



QM/MM Calculations

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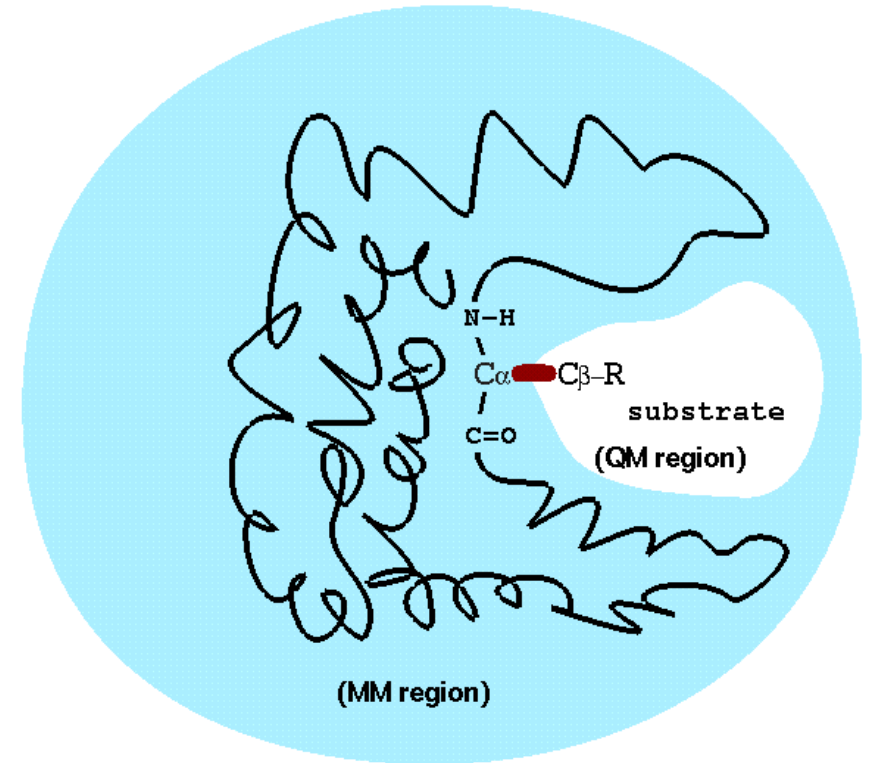
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Outline

- Introduction
- QM/MM energy function
- Boundary approximations
- Long range electrostatics
- QM/MM optimization
- Reaction path calculations
- Chain-of-replica methods
- FEP

Introduction

- Molecular Mechanics (MM): thousands of atoms, no reactions.
- Quantum Mechanics (QM): electronic structure, 1000 atoms at most.
- Solution: Combine both (QM/MM, ONIOM).
- Investigate reaction mechanism, analyze sources of catalysis, compare with experiments.



QM/MM energy function

- The total energy of a QM/MM system can be written as:

$$E_{Total} = E_{QM}(QM) + E_{MM}(MM) + E_{QM/MM}(QM / MM)$$

- where the first and second terms of Eq. 1 correspond to the QM and MM energies of the respective QM and MM subsystems, and the last term represents the interaction according to:

$$E_{QM/MM}(QM / MM) = E_{Coulomb}(QM / MM) + E_{vdW}(QM / MM) \\ + E_{MM-bonded}(QM / MM)$$

- the second and third terms of Eq. 2 are calculated with the force field (FF).

Additive QM/MM

- The first term is calculated together with EQM(QM) from an effective Hamiltonian to polarize the wavefunction,

$$E_{QM}(QM) + E_{Coulomb}(QM/MM) = \langle \psi | H_{eff} | \psi \rangle$$

$$H_{eff} = \frac{1}{2} \sum_i^N \nabla_i^2 + \sum_{i \neq j}^N \frac{1}{r_{ij}} - \sum_i^N \sum_{\alpha \in QM} \frac{Z_\alpha}{r_{\alpha i}} + \sum_{\alpha_1 \neq \alpha_2 \in QM} \frac{Z_{\alpha_1} Z_{\alpha_2}}{r_{\alpha_1 \alpha_2}}$$

