## Reactive force fields: concepts of ReaxFF

#### Adri van Duin

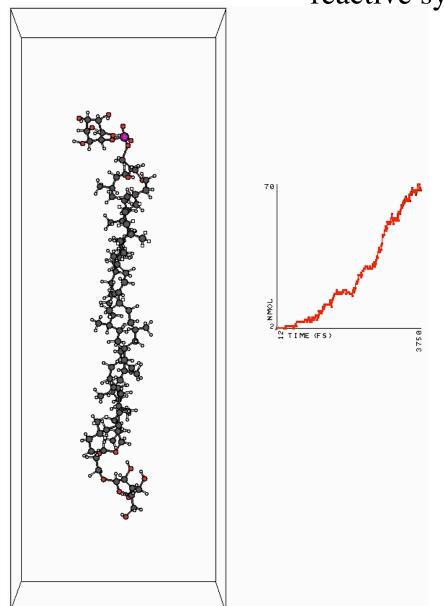
Material and Process Simulation Center, California Institute of Technology

CH-121 lecture February 4 2008





Aim: simulation of the dynamics of large, complicated reactive systems

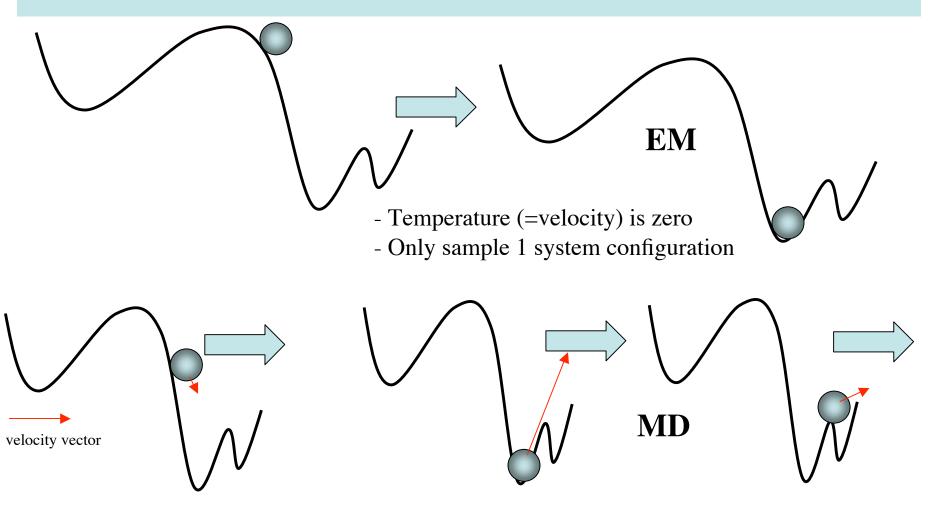


Simulation of the decomposition of a archaeol lipid biomarker by exposure to high-velocity (30eV) N-radicals

## **Outline**

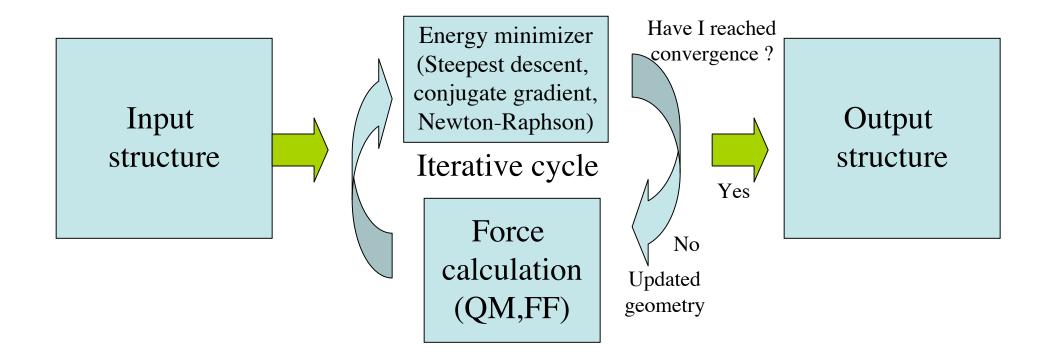
- Energy minimization and molecular dynamics methods
- Simulations on the dynamics of chemical reactions
- How to make a force field reactive: building the ReaxFF reactive force field
  - Concepts of covalent non-reactive force fields
  - Introduction of bond orders
  - Non-bonded interactions in a reactive force field
  - Charge polarization
  - Current status of the ReaxFF method
  - ReaxFF program, in- and output files
- Force field development for Si/SiO systems
- Applications of the Si/SiO reactive force field
  - Hydrogen diffusion in Si/SiO<sub>2</sub> interfaces
  - Thermal decomposition of PDMS polymers

# Energy minimization (EM) and molecular dynamics (MD) methods

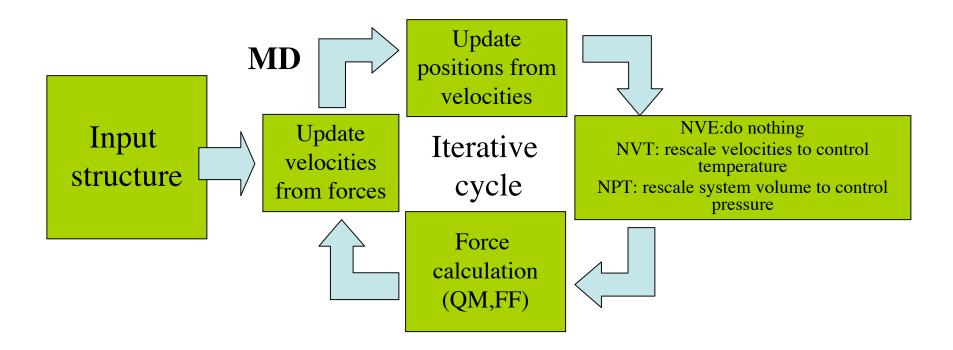


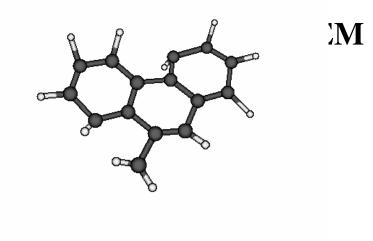
- Non-zero temperature
- Sample configurational space; the higher the temperature the more configurations become available
- Energy conservation:  $E_{kin}+E_{pot}$ =constant

## Energy minimization methods: structure

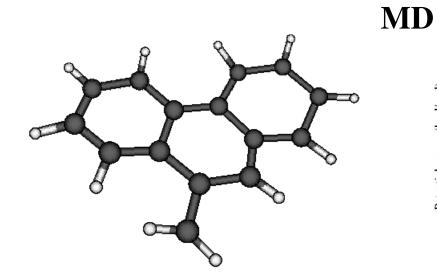


### MD-methods: structure

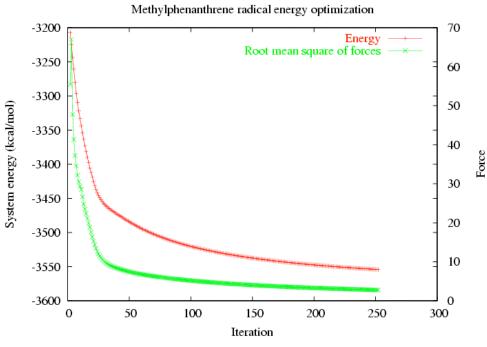


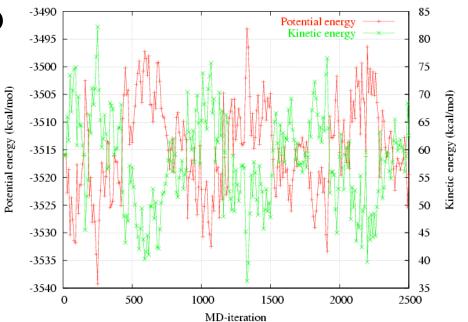


FF energy minimization of a methylphenanthrene radical using a steepest descent method



FF NVE molecular dynamics of a methylphenanthrene radical at T=700K





## Applications of EM and MD

#### EM

- Determine static (0 Kelvin) properties of a single system configuration.
- Can be used to calculate IR, NMR-spectra, geometry information, relative energies.
- Usually employed on a single molecule; not relevant for multimolecular systems.

