CEITEC Central European Institute of Technology Brno, Czech Republic

Structural Bioinformatics and Molecular Modeling

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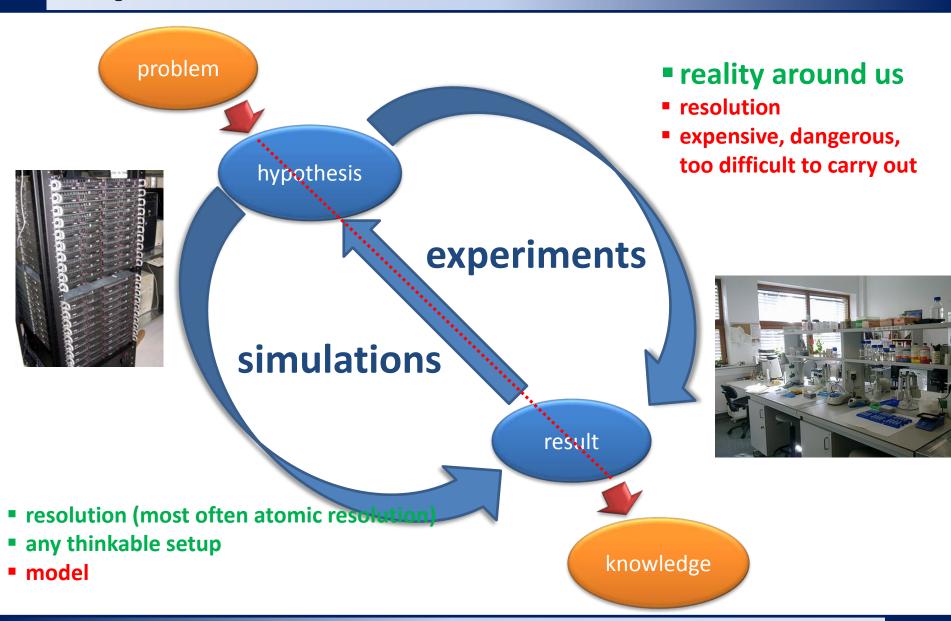
Molecular Modeling

(with computational chemistry as a basis)

Jaroslav Koča

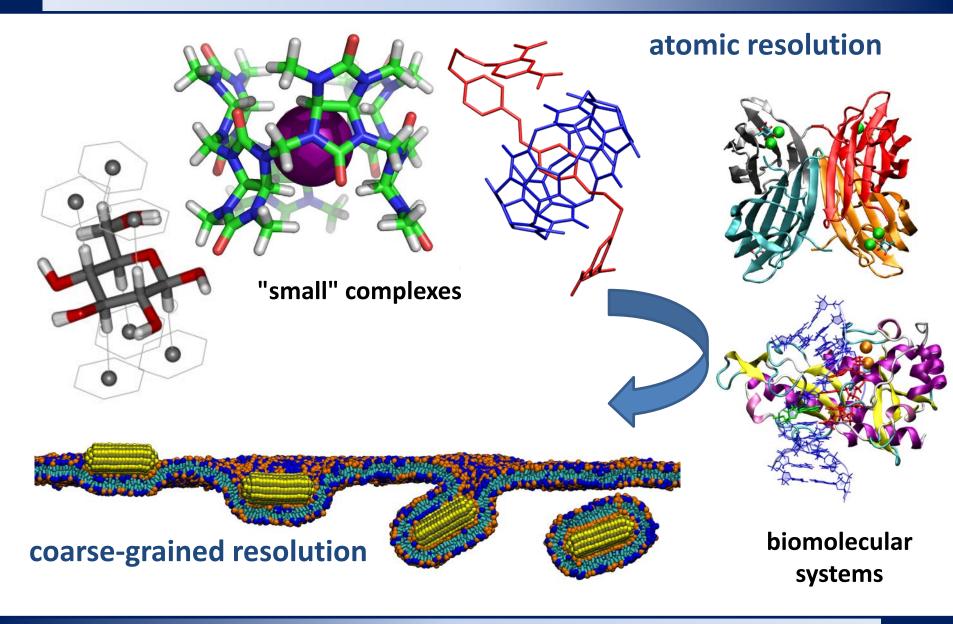
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Experiment vs Simulations

