ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA
A.D. 1088

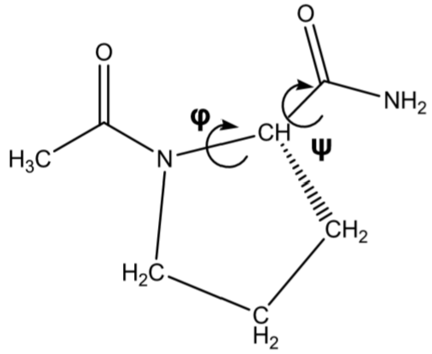
Hybrid methods for computing the electronic structure of complex systems: QM/MM

Importance of environment in chemistry

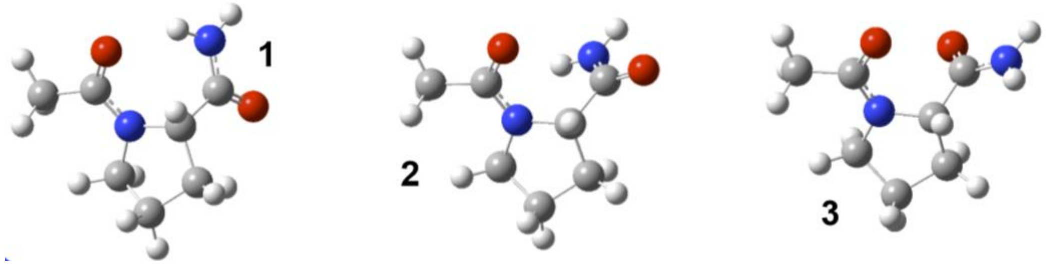
Motivation: solvation

Most chemical reactions occur in a homogeneous, isotropic solution, not in gas-phase

- the conformation can vary depending on the solvent



N-Acetylproline Amide



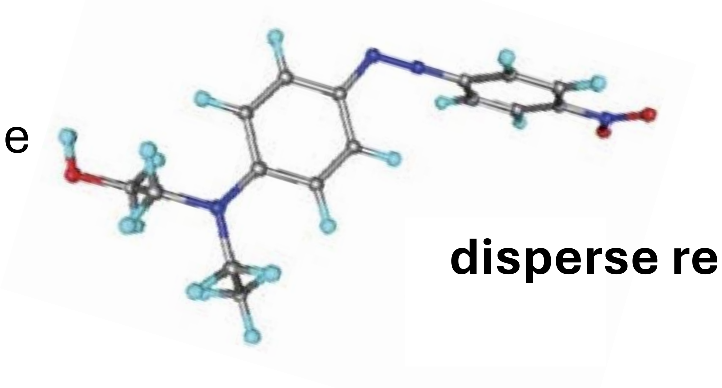
population %

	In gas-phase B3LYP/6-311++G**	In water: PCM B3LYP/ 6-311++G**
1	99	4
2	1	28
3	-	68

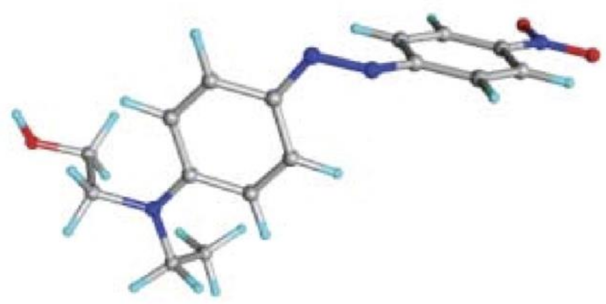
doi: 10.1021/jp711006f

- the reaction mechanism can vary depending on the solvent

TS in gas-phase
(inversion)



disperse red 1



TS in DMSO
(torsion)

doi: 10.1039/c0pp00056f

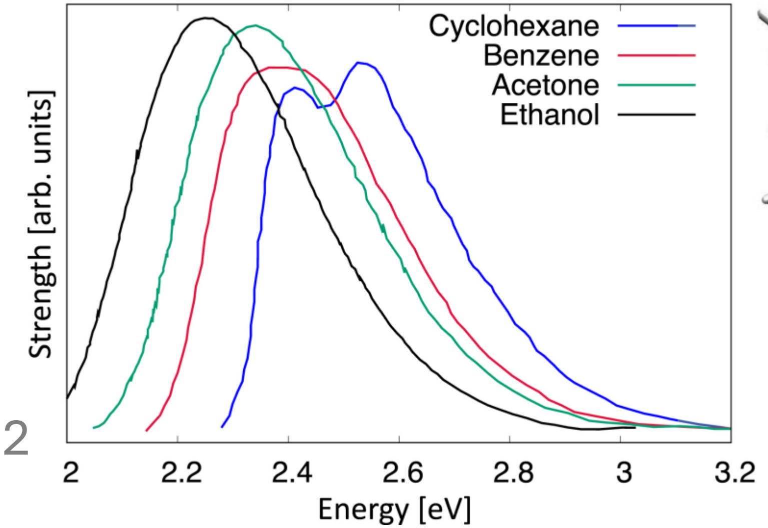
- even if the mechanism is conserved the reaction rate can change

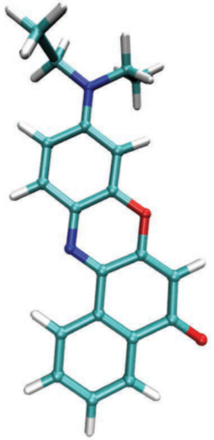
Motivation: solvation

Each excited state is affected differently by solvation

- the larger the dipole moment, the more pronounced the spectral shift
- **solvatochromic effect**: the phenomenon observed when a solution changes color as a function of the solvents

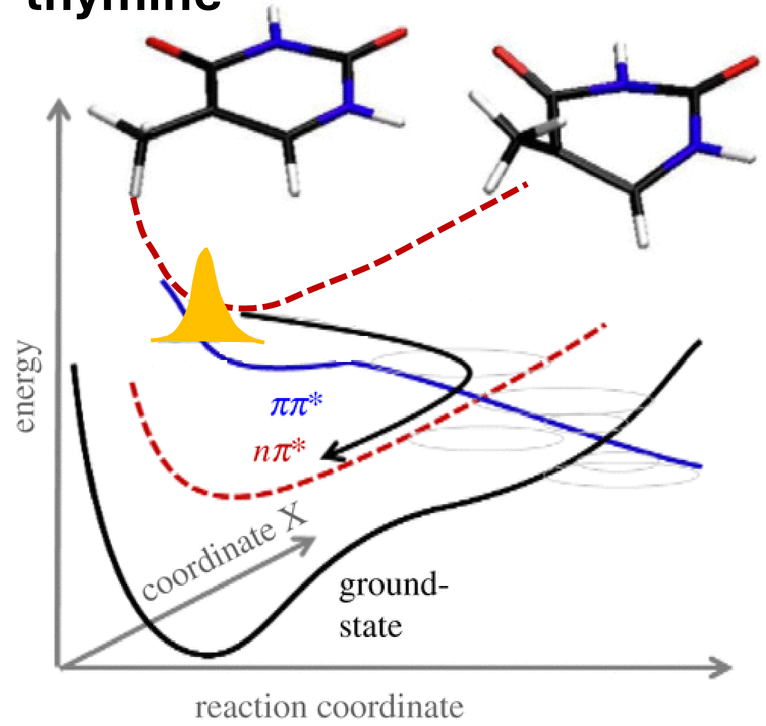
Nile red





arXiv:1809.04152

thymine



10.1098/rsta.2017.0473

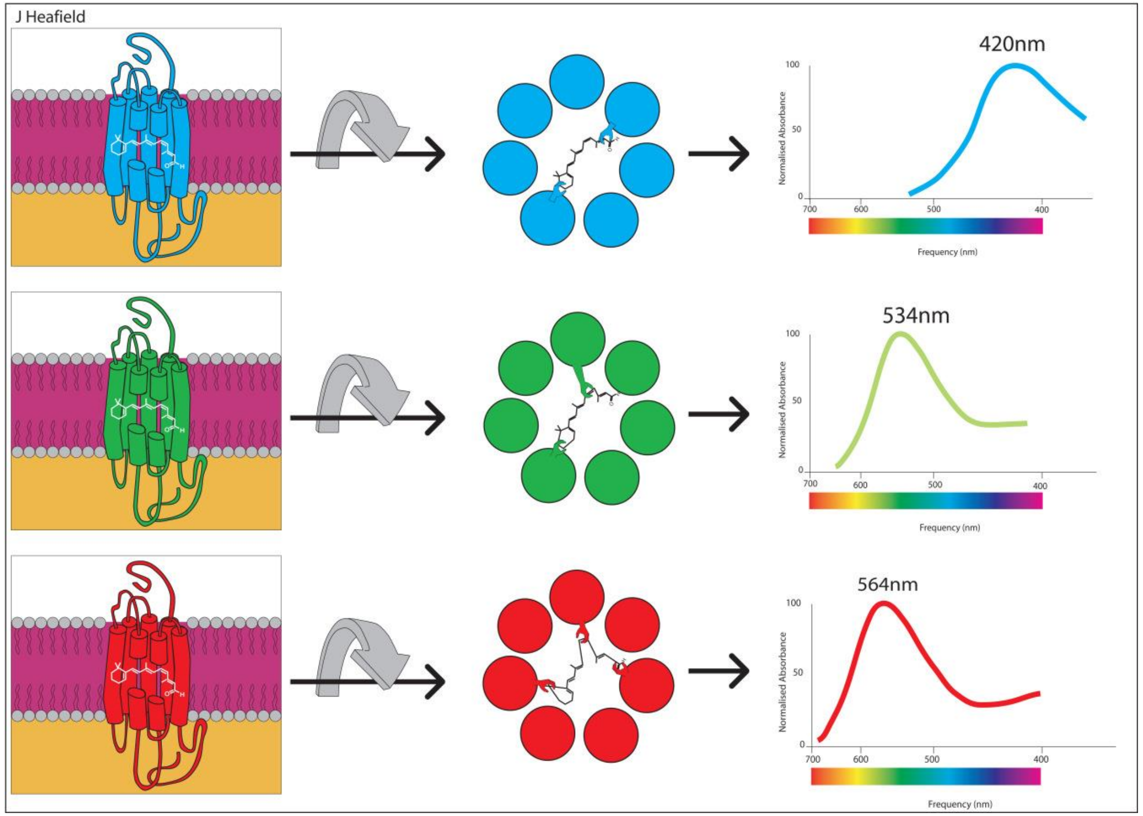
- the reaction mechanism can change with respect to gas-phase

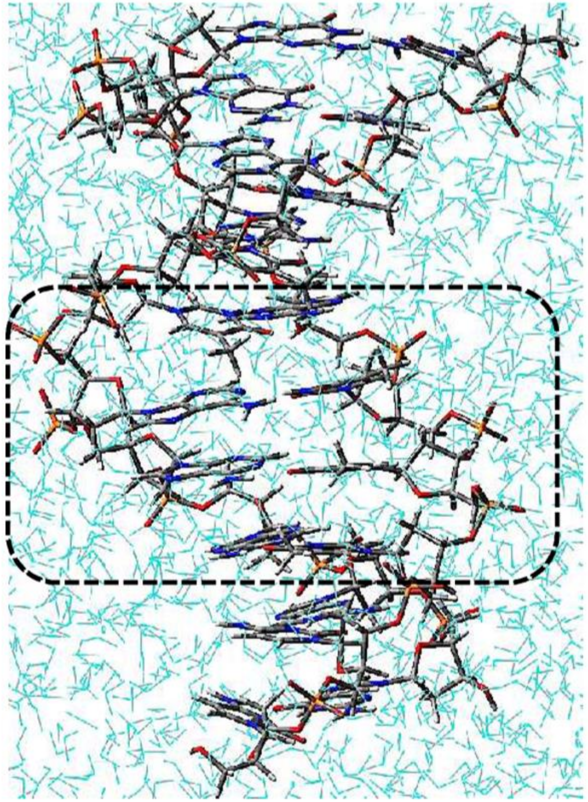
opening of new channels which could trap the ES populations or accelerate the decay to the GS

Motivation: heterogeneous media

Reaction in a heterogeneous, anisotropic environment

- studying reactions catalyzed by proteins





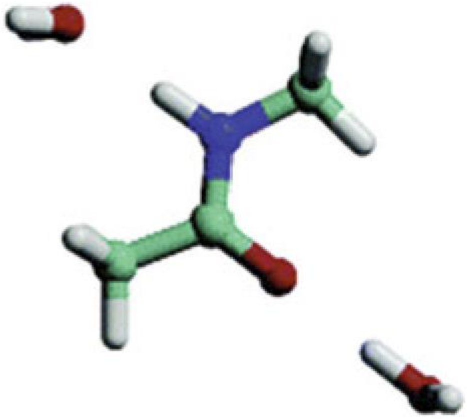
- studying complex molecular structures (DNA, membranes)

Approaches for introducing solvent effects in the calculations

Micro-solvation

micro-solvation: modeling solute-solvent interactions by means of a supermolecule made of an aggregate of the solute and a limited number of solvent molecules

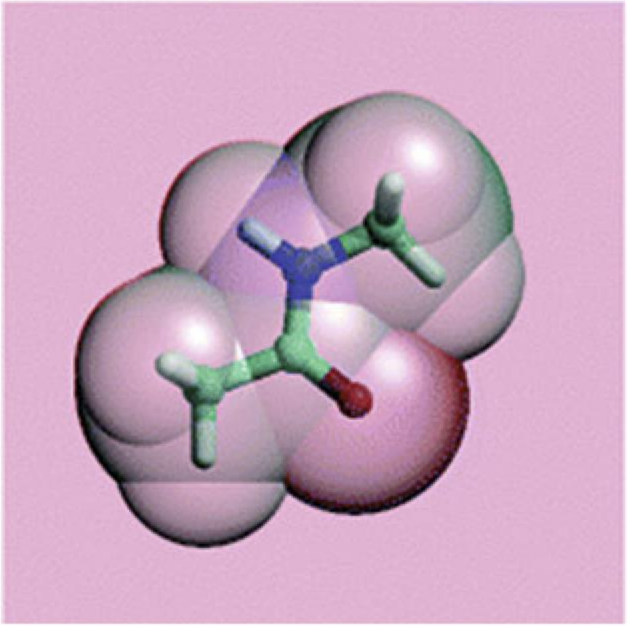
- the entire supermolecule is treated at the QM level
- easy to realize (no coding or external programs necessary)
- suitable for treating strong intermolecular interactions (e.g. H-bonds, solute protonation)
- omits long range electrostatic solute-solvent interactions
- outcome depends strongly on the user's choice regarding the number and positions of solvent molecules