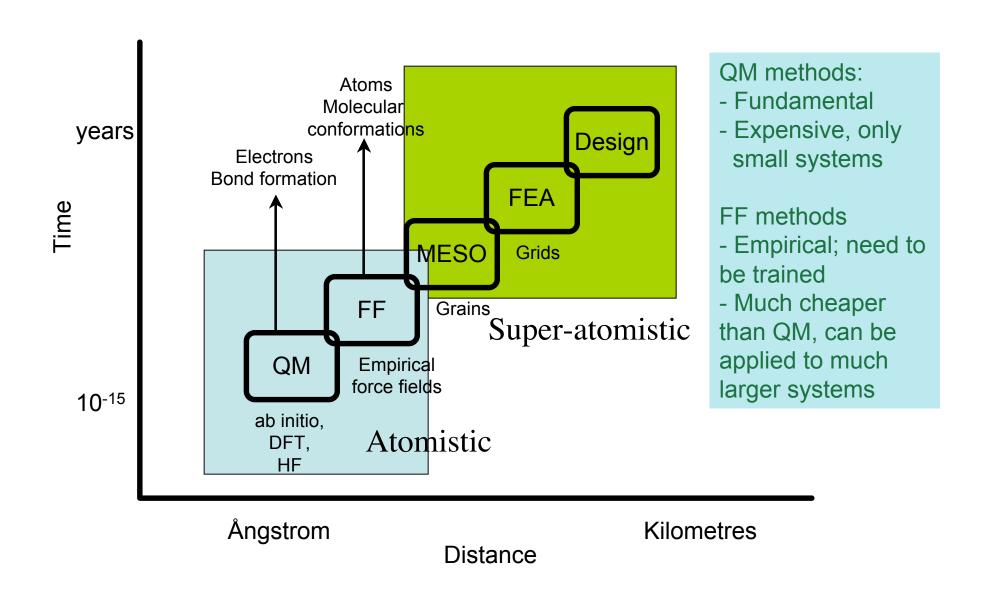
#### MD

- Used to sample the configurational space; average over multiple system configurations.

Fluorimidazole /HTFS system

- Can be used to model temperature and pressure effects
- Can be used to calculate diffusion constants, reaction rates.
- Can be employed on multi-component systems.
- Almost always FF; QM/MD is very expensive

## Simulations on the dynamics of chemical reactions



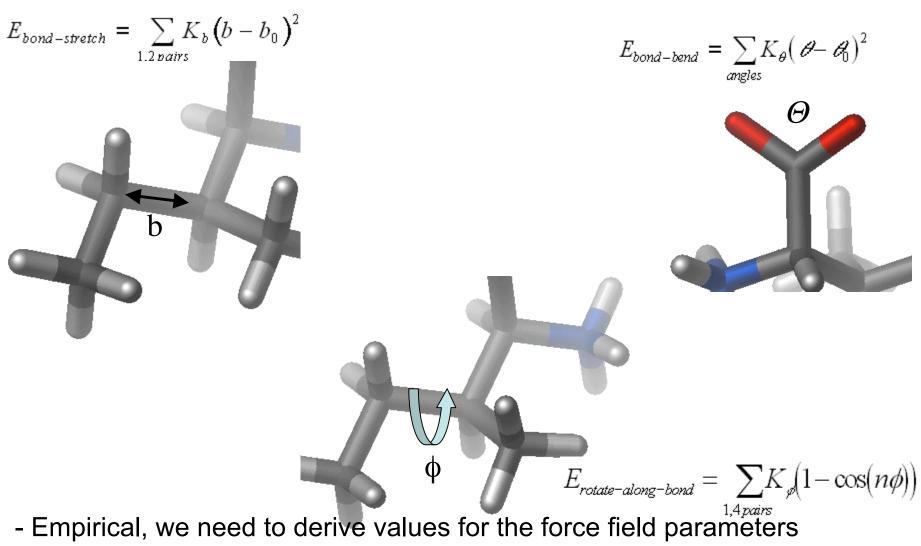
## QM-methods

$$\mathsf{H} = -\sum_{A} \frac{1}{2M_{A}} \nabla_{A}^{2} - \sum_{i} \frac{1}{2} \nabla_{i}^{2} + \sum_{A < B} \frac{Z_{A}Z_{B}}{R_{AB}} - \sum_{i} \sum_{A} \frac{Z_{A}}{R_{Ai}} + \sum_{i < j} \frac{1}{r_{ij}}$$
Kinetic energy Nucleus-Electron attraction

Nucleus-Nucleus Electron-Electron repulsion (analytically unsolvable)

- Allows calculation of atomic interactions First Principles
- Computationally expensive, especially for finding accurate approximations of electron-electron repulsion term

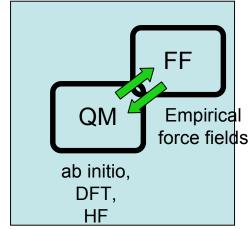
## Force field methods

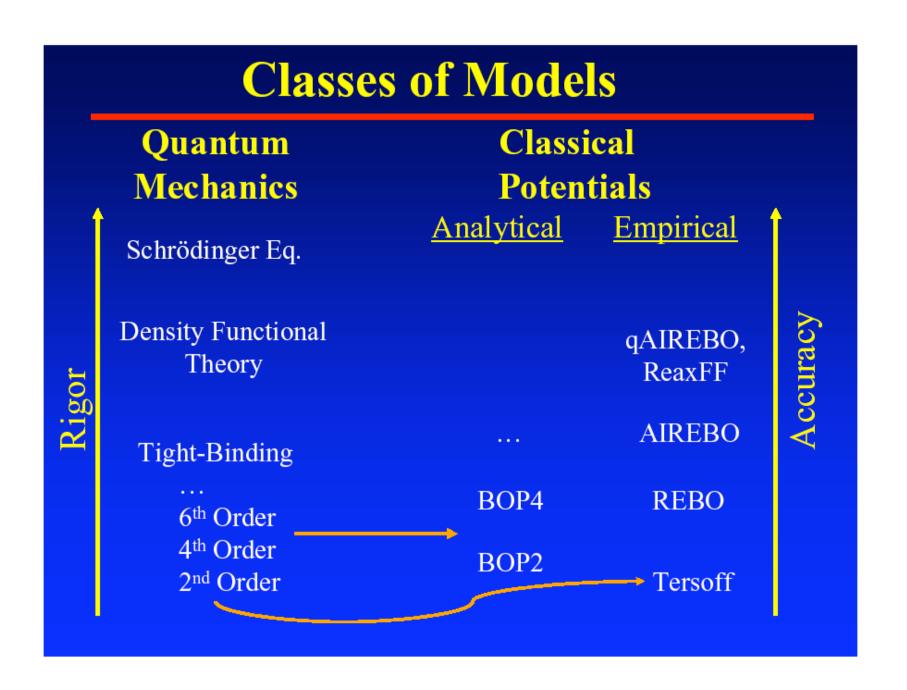


- (intuition, compare to experiment, compare to QM)
- MUCH faster than QM; can be applied to bigger systems

## QM and FF-based approaches to reactive MD

- Option 1: Burn CPUs with QM/MD (e.g. Raty et al., PRL 2005)
- Option 2: use empirical assumptions to make QM faster (semiempirical methods)
  - CINDO/MINDO/AM1/MOPAC (e.g. Pople and Segal, JCP 1966; Stewart, J. Comp. Chem. 1989)
  - Tight-binding (e.g. McMahan and Klepeis, PRB 1997)
  - Analytical Bond Order Potentials (e.g. Pettifor and Oleinik, PRB 1999)
- Option 3: Add ability to simulate reactions to FF-method (empirical bond-order based force fields)
  - Tersoff/Brenner /AIREBO (Tersoff, PRL 1988; Brenner, PRB 1990, Stuart et al., JCP 2000)
  - LCBOP (de Los et al., PRB 2005)
  - EDIP (e.g. Bazant and Kaxiras, PRL 1996)
  - ReaxFF (e.g. van Duin et al. JPC-A 2001)





from Steve Stuart, Clemson University

# How to make a force field reactive: building the ReaxFF reactive force field

- Concepts of covalent non-reactive force fields
- Introduction of bond orders
- Non-bonded interactions in a reactive force field
- Charge polarization
- Current status of the ReaxFF method
- ReaxFF program, in- and output files

## Concepts of covalent non-reactive force fields

$$E_{system} = E_{bond} + E_{angle} + E_{torsion} + E_{vdWaals} + E_{Coulomb}$$

$$E_{bond} = k_b (r - r_o)^2$$

$$E_{angle} = k_v (\varphi - \varphi_o)^2$$

$$E_{torsion} = V_2 \cdot (1 - \cos 2\omega) + V_3 \cdot (1 + \cos 3\omega)$$

$$E_{vdWaals} = D_{ij} \left\{ \exp \left[ \alpha_{ij} \cdot \left( 1 - \frac{r_{ij}}{r_{vdW}} \right) \right] - 2 \cdot \exp \left[ \frac{1}{2} \alpha_{ij} \cdot \left( 1 - \frac{r_{ij}}{r_{vdW}} \right) \right] \right\}$$