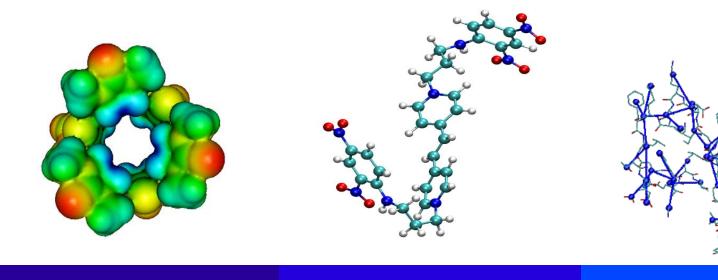


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What can be studied?



Levels of Theory



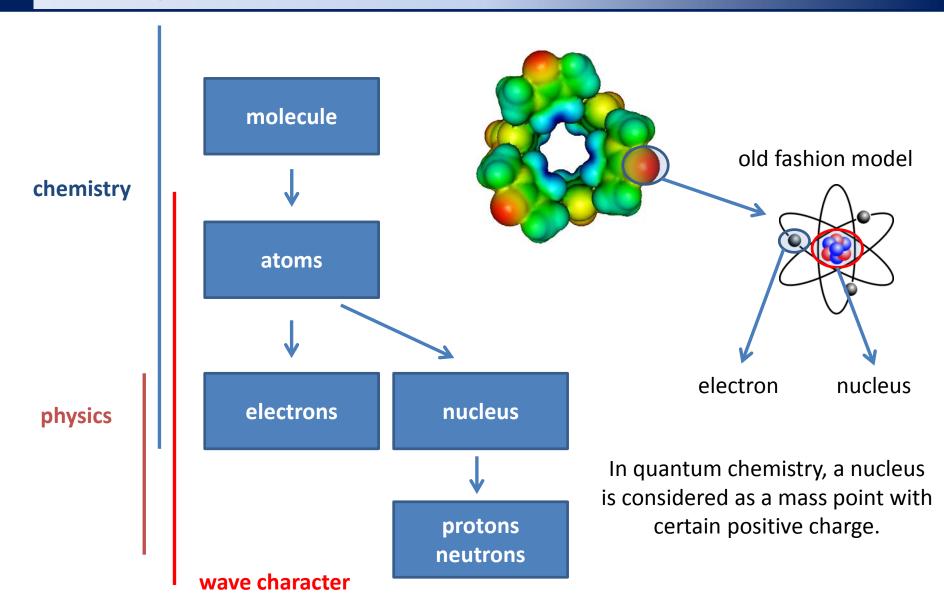
Quantum Mechanics	Molecular Mechanics	Coarse-grained Mechanics
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Atomic F	Bead Resolution	
reactivity	conformational movement	domain movement, folding
up to 1'000 atoms	up to 1'000'000 atoms	up to 1'000'000 beads
up to 100 ps	up to μs	up to ms

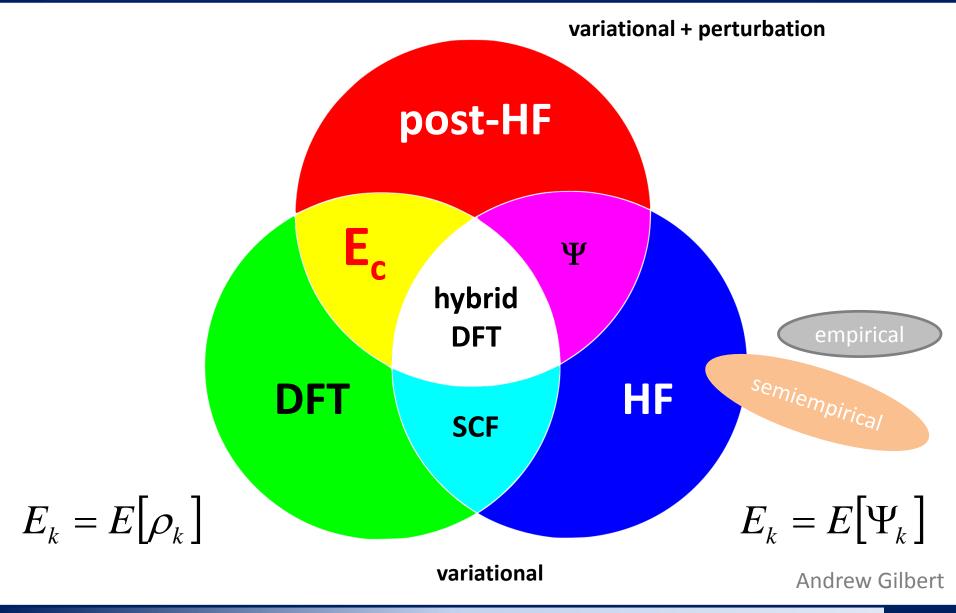
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Quantum Mechanics