The continuum approach

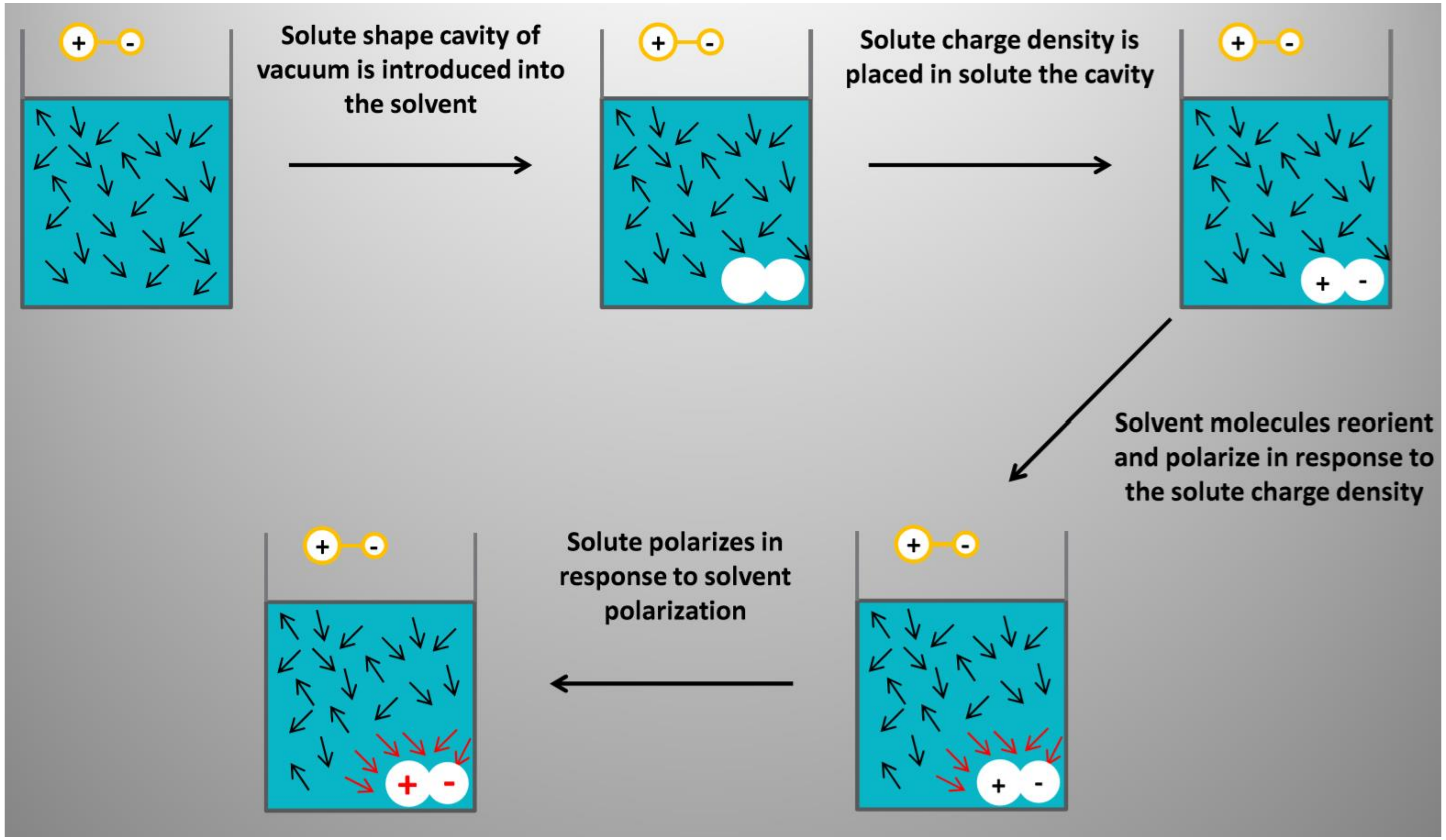
continuum solvation: an environment is replaced by an infinite continuum dielectric around a cavity containing the solute

- the solute is described at a QM level
- in the standard implementation solute-solvent interactions are limited to those of electrostatic origin
- model system is a very dilute solution (composed of a single solute molecule)
- solvent is isotropic, at equilibrium at a given temperature
- not capable of describing anisotropic environment and directional interactions (e.g. H bonds)



The continuum approach: electrostatics and polarization

The charge distribution ρ_M of the solute, inside the cavity, polarizes the dielectric continuum, which in turn polarizes the solute charge distribution. This definition of the interaction corresponds to a **self-consistent process**, which is numerically solved following an iterative procedure



Solute shape cavity of vacuum is introduced into the solvent

Solute charge density is placed in solute the cavity

Solvent molecules reorient and polarize in response to the solute charge density

Solute polarizes in response to solvent polarization

lecture slide: Waldemar Kulig

The hybrid QM/MM approach

Quantum Mechanics (**QM**)/ Molecular Mechanics (**MM**): a hybrid method combining the advantages of both worlds

- **active part** – part of the system involved in a (photo)reaction – described at the **QM level**
- **inactive part** – surrounding which remains in equilibrium – described at the **MM level**

- Quantum Mechanics

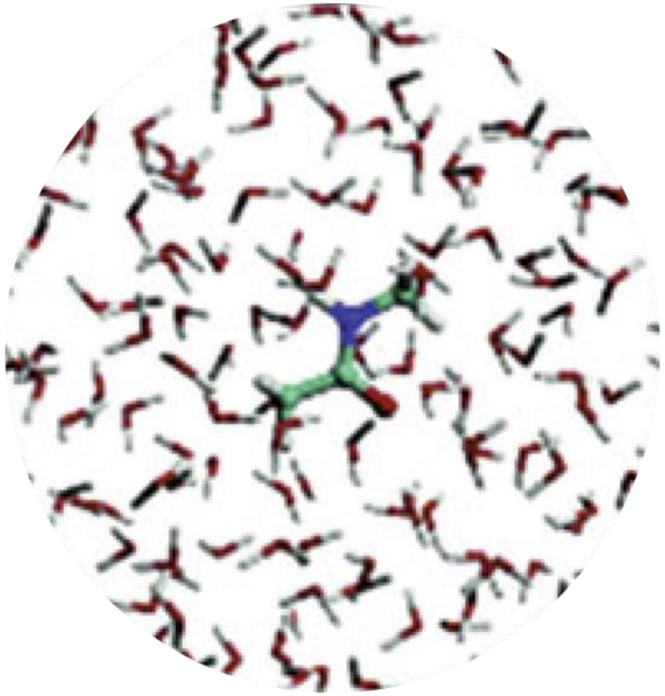
👍 describes bond breaking and forming, excited states, non-equilibrium dynamics

👎 expensive and time-consuming

- Molecular Mechanics

👍 very fast, realiable results around equilibrium

👎 electrons are not treated explicitly, requires parametrization, cannot describe bond breaking or forming



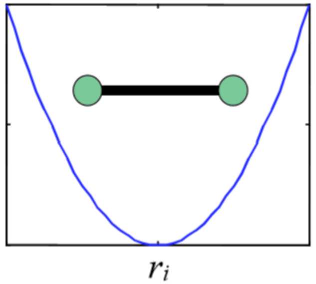
Molecular Mechanics (MM)

Force fields

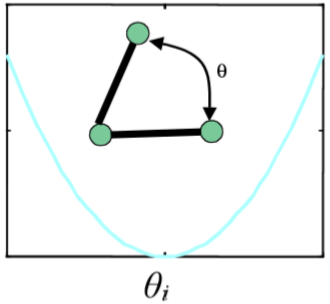
Potential energy surface through **mathematical functions** and **empirical parameters** that describe the energetic contributions of the various interactions between atoms

$$v(\boldsymbol{R}) = E_{bond} + E_{angle} + E_{dihedral} + E_{Coulomb} + E_{VdWaals}$$

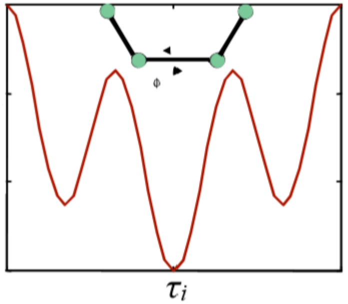
stretching



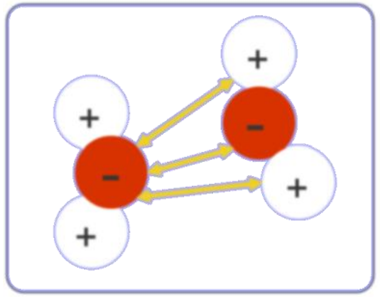
bending



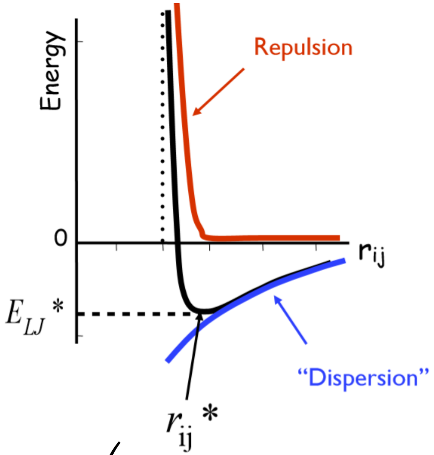
torsion



Coulomb



van der Waals



functional form

$$\frac{1}{2}k_i^b(r_i - r_{i0})^2$$

$$\frac{1}{2}k_i^a(\Theta_i - \Theta_{i0})^2$$

$$\frac{1}{2}\sum_i A_j[1 + (-1)^{j+1}\cos(j\tau_i + \phi)]$$

$$\frac{1}{4\pi\varepsilon_0}\sum_i\sum_{j>i}\frac{q_i q_j}{R_{ij}}$$

$$\sum_i\sum_{j>i}4E_{IJ}\left(\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^{6}\right)$$

Lennard-Jones potential

parameter set: atom-specific parameters ($k_i^b, r_{i0}, k_i^a, \Theta_{i0}, A_j, q_i, E_{IJ}, \sigma_{ij}$, etc.) which depend not only on the atom itself but also on the nearest neighbours

Force Field ≡ functional form + parameter set

Force fields

```
PARM99 for DNA,RNA,AA, organic molecules, Polariz.& LP incl.02/04/99
C  12.01         0.616  !          sp2 C carbonyl group
CA 12.01         0.360             sp2 C pure aromatic (benzene)
CB 12.01         0.360             sp2 aromatic C, 5&6 membered ring junction
CC 12.01         0.360             sp2 aromatic C, 5 memb. ring HIS
CD 12.01         0.360             sp2 C atom in the middle of: C=CD-CD=C
CK 12.01         0.360             sp2 C 5 memb.ring in purines
CM 12.01         0.360             sp2 C  pyrimidines in pos. 5 & 6
CN 12.01         0.360             sp2 C aromatic 5&6 memb.ring junct.(TRP)
CQ 12.01         0.360             sp2 C in 5 mem.ring of purines between 2 N
CR 12.01         0.360             sp2 arom as CQ but in HIS
…
```

atom parameters

```
H  1.008         0.161             H bonded to nitrogen atoms
HC 1.008         0.135             H aliph. bond. to C without electrwd.group
H1 1.008         0.135             H aliph. bond. to C with 1 electrwd. group
H2 1.008         0.135             H aliph. bond. to C with 2 electrwd.groups
H3 1.008         0.135             H aliph. bond. to C with 3 eletrwd.groups
HA 1.008         0.167             H arom. bond. to C without elctrwd. groups
H4 1.008         0.167             H arom. bond. to C with 1 electrwd. group
H5 1.008         0.167             H arom.at C with 2 elctrwd. gr,+HCOO group
…
```

bond parameters

```
C -C    310.0    1.525       Junmei et al, 1999
C -CA   469.0    1.409       JCC,7,(1986),230; (not used any more in TYR)
C -CB   447.0    1.419       JCC,7,(1986),230; GUA
C -CM   410.0    1.444       JCC,7,(1986),230; THY,URA
C -CT   317.0    1.522       JCC,7,(1986),230; AA
C -N    490.0    1.335       JCC,7,(1986),230; AA
C -N*   424.0    1.383       JCC,7,(1986),230; CYT,URA
C -NA   418.0    1.388       JCC,7,(1986),230; GUA.URA
C -NC   457.0    1.358       JCC,7,(1986),230; CYT
C -O    570.0    1.229       JCC,7,(1986),230; AA,CYT,GUA,THY,URA
C -O2   656.0    1.250       JCC,7,(1986),230; GLU,ASP
C -OH   450.0    1.364       JCC,7,(1986),230; (not used any more for TYR
C -OS   450.0    1.323       Junmei et al, 1999
C -H4   367.0    1.080       Junmei et al, 1999
C -H5   367.0    1.080       Junmei et al, 1999
CA-CA   469.0    1.400       JCC,7,(1986),230; BENZENE,PHE,TRP,TYR
CA-CB   469.0    1.404       JCC,7,(1986),230; ADE,TRP
CA-CM   427.0    1.433       JCC,7,(1986),230; CYT
CA-CN   469.0    1.400       JCC,7,(1986),230; TRP
```

angle parameters

```
C -C -O      80.0      120.00     Junmei et al, 1999 acrolein
C -C -OH     80.0      120.00     Junmei et al, 1999
CA-C -CA     63.0      120.00     changed from 85.0  bsd on C6H6 nmodes; AA
CA-C -OH     70.0      120.00     AA (not used in tyr)
CB-C -NA     70.0      111.30     NA
CB-C -O      80.0      128.80
CM-C -NA     70.0      114.10
CM-C -O      80.0      125.30
CT-C -O      80.0      120.40
CT-C -O2     70.0      117.00
CT-C -N      70.0      116.60     AA general
CT-C -CT     63.0      117.00     Junmei et al, 1999
CT-C -OS     80.0      115.00     Junmei et al, 1999
CT-C -OH     80.0      110.00     Junmei et al, 1999
…
```

dihedral parameters

```
X -C -C -X    4   14.50      180.0         2.          Junmei et al, 1999
X -C -CA-X    4   14.50      180.0         2.          intrpol.bsd.on C6H6
X -C -CB-X    4   12.00      180.0         2.          intrpol.bsd.on C6H6
X -C -CM-X    4    8.70      180.0         2.          intrpol.bsd.on C6H6
X -C -CT-X    6    0.00        0.0         2.          JCC,7,(1986),230
X -C -N -X    4   10.00      180.0         2.          AA,NMA
X -C -N*-X    4    5.80      180.0         2.          JCC,7,(1986),230
X -C -NA-X    4    5.40      180.0         2.          JCC,7,(1986),230
X -C -NC-X    2    8.00      180.0         2.          JCC,7,(1986),230
X -C -O -X    4   11.20      180.0         2.          Junmei et al, 1999
X -C -OH-X    2    4.60      180.0         2.          Junmei et al, 1999
X -C -OS-X    2    5.40      180.0         2.          Junmei et al, 1999
…
```

Lennard-Jones parameters

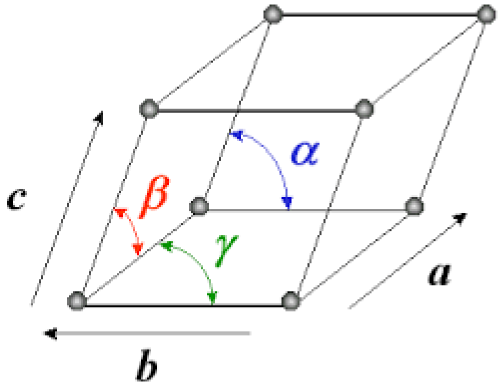
```
H            0.6000  0.0157            !Ferguson base pair geom.
HO           0.0000  0.0000             OPLS Jorgensen, JACS,110,(1988),1657
HS           0.6000  0.0157             W. Cornell CH3SH ⟶ CH3OH FEP
HC           1.4870  0.0157             OPLS
H1           1.3870  0.0157             Veenstra et al JCC,8,(1992),963
H2           1.2870  0.0157             Veenstra et al JCC,8,(1992),963
H3           1.1870  0.0157             Veenstra et al JCC,8,(1992),963
HP           1.1000  0.0157             Veenstra et al JCC,8,(1992),963
HA           1.4590  0.0150             Spellmeyer
```

Force fields

- **Assisted Model Building with Energy Refinement (AMBER,** https://ambermd.org/AmberModels.php) & **Chemistry at Harvard Macromolecular Mechanics** (**CHARMM,** http://mackerell.umaryland.edu/charmm_ff.shtml): two families of force fields for molecular dynamics of **biomolecules** (proteins, DNA, RNA, carbohydrates, lipids)
  - AMBER is also the name for the molecular dynamics software package.
- **The Optimized Potentials for Liquid Simulations (OPLS,** http://zarbi.chem.yale.edu/oplsaam.html) **& Generalized AMBER Force Field** (**GAFF,** https://ambermd.org/antechamber/gaff.html): generalized force fields for organic molecules
- **Universal Force Field (UFF):** a full periodic table force field with extra terms that can be used to calculate single point energies, do geometry optimizations, calculate frequencies… but less optimal for molecular dynamics
- **AMOEBA**: a **polarizable** force field designed to model molecular systems with greater physical realism

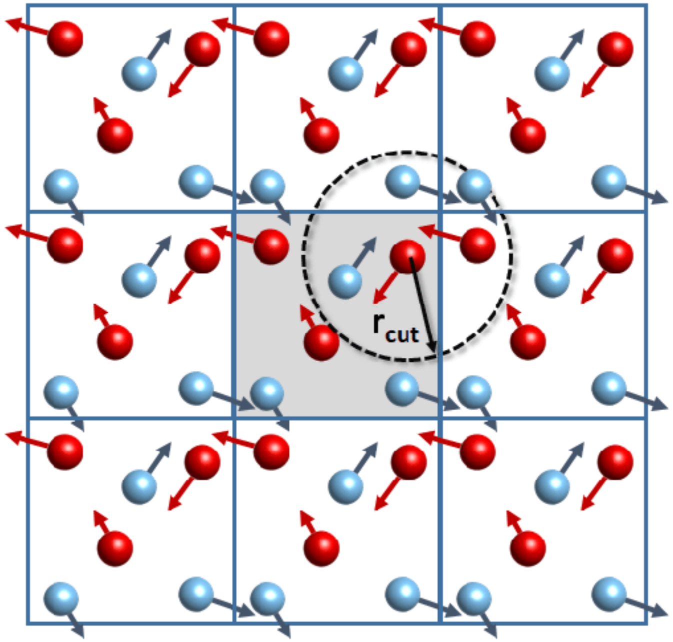
https://doi.org/10.1002/adts.201900135

Periodic boundary conditions



Periodic boundary conditions (PBC): used to limit the negative effects of the small system size

- For each particle with position $\boldsymbol{r}$, we can imagine infinite replicas present at positions $\boldsymbol{r}+\boldsymbol{l}\cdot\boldsymbol{a}+\boldsymbol{m}\cdot\boldsymbol{b}+\boldsymbol{n}\cdot\boldsymbol{c}$, where $\boldsymbol{l},\boldsymbol{m},\boldsymbol{n}$ are integers and $\boldsymbol{a},\boldsymbol{b},\boldsymbol{c}$ are the vectors representing the cell axes.