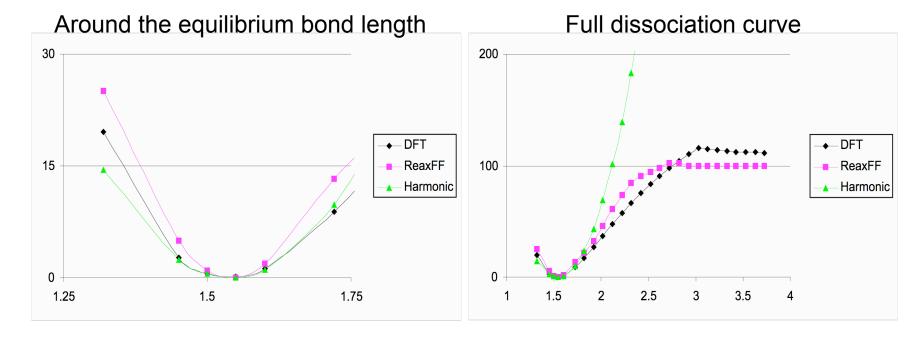
$$E_{Coulomb} = C \cdot \frac{q_i \cdot q_j}{r_{ij}}$$

- Can be parameterized to describe structures and energies close to equilibrium
- Expansion with anharmonic terms improves reliability and application range
- Does not dissociate bonds properly

System energy description for a simple harmonic non-reactive force field

#### Failure of the harmonic model

#### C-C bond stretching in Ethane



- Although the harmonic approximation can describe the bond stretching around the equilibrium it cannot describe the bond dissociation.
- Harmonic force field needs to use multiple atom types to distinguish single, double and triple bonded carbons.

# From non-reactive to reactive force fields: key features of ReaxFF

- -To get a smooth transition from nonbonded to single, double and triple bonded systems ReaxFF employs a bond length/bond order relationship. Bond orders are updated every iteration.
- -All connectivity-dependent interactions (i.e. valence and torsion angles) are made bond-order dependent, ensuring that their energy contributions disappear upon bond dissociation.
- Nonbonded interactions (van der Waals, Coulomb) are calculated between every atom pair, irrespective of connectivity. Excessive close-range nonbonded interactions are avoided by shielding.
- ReaxFF uses a geometry-dependent charge calculation scheme that accounts for polarization effects.

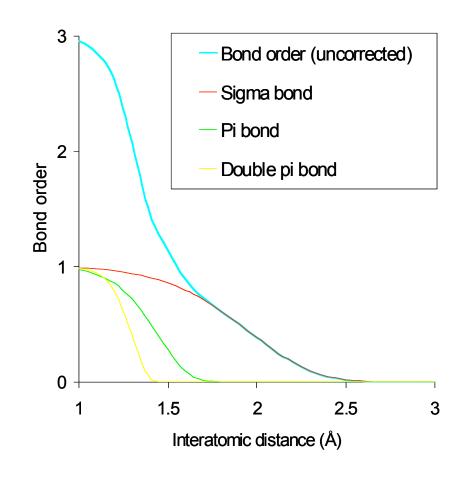
#### Introduction of bond orders

#### Calculation of bond orders from interatomic distances

$$BO'_{ij} = \exp\left[p_{bo,1} \cdot \left(\frac{r_{ij}}{r_o^{\sigma}}\right)^{p_{bo,2}}\right]$$

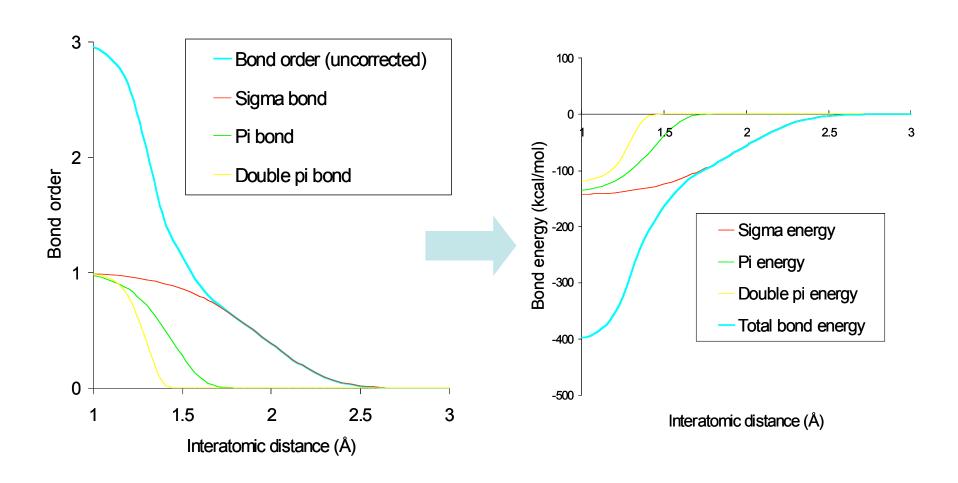
$$+ \exp\left[p_{bo,3} \cdot \left(\frac{r_{ij}}{r_o^{\pi}}\right)^{p_{bo,4}}\right]$$

$$+ \exp\left[p_{bo,5} \cdot \left(\frac{r_{ij}}{r_o^{\pi\pi}}\right)^{p_{bo,6}}\right]$$



#### Calculation of bond energy from bond orders

$$E_{bond} = -D_e^{\sigma} \cdot BO_{ij}^{\sigma} \cdot f(BO_{ij}^{\sigma}) - D_e^{\pi} \cdot BO_{ij}^{\pi} - D_e^{\pi\pi} \cdot BO_{ij}^{\pi\pi}$$



#### Connectivity: differences in program structure

#### Non-reactive force field

1:  $x_1 y_1 z_1$ 

2: x<sub>2</sub> y<sub>2</sub> z<sub>2</sub>

3:  $x_3 y_3 z_3$ 

4: x<sub>4</sub> y<sub>4</sub> z<sub>4</sub>

5: x<sub>5</sub> y<sub>5</sub> z<sub>5</sub>

6:  $x_6 y_6 z_6$ 

Atom positions

1:2 3 4

2:156

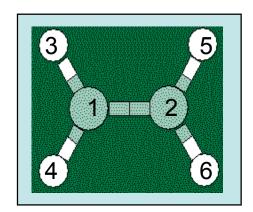
3: 1

4: 1

5: 2

6: 2

Connection table



#### Reactive force field

1:  $x_1 y_1 z_1$ 

2: x<sub>2</sub> y<sub>2</sub> z<sub>2</sub>

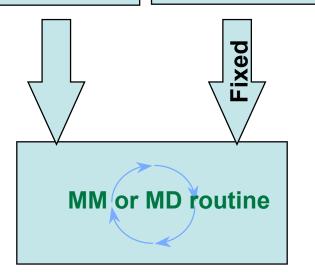
3:  $x_3 y_3 z_3$ 

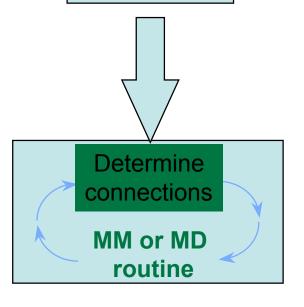
4: x<sub>4</sub> y<sub>4</sub> z<sub>4</sub>

5: x<sub>5</sub> y<sub>5</sub> z<sub>5</sub>

6:  $x_6 y_6 z_6$ 

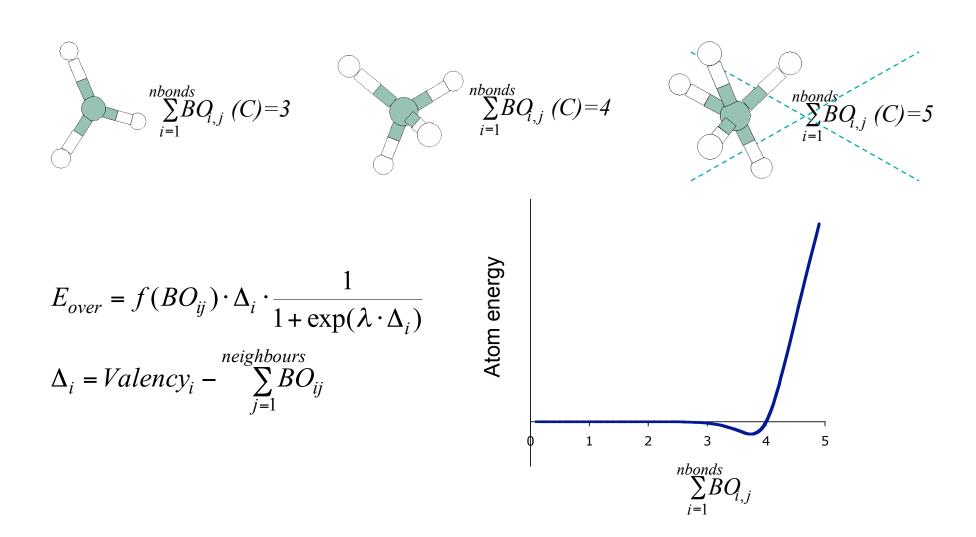
Atom positions





## Dealing with overcoordination

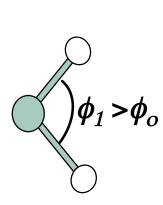
Avoid unrealistically high amounts of bond orders on atoms



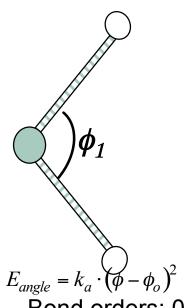
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- -ReaxFF uses a geometry-dependent charge calculation scheme that accounts for polarization effects.

