

The AMOEBA Polarizable Force Field in OpenMM

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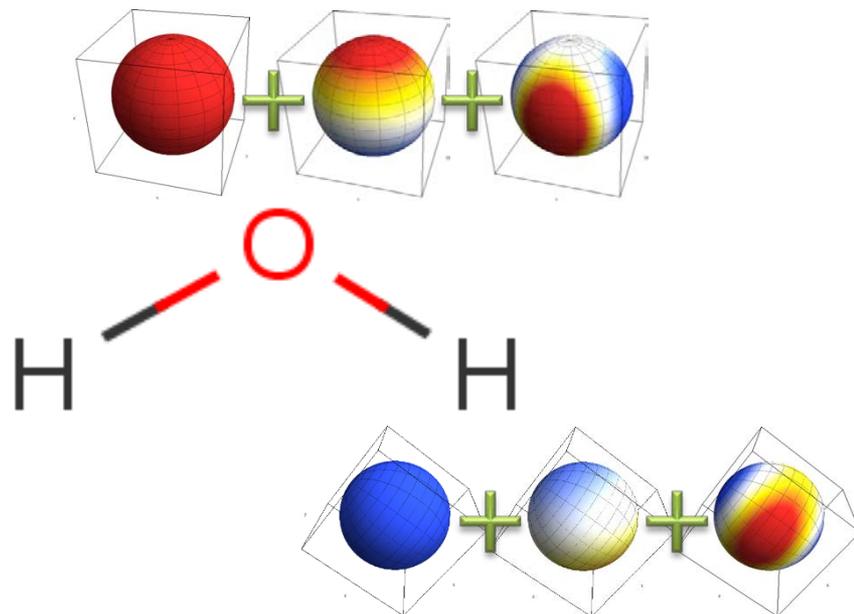
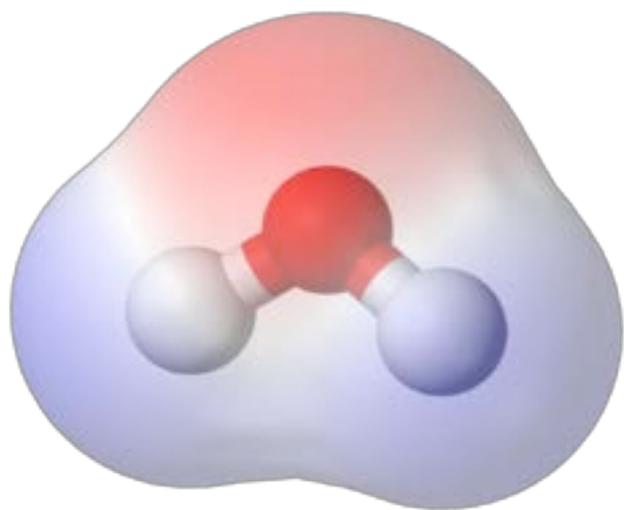
Stanford Department of Chemistry

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Outline

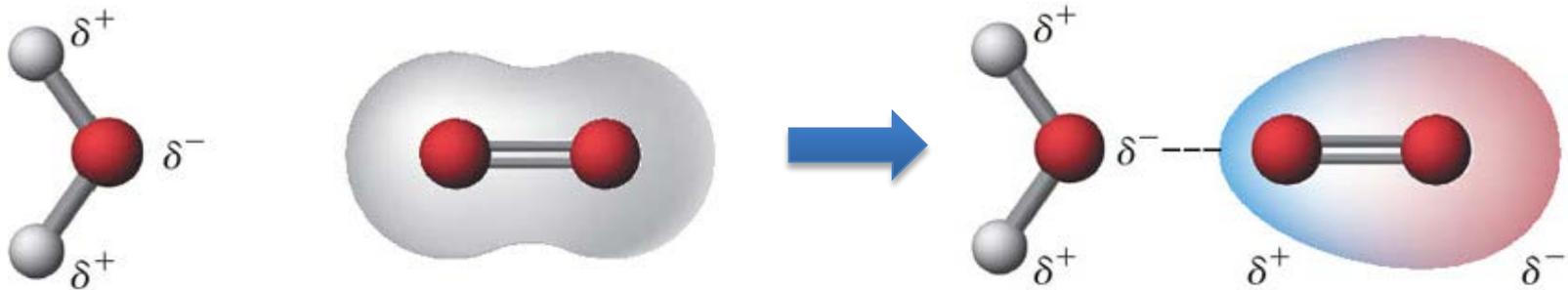
- **Part I: Introduction to the AMOEBA force field**
 - Physical foundations of the AMOEBA force field
 - Validation and comparison to fixed-charge force fields
- Part II: Implementation of AMOEBA in OpenMM
 - Accuracy and performance benchmarks
 - How to set up a simulation