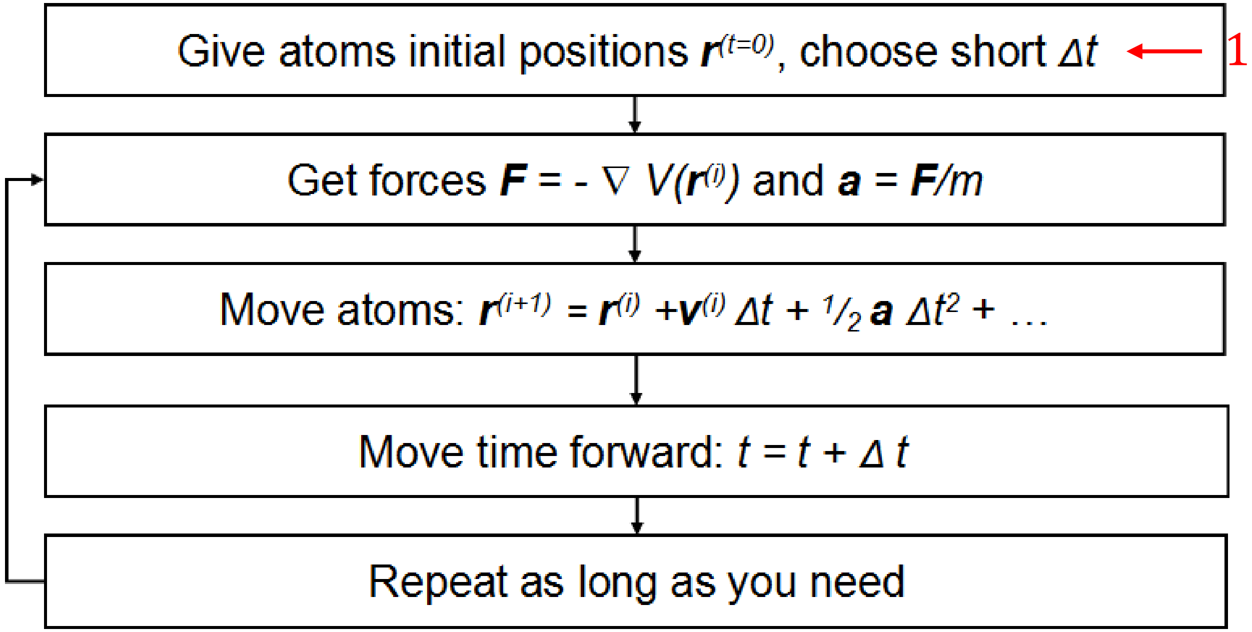
In practice:

- when a particle leaves the box, one of its images re-enters from the opposite side
- when calculating pairwise energy, it is done using the nearest replicas

Molecular dynamics

Molecular dynamics (MD): simulation of the temporal evolution of the system based on the principles of classical mechanics

- consists in solving numerically Newton's equations of motion for each particle



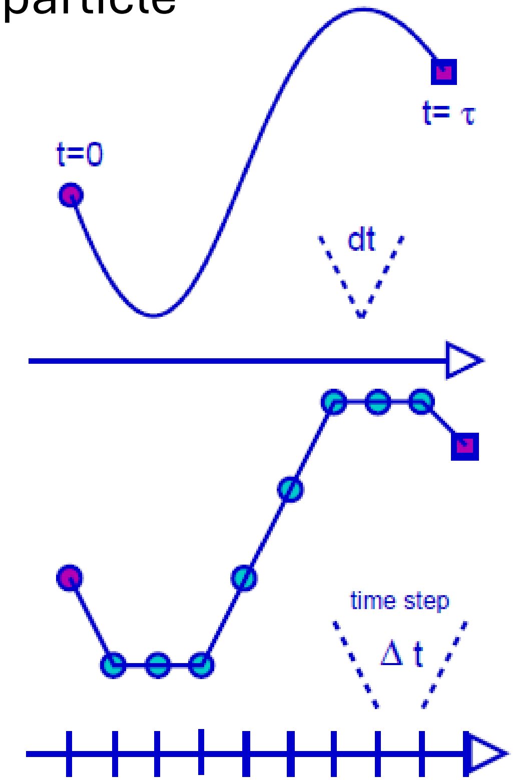
Give atoms initial positions $\mathbf{r}^{(t=0)}$, choose short Δt ← $1 - 2\ fs$

Get forces $\mathbf{F} = -\nabla V(\mathbf{r}^{(i)})$ and $\mathbf{a} = \mathbf{F}/m$

Move atoms: $\mathbf{r}^{(i+1)} = \mathbf{r}^{(i)} + \mathbf{v}^{(i)} \Delta t + \frac{1}{2} \mathbf{a} \Delta t^2 + \ldots$

Move time forward: $t = t + \Delta t$

Repeat as long as you need



- **cutoff radius**: Coulomb interactions are long range ($\propto 1/r$), however it is expensive to consider every pair of interactions in the system → calculate interactions with atoms within cutoff (e.g. 10 Å)
- **shake algorithm**: keep hydrogens fixed during MD. allows for longer time step in the integration schemes (typically $1 - 2\ fs$) → solvent molecules move as rigid bodies (translations and rotations)

Molecular dynamics: heating

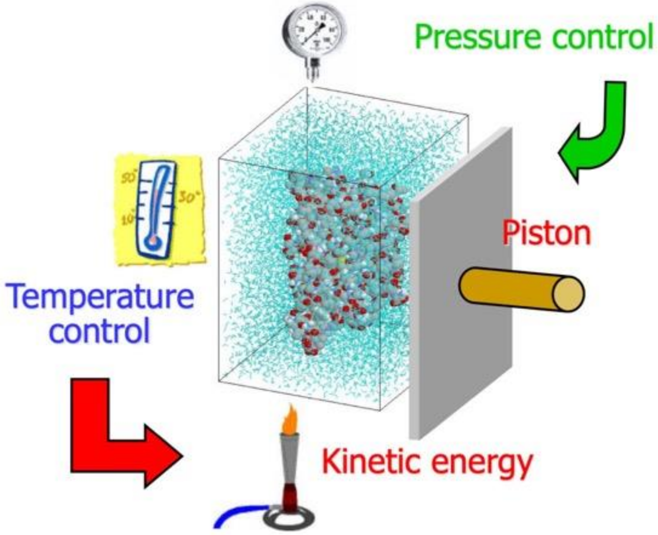
NVE (aka **microcanonical**) ensemble: MD solves the Newton's equations conserving the total energy;

- constant **N**umber of particles, energy **E** and volume **V** ensemble
- closed system (no exchange with environment)

NVT (aka **canonical**) ensemble: emulates energy flowing in/out of the system (thus not conserved) to mimic heat exchange with a bath in a thermal contact

- realized through a **thermostat**: random adjustment of atomic velocities (temperature in MD is related to the average kinetic energy of particles):

$$T \propto \langle v^2 \rangle$$



NpT (aka **isothermic-isobaric**) ensemble: allows the box size and shape to fluctuate to maintain target pressure

- realized through a **barostat**: adjustment of box volume through randomly scaling particle coordinates and forces they experience

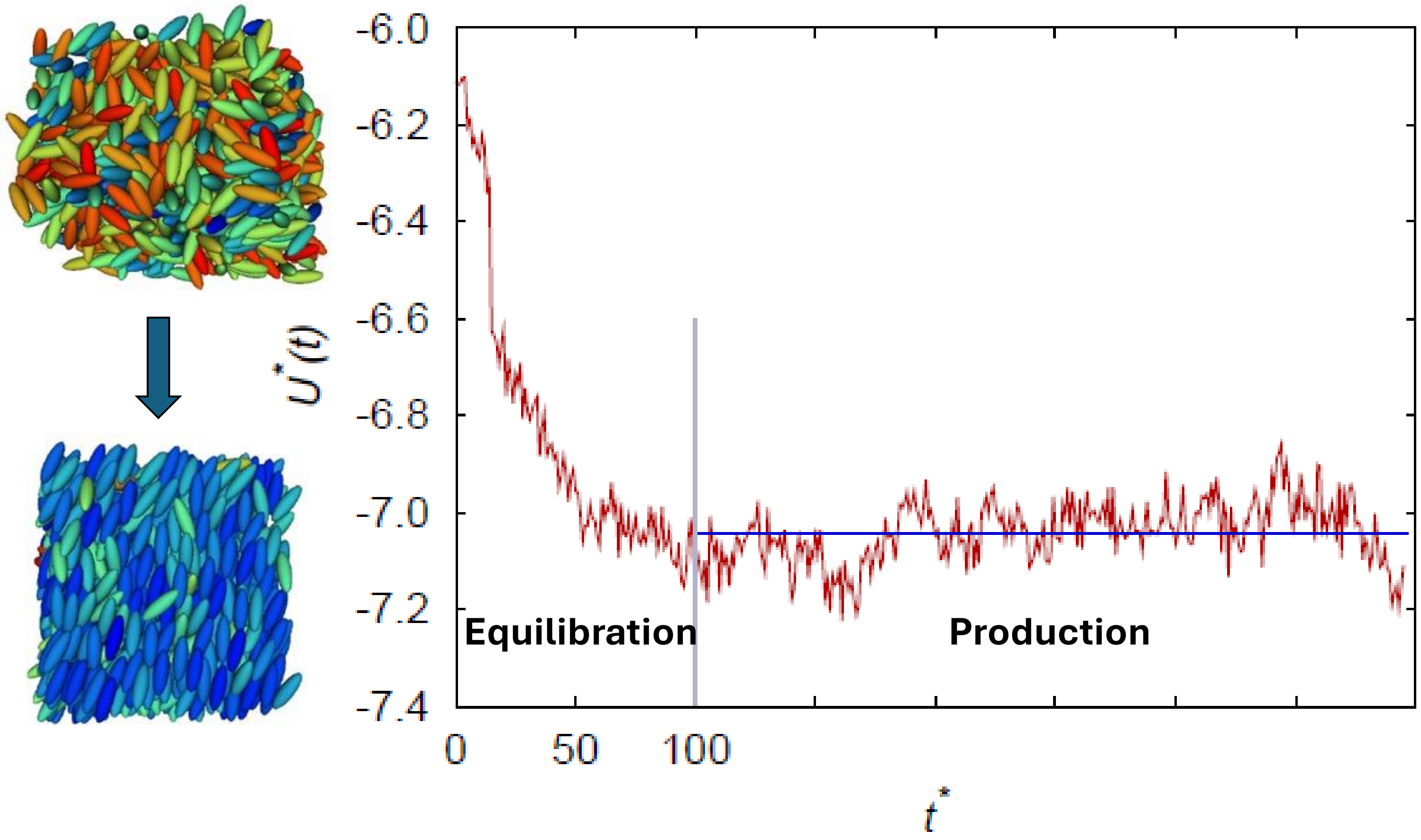
$$p \propto 1/V$$

Molecular dynamics: equilibration & production

Heating: the simulation is run for several hundreds of *ps* until the reaching desired temperature (e.g. 300 K)

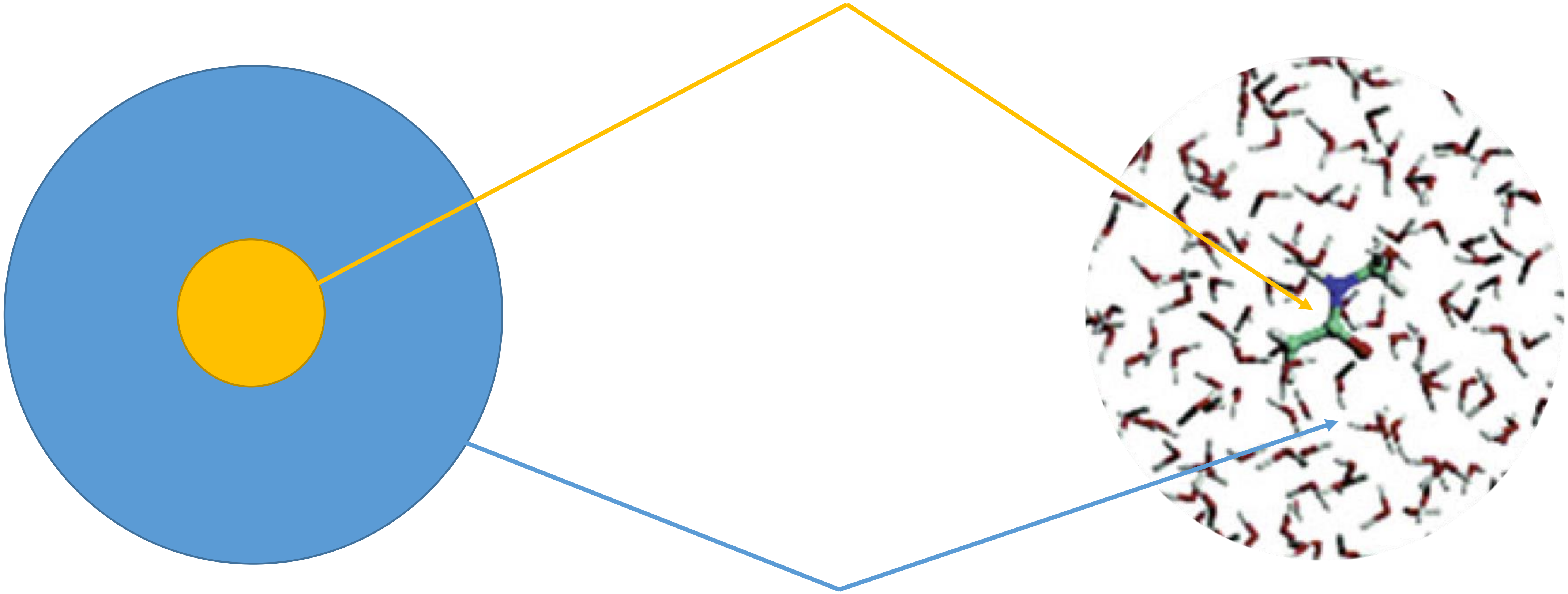
Equilibration: the simulation is run for several *ns* until reaching a stable thermodynamic state that is representative of the desired ensemble

