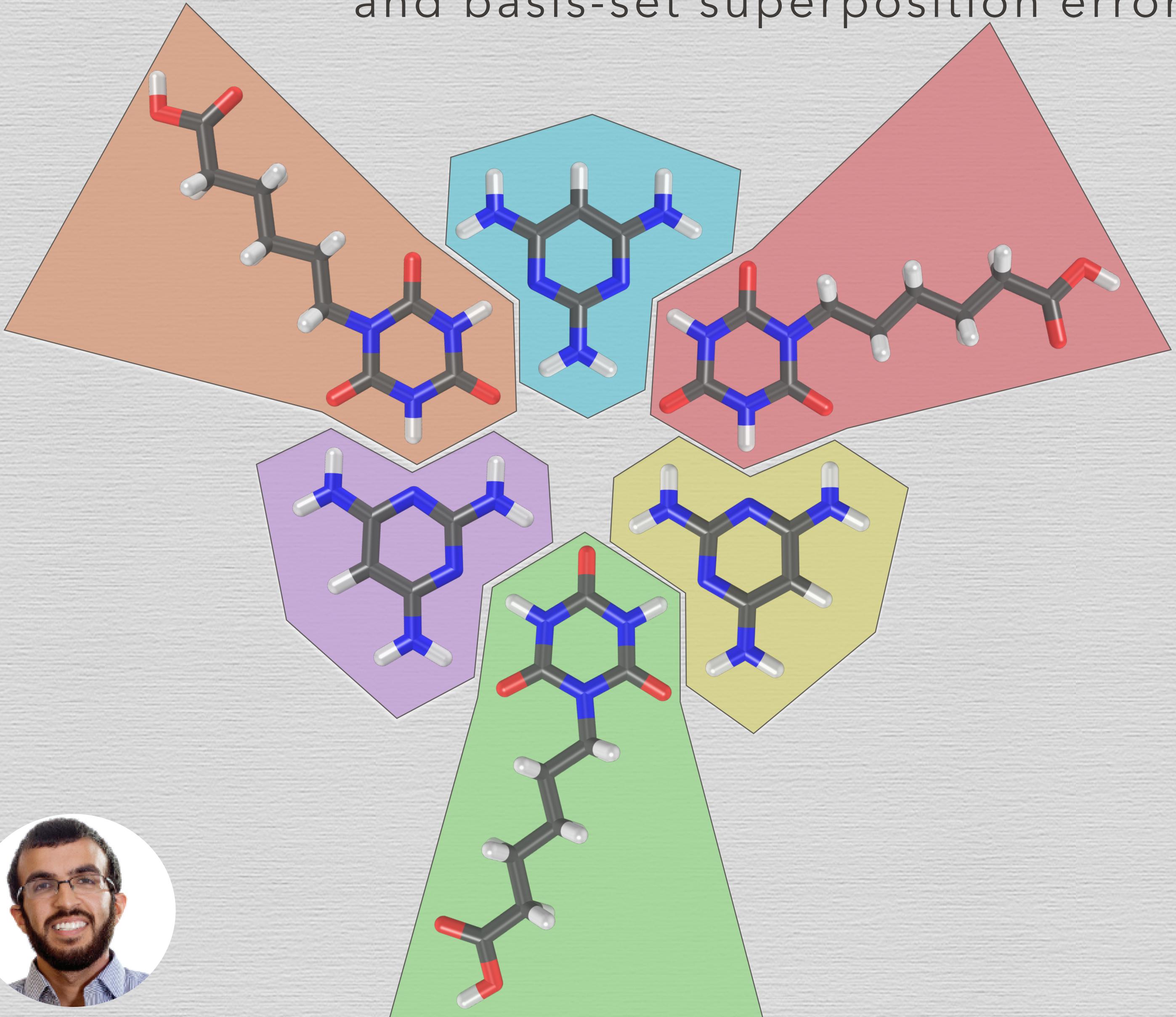
MANY-BODY EXPANSION (MBE)

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MANY-BODY EXPANSION (MBE)

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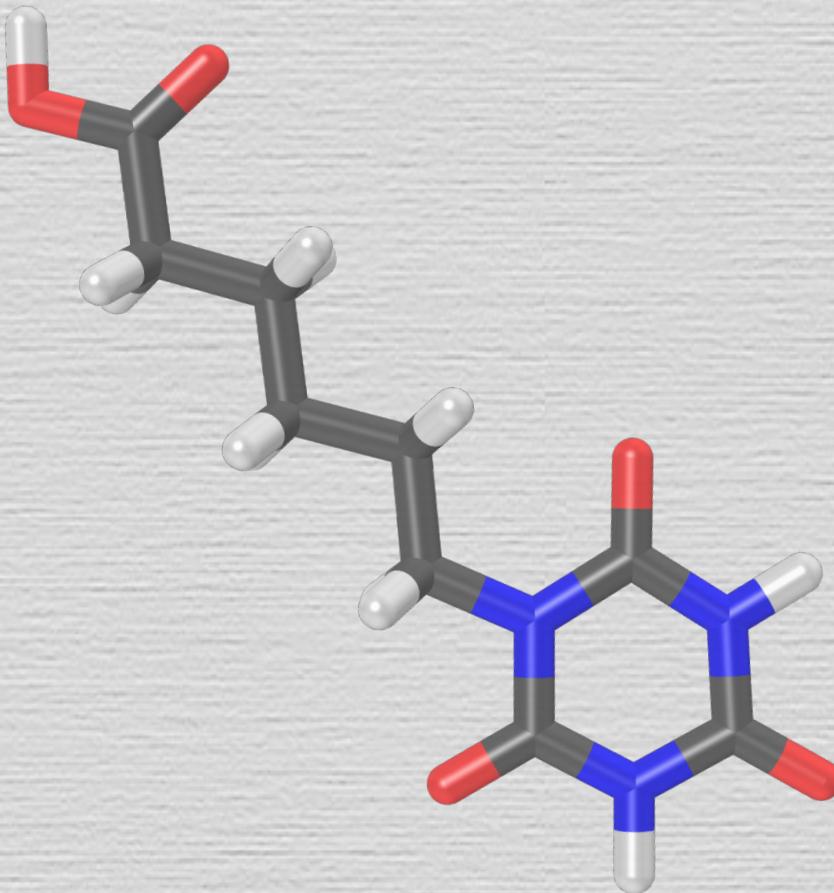


$$E_{\text{hex}} \approx \sum_I E_I$$



MANY-BODY EXPANSION (MBE)

and basis-set superposition error (BSSE) corrections



$$E_{\text{hex}} \approx \sum_I E_I + \sum_{I>J} \Delta E_{IJ}^{(2)}$$



```
psi4.energy("mp2/cc-pvdz", bsse_type="cp", max_nbody=2)
```

MANY-BODY EXPANSION (MBE)

and basis-set superposition error (BSSE) corrections

$$E_{\text{hex}} \approx \sum_I E_I + \sum_{I>J} \Delta E_{IJ}^{(2)} + \sum_{I>J>K} \Delta E_{IJK}^{(3)}$$

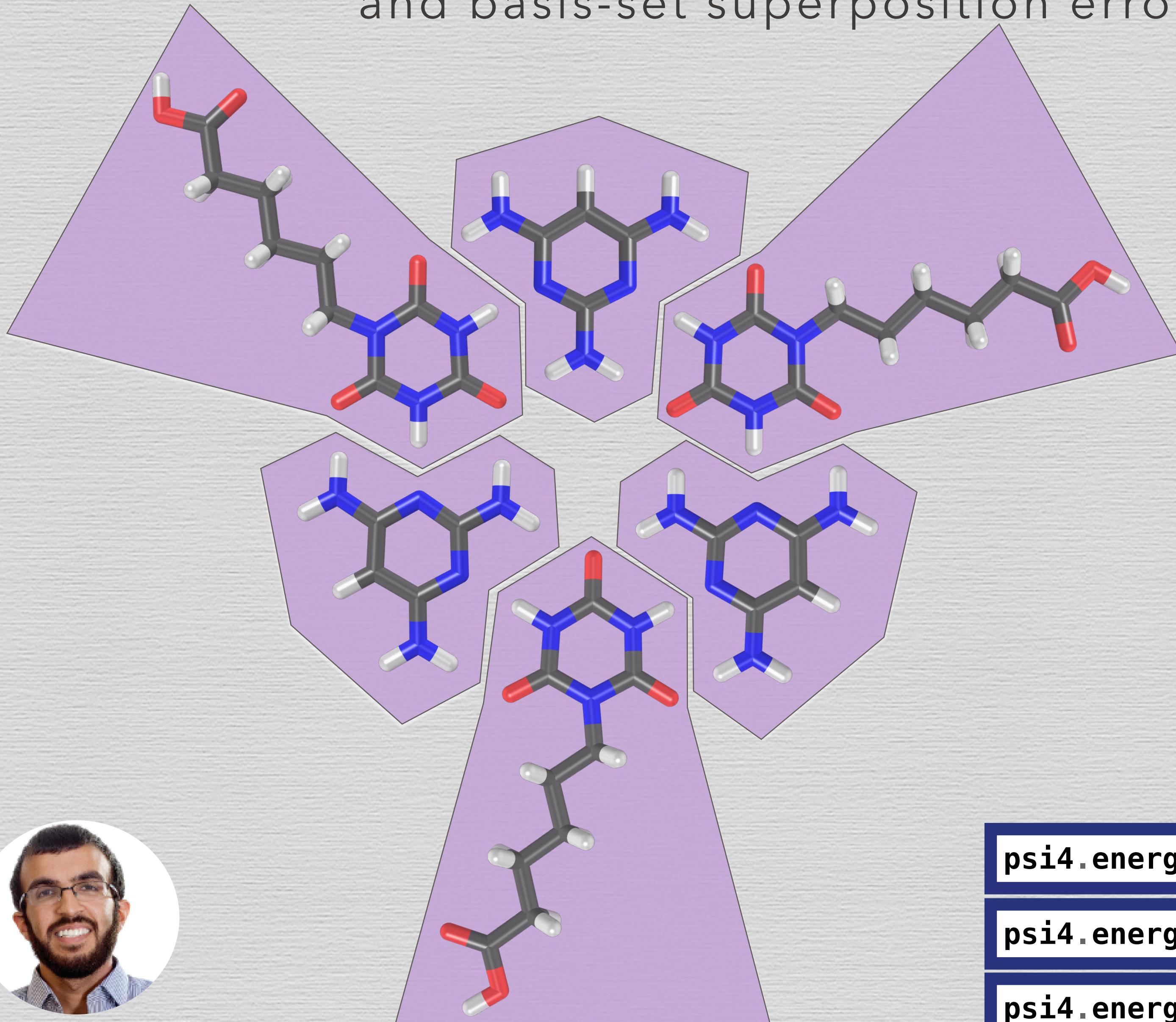
```
psi4.energy("mp2/cc-pvdz", bsse_type="cp", max_nbody=2)
```

```
psi4.energy("mp2/cc-pvdz", bsse_type="cp", max_nbody=3)
```



MANY-BODY EXPANSION (MBE)

and basis-set superposition error (BSSE) corrections



$$E_{\text{hex}} \approx \sum_I E_I + \sum_{I>J} \Delta E_{IJ}^{(2)} + \sum_{I>J>K} \Delta E_{IJK}^{(3)} + \dots$$

```
psi4.energy("mp2/cc-pvdz", bsse_type="cp", max_nbody=2)
```

```
psi4.energy("mp2/cc-pvdz", bsse_type="cp", max_nbody=3)
```

```
psi4.energy("mp2/cc-pvdz", bsse_type="cp")
```



(1) Psi4 COMPOSITE & BSSE BY HAND

flexible but error-prone

```
psi4.energy("mp2/cc-pvtz", molecule=  )
```

```
psi4.energy("mp2/cc-pvtz", molecule=  )
```

```
psi4.energy("mp2/cc-pvtz", molecule=  )
```

```
psi4.energy("ccsd(t)/cc-pvdz", molecule=  )
```

```
psi4.energy("ccsd(t)/cc-pvdz", molecule=  )
```

```
psi4.energy("ccsd(t)/cc-pvdz", molecule=  )
```



Local Compute

- **AVAILABLE** with [Psi4](#) since 2010.
- **SPECIFICATION** through multiple files of slight variation. Procedure [manual](#), so high risk of user error.
- **RATE-LIMITED** by single longest calc since can run [parallel in queue](#).
- **RETRIEVAL** from [filesystem](#) if named systematically.
- **FLEXIBILITY** to mix QC programs to access more or [more efficient](#) methods since separate input files.

(1) Psi4 COMPOSITE & BSSE BY HAND

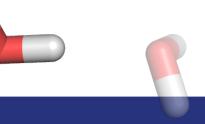
flexible but error-prone

```
psi4.energy("mp2/cc-pvtz", molecule= 
```

```
psi4.energy("mp2/cc-pvtz", molecule= 
```

```
psi4.energy("mp2/cc-pvtz", molecule= 
```

```
psi4.energy("ccsd(t)/cc-pvdz", molecule= 
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psi4.energy("ccsd(t)/cc-pvdz", molecule= 
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psi4.energy("ccsd(t)/cc-pvdz", molecule= 
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- **AVAILABLE** with **Psi4** since 2010.
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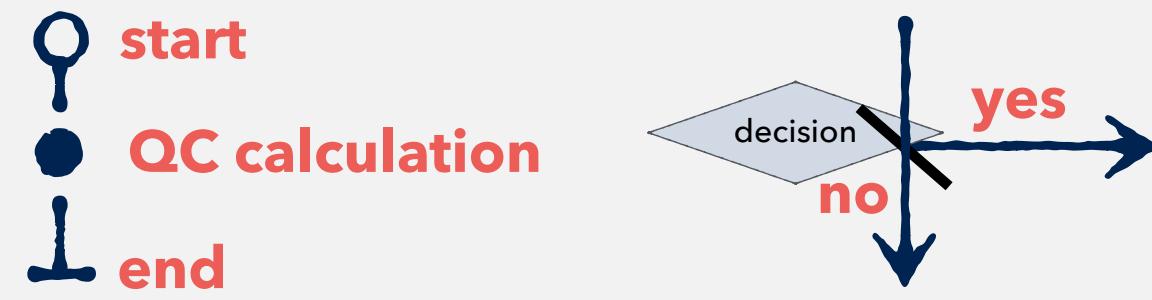
```
def energy(method):
```

```
def gradient(method):
```

```
def hessian(method):
```

PSI4 RECURSIVE DRIVER

capable but complicated



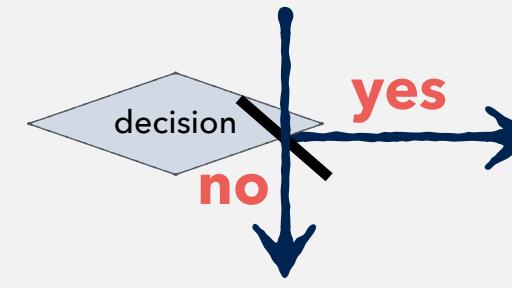
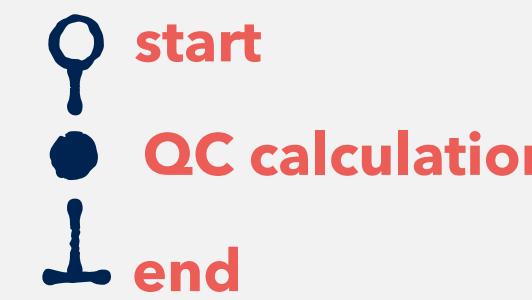
PSI4 RECURSIVE DRIVER

capable but complicated

```
def energy(method):
```

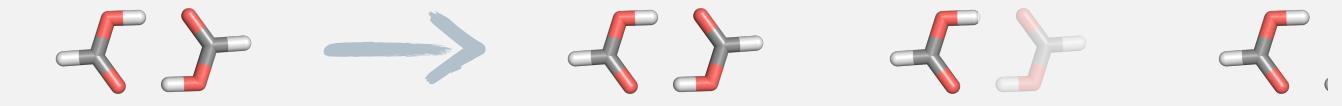
```
def gradient(method):
```

```
def hessian(method):
```



```
def manybody():
```

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



RUN

for frag in fragments:

energy
gradient (method, frag)
hessian

Assemble n-body & interaction results from fragments.

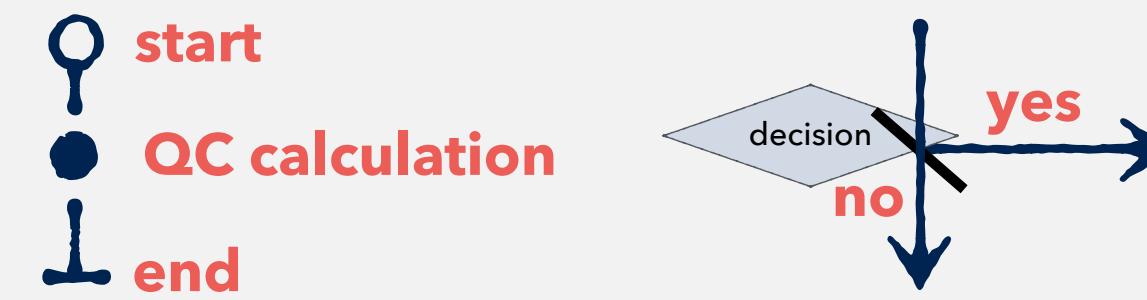
PSI4 RECURSIVE DRIVER

capable but complicated

```
def energy(method):
```

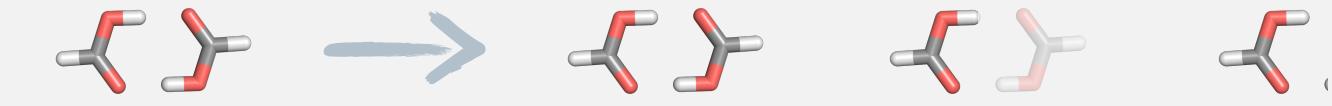
```
def gradient(method):
```

```
def hessian(method):
```



```
def manybody():
```

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



RUN

```
for frag in fragments:
```

energy
gradient(method, frag)
hessian

Assemble n-body & interaction results from fragments.

```
def findif():
```

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



RUN

```
for disp in displacements:
```

energy
gradient(method, disp)
hessian

Assemble derivative results from displacements.

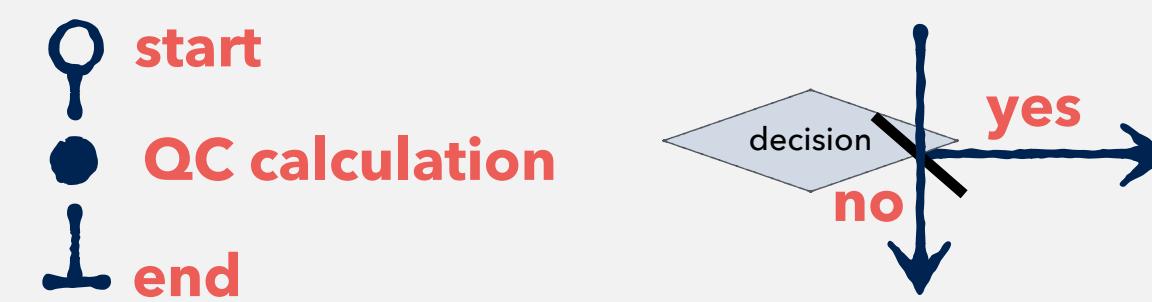
PSI4 RECURSIVE DRIVER

capable but complicated

```
def energy(method):
```

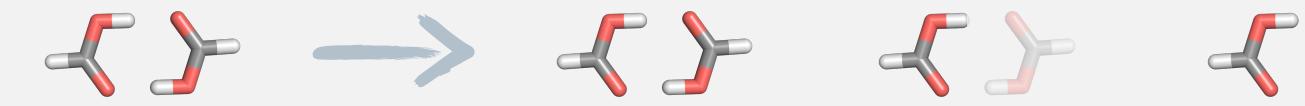
```
def gradient(method):
```

```
def hessian(method):
```



```
def manybody():
```

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



RUN

```
for frag in fragments:
```

energy
gradient(method, frag)
hessian

Assemble n-body & interaction results from fragments.

```
def findif():
```

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



RUN

```
for disp in displacements:
```

energy
gradient(method, disp)
hessian

Assemble derivative results from displacements.

```
def composite():
```

Separate **method** into method, basis, & extrapolations.
molecule unchanged.

mp2/cc-pv[tq]z →

MP2 TOTAL ENERGY/cc-pVTZ
MP2 TOTAL ENERGY/cc-pVQZ

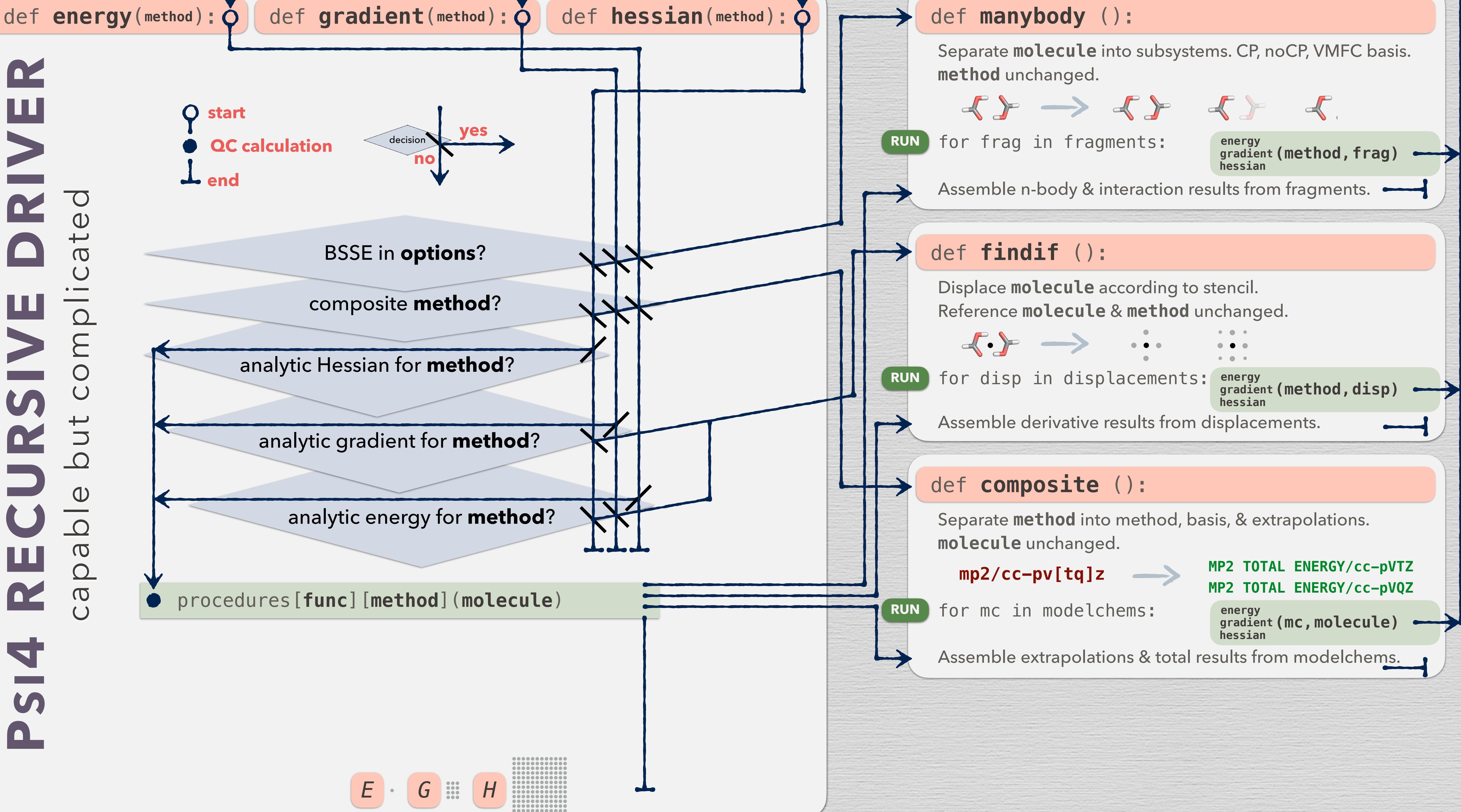
RUN

```
for mc in modelchems:
```

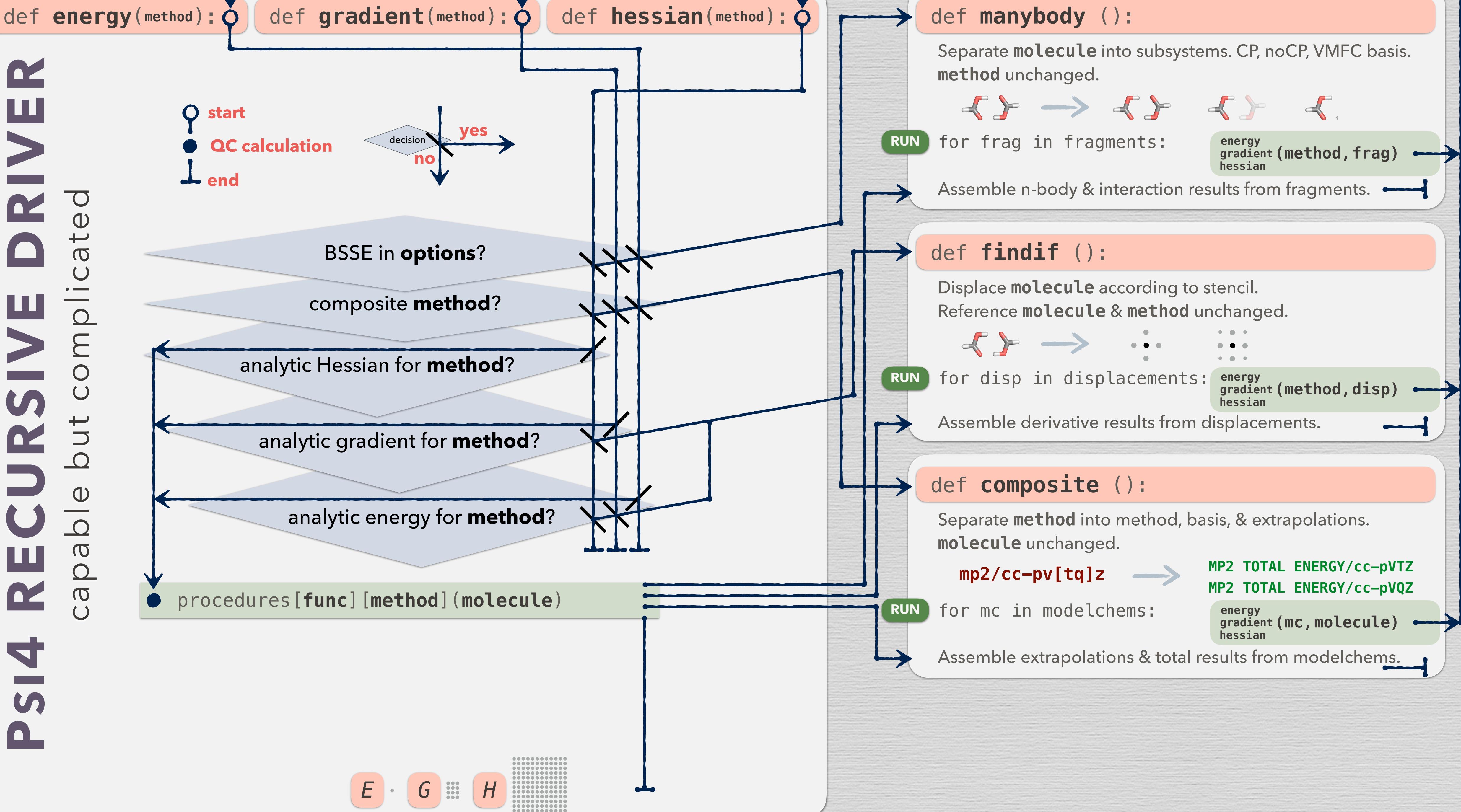
energy
gradient(mc, molecule)
hessian

Assemble extrapolations & total results from modelchems.

PSI4 RECURSIVE DRIVER

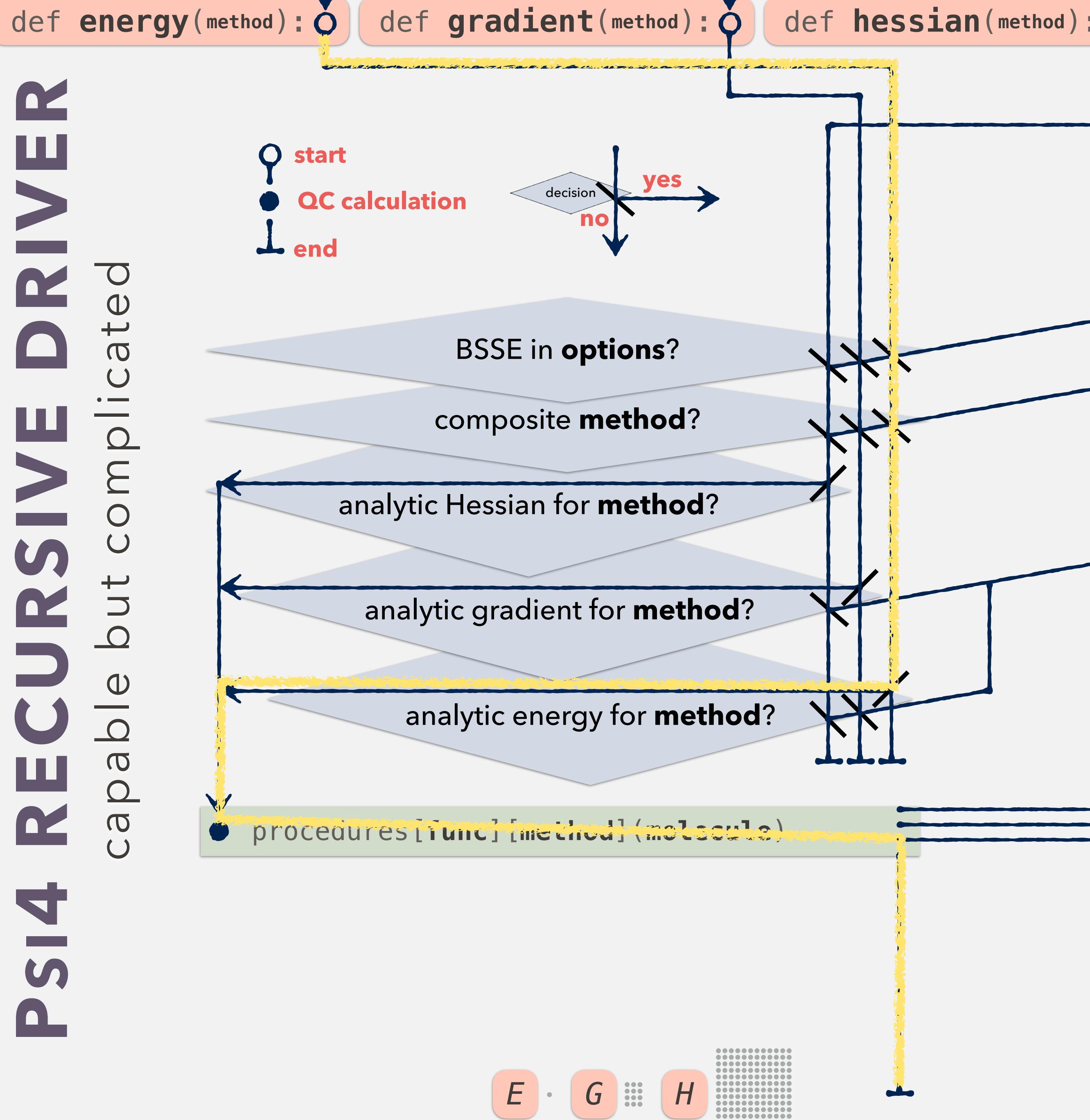


PSI4 RECURSIVE DRIVER



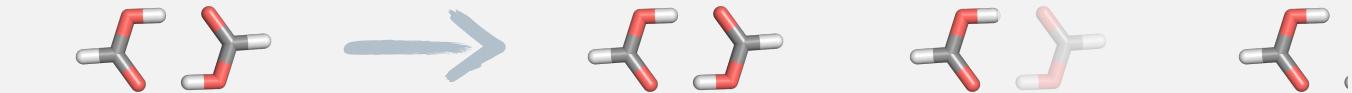
PSI4 RECURSIVE DRIVER

capable but complicated



`def manybody ():`

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



`for frag in fragments:`

Assemble n-body & interaction results from fragments.

`energy
gradient (method, frag)
hessian`

`def findif ():`

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



`for disp in displacements:`

Assemble derivative results from displacements.

`energy
gradient (method, disp)
hessian`

`def composite ():`

Separate **method** into method, basis, & extrapolations.
molecule unchanged.

`mp2/cc-pv[tq]z`

`for mc in modelchems:`

Assemble extrapolations & total results from modelchems.

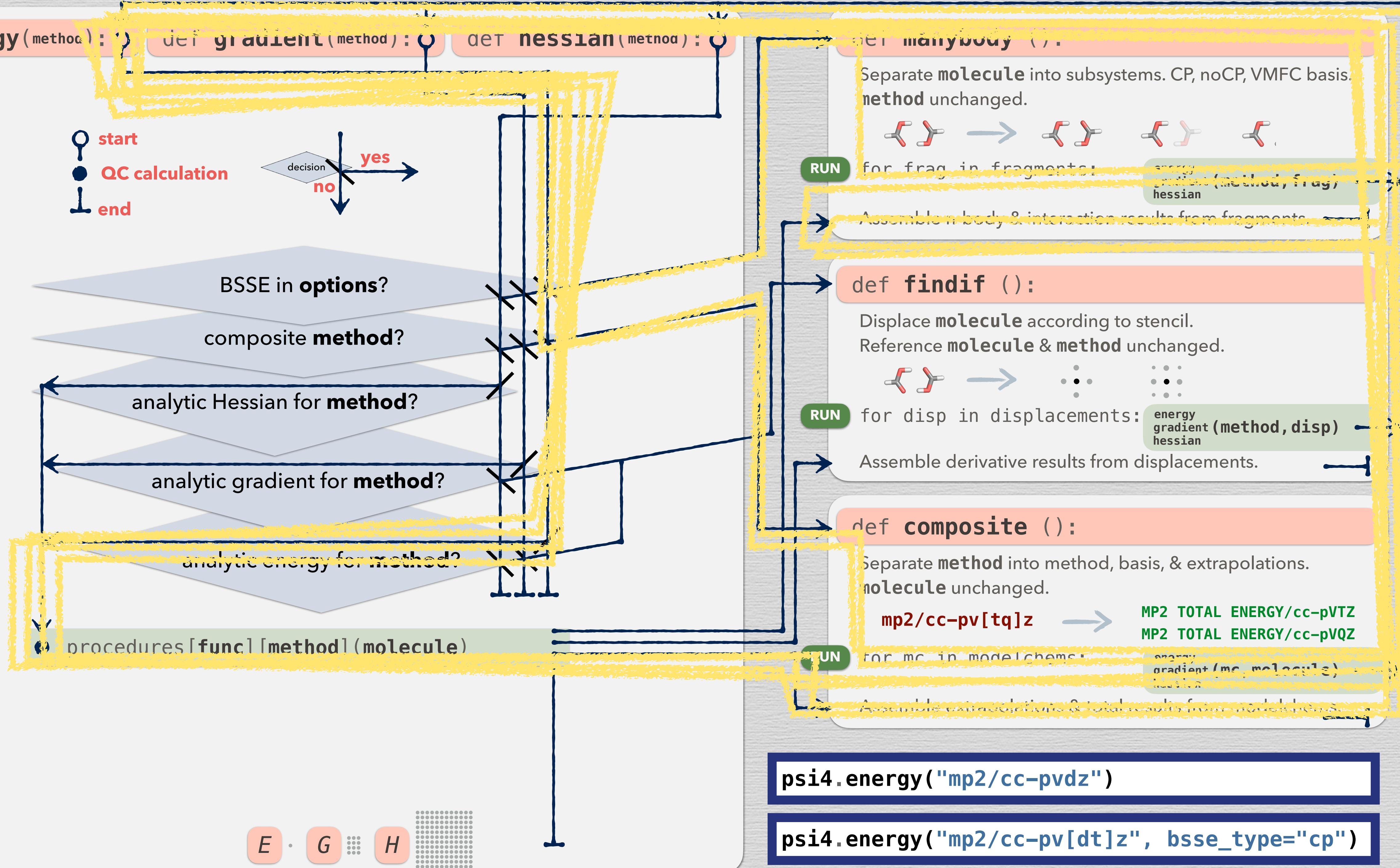
`MP2 TOTAL ENERGY/cc-pVTZ
MP2 TOTAL ENERGY/cc-pVQZ`

`energy
gradient (mc, molecule)
hessian`

`psi4.energy("mp2/cc-pvdz")`

PSI4 RECURSIVE DRIVER

capable but complicated



(2) PSI4 RECURSIVE DRIVER, INTERNAL

capable but complicated

