CHE501 Lecture Notes

see also part 1 (CHE502) and supplementary materials and examples from previous years

see http://loriot.ism.u-bordeaux.fr/vistec2019.1/vistec2019.1.html

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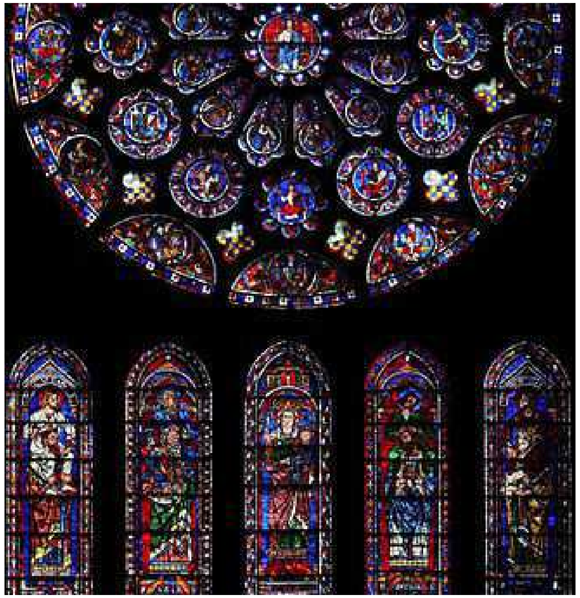
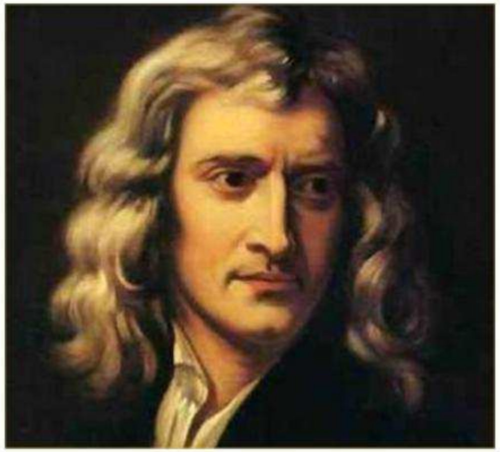
Wenn wir wüssten, was wir tun,
würde man es nicht Forschung nennen.

(If we knew what we are doing
it would not be called research)

Albert Einstein





"If I have seen farther than others, it is because
I have stood on the shoulders of giants."

Sir Isaac Newton (1642 – 1727) Physicist

Grades (American English) or Marks (British English)

50%: Written open-book exam of $\approx$ 2 hours on the last day (Feb. 15)
$+$
50%: Doing a small ($\lessapprox 50$ lines) coding exercise on an MD-related problem as a take-home exam on the last 3 days
(Feb. 12-14 (or so)) of the course

Part 1: We try to remember CHE502

— a little bit of Quantum Mechanics (QM)

— a little bit of Statistical Mechanics

Part 2: Statistical Mechanics via molecular simulations (MD & MC)

— Modeling

— A Few Necessary Approximations & Tricks

Part 3: Extracting Information from Simulations

— Statics (thermodynamics)

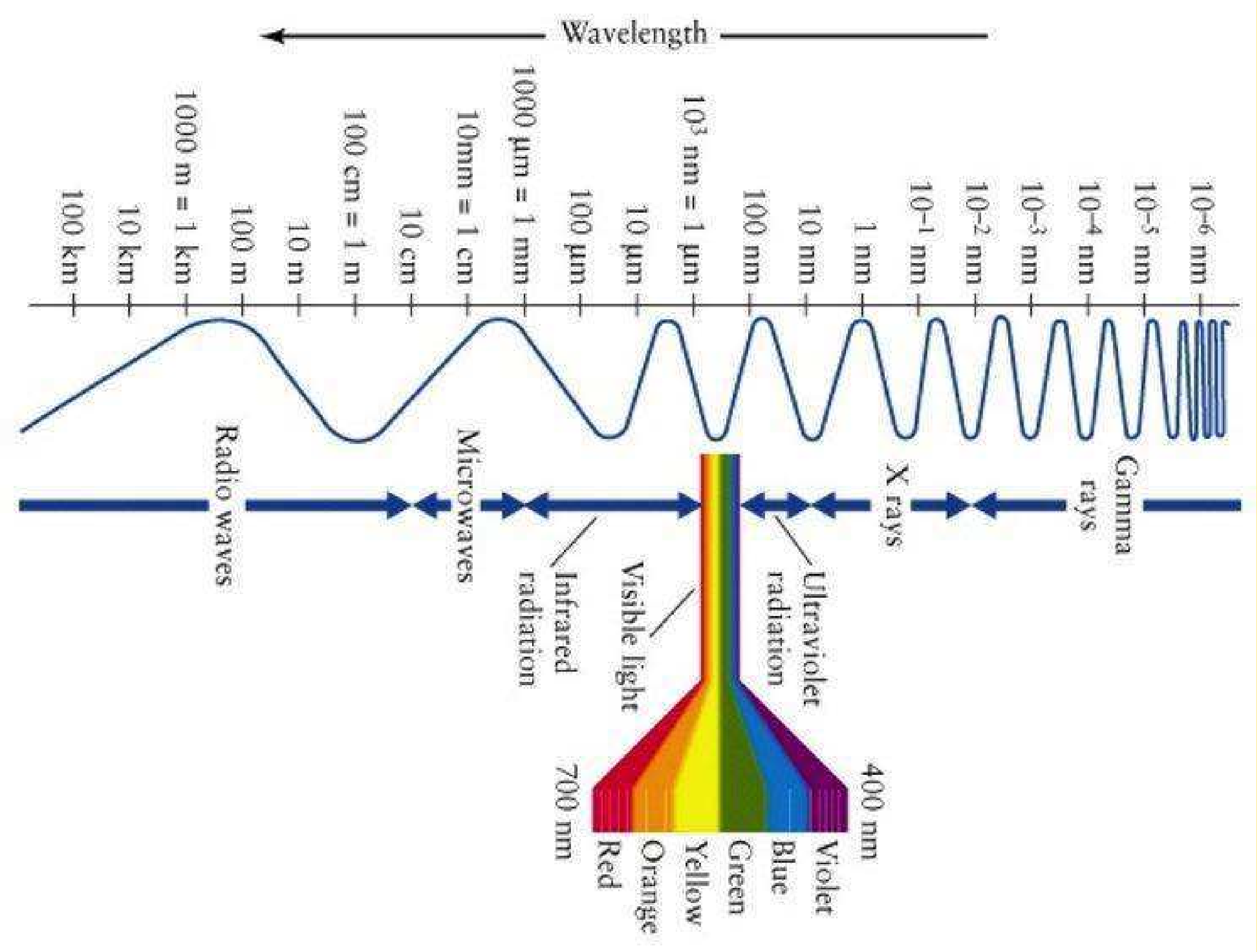
— Dynamics (kinetics)

Part 4: Other Simulation Methods

Part 5: Examples, Computer Lab

Part 1 CHE502

— Quantum Mechanics



Time independent Schrödinger Equation

$$\hat{H}\ \Psi_{i_1,i_2,i_3,...}(x_1,x_2,x_3,...) = E_{i_1,i_2,i_3,...} \cdot \Psi_{i_1,i_2,i_3,...}(x_1,x_2,x_3,...)$$

$\hat{H}$: 0 (describes the system (atom, molecule, ...))
$\Psi_{i_1,i_2,i_3,...}(x_1,x_2,x_3,...)$: Wavefunction, eigenfunction, also called state,
with n independent variables x_j and n quantum numbers i_j
$E_{i_1,i_2,i_3,...}$: Energy eigenvalues

Hamiltonian $\hat{H}$	Eigenvalues E	Eigenfunctions Ψ
particle in box	$E_n = h^2/(8mL^2) \cdot n^2, n = 1,2,3...$	Cosine
harmonic oscillator	$E_v = \hbar\omega(v+1/2) \quad , v = 0,1,2,..$	Hermite·Gaussian
rigid rotor	$E_l = \hbar^2/(2I)l(l+1), l = 0,1,2...$	spherical harmonics (l,m)
hydrogenoid	$E_n = -\mathcal{R} \cdot 1/n^2, n = 1,2,3...$	*
....	......	...

— Statistical Mechanics

If we know (or can construct to a good approximations) all
(or at least a "representative sample") of the (micro-)states of a system
that are compatible with our macroscopic state
(e.g. NVE, NVT, NpT, μVT, ...)
then we can (in principle, if not practically) compute its partition function
(called Ω, Q (Z), Ξ, ...)

We have studied a few cases, where the ratio of partition functions
($=$ the equilibrium constant k of a gas-phase reaction)
can be obtained to a good approximation using only the first term of the partition function
(i.e. only one of the very large number of possible states)

This is, however, quite exceptional, and in most cases we have to do a more careful job.

Q, the canonical partition function (sum of states Z)

$$Q = \sum_{\textbf{all states } i} \exp(\frac{-E_i(N,V,T)}{k_\mathrm{B}T})$$

The average value $\langle ... \rangle$ of any quantity (observable) A over the given ensemble (NVE, NVT , etc.) is given by (just two examples):

$$\langle A \rangle_T = \frac{1}{Q} \int_{\mathrm{all}\ p,q} A(p,q) \cdot \exp \frac{-E(p,q)}{k_\mathrm{B}T} \, \mathrm{d}p \, \mathrm{d}q$$

where q stands for all positions variables $(x_1, y_1, z_1, x_2.y_2, ..., z_N)$
and p for all velocity variables $(vx_1, vy_1, ..., vz_N)$

So the integrals are $6N$-fold integrals ($\int \int \int ...... \int$) over the (q,p)-space, which is called **phase space**

From Ω (NVE), it is

$$\langle A \rangle_E = \frac{1}{\Omega} \int_{\text{all } p,q} A(p,q) \cdot \delta(E(p,q) - E_0) \, \mathrm{d}p \, \mathrm{d}q \qquad (\mathrm{Av}\Omega)$$

In both cases (and in all other cases):

$\Rightarrow$ not really doable (too many $\int \iint \iiint \iiiint \ldots \mathrm{d}x_1 \mathrm{d}x_2 \mathrm{d}x_3 \mathrm{d}\ldots \mathrm{d}v_1 \mathrm{d}v_2 \mathrm{d}\ldots$)

$\Rightarrow$ simulations

Part 2 Basic Ideas

Instead of doing systematically all the $\int\int\int\int$ over all the q and p, we try to select beforehand those q and p which contribute markedly to the integral for $\langle A \rangle$.