Production: once equilibrium is reached statistical data are collected



Basics of QM/MM

QM/MM partitioning



QM level: inner region (active site, chromophore)

MM level: outer region (explicit solvent, protein)

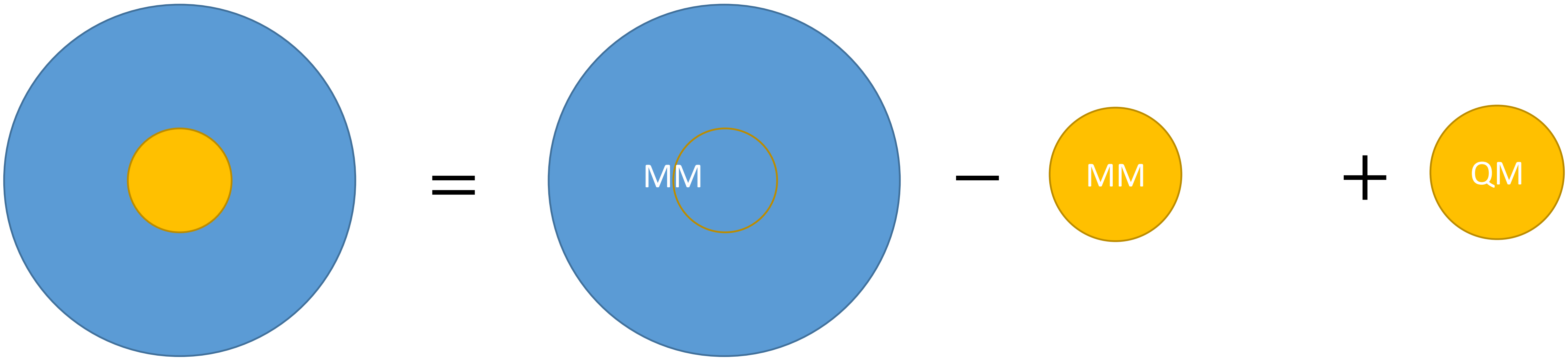
droplet: since PBC algorithms are missing in most QM programs, a cavity solvation model is usually used in QM/MM schemes

- follows shape of solute
- avoids possible anisotropic charge screening

QM/MM partitioning schemes: subtractive scheme

Subtractive scheme for QM/MM calculations involve:

- an MM calculation of the entire system
- an MM calculation of the inner region
- a QM calculation of the inner region

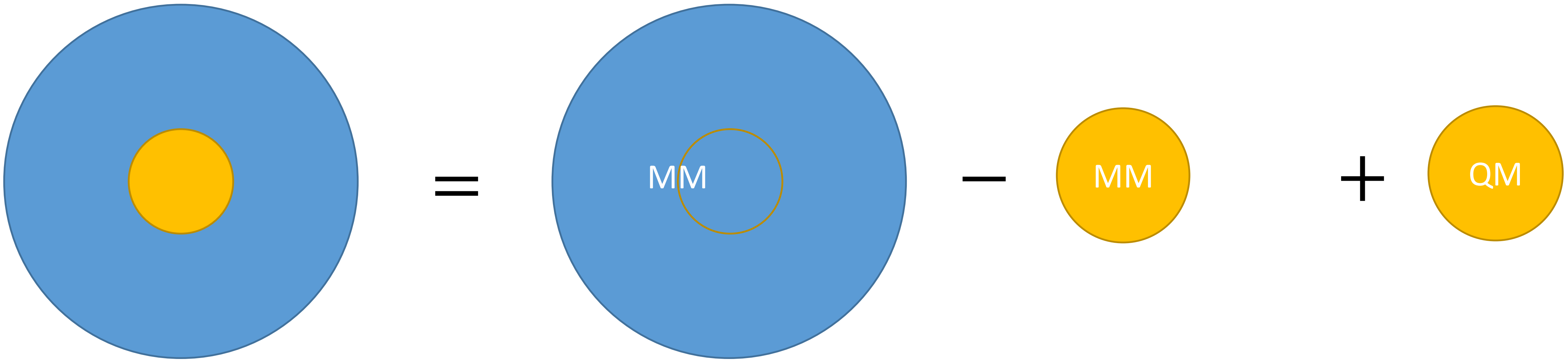


$$E_{tot} = E_{tot}^{MM} - E_{in}^{MM} + E_{in}^{QM}$$

QM/MM partitioning schemes: subtractive scheme

mechanical embedding: electron density of QM atoms represented as point charges in the MM calculation

- point charges can be updated in every step from fitting the electrostatic potential generated by the QM density
- QM calculation is conducted <u>in the absence</u> of the outer region (environment cannot polarize the electron density of the solute)



$$E_{tot} = E_{tot}^{MM} - E_{in}^{MM} + E_{in}^{QM}$$

QM/MM partitioning schemes: subtractive scheme

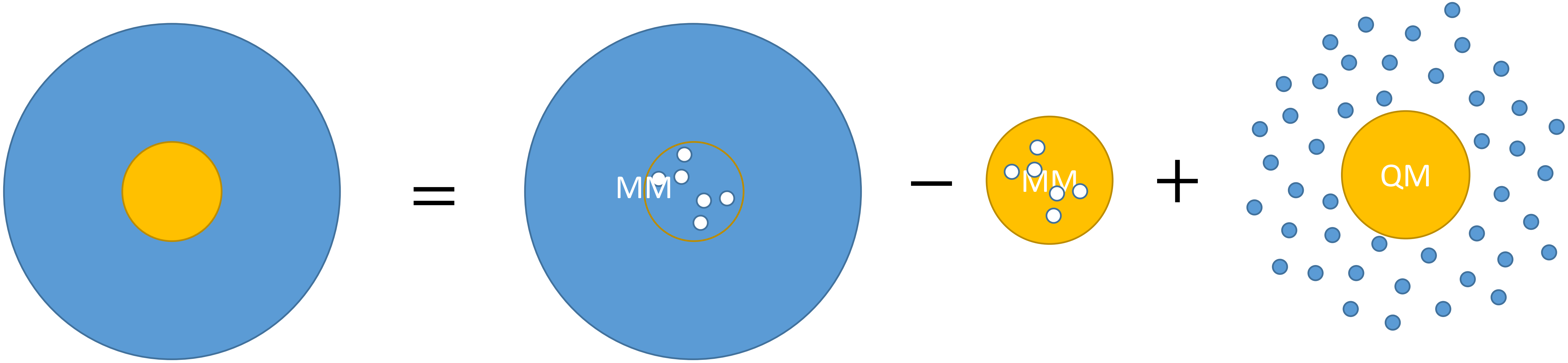
electrostatic embedding: MM atoms represented as point charges in the QM calculation

- introduce additional terms in the Hamiltonian operator

$$\hat{H}^{electr}_{QM/MM} = -\sum_{i\in inner}\sum_{j\in outer}\frac{q_j}{|r_i-R_j|}+\sum_{A\in inner}\sum_{j\in outer}\frac{q_jZ_A}{|r_A-R_j|}$$

i: electrons in the QM layer
A: nuclei in the QM layer
j: atoms (point charges) in the MM layer

- solvent can polarize the electron density of the solute



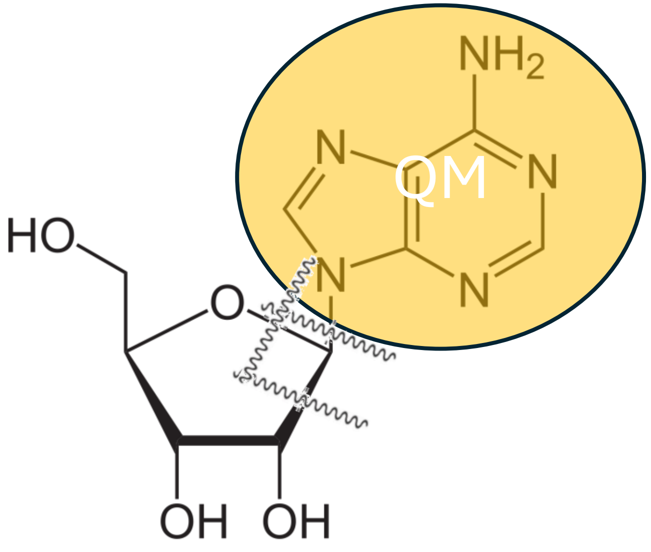
$$E_{tot} = E^{MM}_{tot-in_{ch}} - E^{MM}_{in-in_{ch}} + E^{QM}_{in+out_{ch}}$$

Definition of QM and MM systems: where to put the cut?

Rules of thumb for QM/MM partitioning

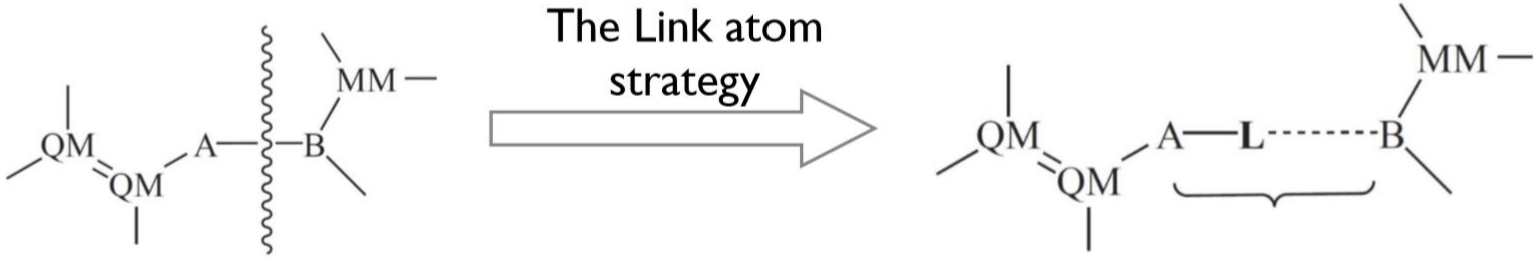
- the QM layer should include the bonds which are formed / broken OR entire photoresponsive system
- no cuts through double or higher order bonds
- cut should be “sufficiently” far from the active center (optimal balance between cost and accuracy)
- the fewer number of cuts, the better

Partitioning along “innocent” C(sp^3)-C(sp^3) bonds should be preferred



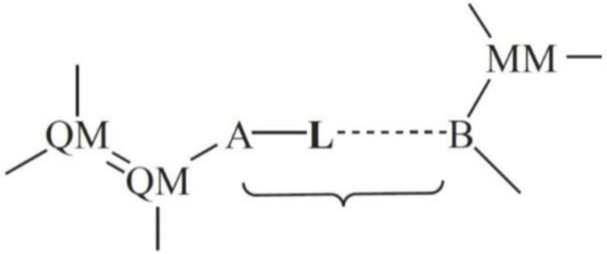
Treatment of QM/MM cuts along covalent bonds

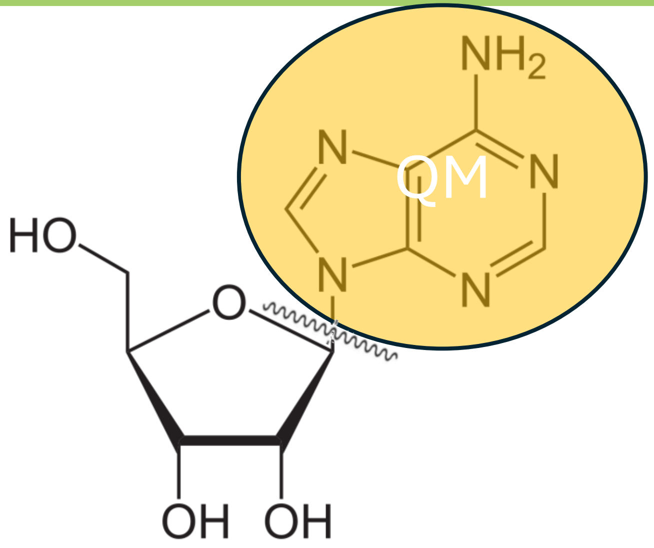
The **link atom strategy**:



- **link atom**: an additional atomic center **L** that is not part of the real system is introduced. It is covalently bound to the QM atom **A** and saturates its free valence
- the link atom **L** is in most cases a hydrogen atom, but any monovalent atom or group might be used (e.g. CH_3)
- QM calculations are performed on an electronically saturated system consisting of the inner subsystem and the link atom(s)
- the real bond **A-B** is described at the MM level

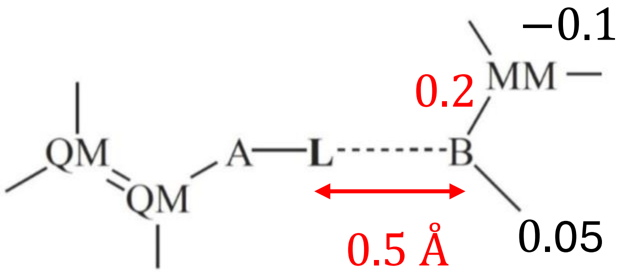
Charge neutrality of QM and MM layers



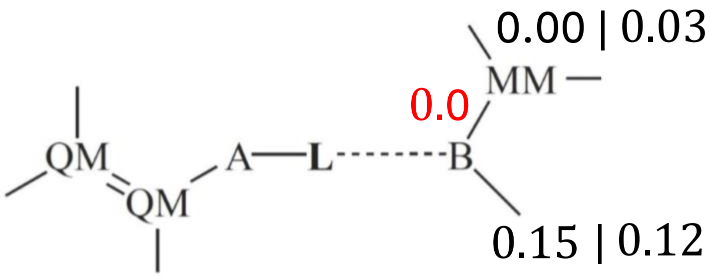


- QM layer has unit charge by definition
- MM layer is built out of units / residues (e.g. nucleosides , amino acids, etc.) which have unit charges
  - if the QM/MM cut is applied at the bond between two residues (rarely the case) then also the MM layer has unit charge
  - if the QM/MM cut is applied at a bond from a residue the MM layer (usually) does not have a unit charge
    - rescaling of the residue charges to assure unit charge