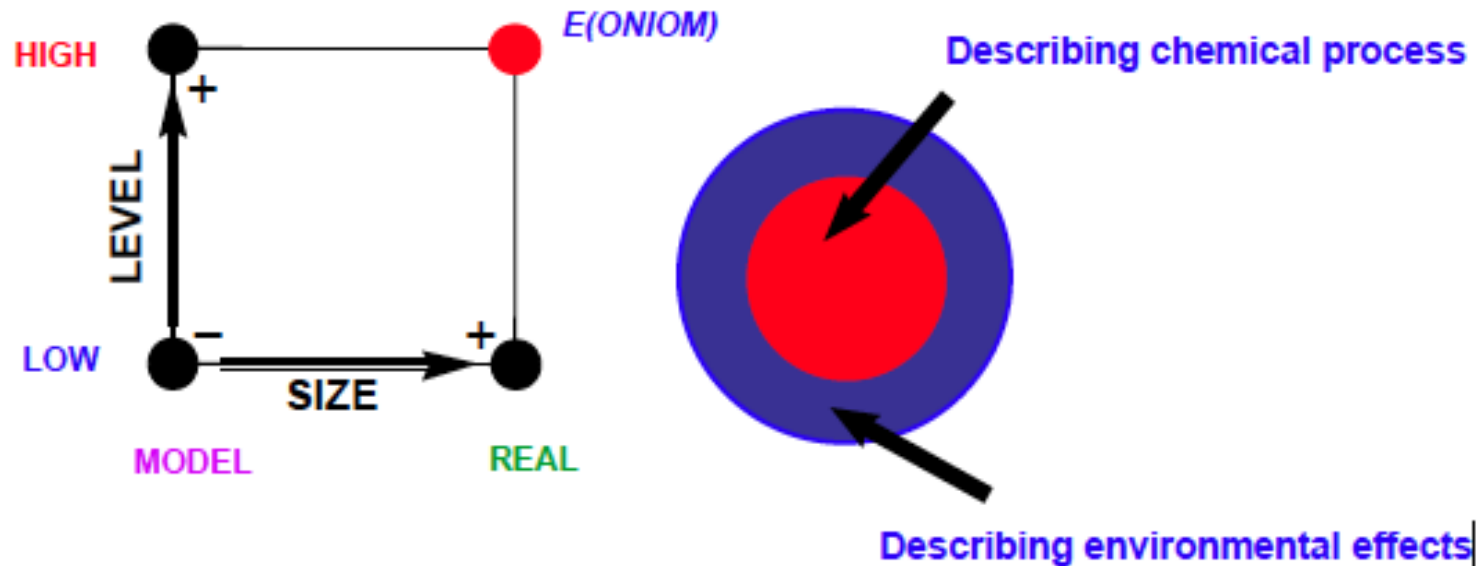
$$- \sum_i^N \sum_{\beta \in MM} \frac{q_B}{r_{iB}} + \sum_{\alpha_1 \in QM, B \in MM} \frac{Z_{\alpha_1} q_B}{r_{\alpha_1 B}}$$

- Hamiltonian can be semiempirical or *ab initio*

Subtractive QM/MM

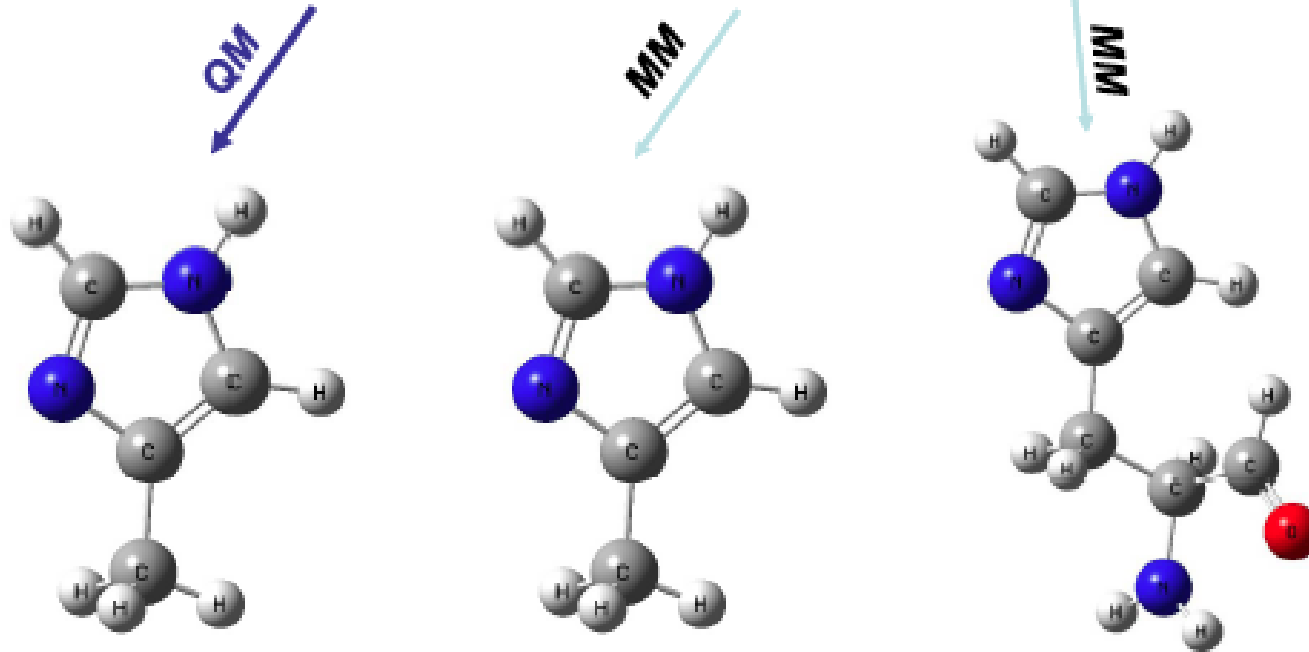
ONIOM method

$$\begin{aligned}
 E(\text{HIGH}, \text{REAL}) &\approx E(\text{ONIOM}) \\
 &= E(\text{LOW}, \text{MODEL}) + [E(\text{LOW}, \text{REAL}) - E(\text{LOW}, \text{MODEL})] + \\
 &\quad [E(\text{HIGH}, \text{MODEL}) - E(\text{LOW}, \text{MODEL})]
 \end{aligned}$$