Overview of polarizable force fields

Electronic polarization is a critical part of how a molecule responds to its environment.

Polarization is responsible for *(ion / dipole)-induced dipole* forces



- Electronic polarization happens almost instantly (faster than time step)
- Most force fields use fixed point charges and *cannot describe polarization*
- Point charges are increased from their intrinsic values to describe “average” polarization in the environment
- Thus, point-charge force fields are inherently inaccurate when transferred to different environments! (e.g. water in bulk vs. near a protein)

Introducing the AMOEBA force field

AMOEBA is one of several force fields with the ability to describe electronic polarization.

Some flavors of polarizable force fields:

- Charge-on-spring (a.k.a. Drude) models
- Fluctuating-charge models
- Polarizable point dipoles



AMOEBA belongs to the 3rd category and stands for:

Atomic **M**ultipoles **O**ptimized **E**nergetics for **B**iomolecular **A**pplications

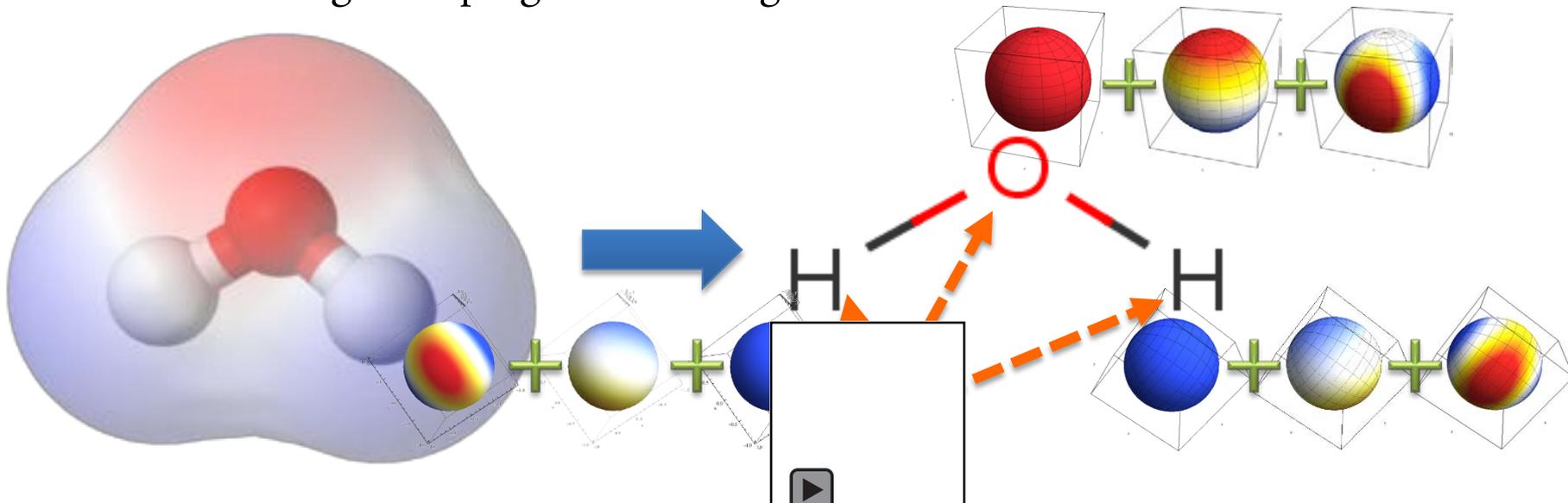
- Developed mainly by Pengyu Ren and Jay Ponder
- Original implementation in TINKER software
- Optimized implementation in OpenMM (topic of this talk)

Polarizable atomic multipoles in AMOEBA

AMOEBA treats electrostatics using a combination of fixed and polarizable multipoles.