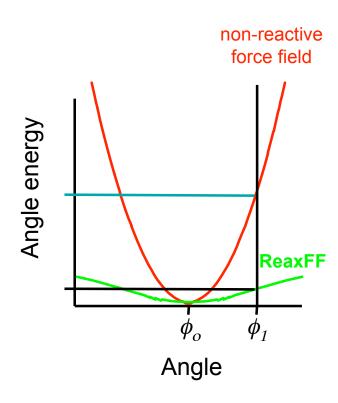
## Valence angles



Bond orders: 1



Bond orders: 0.4



Non-reactive:  $E_{angle} = k_a \cdot (\phi - \phi_o)^2$ 

Reactive: 
$$E_{angle} = \left[1 - \exp(\lambda_3 \cdot BO_a^3)\right] \left[1 - \exp(\lambda_3 \cdot BO_b^3)\right] \left\{k_a - k_a \exp[-k_b \cdot (\phi - \phi_o)^2]\right\}$$

$$BO_a = \text{Bond ord}$$

Bond-order dependent part

$$BO_a$$
 = Bond order a  
 $BO_b$  = Bond order b  
 $\phi$  = Angle  
 $\phi_o$  = Equilibrium angle

## Torsion and conjugation

#### - Torsion angle energy term

$$E_{tors} = f_{10}(BO_{ij}, BO_{jk}, BO_{jk}) \cdot \sin\Theta_{ijk} \cdot \sin\Theta_{jkl} \cdot \left[\frac{1}{2}V_1 \cdot \left(1 + \cos\omega_{ijkl}\right) + \frac{1}{2}V_2 \cdot \exp\left\{p_{tor1} \cdot \left(2 - BO_{jk}^{\pi} - f_{11}(\Delta_j, \Delta_k)\right)^2\right\} \cdot \left(1 - \cos2\omega_{ijkl}\right) + \frac{1}{2}V_3 \cdot \left(1 + \cos3\omega_{ijkl}\right)\right]$$

#### - 4-body (torsion) conjugation term

$$E_{conj} = f_{12}(BO_{ij}, BO_{jk}, BO_{kl}) \cdot p_{\cot 1} \cdot \left[ 1 + \left( \cos^2 \omega_{ijkl} - 1 \right) \cdot \sin \Theta_{ijk} \cdot \sin \Theta_{jkl} \right]$$

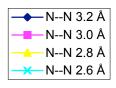
- Bond order dependent
- Tested against a large database of PAH heats of formation

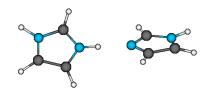
#### - 3-body (angle) conjugation term

$$E_{coa} = p_{coa1} \cdot \frac{1}{1 + \exp\left(p_{coa2} \cdot \Delta_{j}^{val}\right)} \cdot \exp\left[-p_{coa3} \cdot \left(-BO_{ij} + \sum_{n=1}^{neighbours(i)} BO_{in}\right)^{2}\right] \cdot \exp\left[-p_{coa3} \cdot \left(-BO_{jk} + \sum_{n=1}^{neighbours(i)} BO_{kn}\right)^{2}\right] \cdot \exp\left[-p_{coa4} \cdot \left(BO_{ij} - 1.5\right)^{2}\right] \cdot \exp\left[-p_{coa4} \cdot \left(BO_{ij} - 1.5\right)^{2}\right]$$

## Hydrogen bonds

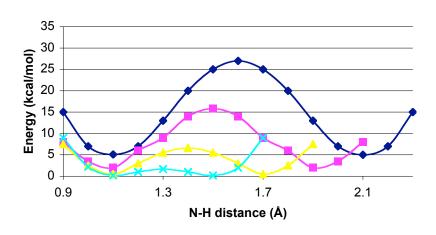
$$E_{Hbond} = p_{hb1} \cdot \left[ 1 - \exp(p_{hb2} \cdot BO_{XH}) \right] \cdot \exp\left[ p_{hb3} \left( \frac{r_{hb}^{o}}{r_{HZ}} + \frac{r_{HZ}}{r_{hb}^{o}} - 2 \right) \right] \cdot \sin^{8} \left( \frac{\Theta_{XHZ}}{2} \right)$$



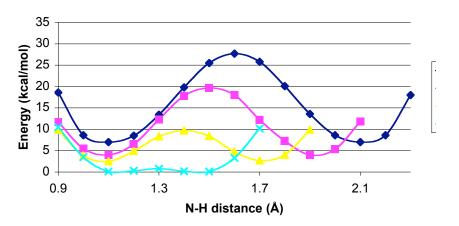


- Bond order dependent
- Tested for a wide range of hydrogen transfer reactions
- Tested for bulk water and proton diffusion in water

#### H-transfer in [Im-Im]+: QM-data



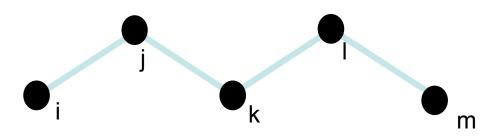
#### H-transfer in [Im-Im]+: ReaxFF-data



## Key features

- -To get a smooth transition from nonbonded to single, double and triple bonded systems ReaxFF employs a bond length/bond order relationship. Bond orders are updated every iteration.
- All connectivity-dependent interactions (i.e. valence and torsion angles) are made bond-order dependent, ensuring that their energy contributions disappear upon bond dissociation.
- Nonbonded interactions (van der Waals, Coulomb) are calculated between every atom pair, irrespective of connectivity. Excessive close-range nonbonded interactions are avoided by shielding.
- -ReaxFF uses a geometry-dependent charge calculation scheme that accounts for polarization effects.

#### Nonbonded interactions



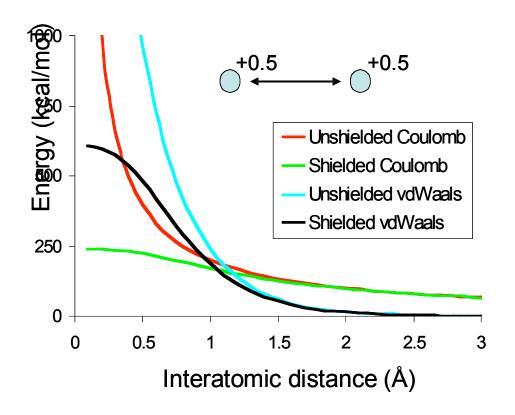
Non-reactive force field: ignore vdWaals and Coulomb interactions between atoms sharing a bond (I-j, j-k, k-l and l-m) or a valence angle (I-k, j-l and k-m).

These exception rules are very awkward when trying to describe reactions.

ReaxFF: calculate nonbonded interactions between *all* atom pairs, regardless of connectivity.

To avoid excessive repulsive/attractive nonbonded interactions at short distances both Coulomb and van der Waals interactions are shielded in ReaxFF.

#### Shielded vdWaals and Coulomb interactions



$$E_{Coulomb} = C \cdot \frac{q_i \cdot q_j}{\left\{r_{ij}^3 + \left(1/\gamma_{ij}\right)^3\right\}^{1/3}}$$

Shielded Coulomb potential

vdWaals: Shielded Morse potential

- For metals ReaxFF only uses bond energy, overcoordination, vdWaals and Coulomb-terms (no angle or dihedrals)
- vdWaals and overcoordination terms serve as a density-dependent repulsive term (as used in EAM-potentials [Daw and Baskes, PRB 1984] ), allowing ReaxFF to describe bulk metals

## Key features

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- ReaxFF uses a geometry-dependent charge calculation scheme that accounts for polarization effects.

## Charge polarization

- Assign one electronegativity and hardness to each element; optimize these parameters against QM-charge distributions

- Use system geometry in solving electronegativity equilibration equations in every iteration

$$\frac{\partial E}{\partial q_1} = \chi_1 + 2q_1\eta_1 + C \cdot \sum_{j=1}^{n} \frac{q_j}{\left(r_{1,j}^3 + \left(\frac{1}{\gamma_{1,j}}\right)^3\right)^{\frac{1}{3}}}$$

$$\frac{\partial E}{\partial q_2} = \chi_2 + 2q_2\eta_2 + C \cdot \sum_{j=1}^n \frac{q_j}{\left(r_{2,j}^3 + \left(\frac{1}{\gamma_{2,j}}\right)^3\right)^{\frac{1}{3}}}$$

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$$\frac{\partial E}{\partial q_n} = \chi_n + 2q_n \eta_n + C \cdot \sum_{j=1}^n \frac{q_j}{\left(r_{n,j}^3 + \left(\frac{1}{\gamma_{n,j}}\right)^3\right)^{\frac{1}{3}}}$$

$$\sum_{i=1}^{n} q_i = 0$$

EEM-method (Mortier et al., JACS 1986); shielding: Janssens et al. J.Phys.Chem. 1995.