Composition of Molecules



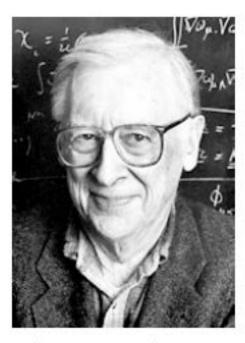
Classifications of Methods



The Nobel Prize in Chemistry 1998



Walter Kohn



John A. Pople

The Nobel Prize in Chemistry 1998 was divided equally between **Walter Kohn** "for his development of the **density-functional theory**" and **John A. Pople** "for his development of **computational methods in quantum chemistry**"

http://www.nobelprize.org/nobel_prizes/chemistry/laureates/1998/

Computational Complexity

Formal Scaling	Methods			
	HF	CI metods	MP metods	CC metods
$N^4 -> N^2 -> N^1$	HF, DFT			
N^5			MP2	CC2 (iterative)
N^6		CISD	MP3, MP4(SDQ)	CCSD (iterative)
N^7			MP4	CCSD(T), CC3 (iterative)
N^8		CISDT	MP5	CCSDT
N^9			MP6	
N ¹⁰		CISDTQ	MP7	CCSDTQ (iterative)

Legend

HF – Hartree-Fock method

DFT – density functional theory methods

CI – configuration interaction methods

MP - Møller–Plesset perturbation methods

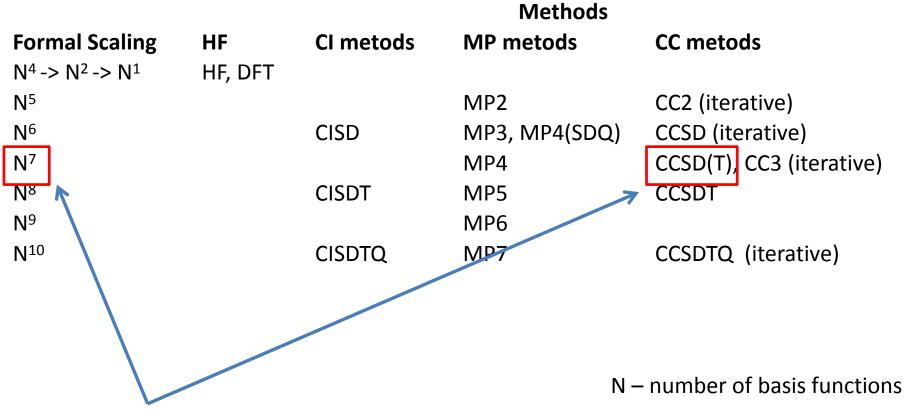
CC – coupled cluster methods

N – number of basis functions

$$N \approx N_A \overline{N_{BF}}$$

Methods highlighted in the box can provide results, which include part of omitted correlation energy.

Complexity & Accuracy



Coupled cluster methods are able to reach chemical **accuracy** but only for small molecules.