Difference between AMOEBA and fixed charge force fields:

- Conventional force fields have point charges on each atom
- AMOEBA puts a point charge, dipole, and quadrupole on each atom
 - Each atom needs to have its own coordinate system
- AMOEBA also adds a polarizable dipole to each atom
 - Short-range damping to avoid singularities



Summary of interactions in AMOEBA

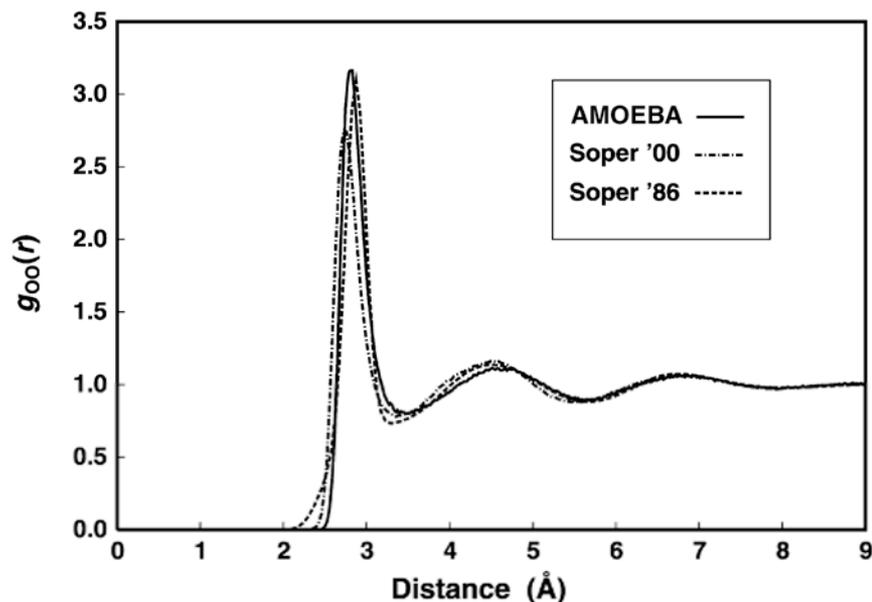
All interaction terms (van der Waals, torsions, etc.) are treated at a higher level of detail.



