# pyfragment Documentation

Release 0.1

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**CHAPTER** 

ONE

#### BACKGROUND

PyFragment is a collection of Python modules that facilitate the setup and parallel execution of *embedded-fragment* calculations on molecular clusters, liquids, and solids.

### 1.1 Theory

The *embedded-fragment* methods are rooted in the many body expansion (MBE), which expresses the total energy of a molecular system as

$$E = \sum_{i} E_{i}$$

```
drivers.energy_driver()
 SP energy
```

### 1.2 Implementation

A series of modules are available. Please check:

#### 1.2.1 Codes

```
class ChargeState . ChargeState (fragments, fragment_charges)
```

Base class for VB CT state

```
coupling_dimer_gs (state2, embed_flag=None)
```

-sqrt(  $[E_(AB) + - E_(A+B)]*[E_(AB) + - E_(AB+)]$ )  $E_(AB) + ==$  the relaxed, correlated charged dimer  $E_(A+B) ==$  non-stationary HF energy of the charge-local dimer

plus monomer correlation energies of E\_A+ and E\_B

For a dimer system, this method reproduces the exact E by construction

#### coupling\_dimer\_gs\_no\_embed(state2)

Wraps the above dimer\_gs coupling, but the two monomers do not polarize each other in monomerSCF. Hence, it does not exactly reproduce the dimer GS energy by construction

```
coupling_dimer_gs_overlapHOMO (state2)
```

 $S*E_(AB)+ - sqrt([E_(AB)+ - E_(A+B)]*[E_(AB)+ - E_(AB+)])$  Second term is same as coupling\_dimer\_gs First term is overlap of monomer HOMO's times relaxed dimer energy This method also reproduces energy of a dimer by construction; it just makes the overlap matrix non-identity

#### diag\_chargelocal\_dimers (subcomm=None)

return E1 + E2, the BIM energy of this charge-transfer configuration E1: sum of monomer correlated energies E2: sum of dimer interaction energies  $(E_AB - E_A - E_B)$ 

interaction INCLUDES correlation for relaxed dimers (when A&B have same charge) but it's just the non-stationary HF energy for charge-local dimers

### **CHAPTER**

# TWO

# **INDICES AND TABLES**

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# **PYTHON MODULE INDEX**

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