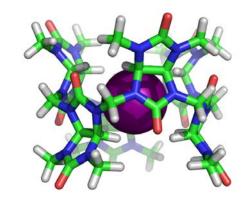
On currently available hardware, it is possible to apply the CCSD(T) method to systems containing up to **50 atoms**.

$$N \approx N_A \overline{N_{BF}}$$

Accuracy

Small Numbers from Big Numbers

RI-BLYP-d3/def2-TZVPP (vacuum)



bambus[6]uril/anion interaction (139 atoms)

"Chemical" Accuracy

error < 1 kcal mol⁻¹

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Accuracy

Small Numbers from Big Numbers

RI-BLYP-d3/def2-TZVPP (vacuum)



bambus[6]uril/anion interaction (139 atoms)

"Chemical" Accuracy

error < 1 kcal mol⁻¹

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Take Home Message

Quantum Mechanics

- due to dual character (particles/waves) of electrons and nuclei, any chemical system has to be described by the Schrödinger equation (SE)
- albeit very simple notation of SE, its analytical solution is not impossible even for simple chemical systems (two and more electrons)
- > several approximations were introduced that make numerical solution of SE possible but some of them introduces very serious errors (correlation energy)
- it is possible to fix these errors but procedures are very computationally demanding even for small systems (up to 50 atoms)
- once approximate solution of SE is known then any property (including energy) can be easily obtained from wavefunction of given state
- SE is naturally able to describe chemical reactions

Molecular Mechanics

Can we make calculations faster?

Molecular Mechanics

Schrodinger equation - quantum mechanical description

$$\hat{H}\psi_k^{\mathbf{R}}(\mathbf{r}_e) = E_k(\mathbf{R})\psi_k^{\mathbf{R}}(\mathbf{r}_e)$$



approximation
electron motions is omitted
(electron motions is implicitly included in empirical parameters)

$$E_{k}(\mathbf{R}) = E_{bonds} + E_{angles} + E_{torsions} + E_{ele} + E_{vdw} + \dots$$

bonded contributions

non-bonded contributions

Classical physics - mechanical description

Bonded Contributions

Bonds

$$E_{bonds} = \sum_{b=1}^{bonds} \frac{1}{2} K_b (d_b - d_{b0})^2$$

Angles

$$E_{angles} = \sum_{a=1}^{angles} \frac{1}{2} K_a (\theta_a - \theta_{a0})^2$$

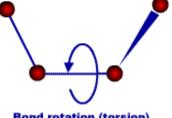
Torsion angles

$$E_{torsions} = \sum_{t=1}^{torsions} \sum_{n} \frac{V_{t,n}}{2} (1 + \cos[n\varphi_t - \delta_{t,n}])$$









Bond rotation (torsion)

empirical parameters

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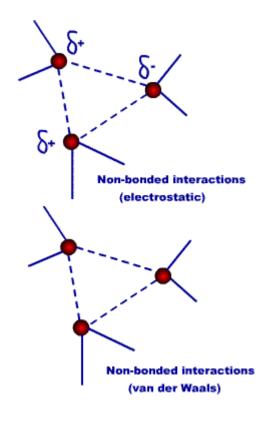
Non-bonded Contributions

Electrostatic interactions

$$E_{ele} = \sum_{i=1}^{N} \sum_{j=i+1}^{N} \frac{1}{4\pi\varepsilon_o} \frac{q_i q_j}{r_{ij}}$$

van der Waals interactions

$$E_{ele} = \sum_{i=1}^{N} \sum_{j=i+1}^{N} 4\varepsilon_{ij} \begin{bmatrix} \sigma_{ij} \\ r_{ij} \end{bmatrix}^{12} - \begin{bmatrix} \sigma_{ij} \\ r_{ij} \end{bmatrix}^{6}$$



PME – particle meshed Ewald (N log, N)

N – number of atoms

empirical parameters

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Take Home Message

Molecular Mechanics

- based on classical mechanics, accuracy is compromised
- empirical parameters (parameter set, force field) derived from experimental or highlevel QM calculations are required
- parameter transferability problems, parameters are derived for limited set of systems (proteins, nucleic acids, lipids, saccharides, etc), no general parameter set yet
- > very fast calculations of systems containing up to millions of atoms
- electrons are not explicitly accounted in the theory thus it is not possible to describe chemical reaction (exceptions: ReaxFF, EVB)
- suitable for study of conformational changes and structure