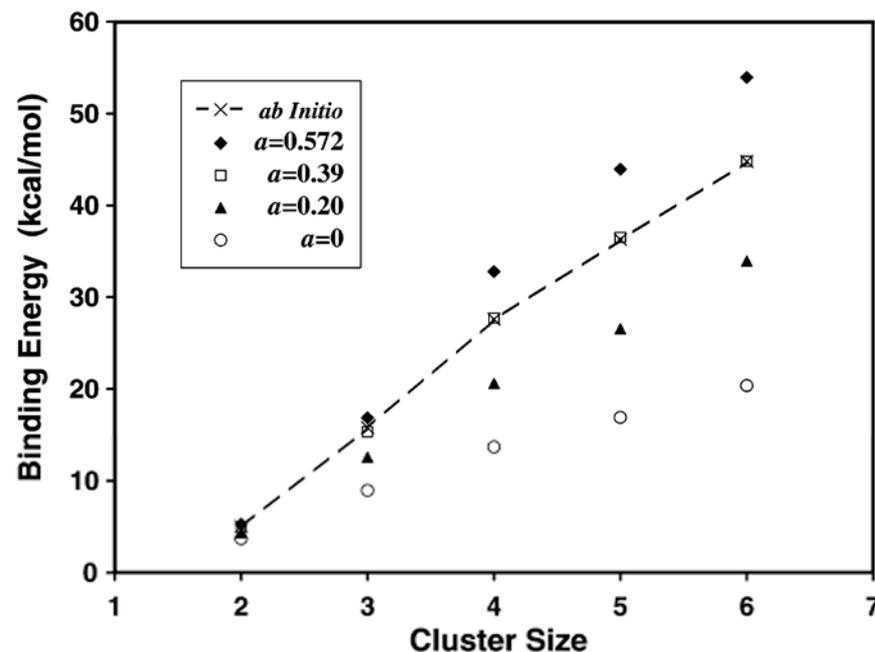
The AMOEBA water model

The AMOEBA water model is capable of describing water in both vapor and liquid phases.

O–O radial distribution function compared to experiment



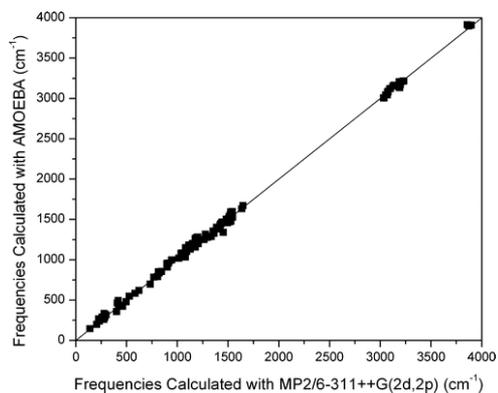
Binding energy of water clusters
(perfect agreement with x's and squares)



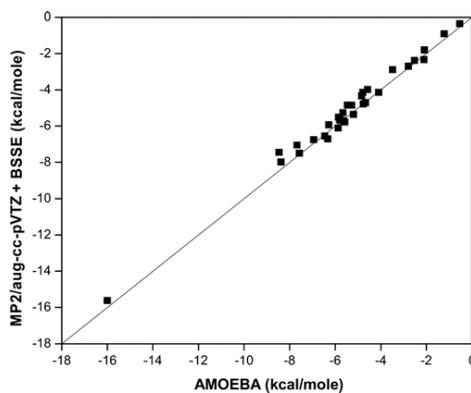
Organic molecules in the AMOEBA force field

A force field for organic molecules has been developed with some validation in the literature.