Subtractive QM/MM (cont.)

$$\text{Energy(ONIOM)} = E(\text{high, model}) - E(\text{low, model}) + E(\text{low, real})$$



Boundary Approximations

Boundary problem in QM/MM: cutting chemical bonds

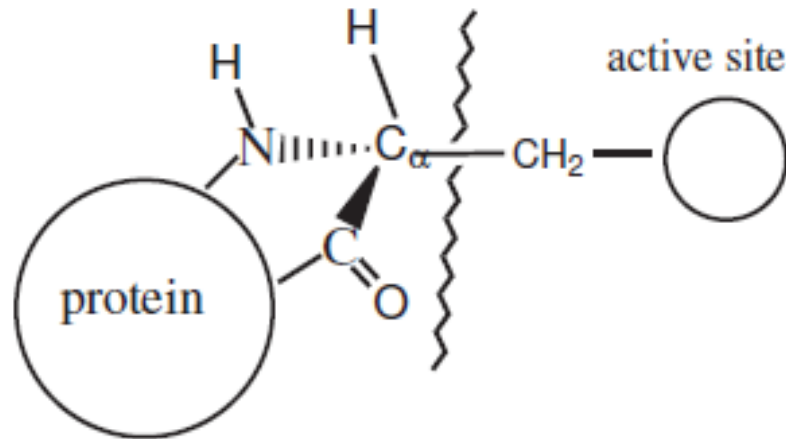
- Link atom (single and double)
- Localized self-consistent field (LSCF)
- Generalized hybrid orbital (GHO)
- Pseudobond

Advantages and disadvantages to each, e.g., excluded partial charges, distributed gaussian, etc.

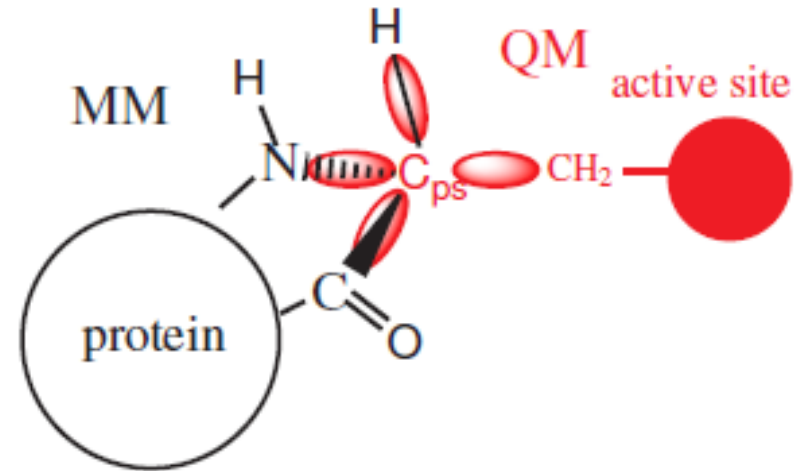
König *et al.*, JPCB, **109**, 9082, (2005).

Pseudobond Method

how to cut a chemical bond?



The pseudobond approach



- *Cps*: pseudoatom with one free valence, composed of a minimal basis set and pseudopotential.
- The pseudopotential is “tailored” to reproduced C-C or C-N bond length, angle, force.

Long range interactions

In general QM/MM calculations are performed with stochastic boundary conditions and the FF are non-polarizable. Recently:

- Generalized solvent boundary potential (PB charges outside cutoff range). Schaefer *et al.*, JCP, **123**, 014905, (2005).
- QM/MM-Ewald (approximate QM ESP by Mulliken charges for reciprocal space). Nam, Gao and York, JCTC, **1**, 2, (2005).
- QM/MM-Ewald improved (represent QM charge density for reciprocal space). Giese and York, JCTC, **12**, 2611, (2016).

Long range interactions

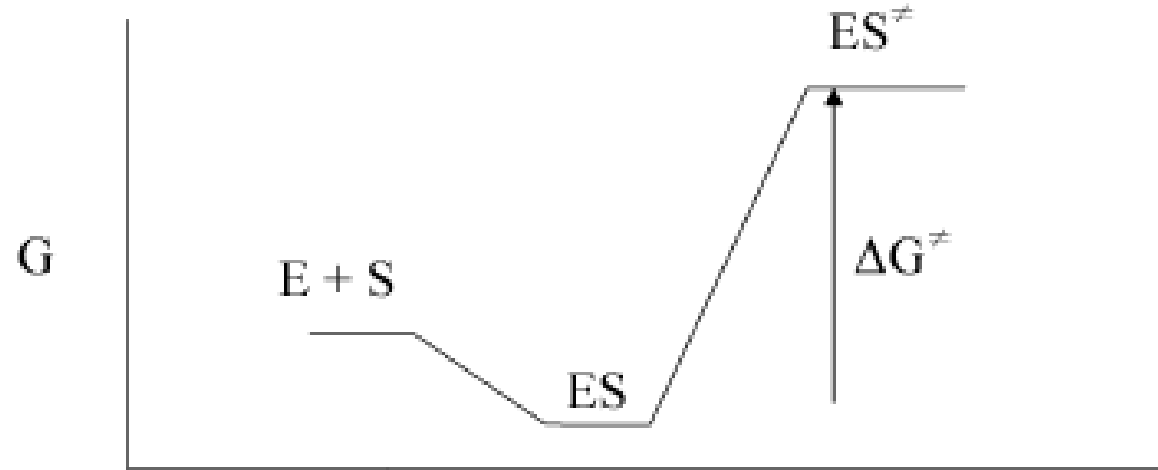
- QM/MM lattice summation (use Ladd lattice summation). Dehez *et al.*, JCP, **122**, 234503, (2005).
- Potential (or its force) displacement or reduction (use functions to change the potential in the boundary). McCann *et al.*, JCTC, **9**, 944, (2013).
- Smoothing functions. Fang *et al.*, JCP, **143**, 044103, (2015). Kratz *et al.*, TCA, 135:166 (2016).