```
psi4.energy("mp2/cc-pv[dt]z+d:ccsd(t)/cc-pvdz", bsse_type="cp", molecule= 
```



Local Compute

- **AVAILABLE** with [PSI4](#) in current form since 2016.
- **SPECIFICATION** through single file. Procedure [automated](#), so low risk of user error.
- **RATE-LIMITED** by sum of all calcs since run [sequentially](#).
- **RETRIEVAL** from filesystem difficult since many calcs in [aggregated outfile](#).
- **FLEXIBILITY** limited to PSI4 only.

PSI4 DISTRIBUTED DRIVER

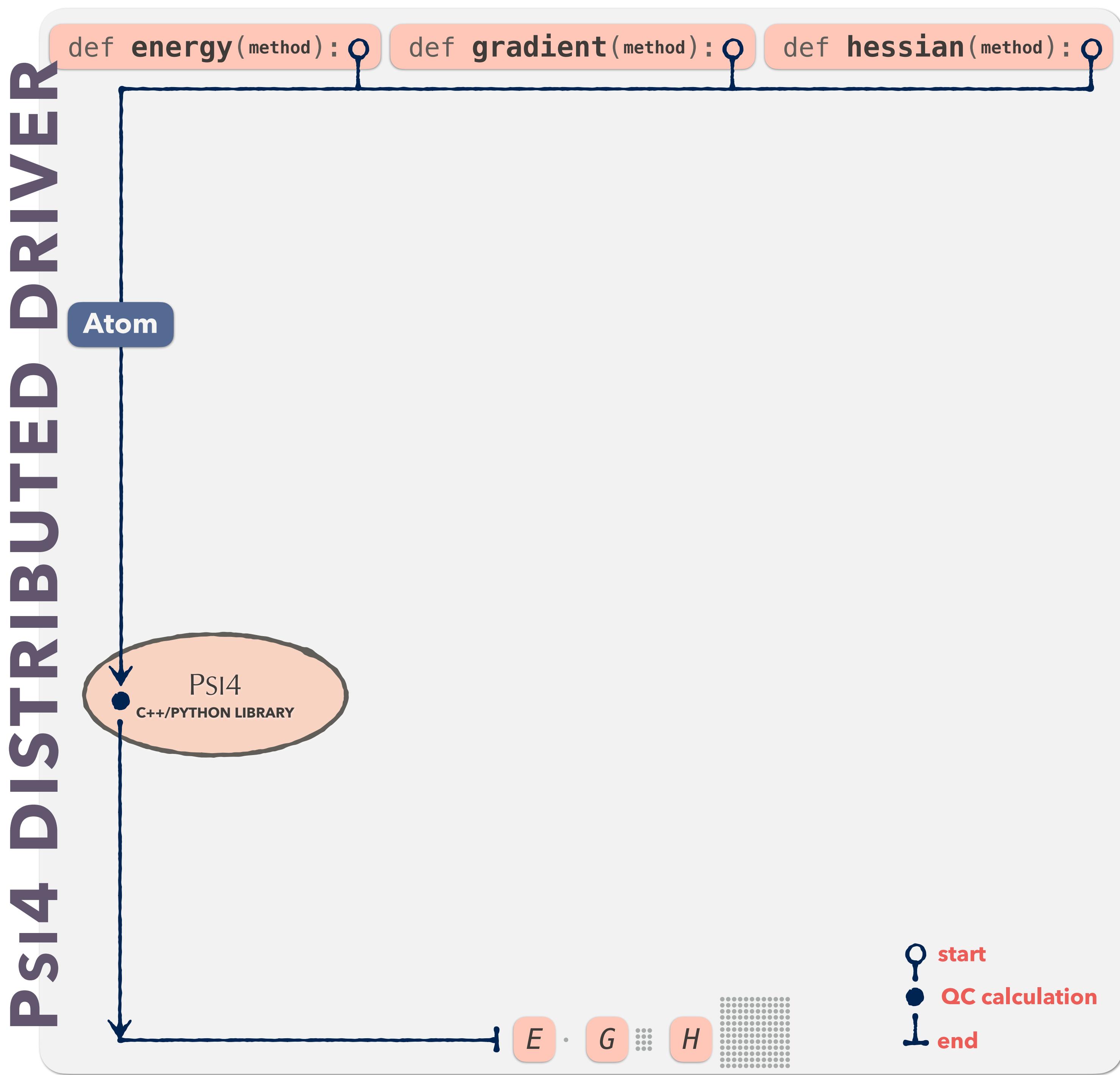
```
def energy(method):
```