Doing this is a **"simulation"**

→ We construct a **sample** of qs and ps compatible with our conditions (NVE, NVT, etc.)

→ The computation of the averages is thus much simpler:

Thermodynamic average from simulations (**much simpler!**)

$$\mathrm{MD:}\quad \langle A \rangle_E = \frac{1}{N}\sum_{i=1}^{N} A(\mathcal{P}_i)$$

$$(\ \mathrm{and\ for\ later:}\quad \mathrm{MC:}\quad \langle A \rangle_T = \frac{1}{N}\sum_{i=1}^{N} A(\mathcal{C}_i)\quad)$$

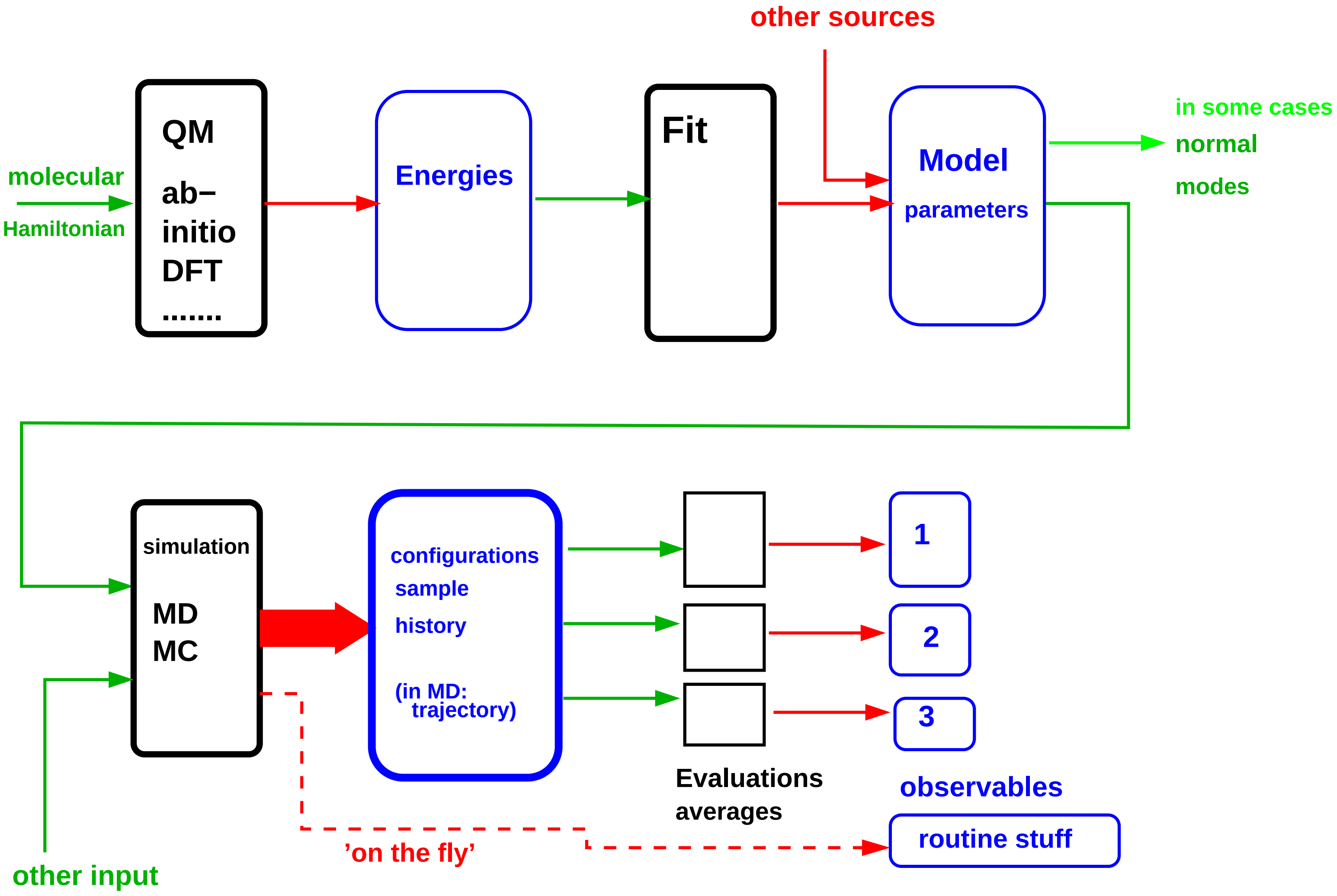
---

where $\mathcal{P}_i$ (which stands for all the q and p) is called the ith configuration (from the sample) in **phase space**
and $\mathcal{C}_i$ (all the q only) is the ith configuration (from the sample) in **configuration** space)

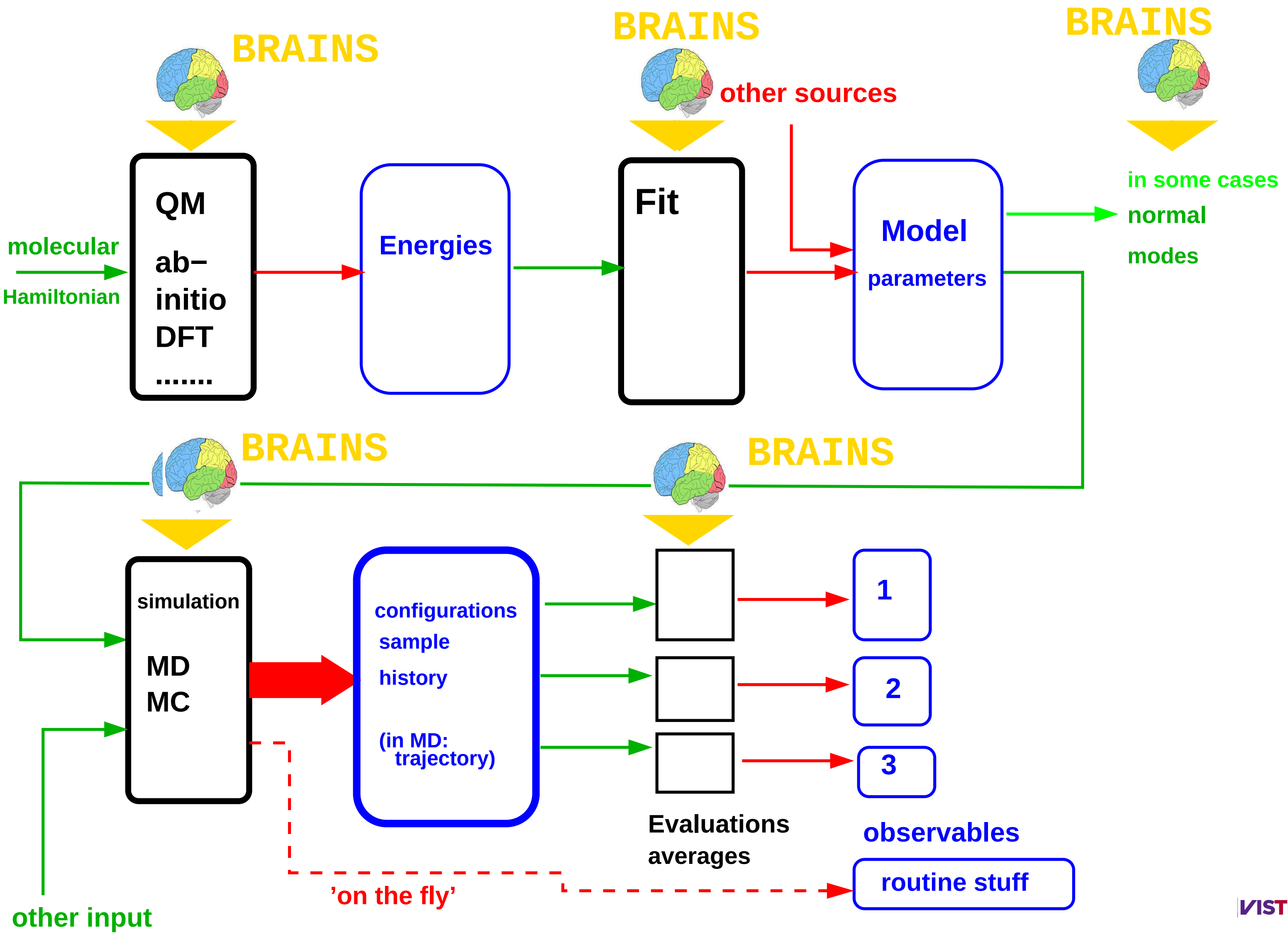
$\Rightarrow$ more later

Statistical Mechanics via MD-Simulations

Flowchart



Each step needs critical thinking nothing is 'automatic'
there are no 'standard' procedures (chemists,engineers, remember this)



- **REMINDER**: Born Oppenheimer (BO) **approximation**

Let's look at a molecule.
Its Hamiltonian $\hat{H}$ will depend on the positions of the nuclei $\mathcal{R}$ and electrons r,
and so will the Eigenvalues (energies) and Eigenfunctions (states)
let's call them $\Psi(\mathcal{R}, r)$

We do the usual product-ansatz (BO approximation):

$$\Psi(\mathcal{R}, r) = \psi^{\mathrm{electronic}}(r) \cdot \varphi^{\mathrm{nuclei}}(\mathcal{R})$$

– Solving the equations for the electrons, at fixed positions of the nuclei (which appear in the Hamiltonian of the electronic equation as parameters) is the topic of quantum chemistry.
From this we get the **Potential Energy Surface (PES)**

The Schrödinger equation for the nuclei can in many cases (but not always!) be replaced by classical mechanics (MD): Newton's equation

For all masses larger than Hydrogen and
temperatures $\geq$ room temperature
classical mechanics (Newton's equation) is a good approximation.