QM/MM optimization

How to optimize a QM/MM system?

- Start by optimizing QM subsystem in field of MM subsystem keeping MM fixed (quasi-Newton, redundant internal coordinates).
- Once QM converges, optimize MM subsystem with QM fitted charges (MK) keeping QM fixed (truncated Newton, cartesian coordinates).
- Iterate until neither subsystem changes

Modeling enzyme reactions



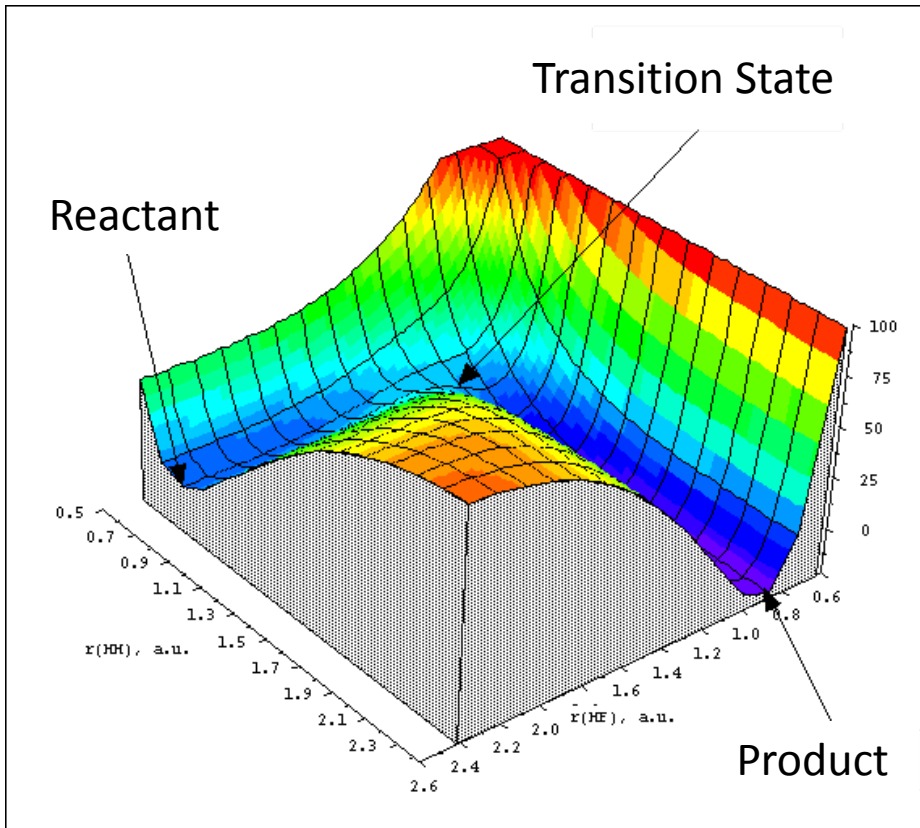
- Classical reaction rate (Eyring's Transition State Theory):

$$k = \kappa \frac{1}{\beta h} \exp(-\beta \Delta G^{\ddagger})$$

ΔG^{\ddagger} = free energy activation barrier

κ = transmission coefficient

Reaction Paths



- Minimum energy path (MEP): steepest descent path connecting reactants and products, or reaction path at “0K”.
- Free energy can further be calculated by including the fluctuations around the MEP.

$$\frac{dX_i}{ds} = c \frac{\partial E}{\partial X_i}$$

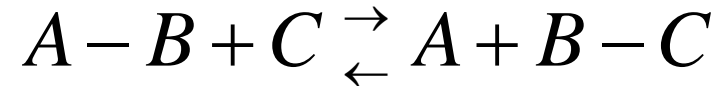
$s = \text{Reaction coordinate}$

$$\frac{dX_i}{ds} = \text{Tangent to path}$$

$$\frac{\partial E}{\partial X_i} = \text{Energy gradient}$$

Calculation of the MEP

- One-dimensional case:



Reaction coordinate driving method: use restraint potential to drive system from reactant to product