```
def gradient(method):
```

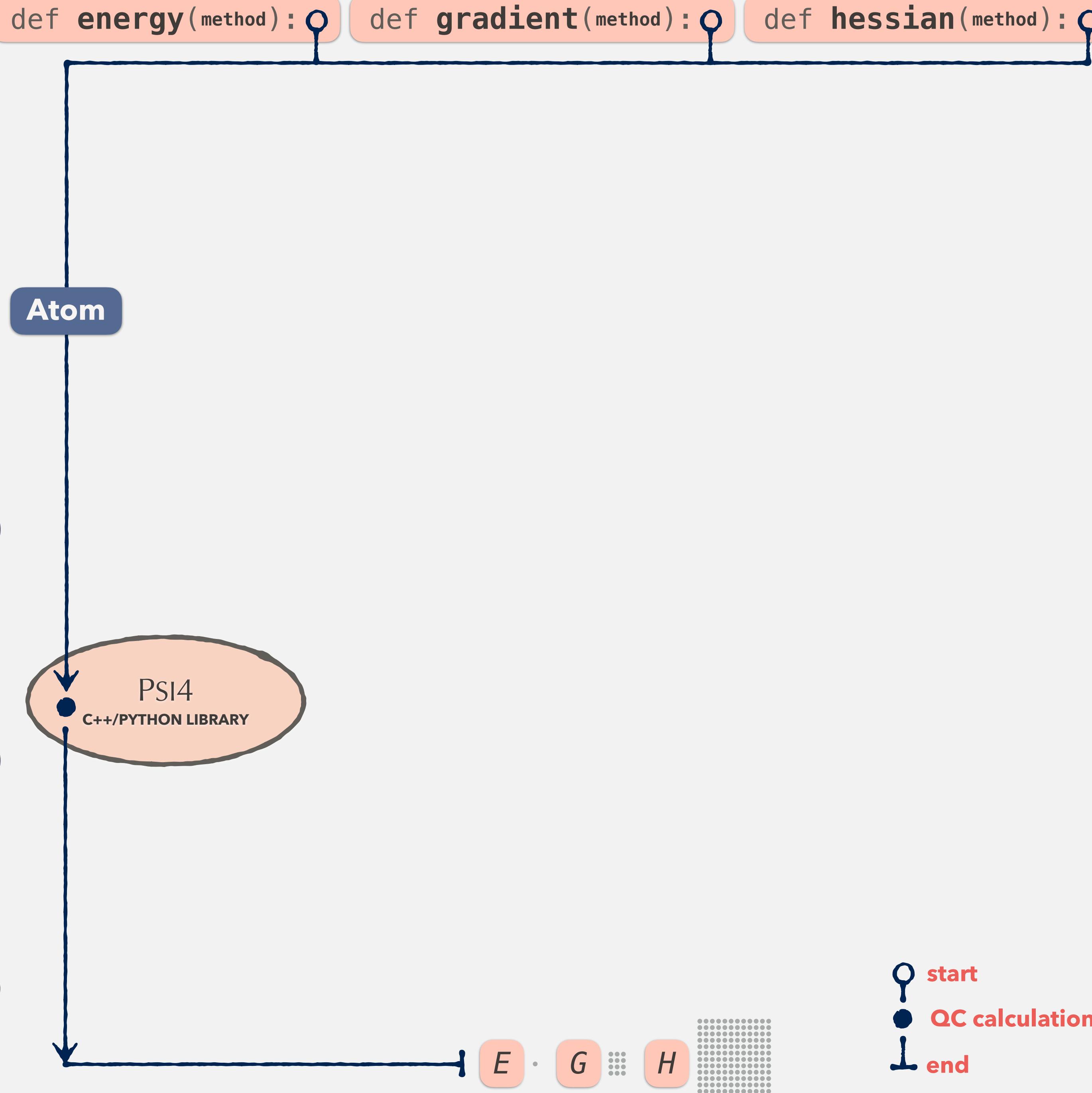
```
def hessian(method):
```

E • G H

start
 QC calculation
 end

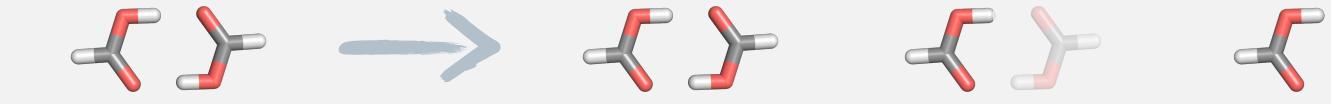


PSI4 DISTRIBUTED DRIVER

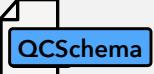


`class ManyBodyComputer ():`

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.

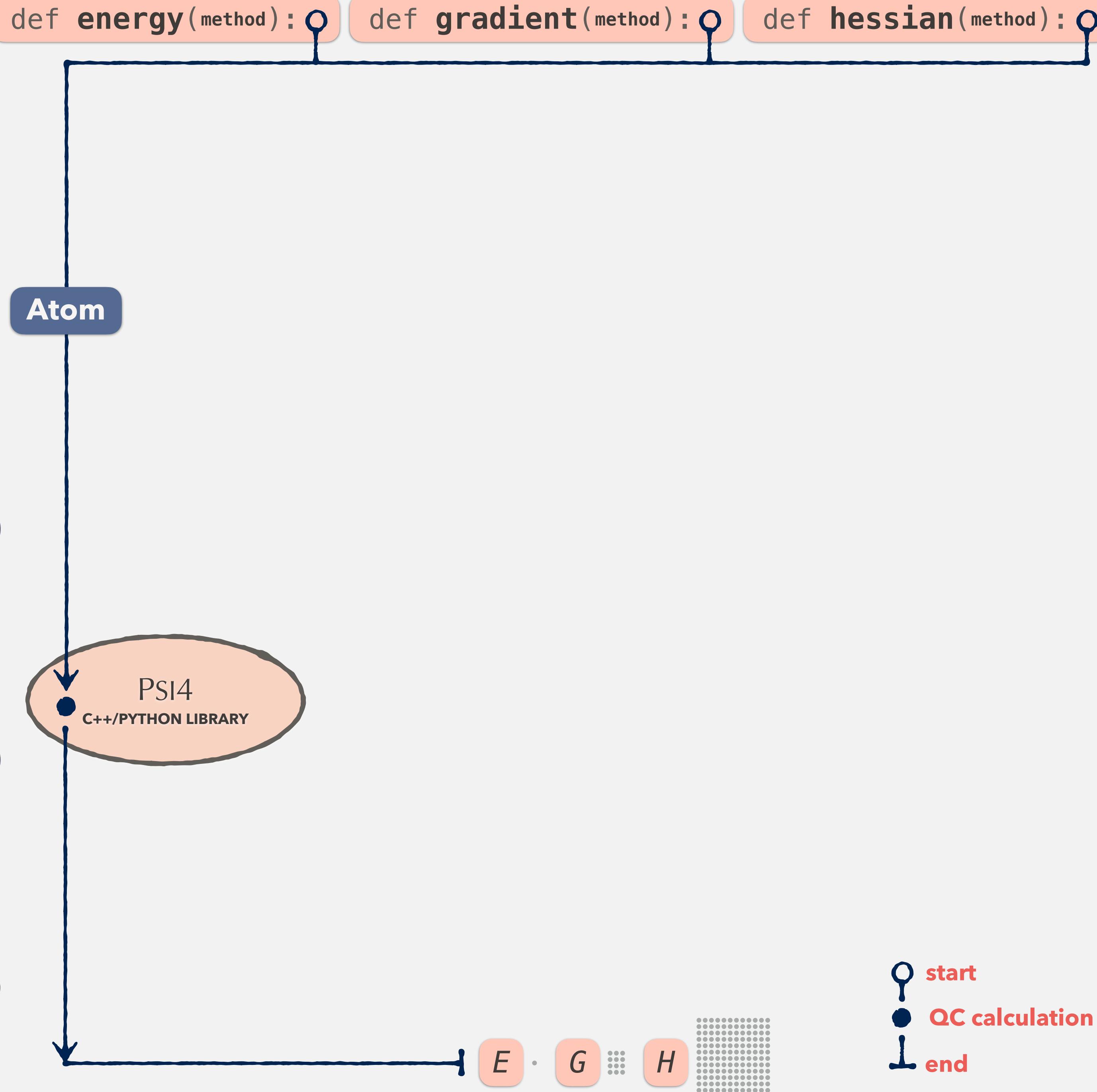


for frag in fragments: return qcschema



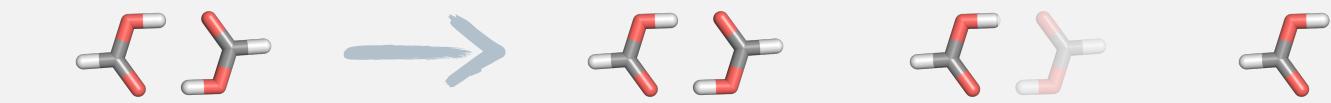
ASM Assemble n-body & interaction results from fragments.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.

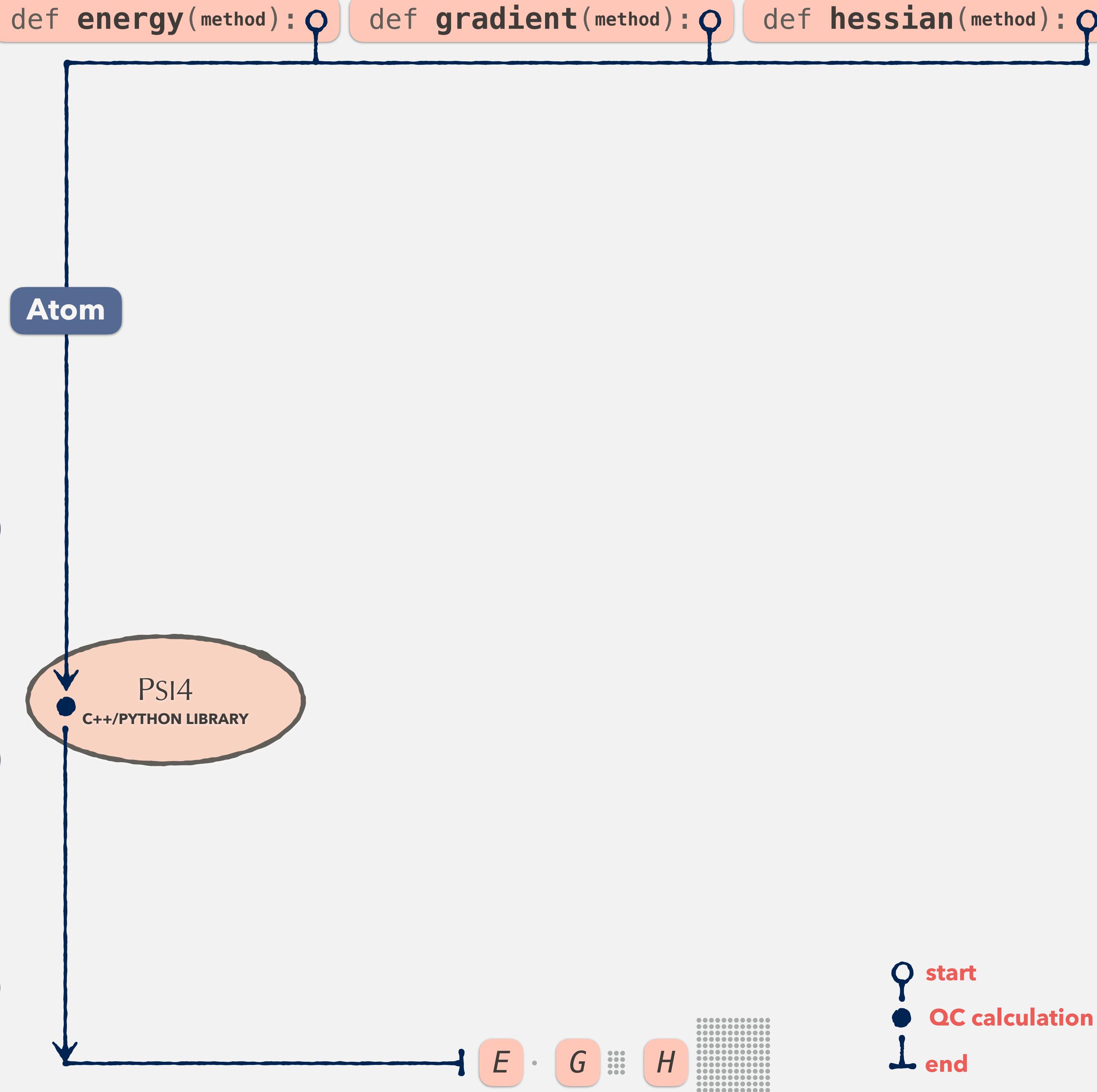


for disp in displacements: return qcschema



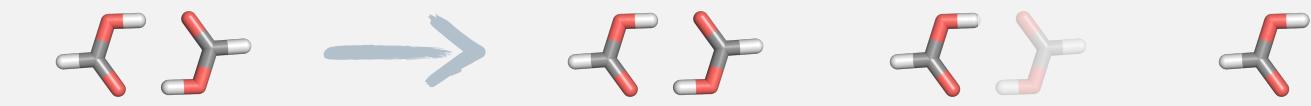
ASM Assemble derivative results from displacements.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema



ASM Assemble derivative results from displacements.

class CompositeComputer ():

PLAN Separate **method** into method, basis, & extrapolations.
molecule unchanged.

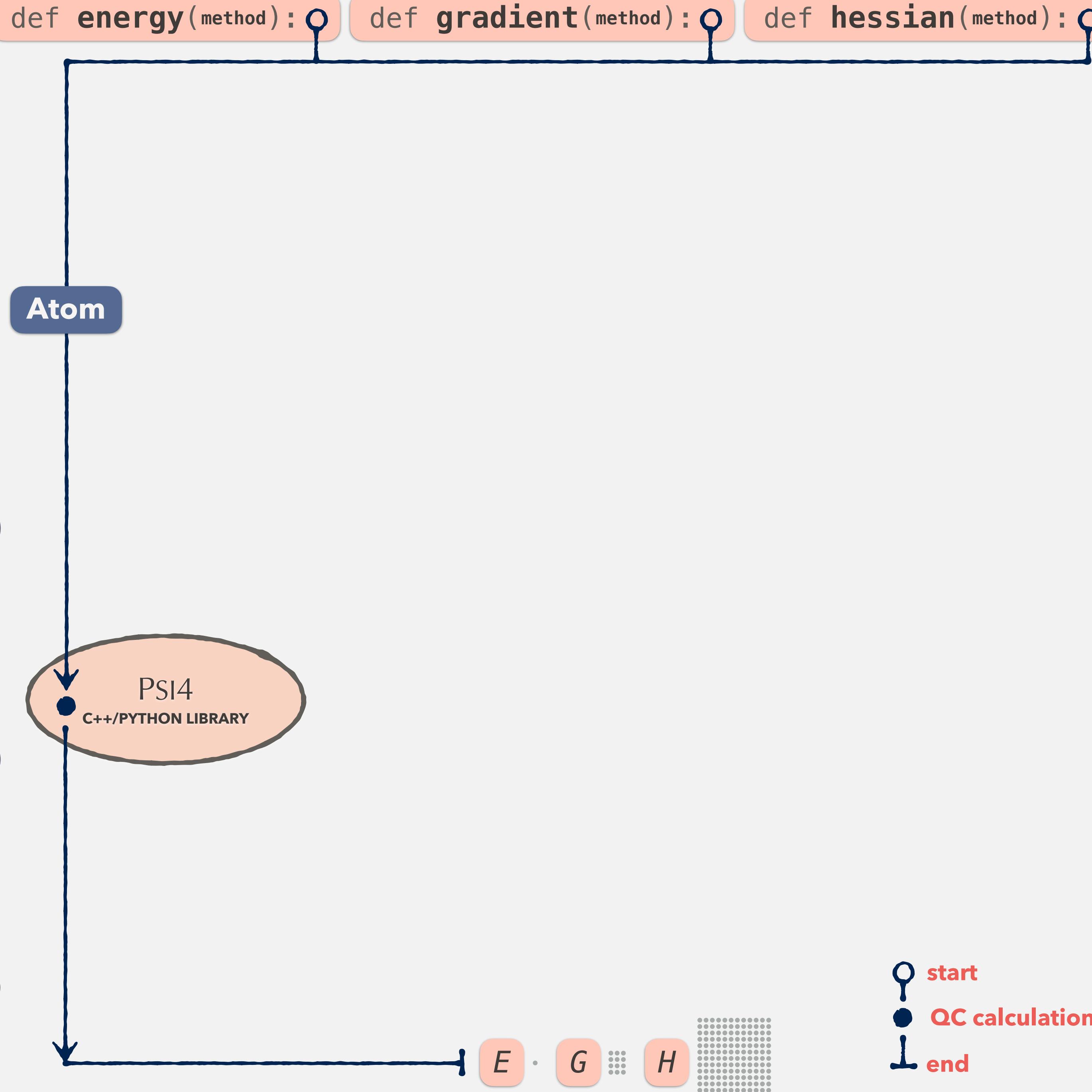
mp2/cc-pv[tq]z → MP2 TOTAL ENERGY/cc-pVTZ
MP2 TOTAL ENERGY/cc-pVQZ

for mc in modelchems: return qcschema



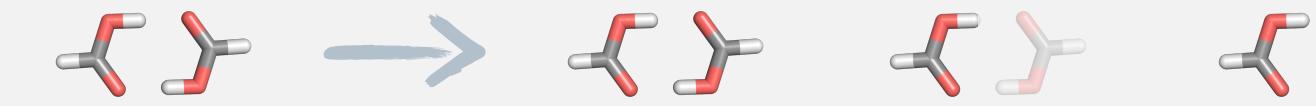
ASM Assemble extrapolations & total results from modelchems.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema



ASM Assemble derivative results from displacements.

class CompositeComputer ():

PLAN Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



ASM Assemble extrapolations & total results from modelchems.

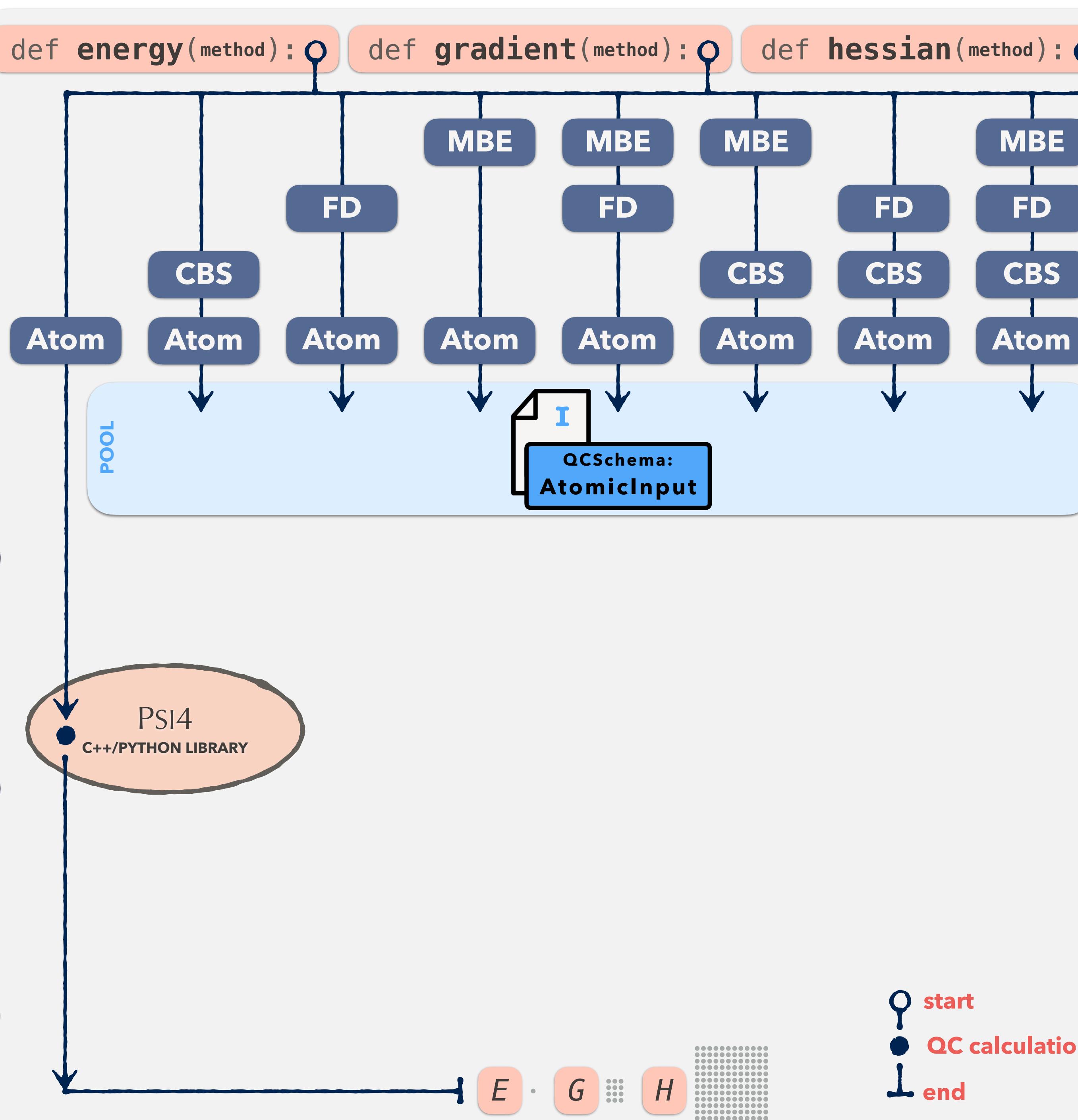
class AtomicComputer ():

PLAN **molecule** & **method** unchanged. return qcschema



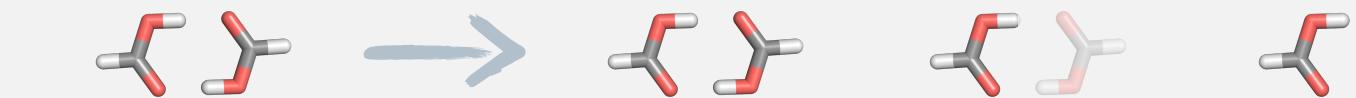
ASM Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

PLAN Separate molecule into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace molecule according to stencil.
Reference molecule & method unchanged.



for disp in displacements: return qcschema



ASM Assemble derivative results from displacements.

class CompositeComputer ():

PLAN Separate method into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



ASM Assemble extrapolations & total results from modelchems.

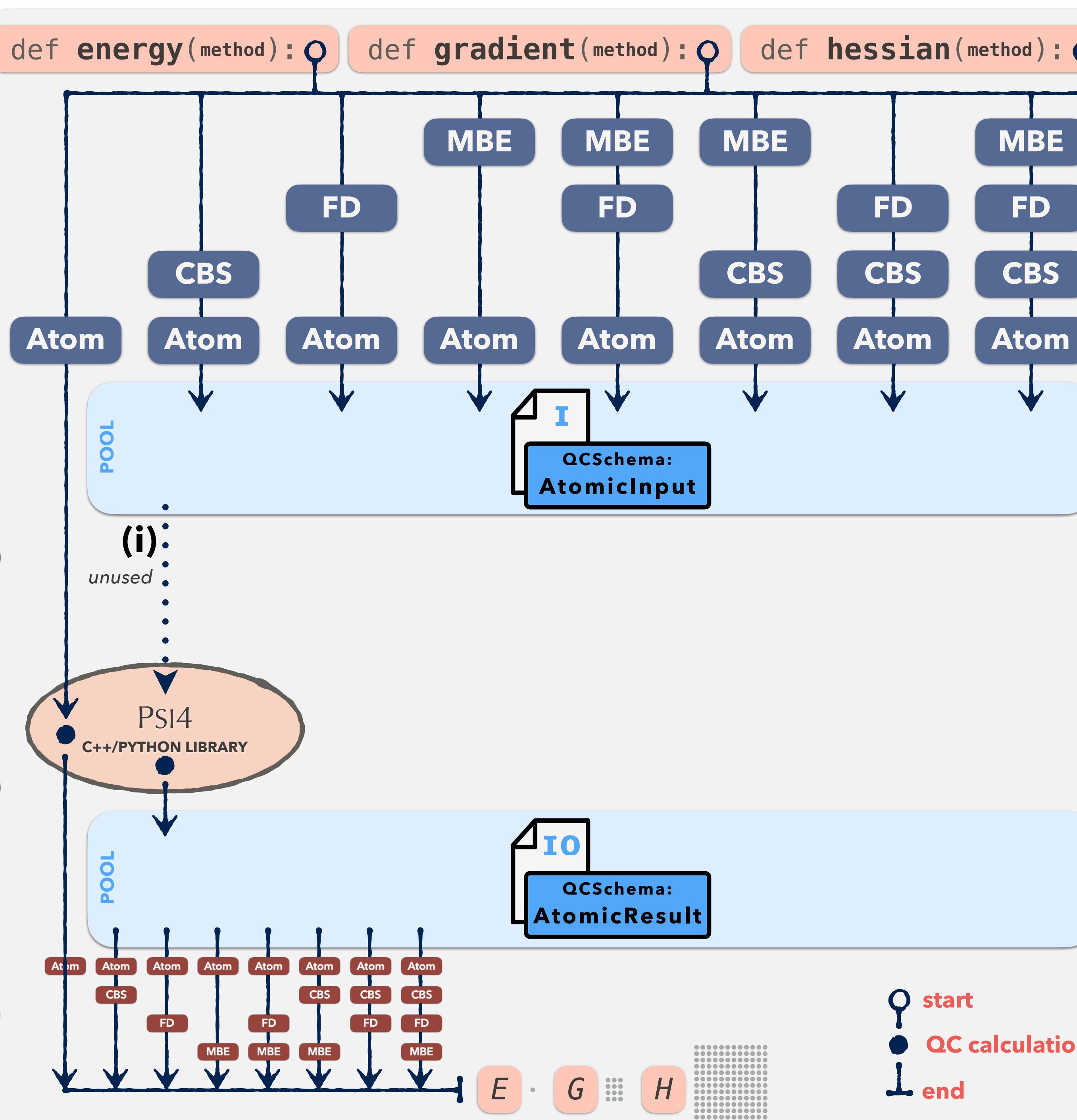
class AtomicComputer ():

PLAN molecule & method unchanged. return qcschema



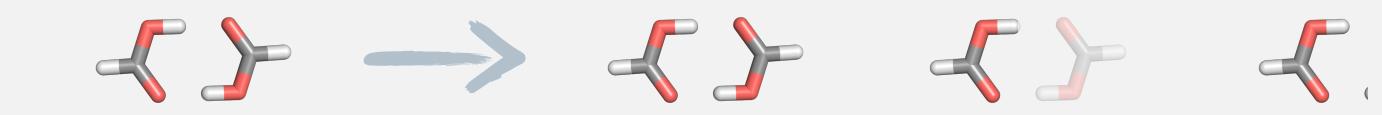
ASM Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER

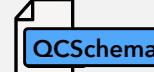


class ManyBodyComputer ():

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



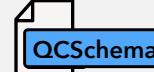
ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace **molecule** according to stencil.
Reference molecule & method unchanged.



for disp in displacements: return qcschema



ASM Assemble derivative results from displacements.

class CompositeComputer ():

PLAN Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



ASM Assemble extrapolations & total results from modelchems.

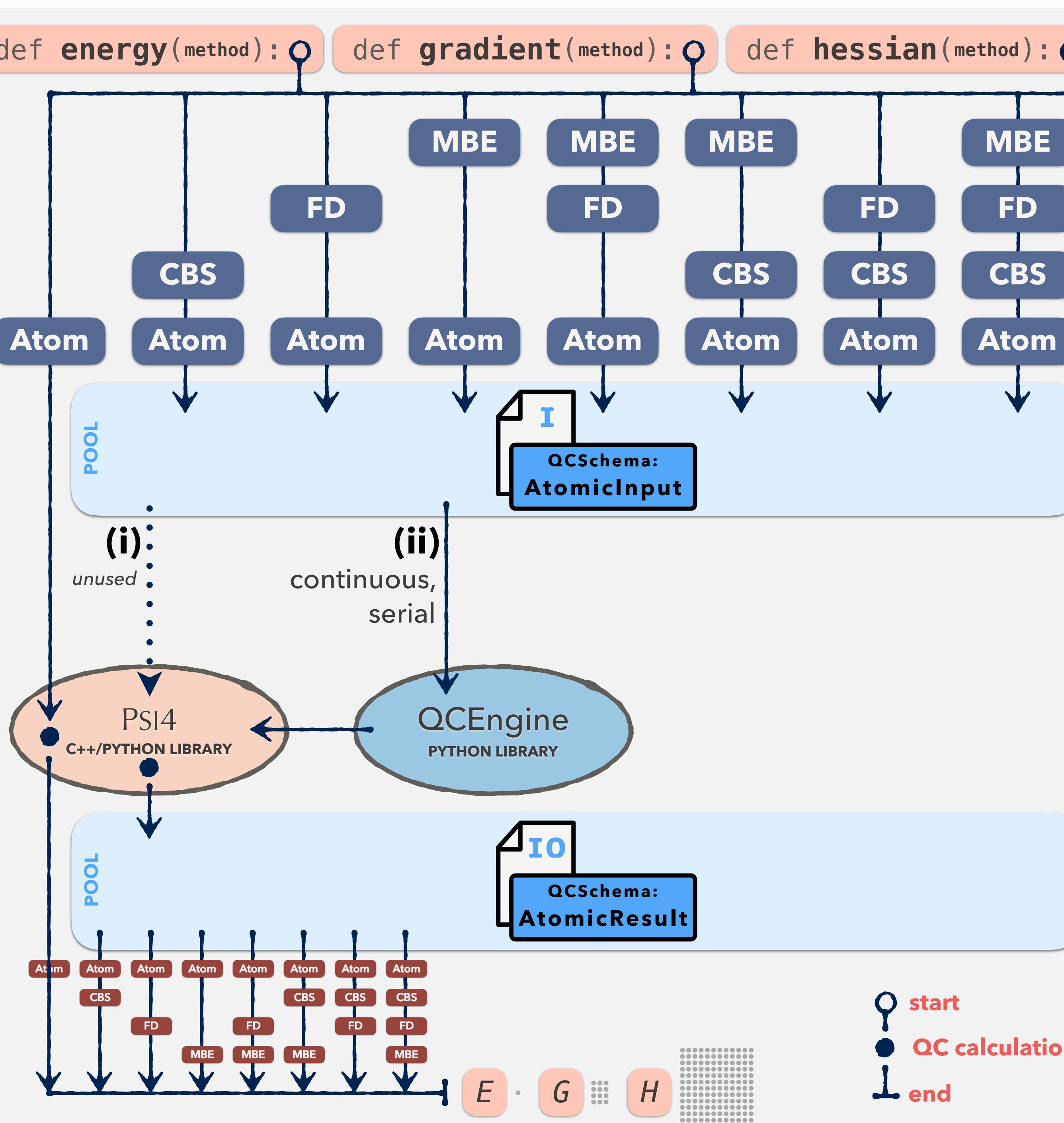
class AtomicComputer ():

molecule & method unchanged. return qcschema



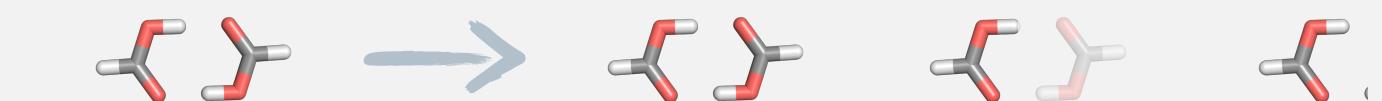
ASM Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema

.....
Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema

.....
Assemble derivative results from displacements.

class CompositeComputer ():

Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema

.....
Assemble extrapolations & total results from modelchems.

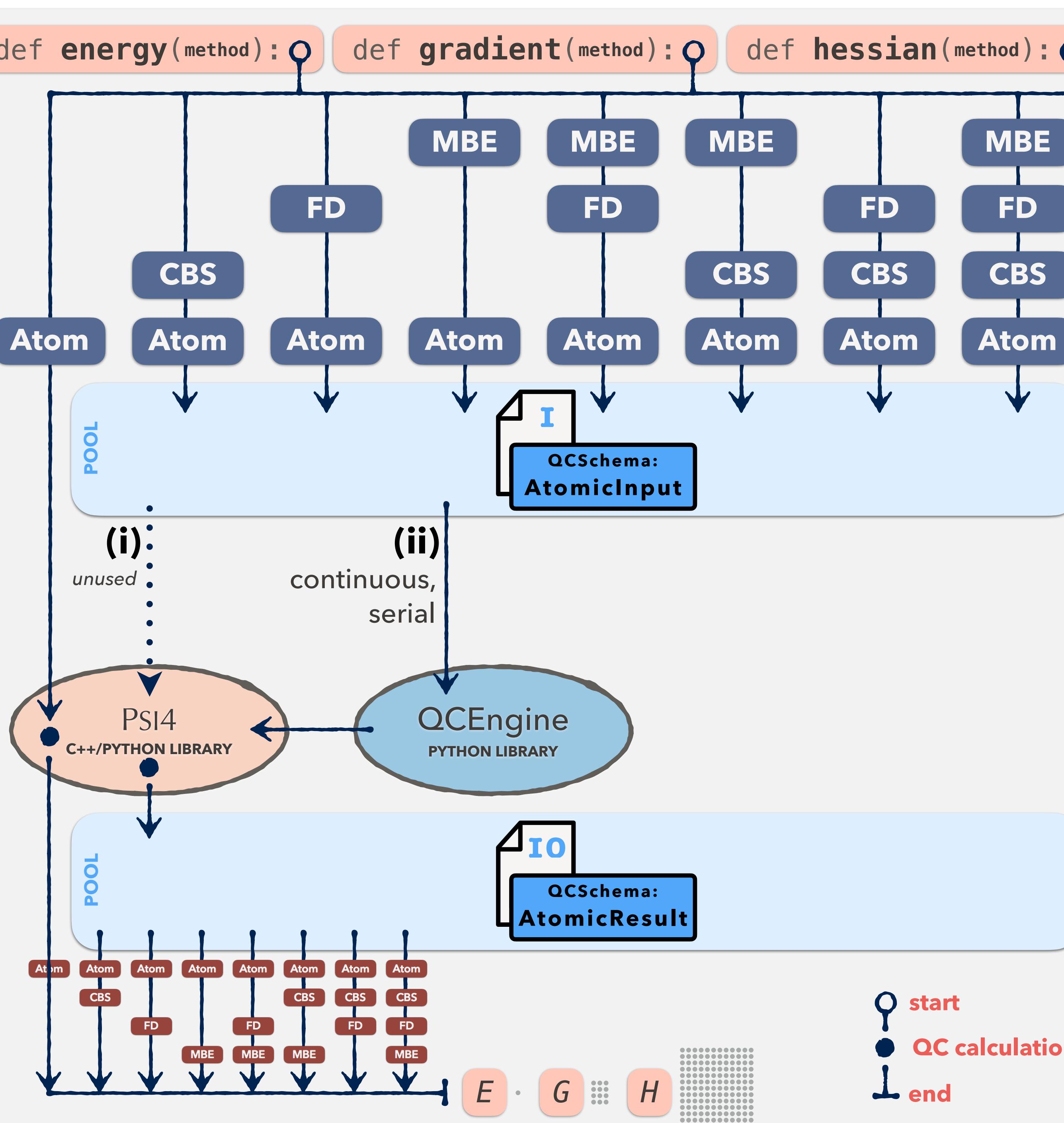
class AtomicComputer ():

molecule & **method** unchanged. return qcschema



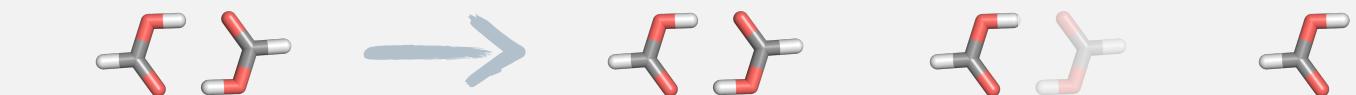
Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER



class ManyBodyComputer ():

Separate **molecule** into subsystems. CP, noCP, VMFC basis. **method** unchanged.



for frag in fragments: return qcschema

Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

Displace **molecule** according to stencil. Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema

Assemble derivative results from displacements.

class CompositeComputer ():

Separate **method** into method, basis, & extrapolations. **molecule** unchanged.



for mc in modelchems: return qcschema

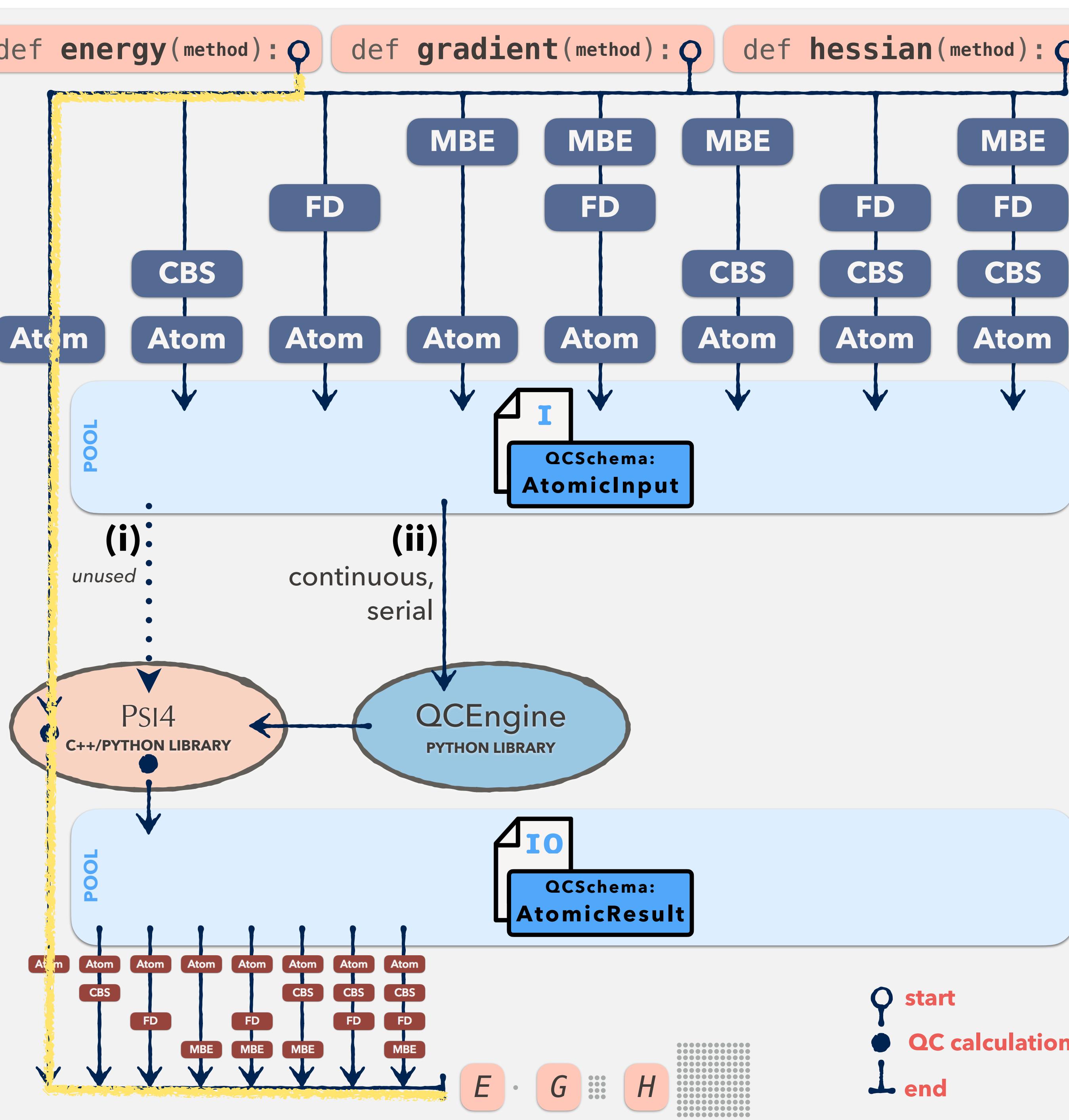
Assemble extrapolations & total results from modelchems.

class AtomicComputer ():

molecule & **method** unchanged. return qcschema

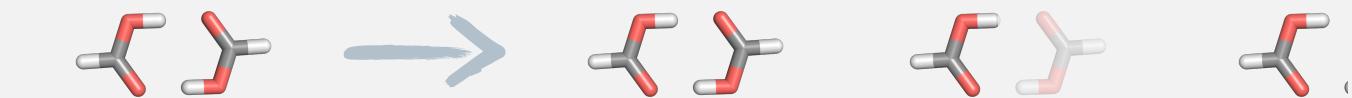
Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER

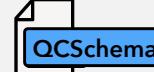


`class ManyBodyComputer ():`

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



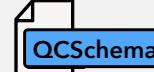
Assemble n-body & interaction results from fragments.

`class FiniteDifferenceComputer ():`

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema



Assemble derivative results from displacements.

`class CompositeComputer ():`

Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



Assemble extrapolations & total results from modelchems.

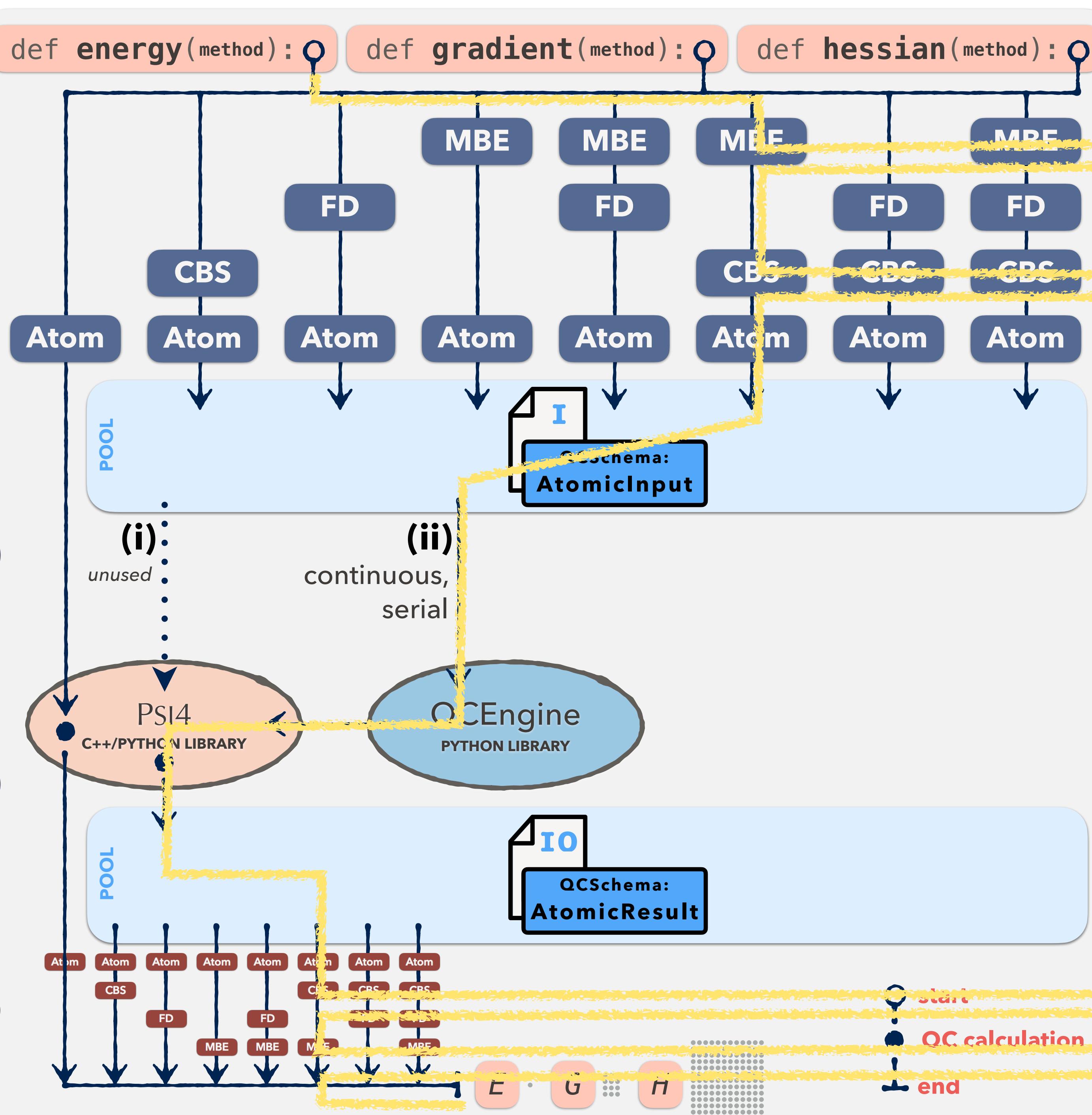
`psi4.energy("mp2/cc-pvdz")`

PLAN molecule & method unchanged. return qcschema



ASM Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER



`class ManyBodyComputer ():`

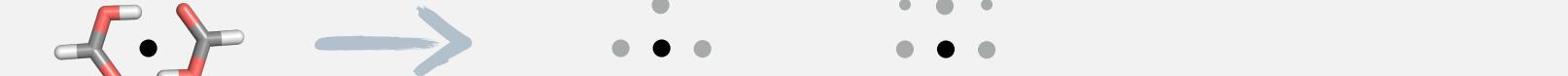
PLAN Separate molecule into subsystems. CP, noCP, VMFC basis.
method unchanged.



PLAN Assemble n-body & interaction results from fragments.

`class FiniteDifferenceComputer ():`

PLAN Displace molecule according to stencil.
Reference molecule & method unchanged.



for disp in displacements: return qcschema

ASM Assemble derivative results from displacements.

`class CompositeComputer ():`

PLAN Separate method into method, basis, & extrapolations.
molecule unchanged.

`mp2/cc-pv[tq]z` → MP2 TOTAL ENERGY/cc-pVTZ
MP2 TOTAL ENERGY/cc-pVQZ

for inc in modelScheme: return qcschema

ASM Assemble extrapolations & total results from modelscheme.

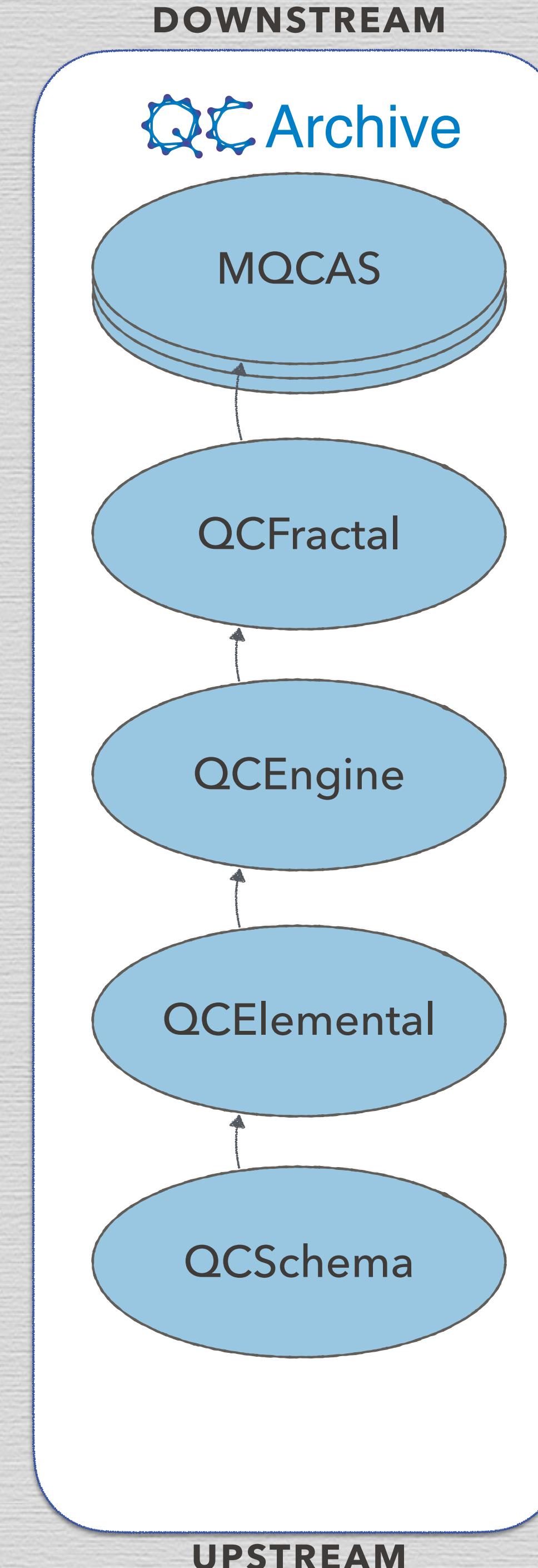
`psi4.energy("mp2/cc-pvdz")`

PLAN molecule & method unchanged return qcschema

`psi4.energy("mp2/cc-pv[dt]z", bsse_type="cp")`

QCARCHIVE STACK

qcarchive.molssi.org/



- database, universally queryable for CMS results
- MolSSI QC Archive Server ("em-quacks")
- batch (parallel) compute setup & management
- database storage & query of QC results
- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs
- Python QCSchema implementations & validation
- NIST periodic table & physical constants
- molecule parsing, validation, export
- QC data layout & descriptions
- e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

QCARCHIVE STACK

qcarchive.molssi.org/

github.com/MoSSI/QCFractal

pip install qcfractal

conda install qcfractal -c conda-forge

github.com/MoSSI/QCEngine

pip install qcengine

conda install qcengine -c conda-forge

github.com/MoSSI/QCElemental

pip install elemental

conda install qcelemental -c conda-forge

github.com/MoSSI/QCSchema

DOWNSTREAM

 QC Archive

MQCAS

QCFractal

QCEngine

QCElemental

QCSchema

 QC Archive
Infrastructure

UPSTREAM

- database, universally queryable for CMS results
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- batch (parallel) compute setup & management
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- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs

- Python QCSchema implementations & validation
- NIST periodic table & physical constants
- molecule parsing, validation, export

- QC data layout & descriptions
- e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

QCARCHIVE STACK

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github.com/MoSSI/QCFractal

pip install qcfractal

conda install qcfractal -c conda-forge

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pip install qcengine

conda install qcengine -c conda-forge

github.com/MoSSI/QCElemental

pip install elemental

conda install qcelemental -c conda-forge

github.com/MoSSI/QCSchema

DOWNSTREAM

 QC Archive

MQCAS

QCFractal

QCEngine

QCElemental

QCSchema

 QC Archive
Infrastructure

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- database, universally queryable for CMS results
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- batch (parallel) compute setup & management
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- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs

- Python QCSchema implementations & validation
- NIST periodic table & physical constants
- molecule parsing, validation, export

- **QC data layout & descriptions**
- e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

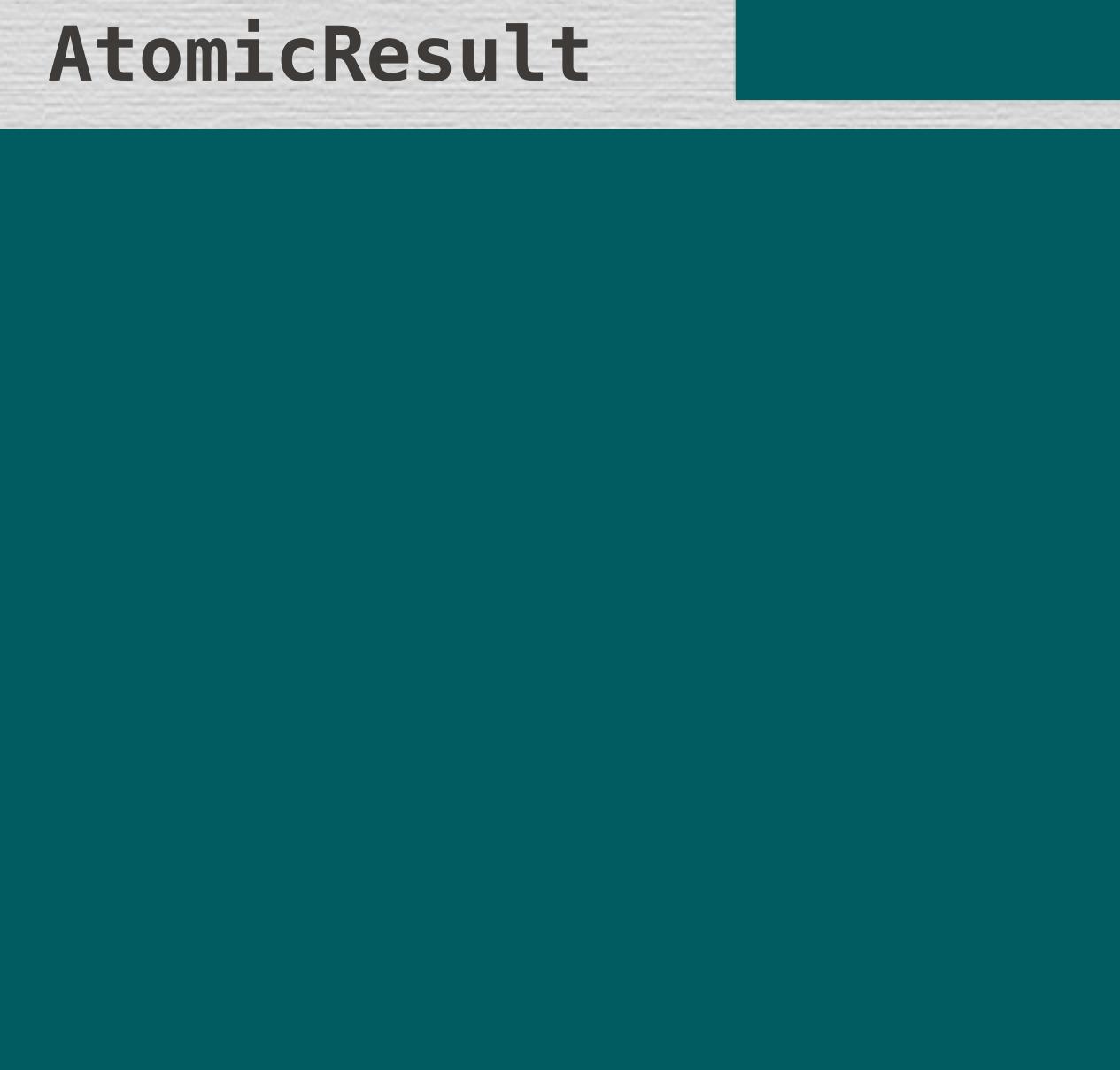
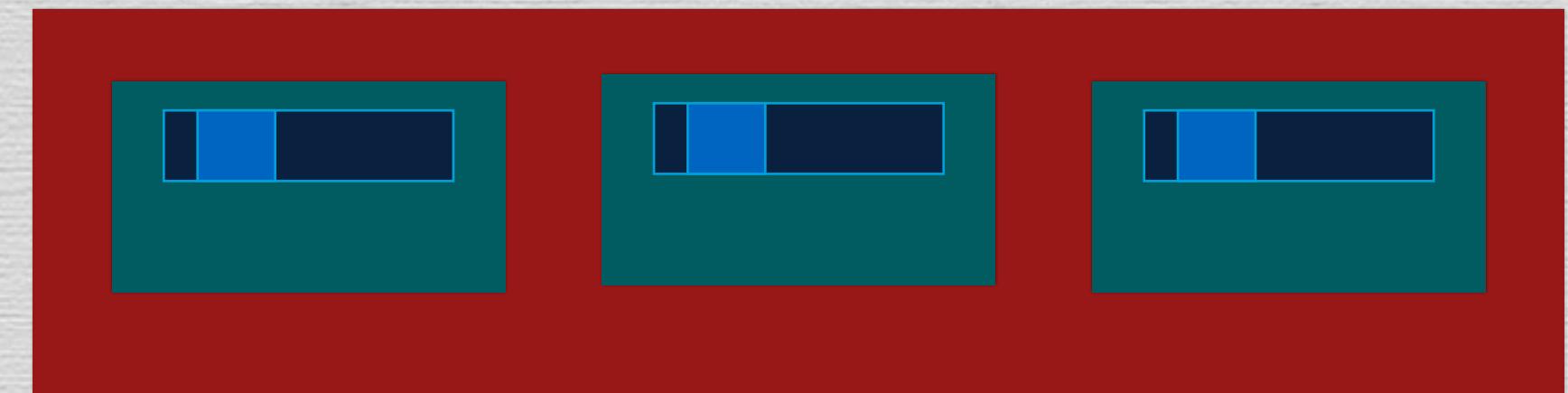
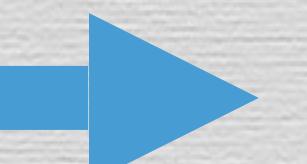
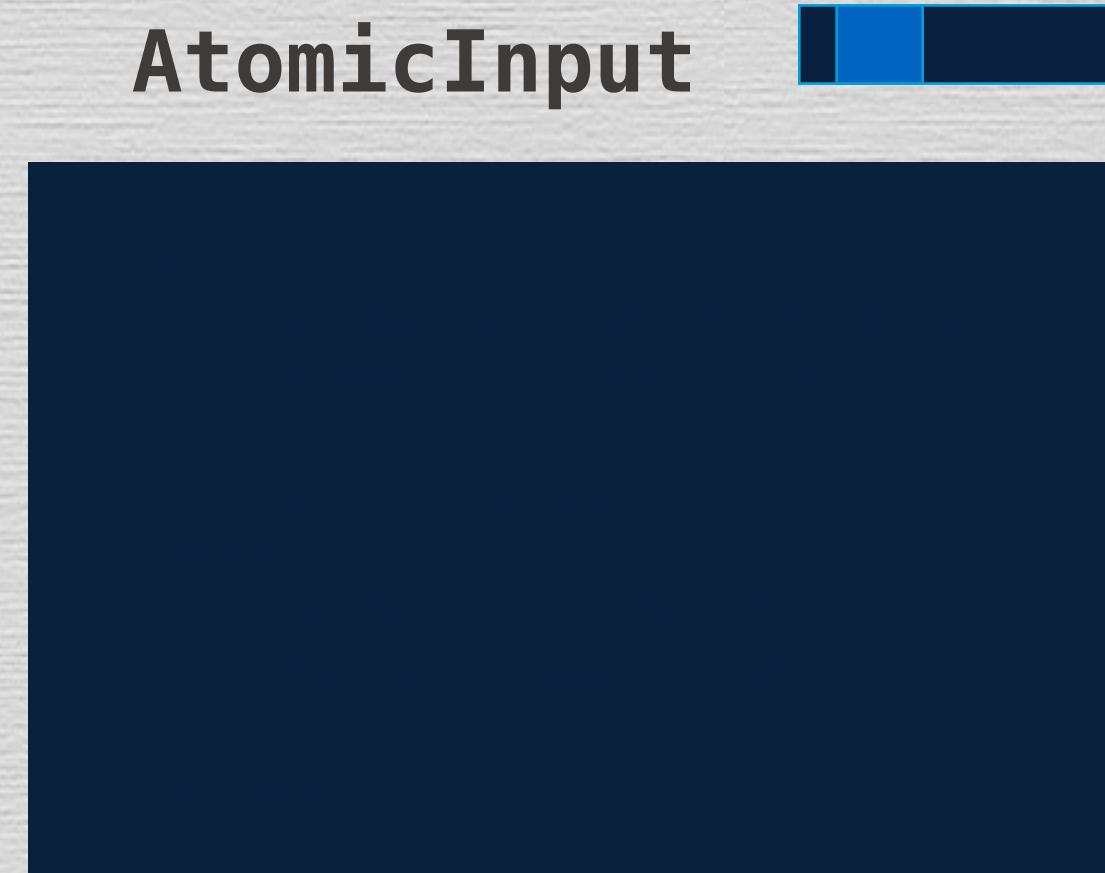
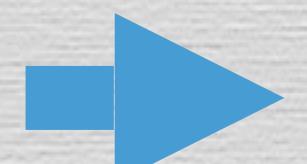
QUANTUM CHEMISTRY SCHEMA

github.com/MolSSI/QCSchema

- **COMMUNICATION** channel between all pieces of the ecosystem.
- **COMMUNITY** project useful for many aspects of quantum chem.
- **JSON** nominally, but any key/value/array language like MessagePack/BSON/XML/YAML ok.
- **TIMELINE** development stage since 2017. Most changes for QCA. More community participation desired but little momentum.
- **PRIOR ART** present but varied. Inviting all of the groups.
- **SCHEMA** defined in Python module but not used directly in QCA.

Molecule ■

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```



QUANTUM CHEMISTRY SCHEMA

primary schemas defined thus far

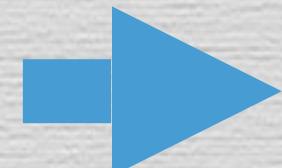
- **MOLECULE** Cartesian, atomic units (AU) based specification.
- **ATOMICINPUT** job directive for analytic single-point – energy, gradient, Hessian, or property – as defined by **DRIVER**.
- **ATOMICRESULT** append to **ATOMICINPUT** with output, simple scalar and array results, and wavefunction results.
- **PROVENANCE** who wrote the data – program, version, module, computer system information.
- **BASISSET** similar to BSE. allows **WAVEFUNCTION** data in CCA ordering.
- **OPTIMIZATIONINPUT & OPTIMIZATIONRESULT** job directive for abstract generic optimizer call generic QC program for gradient computation.

Molecule

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```