Similar to Qeq-method (Rappe and Goddard, J. Phys. Chem. 1991) with empirical shielding correction.

 $\chi$ : atom electronegativity

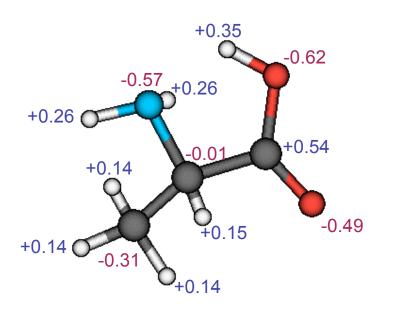
η: atom hardness

γ: shielding parameter

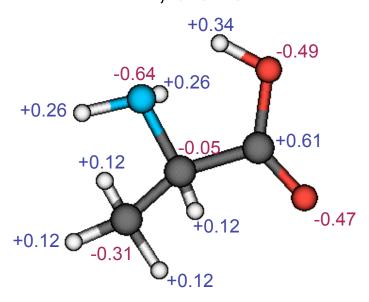
*r*: interatomic distances

q:atom charge

ReaxFF charges



QM Mulliken charges DFT; 6-31G\*\*

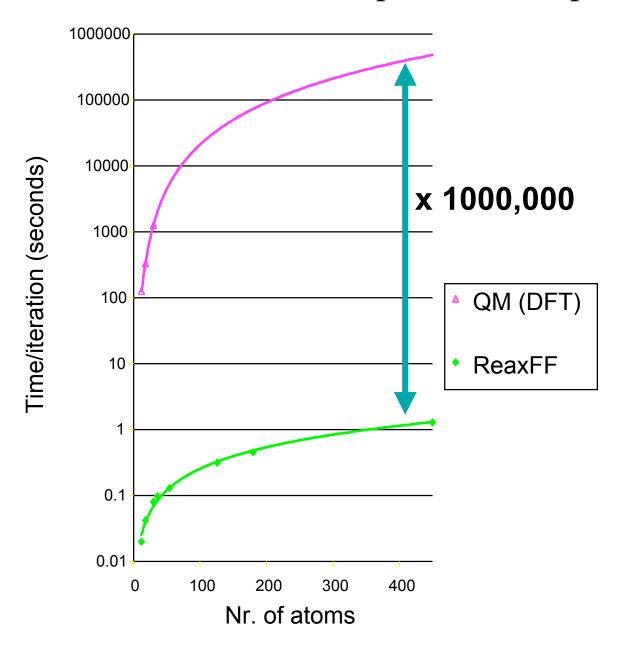


- Good reproduction of Mulliken charges (similar concepts)
- Combined with 1-2 Coulomb-interactions, this enables ReaxFF to simulate polarization effects on local chemistry
- EEM/Qeq methods work well around equilibrium; incorrect description of charge flow at high compression and dissociation (Chen and Martinez, Chem.Phys.Lett. 2006)
- Most expensive part of the reactive force field; needs to be updated every MD-step and forces sub-femtosecond steps

#### General rules for ReaxFF

- MD-force field; no discontinuities in energy or forces even during reactions.
- User should not have to pre-define reactive sites or reaction pathways; potential functions should be able to automatically handle coordination changes associated with reactions.
- Each element is represented by only 1 atom type in the force field; force field should be able to determine equilibrium bond lengths, valence angles etc. from chemical environment.

## ReaxFF Computational expense

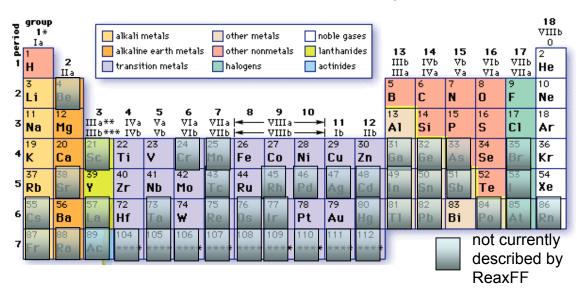


- -ReaxFF allows for reactive MD-simulations on systems containing more than 1000 atoms
- ReaxFF is 10-50 times slower than non-reactive force fields
- Better scaling than QM-methods (NlogN for ReaxFF, N³ (at best) for QM

## Current development status of ReaxFF

- ReaxFF combines covalent, metallic and ionic elements allowing applications all across the periodic table
- All ReaxFF descriptions use the same potential functions, enabling application to interfaces between different material types
- Code has been distributed to over 60 research groups
- Parallel ReaxFF (GRASP/Reax and USC/Reax) available

#### ReaxFF transferability



#### Some ReaxFF publications

- -C/H:van Duin et al, JPC-A 2001, 105, 9396; Org. Geochem.2003, 34, 515; Chen et al, PR-B 2005, 72, 085416, Han et al. Appl. Phys. Lett. 2005, 86, 203108.
- C/N/O/H:Strachan et al, PRL 2003,91,09301;
   JCP 2005,122,054502; van Duin et al, JACS 2005, 127, 11053
- -Metals: Zhang et al, PRB 2004,69,045423; Nielson et al., JPC-A 2005, 109, 493; Su et al., PRB 75, 2007; Ludwig et al, JPC-B 2006; Cheung et al, JPC-A 2005, 109, 851
- Si/SiO/SiC: van Duin et al., JPC-A 2003,
  107, 3803; Chenoweth et al., JACS 2005,
  127, 7192; Buehler et al., PRL 2006, 96,
  095505; Buehler et al, PRL 2007.

## Parallel ReaxFF: GRASP/ReaxFF

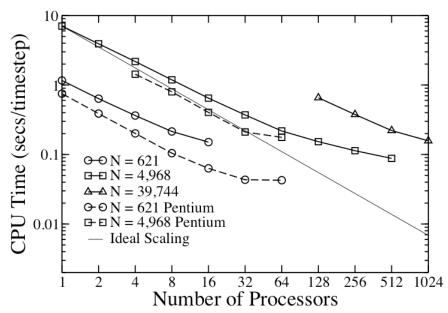
- ReaxFF is incorporated in the Grasp-framework (Aidan Thompson, Sandia) allowing parallel ReaxFF-simulations.

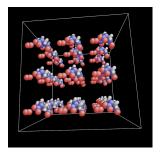
#### **GRASP Performance on BG/L with ReaxFF**

Comparison with Liberty Cluster (3GHz Pentium+Myrinet)

## RDX Explosive with Oxygen

ReaxFF force field with charge equilibration



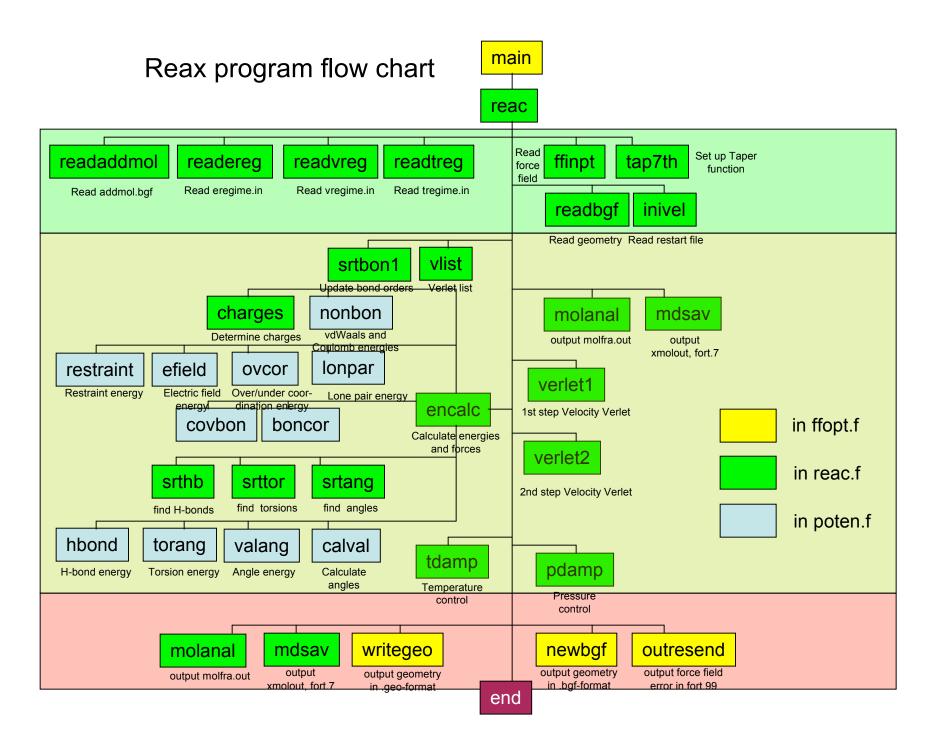


- ReaxFF enables reactive modelling
- •Si/SiO<sub>2</sub>, Explosives, film growth
- •Each process computes energy and forces for a virtual non-periodic cluster
- Low communication, duplicated computation ~ P(N/P)<sup>2/3</sup>
- •Uses Van Duin's Fortran subroutines for force calculation.
- Good strong scaling
- Sweet spot: 5000 atoms/processor