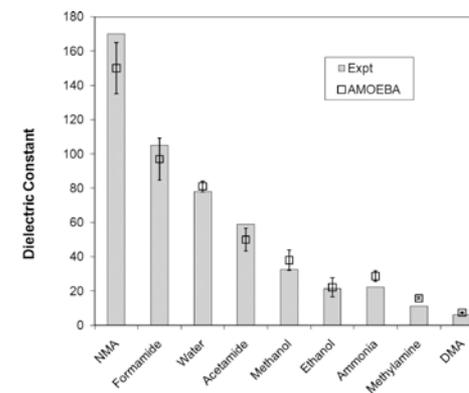
Vibrational frequencies



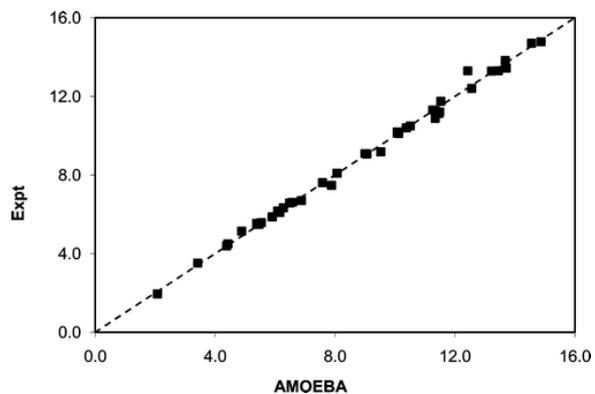
Dimer binding energies



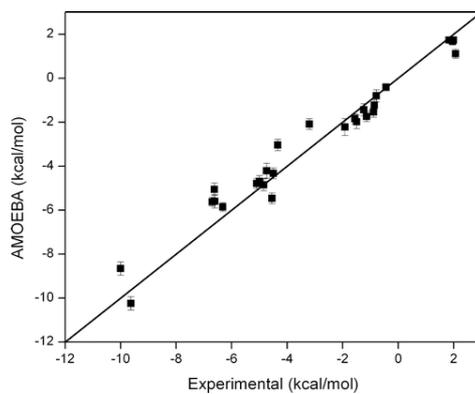
Dielectric constants



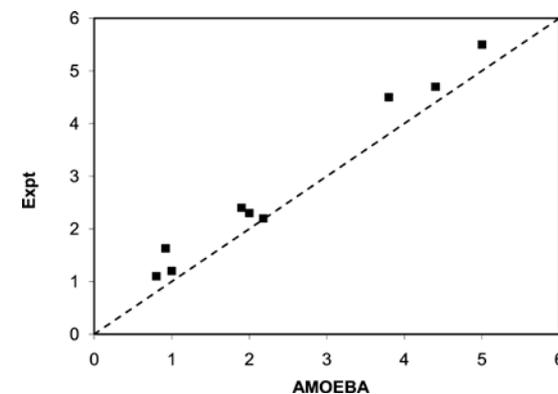
Heats of vaporization



Free energies of solvation

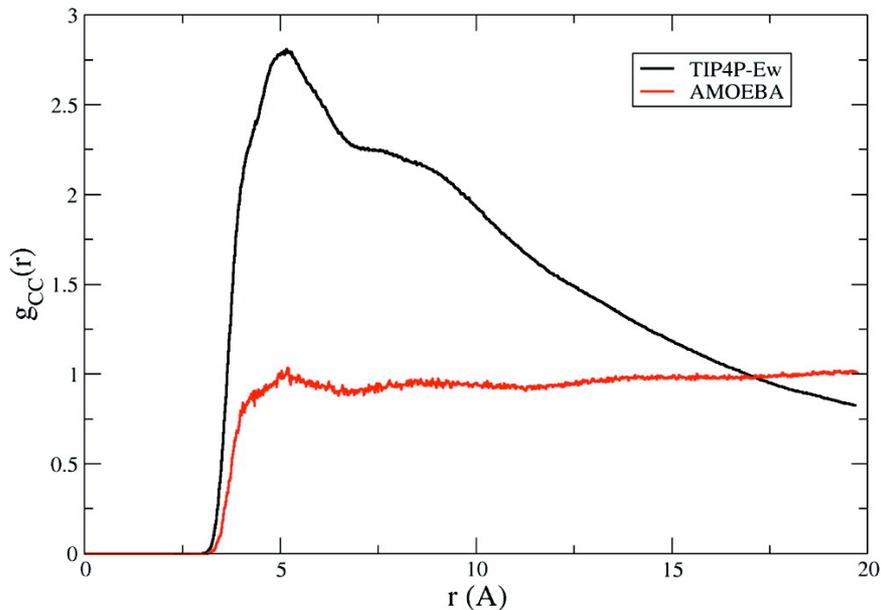


Diffusion constants

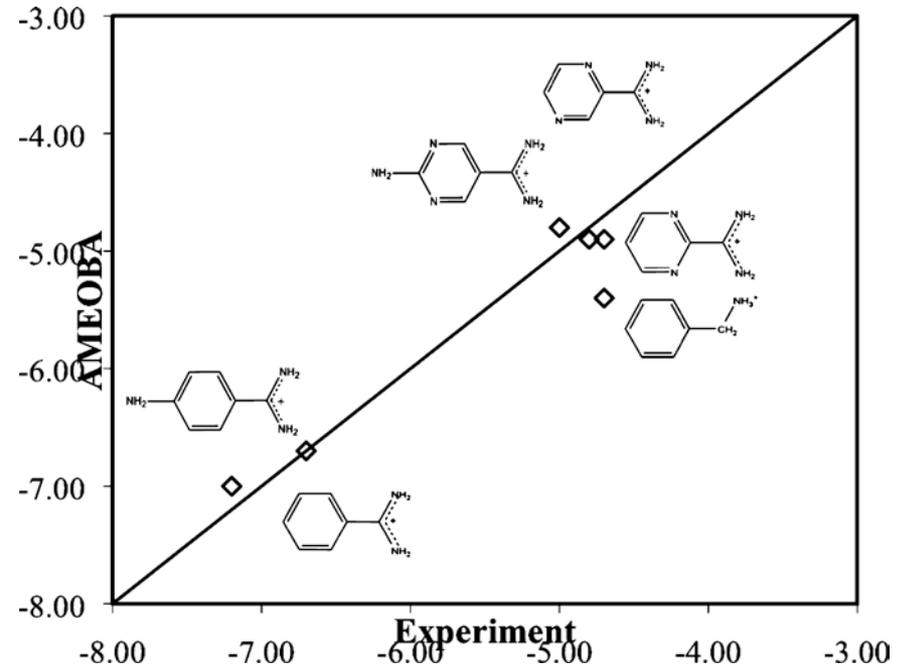