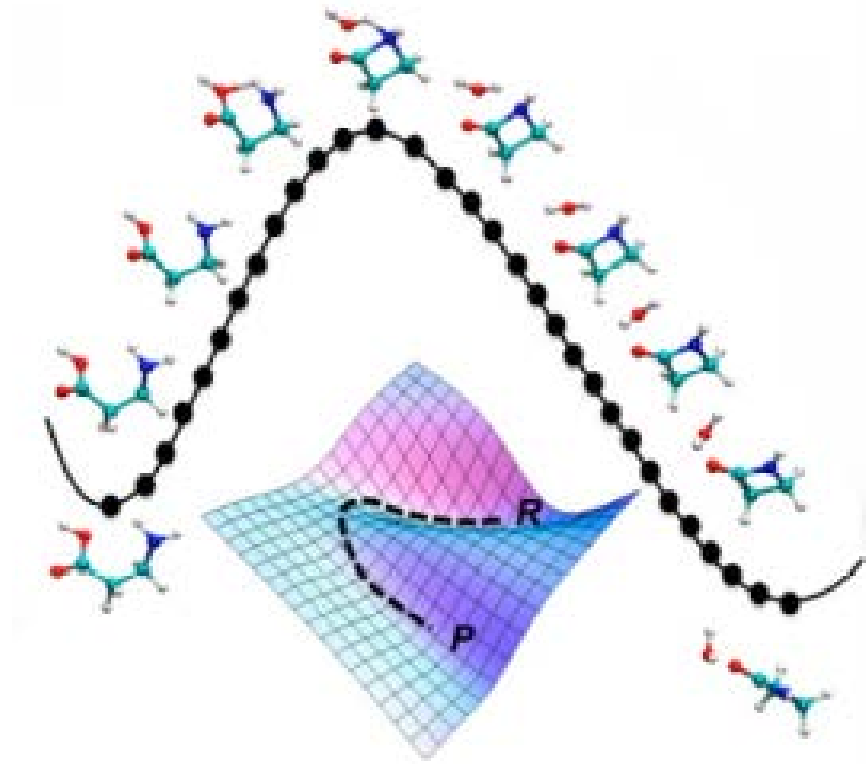
$$V_{restraint} = k(s - s_0)^2$$

$$s = R_{BC} - R_{AB}$$

- Multi-dimensional case:

s may be hard to identify, multidimensional mapping is computationally expensive.

Chain-of-replicas



- Given the information of the reactant, (intermediate) and product, a discretized chain of points can be obtained along the path.
- All the points can be optimized to the MEP simultaneously by using the force perpendicular to the path tangent.
- Points are kept spaced by imposing an equidistant constraint.

Nudged Elastic Band (NEB)

1st order methods use only energies and gradients to optimize MEP.

- “Spring” between atoms.
- Projection of spring forces (parallel to MEP).
- Add perpendicular force to spring force.
- Minimize in direction of force (velocity Verlet).

2nd order methods

Include approximate Hessians to optimize MEP.

- QSM. Burger and Yang, JCP, **124**, 054109
 - Adaptive step–size integration (Runge–Kutta).
 - Use quadratic surface approx. by damped BFGS
 - Updated Hessian.
 - Reaction path approximated by 3rd order B–spline.
- 2nd order path optimizer. Ayala and Schlegel, JCP, **107**, 375
 - Explicit critical point optimizer.
 - Hessian update with BFGS/Powell mixture.
 - Reaction path approximated by arc of circle to calculate tangents.

Enzyme reaction paths

For QM/MM calculations it is possible to do a combined iterative procedure to reduce time.

- 1) Start optimization with NEB.
- 2) At each NEB step, do MM optimization with restraints.
- 3) Once NEB converged, finish with 2nd order method.

4OT example: 348 (765); 306(618) for first and second steps with combined procedure (2nd order only).

QM/MM-FEP

- Average fluctuations of the enzyme can be included:

$$\Delta G = \Delta E_{QM}^+ + \Delta G_{QM/MM}^+$$

$$\begin{aligned} \Delta G_{QM/MM}^+ &= \sum \Delta G^{i \rightarrow i+1} \\ &= \sum \left\{ -\frac{1}{\beta} \left\langle \exp(-\beta \Delta E_{QM/MM}^{i \rightarrow i+1}) \right\rangle_i \right\} \end{aligned}$$

- MEP obtained in enzyme environment.
- FEP due to QM fluctuations can be included.

Other methods for Free Energy calculations

Recently other methods have been proposed to determine FE of reaction with QM/MM:

- Minimum free energy path (QM/MM–MFEP)
 - Thermodynamics of the reaction described by a PMF
 - MM is sampled and averaged, followed by optimization of QM on average MM field (PMF)
- Born-Oppenheimer MD (QM/MM–BOMD)
 - On–the–fly BOMD with QM/MM
 - Umbrella sampling used for high energy regions of PES

Applications and calculations using LICHEM

Electrostatic models

- Point-charges
- Point-multipoles
- Polarizable sites
- Diffuse charge density
- AMBER/CHARMM: point-charge based models
- Core-Shell/COS: point-charge and polarization
- AMOEBA: point-multipoles and polarization
- Gaussian electrostatic model (GEM): charge density and polarization

LICHEM: Layered Interacting CHEmical Models



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kratman Eigen update	Latest commit 7084bdb on Jun 14
Eigen3	Eigen update a month ago
doc	A lot of updates for code clean up a year ago
include	Minor updates 8 months ago
src	Eigen and doxygen updates 3 months ago
tests	Test update 6 months ago
.travis.yml	OSX build fix 5 months ago
Makefile	OSX build fix 5 months ago
README.md	Minor doc. update 8 months ago