## ReaxFF program, in- and output files

#### ReaxFF program structure

- Written in Fortran-77
- Library independent
- Text-based interface (graphical interface is developed within CMDF)
- Installed on various computers and operating systems (Linux, Windows, Macs)
- Code divided in 6 parts:
  - reac.f (10640 lines): general MD routines
  - poten.f (3034 lines): energy equations
  - ffopt.f (1581 lines): force field optimization
  - shanno (1718 lines): energy minimization
  - vibra.f (1194 lines): vibrational frequencies
  - blas.f (613 lines): BLAS-routines
  - program parameters in cbka.blk



### Overview ReaxFF in- and output files

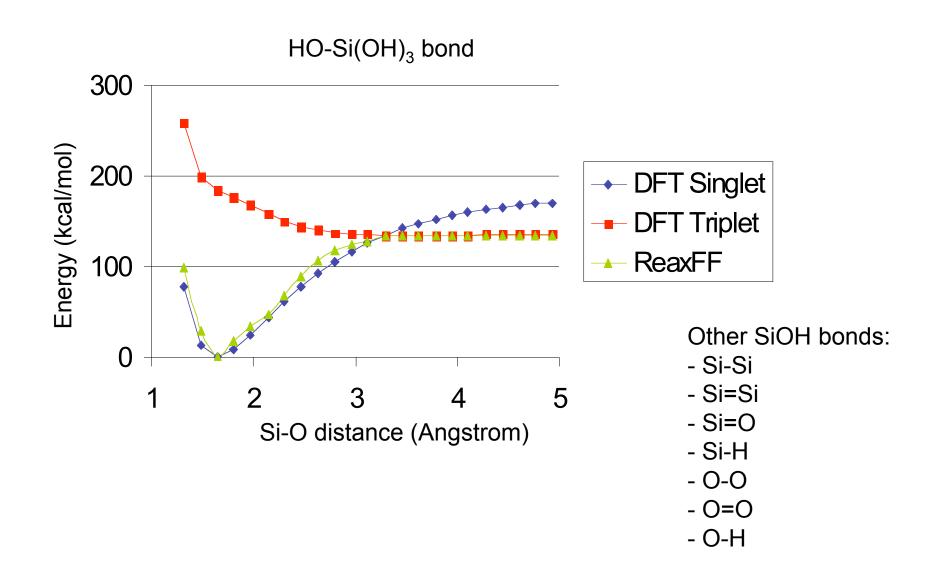
#### Mandatory input files

- geo (input geometry)
- control (run control parameters)
- ffield (force field parameters)
- exe (UNIX-script)

### Force field development for Si/SiO systems

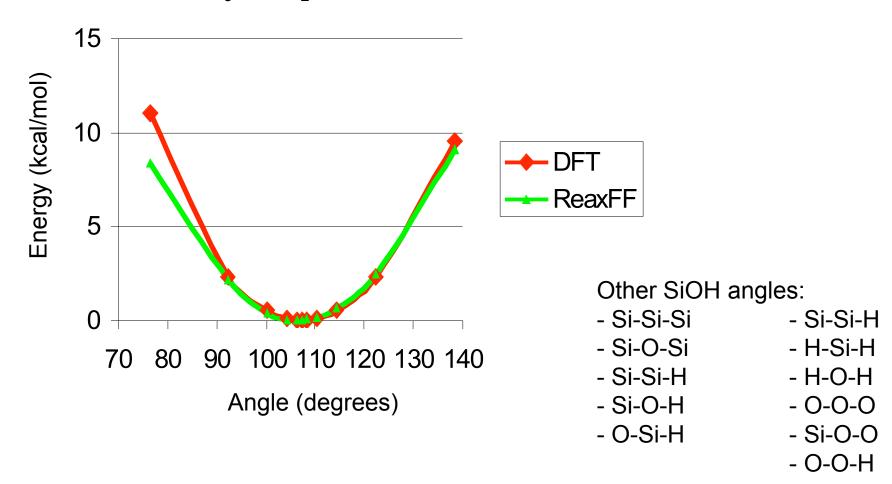
- Concept: build a QM-based database (training set) that described reactive and non-reactive aspects of the material and optimize ReaxFF to reproduce these QM-data.
- Bigger (more extensive) training sets yield more transferable force fields (but longer development time!)
- Things to include in training sets
  - Bond dissociation
  - Angle bending
  - Under/overcoordination
  - Key reactions, including transition states
  - Charges
  - Condensed phase data: Equations of state, heats of formation (experiment)

### Bond energy

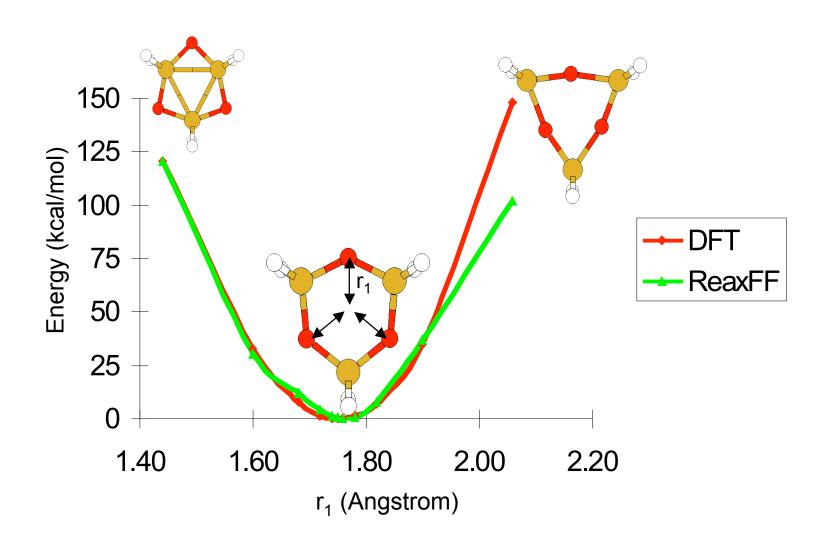


## Valence angle bending 1. Individual valence angles

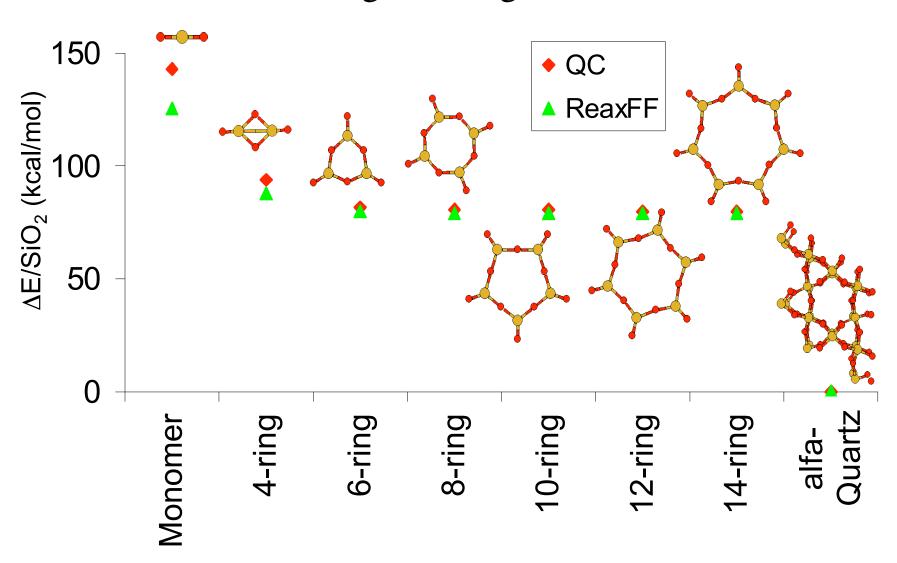
H<sub>3</sub>Si-SiH<sub>2</sub>-OH angle