```
0 0 0 0  
H 2 0 0  
--  
@22Ne 5 0 0  
units bohr
```

Snippet 1:



```
{"atom_labels": ["", "", ""],  
 "atomic_numbers": [ 8,  1, 10],  
 "fix_com": False,  
 "fix_orientation": False,  
 "fragment_charges": [0.0, 0.0],  
 "fragment_multiplicities": [2, 1],  
 "fragments": [[0, 1], [2]],  
 "geometry": [[[0., 0., 0.],  
              [2., 0., 0.],  
              [5., 0., 0.]],  
             "mass_numbers": [16, 1, 22],  
             "masses": [15.99491462, 1.00782503, 21.99138511],  
             "molecular_charge": 0.0,  
             "molecular_multiplicity": 2,  
             "name": "HNeO",  
             "provenance": {"creator": "QCElemental",  
                           "routine": "qcelemental.molparse.from_schema",  
                           "version": "v0.8.0"},  
             "real": [ True,  True, False],  
             "schema_name": "qcschema_molecule",  
             "schema_version": 2,  
             "symbols": ["O", "H", "Ne"],  
             "validated": True}]
```

Snippet 2: QCSchema Molecule from Snippet 1.

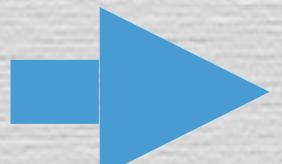
QUANTUM CHEMISTRY SCHEMA

primary schemas defined thus far

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- **ATOMICRESULT** append to **ATOMICINPUT** with output, simple scalar and array results, and wavefunction results.
- **PROVENANCE** who wrote the data – program, version, module, compute information.
- **BASISSET** similar to BSE. allows **WAVEFUNCTION** data in CCA ordering.
- **OPTIMIZATIONINPUT & OPTIMIZATIONRESULT** job directive for abstract generic optimizer call generic QC program for gradient computation.

Molecule 

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```



AtomicInput 

```
{  
    "molecule": {  
        "geometry": [0, 0, 0, 0, 0, 1],  
        "symbols": ["He", "He"]  
    },  
    "driver": "energy",  
    "model": {  
        "method": "CCSD(T)",  
        "basis": "aug-cc-pVDZ",  
    },  
    "keywords": {},  
}
```

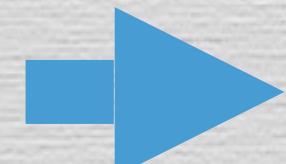
QUANTUM CHEMISTRY SCHEMA

primary schemas defined thus far

- **MOLECULE** Cartesian, atomic units (AU) based specification.
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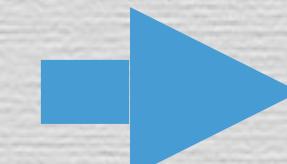
Molecule

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```



AtomicInput

```
{  
    "molecule": {  
        "geometry": [0, 0, 0, 0, 0, 1],  
        "symbols": ["He", "He"]  
    },  
    "driver": "energy",  
    "model": {  
        "method": "CCSD(T)",  
        "basis": "aug-cc-pVDZ",  
    },  
    "keywords": {},  
}
```



AtomicResult

```
{  
    ... AtomicInput ...  
    "provenance": {  
        "creator": "My QM Program",  
        "version": "1.1rc1",  
    },  
    "properties": {  
        "calcinfo_nalpha": 5,  
        "scf_total_energy": -5.433191881443323,  
        "nuclear_repulsion_energy": 2.11670883436,  
        "scf_iterations": 8.0,  
    },  
    "error": null,  
    "return_result": -6.5432123456,  
    "success": true,  
    "stdout": "...",  
    "wavefunction": "..."  
}
```

QUANTUM CHEMISTRY SCHEMA

primary schemas defined thus far

- **MOLECULE** Cartesian, atomic units (AU) based specification.
- **ATOMICINPUT** job directive for analytic single-point – energy, gradient, Hessian, or property – as defined by **DRIVER**.
- **ATOMICRESULT** append to **ATOMICINPUT** with output, simple scalar and array results, and wavefunction results.
- **PROVENANCE** who wrote the data – program, version, module, compute information.
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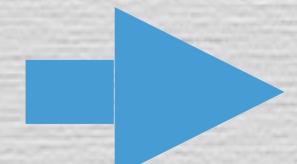
- orbitals_a
- orbitals_b
- density_a
- density_b
- fock_a
- fock_b
- eigenvalues_a
- eigenvalues_b
- occupations_a
- occupations_b



AtomicResult

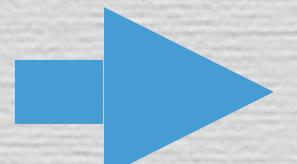
Molecule

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```



AtomicInput

```
{  
    "molecule": {  
        "geometry": [0, 0, 0, 0, 0, 1],  
        "symbols": ["He", "He"]  
    },  
    "driver": "energy",  
    "model": {  
        "method": "CCSD(T)",  
        "basis": "aug-cc-pVDZ",  
    },  
    "keywords": {},  
}
```



```
{  
    ... AtomicInput ...  
    "provenance": {  
        "creator": "My QM Program",  
        "version": "1.1rc1",  
    },  
    "properties": {  
        "calcinfo_nalpha": 5,  
        "scf_total_energy": -5.433191881443323,  
        "nuclear_repulsion_energy": 2.11670883436,  
        "scf_iterations": 8.0,  
    },  
    "error": null,  
    "return_result": -6.5432123456,  
    "success": true,  
    "stdout": "...",  
    "wavefunction": "..."  
}
```

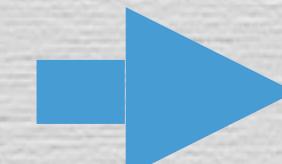
QUANTUM CHEMISTRY SCHEMA

primary schemas defined thus far

- **MOLECULE** Cartesian, atomic units (AU) based specification.
- **ATOMICINPUT** job directive for analytic single-point – energy, gradient, Hessian, or property – as defined by **DRIVER**.
- **ATOMICRESULT** append to **ATOMICINPUT** with output, simple scalar and array results, and wavefunction results.
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- **OPTIMIZATIONINPUT & OPTIMIZATIONRESULT** job directive for abstract generic optimizer call generic QC program for gradient computation.

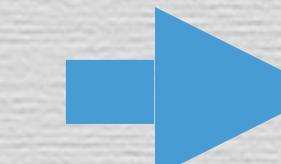
Molecule

```
{  
    "geometry": [0, 0, 0, 0, 0, 1],  
    "symbols": ["He", "He"],  
    ...  
}
```



AtomicInput

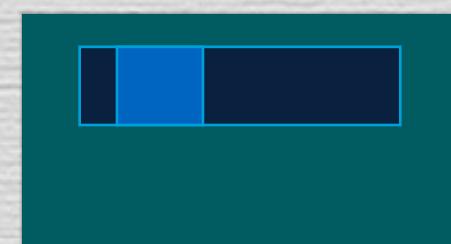
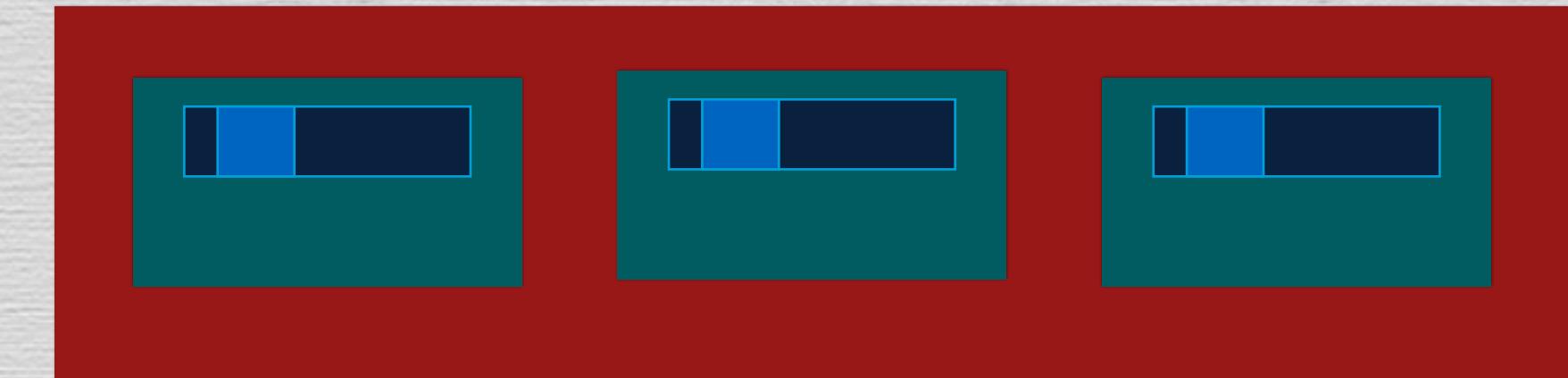
```
{  
    "molecule": {  
        "geometry": [0, 0, 0, 0, 0, 1],  
        "symbols": ["He", "He"]  
    },  
    "driver": "energy",  
    "model": {  
        "method": "CCSD(T)",  
        "basis": "aug-cc-pVDZ",  
    },  
    "keywords": {},  
}
```



AtomicResult

```
{  
    ... AtomicInput ...  
    "provenance": {  
        "creator": "My QM Program",  
        "version": "1.1rc1",  
    },  
    "properties": {  
        "calcinfo_nalpha": 5,  
        "scf_total_energy": -5.433191881443323,  
        "nuclear_repulsion_energy": 2.11670883436,  
        "scf_iterations": 8.0,  
    },  
    "error": null,  
    "return_result": -6.5432123456,  
    "success": true,  
    "stdout": "...",  
    "wavefunction": "..."  
}
```

OptimizationResult



QCSchema DEFINES DATA LAYOUTS

and text advice, nothing more

- **LAYOUT** JSON Schema defines a data layout and some minimal type and count checking.
- **CONVENTIONS** JSON Schema can't check conventions you rely upon like AU units, CCA ordering, center-of-mass positioning

DOMAIN-SPECIFIC ASCII

```
$ccinp ncore=0 $end
$basis gbasis=accd $end
$contrl cctyp=ccsd
coord=prinaxis
icharg=0 ispher=1
runtyp=energy scftyp=rohf
units=bohr mult=2 $end
$data

C1
N 7  0.000  0.000 -0.146
H 1  0.000 -1.511  1.014
H 1  0.000  1.511  1.014
$end
```

GAMESS Input

DATA LAYOUT TRANSLATION



QCSchema: AtomicInput

```
{
  'molecule': {
    'symbols': [ ],
    'geometry': [ ],
    'molecular_multiplicity':  },
  'driver': ' ',
  'model': {
    'method': ' ',
    'basis': ' '},
  'keywords': {
    }
  },
```

QCSchema DEFINES DATA LAYOUTS

and text advice, nothing more

- **LAYOUT** JSON Schema defines a data layout and some minimal type and count checking.
- **CONVENTIONS** JSON Schema can't check conventions you rely upon like AU units, CCA ordering, center-of-mass positioning

DOMAIN-SPECIFIC ASCII

```
$ccinp ncore=0 $end
$basis gbasis=accd $end
$contrl cctyp=ccsd
coord=prinaxis
icharg=0 ispher=1
runtyp=energy scftyp=rohf
units=bohr mult=2 $end
$data

C1
N 7  0.000  0.000 -0.146
H 1  0.000 -1.511  1.014
H 1  0.000  1.511  1.014
$end
```

GAMESS Input

DATA LAYOUT TRANSLATION

MOL & DRIVER STANDARDIZATION

BASIS & KEYWORDS STANDARDIZATION

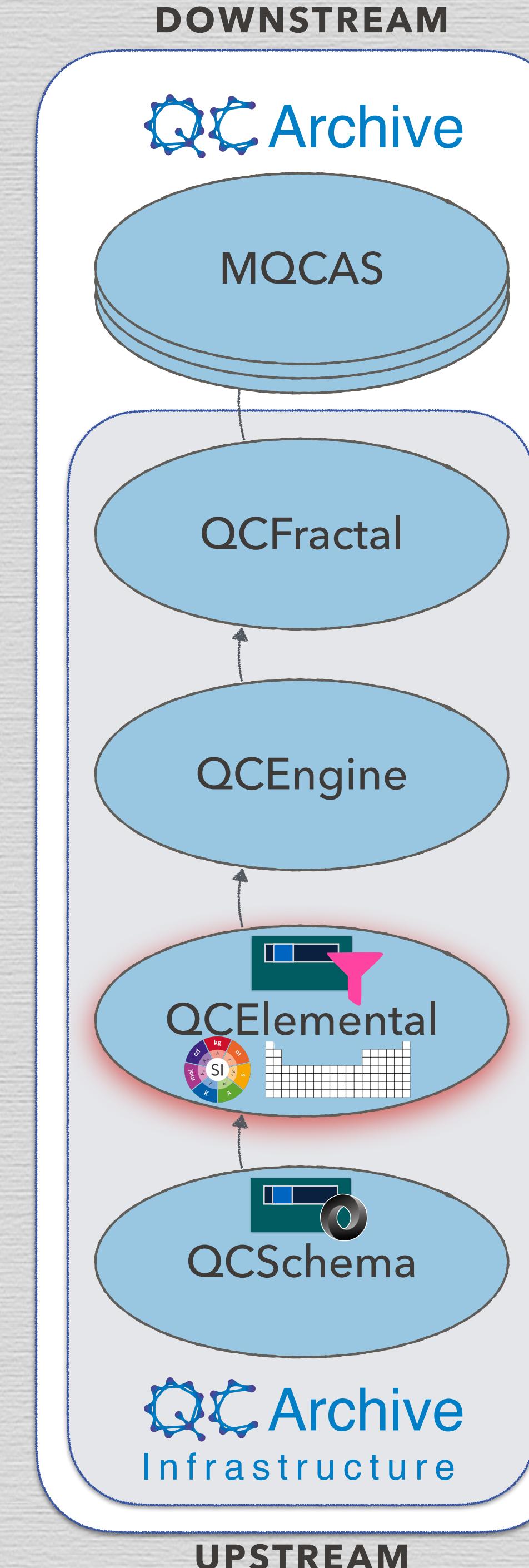
QCSchema: AtomicInput

```
{
  'molecule': {
    'symbols': [ 'N', 'H', 'H' ],
    'geometry': [ 0.000, ..., 1.014 ],
    'molecular_multiplicity': 2 },
  'driver': 'energy',
  'model': {
    'method': 'ccsd',
    'basis': 'accd' },
  'keywords': {
    'contrl_ispher': 1,
    'contrl_scftyp': 'rohf',
    'ccinp_ncore': 0 },}
```

GAMESS QC Engine Input

QCARCHIVE STACK

qcarchive.molssi.org/



- database, universally queryable for CMS results
- MolSSI QCArchive Server ("em-quacks")

- batch (parallel) compute setup & management
- database storage & query of QC results

- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs

- **Python QCSchema implementations & validation**
- **NIST periodic table & physical constants**
- **molecule parsing, validation, export**

- QC data layout & descriptions
- e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

QCELEMENTAL IMPLEMENTS QCSHEMA

with strong validation through pydantic

SIX FLAWED MOLECULES

```
> Molecule(geometry=[5, 6], symbols=['O'])
```

```
ValueError: cannot reshape array of size 2 into shape (3)
```

```
> Molecule(geometry=[4, 4, 4], symbols=['Z'])
```

```
NotAnElementError: Z
```

```
> Molecule(geometry=[0, 1, 2, 3, 4, 5], symbols=['H', 'H', 'H'])
```

```
ValidationError: dropped atoms! nat = 3 != 2
```

```
> Molecule(geometry=[0, 0.001, 0, 0, 0, 0], symbols=['N', 'N'])
```

```
ValidationError: Following atoms are too close: [(0, 1, 0.001)]
```

```
> Molecule(geometry=[0, 0, 0], symbols=['He'], molecular_charge=0, molecular_multiplicity=2)
```

```
ValidationError: Inconsistent or unspecified chg/mult: sys chg: 0, frag chg: [None], sys mult: 2, frag mult: [None]
```

```
> Molecule(geometry=[0, 0, 0], symbols=['He'], fragments=[[0], [1]])
```

```
ValidationError: dropped atoms! nat = 2 != 1
```

THAT RAISE HELPFUL ERRORS IN QCElemental

QCELEMENTAL PROVIDES DATASETS

NIST CODATA, covalent and vdW radii, Periodic Table

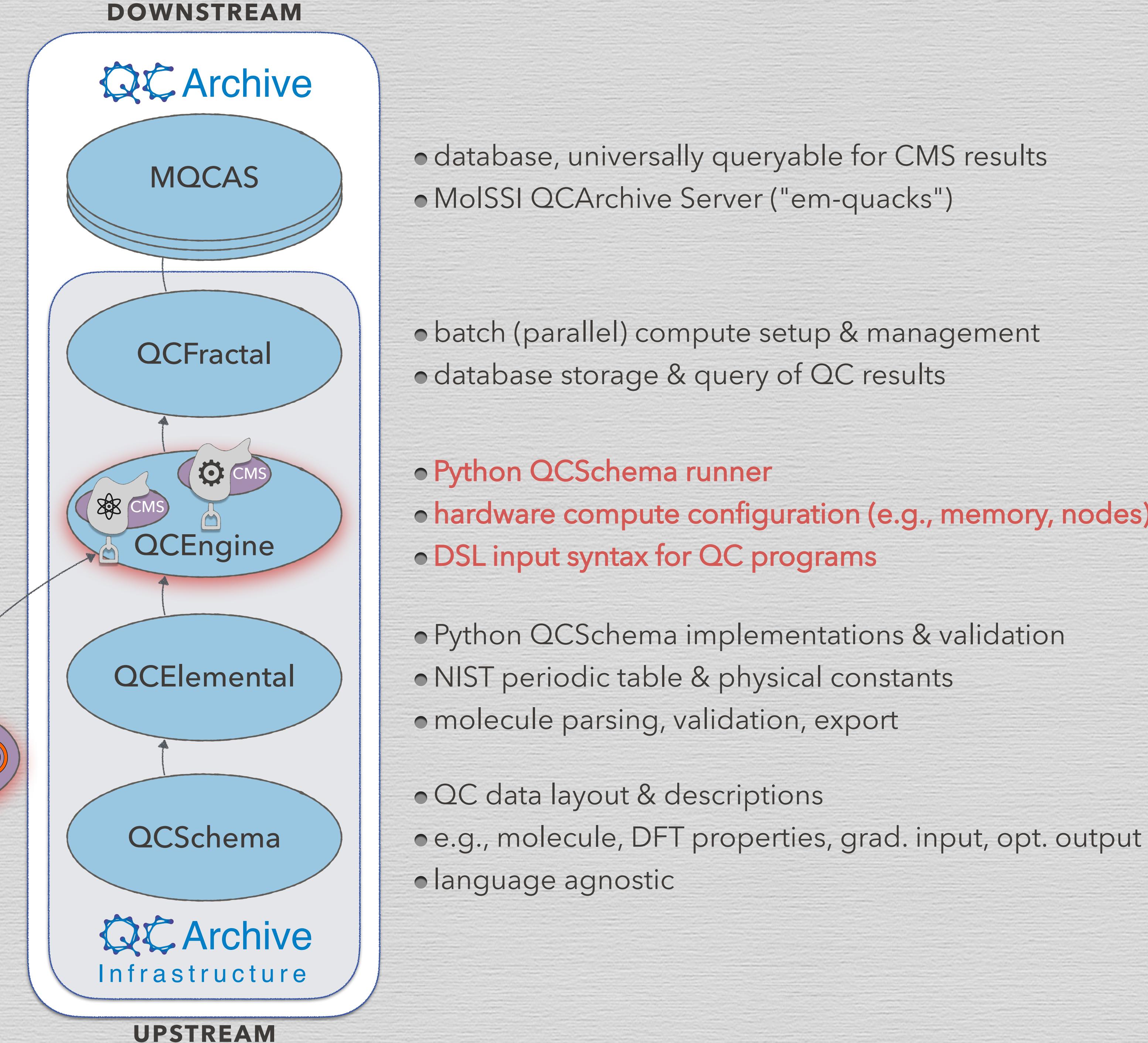
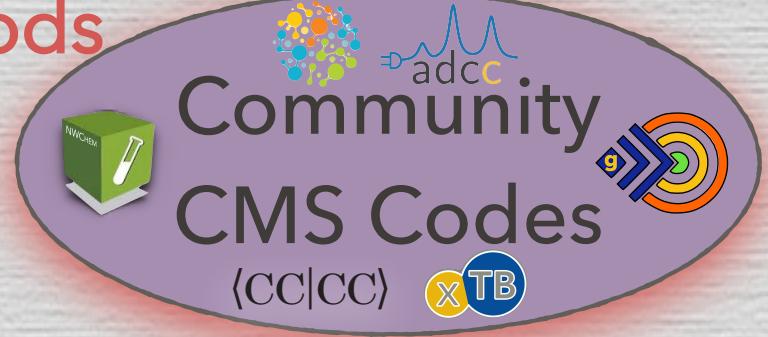
- **STRUCTURED DATA** processed into light Python API directly from NIST structured data, if available.
- **PRECISION** original significant figures value always available
- **VERSIONED** store& upgrade: when reproducibility demands old versions, accessing both helps transitions.
- **CONVERSION** with pint module, internally consistent unit conversions available.
- **STORAGE/USER UNITS** maintain AU in QCSchema, while presenting results in customary units.

```
>>> import qcelemental as qcel
>>> qcel.constants.Hartree_energy_in_eV
27.21138602
>>> pc = qcel.constants.get('hartree ENERGY in ev', return_tuple=True)
>>> pc.label
'Hartree energy in eV'
>>> pc.data
Decimal('27.21138602')
>>> pc.units
'eV'
>>> pc.comment
'uncertainty=0.000 000 17'
>>> qcel.constants.conversion_factor("bohr", "miles")
3.2881547429884475e-14
```

```
>>> import qcelemental as qcel
>>> qcel.periodictable.to_E('KRYPTON')
'Kr'
>>> qcel.periodictable.to_element(36)
'Krypton'
>>> qcel.periodictable.to_Z('kr84')
36
>>> qcel.periodictable.to_A('Kr')
84
>>> qcel.periodictable.to_mass('Kr86')
85.9106106269
```

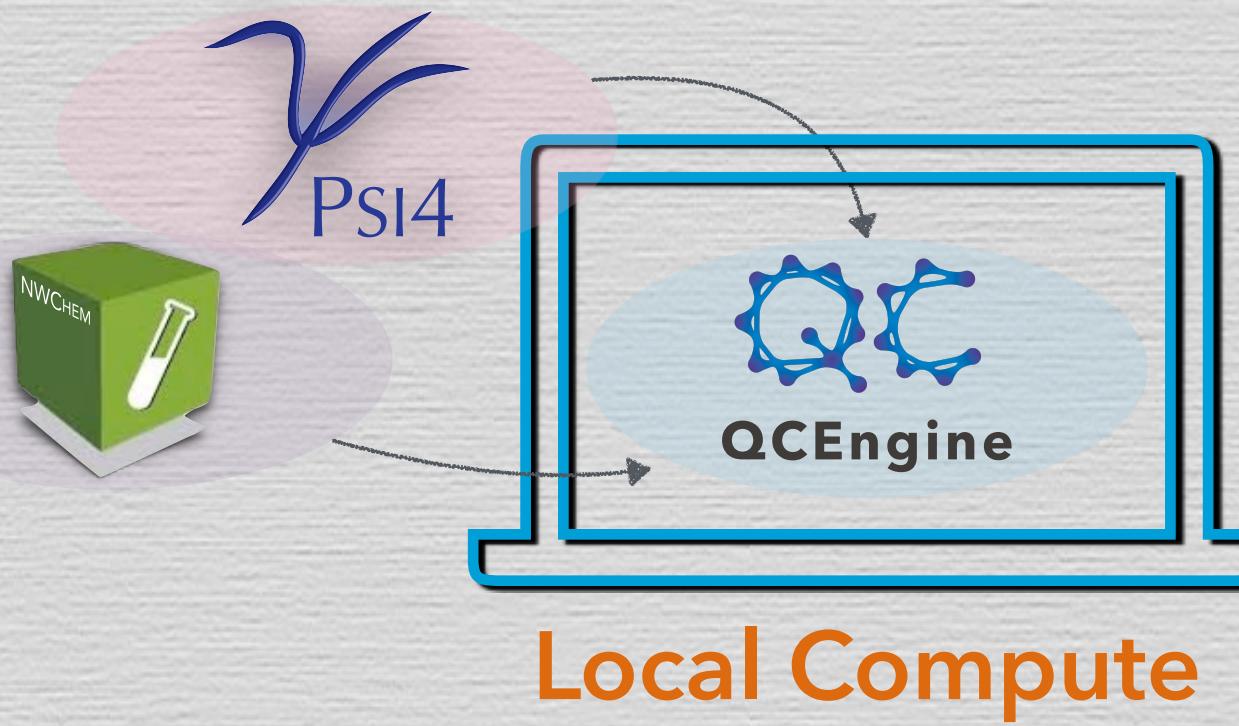
QCARCHIVE STACK

- the difficult part – coded QC methods
- structured output uncommon
- DSL input; API/schema uncommon



QCENGINE: PYTHON QCSCHEMA RUNNER

github.com/MoSSI/QCEngine



CMDLINE

```
> qcengine run cfour  
          molpro atomicinput  
          psi4  
          dftd4
```

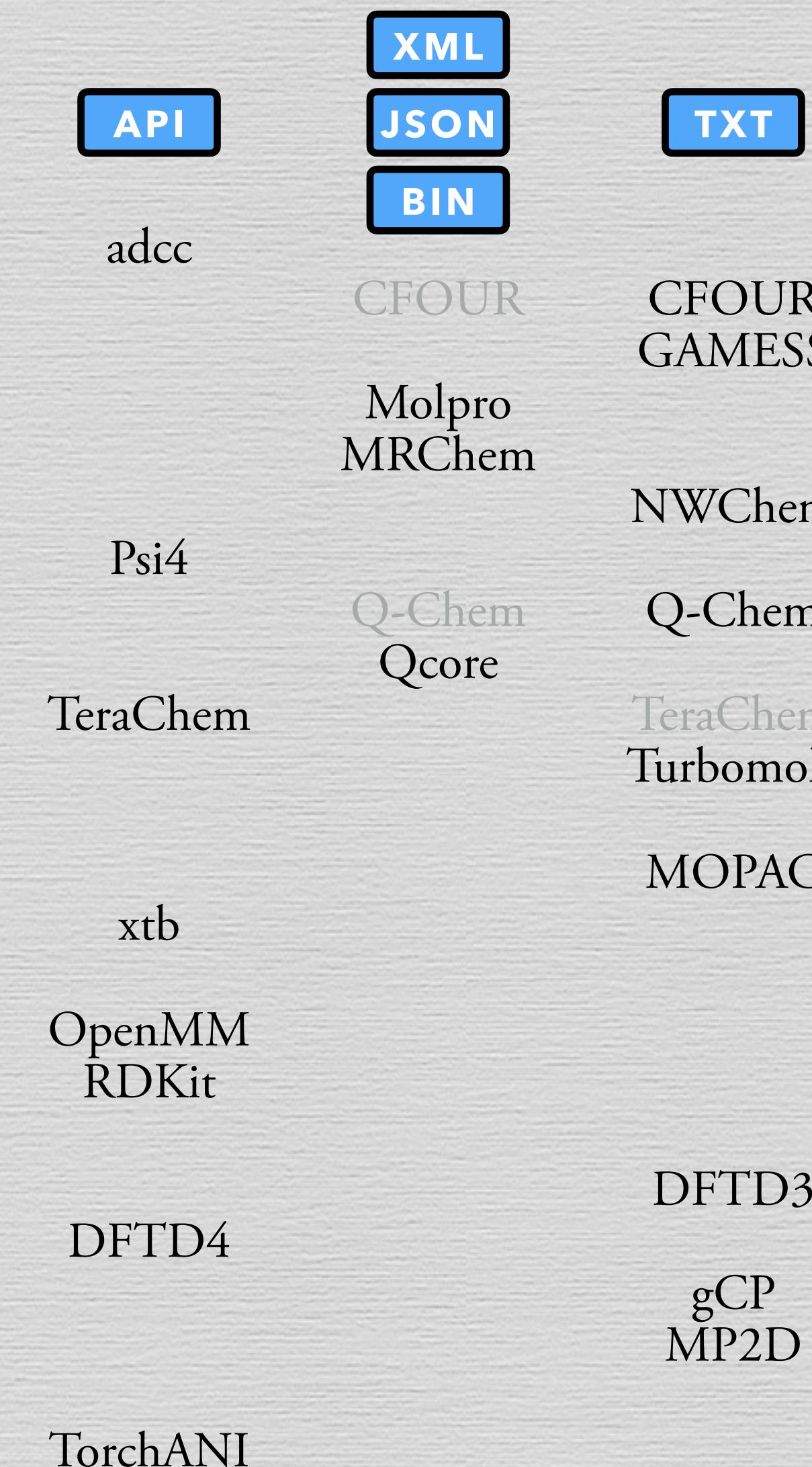
PYAPI