The problem of overpolarization of the link atom

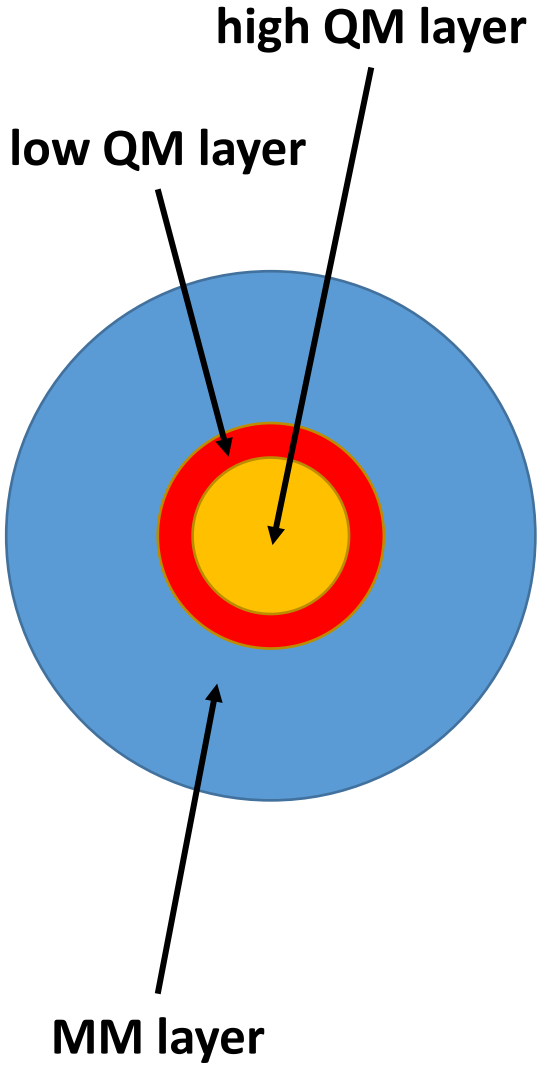


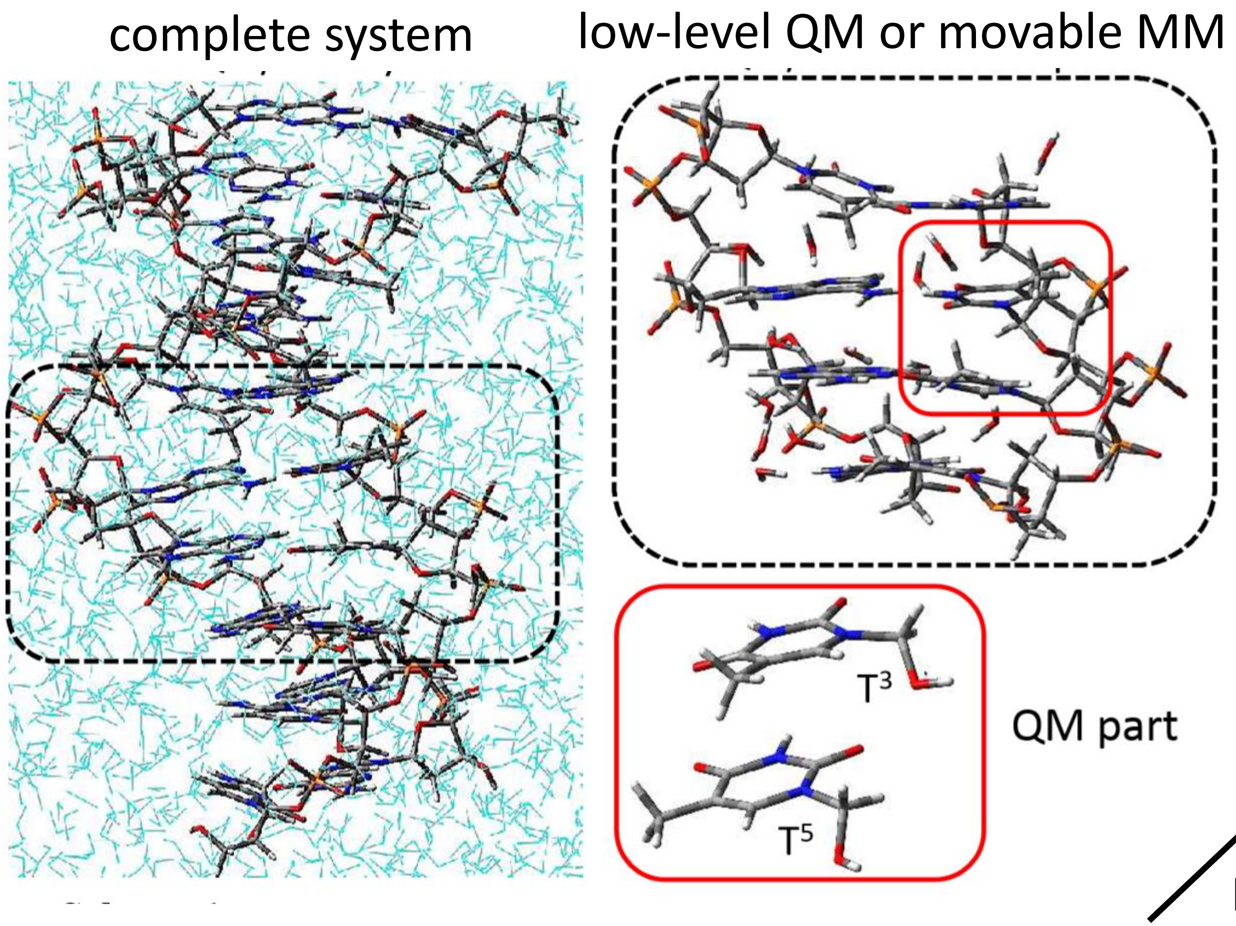
- due to the short **B**--**L** distance, the charge of the close-by atom **B** of the MM layer may overpolarize the QM system
- remedy: redistribute the charge of atom **B** onto the nearby MM atoms (nearest neighbours)
  - v1: equal amounts
  - v2: weighted according to the original charges of the MM atoms

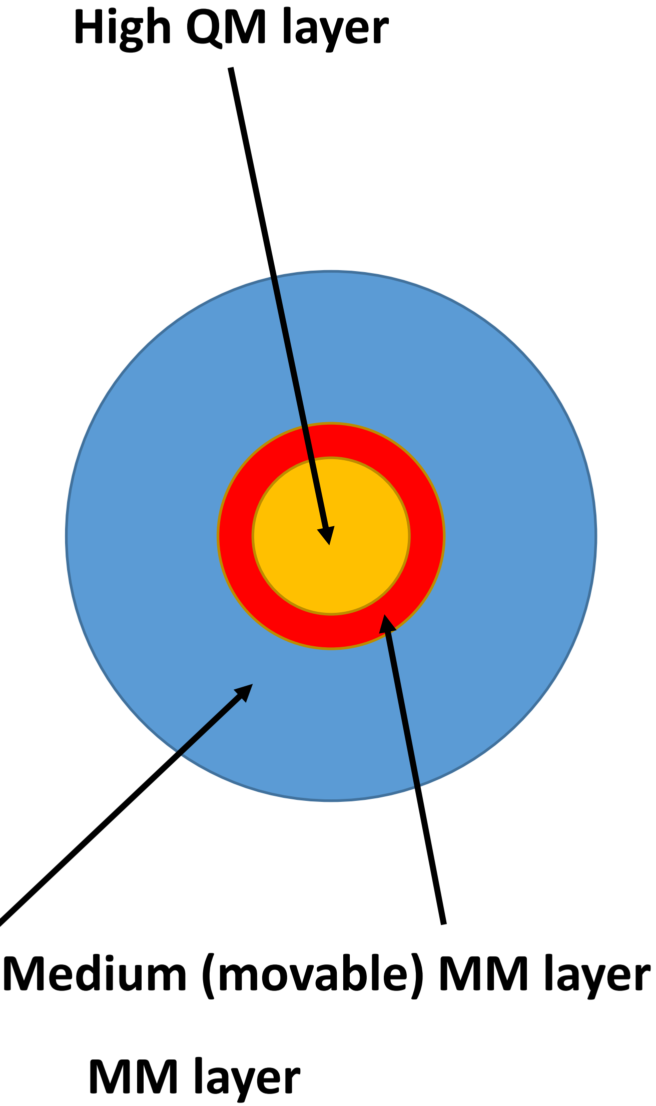


Multi layer schemes

Multi-layer schemes: increase the level of theory / flexibility for atoms in the immediate vicinity of the QM layer





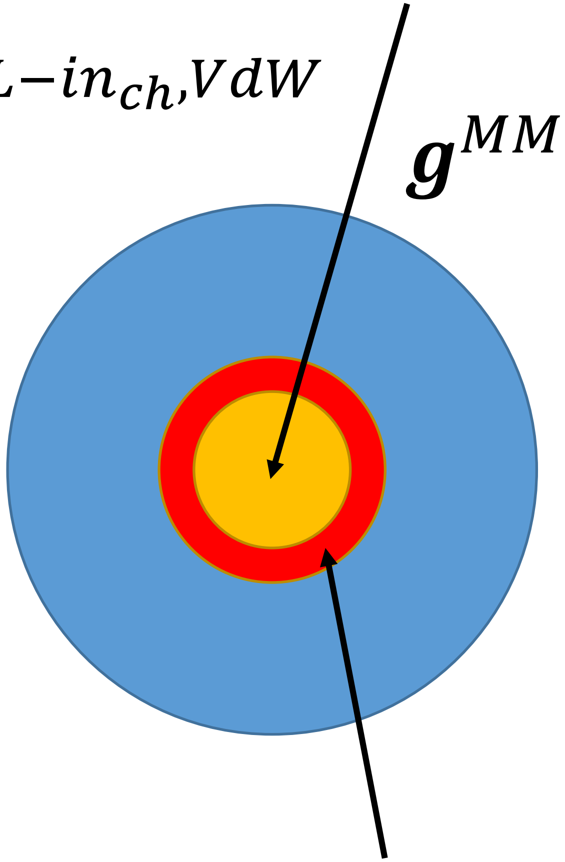


Energy gradients and NACs

$$\boldsymbol{g}_{i}^{QM} = \boldsymbol{g}_{i,H+out_{ch}}^{QM} + \boldsymbol{g}_{HML-in_{ch},VdW}^{MM}$$

- $\boldsymbol{g}_{\boldsymbol{i},H}^{QM}$: gradient of the i-th electronic state of the High layer computed at the QM level
- $\boldsymbol{g}_{HML,VdW}^{MM}$: non-bonding interactions between High and Medium/Low layer computed at the MM level
- link atom gradient projected onto next neighbours High and Medium layer atoms

High QM layer



Medium (movable) MM layer

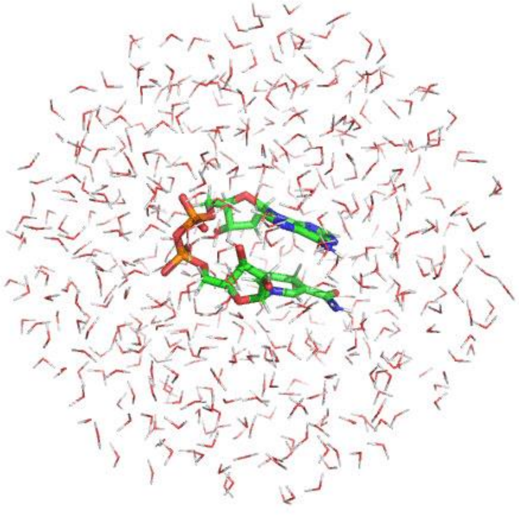
$$\boldsymbol{g}^{MM} = \boldsymbol{g}_{HML-in_{ch}}^{MM} + \sum_{k}^{K} -\boldsymbol{E}_{i,H}^{QM}(\boldsymbol{r}_k)q_k$$

- $\boldsymbol{g}_{HML}^{MM}$: gradient of the Medium layer atoms computed at the MM level
- $\boldsymbol{E}_{i,H}^{QM}(\boldsymbol{r}_i)$: value of the electric field due to the electron density of the i-th electronic state of the High layer at the coordinates of the k-th point charge

NAC computed only for High layer!

- assumed that MM atoms do not induce non-adiabatic couplings (approx. justified as long as link atom sufficiently far from photoresponsive center)

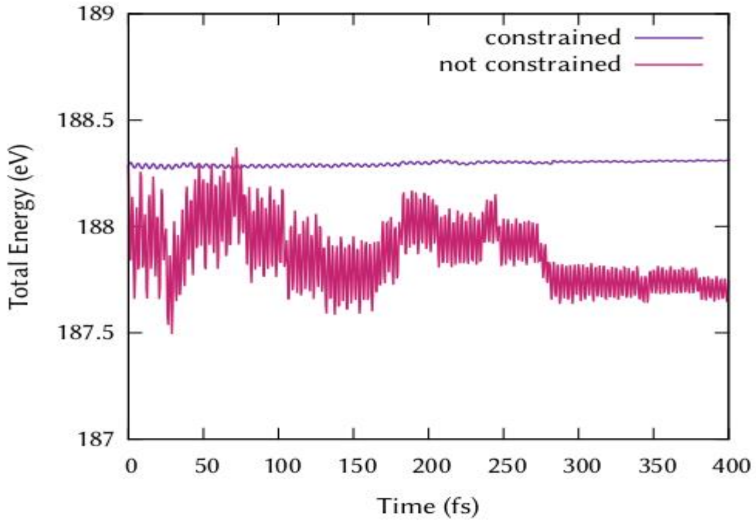
Considerations on dynamics



Wigner sampling

- equilibrate MM atoms around each <u>fixed</u> Wigner sampled geometry for 10 ps (takes care of static disorder across ensemble)
- use Wigner sampled velocities for High layer and MM velocities at last step of equilibration for Medium layer

Rattle



- correction of solvent molecules' velocities in the Velocity Verlet algorithm
- constrain internal DOFs of solvent molecules (keep only translations and rotations)
- as an alternative: use flexible force fields which describe non-equilibrium solvent

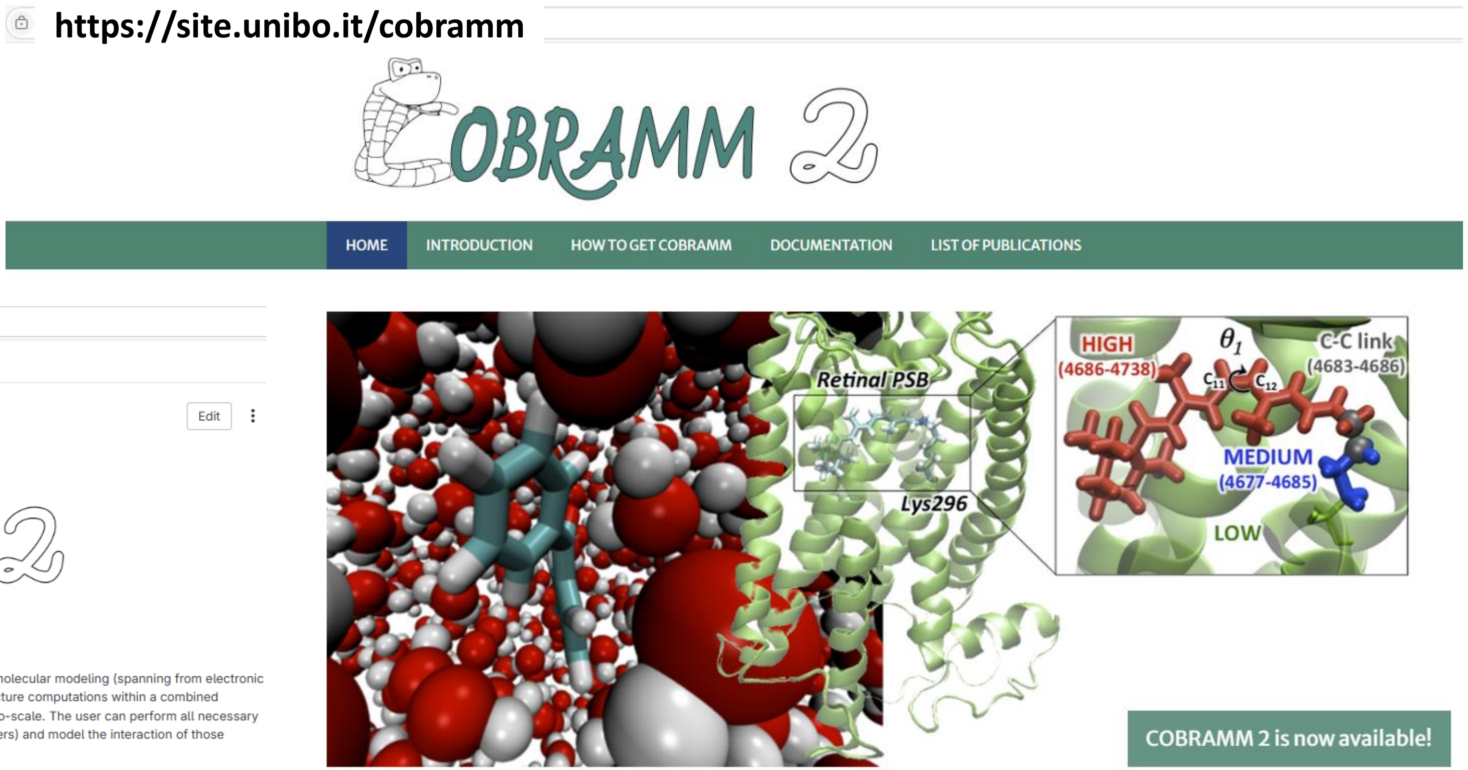
Velocity rescaling

- when using NAC vector, by default only velocities of High layer atoms are adjusted after hopping
- when using GD vectors, make sure that only velocities of High layer atoms are adjusted after hopping

QM/MM with COBRAMM

COBRAMM: Cobramm is Optimized in Bologna to Run Ab-initio and Molecular Mechanics

https://site.unibo.it/cobramm



https://gitlab.com/cobrammgroup/cobramm

Home

Last edited by **Flavia Aleotti** 4 months ago

Welcome to the **COBRAMM** wiki pages!