Hydrogen is 'borderline' (de Broglie wavelength $\approx$ particle dimension)

Reminder: relation of QM to classical mechanics

the larger the mass, the higher the temperature, the more 'classical',
see "de Broglie (thermal) wavelength":

$$\lambda = \frac{h}{p} \;, \quad \text{with } p \text{ from } < E_{\text{kin}} > \quad \Rightarrow \; \lambda = \frac{h}{\sqrt{2\pi m k_{\text{B}} T}}$$

Thus:

$$\text{For each particle } i \ : \ m_i \cdot \frac{\partial^2 \vec{r}}{\partial t^2} = \vec{F}_i = -\vec{\text{grad}}_i(\text{PES})$$

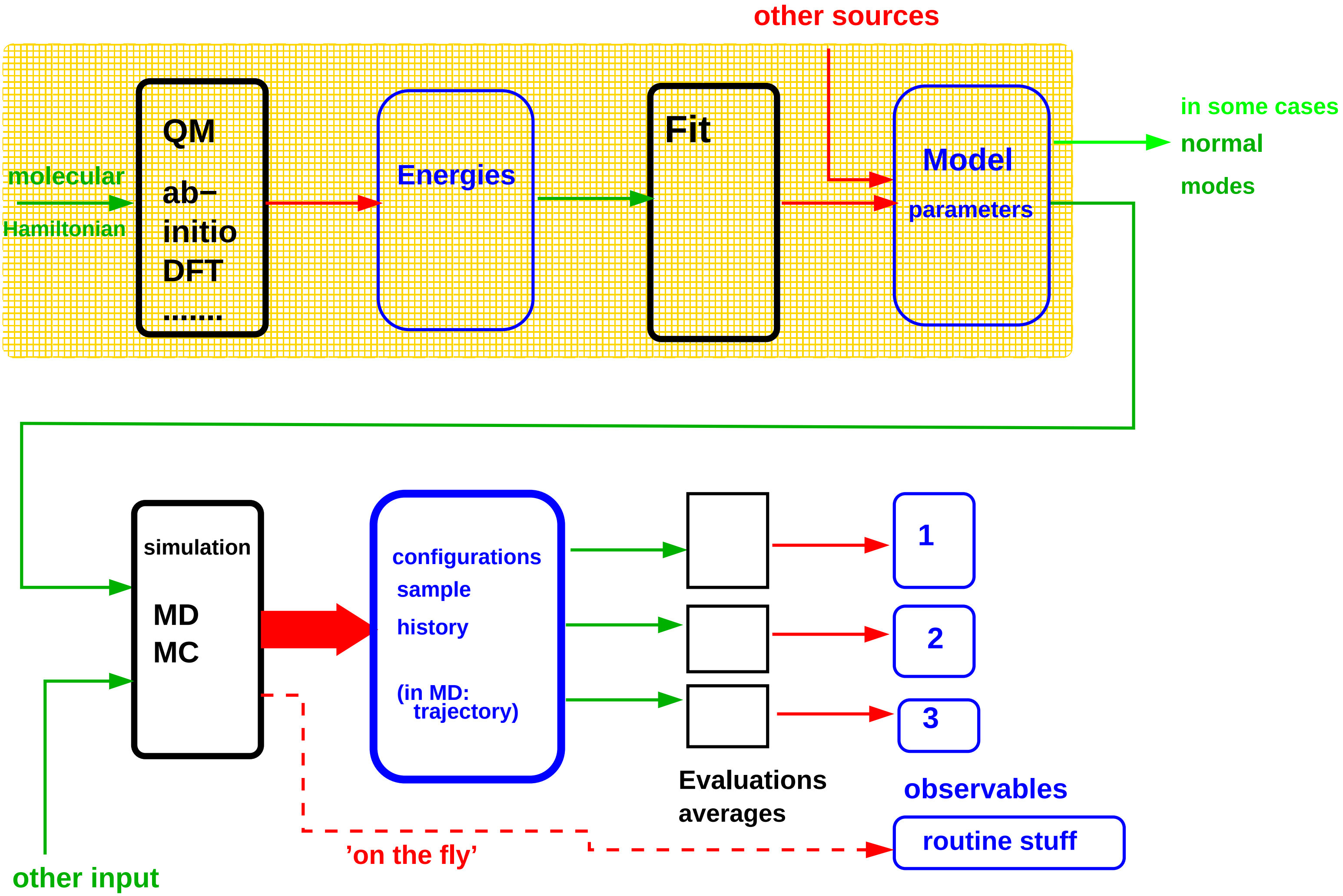
For N particles, this is a system of
– $3N$ coupled 2nd order partial differential equations, or
– $6N$ coupled 1st order partial differential equations

(coupled because "$\vec{\text{grad}}_i(\text{PES})$" depends also on all other particles j)

Before we discuss how to solve such differential equations,
we will deal with the description of the PES

$$\text{PES} = V(\mathcal{R}) = V(R_1, R_2, R_3, ..., R_N)$$

Interaction Models (PES) ⇔ CHE502,
some reminder and additional material below
(also called molecular Modeling, Force Field Development .....)



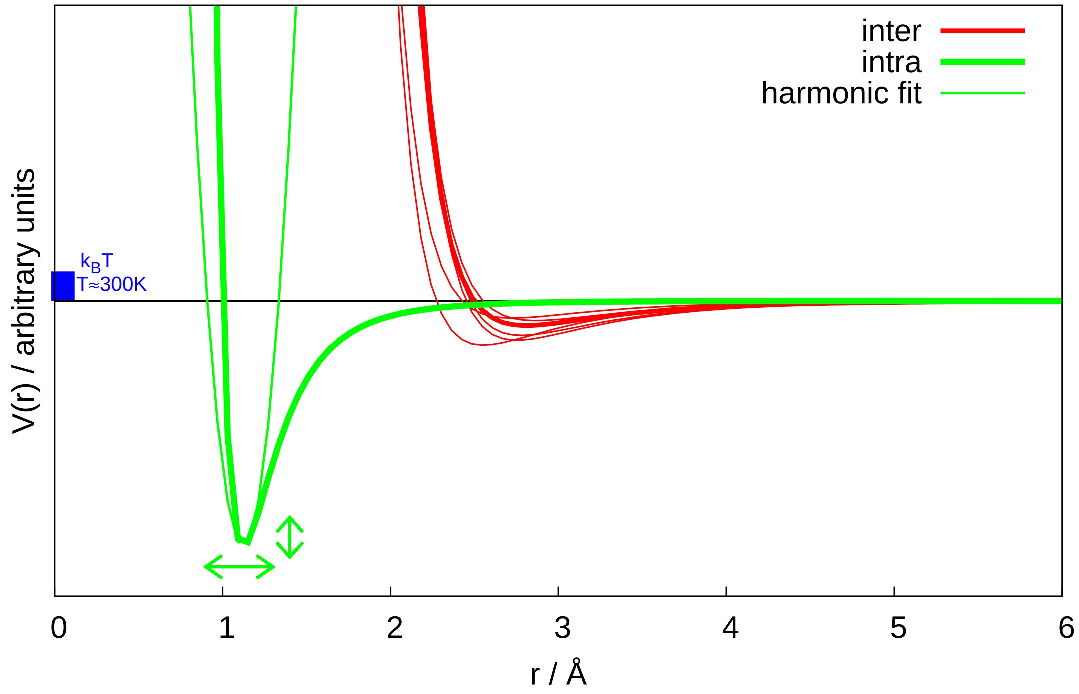
PES, recap from a slightly different viewpoint:

We distinguish first between:
Inter– *(between)* and intra– *(inside)* molecular interactions

$$V^{\text{total}} = V^{\text{inter}} + V^{\text{intra}} \qquad \underbrace{+ \quad V^{\text{inter}-\text{intra}} \quad ?}$$

Remember:

typical intra− and intermolecular potentials / k_BT (T≈300K)



(1) Intermolecular Interactions

Keywords:
Pairwise additive (or simply **pair**) potentials

Many-body potentials, polarizabilities and polarization

(2) Intramolecular Interactions

Keywords:
Internal coordinates (bond-**stretch**, angle-**bend**, **torsion** ...)

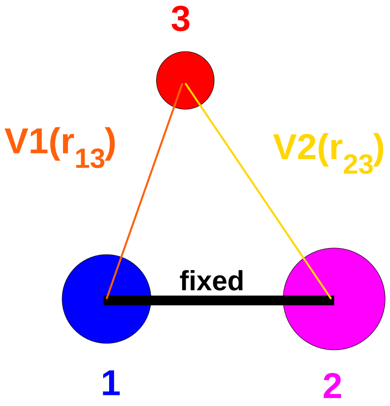
"bonded" and **"non-bonded"** interactions

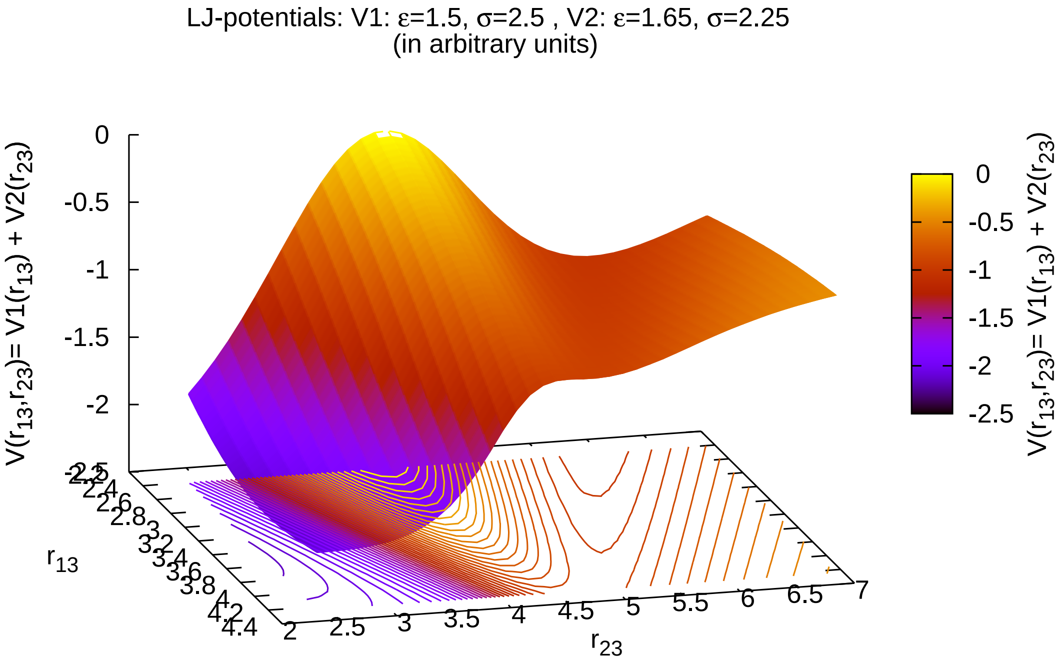
So why do we (usually) use different mathematical representations for the inter- and intramolecular interactions (inter- and intramolecular PES) ?

(1) Intermolecular

Usually this PES V is a function of many variables: $V(r_1, r_2, r_3, r_4, ...)$
($\approx 3N$ variables for N particles)
and one struggles to get a meaningful representation.