Potential Energy Surface

Configuration Space

$$E(\mathbf{R})$$

R = point in 3N-dimensional space (N is number of atoms)

$$\mathbf{R} = \{x_1, y_1, z_1, x_2, y_2, z_2, \dots, x_N, y_N, z_N\}$$

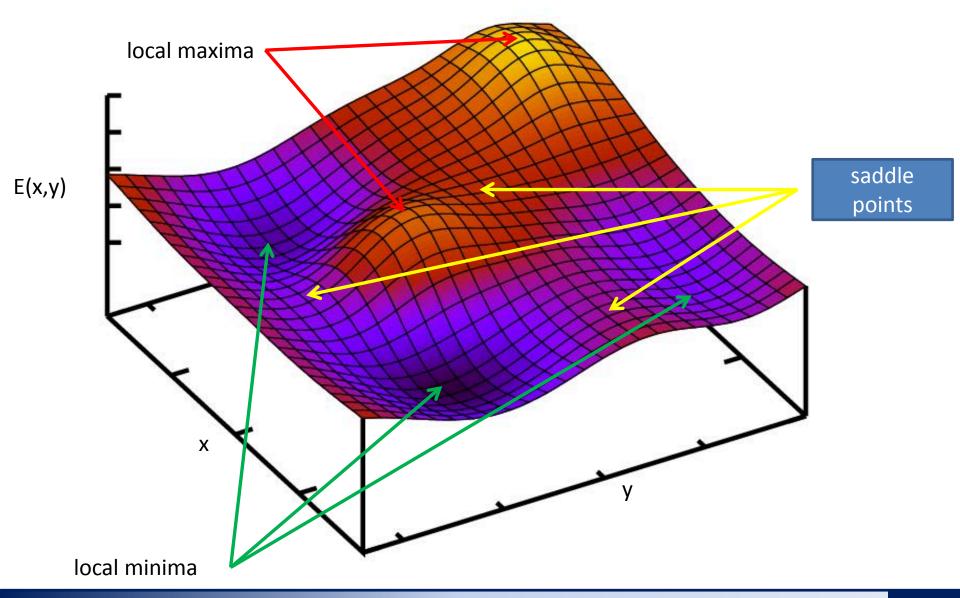
Cartesian coordinates of the first atom

Individual points form the configuration space.

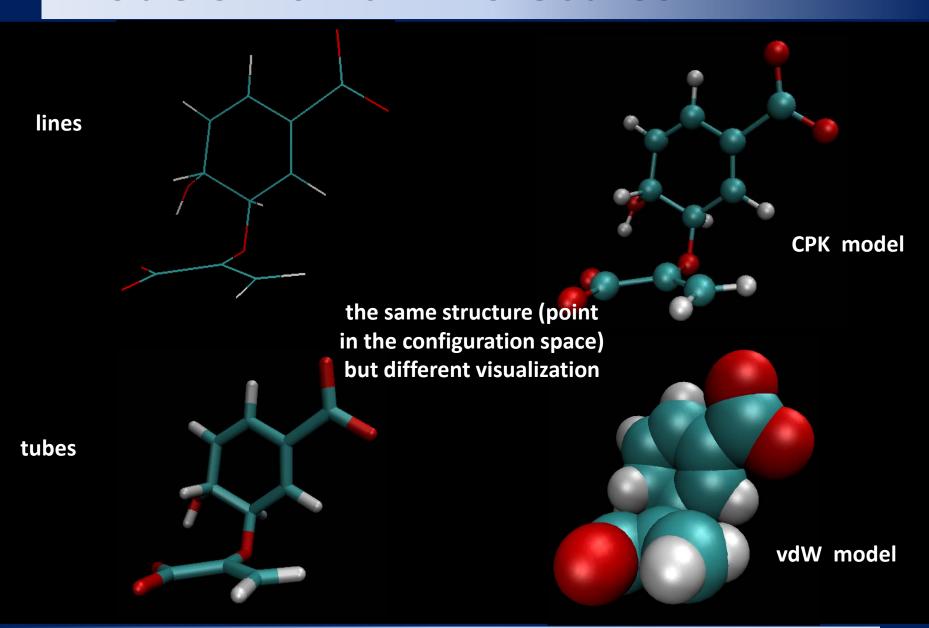
Every point in the configuration space represents a unique structure of studied system.