```
qcengine.compute(atomicinput, "molpro", local_options({"nnodes": 4, "memory": 10})  
                  cfour  
                  psi4  
                  dftd4)
```

QCENGINE: AVAILABLE PROGRAM HARNESSSES

github.com/MoSSI/QCEngine

CMS Program	QCENGINE				
	E	G	H	Prop.	Wfn
Quantum Chemistry					
ADCC	✓	✗	✗	✓	✗
CFOUR	✓	✓	✓	✓	✗
GAMESS	✓	✓	✗	✓	✗
MOLPRO	✓	✓	✗	✓	✗
MRCHEM	✓	✗	✗	✓	✗
NWCHEM	✓	✓	✓	✓	✗
Psi4	✓	✓	✓	✓	✓
Q-CHEM	✓	✓	✓	✗	✗
QCORE	✓	✓	✓	✗	✓
TERACHEM	✓	✓	✗	✓	✗
TURBOMOLE	✓	✓	✓	✗	✗
Semi-Empirical					
MOPAC	✓	✓	✗	✓	✗
XTB	✓	✓	✗	✓	✗
Molecular Mechanics					
OPENMM	✓	✓	✗	✓	
RDKit	✓	✓	✗	✓	
Analytical Corrections					
DFTD3	✓	✓	✗	✗	
DFTD4	✓	✓	✗	✗	
gCP	✓	✓	✗	✗	
MP2D	✓	✓	✗	✗	
Machine Learning Inference					
TORCHANI	✓	✓	✓	✓	

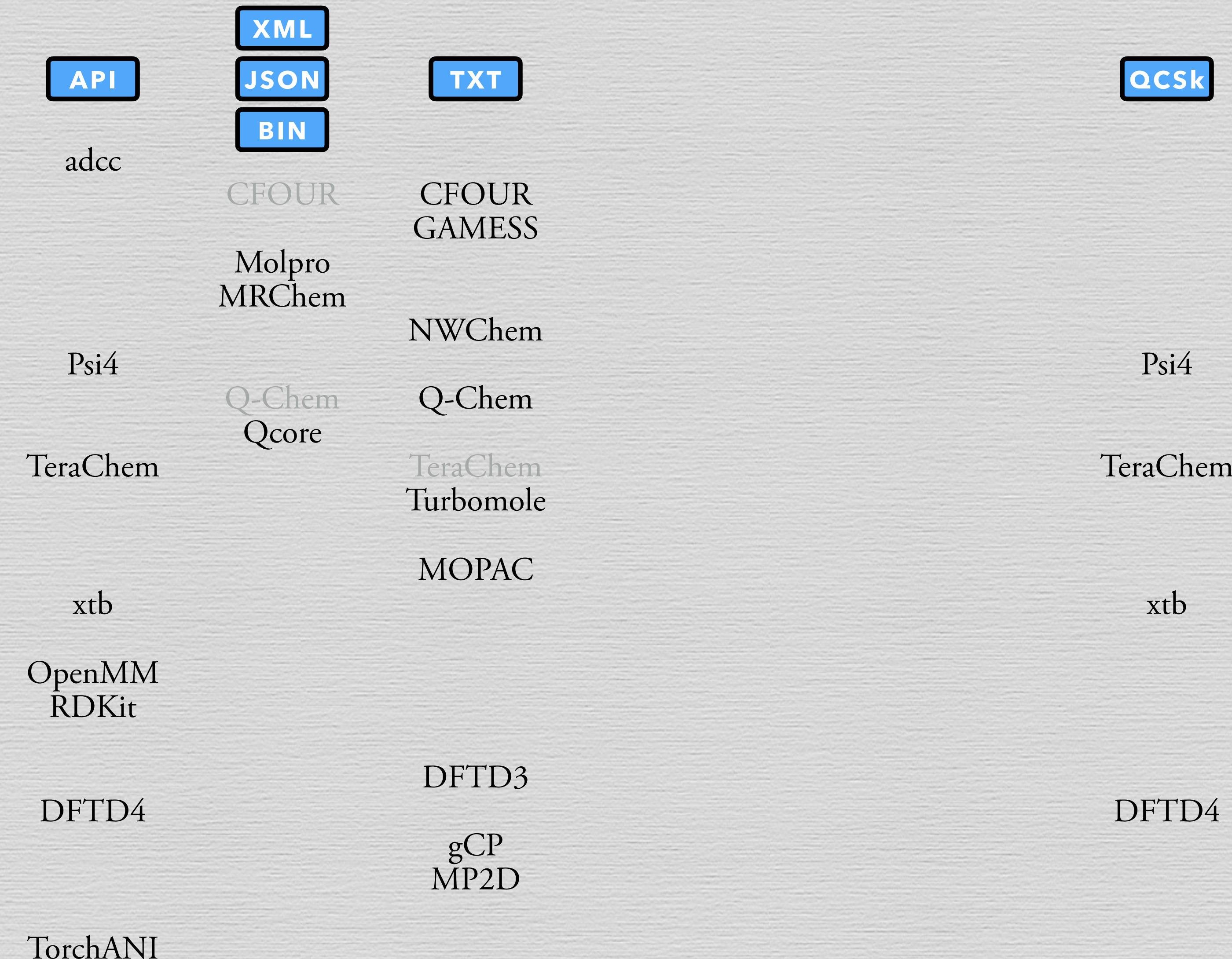


- **SCHEMA** runner
- **PROGRAMS** any analytic single point from CMS code
- **PROCEDURES** anything except analytic single point. Only optimizers so far.
- **PROGRAM CHECKS** indicate some methods accessible through QCSchema
- **CMS** primarily QM but also SE, MM, partial, or ML
- **INTERFACE** in variety of ways from API to structured data to regex. Former preferred for numerical precision.

QCENGINE: AVAILABLE PROGRAM HARNESSSES

github.com/MoSSI/QCEngine

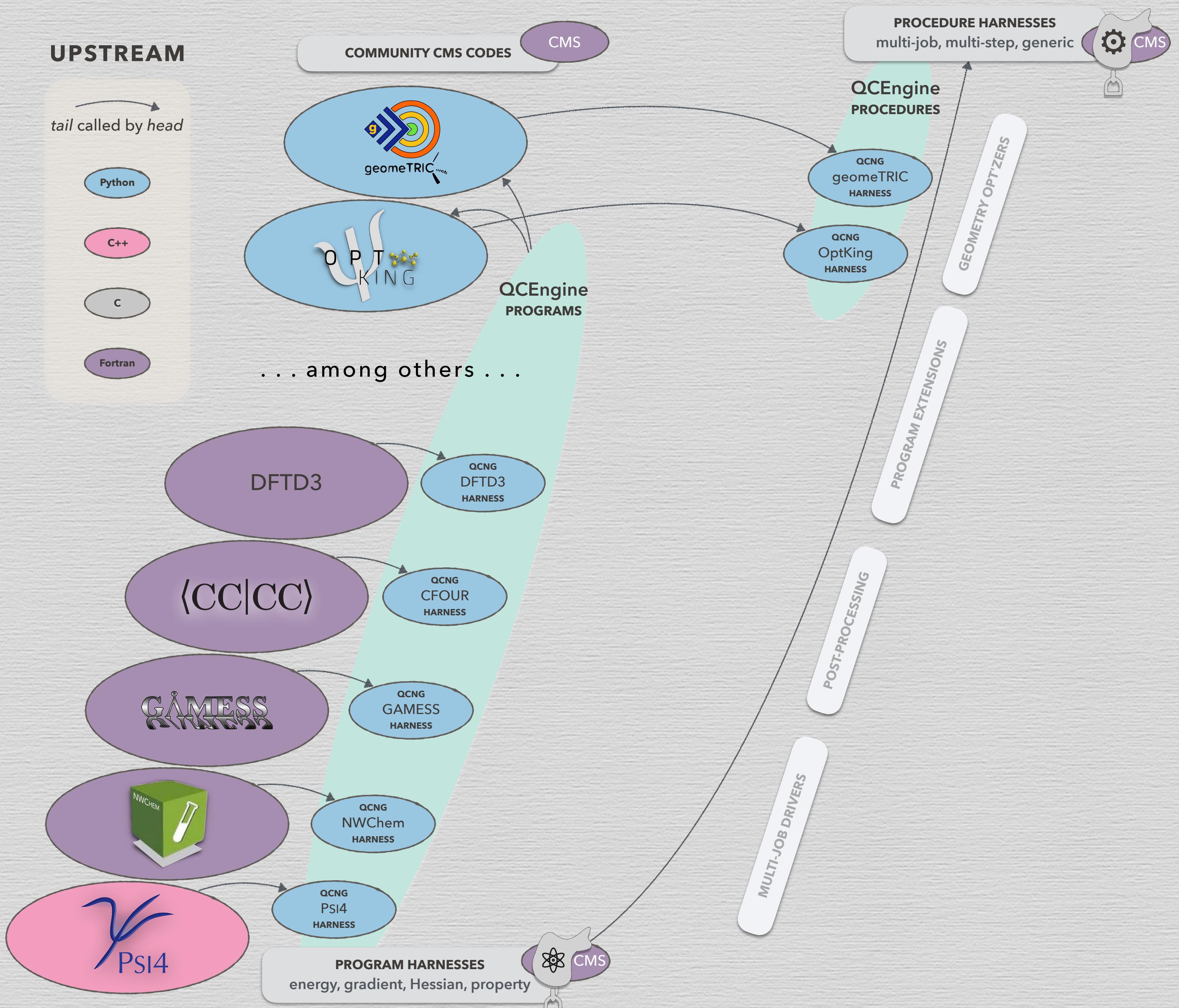
CMS Program	QCENGINE				
	E	G	H	Prop.	Wfn
Quantum Chemistry					
ADCC	✓	✗	✗	✓	✗
CFOUR	✓	✓	✓	✓	✗
GAMESS	✓	✓	✗	✓	✗
MOLPRO	✓	✓	✗	✓	✗
MRChem	✓	✗	✗	✓	✗
NWChem	✓	✓	✓	✓	✗
Psi4	✓	✓	✓	✓	✓
Q-Chem	✓	✓	✓	✗	✗
Qcore	✓	✓	✓	✗	✓
TeraChem	✓	✓	✗	✓	✗
Turbomole	✓	✓	✓	✗	✗
Semi-Empirical					
MOPAC	✓	✓	✗	✓	✗
xtb	✓	✓	✗	✓	✗
Molecular Mechanics					
OpenMM	✓	✓	✗	✓	
RDKit	✓	✓	✗	✓	
Analytical Corrections					
DFTD3	✓	✓	✗	✗	
DFTD4	✓	✓	✗	✗	
gCP	✓	✓	✗	✗	
MP2D	✓	✓	✗	✗	
Machine Learning Inference					
TorchANI	✓	✓	✓	✓	



QCENGINE:

INTERNAL MAP

github.com/MoSSI/QCEngine



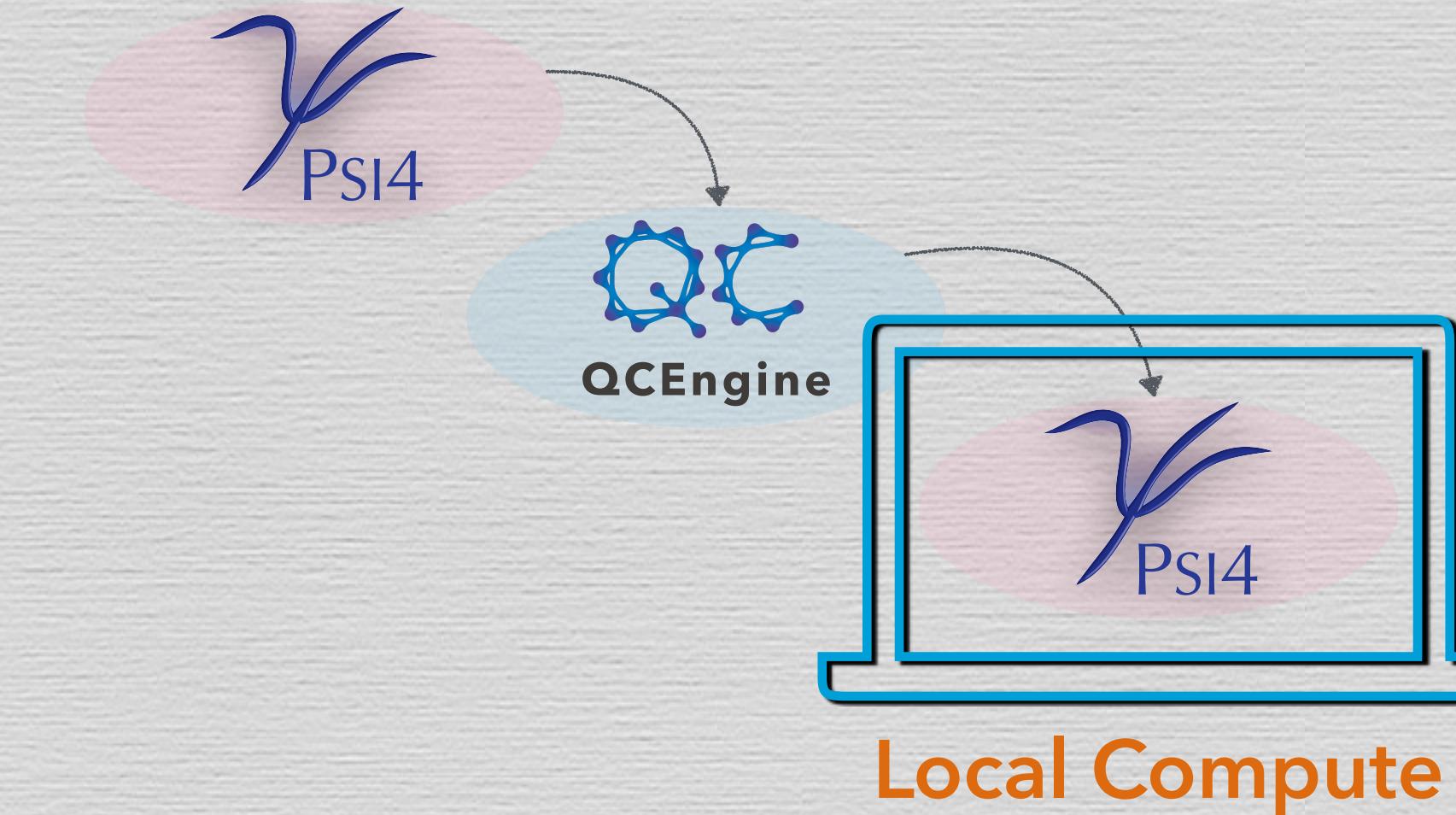
- **SCHEMA** runner
- **PROGRAMS** any analytic single point from CMS code
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- **CMS** primarily QM but also SE, MM, partial, or ML
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DOWNSTREAM

(3) Psi4 DISTRIBUTED DRIVER, INTERNAL

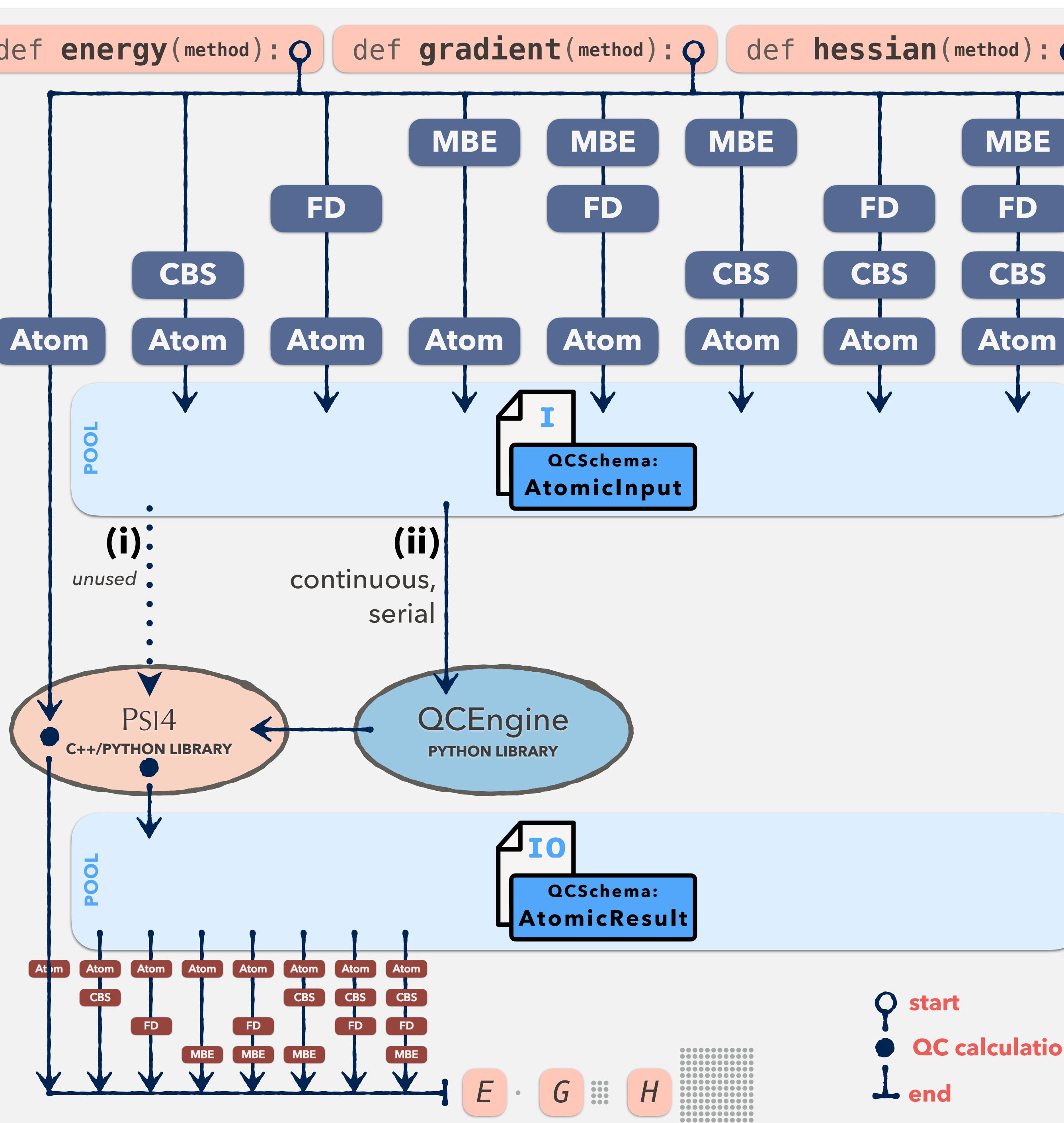
still capable, now orderly and extensible