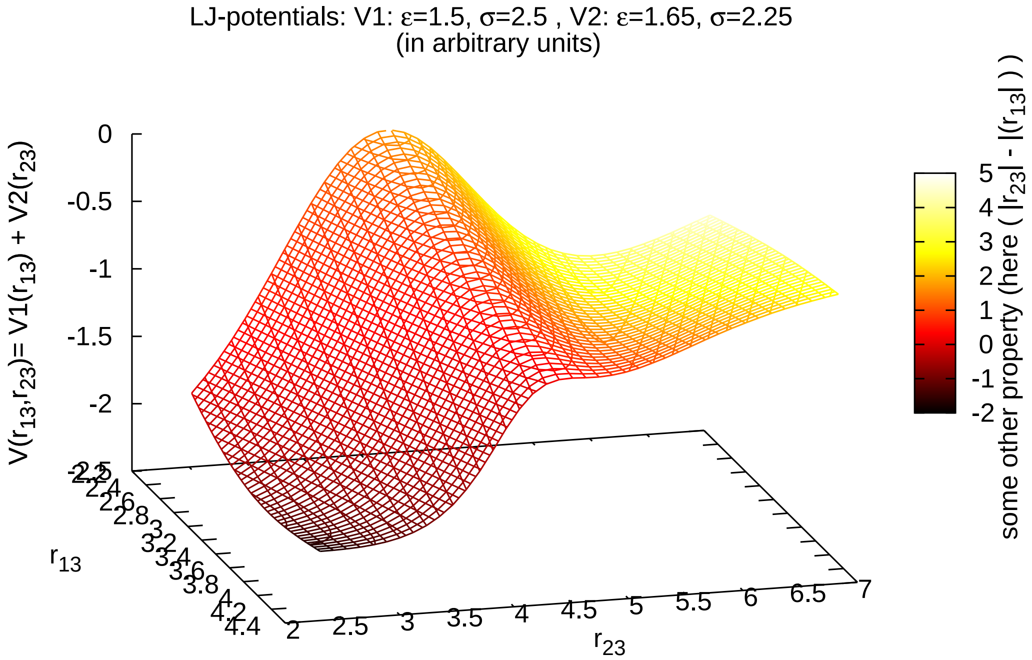
Example: Two Lennard-Jones (LJ) potentials $V1$ and $V2$





3Dplot, color coded (redundant here)
Contour plot

Exploring a PES in more than 1 dimension is very difficult !

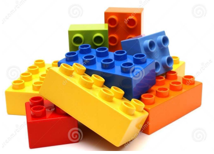


same, color coded for some **other** property

We discussed this already a lot in CHE502;
see also the little example (FORTRAN and gnuplot)
(scripting and plots with the `gnuplot` free software)

describing a PES: “Salami tactics“

Put together $V^{\text{inter}}(\{R_I^{\text{nuclei}}\})$ from smaller pieces
($\{R_I^{\text{nuclei}}\}$=all nuclear coordinates)
(in some way like a LEGO)



However, there is a price (*There is no free lunch*!)
as we shall shortly see.

Most frequently made approximation:
The pair potential approximation

The pair potential approximation

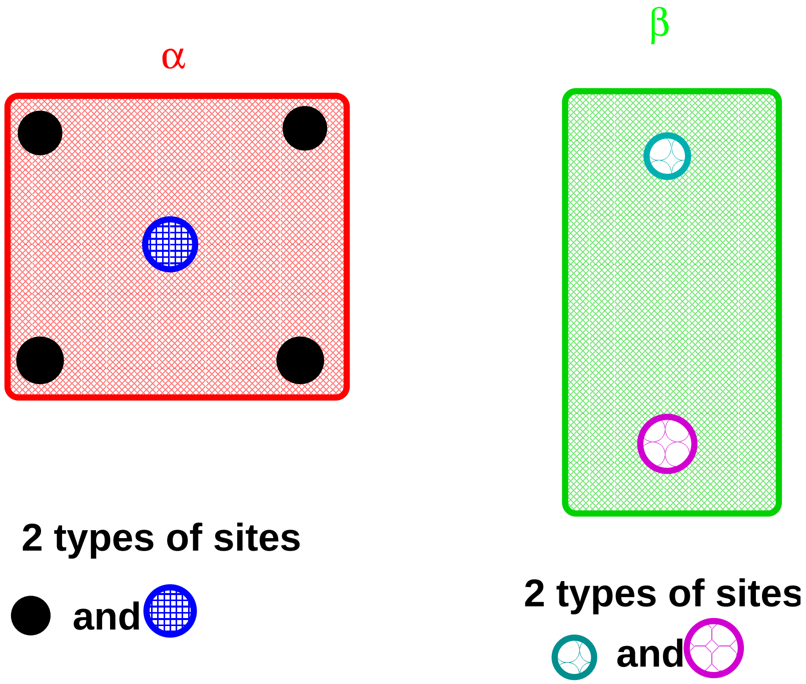
We will assume that:

$$V^{\text{inter}}(\{R_I^{\text{nuclei}}\}) = \sum_{i_\alpha, j_\beta} U_{ij}(r_{ij})$$

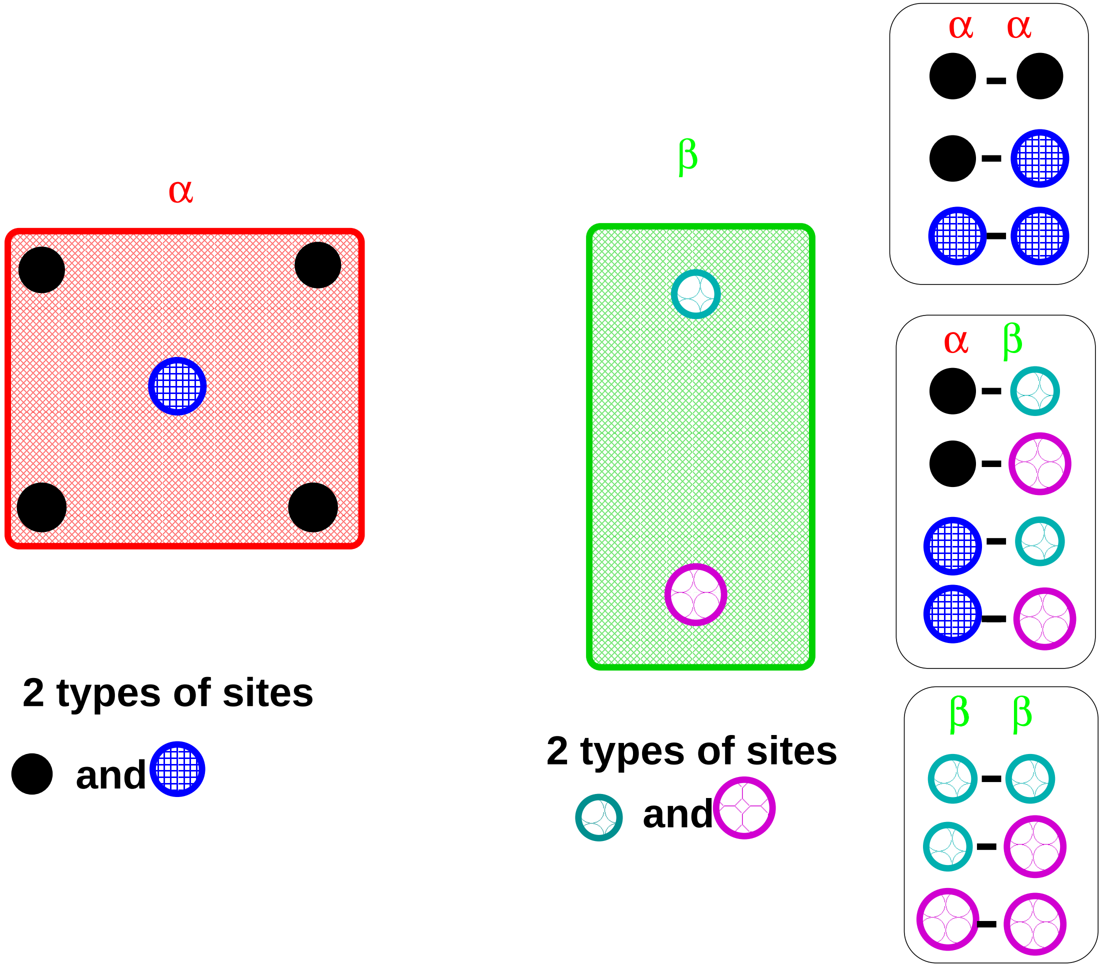
where i_α is a site on a molecule α and j_β is a site on a (usually different) molecule β.
r_{ij} is the absolute value (modulus) of the distance between the two sites i and j: $r_{ij} = |\vec{r}_i - \vec{r}_j|$
U_{ij} is the pair potential between the sites i and j.

The pair potential approximation is a **very drastic** assumption
so let's look at it again very quickly since most of this was already discussed in CHE502

Let us first assume that molecules are **“rigid bodies“**, i.e. that there are **no deformations, no intramolecular motions** (vibrations) etc.



10 types of pair potential U_{ij}



For two molecules:

16 terms

8 terms

1 term

4 terms

4 terms

1 term

1 term

1 term

2 terms

1 term

The question now is: **How to find the different U_{ij}s?**

.. via the PES from quantum chemistry:

Step 1): You make many ($\approx$ 100 - 1000) single point quantum chemical calculations for ‘super-molecules‘ consisting of one red and one green molecule with **all** possible mutual distances and orientations, keeping the molecular geometries constrained.

Step 2): You chose sites on the molecule. In most cases, you locate the sites on the atoms. Sometimes, you use one site for several atoms (e.g. a CH_2-group, or a CH_3 group and such).
This is called the "united atom" approach, see below.

Step 3): Once you have determined the sites, you know how many different site-site pair potentials U_{ij} you will need.
You make an Ansatz* for the U_{ij}
e.g.
U_{ij} = electrostatic attraction or repulsion + short range repulsion + ...

* Ansatz, German word, plural Ansätze: What you put in initially in a chemical reaction; what you start out with, assuming that it will work

The most frequently used mathematical expression is:

$$U_{ij}(r_{ij}) = \frac{1}{4\pi\epsilon_0} \cdot \frac{q_i \cdot q_j}{r_{ij}} + 4 \cdot \epsilon_{ij} \cdot \left((\frac{\sigma_{ij}}{r_{ij}})^{12} - (\frac{\sigma_{ij}}{r_{ij}})^{6} \right) \; = U^{\mathrm{Coulomb}} + U^{\mathrm{Lennard-Jones}}$$

with
$\frac{1}{4\pi\epsilon_0}$ a constant depending on which unit system you use,
q_i and q_j partial electric charges on the sites i and j
and ϵ_{ij} and σ_{ij} two (Lennard-Jones) constants depending on the type of interaction (black-black, black-blue, blue-blue, etc.)