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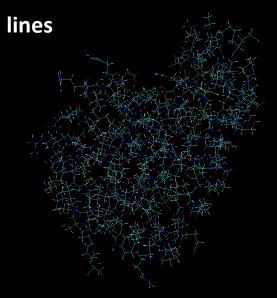
Two-dimensional Case

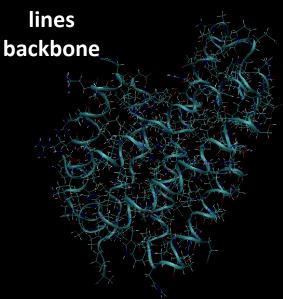


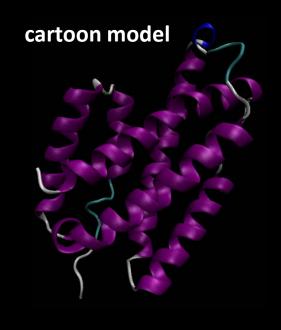
Models – small molecules

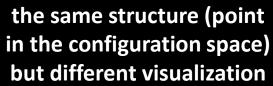


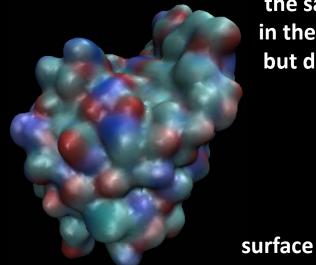
Models - biomolecules











Different visualization models are used to depict various structural features or internal properties of molecules or molecular assemblies, which then improve perceptions of studied systems/problems.

Take Home Message

Potential Energy Surface

- stationary points (local minima and saddle points) are very important for description of reactivity and kinetics of small molecular systems
- > stationary points represents unique structures of molecular system

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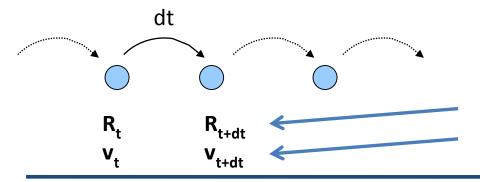
Molecular Dynamics

How to get thermodynamical parameters of complex systems ...

Molecular Dynamics







integration time step (determined by fastest motions in system)

atom positions atom velocities

trajectory

Equation of Motions

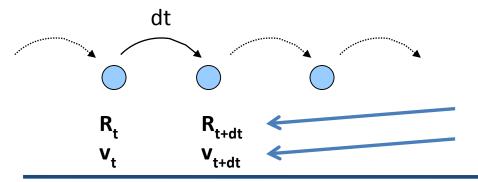
$$-\frac{\partial^2 E(\mathbf{R})}{\partial \mathbf{r}_i^2} = m_i \frac{d^2 \mathbf{r}_i}{dt^2}$$

$$\mathbf{F}_i = m_i \mathbf{a}_i$$

Molecular Dynamics

Evolution of system in time





integration time step (determined by fastest motions in system)

atom positions atom velocities

trajectory

Sampling problem

$$1 \mu s = 10^9 fs$$

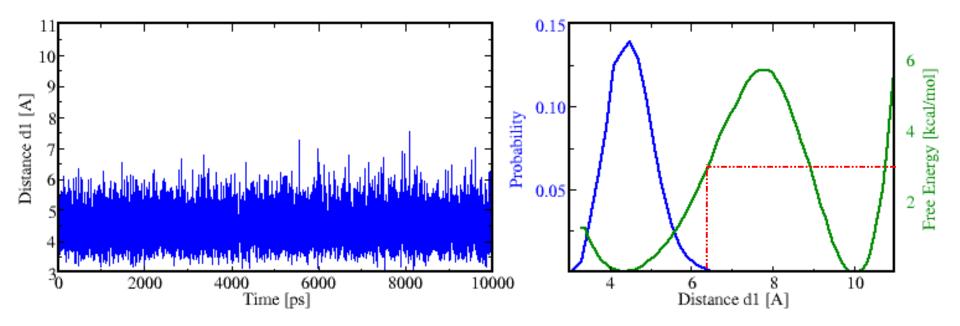
1631 atoms, AMBER, GPU acceleration

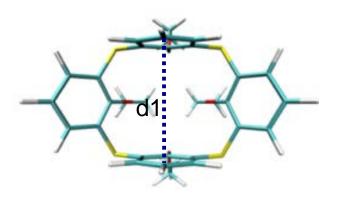
1 step ~ 1 ms CPU/GPU time 10⁹ steps ~ 12 days CPU/GPU time