COBRAMM is a program package interfacing widely known commercial & academic softwares for molecular modeling (spanning from electronic structure to molecular mechanics computations). It allows ground and excited state electronic structure computations within a combined quantum mechanical/molecular mechanical (QM/MM) framework to bridge the atomistic to the nano-scale. The user can perform all necessary steps to simulate chemical reactions in complex environments (ranging from solvents to bio-polymers) and model the interaction of those systems with light to simulate their spectroscopy, as well as their photoinduced dynamics.

A detailed description of the QM/MM methodology and the capabilities of the code is available in the following publication: O. Weingart, A. Nenov, P. Altoè, I. Rivalta, J. Segarra-Martí, I. Dokukina, M. Garavelli, *COBRAMM 2.0 -- A software interface for tailoring molecular electronic structure calculations and running nanoscale (QM/MM) simulations*, J. Mol. Model. 24, 271 (2018).

Requirements and installation

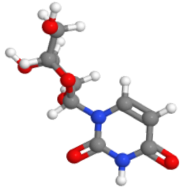
To install COBRAMM on your machine, you can follow the instructions of the brief installation guide contained in the wiki.

COBRAMM Manual

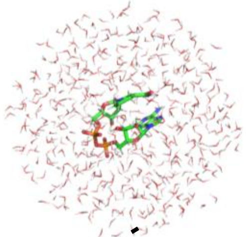
1. Introduction
   1. The QM/MM partitioning scheme
   2. The boundary region
   3. Handling QM/MM non-bonding cross-terms
   4. The COBRAMM code
2. Basic guide to COBRAMM
   1. Input Files Description
   2. Input preparation
   3. Running COBRAMM
   4. Working with COBRAMM numerical routines
   5. Post-processing utilities
3. Task-based manual
4. Software-based manual

COBRAMM features

gas-phase geometry



Conformational Dynamics



Crystal Structure

COBRAMM

Potential energy surface exploration

$$\hat{\mathcal{H}}\Psi = \mathcal{E}\Psi$$

Multiconfiguration WF theory

Density functional theory

COBRAMM: High / Medium / Low layer partitioning

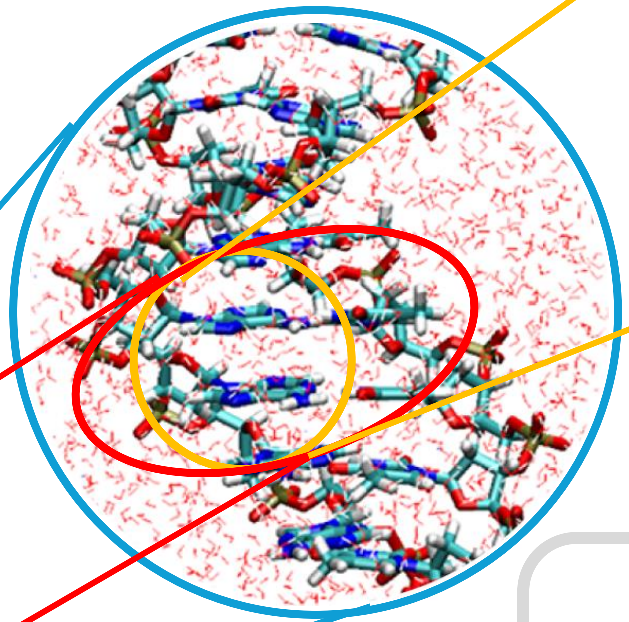
quantum mechanics

OPEN MOLCAS

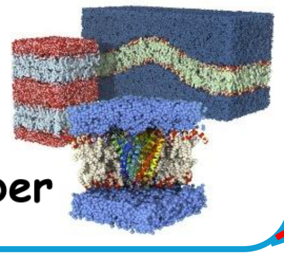
Molpro

OpenQP

COBRAMM



molecular mechanics

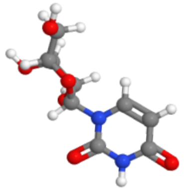

Amber

- geometry optimizations (minima, TS, CoIn)
- normal modes and frequencies
- minimum energy paths
- relaxed and frozen scans

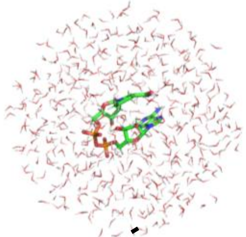
ORCA

COBRAMM features

gas-phase geometry



Conformational Dynamics



Crystal Structure

Multiconfiguration WF theory

Density functional theory

Potential energy surface exploration

$$\hat{\mathcal{H}}\Psi = \mathcal{E}\Psi$$

COBRAMM

Non-Adiabatic Dynamics

on-the-fly dynamics (Tully’s FSSH)

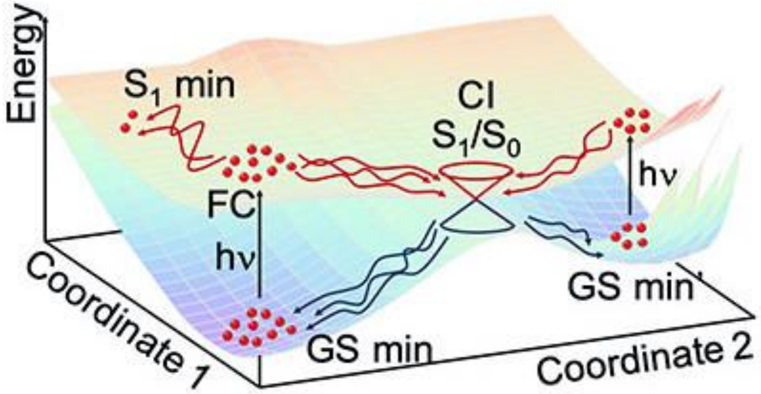
quantum dynamics (model Hamiltonians)

$$\frac{\partial|\psi(t)\rangle}{\partial t} = -\frac{i}{\hbar}\hat{H}|\psi(t)\rangle$$

Excited state non-adiabatic dynamics

Mixed quantum-classical dynamics in explicit movable solvent

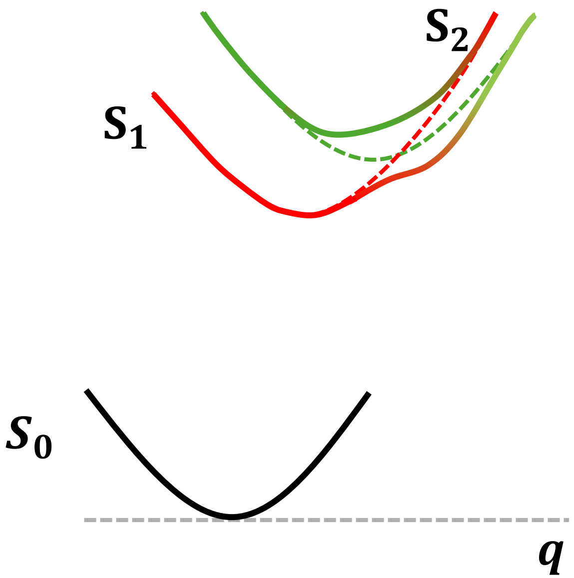
(MQCD/MM)



- Tully Fewest Switches Surface Hopping
  - hopping probability estimated through non-adiabatic or time-derivative couplings
- CASSCF/CASPT2 (Molcas, Molpro)
- TD-DFT (Gaussian, Turbomole)
- MR-DFT (OpenQP, only in vacuo)

Full-Dimensional Quantum dynamics in explicit movable solvent

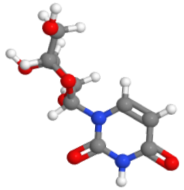
(QD/MM)



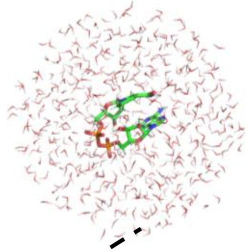
- Hamiltonian of High Layer approximated by a Linear Vibronic Coupling model (rigid systems, fast dynamics)
- quantum-classical interaction treated by a mean field approach
- COBRAMM-Quantics (MCTDH) interface
- fully automatized parametrization at CASPT2 level (through Molcas)

COBRAMM features

gas-phase geometry



Conformational Dynamics



Crystal Structure

Multiconfiguration WF theory

Density functional theory

Potential energy surface exploration

$$\hat{\mathcal{H}}\Psi = \mathcal{E}\Psi$$

COBRAMM

Transient Spectroscopy

$$\boldsymbol{P}^{(3)}(t) = R^{(3)}(t_3, t_2)$$

transient spectroscopy

post-processing & analysis

Non-Adiabatic Dynamics

$$\frac{\partial|\psi(t)\rangle}{\partial t} = -\frac{i}{\hbar}\hat{H}|\psi(t)\rangle$$

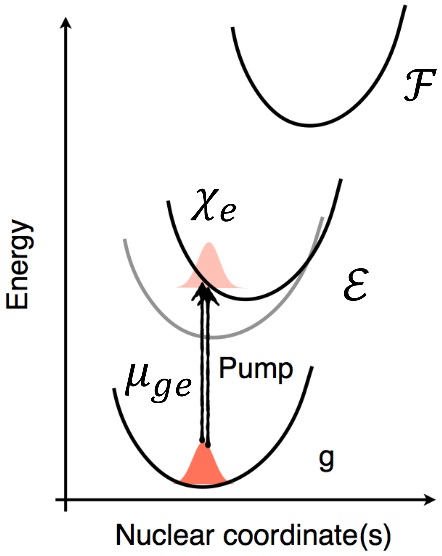
on-the-fly dynamics (Tully’s FSSH)

quantum dynamics (model Hamiltonians)

Transient spectroscopy

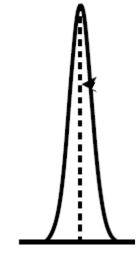
$$\Psi(r,R,t) = \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)|\chi_i(R,t)\rangle|\psi_i(r)\rangle$$

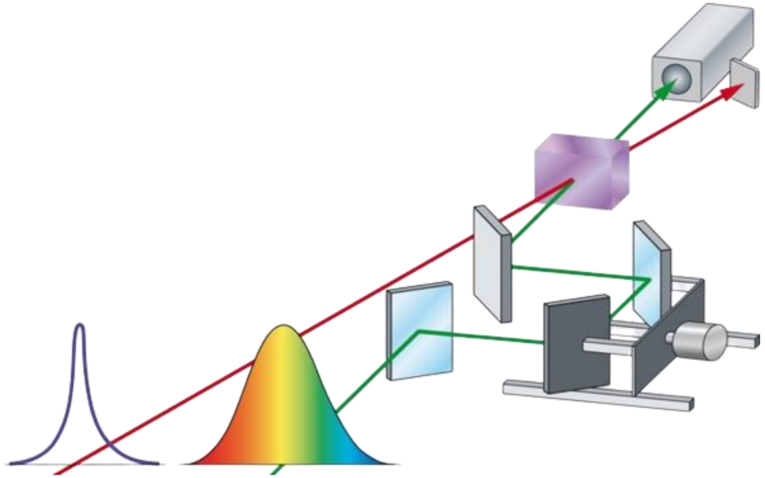
Pump: g → $\mathcal{E}$ wave packet projection



t_2 t_3

pump



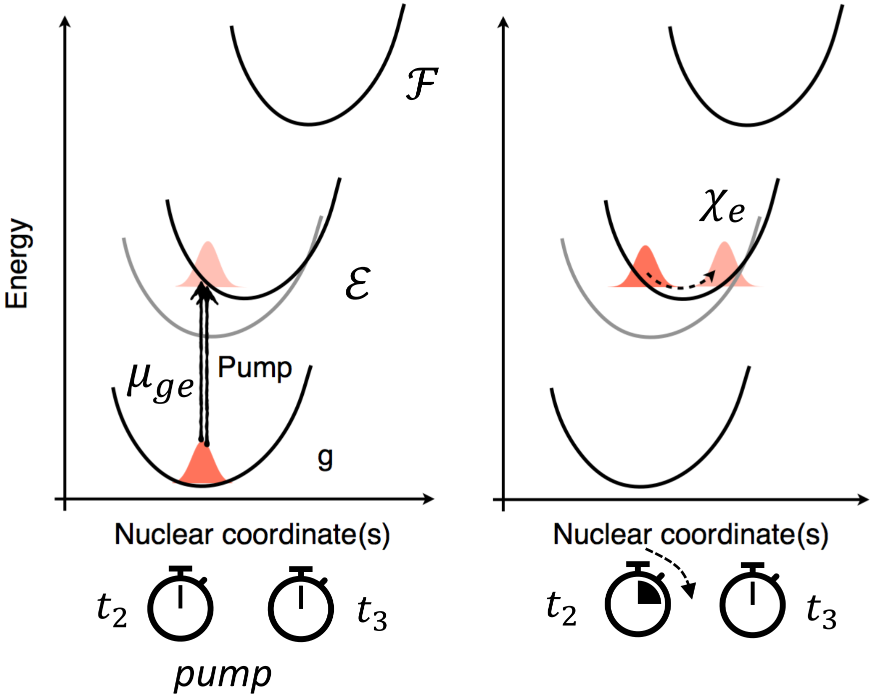


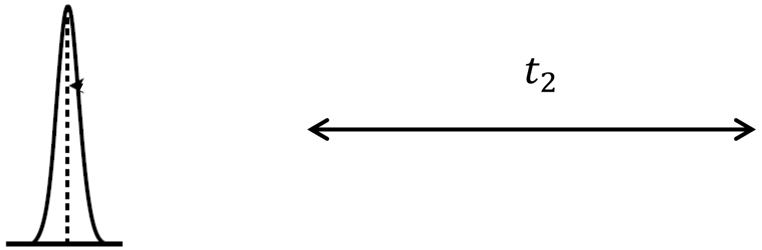
Transient spectroscopy

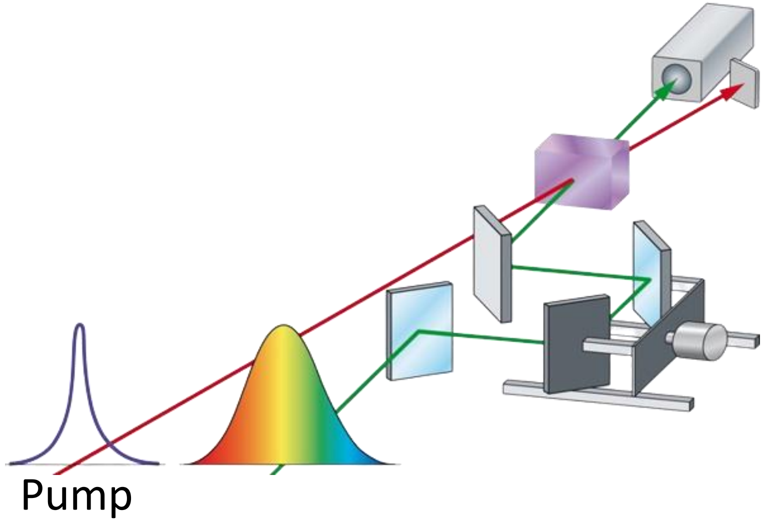
$$\Psi(r,R,t) = \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)|\chi_i(R,t)\rangle|\psi_i(r)\rangle$$

Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2







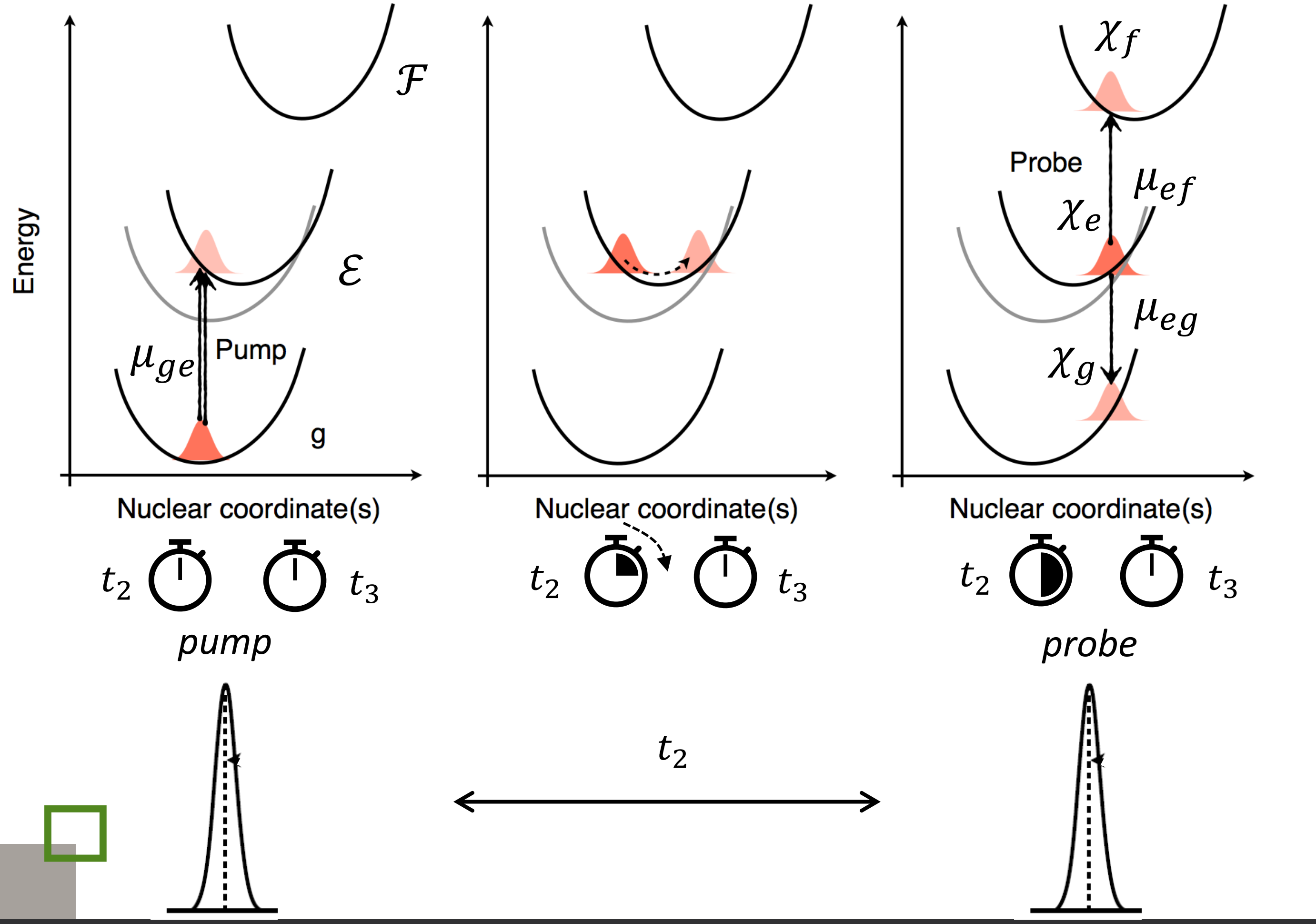
Transient spectroscopy

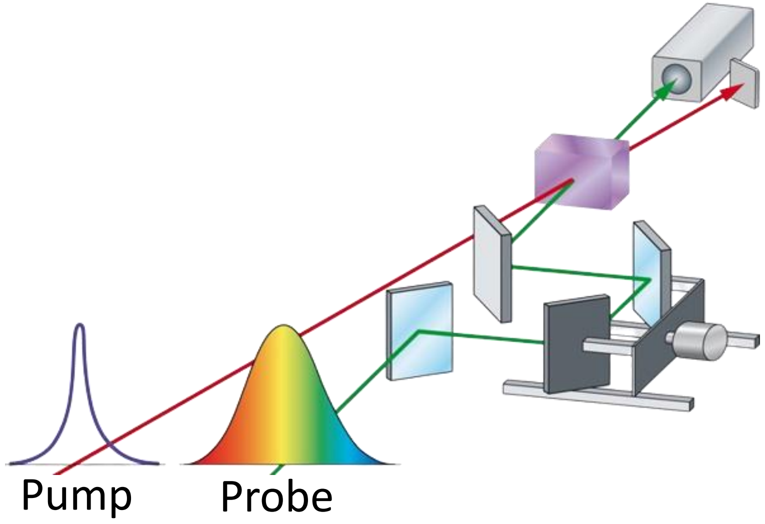
$$\Psi(r,R,t) = \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)|\chi_i(R,t)\rangle|\psi_i(r)\rangle$$

Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2

Probe: $\mathcal{E}$ → g/$\mathcal{F}$ wave packet projection





Transient spectroscopy

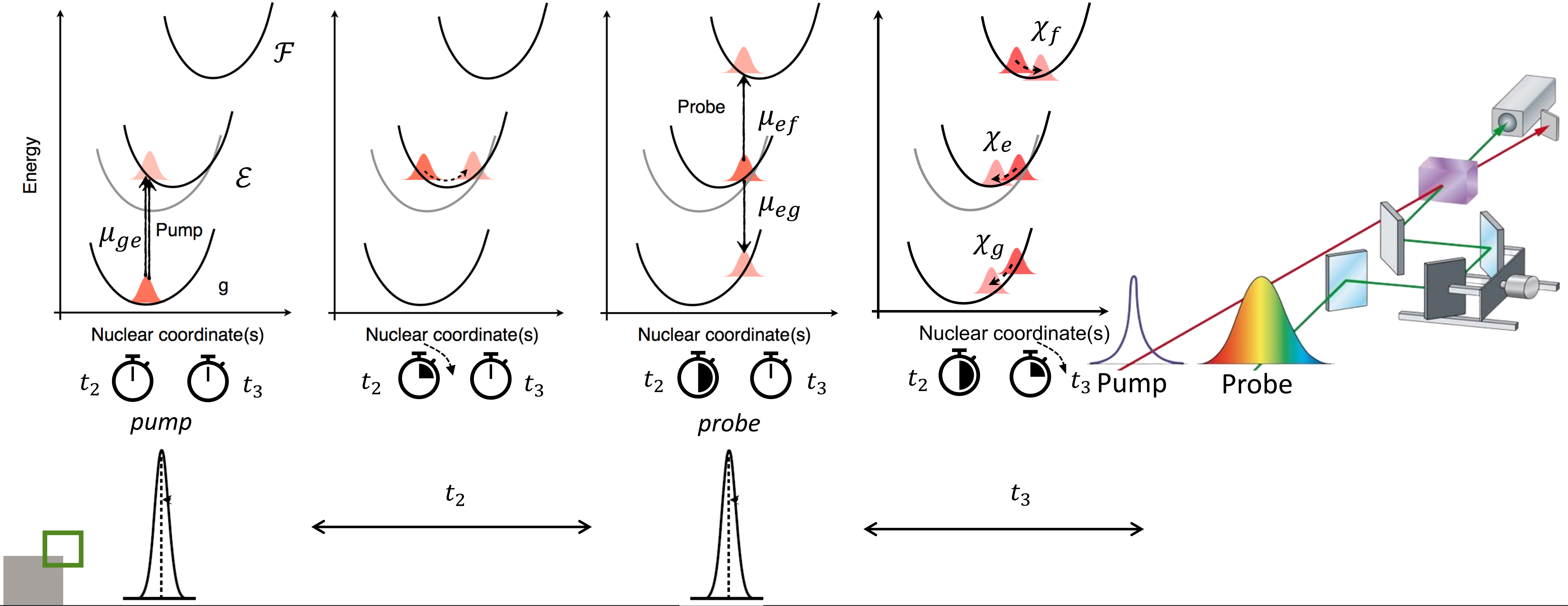
$$\Psi(r,R,t) = \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)|\chi_i(R,t)\rangle|\psi_i(r)\rangle$$

Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2

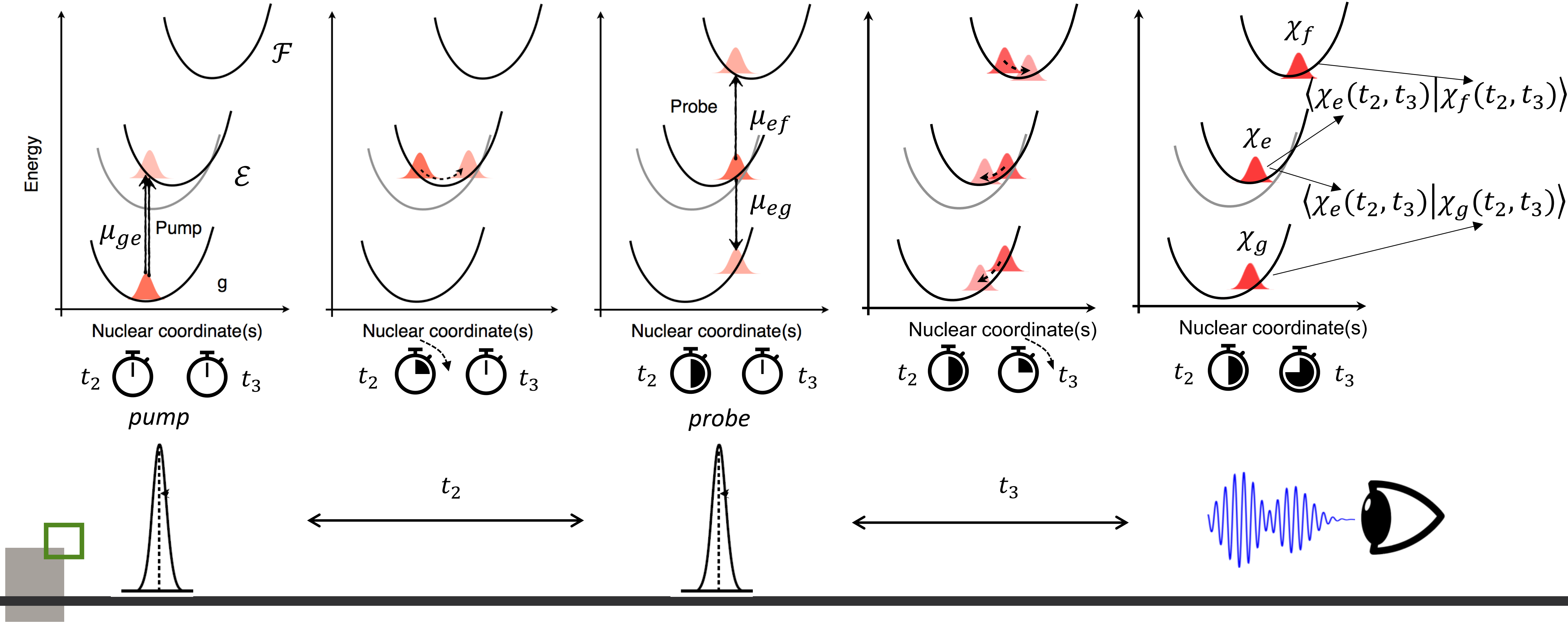
Probe: $\mathcal{E}$ → g/$\mathcal{F}$ wave packet projection

coherence evolution during t_3



Transient spectroscopy

$$\Psi(r,R,t) = \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)|\chi_i(R,t)\rangle|\psi_i(r)\rangle$$



Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2

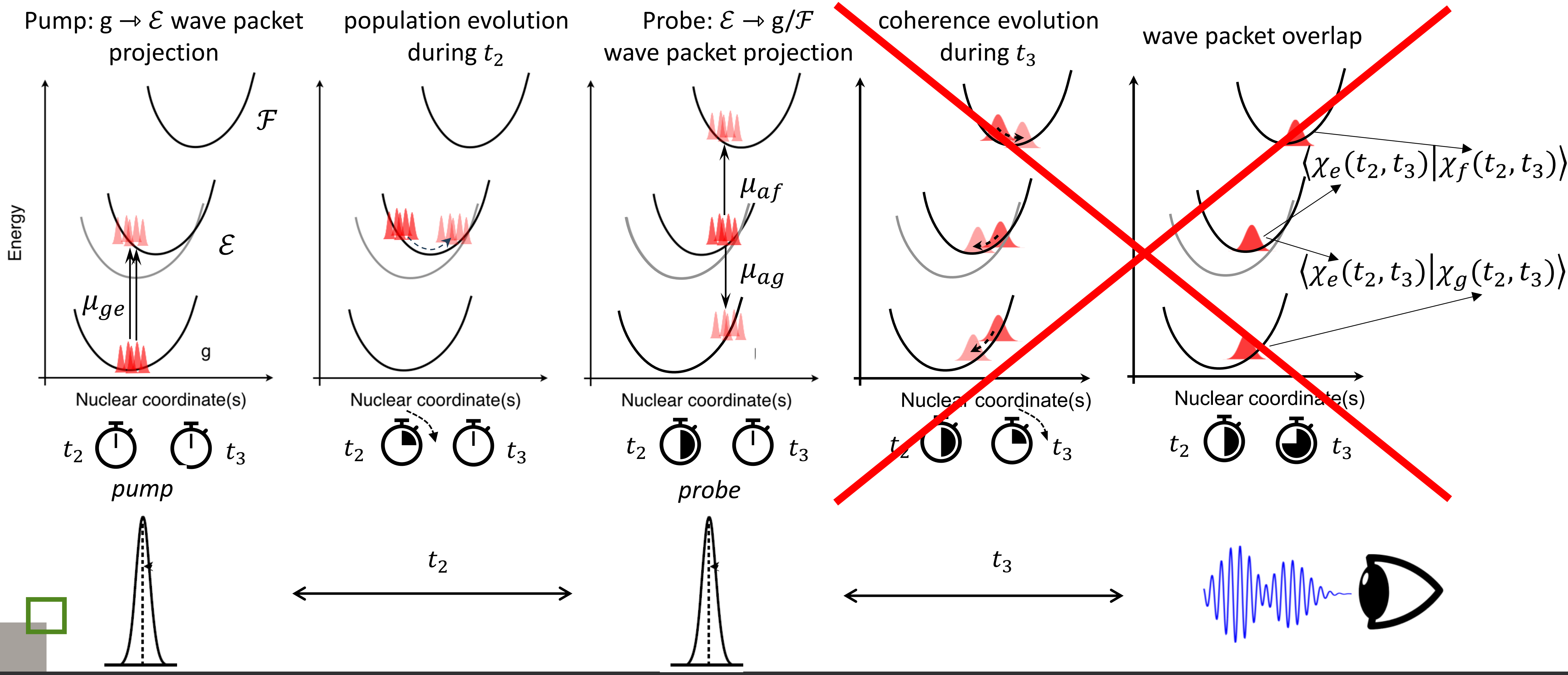
Probe: $\mathcal{E}$ → g/$\mathcal{F}$ wave packet projection

coherence evolution during t_3

wave packet overlap

Transient spectroscopy from on-the-fly dynamics

$$\Psi(r,R,t) \approx \sum_{n} \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)\delta_n(R_n,t)|\psi_i(r)\rangle$$



Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2

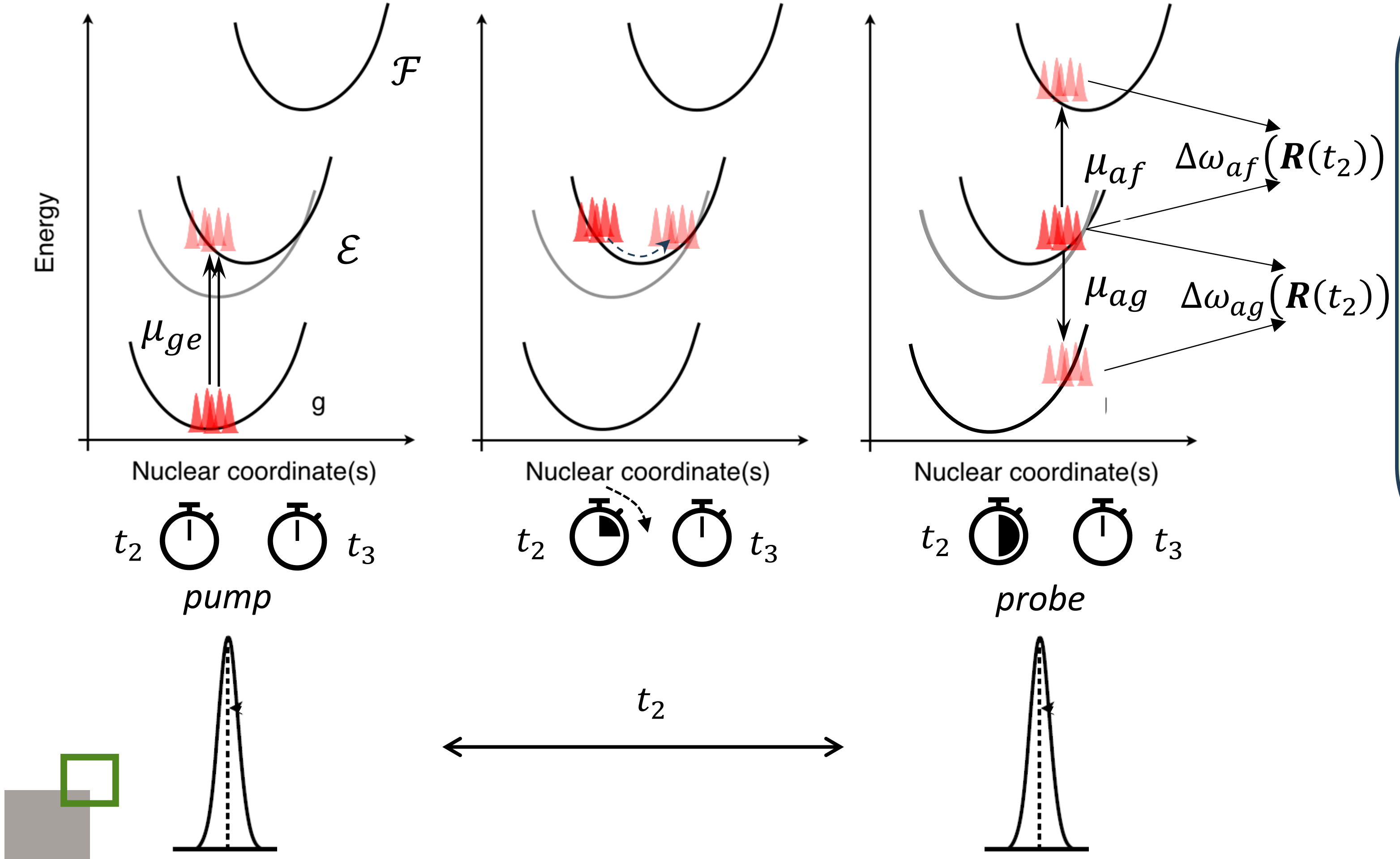
Probe: $\mathcal{E}$ → g/$\mathcal{F}$ wave packet projection

coherence evolution during t_3

wave packet overlap

Transient spectroscopy from on-the-fly dynamics

$$\Psi(r,R,t) \approx \sum_{n} \sum_{i\in g,\mathcal{E},\mathcal{F}} c_i(t)\delta_n(R_n,t)|\psi_i(r)\rangle$$



Pump: g → $\mathcal{E}$ wave packet projection

population evolution during t_2

Probe: $\mathcal{E}$ → g/$\mathcal{F}$ wave packet projection

3rd order nonlinear response

$$I(\omega,t_2) =$$

$$-\sum_{n} |\mu^n_{gb}|^2 |\mu^n_{gb}|^2 e^{-\frac{\left(\omega-\Delta\omega^n_{gb}(\boldsymbol{R}_n(t_2=0)\right)^2}{2\sigma^2}} \quad \boxed{\text{GSB}}$$

$$-\sum_{n} |\mu^n_{gb}|^2 |\mu^n_{ag}|^2 e^{-\frac{\left(\omega-\Delta\omega^n_{ag}(\boldsymbol{R}_n(t_2))\right)^2}{2\sigma^2}} \quad \boxed{\text{SE}}$$

$$+\sum_{n} \sum_{i\in\mathcal{F}} |\mu^n_{gb}|^2 |\mu^n_{ai}|^2 e^{-\frac{\left(\omega-\Delta\omega^n_{ai}(\boldsymbol{R}_n(t_2))\right)^2}{2\sigma^2}} \quad \boxed{\text{ESA}}$$

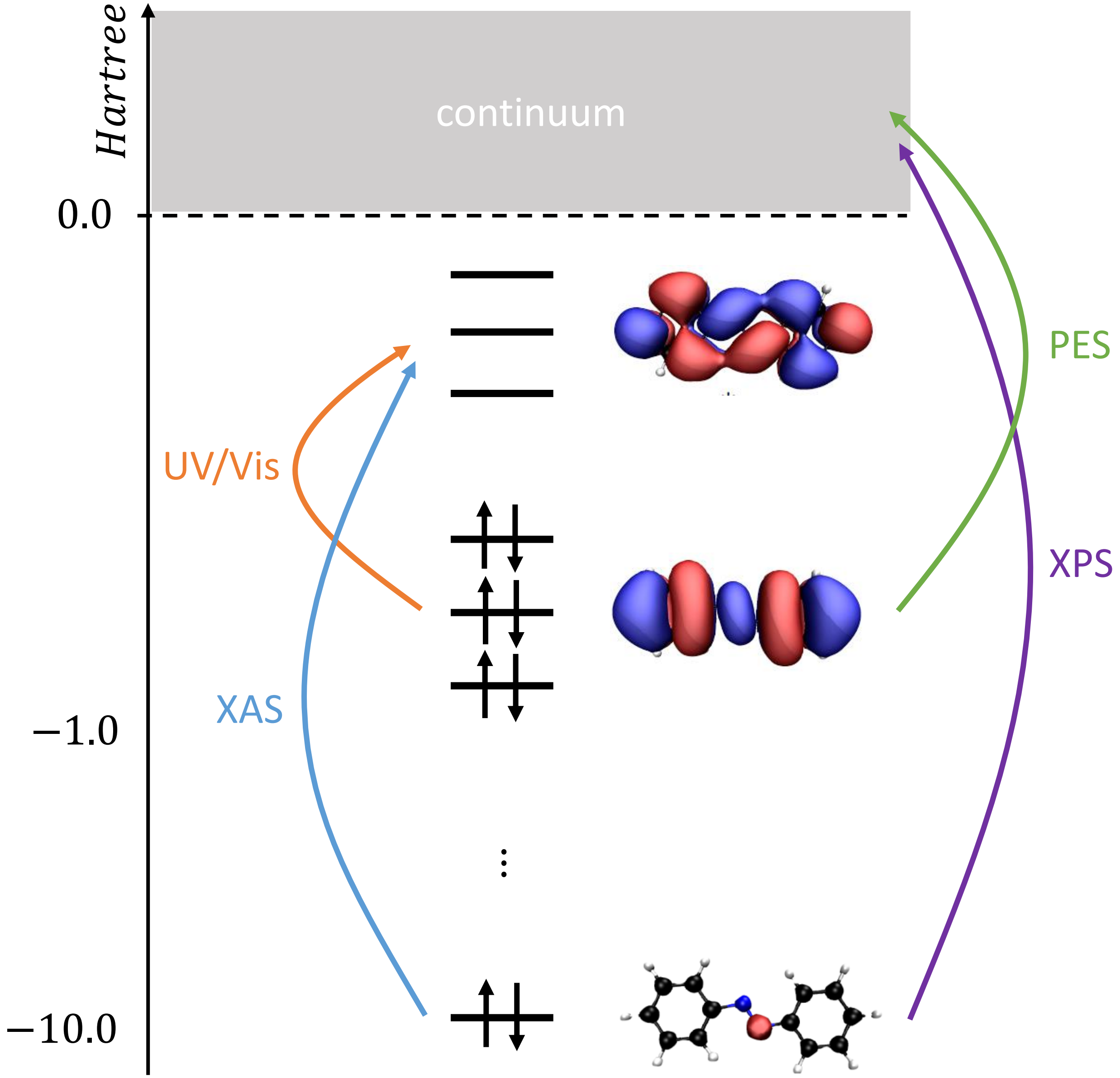
active state

phenomenological broadening

bright state

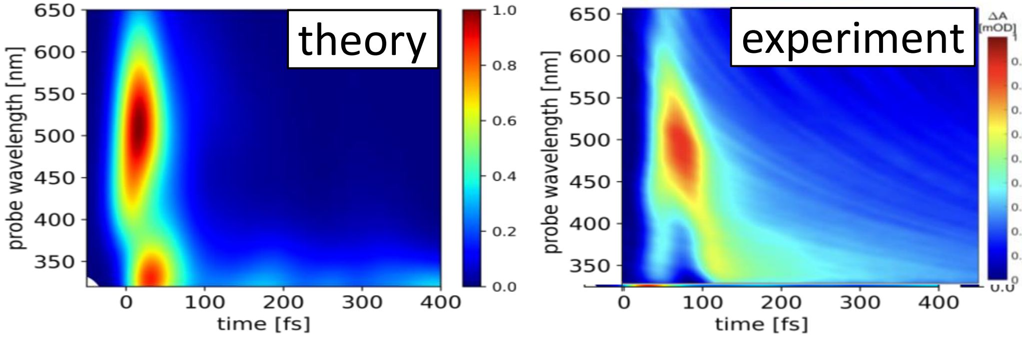
Transient Spectroscopy

- UV/Vis ($1.5 - 6\ eV$, valence → valence* orbitals)
- far UV ($6 - 20\ eV$, ionization from valence MO)
  - **P**hoto-**E**lectron **S**pectroscopy (PES)
- X-ray ($> 20\ eV$, transitions and ionization from core-orbitals)
  - **X**-ray **A**bsorption **S**pectroscopy (XAS)
  - **X**-ray **P**hoto-**E**lectron **S**pectroscopy (XPS)

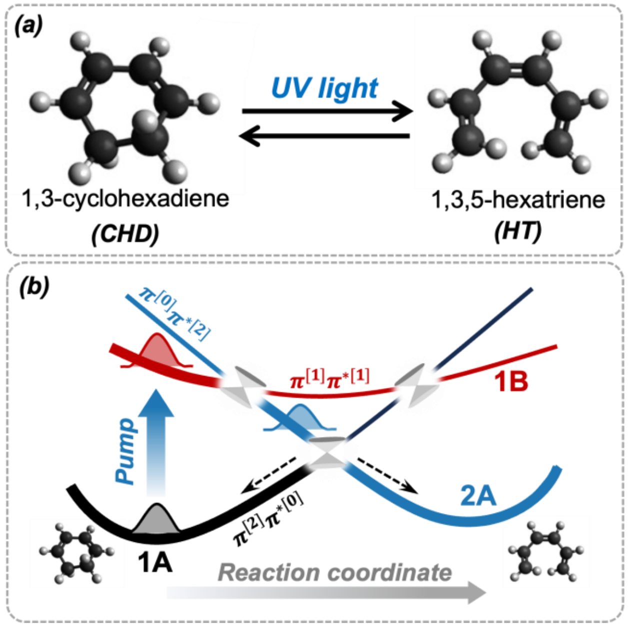


Transient spectroscopy in COBRAMM

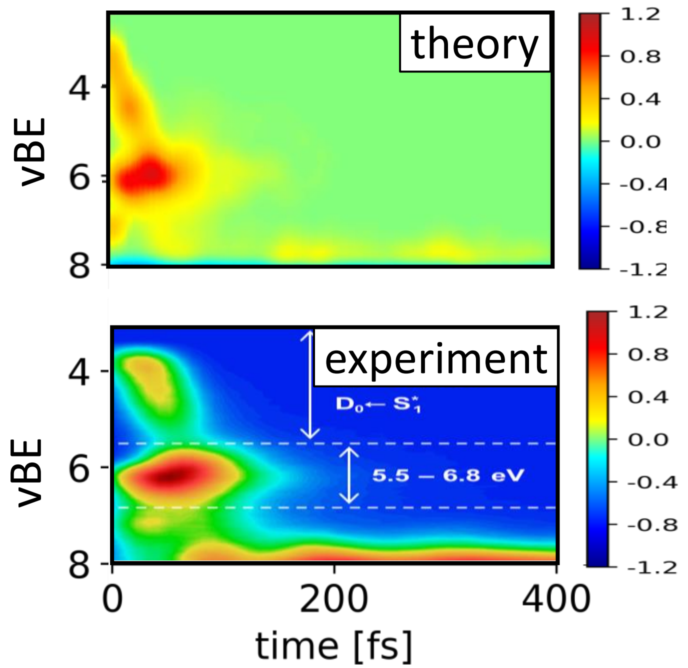
Transient UV/Vis Absorption



- TD-DFT
- RASSCF/RASPT2
- TD-DFT//RASPT2

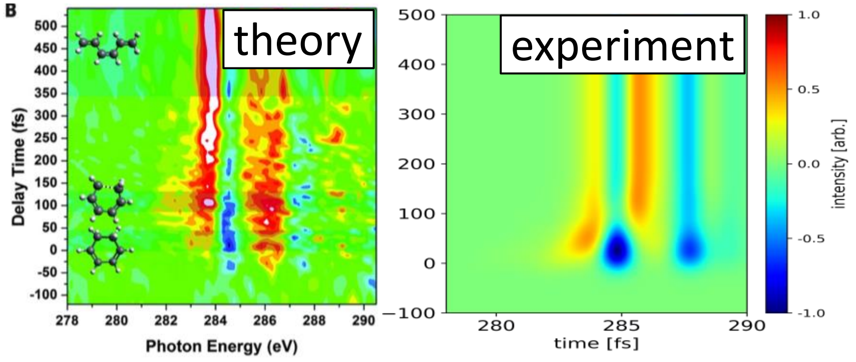


Transient Photo-Emission



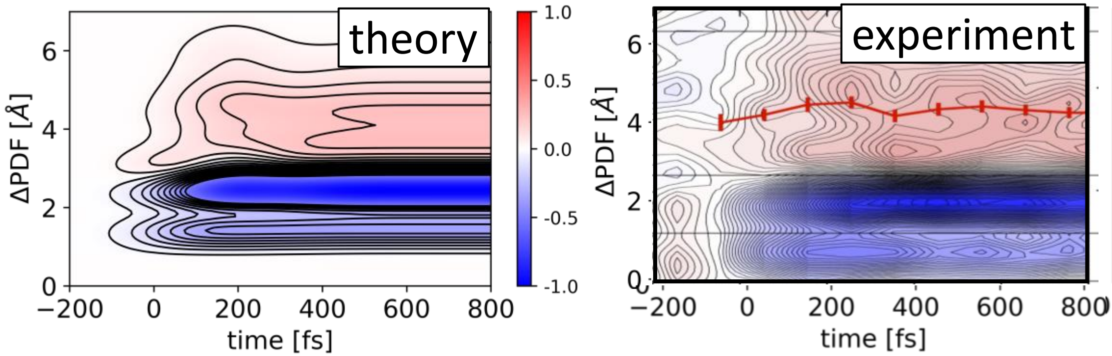
- RASSCF/RASPT2

Transient X-ray Absorption



- RASSCF/RASPT2

Transient Ultrafast Electron Diffraction



- TD-DFT
- RASSCF/RASPT2