```
psi4.energy("mp2/cc-pv[dt]z+d:ccsd(t)/cc-pvdz", bsse_type="cp", molecule=ဆ)
```



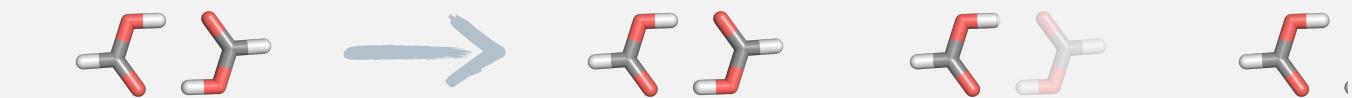
- **AVAILABLE** now with **Psi4 dev branch** & **QCEngine** (already a Psi4 dep).
- **SPECIFICATION** through single file. Procedure **automated**, so low risk of user error.
- **RATE-LIMITED** by sum of all calcs since run **sequentially**.
- **RETRIEVAL** from filesystem difficult since many calcs in **aggregated outfile**.
- **FLEXIBILITY** limited to Psi4 only.

PSI4 DISTRIBUTED DRIVER

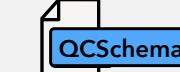


class ManyBodyComputer ():

PLAN Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



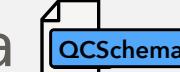
ASM Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

PLAN Displace **molecule** according to stencil.
Reference molecule & method unchanged.



for disp in displacements: return qcschema



ASM Assemble derivative results from displacements.

class CompositeComputer ():

PLAN Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



ASM Assemble extrapolations & total results from modelchems.

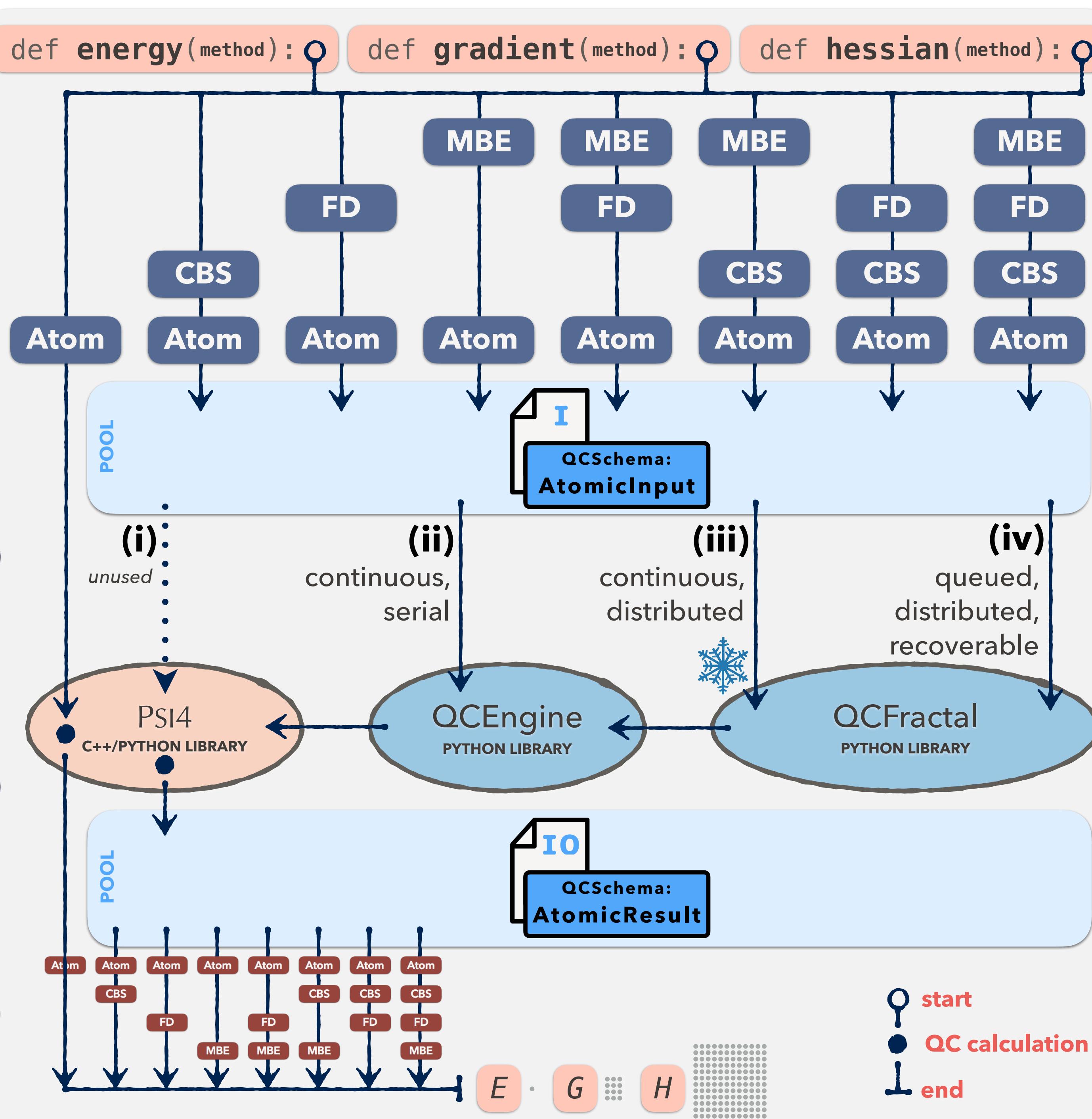
class AtomicComputer ():

molecule & method unchanged. return qcschema



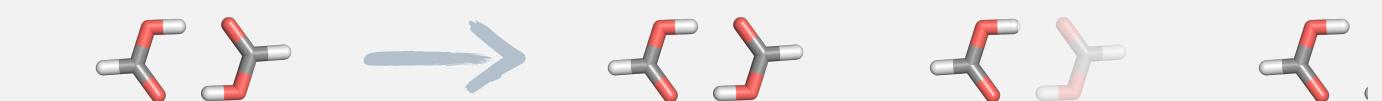
ASM Return analytic energy, gradient, or Hessian.

PSI4 DISTRIBUTED DRIVER

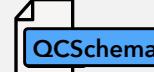


class ManyBodyComputer ():

Separate **molecule** into subsystems. CP, noCP, VMFC basis.
method unchanged.



for frag in fragments: return qcschema



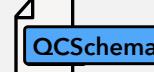
Assemble n-body & interaction results from fragments.

class FiniteDifferenceComputer ():

Displace **molecule** according to stencil.
Reference **molecule** & **method** unchanged.



for disp in displacements: return qcschema



Assemble derivative results from displacements.

class CompositeComputer ():

Separate **method** into method, basis, & extrapolations.
molecule unchanged.



for mc in modelchems: return qcschema



Assemble extrapolations & total results from modelchems.

class AtomicComputer ():

molecule & **method** unchanged. return qcschema

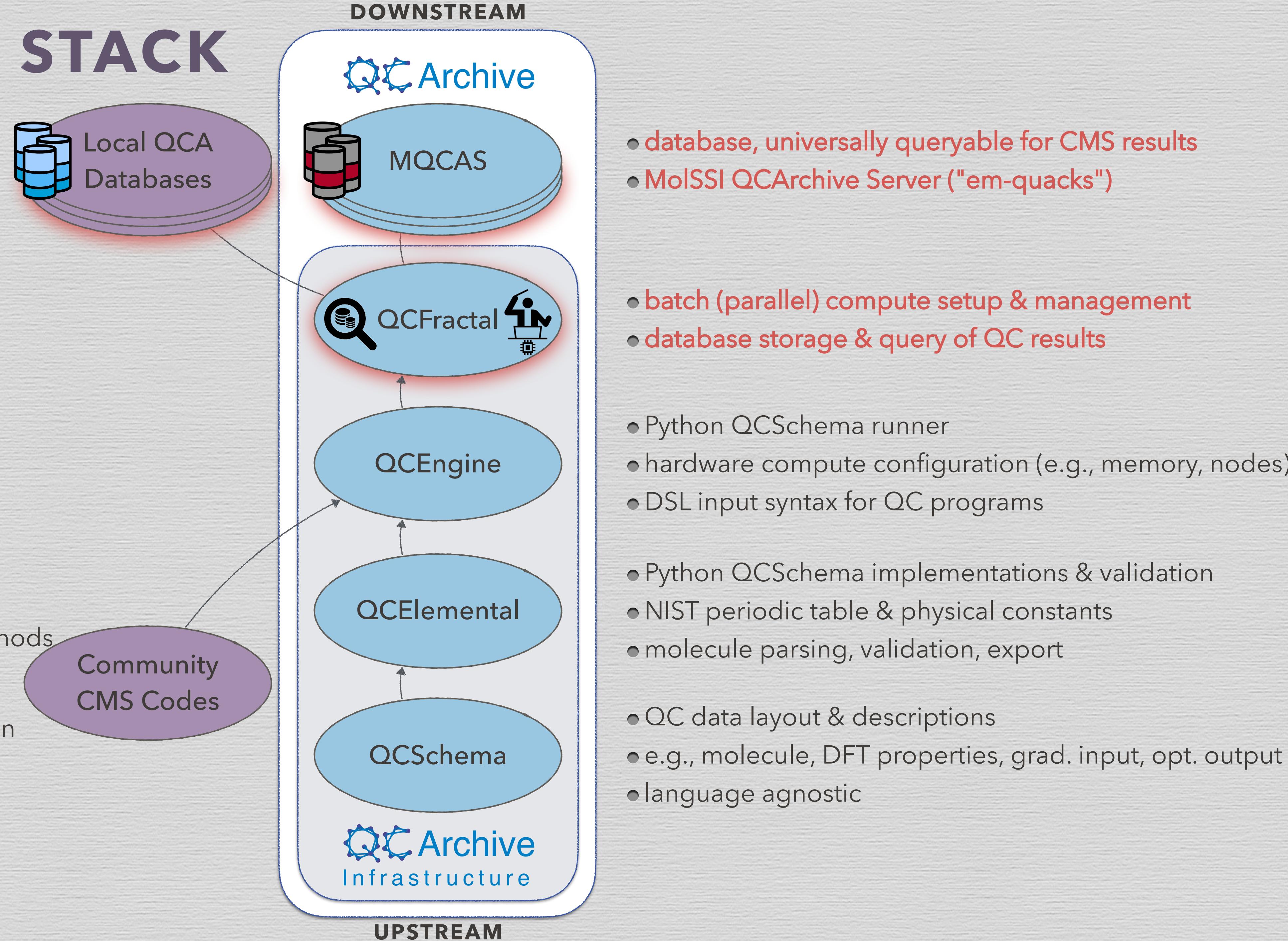


Return analytic energy, gradient, or Hessian.

QCARCHIVE STACK

- database, permissioned query
- fully powerful as MQCAS but locally controlled

- the difficult part – coded QC methods
- structured output uncommon
- DSL input; API/schema uncommon



- database, universally queryable for CMS results
- MolSSI QCArchive Server ("em-quacks")

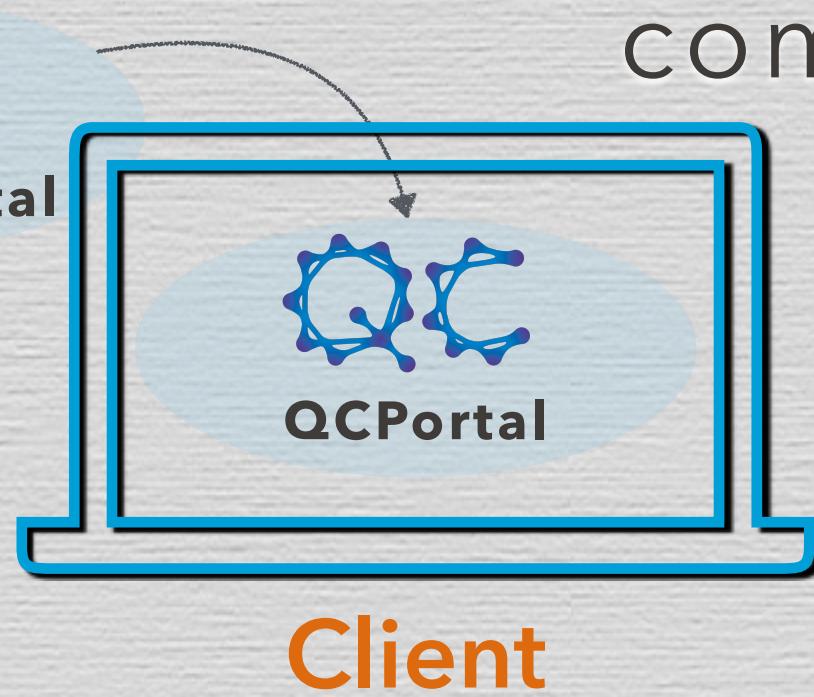
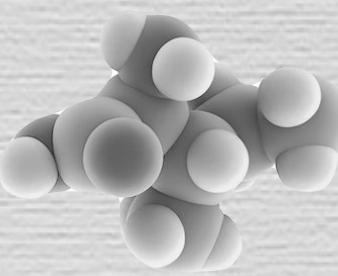
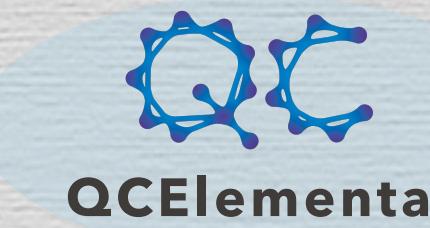
- batch (parallel) compute setup & management
- database storage & query of QC results

- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs

- Python QCSchema implementations & validation
- NIST periodic table & physical constants
- molecule parsing, validation, export
- QC data layout & descriptions
 - e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

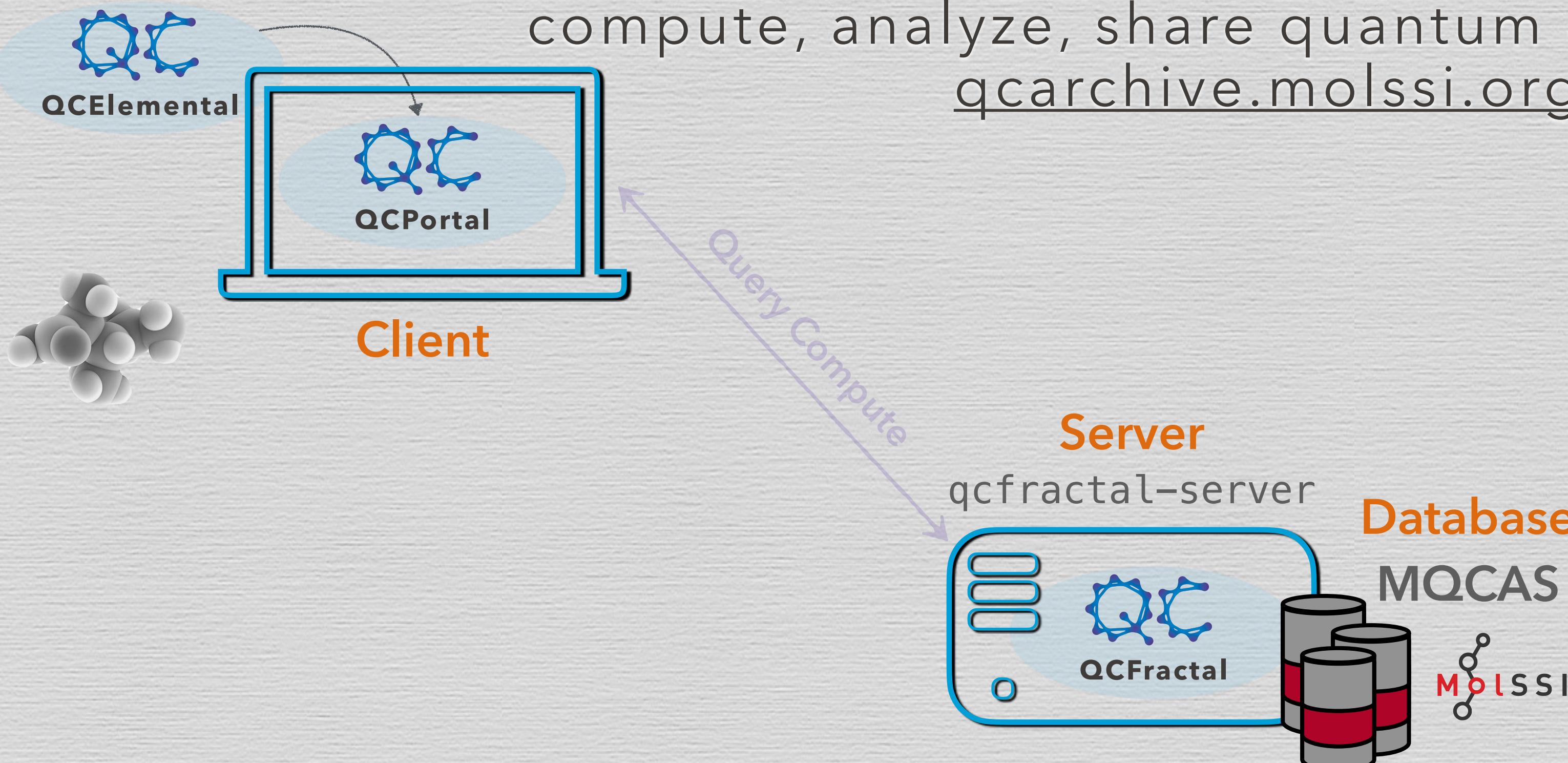
QCARCHIVE OVERVIEW

compute, analyze, share quantum chemistry data
qcarchive.molssi.org



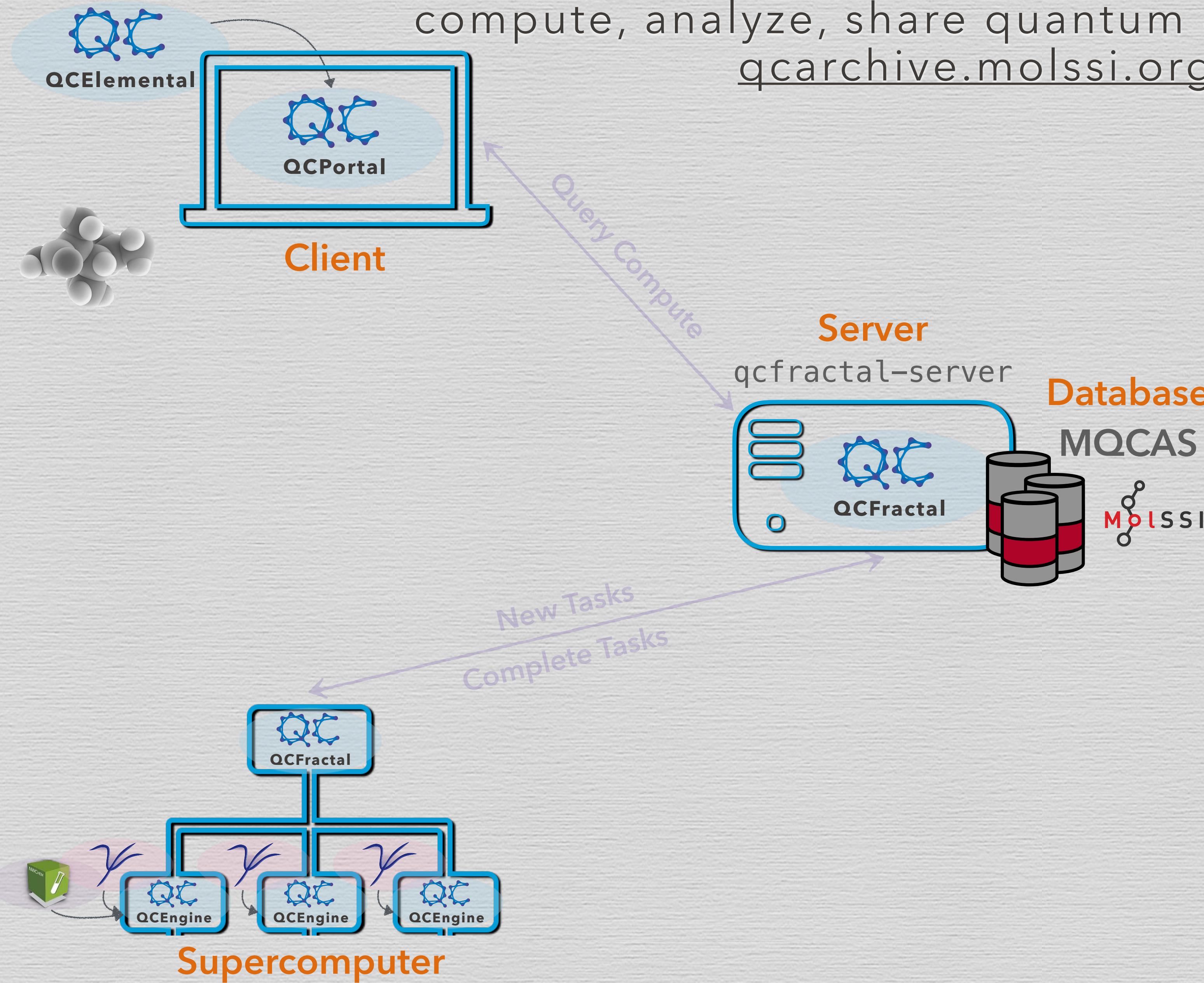
- hybrid **COMPUTE** and **DATA** management tool for quantum chemistry
- **SHARE** and **COLLABORATE** structured data
- **EASE OF USE** for non-specialist
- Completely installable from **CONDA**
- **MULTI-PHYSICAL-SITE** compute
- **SCALE** - Up to 500 tasks/second, 300,000 concurrent tasks
- **ELASTIC** - Runs on laptops, campus clusters, and leadership-class supercomputers

QCARCHIVE OVERVIEW



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QCARCHIVE OVERVIEW

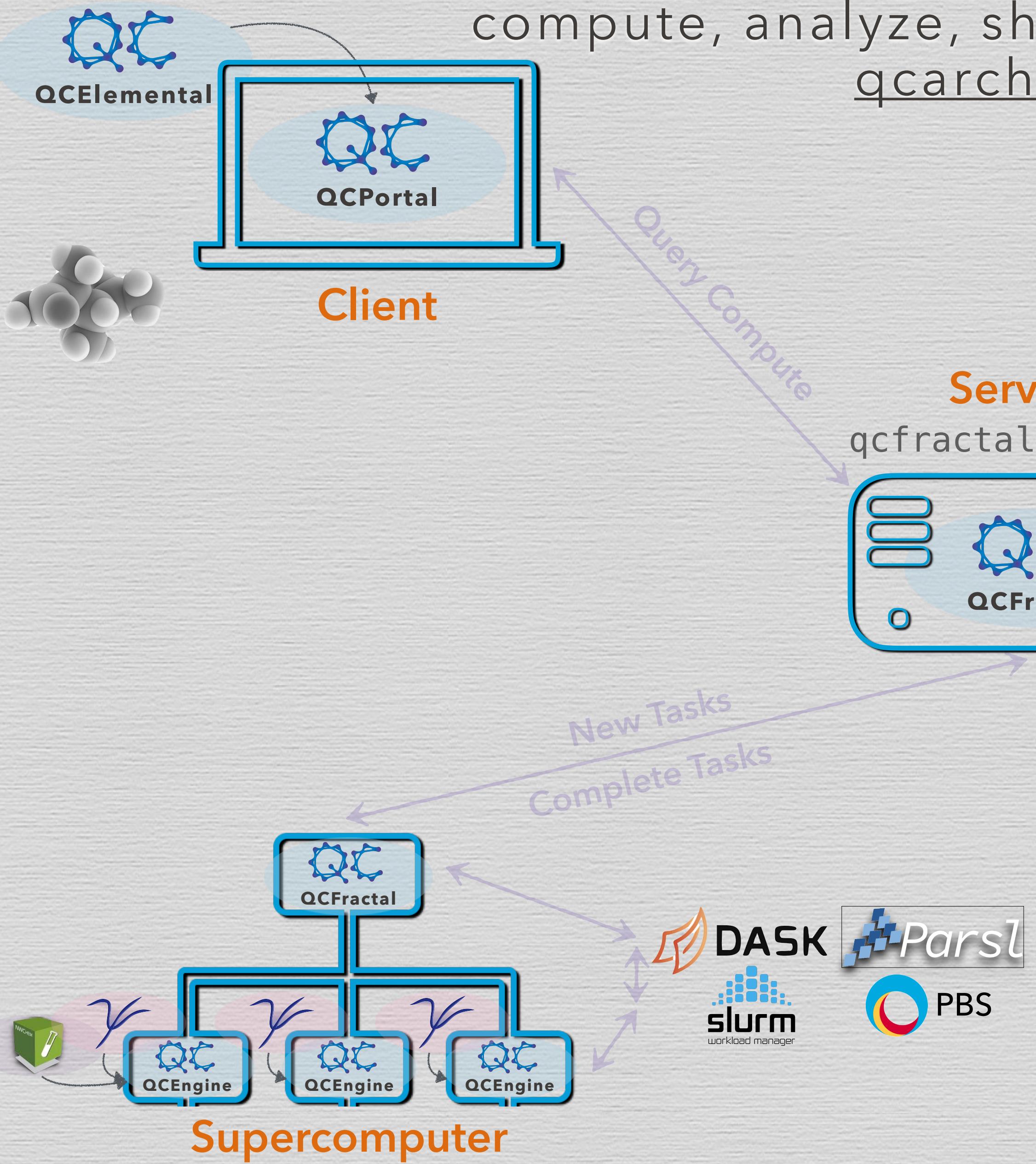


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qcfractal-manager **Distributed Compute**

worker **Compute Nodes**

QCARCHIVE OVERVIEW

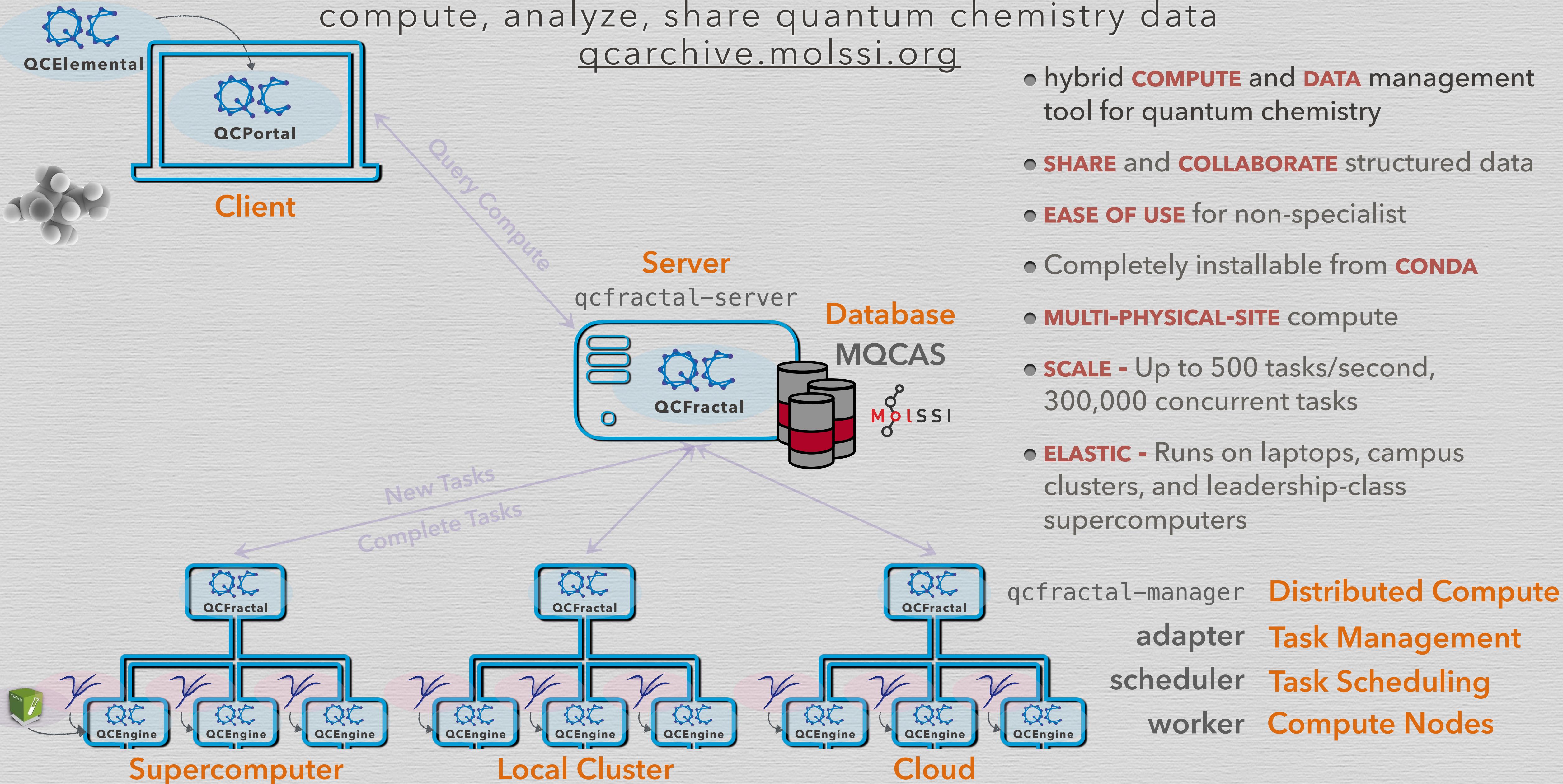


compute, analyze, share quantum chemistry data
qcarchive.molssi.org

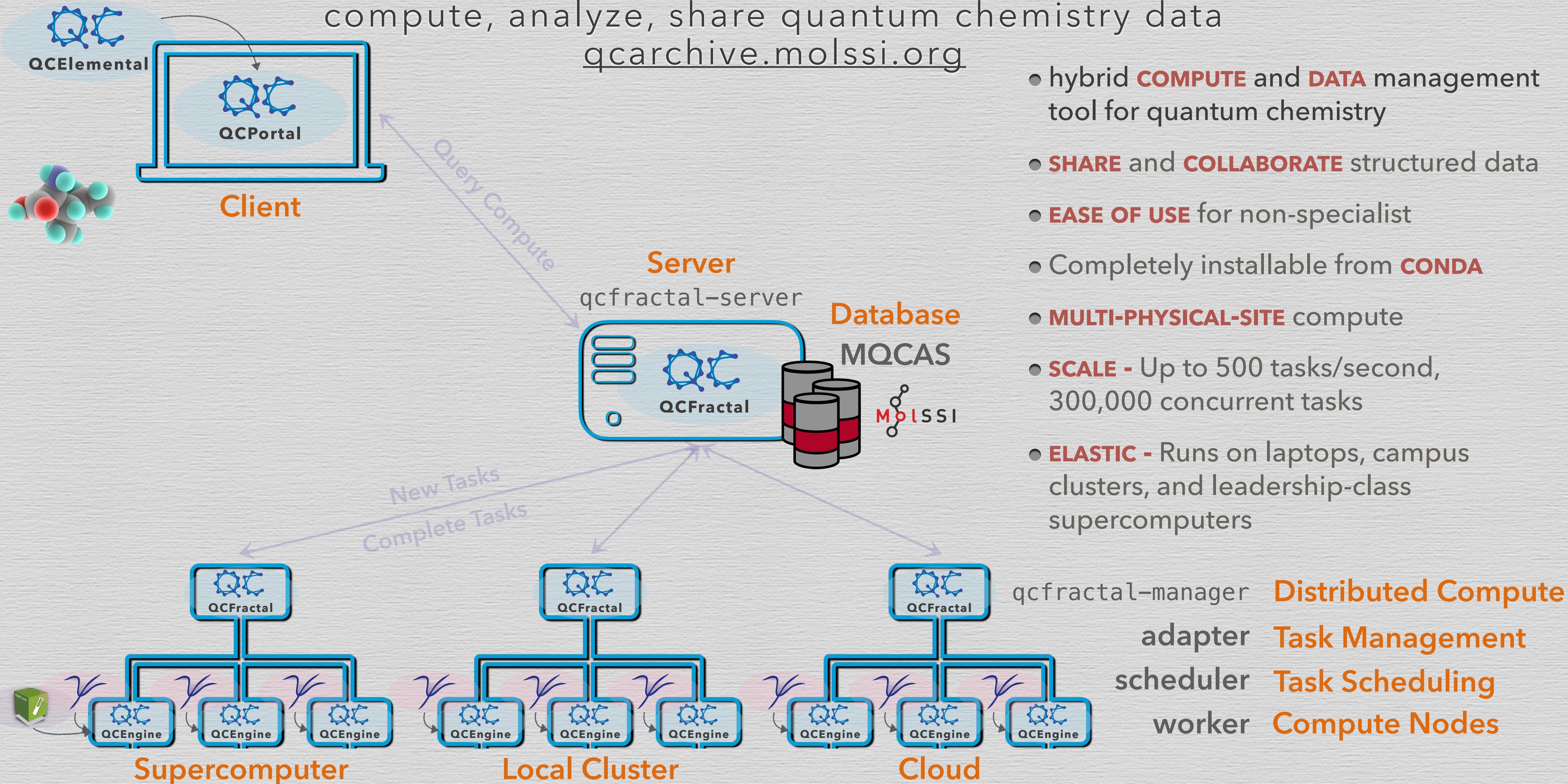
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qcfractal-manager	Distributed Compute
adapter	Task Management
scheduler	Task Scheduling
worker	Compute Nodes

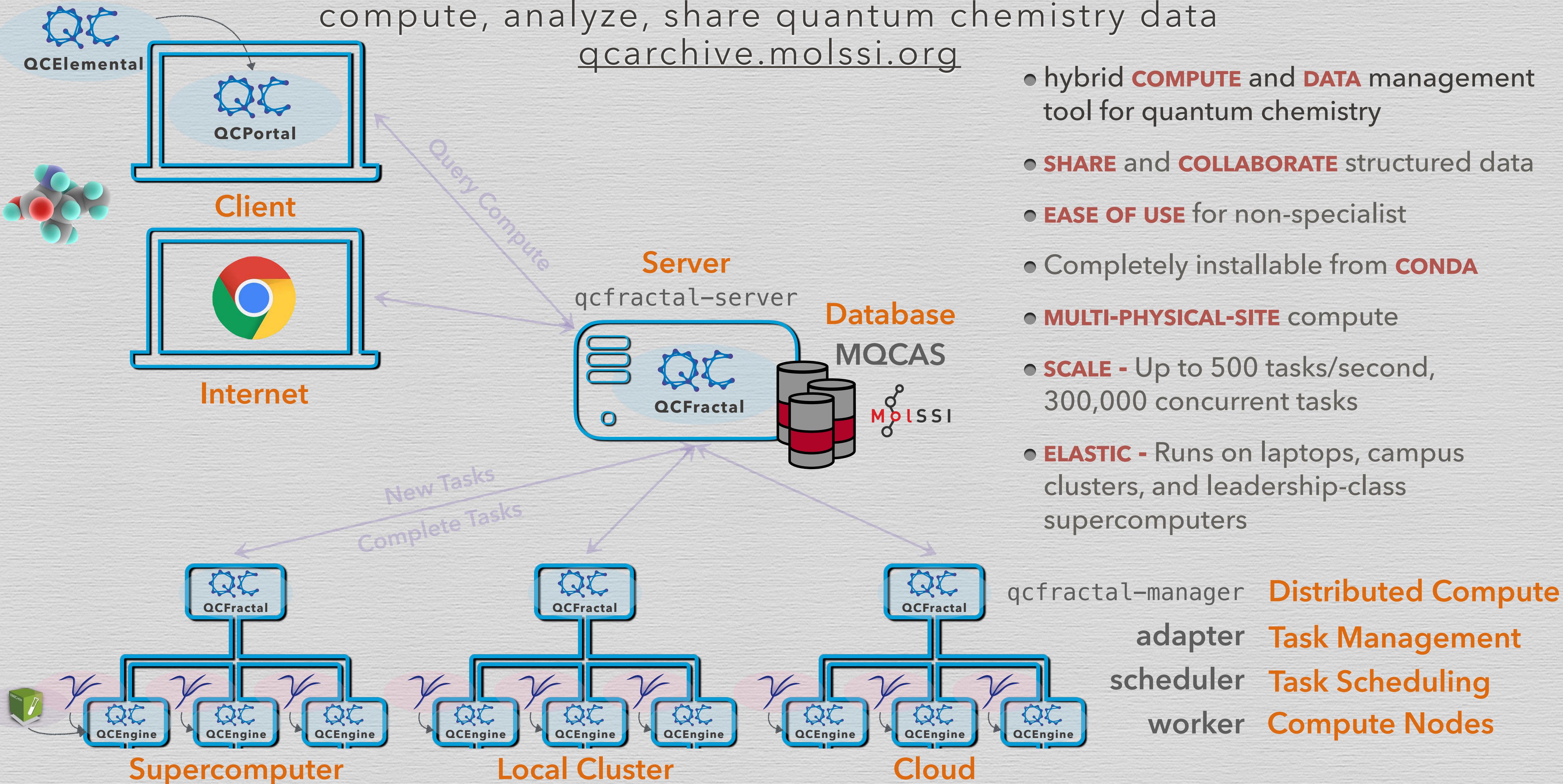
QCARCHIVE OVERVIEW



QCARCHIVE OVERVIEW

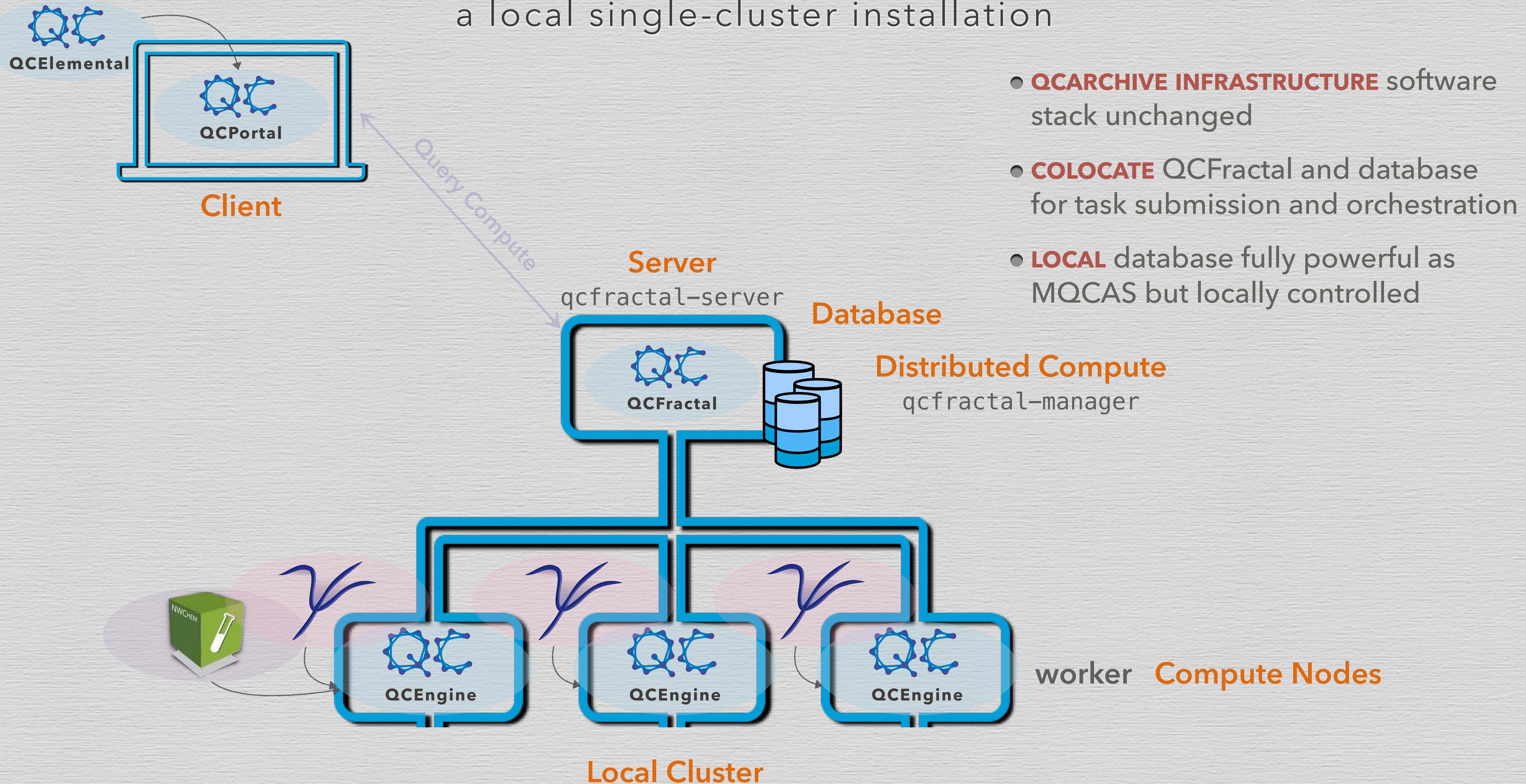


QCARCHIVE OVERVIEW



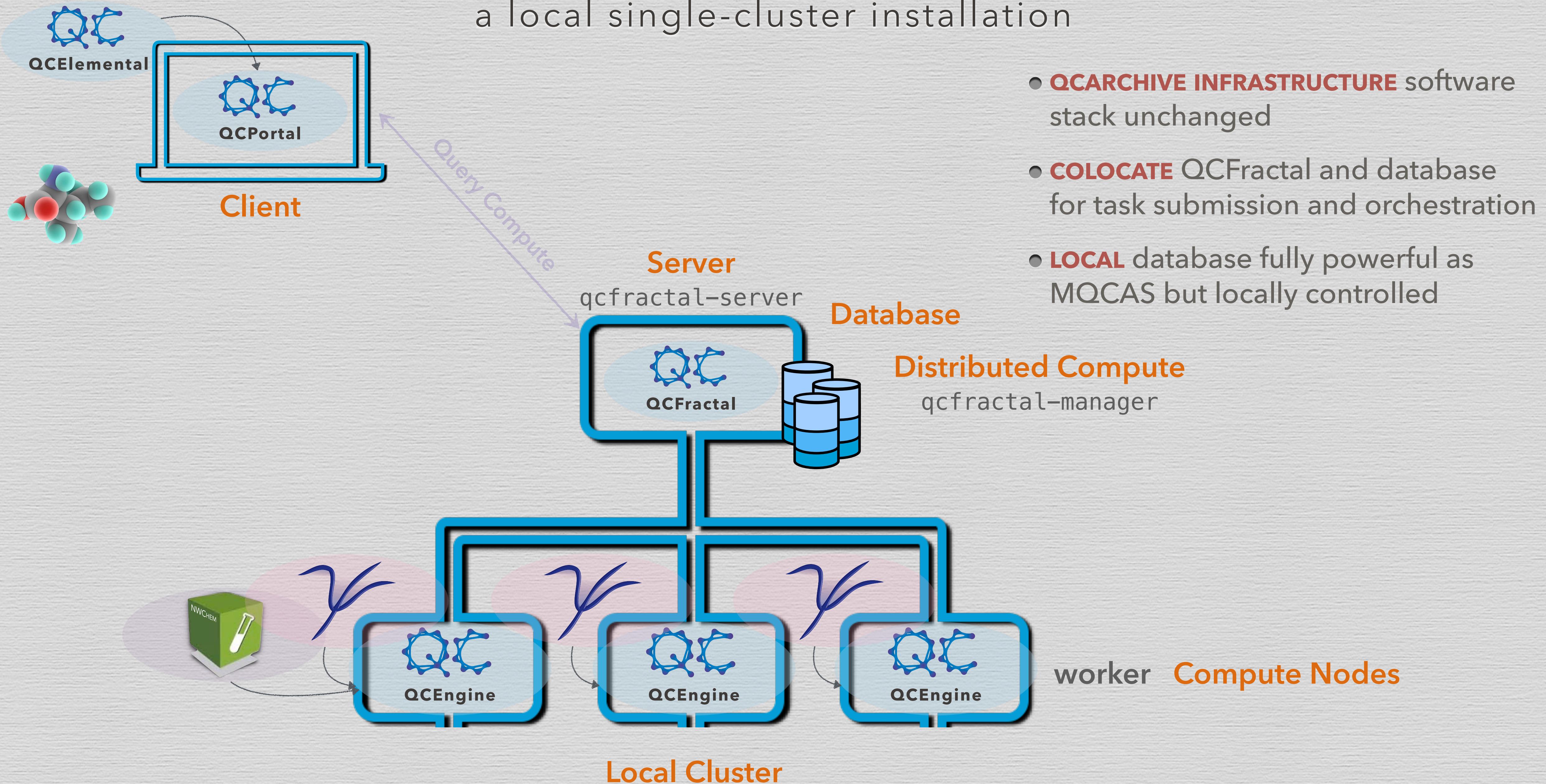
QCARCHIVE, SMALLER

a local single-cluster installation



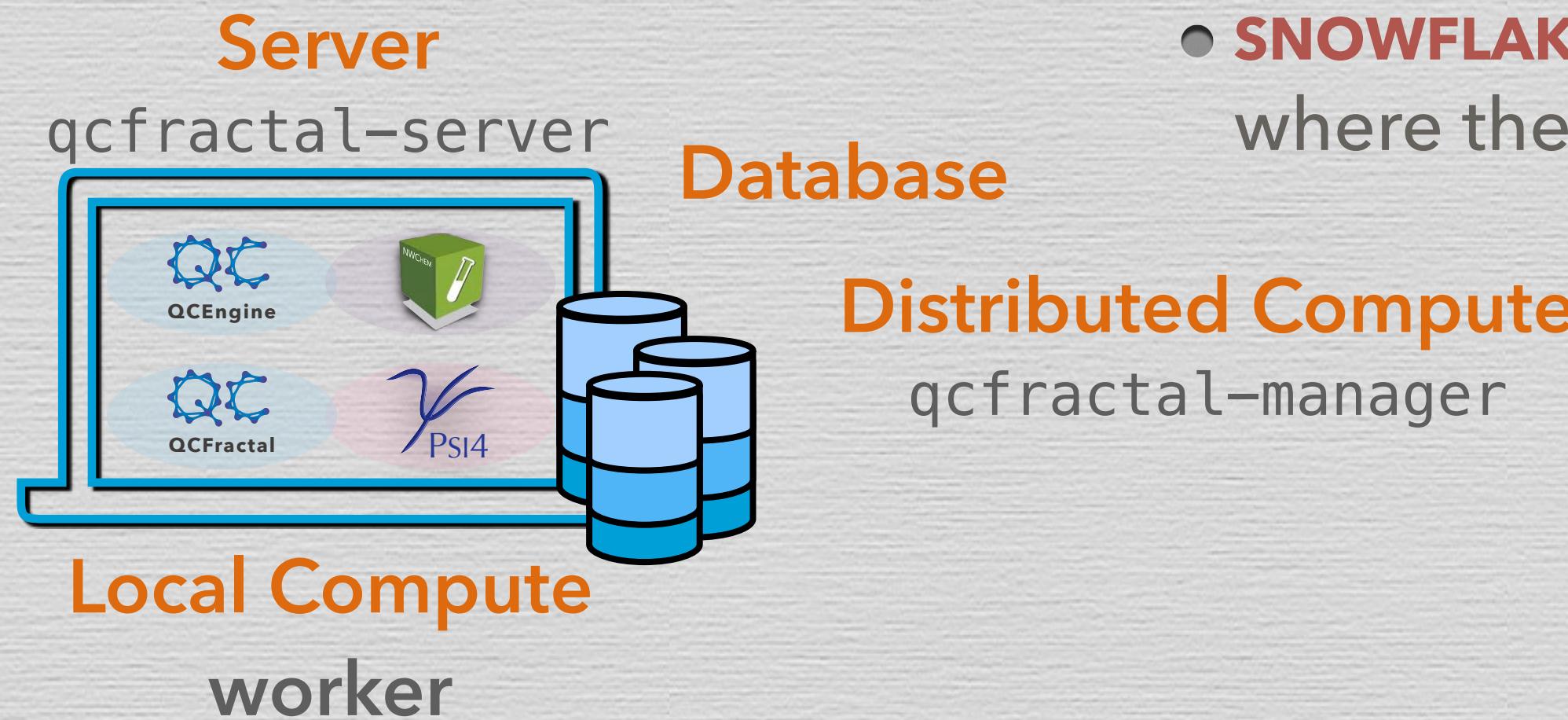
QCARCHIVE, SMALLER

a local single-cluster installation



QCARCHIVE, SMALLEST

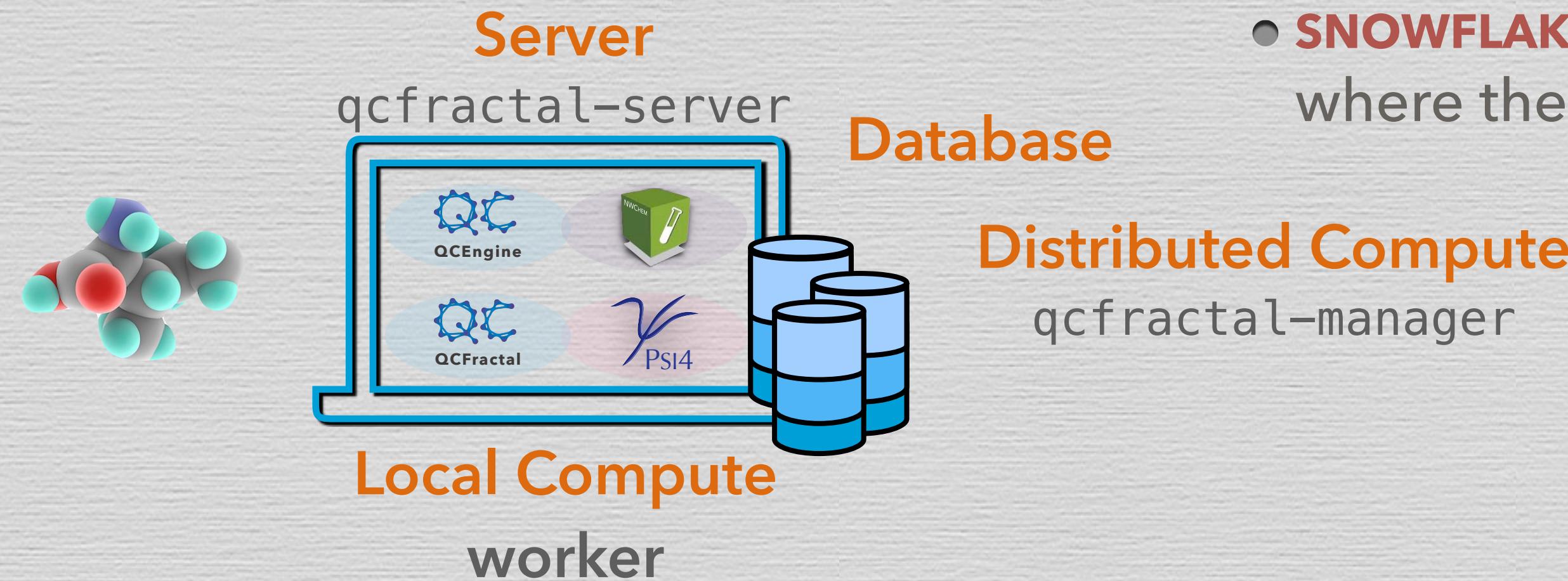
a local single-box installation



- **QCARCHIVE INFRASTRUCTURE** software stack unchanged
- **COLOCATE** QCFractal, database and QC codes for self-contained setup
- **SNOWFLAKE** a still-simpler mode where the database does not persist

QCARCHIVE, SMALLEST

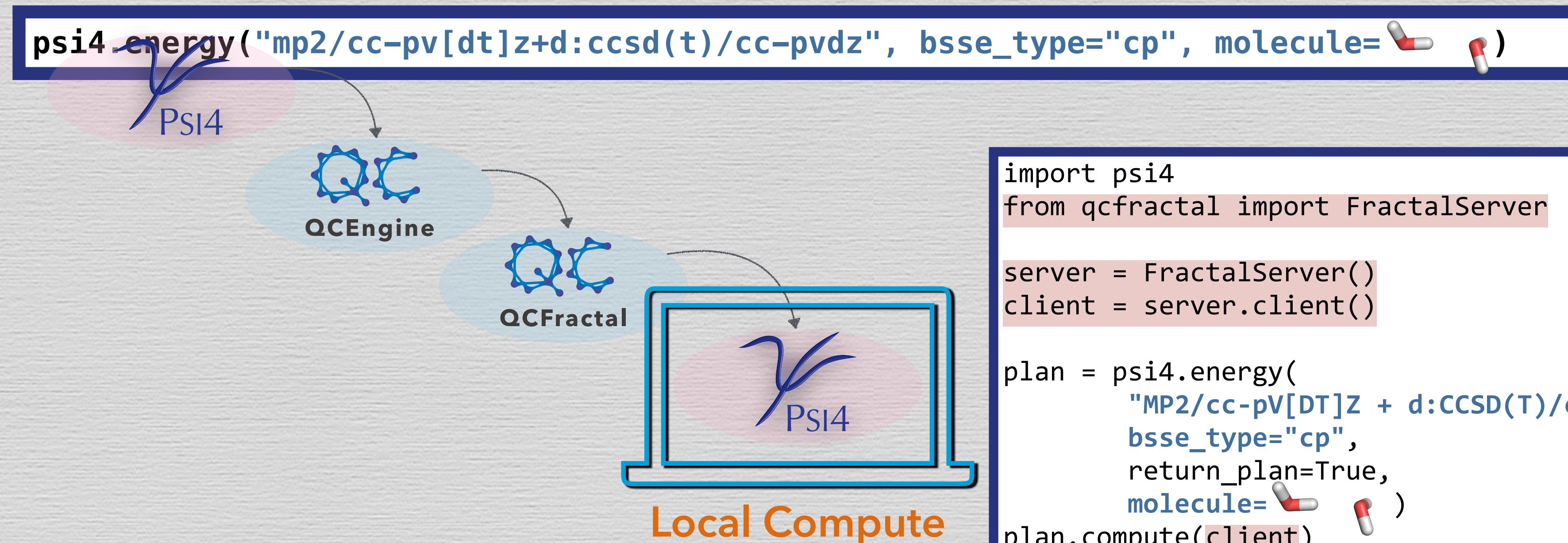
a local single-box installation



- **QCARCHIVE INFRASTRUCTURE** software stack unchanged
- **COLOCATE** QCFractal, database and QC codes for self-contained setup
- **SNOWFLAKE** a still-simpler mode where the database does not persist

(4) Psi4 DISTRIBUTED DRIVER, QCARCHIVE

distributed, searchable, and error-resistant