README.md

LICHEM: Layered Interacting CHEmical Models

By: Eric G. Kratz

Symbiotic Computational Chemistry

LICHEM

- Design principles:
 - Primarily an interface
 - A single executable
 - Open source

Mode	Potential	QM wrapper	MM wrapper	Calc. type
File conv.	Point-charge	Gaussian	TINKER	Energies
QM only	Mtp/pol	NWChem	TINKER-HP	Optimization
MM only	Pseudo-bond	PSI4	LAMMPS	PIMC
QM/MM	Diffuse charge		AMBER	Monte Carlo
	GEM			Reaction Path
				Dynamics
				Frequencies

Multipole moments

- Few QM packages can include atomic multipole moments
- Most QM packages can include point-charges
- Why not convert the atomic multipole moments to point-charges?

Simplifying multipoles

- Spherical harmonic multipoles can be converted to six point-charges (Devereux et al., JCTC, 10, 4229, 2014).
- Now nearly any QM package can be used for calculations with multipole moments
- Of course, this is only needed for QM packages which do not support external multiple moments

$$q_{\pm x} = \frac{Q_{00}}{6} \pm \frac{Q_{11c}}{2d} - \frac{Q_{20}}{6d^2} + \frac{Q_{22c}}{2\sqrt{3}d^2}$$

$$q_{\pm y} = \frac{Q_{00}}{6} \pm \frac{Q_{11s}}{2d} - \frac{Q_{20}}{6d^2} + \frac{Q_{22c}}{2\sqrt{3}d^2}$$

$$q_{\pm z} = \frac{Q_{00}}{6} \pm \frac{Q_{10}}{2d} + \frac{Q_{20}}{6d^2} + \frac{Q_{22c}}{2\sqrt{3}d^2}$$

Polarization

- Polarizable QM/MM requires two coupled SCF (wfn/μ_{ind}) (Lipparini et al. J. Chem. Phys, 141, 184108, 2014)

- The polarization energy can be expressed as:

$$E_{pol} = E_{pol}^{QM} + E_{pol}^{QM/MM} + E_{pol}^{MM}$$

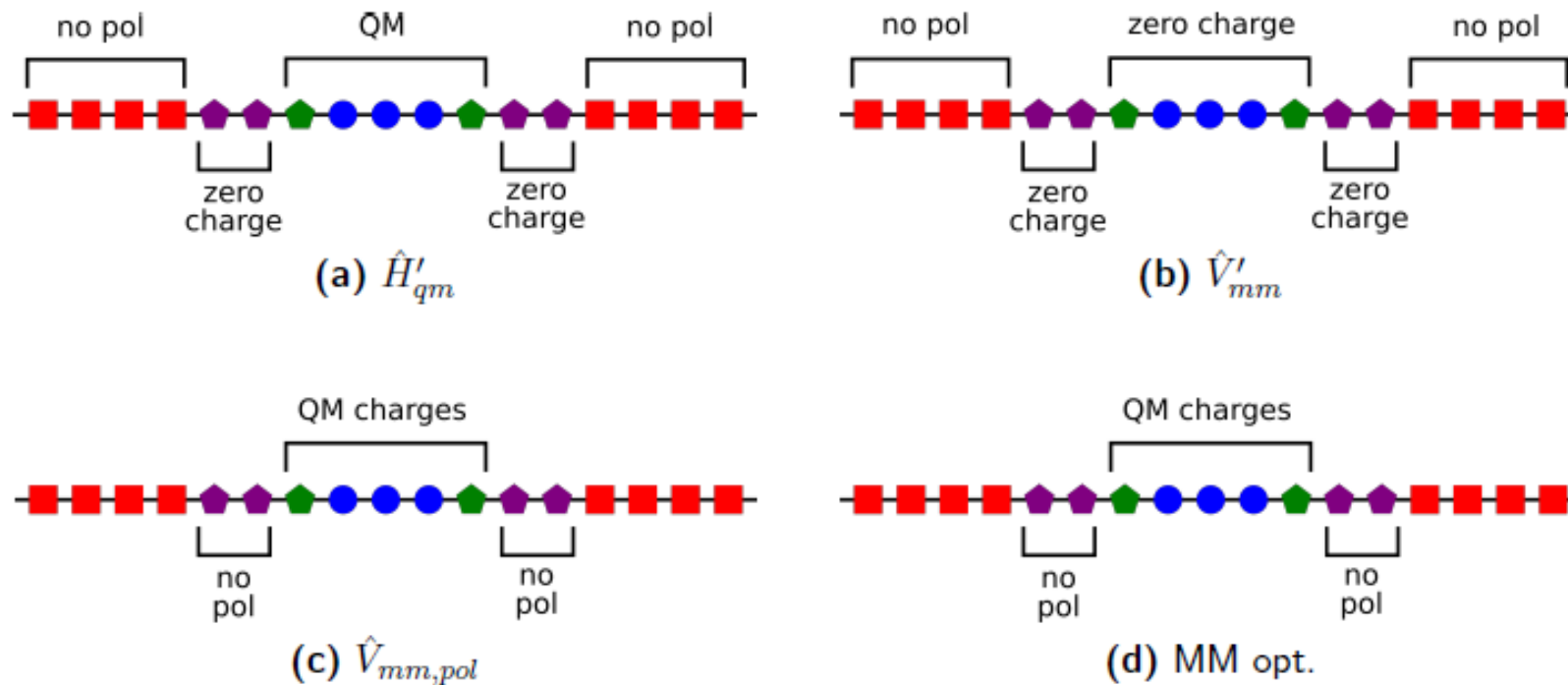
- ~80% of the polarization energy comes from interactions with the static field (Wang et al., J. Phys. Chem. B, 117, 9956, 2013)
- The polarization energy is approximated by neglecting μ_{ind}^{MM} in H_{eff} during the QM evaluation