Proteins in the AMOEBA force field

A force field for proteins has also been developed with some validation.



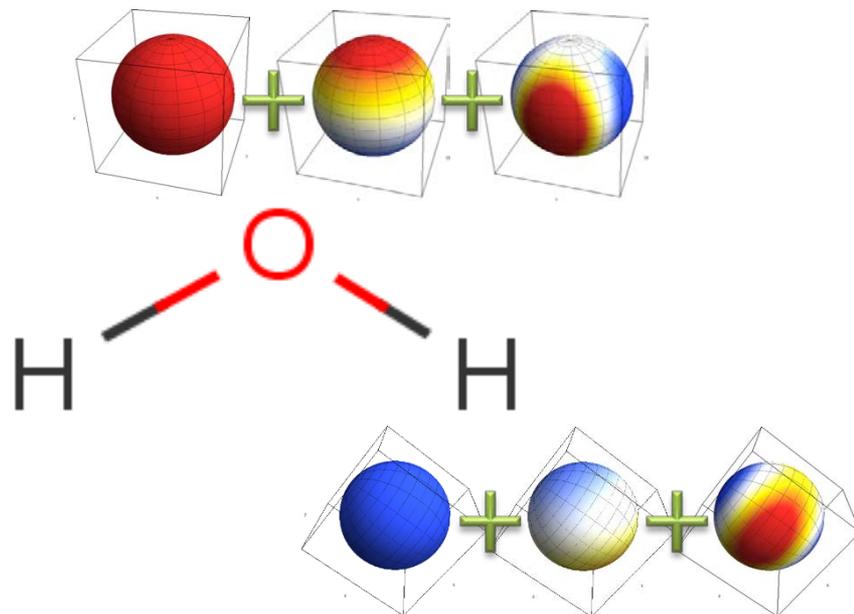
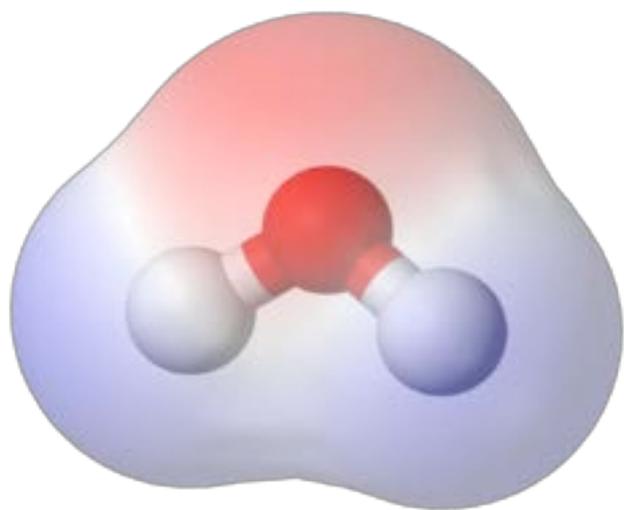
Point-charge force field (black)
wrongly predicts peptide aggregation,
AMOEBA (red) gives correct result



Protein–ligand binding free energies

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Accuracy of the AMOEBA force field