```
import psi4
from qcfractal import FractalServer

server = FractalServer()
client = server.client()

plan = psi4.energy(
    "MP2/cc-pV[DT]Z + d:CCSD(T)/cc-pVDZ",
    bsse_type="cp",
    return_plan=True,
    molecule=CH2 )
plan.compute(client)

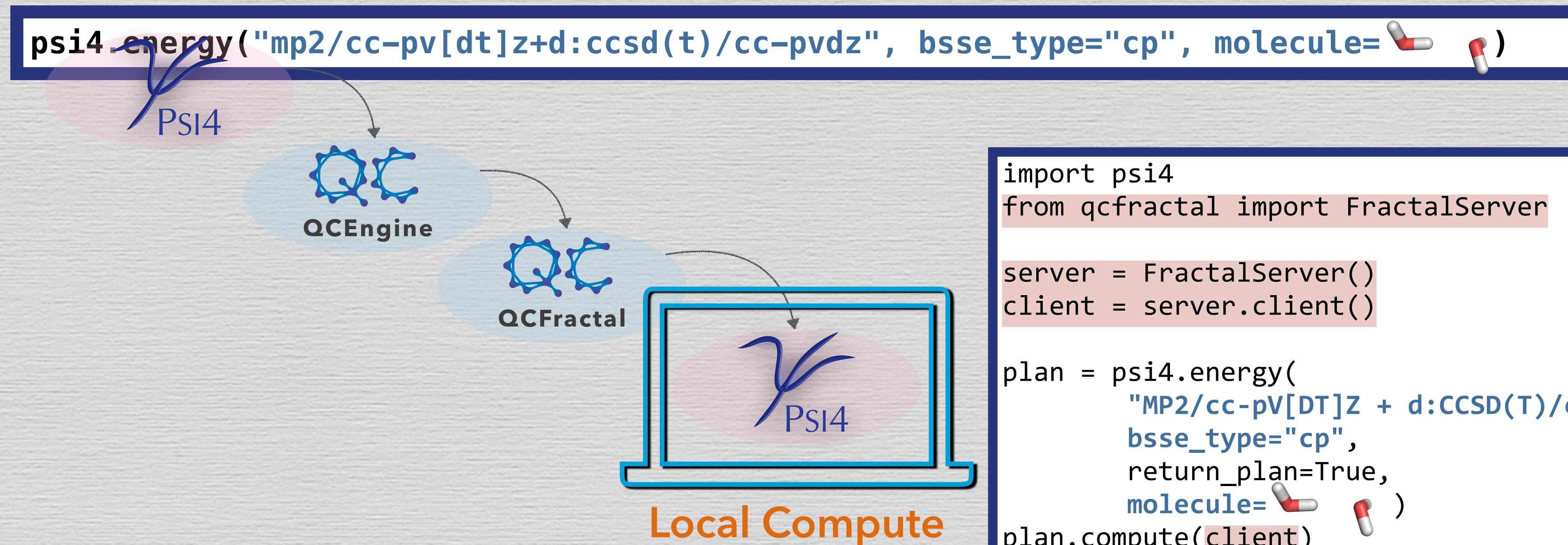
# re-run file after jobs complete for final processing

qcsk = plan.get_results(client)
print(qcsk.return_result) # CP IE
```

- **AVAILABLE** now with **Psi4 dev branch** & **QCEngine** & **QCFractal**
- **SPECIFICATION** through single file. Procedure **automated**, so low risk of user error.
- **RATE-LIMITED** by single longest calc since QCFractal runs **parallel in queue**.
- **RETRIEVAL** from QCArchive **database** with query.
- **FLEXIBILITY** limited to Psi4 only.

(4) Psi4 DISTRIBUTED DRIVER, QCARCHIVE

distributed, searchable, and error-resistant



- **AVAILABLE** now with **Psi4 dev branch** & **QCEngine** & **QCFractal**
- **SPECIFICATION** through single file. Procedure **automated**, so low risk.
- **RATE-LIMITED** by single longest calc since QCFractal runs **parallel** instead.
- **RETRIEVAL** from QCArchive **database** with query.
- **FLEXIBILITY** limited to Psi4 only.

```
import psi4
from qcfractal import FractalServer

server = FractalServer()
client = server.client()

plan = psi4.energy(
    "MP2/cc-pV[DT]Z + d:CCSD(T)/cc-pVDZ",
    bsse_type="cp",
    return_plan=True,
    molecule=)
plan.compute(client)

# re-run file after jobs complete for final processing

qcsk = plan.get_results(client)
print(qcsk.return_result) # CP IE
```

```
plan = psi4.energy("CCSD(T)/cc-pVDZ",
                    return_plan=True,
                    molecule=)
plan.compute(client) # free! calcs in database

qcsk = plan.get_results(client)
print(qcsk.return_result) # CCSD(T) energy
```

(4) PSI4 DISTRIBUTED DRIVER, QCARCHIVE

distributed, searchable, and error-resistant

```
psi4.energy("mp2/cc-pv[dt]z+d:ccsd(t)/cc-pvdz", bsse_type="cp", molecule=
```

```
psi4.gradient("mp2/cc-pv[dt]z+d:ccsd(t)/cc-pvdz", bsse_type="cp", molecule=
```

```
psi4.hessian("mp2/cc-pv[dt]z+d:ccsd(t)/cc-pvdz", bsse_type="cp", molecule=
```



```
import psi4  
server = FractalServer()  
client = server.client()  
  
plan = psi4.energy(  
    "MP2/cc-pV[DT]Z + d:CCSD(T)/cc-pVDZ",  
    bsse_type="cp",  
    return_plan=True,  
    molecule= )  
plan.compute(client)  
  
# re-run file after jobs complete for final processing  
  
qcsk = plan.get_results(client)  
print(qcsk.return_result) # CP IE  
  
plan = psi4.energy("CCSD(T)/cc-pVDZ",  
                   return_plan=True,  
                   molecule= )  
plan.compute(client) # free! calcs in database  
  
qcsk = plan.get_results(client)  
print(qcsk.return_result) # CCSD(T) energy
```

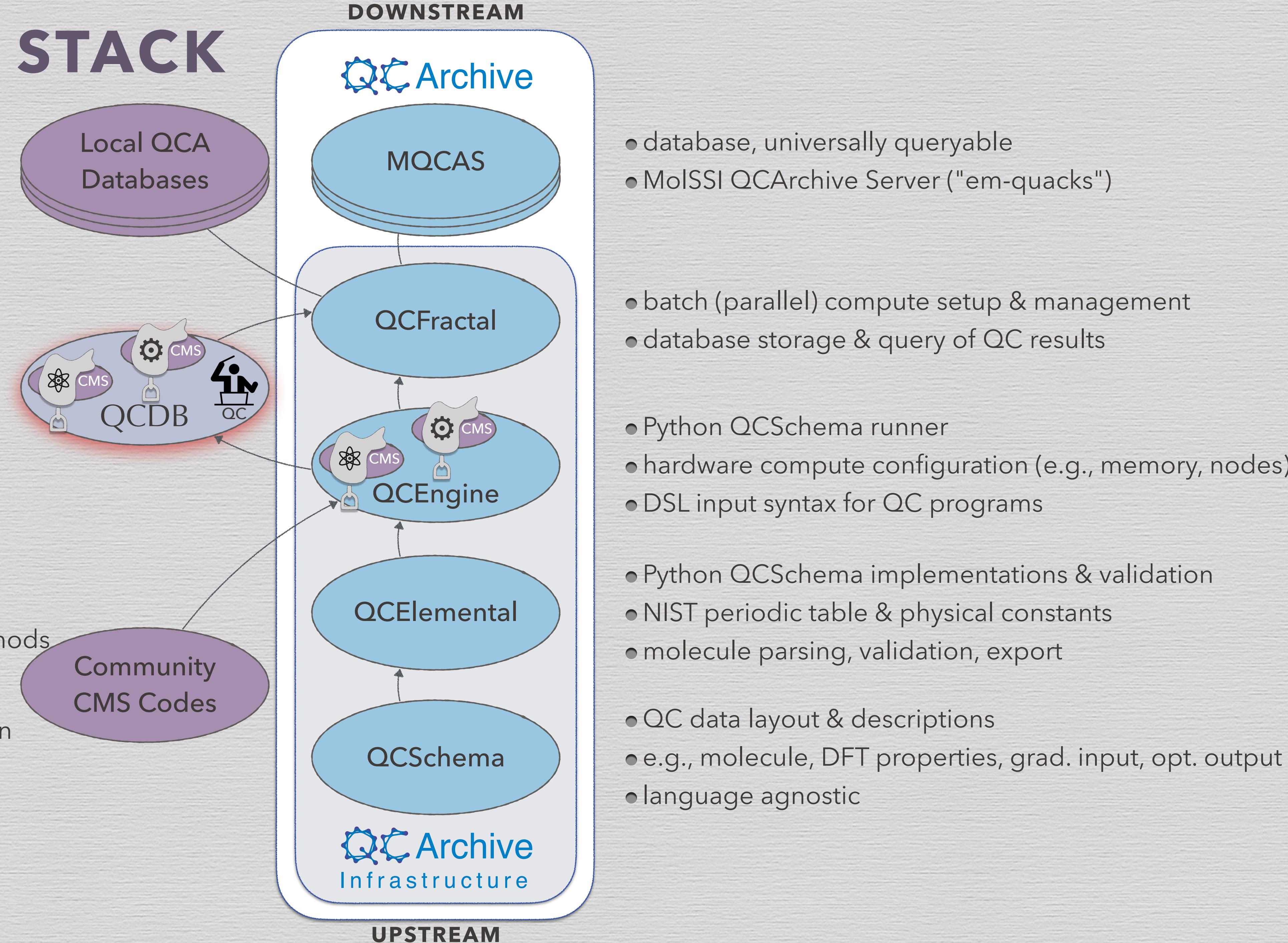
- **AVAILABLE** now with **PSI4 dev branch** & **QCEngine** & **QCFractal**
- **SPECIFICATION** through single file. Procedure **automated**, so low risk.
- **RATE-LIMITED** by single longest calc since QCFractal runs **parallel** in background.
- **RETRIEVAL** from QCArchive **database** with query.
- **FLEXIBILITY** limited to PSI4 only.

QCARCHIVE STACK

- database, permissioned query
- fully powerful as MQCAS but locally controlled

- **DSL or unified input syntax**
- **multi-QCprogram workflows**
- **standardization layers**

- the difficult part – coded QC methods
- structured output uncommon
- DSL input; API/schema uncommon



QCSchema DEFINES DATA LAYOUTS

QCDB unifies data contents

- **LAYOUT** JSON Schema defines a data layout and some minimal type and count checking.
- **CONVENTIONS** JSON Schema can't check conventions you rely upon like AU units, CCA ordering, center-of-mass positioning

DOMAIN-SPECIFIC ASCII

```
$ccinp ncore=0 $end
$basis gbasis=accd $end
$contrl cctyp=ccsd
coord=prinaxis
icharg=0 ispher=1
runtyp=energy scftyp=rohf
units=bohr mult=2 $end
$data

C1
N 7  0.000  0.000 -0.146
H 1  0.000 -1.511  1.014
H 1  0.000  1.511  1.014
$end
```

QCSchema: AtomicInput

```
{
  'molecule': {
    'symbols': ['N', 'H', 'H'],
    'geometry': [0.000, ..., 1.014],
    'molecular_multiplicity': 2},
  'driver': 'energy',
  'model': {
    'method': 'ccsd',
    'basis': 'accd'},
  'keywords': {
    'contrl_ispher': 1,
    'contrl_scftyp': 'rohf',
    'ccinp_ncore': 0},
```

GAMESS Input

GAMESS QCEngine Input

DATA LAYOUT
TRANSLATION

MOL & DRIVER
STANDARDIZATION

QCSchema DEFINES DATA LAYOUTS

QCDB unifies data contents

- **LAYOUT** JSON Schema defines a data layout and some minimal type and count checking.
- **CONVENTIONS** JSON Schema can't check conventions you rely upon like AU units, CCA ordering, center-of-mass positioning
- **QCDB UNIFIED CONTROL & KEYWORD TRANSLATION** allows users to focus on scientific choices, not DSL.
- **LOWER BARRIERS** to using a variety of codes, many with unique features.

DOMAIN-SPECIFIC ASCII