Characteristic timescales:

- Protein folding (ms)
- Chemical reactions (ms, s, h)

Sampling Problem





10 ns long simulation is able to discover free energy landscape with depth only about **3 kcal/mol**.

Multiscale Methods QM/MM Methods

How to describe reactivity occurring in biomolecules (enzymes)?

Enzymatic Reactions

MutH Enzyme: ~4,300 atoms Water: ~42,000 atoms Total: $\sim 46,500$ atoms

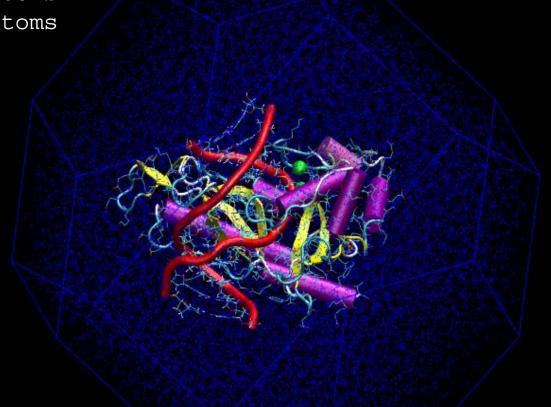
Enzymatic Reactions

Enzyme: $\sim 4,300$ atoms

Water: \sim 42,000 atoms

Total: $\sim 46,500$ atoms

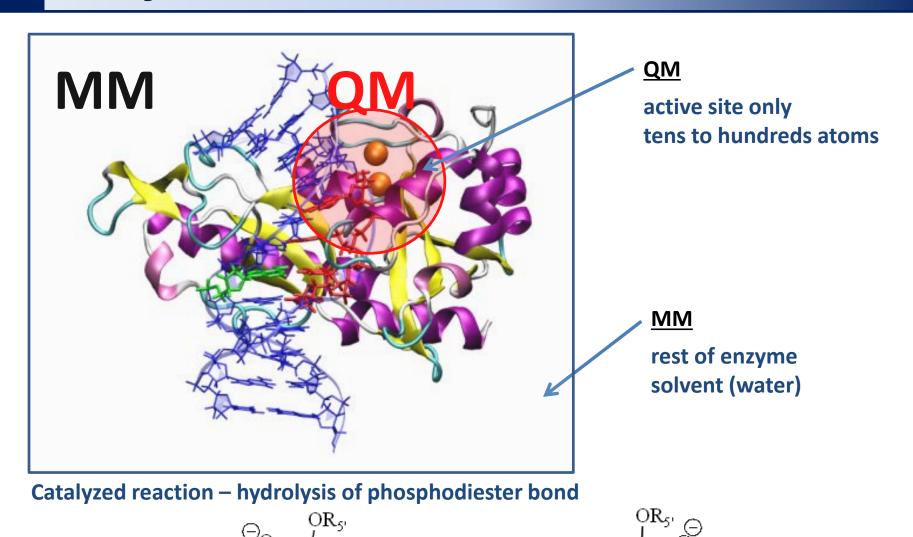
MutH



Beyond any QM method!