# Valence angle bending 2. Ring deformation



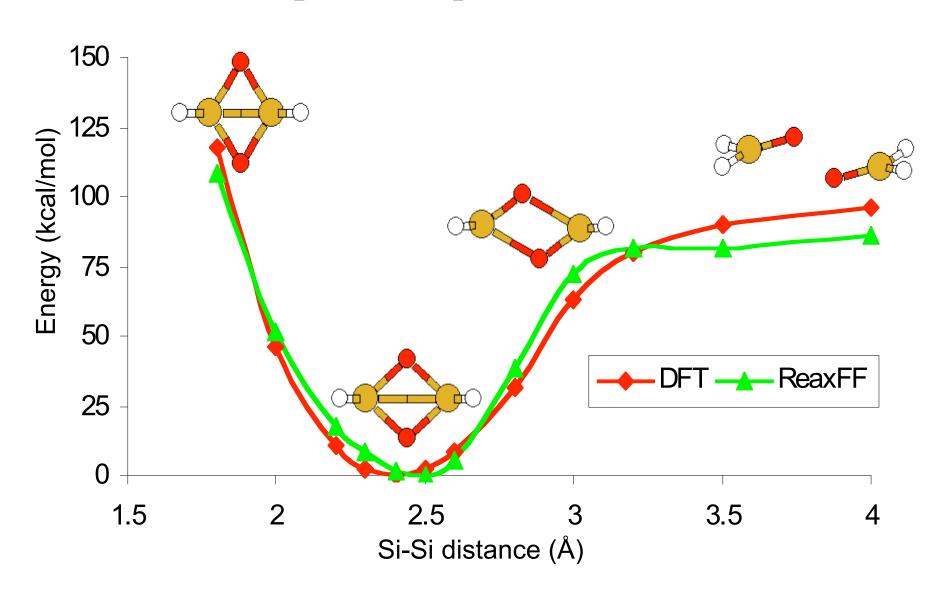
# Valence angle bending 3. Ring size/ring strain



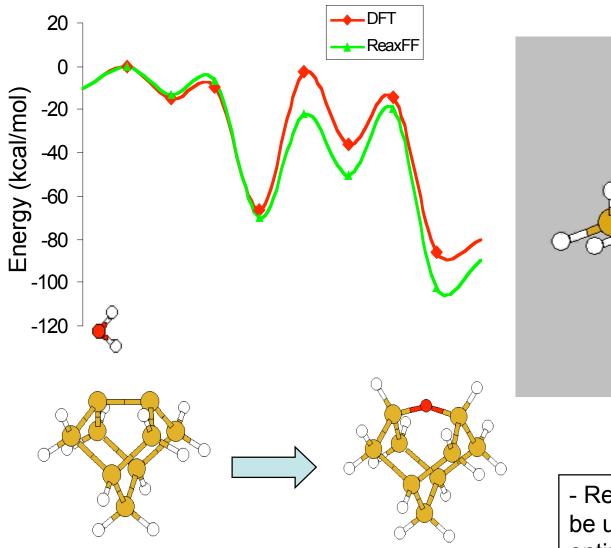
### Over/undercoordination

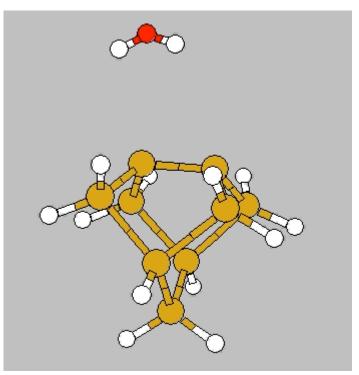
$$\Delta E (DFT)$$
  $\Delta E (ReaxFF)$   
Si(OH)<sub>4</sub>+ HO-OH  $\longrightarrow$  Si(OH)<sub>6</sub> +60.9 kcal/mol +48.2 kcal/mol +3Si-O-SiH<sub>3</sub>+ H<sub>3</sub>Si-SiH<sub>3</sub>  $\longrightarrow$  O(SiH<sub>3</sub>)<sub>4</sub> +102.5 kcal/mol +87.4 kcal/mol

Reactions
1.  $H_2Si=O + H_2Si=O \rightarrow 4$ -ring

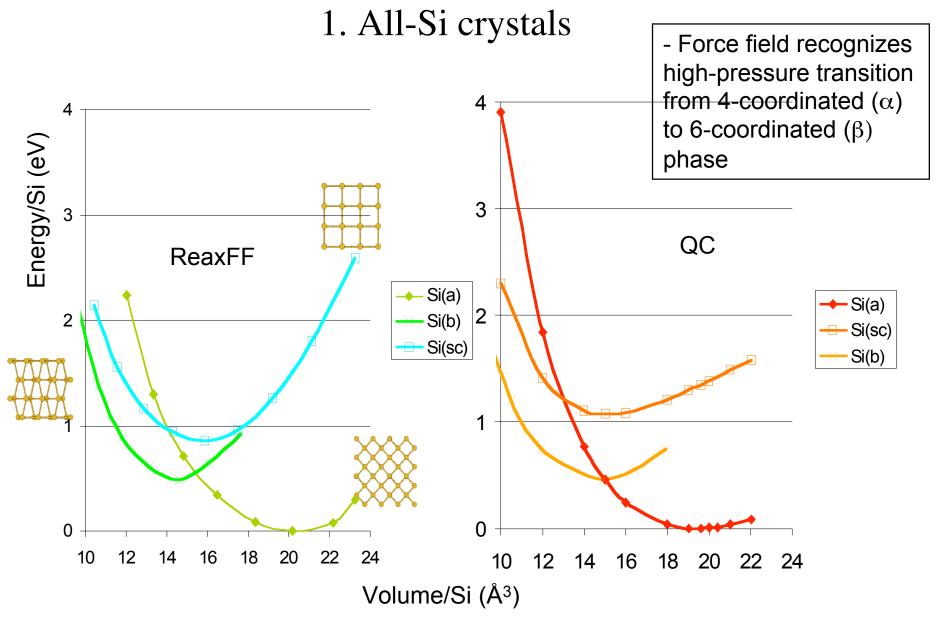


# Reactions 2. H<sub>2</sub>O- incorporation in a Si-cluster

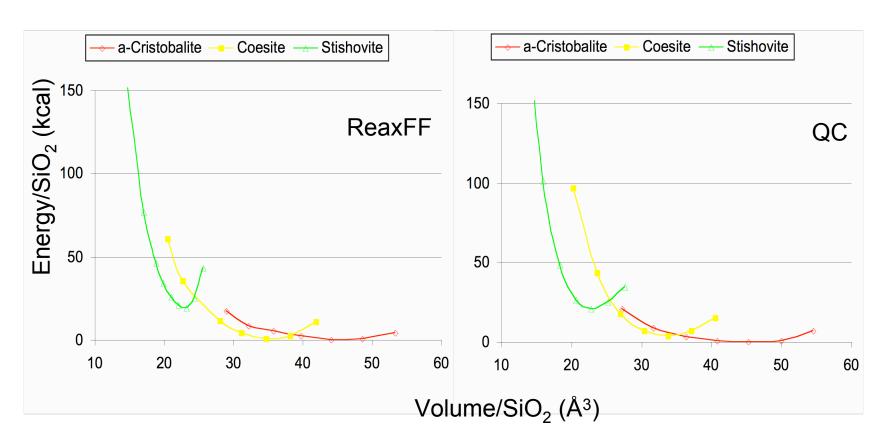




- Reactive force field can be used to simulate the entire reaction pathway Equations of state crystals

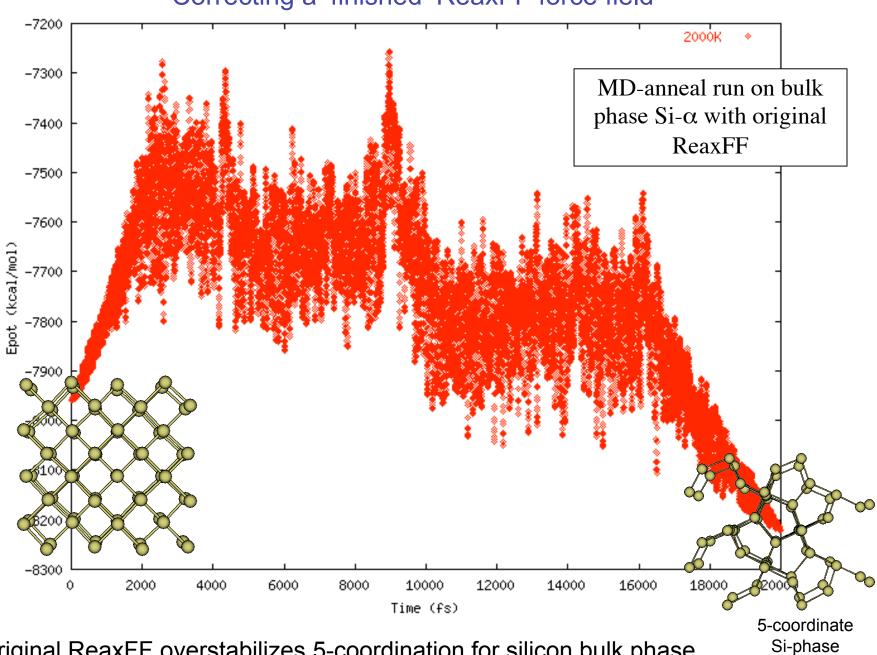


# Compression/expansion crystals 2. Silicon oxide crystals



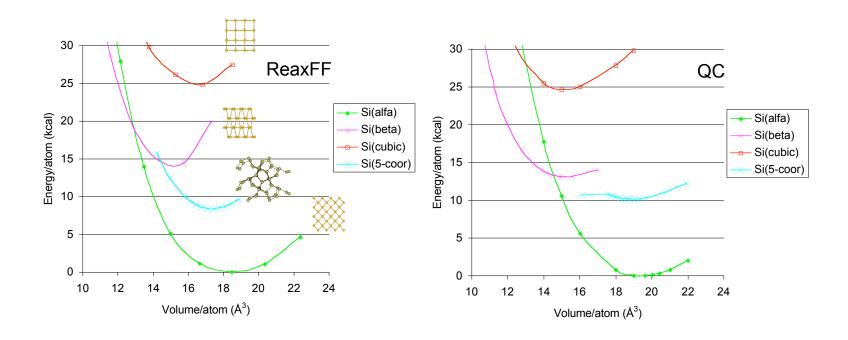
- ReaxFF reproduces the QC-data for both the clusters as well as the condensed phases.