In our example (red and green molecules) we would thus have 4 different partial charges q_i (4 types of sites), 10 ϵ_{ij}s and 10 σ_{ij}s,
a total of 24 parameters.

Step 4): Determine these 24 parameters by **fitting** the 10 U_{ij} Ansatz-functions to reproduce as well as possible the 100-1000 interaction energies determines in Step 1 by quantum chemical calculations.

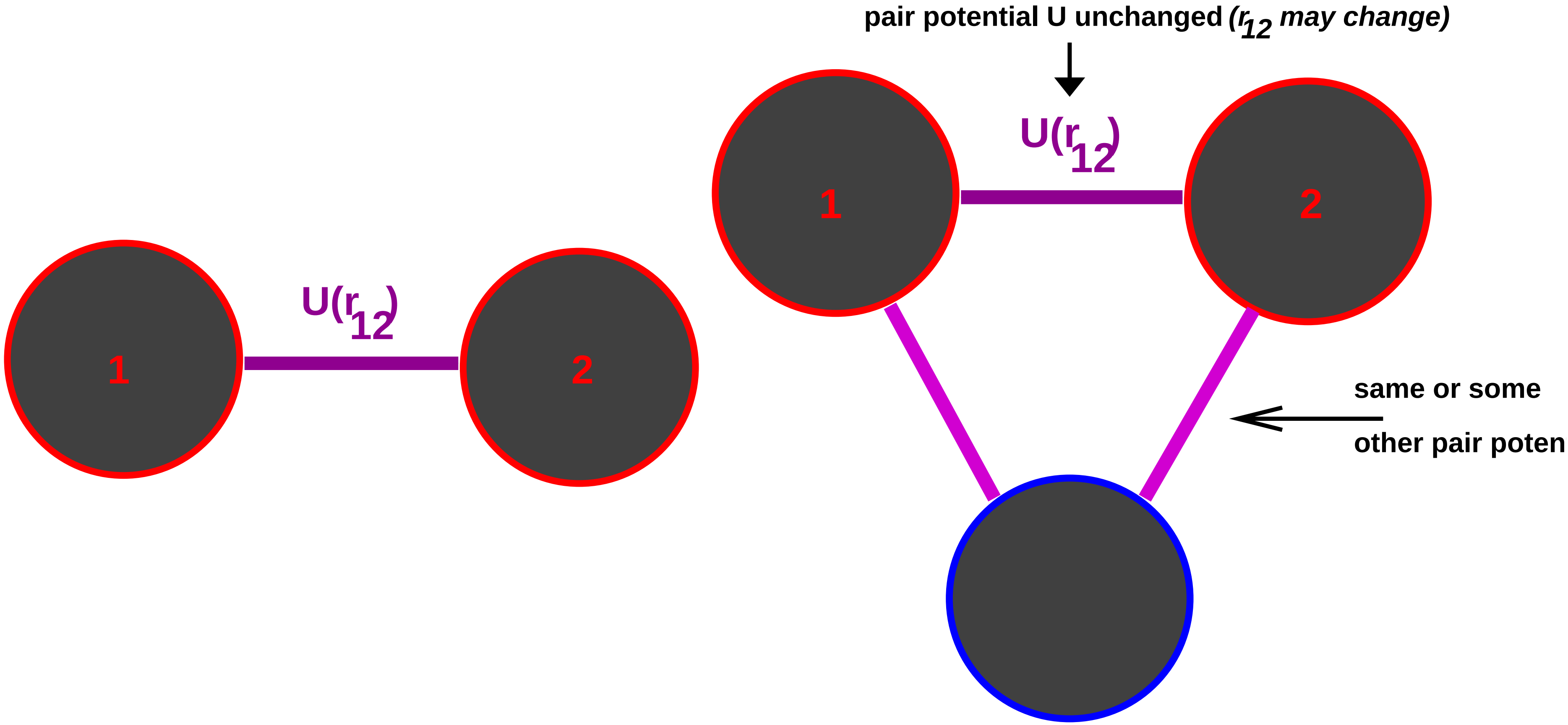
Making these fits is difficult, and many tricks must be used.
Sometimes additional constraints must be applied
This is ongoing research work

We note that if we want to compute the total energy of an ensemble of N molecules, each of which contains M sites, the total number of pair interactions to compute will increase $\propto (N \cdot M)^2$ - a little something. (Because every site will interact with every other site except itself and sites on the same molecule.)

Let's now ask:

What is the price of the "pair potential approximation"?
i.e. **What do we miss? What do we leave out? ...**

Pair potential approximation



You miss the influence that a third particle (in blue) may have on the (shape, strength, ... of the) interaction U between 1 and 2

Summary: intermolecular interactions

In the pair potential approximation V^{inter} will thus be a simple sum of Us, and each U will depend only of the distance ($r_{ij} = |\vec{r}_i - \vec{r}_j|$, i.e. a scalar, not the **vectors**)
of only two sites i and j:

$$V^{\mathrm{inter}} = \sum U_{ij}(r_{ij})$$

$\rightarrow$ "Rigid" molecules are not always a reasonable approximation (think e.g. of polymers)

So we need to describe the fact that molecules can change their shape, vibrate, ...

This is done by means of intramolecular potentials V^{intra} (*intra means "inside"*)

(2) Intramolecular interactions

Main features
Deep (compared to $k_{\mathrm{B}}T$) potential wells
Stable molecules (no dissociation)

$\Rightarrow$ model potential can diverge at small and large values of the argument (e.g. distance)

$\Rightarrow$ harmonic (bilinear) ansatz:

$$V^{\mathrm{intra}} = \sum k_{ij}\ \rho_i\ \rho_j \qquad \rho = \text{internal (or Wilson's) coordinate}$$

$\text{types of }\rho : \text{bond stretch} : \delta r = ((r_{\alpha\beta}) - (r^0_{\alpha\beta}))$
$\text{angle bend} : \delta\alpha = ((\alpha_{\alpha\beta\gamma}) - (\alpha^0_{\alpha\beta\gamma}))$,
α, β, γ (adjacent) atoms (sites) on the same molecule;
$\text{torsion} : \delta\Theta = ((\Theta_{\alpha\beta\gamma\delta}) - (\Theta^0_{\alpha\beta\gamma\delta}))$,
$\alpha, \beta, \gamma\delta$ (adjacent) atoms (sites) on the same molecule;

^{0}: equilibrium value
This is a generalization of the Hook's law spring model

($\rightarrow$ Torsions : harmonic not always suitable. Why?)

$$V^{\text{intra}} = \sum_{l \le m} f_{lm} \cdot \rho_l \cdot \rho_m$$

where f_{lm} is the force constant (or element of the F-matrix),
the ρ are Wilson's internal displacement coordinates.
Warning: *The sum goes either as written here (1-1, 1-2, 1-3, but not 2-1, 3-1, 3-2, ... (i.e. no double counting)), but definitions vary.*

Many 'types' of ρ, here only 3 are given:

Type "stretch": $\rho^{\text{stretch}} = r_{ij} - r_{ij}^0$
Type "bend": $\rho^{\text{bend}} = \alpha_{ijk} - \alpha_{ijk}^0$
Type "torsion": $\rho^{\text{torsion}} = \phi_{ijkl} - \phi_{ijkl}^0$
where r_{ij} is the distance between two sites (here always site = atom!)
α_{ijk} is the angle between r_{ji} and r_{jk} at atom j
ϕ_{ijkl} is the angle between the plane defined by atoms i,j,k and the plane defined by atoms j,k, and l

Note:

1) You see that the definitions of the ρ already contain parameters, the “equilibrium values“

2) You can easily extend V^{intra} up to higher orders in ρ (anharmonicities):

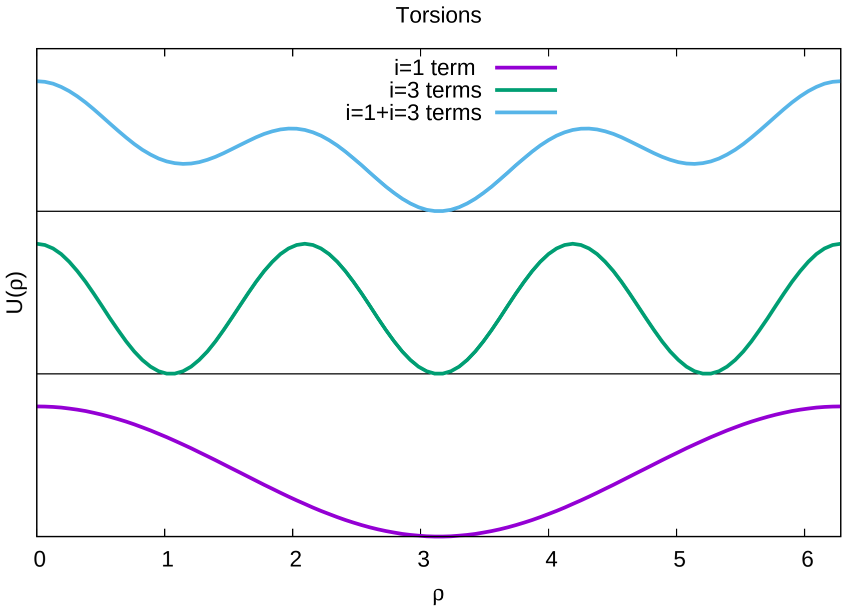
$$V^{\text{intra}} = \sum_{l \le m} f_{lm} \cdot \rho_l \cdot \rho_m + \sum_{k \le m \le n} k_{klm} \cdot \rho_k \cdot \rho_l \cdot \rho_m + \ldots\ldots$$

3) The computation of such V^{intra} is “technically“ more complicated than the simple sum or pair-potentials U, **but**
In our system with N molecules with M sites each,
we define a number of ρs between the M sites of each molecule,
say M_ρ, and the total number of interactions to compute will be
$N \cdot M_\rho$, which increases $\propto N$
and not $\propto N^2$ (like intermolecular interactions)
when we increase the “system size“.