Polarization

- QM charges effectively include the induced atomic dipoles
- E_{pol} includes full polarization from the MM and QM terms and the QM/MM interaction includes polarization from static MM field
- In essence this approximation captures $\geq 80\%$ of the mutual QM/MM polarization energy

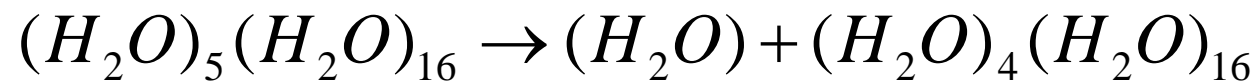
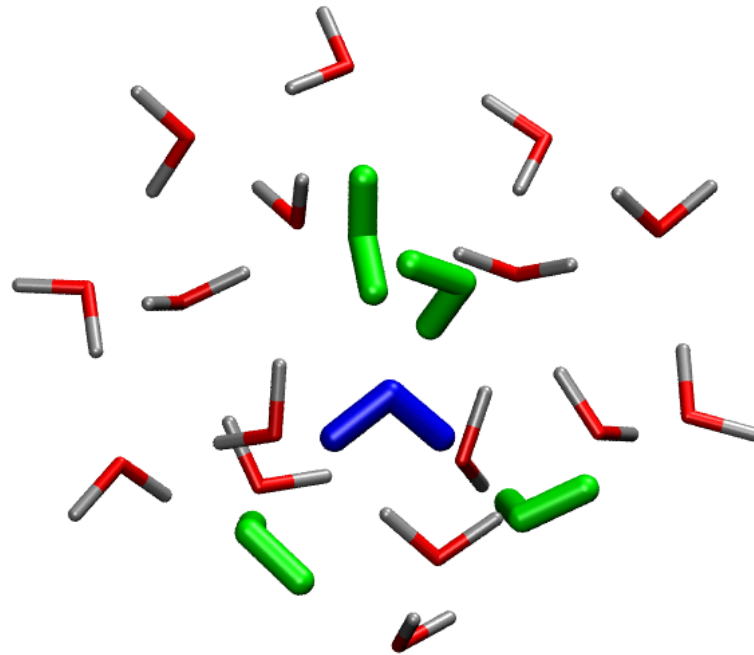
Polarizable pseudo-bond method

- Regions: QM, MMM, pseudo-bond atoms (PB), boundary atoms (BA)



Importance of Polarization

- Testing QMMM polarization requires properties that can easily be calculated with full QM



$$E_{solv} = E_{5,16} - E_{4,16} - E_{1,0}$$

Importance of Polarization

<i>QM*</i>	<i>MM</i>	<i>E_{Solv}(eV)</i>
MP2	-	-1.5730
B97D	-	-1.5239
B97D	AMOEBA	-1.4663
B97D	TIP3	-1.2817
B97D	AMOEBA**	-1.2387
PBE0	-	-1.5166
PBE0	AMOEBA	-1.5814
PBE0	TIP3	-1.3999
PBE0	AMOEBA**	-1.3575
-	AMOEBA	-1.5419
-	TIP3	-1.1948
-	AMOEBA**	-0.5091

*= 6-311++G(d,p)