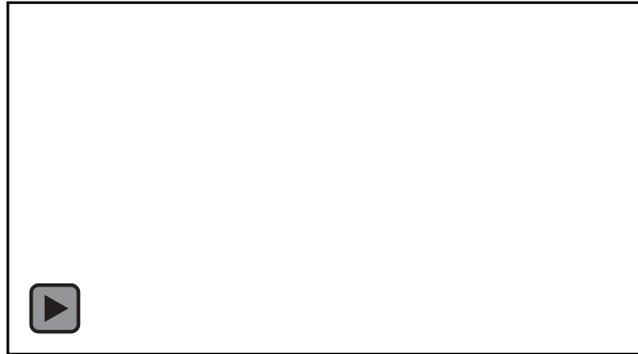
We used AMOEBA in OpenMM to compute the energies of these geometries.



A series of constrained geometry optimizations using MP2/aug-cc-pVTZ

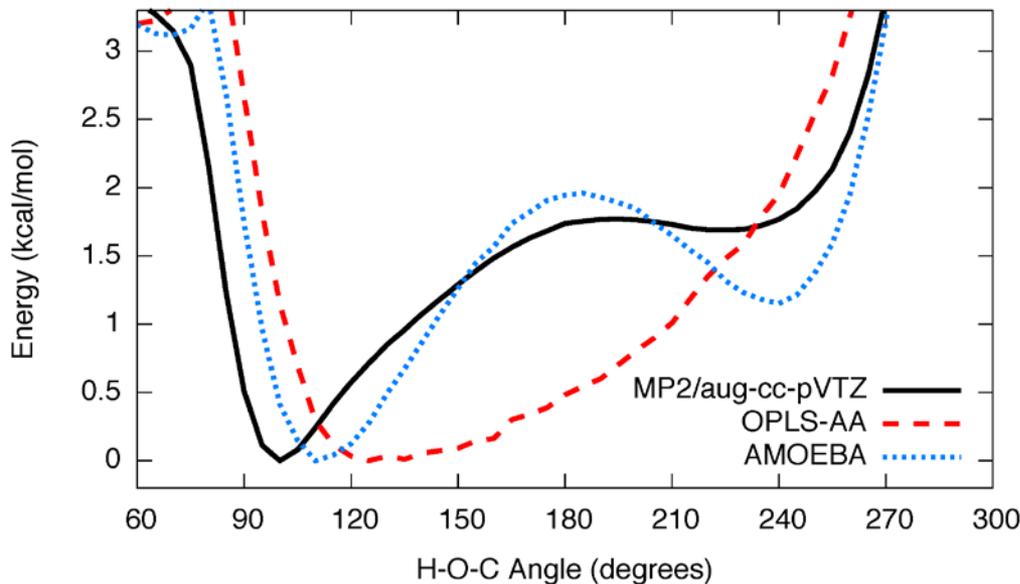
Accuracy of the AMOEBA force field

AMOEBA gives improved agreement with the *ab initio* gold standard.