4) Torsions:

If the barriers are not very hight compared to $k_\mathrm{B}T$, torsional potentials should be written as something like:

$$V^{\text{intra tors}}(\rho) \propto \sum_i (\cos(i\rho) + 1)$$



Let's put everything together and write:

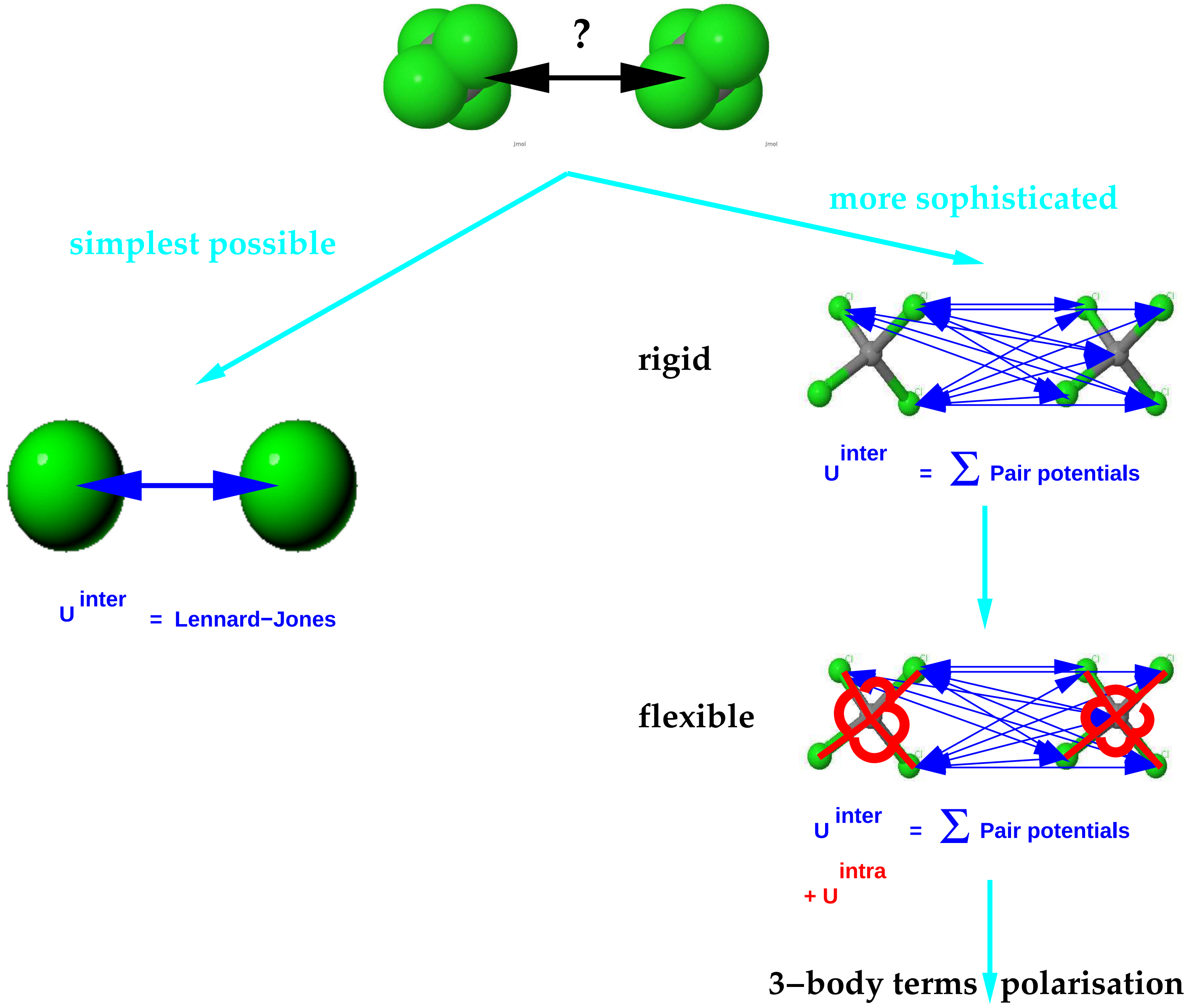
$$V^{\text{total}} = V^{\text{inter}} + V^{\text{intra}}$$

and look at two examples:

- Various classes of model**s** for CCl_4
- Model potentials (models) for water

This can also be seen as an exercise in
coarse graining

Example **Modeling CCl_4**



?

simplest possible

more sophisticated

rigid

$U^{inter} = \sum$ Pair potentials

U^{inter} = Lennard−Jones

flexible

$U^{inter} = \sum$ Pair potentials

$+ U^{intra}$

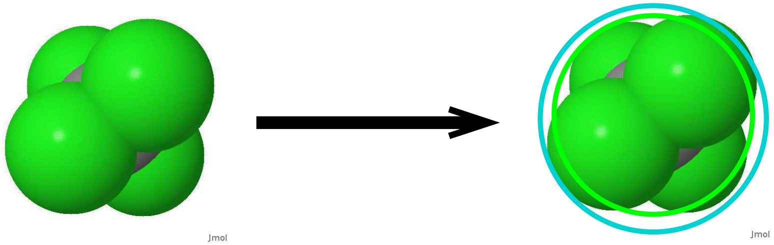
3−body terms polarisation

Coarse-graining often involves replacing a feature by its average value

e.g. : united atom
replace several atoms (sites) by one pseudo-atom (site),
e.g.: CH_3 = "Me", CH_2= xx, CCl_4 = carbon-tet (our example)

This saves a lot of computer time, e.g. for N CCl_4-molecules :
$\approx 25N^2$ interactions for the all-atom model
$\approx \quad N^2$ interactions for the united atom model

Difficulty: Which 'average' to use?
Average energy (of some sort)? Average 'size' (whatever that may be)?
Average ...?



Which is the 'correct' radius ?

Intramolecular potential for water:

A) Define the internal coordinates:

$$\rho_1 = r_{\mathrm{OH}_1} - r^0_{\mathrm{OH}_1} \quad , \quad \rho_2 = r_{\mathrm{OH}_2} - r^0_{\mathrm{OH}_2} \quad , \quad \rho_3 = \alpha_{\mathrm{H}_1\mathrm{OH}_2} - \alpha^0_{\mathrm{H}_1\mathrm{OH}_2}$$

ρ_1 and ρ_2 are of type “stretch“, ρ_3 is of type “bend“.
$r^0_{\mathrm{OH}_1} = r^0_{\mathrm{OH}_2} \approx$ 0.98 Å,
$\alpha^0_{\mathrm{H}_1\mathrm{OH}_2} \approx$ 109 degrees.
(*Other definitions are possible, we can also use more than 3 coordinates*)

B) For symmetry reasons, the potential then must be written as:

$$\begin{aligned} V^{\mathrm{intra}} \quad = \quad & f_{11} \cdot (\rho_1^2 + \rho_2^2) \; + \; f_{33} \cdot \rho_3^2 \\ & + \; f_{12} \cdot \rho_1 \cdot \rho_2 \; + \; f_{13} \cdot \rho_3 \cdot (\rho_1 + \rho_2) \end{aligned}$$

We have thus 4 independent constants (i.e. $f_{11} = f_{22}$ etc.)
f_{11} is called the (diagonal) O-H stretching force constant (Hook’s law),
f_{33} is the (diagonal) HOH bending force constant,
f_{12} and f_{13} are the stretch-stretch and stretch-bend coupling constants, respectively.

In other terms (nomenclature more like the one used in spectroscopy):
Water, c_{2v} symmetry, harmonic potential, thus:

$$\rho_1 = \delta r_{\mathrm{O-H_1}} \quad \rho_2 = \delta r_{\mathrm{O-H_2}} \quad \rho_3 = \delta \Theta_{\mathrm{H_1-O-H_2}}$$

$$V(\rho_1, \rho_2, \rho_3) = k_{11} \cdot (\rho_1^2 + \rho_2^2) + k_{33} \cdot \rho_3^2 + k_{12} \cdot \rho_1 \cdot \rho_2 + k_{13} \cdot (\rho_1 \rho_3 + \rho_2 \rho_3)$$

$$\leftrightarrow (\rho_1, \rho_2, \rho_3) \cdot \begin{pmatrix} k_{11} & k_{12} & k_{13} \\ k_{12} & k_{11} & k_{13} \\ k_{13} & k_{13} & k_{33} \end{pmatrix} \cdot \begin{pmatrix} \rho_1 \\ \rho_2 \\ \rho_3 \end{pmatrix} \qquad (\text{factors} \frac{1}{2} \;\; !)$$

The matrix is called the F-matrix (!) (remember chi502)
(it is symmetric,
be careful, there are different ways in the literature to write this)
here it contains 4 independent constants k.

Water: Models for the intermolecular interaction:

Just for water (H_2O), there are probably about 50 reasonably good, but quite different models in the literature.
They are known by acronyms like BNS, ST2, MCY, TIPS, TIP3P, TIP4P, CF2, CF3, BJH, SPC, SPC/E, etc. etc. etc.

– "rigid" (V^{intra} replaced by constraints) or "flexible" models
– 3, 4, 5 or more sites
– "polarizable" ($\vec{\mu} \propto \overset{\leftrightarrow}{\alpha} \vec{E}$) and "non-polarizable"
– from Quantum-Chemical PES (ab-initio, DFT, ... of various qualities)
or fitted to reproduce certain properties
(structure ($g(r)$s), thermodynamics, phase diagrams, spectroscopy,
solvent properties, ...)

One more reminder

If the potential is 'narrow' (Δx small in the uncertainty relation)
the frequencies ω can still be obtained to a very good approximation classically
(and then used to compute the 'quantum' energy levels of this 'oscillator system', (i.e., for example, without diffusion))

So if we have again a system of $i = 1, ..., N$ interacting particles
(here via a very specific potential energy function)

$$m_i \, \frac{\partial^2 \vec{r}_i}{\partial t^2} = \vec{\mathrm{grad}}_i V = \vec{F}_i \quad , \; i = 1, N$$

Such a system of **coupled**
(because $\vec{F}_i$ depends in general not only on $\vec{r}_i$ but also on all other $\vec{r}_j$s)
differential equations generally **does not have 'analytical'** solutions
(Henri Poincaré)

However, in this particular case ($\Rightarrow$ 'harmonic' problem), it has,
and the solutions are called **"normal modes"**.

Systems which have analytical solutions
(i.e. mathematical expressions, like sin(..), cos(...), exp(..), ...)
are called **’regular’** (or **linear**) systems,
the others are **’irregular’**, **non-linear’** or **’chaotic’**

Studying non-linear systems is a branch of mathematics (chaos theory)

See ’normal modes’ in the supplementary material for the usual way to study harmonic (a class of linear or regular) systems.