#### Correcting a 'finished' ReaxFF force field

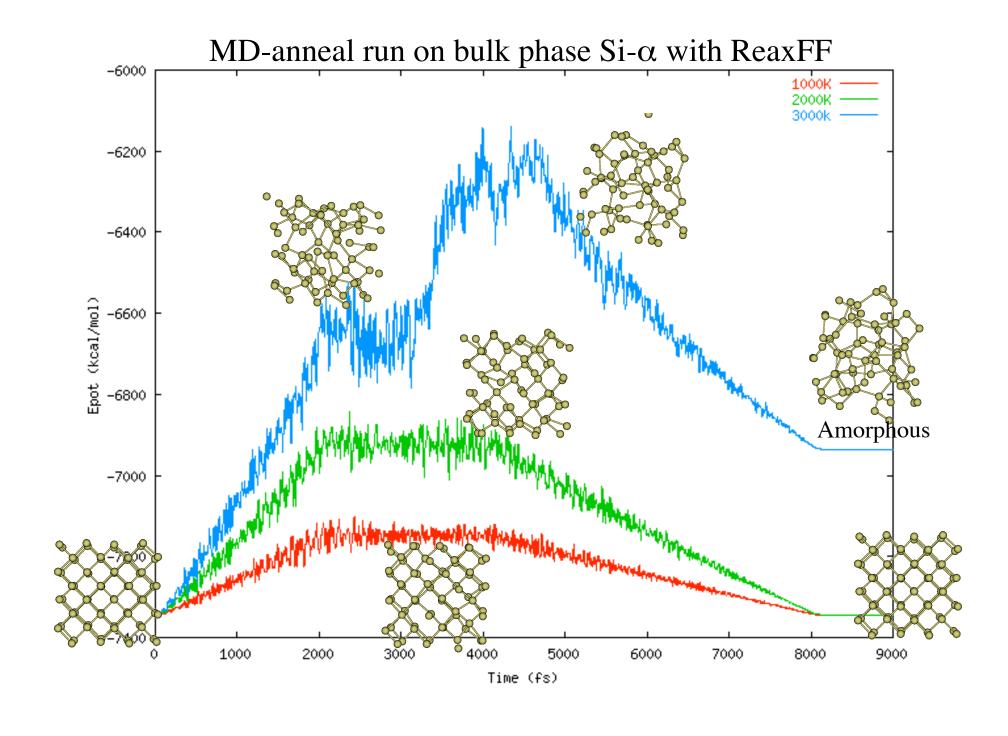


- Original ReaxFF overstabilizes 5-coordination for silicon bulk phase

#### Re-optimize ReaxFF with equation of state for 5-coordinate Si-phase



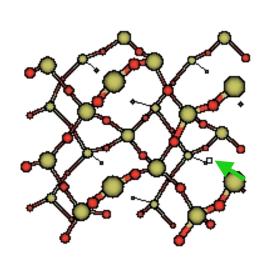
- Re-optimized ReaxFF gets proper stability for 5-coordinate Si-phase
- 5-coordinate phase is more stable than 6-coordinate  $Si(\beta)$ !
- 5-coordinate Si might be important in amorphous Si

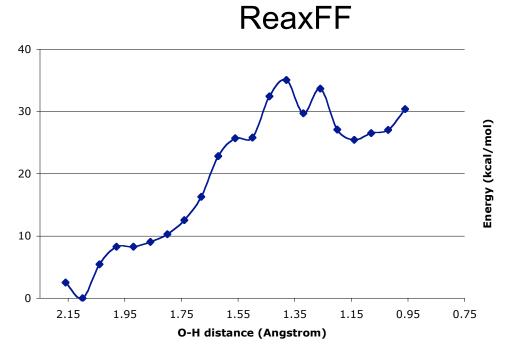


### Applications of the Reax Si/SiO force field

- Hydrogen diffusion in Si/SiO<sub>2</sub> interfaces
- Stability of PDMS polymers

# ReaxFF simulations on H-diffusion and bonding in $\alpha$ -quartz





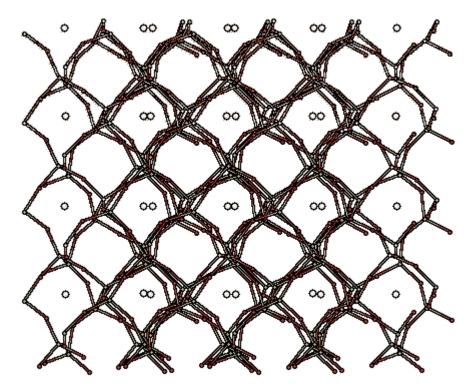
Hydrogen radical in 72-atom α-quartz T=100K; reaction enforce by a moving restraint

Seqquest: E(quartz\_H)-E(quartz+H)= +24 kcal/mol

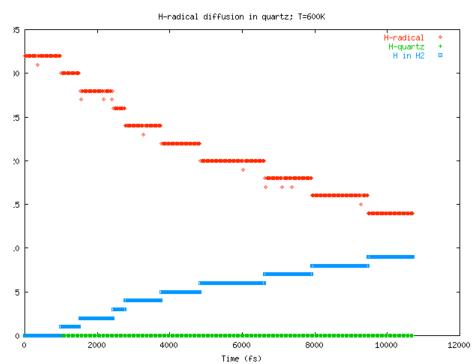
-Good agreement between Reax and SeqQuest reaction energies

## ReaxFF simulations on H-radical diffusion through $\alpha$ -quartz

#### T=600K

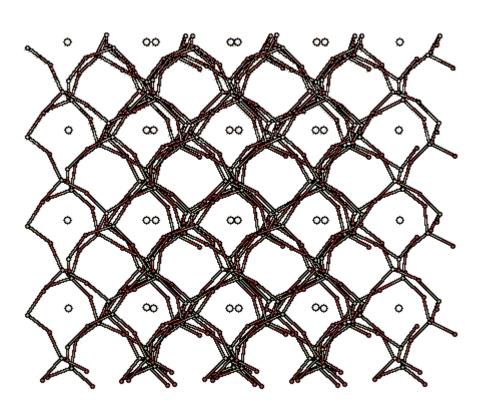


32 H-radicals in 576-atom  $\alpha$ -quartz system



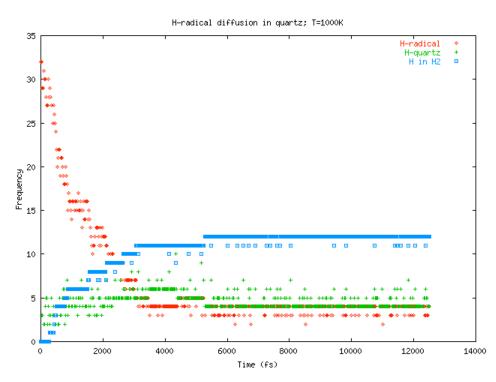
No reaction of H-radicals with lattice oxygens; all H-radicals diffuse and form  $H_2$ 

## ReaxFF simulations on H-radical diffusion through $\alpha$ -quartz



32 H-radicals in 576-atom  $\alpha$ -quartz system

#### T=1000K



-Elevated temperatures result in H-reaction with lattice oxygens. H<sub>2</sub> formation still dominates

#### Conclusions

- ReaxFF has proven to be transferable to a wide range of materials and can handle both complex chemistry and chemical diversity. Specifically, ReaxFF can describe covalent, metallic and ionic materials and interactions between these material types.
- The low computational cost of ReaxFF (compared to QM) makes the method suitable for simulating reaction dynamics for large (>> 1000 atoms) systems (single processor). ReaxFF has now been parallelized, allowing reactive simulations on >>1000,000 atoms.