Enzymatic Reactions

 H_2O

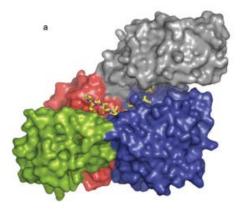


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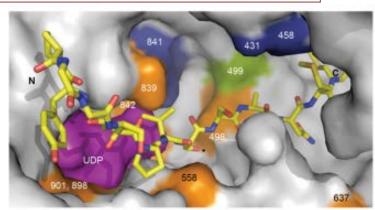
HO —R₃₁

Introduction - OGT glycosyltransferase

- \bullet Uridine diphospho-*N*-acetylglucosamine: polypeptide β-N-acetylaminyltransferase; PDB ID: 3PE4
- ❖ Enzymatic transfer of N-acetylglucosamine molecule on Ser/Thr residue of protein
- ❖ Inverting glycosyltransferase of the GT-B family
- Post-translational modification: first reported in 1984



OGT Crystal Structure (Walker et al, 2011)



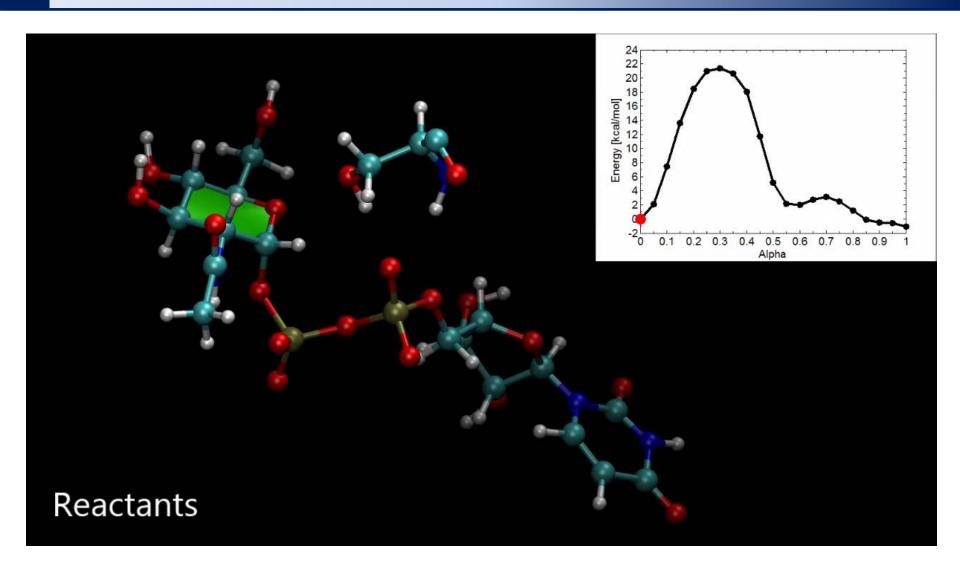
OGT Catalytic Site

Different Mechanisms Proposed for OGT

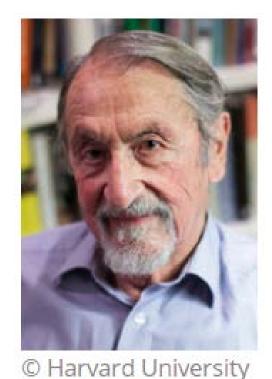
- His498 as catalytic base (M_{His}) (Lazarus et al. 2011 Tvaroska et al. 2012)
- 2. α-phosphate as base (MPO4) (Schimpl et al. 2012)

3. Water molecule for shunting proton to ASP554 (MAsp) (Lazarus et al. 2012)

Most Probable Reaction Path – M_{PO4}



Nobel Laureates in Chemistry 2013



Martin Karplus

Université de Strasbourg, Strasbourg, France, Harvard University, Cambridge, MA, USA



Photo: © S. Fisch Michael Levitt

Stanford University School of Medicine, Stanford, CA, USA



Photo: Wikimedia Commons

Arieh Warshel

University of Southern California, Los Angeles, CA, USA

http://www.nobelprize.org/nobel_prizes/chemistry/laureates/2013/

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Take Home Message





Figure 2. Newton and Schrödinger's cat. Previously, classical physics and quantum chemistry belonged to rivalling worlds. The Nobel Laureates in Chemistry 2013 have opened a gate between those worlds and have brought about a flourishing collaboration.

- study of chemical reactions occurring in very large molecular assemblies is possible by QM/MM methods ("routine" calculations)
 - enzymatic reactions (drug development)
 - catalysis in solid state (zeolites, industry)
- many unresolved issues (QM accuracy, MM polarization, boundary problems, ...)

http://www.nobelprize.org/nobel_prizes/chemistry/laureates/2013/

Thank you for your attention!

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