Normal Modes

In some cases, Newton's coupled differential equations of motion:

$$m_i \, \frac{\partial^2 r_i}{\partial t^2} = \mathrm{grad}_i V = F_i \quad , \; i = 1, N$$

do have an analytical solution.

The most famous case are 'normal modes'
(physicists talk about 'group coordinates'),
which exist ONLY if the right hand side
(rhs, i.e. the potential V and forces F)
have a very special form and the motions are 'infinitesimally small' around
an extremum (usually minimum, however, → transition states).

Normal modes are a generalization of the well-know
harmonic oscillator problem
(*which you have studied over and over*)

Reminder:

$$\omega = \sqrt{\frac{k}{m}} \quad , \quad E_v = \hbar\, \omega\, (v + \frac{1}{2})$$

m: the mass; k: the force constant (2nd derivative of potential)
ω: frequency, v **vibrational quantum number**

(Note again the the frequency computed from classical mechanics is used in the expression for the quantum energies)

Classical solution:

$$\Delta x(t) = A \cdot \cos(\omega t) + B \cdot \sin(\omega t) = C \cdot \cos(\omega t + \delta)$$

$\Delta x(t) = x(t) - x_0$: a displacement with respect to an equilibrium position
A, B, C, δ from the initial conditions

for two masses m and M (and one 'spring') on has:

$$\omega = \sqrt{\frac{k}{\mu}} \quad , \quad \frac{1}{\mu} = \frac{1}{m} + \frac{1}{M} \quad , \quad \text{and still } E_v = \hbar\ \omega\ (v + \frac{1}{2})$$

Spring: Hooke's law $V(x) = k \cdot (x - x_0)^2$
(often written as $V(x) = k/2 \cdot (x - x_0)^2$

For more masses and 'springs', we generalize the springs as:

$$V = \sum_{ij} k_{ij} \rho_i \rho_j \ \ (which\ can\ be\ expanded\ as\ V = \sum_{kl} c_{kl}\ u_k^{x,y,z} u_l^{x,y,z} \ \ )$$

k_{ij} are (generalized) force constants (force field),
ρ internal (Wilson) coordinates (stretch, bend, torsion ...)
$u_k^{x,y,z}$ are (infinitesimally) small displacements
of particle k in x, y or z direction

Such a 'harmonic' potential can be obtained by expanding any potential
around an extremum (minimum)
This is what the quantum chemistry codes do.

With this potential (bilinear form) Newton's equations of motion can be solved analytically
(*see Wilson, Decius and Cross*)
and one gets for the motions of particle i:

$$\vec{r}_i(t) - \vec{r}_i^{\,0} = \sum_{J=1}^{\mathcal{N}} A_J \cdot \vec{Q}_i^{J} \cdot \cos\left(\Omega_J \cdot t + \delta_J\right)$$

There are (if ....) $\mathcal{N} = 3N - 6$ normal modes for a system (molecule) of N masses, $\mathcal{N} = 3N - 5$ for linear systems (molecules)

A_j and δ_J are arbitrary amplitude and phase factors
(which depend on the initial conditions)

$\vec{Q}_i^{J}$ are vectors (the normal modes) describing the relative motion of atom i under mode J.

Properties of normal modes:

- All atoms i in a normal mode J move 'in phase' (or anti-phase), the A and δ depend only on J, not on i

- Normal modes are 'orthogonal' (or adiabatic) to each other, this means a mode J will not transfer vibrational energy to another mode (*you know that e.g. in molecules this is not entirely true*)

- Normal modes are the main tool to assign and interpret vibrational spectra (IR, Raman)
the symmetry of the normal modes is related to the selection rules

The quantum energies are, since the modes are independent:

$$E_{v_1,v_2,v_3,\ldots,v_{\mathcal{N}}} = \hbar\Big(\Omega_1(v_1+\frac{1}{2})+\Omega_2(v_2+\frac{1}{2})+\Omega_3(v_3+\frac{1}{2})+\ldots+\Omega_{\mathcal{N}}(v_{\mathcal{N}}+\frac{1}{2})\Big)$$

Beware:

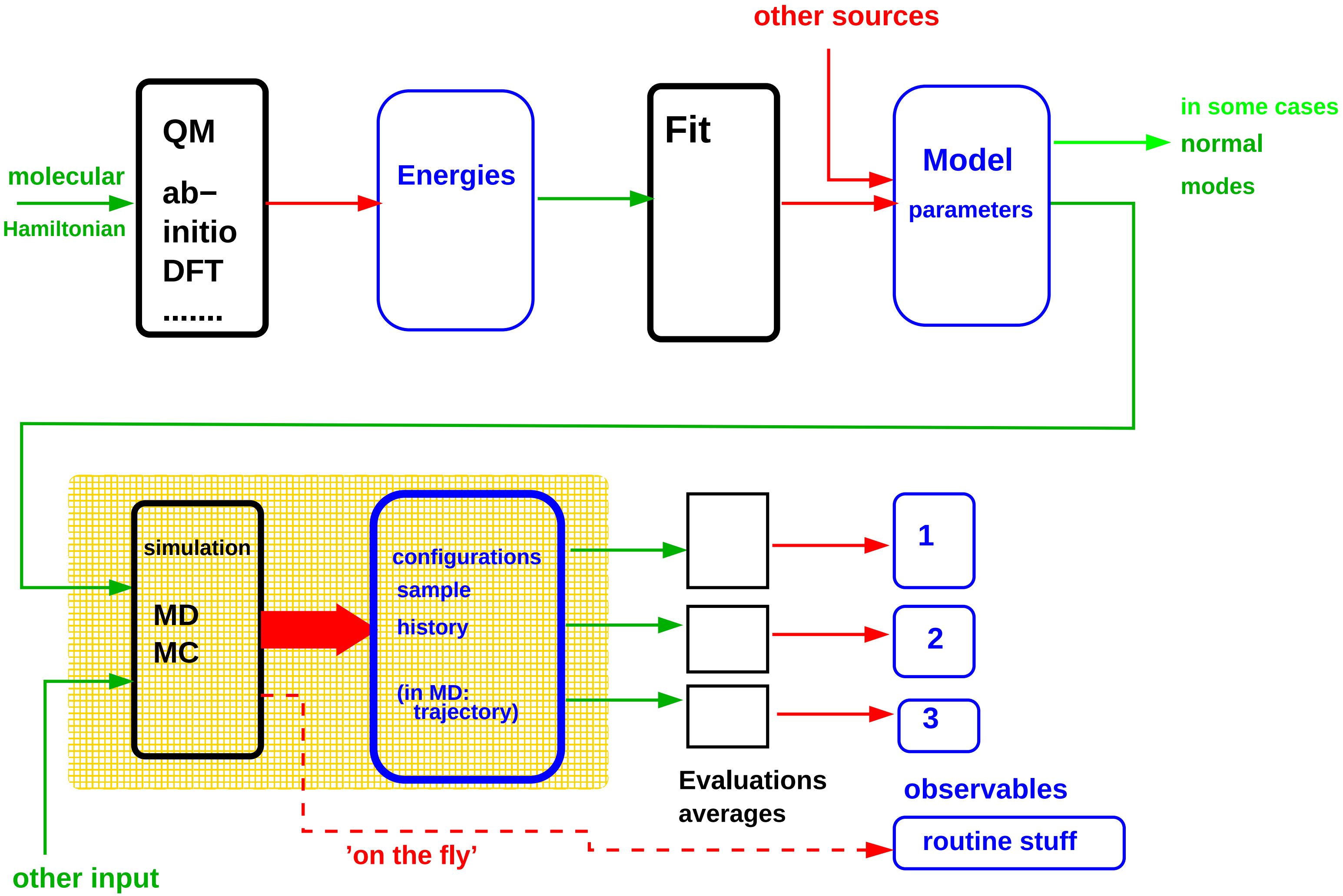
Since normal modes are independent, i.e. do not exchange energy, a normal mode system will not evolve toward thermodynamic equilibrium!

→ Your spectroscopy class

In the general case,
i.e. when normal modes cannot be computed,
the eqs. of motion of an N-particle problem
MUST be solved numerically

→ MD-simulations
→ Statistical mechanics (use Ω for partition function)
→ MC-simulations

Simulations: MD and MC: A few (essential!) ”tricks”



other sources

molecular

Hamiltonian

QM

ab–initio

DFT

....

Energies

Fit

Model

parameters

in some cases

normal

modes

simulation

MD

MC

configurations

sample

history

(in MD: trajectory)

other input

’on the fly’

Evaluations

averages

1

2

3

observables

routine stuff

Let's remember some of our goals

- study matter, mostly **disordered** condensed phases (e.g. liquids), at **finite temperatures**, from a molecular (microscopic) standpoint
- **understand** the links between molecular properties and the macroscopic observables
- study matter under conditions (pressure (density), temperature, ...) not easily attainable in the laboratory
- try avoid as much as possible 'unnecessary experiments' (e.g. in the pharmaceutical industry)
- gain some predictive power

The properties of condensed matter
(e.g. its structure, internal energy, viscosity, diffusion, ...)
in particular at finite temperatures $T > 0$ K
cannot be related to the properties of a single molecule alone.
Such properties are properties of ensembles of many (how many?) molecules.

Many methods in theoretical chemistry consider only the (potential) energies at $T = 0$ K an thus neglect the influence of the kinetic energy (entropy).

This is sufficient in many cases, e.g. in reactions where the energy differences between the reactants (educts) and the products are large.

Remember the examples from CHI502

However, many reactions, e.g. in biology, are so fine-tuned that **temperature becomes a very important factor**
and we need much better approximation to the partition function(s)

$\Rightarrow$ partition function approximated well enough by a single term
$\Rightarrow$ **statistical mechanics**

(*Statistical mechanics*
$\approx$ *statistical thermodynamics*
$\approx$ *statistical physics*
$\approx$ *many particle physics*
$\approx$ ...)