**= Without polarization

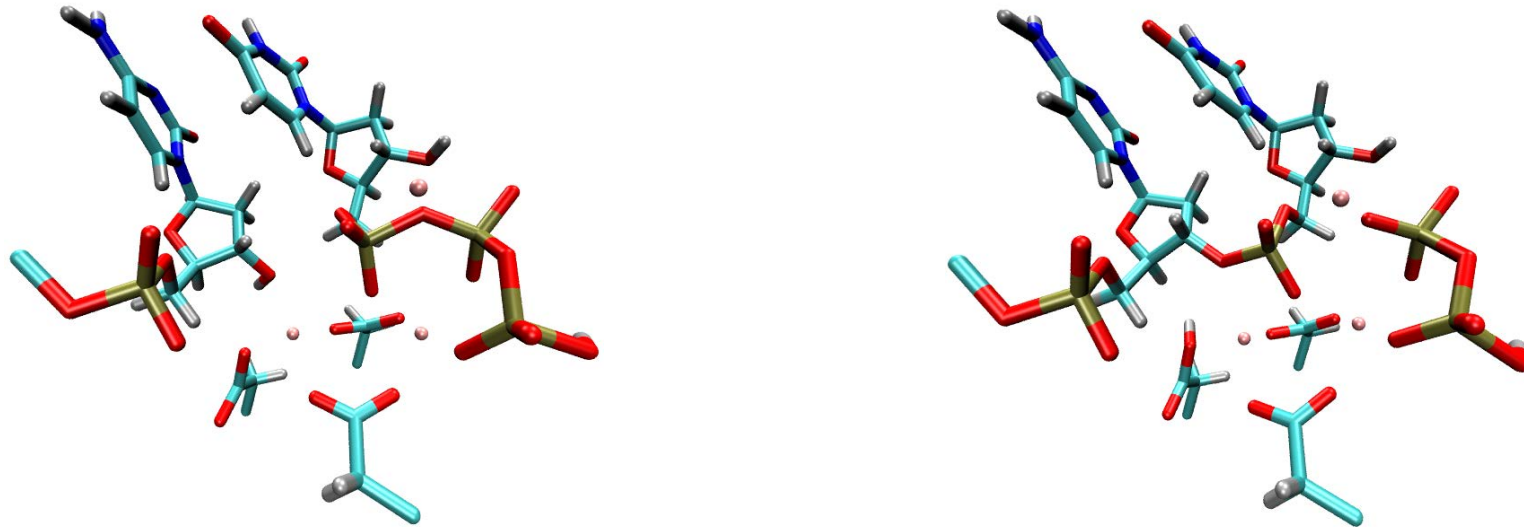
DNA polymerase λ (*Pol* λ)

Brief synopsis of (*Pol* λ) :

- Human DNA polymerase λ is an enzyme which replicates DNA and is one of several enzymes involved in the DNA repair mechanisms
- The ions in the active site are transient and play a large role in the efficiency of the reaction
- *Pol* β and *Pol* μ have been shown to have 3 Mg^{2+} ions in the active site
- Only 2 Mg^{2+} ions have been observed in the *Pol* λ active site

Pol λ

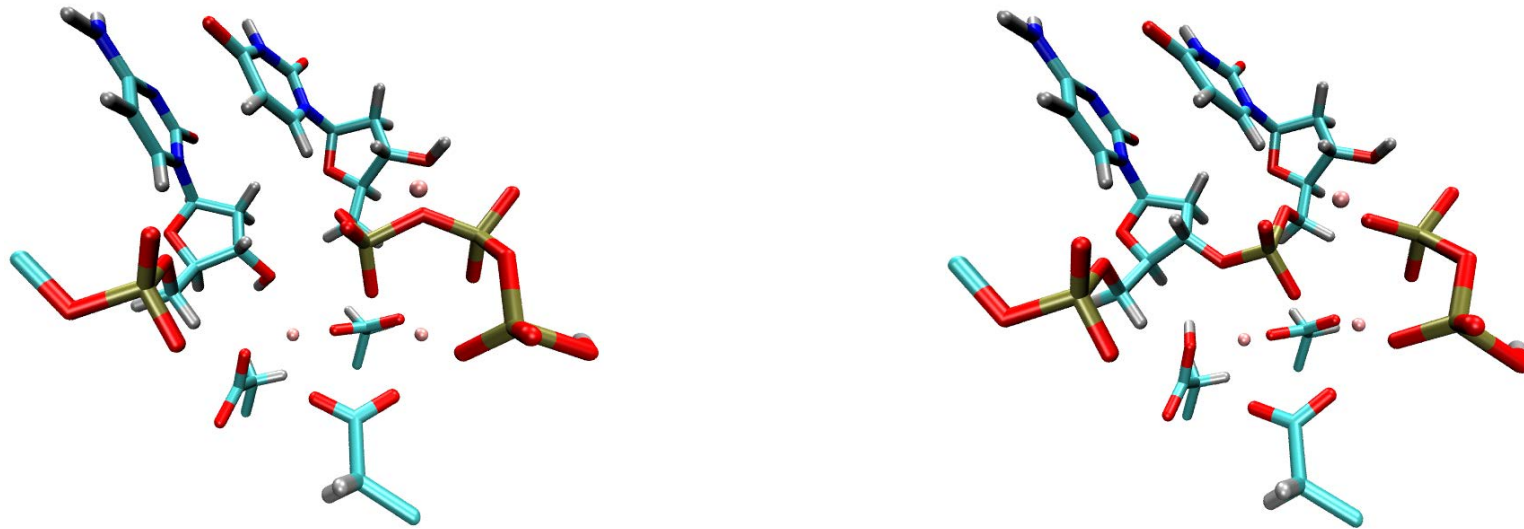
- Addition of a dUTP to the nascent DNA chain



- The pseudo-bond method can be used to describe bonds between the QM and MM regions
 - Method: B97D/6-31G(d)/AMBER99
 - 102 QM atoms, 4 pseudo-bonds, 18 boundary atoms, 18401 MM atoms

Pol λ

- Preliminary QMMM results predict that 3 Mg^{2+} ions are vital to the *Pol λ* reaction
- Our previous results (without the 3rd ion) predicted that the reaction was endothermic



- Calculations with LICHEM suggest that the reaction is only exothermic when the third Mg^{2+} ion is present

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