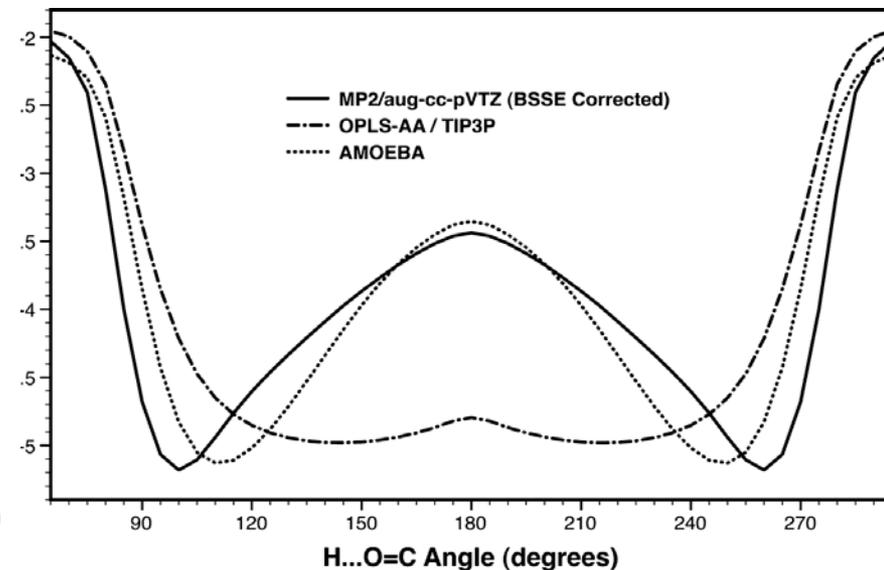


Our graph matches the left side of the literature plot and also reveals a previously hidden asymmetry!

OpenMM result



Original publication



Acceleration of AMOEBA in OpenMM

Polarizable force fields have high computational cost.

Main components of increased computational cost:

- Local coordinate systems for atomic multipoles
- Iterative solution of mutually induced dipoles
- Increased complexity of bonds, angles, dihedrals and VdW terms

$$\sum_{i < j} \frac{q_i q_j}{r_{ij}}$$

Point charge electrostatics

$$\lambda_3 = 1 - \exp(-au^3)$$

$$\lambda_5 = 1 - (1 + au^3) \exp(-au^3)$$

$$\lambda_7 = 1 - \left(1 + au^3 + \frac{3}{5}a^2u^6\right) \exp(-au^3)$$

$$\lambda_9 = 1 - [1 + au^3 + (18a^2u^6 + 9a^3u^9)/35] \exp(-au^3)$$

$$\mu_{j,\alpha}^{\text{ind}}(n+1) = (1 - \omega)\mu_{j,\alpha}^{\text{ind}}(n) + \omega[\mu_{j,\alpha}^{\text{ind}}(n) + \alpha_i \sum_{\beta \in \mathcal{U}} T_{\alpha\beta}^{ij} \mu_{j,\beta}^{\text{ind}}(n)]$$

AMOEBA electrostatics

(above equation must be solved iteratively)

$$T_{\alpha\beta}^{\text{D}} = \lambda_5 \frac{3R_\alpha R_\beta}{R^5} - \lambda_3 \frac{\delta_{\alpha\beta}}{R^3}$$

$$T_{\alpha\beta\gamma}^{\text{D}} = -\lambda_7 \frac{15R_\alpha R_\beta R_\gamma}{R^7} + \lambda_5 \frac{3(R_\alpha \delta_{\beta\gamma} + R_\beta \delta_{\alpha\gamma} + R_\gamma \delta_{\alpha\beta})}{R^5}$$

$$T_{\alpha\beta\gamma\eta}^{\text{D}} = \lambda_9 \frac{105R_\alpha R_\beta R_\gamma R_\eta}{R^9} -$$

$$\lambda_7 \frac{15(R_\alpha R_\beta \delta_{\gamma\eta} + R_\alpha R_\gamma \delta_{\beta\eta} + R_\alpha R_\eta \delta_{\beta\gamma} + R_\beta R_\gamma \delta_{\alpha\eta} + R_\beta R_\eta \delta_{\alpha\gamma} + R_\gamma R_\eta \delta_{\alpha\beta})}{R^7} + \lambda_5 \frac{3(\delta_{\alpha\beta} \delta_{\gamma\eta} + \delta_{\alpha\gamma} \delta_{\beta\eta} + \delta_{\alpha\eta} \delta_{\beta\gamma})}{R^5} \quad (4)$$

Acceleration of AMOEBA in OpenMM

OpenMM uses the GPU to evaluate the AMOEBA interactions for an enormous performance increase.

- Performance measured in ns/day with a 1 fs timestep (i.e. 1,000,000 steps)
- TINKER uses one CPU core* (Intel Core i7 @ 2.67 GHz)
- OpenMM uses one GPU (NVIDIA GeForce GTX TITAN)

System	Solvent	Atoms	OpenMM	TINKER	Speedup
DHFR	Explicit	23,558	1.10	0.012	92

* 2-3x speedup possible in TINKER using multiple cores, not tested here.