```
$ccinp ncore=0 $end
$basis gbasis=accd $end
$contrl cctyp=ccsd
coord=prinaxis
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  'molecule': {
    'symbols': ['N', 'H', 'H'],
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    'molecular_multiplicity': 2},
  'driver': 'energy',
  'model': {
    'method': 'ccsd',
    'basis': 'accd'},
  'keywords': {
    'contrl_ispher': 1,
    'contrl_scftyp': 'rohf',
    'ccinp_ncore': 0},
```

GAMESS Input

GAMESS QCEngine Input

DATA LAYOUT TRANSLATION

MOL & DRIVER STANDARDIZATION

BASIS & KEYWORDS STANDARDIZATION

QCSchema: AtomicInput

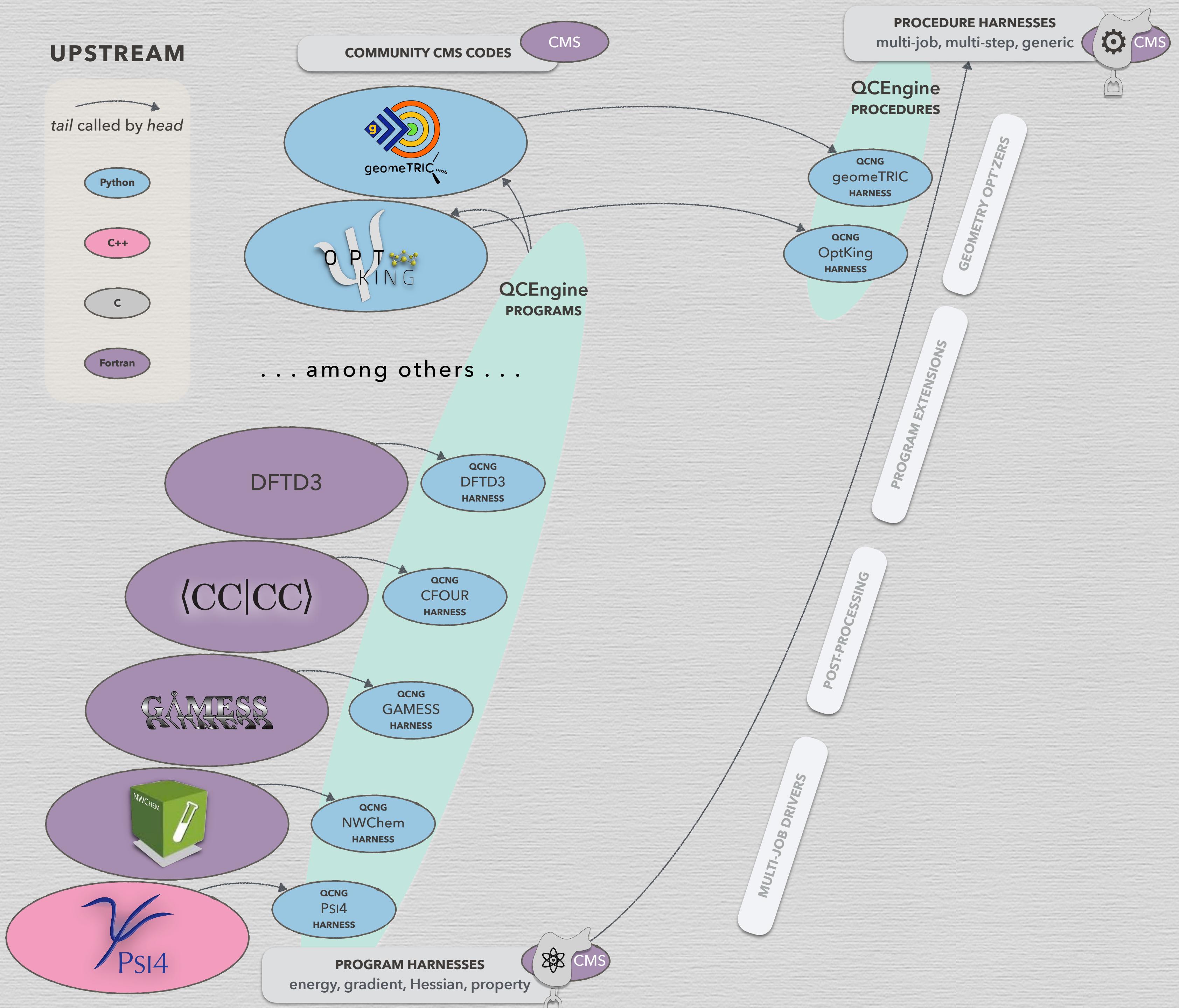
```
{
  'molecule': {
    'symbols': ['N', 'H', 'H'],
    'geometry': [0.000, ..., 1.014],
    'molecular_multiplicity': 2},
  'driver': 'energy',
  'model': {
    'method': 'ccsd',
    'basis': 'aug-cc-pvdz'},
  'keywords': {
    'reference': 'rohf',
    'freeze_core': False}}
```

QCDB Input

QCENGINE:

INTERNAL MAP

github.com/MoSSI/QCEngine



- **SCHEMA** runner
- **PROGRAMS** any analytic single point from CMS code
- **PROCEDURES** anything except analytic single point. Only optimizers so far.
- **PROGRAM CHECKS** indicate some methods accessible through QCSchema
- **CMS** primarily QM but also SE, MM, partial, or ML
- **INTERFACE** in variety of ways from API to structured data to regex. Former preferred for numerical precision.

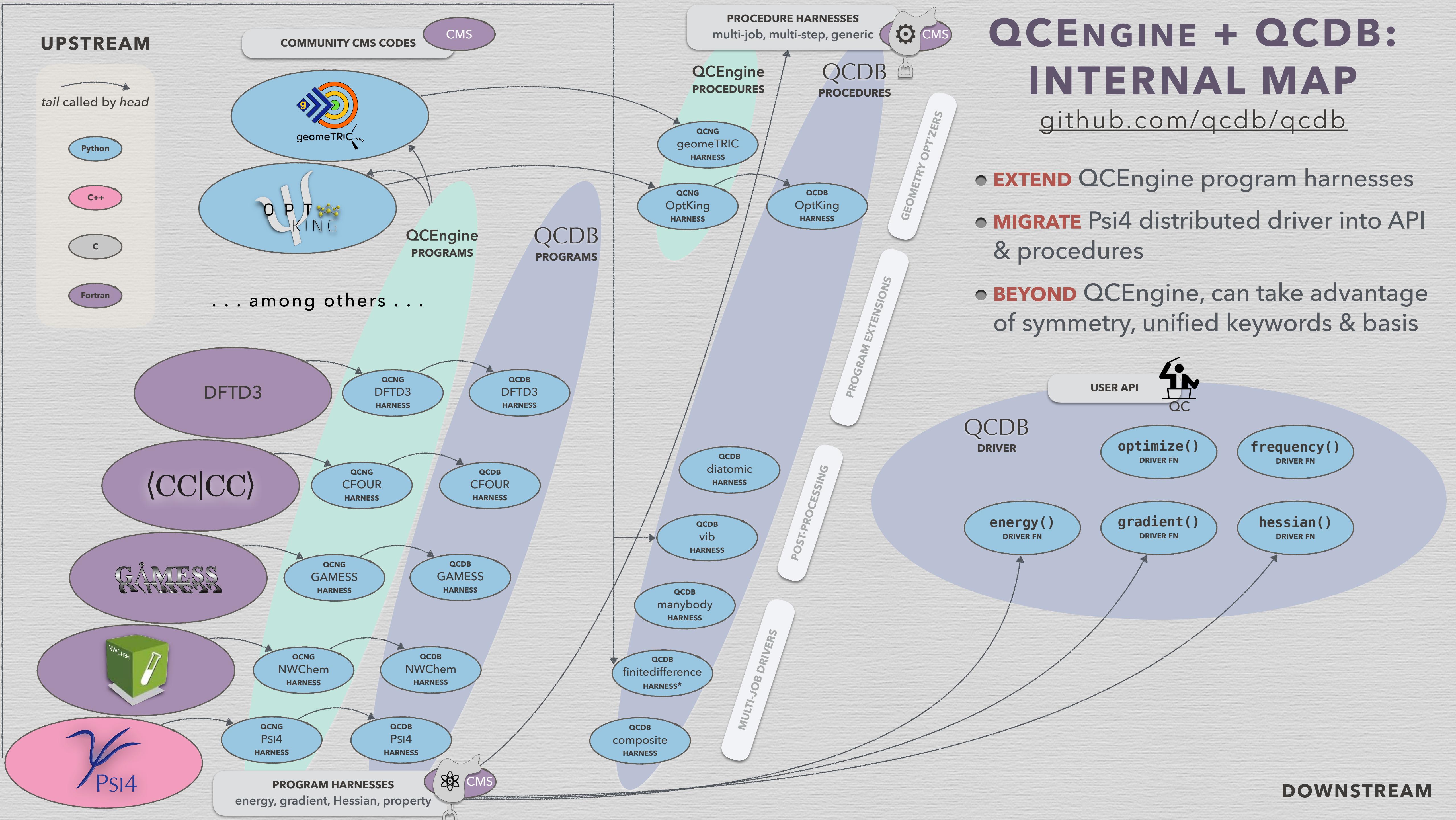
DOWNSTREAM

QCENGINE + QCDB:

INTERNAL MAP

github.com/qcdb/qcdb

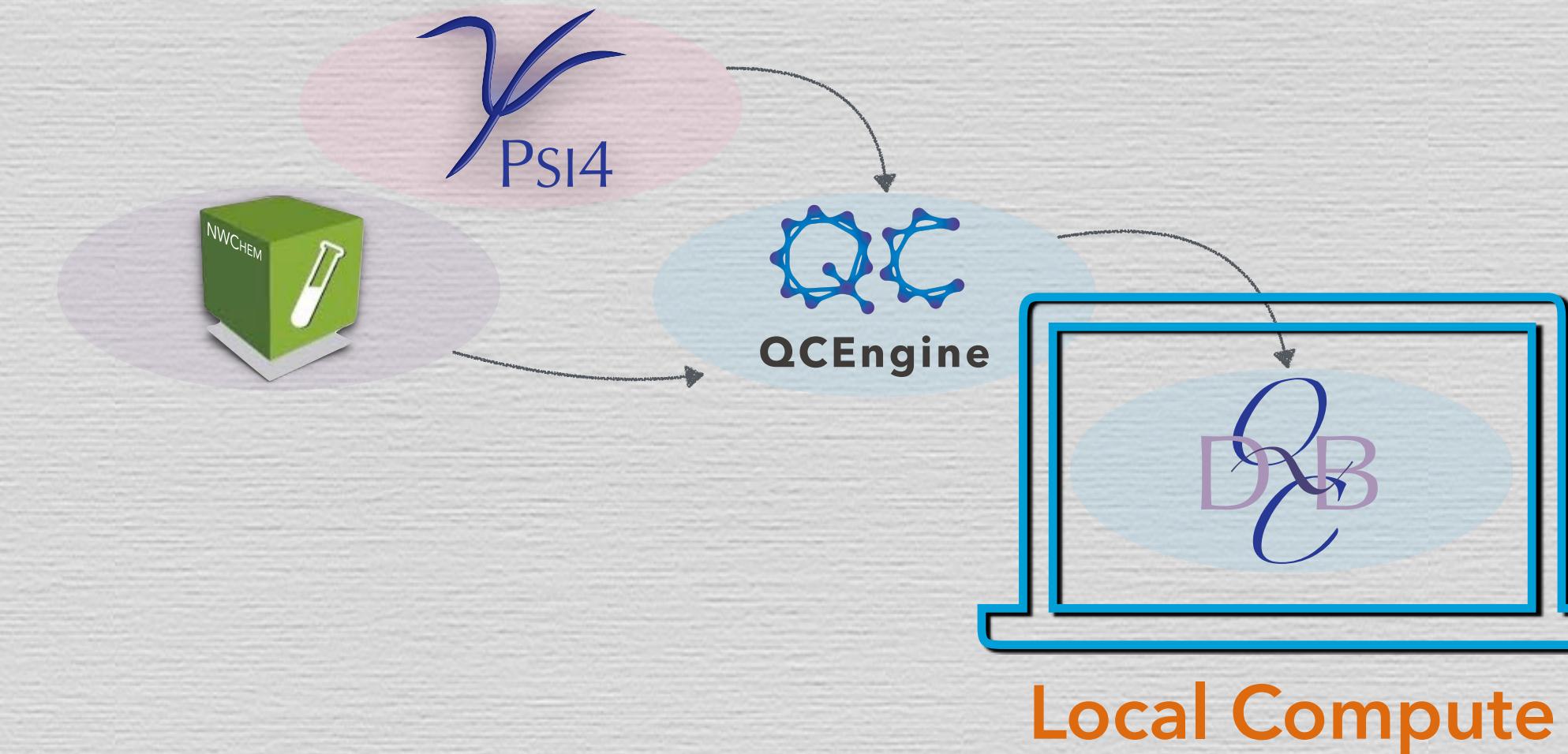
- **EXTEND** QCEngine program harnesses
- **MIGRATE** Psi4 distributed driver into API & procedures
- **Beyond** QCEngine, can take advantage of symmetry, unified keywords & basis



(5) QCDB DISTRIBUTED DRIVER, INTERNAL

PSI4 procedures generalized to other QC programs

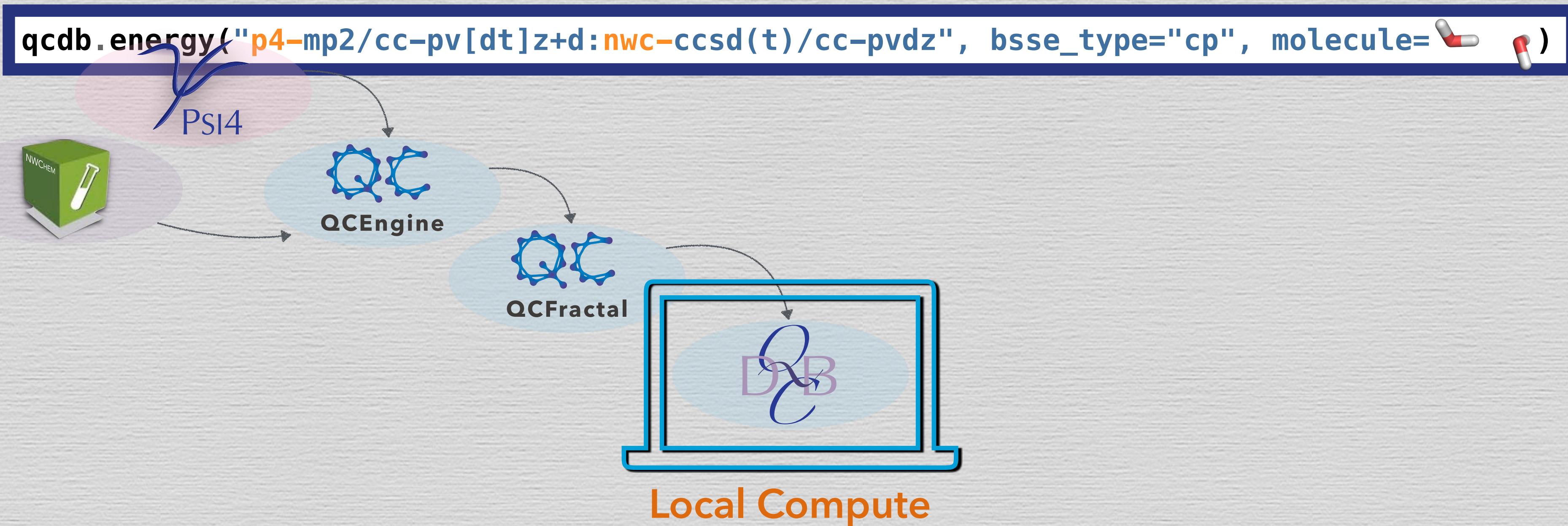
```
qcdb.energy("p4-mp2/cc-pv[dt]z+d:nwc-ccsd(t)/cc-pvdz", bsse_type="cp", molecule= )
```



- **AVAILABLE** now with **QCDB dev branch** & **Psi4** & **QCEngine** & **NWChem** (or CFOUR or GAMESS).
- **SPECIFICATION** through single file. Procedure **automated**, so low risk of user error.
- **RATE-LIMITED** by sum of all calcs since run **sequentially**.
- **RETRIEVAL** from filesystem difficult since many calcs in **aggregated outfile**.
- **FLEXIBILITY** to mix QC programs to access more or **more efficient** methods.

(6) QCDB DISTRIBUTED DRIVER, QCARCHIVE

distributed, searchable, error-resistant, and generalized



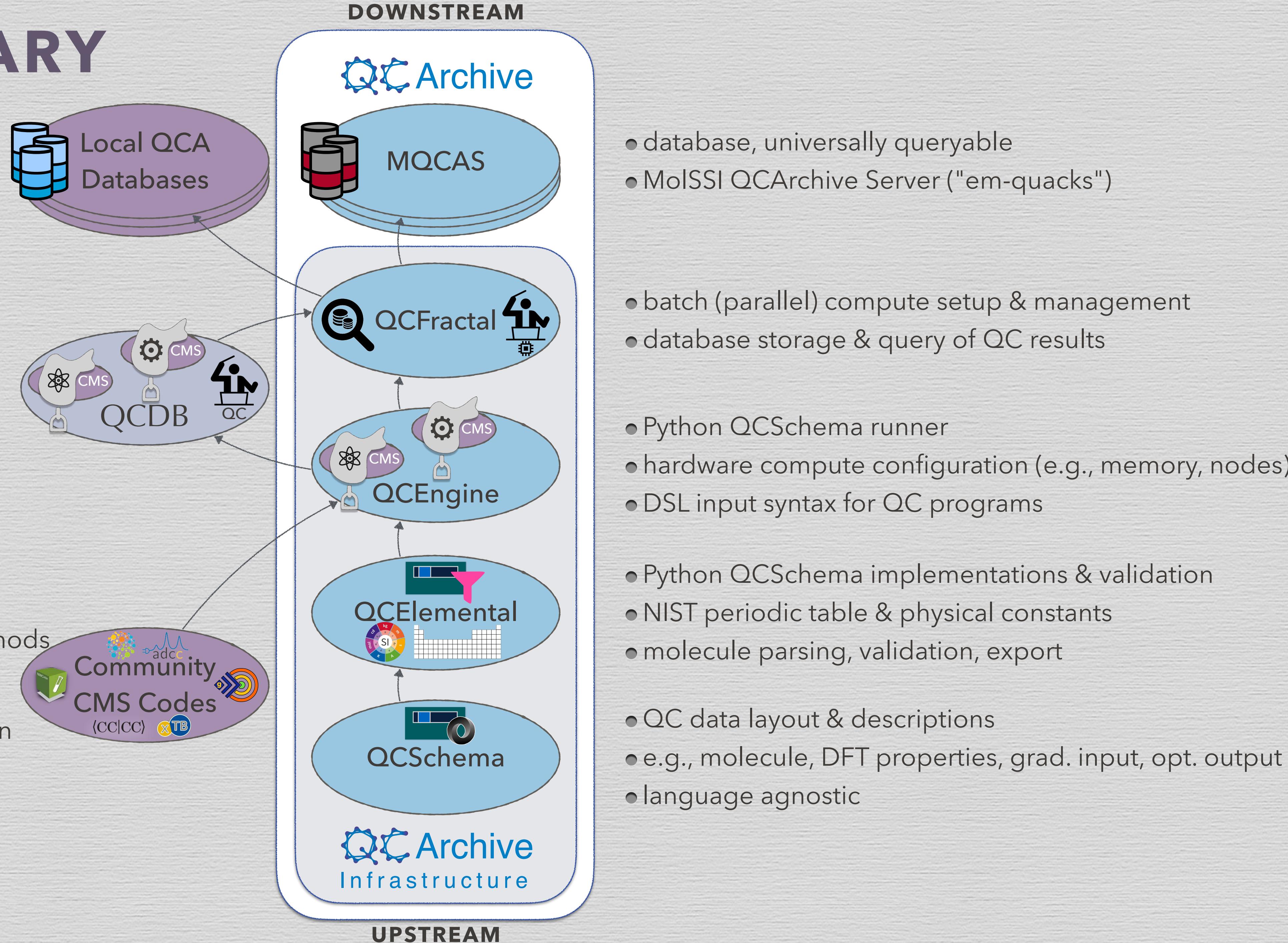
- **AVAILABLE** untested with QCDB dev branch & PSI4 & QC Engine & QC Fractal & NWChem (or CFOUR or GAMESS).
- **SPECIFICATION** through single file. Procedure **automated**, so low risk of user error.
- **RATE-LIMITED** by single longest calc since QC Fractal runs **parallel in queue**.
- **RETRIEVAL** from QC Archive **database** with query.
- **FLEXIBILITY** to mix QC programs to access more or **more efficient** methods.

SUMMARY

- database, permissioned query
- fully powerful as MQCAS but locally controlled

- DSL or unified input syntax
- multi-QC program workflows
- standardization layers

- the difficult part – coded QC methods
- structured output uncommon
- DSL input; API/schema uncommon



- database, universally queryable
- MolSSI QC Archive Server ("em-quacks")

- batch (parallel) compute setup & management
- database storage & query of QC results

- Python QCSchema runner
- hardware compute configuration (e.g., memory, nodes)
- DSL input syntax for QC programs

- Python QCSchema implementations & validation
- NIST periodic table & physical constants
- molecule parsing, validation, export

- QC data layout & descriptions
- e.g., molecule, DFT properties, grad. input, opt. output
- language agnostic

QCARCHIVE



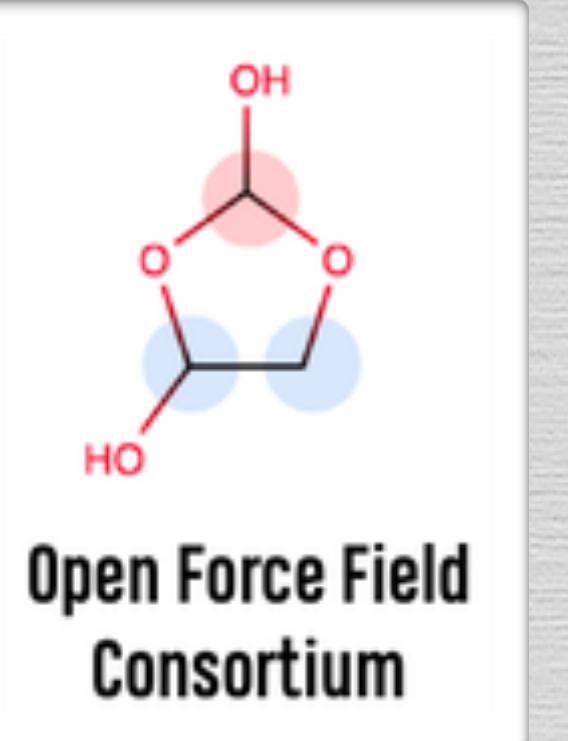
QCARCHIVE ACKNOWLEDGEMENTS



MOLSSI



QCSHEMA



openforcefield.org/

qcarchive.molssi.org

The MolSSI logo, which consists of a stylized molecular structure icon followed by the acronym "MolSSI" in a bold, sans-serif font.



ADCC



Maximilian Scheurer
Heidelberg

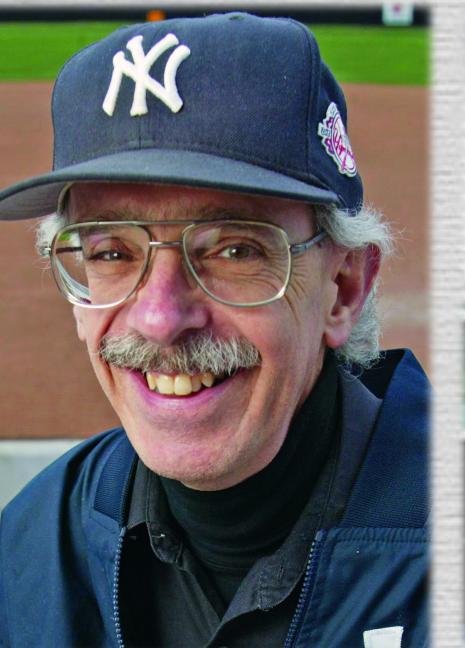


Michael Herbst
Aachen



Andreas Dreww
Heidelberg

GAMESS



Mark Gordon
Iowa State



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TERACHEM



Fang Liu
Emory



Heather Kulik
MIT



Colton Hicks
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Todd Martínez
Stanford

MRCHEM



Roberto Di Remigio
Uppsala



Daniel Smith
MolSSI → Entos



Lori Burns
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David Sherrill
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Justin Turney
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Zach Glick
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Johannes Steinmetzer
Friedrich Schiller U

TURBOMOLE



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Annabelle Lolinco
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Logan Ward
Argonne



Adrian Hurtado
Stony Brook

MOLPRO



Sebastian Lee
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John Stanton
UFL



Devin Matthews
SMU

NWCHEM

HIST./DB/TEST OPTIMIZERS



John Chodera
MSKCC



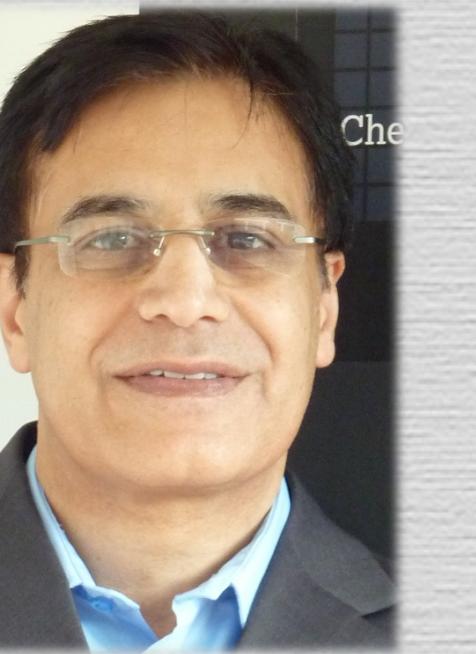
Jeffrey Wagner
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David Dotson
UC Boulder



Joshua Horton
Newcastle



Jamshed Anwar
Lancaster

Che



Lee-Ping Wang
UC Davis



Jan Hermann
Free U Berlin



Alexander Heide
UGA



Rollin King
Bethel

PROCEDURES



Nick Petosa
GaTech → Two Sigma



Daniel Nascimento
U Memphis

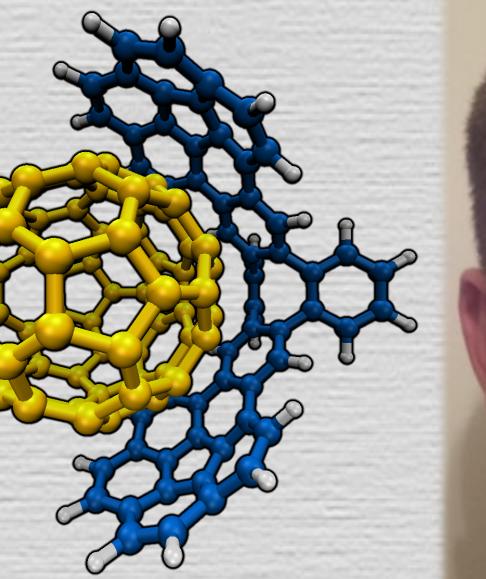


Dom Sirianni
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Chaya Stern
MSKCC

SE / DISP.



Sebastian Ehlert
Bonn



Holger Kruse
Czech Acad. Sci.



Jirí Šponer
Czech Acad. Sci.



Farhad Ramezanghorbani
UFL → Schrödinger

ENGINES



Taylor Barnes
MolSSI



Asim Alenaizan
GaTech



Peter Kraus
Curtin



Jonathon Misiewicz
Emory



Jeff Schriber
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Carlos Borca
Princeton

PSI4 DEVELOPERS



Jerome Gonthier
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Rob Parrish
Stanford



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Rollin King
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Alexander Sokolov
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Eugene DePrince
FSU



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NATIONAL INSTITUTES
OF HEALTH



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MolSSI



Jonathon Misiewicz
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Ed Valeev
VaTech



Andy Simmonett
NIH



Ed Hohenstein
CCNY



Roberto Di Remigio
Tromso

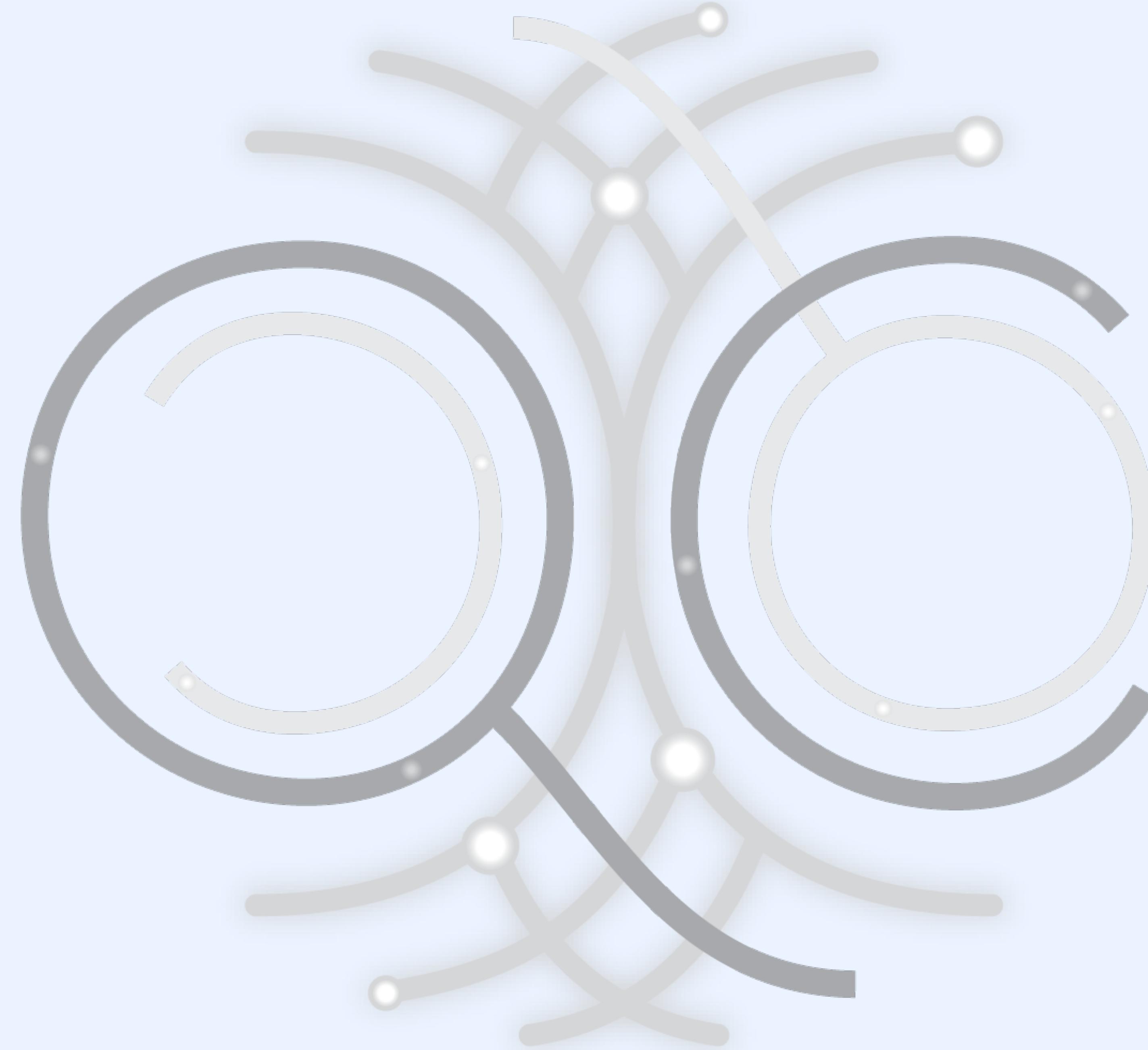


Ugur Bozkaya
Hacettepe



Peter Kraus
Curtin





PUBLICATIONS



Advanced Review

The MolSSI QCARCHIVE project: An open-source platform to compute, organize, and share quantum chemistry data

Daniel G. A. Smith Doaa Altarawy, Lori A. Burns, Matthew Welborn, Levi N. Naden, Logan Ward, Sam Ellis, Benjamin P. Pritchard, T. Daniel Crawford

First published: 31 July 2020 | <https://doi.org/10.1002/wcms.1491> | Cita

[Home](#) > [The Journal of Chemical Physics](#) > Volume 152, Issue 18 > 10.1063/5.0006002

No Access • Submitted: 26 February 2020 • Accepted: 12 April 2020 • Published Online: 13 May 2020

PREV NEXT

PSI4 1.4: Open-source software for high-throughput quantum chemistry

J. Chem. Phys. **152**, 184108 (2020); <https://doi.org/10.1063/5.0006002>

Daniel G. A. Smith¹, Lori A. Burns², Andrew C. Simmonett³, Robert M. Parrish², Matthew C. Schieber², Raimondas Galvelis⁴, Peter Kraus⁵, Holger Kruse⁶, Roberto Di Remigio⁷, Asem Alenaizan², Andrew M. James⁸, Susi Lehtola⁹, Jonathon P. Misiewicz¹⁰, Maximilian Scheurer¹¹, Robert A. Shaw¹², Jeffrey B. Schriber², Yi Xie², Zachary L. Glick², Dominic A. Sirianni², Joseph Senan O'Brien², Jonathan M. Waldrop¹³, Ashutosh Kumar⁸, Edward G. Hohenstein¹⁴, Benjamin P. Pritchard¹, Bernard R. Brooks³, Henry F. Schaefer III¹⁰, Alexander Yu. Sokolov¹⁵, Konrad Patkowski¹³, A. Eugene DePrince III¹⁶, Uğur Bozkaya¹⁷, Rollin A. King¹⁸, Francesco A. Evangelista¹⁹, Justin M. Turney¹⁰, T. Daniel Crawford^{1,8}, and C. David Sherrill^{2,a)}

[Home](#) > [The Journal of Chemical Physics](#) > Volume 155, Issue 20 > 10.1063/5.0059356

No Access • Submitted: 08 June 2021 • Accepted: 01 October 2021 • Published Online: 22 November 2021

PREV

Quantum Chemistry Common Driver and Databases (QCDB) and Quantum Chemistry Engine (QCENGINE): Automation and interoperability among computational chemistry programs

J. Chem. Phys. **155**, 204801 (2021); <https://doi.org/10.1063/5.0059356>

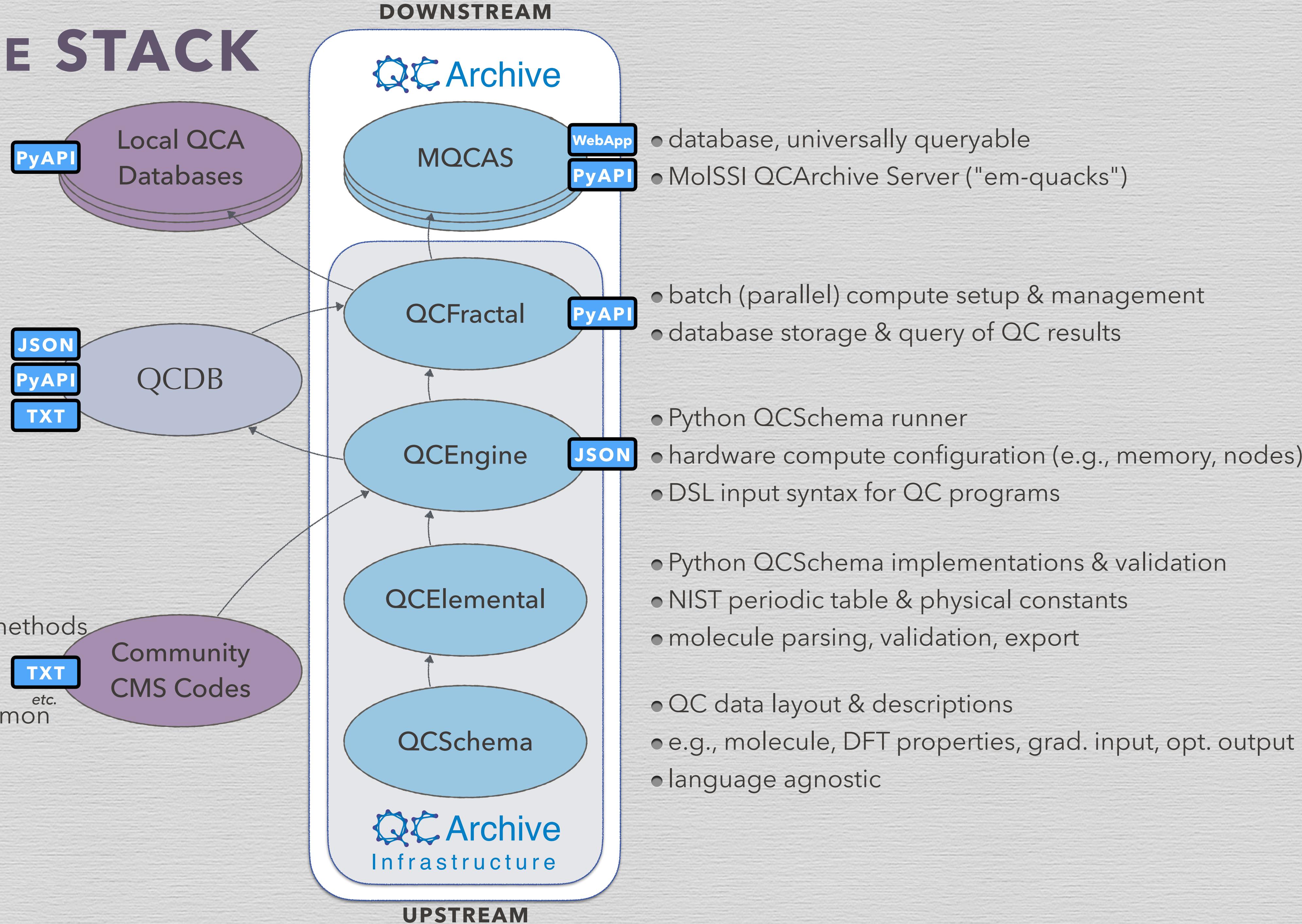
Daniel G. A. Smith^{1,a)}, Annabelle T. Lolino², Zachary L. Glick³, Jiyoung Lee^{2,b)}, Asem Alenaizan^{3,c)}, Taylor A. Barnes¹, Carlos H. Borca³, Roberto Di Remigio^{4,d)}, David L. Dotson⁵, Sebastian Ehlert⁶, Alexander G. Heide⁷, Michael F. Herbst⁸, Jan Hermann⁹, Colton B. Hicks^{10,11}, Joshua T. Horton¹², Adrian G. Hurtado¹³, Peter Kraus¹⁴, Holger Kruse¹⁵, Sebastian J. R. Lee¹⁶, Jonathon P. Misiewicz^{7,e)}, Levi N. Naden¹, Farhad Ramezanghorbani¹⁷, Maximilian Scheurer¹⁸, Jeffrey B. Schriber³, Andrew C. Simmonett¹⁹, Johannes Steinmetzer²⁰, Jeffrey R. Wagner^{5,21}, Logan Ward²², Matthew Welborn^{1,a)}, Doaa Altarawy^{1,23}, Jamshed Anwar¹², John D. Chodera²⁴, Andreas Dreuw¹⁸, Heather J. Kulik²⁵, Fang Liu^{25,e)}, Todd J. Martínez^{10,11}, Devin A. Matthews^{26,f)}, Henry F. Schaefer III⁷, Jiří Šponer¹⁵, Justin M. Turney⁷, Lee-Ping Wang²⁷, Nuwan De Silva^{2,9}, Rollin A. King²⁸, John F. Stanton²⁹, Mark S. Gordon³⁰, Theresa L. Windus³⁰, C. David Sherrill³, and Lori A. Burns^{3,h)}

QCARCHIVE STACK

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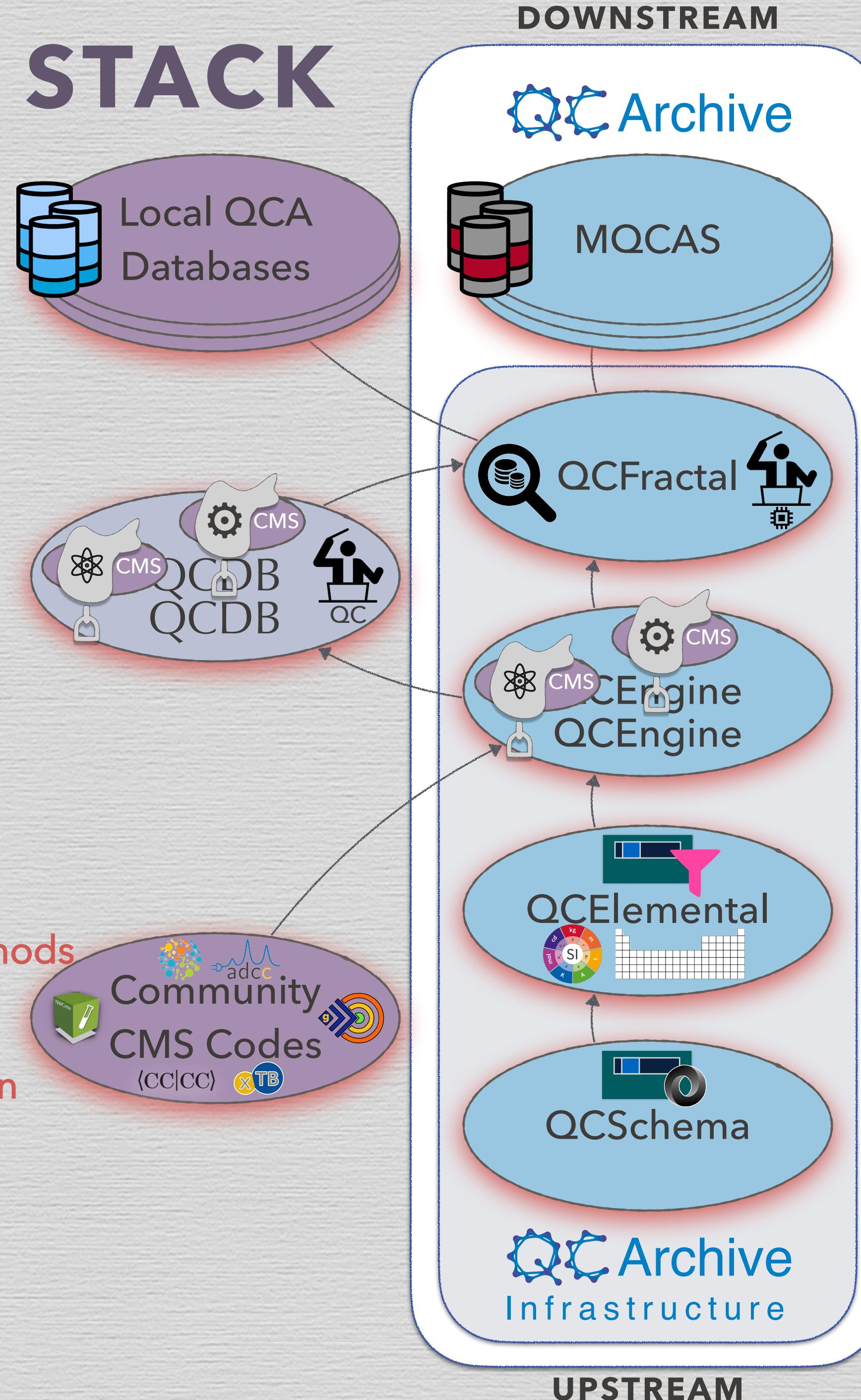


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