– Molecular simulations (MD MC)

Molecular **D**ynamics (**MD**) , **M**onte **C**arlo (**MC**)

allow to go beyond simple (e.g. harmonic) potentials
and the few 'academic' cases that can be treated 'analytically'

Basic idea of molecular simulations:

Since it is impossible to compute the partition functions $(\Omega, Q, \Xi$ ... $)$
(i.e. **all** states compatible with a set of external conditions (e.g. (NVE)),
we will construct a **representative sample**

This is called a **simulation**

Here we shall briefly look at the two main simulation methods:
Molecular Dynamics (MD)
(Metropolis) **Monte Carlo (MC)**
(*and there are several others, to be discussed if we have time*)

Historical remarks:

Numerical work (e.g. MD, MC) was not possible before computer became generally available (1970ies with some precursors
(Edward Teller, Bernie Alder ...) since the 1940ies (Manhattan Project))

Theoreticians were used to search for 'analytical solutions'
(i.e. finding mathematical solutions of
(usually differential or integral) equations)

Simulations required a different way of thinking,
they were thus often called **computer experiments**

Basic Idea of MD (many of which also for MC)

We first remember, from classical mechanics:
If the potential V (and thus forces $\vec{F}$) in Newton's equation depend ONLY on the relative positions ($\vec{r}$s) of the particles
(and not e.g. on some 'external' variables)
the total energy of this system (and the momenta)
will remain constant along the trajectory
(conservation of total energy, independently whether this trajectory can be found analytically or not).

Quantities which remain constant along the trajectory (energy, momenta) are called (first) 'integrals' of the system

We will make use of this when we construct the (NVE) ensemble using MD simulations.

In MC, we usually construct the (NVT) ensemble

However, many assumptions (and tricks) are common to MD and MC (MC needs fewer, but also yields fewer results!)
We talk first mainly about MD and about MC later

Definitions:
In MD, we used the term configuration to designate the ensemble of the nuclear positions ($\{R^{\text{nuclei}}\}$) and velocities ($\{\dot{R}^{\text{nuclei}}\}$)
of **all particles** in a system at **a given time** t_j.

In statistical mechanics, this is called a phase space point.
We shall call such a phase space point $\mathcal{P}(t)$, or simply $\mathcal{P}$.

The ensemble of all the $\mathcal{P}$, $\{\mathcal{P}\}$, that we compute, is the sample of thermodynamics states; it is a part of the corresponding thermodynamic ensemble.

Since we obtain the sample by integrating the equations of motion (see below), the sample is (a part of) the trajectory of the system.

Let us **assume** that we know one phase space point $\mathcal{P}$ that belongs to the ensemble of microstates compatible with the MACROSTATE we are interested in.
(*We just assume that we have this $\mathcal{P}$, we don't know (yet!) how/where to get it, how to generate it ...*)

Reminder: we **assume** that our particles ($=$ atoms or molecules) are heavy enough and/or the temperature high enough so that the particles' "de Broglie wavelength" is small (compared e.g. with the particles' dimensions), then we can replace the **(time dependent) Schrödinger equation** for the particle motions by **Newton's equation**.
(*This is almost always true in "chemistry",*
i.e. with masses $\geq m_{\mathrm{H}}$ *and* $T \approx 300$ *K.*)

Example: Standard (NVE)-MD

We will now consider a system of N particles,
restricted to a volume V
(*i.e. the particle positions are all inside the volume*).

We want to assume that we have one configuration $\mathcal{P}$ for our N particles in this volume V).
We shall call it $\mathcal{P}(t_0)$, it corresponds to **some** MACROSTATE $(NV?)$.

Can we fully characterize the MACROSTATE?

Answer: **Yes**, because we know how to compute the total energy E of $\mathcal{P}(t_0)$:

$$E \ = \ E^{\text{total}} \ = \ T \ + \ V \quad ; \quad T = E^{\text{cin}} \quad ; \quad V = E^{\text{pot}}$$

T we can compute because $\mathcal{P}(t_0)$ contains all velocities
V we can compute from our model because $\mathcal{P}(t_0)$ contains all positions

Thus $\mathcal{P}(t_0)$ is one (micro)state compatible with the MACROSCOPIC values of N, V, and E.

We write the N Newton's equations for all particles i in the configuration $\mathcal{P}(t_0)$:

$$m_i \cdot \ddot{\vec{r}}_i = -\,\overrightarrow{\mathrm{grad}}_i V = \vec{F}_i \quad , \quad i = 1, 2, 3, ..., N$$

where m_i is the mass of particle i, $\vec{R}_i$ its position, $\overrightarrow{\mathrm{grad}}_i V$ is the gradient of V with respect to the coordinates of i, and $\vec{F}_i$ the force acting on i.
(*Note that this equation is for simple point masses.*
If the particles are rigid bodies, the equations are more complicated.)

Imagine that we can somehow (not analytically) solve this system of N 2^{nd} order differential equations
starting from $\mathcal{P}(t_0)$ (the **initial conditions**)
Then we could get after some time δt a new configuration $\mathcal{P}(t_0 + \delta t)$

So we have now:
$\mathcal{P}(t_0)$ characterized by N, V, E
$\mathcal{P}(t_0 + \delta t)$ characterized by:

N because Newton's equations do not change particle numbers
V because the particles are always restricted to this volume
(We'll have to make sure that this is so → PBC)
E because the total energy is a constant of motion in a Newtonian system without external interactions and all the interactions in our model are internal to the system (e.g. no external fields)

So if $\mathcal{P}(t_0)$ is a microstate belonging to a certain MACROSTATE,
$\mathcal{P}(t_0 + \delta t)$ is also a microstate belonging to **the same** MACROSTATE.

We are halfway there, yet

We still need to know:

(a) How to deal with the volume restriction

(b) How to deal with the integration of Newton's equations

(c) How to find $\mathcal{P}(t_0)$

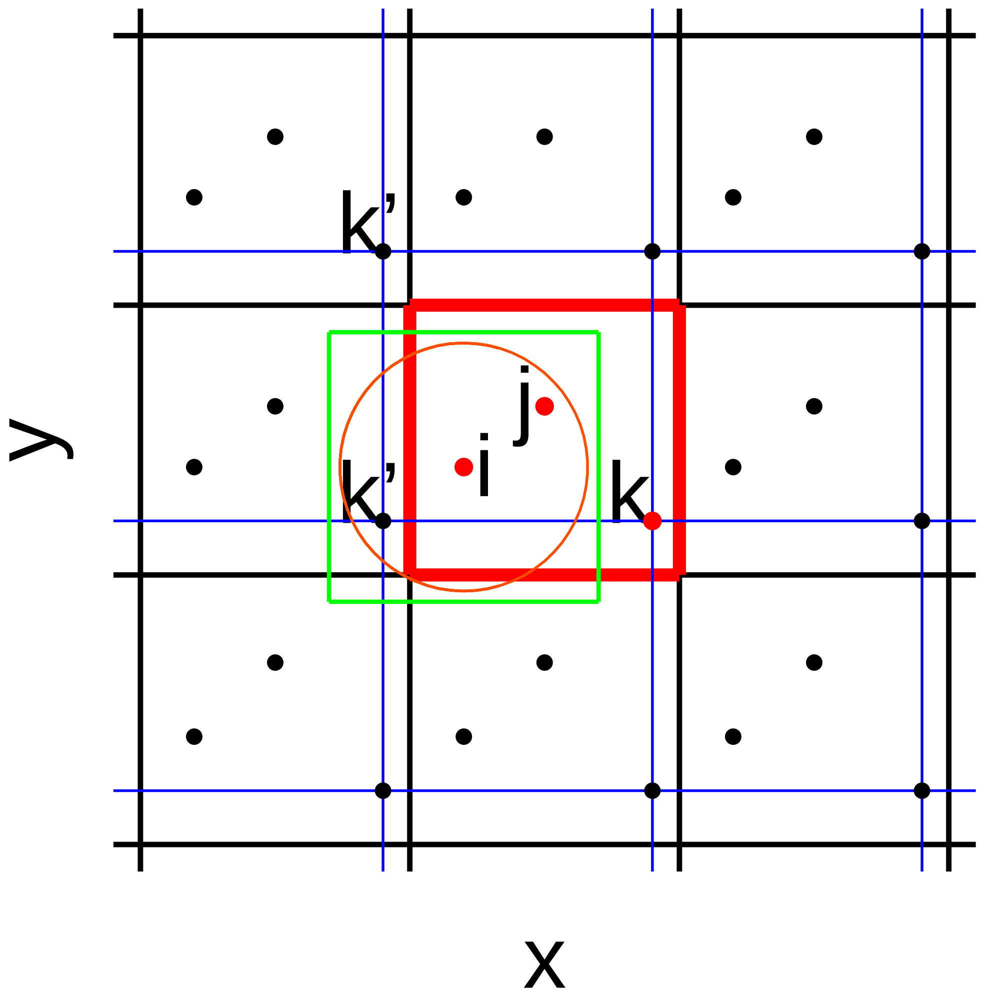
Question (a): Volume restriction
How to make sure that the particle positions are always restricted to inside the volume V ?

Answer: Use Periodic Boundary Conditions (PBC)
with the Minimum Distance Convention to compute the interactions

$\Rightarrow$ **(Almost) the same tricks are used in MC !**

(In MD one needs to compute the interaction energies AND the forces
In MC ONLY the energies are needed)

PBC



'basic box'
containing 'real' particles

'periodic' boxes
containing 'mirror' particles

box centered on
particle i containing
its interaction partners
(minimum distance
convention)

"cut-off" sphere around
i

k and all k'

Interactive Java script:
http://research.chem.psu.edu/shsgroup/chem647/project6/project6.html

Advantages/consequences of periodic boundary conditions
and minimum distance convention:

1) There will always be N particles in the basic box
(because if one particle, say k, leaves the box on one side
a mirror particle k' will enter from the other side).

2) Each particle will be in the center of all its interaction partners
(green box)
The will thus be no surface at the limits of the red box
(nor anywhere else in the system)
In other words:
each particle sits in the center of all other particles
(as far as the computation of the interactions is concerned)

Question (b): How to deal with the integration of Newton's equations?

What is actually the problem with the equations on page 51?:

$$m_i \cdot \ddot{\vec{r}}_i = -\overrightarrow{\mathrm{grad}}_i V = -\overrightarrow{\mathrm{grad}}_i V\left(\vec{r}_1, \vec{r}_2, \vec{r}_3, \ldots.., \vec{r}_N\right) \quad , \quad i = 1, 2, 3, \ldots, N$$

The N 2nd order differential equations are all coupled through their right hand sides.
There is no analytic solution* for this problem
(except in a few special cases e.g. → normal modes)

---

* Analytic solution: You can write the trajectory $R_i(t)$ of a particle i as some mathematical function, e.g.:

$$\vec{R}_i(t) = A \cdot \cos\left(\Omega \cdot t\right) + \ldots. \text{ or whatever other function}$$

Answer (b): Do a numerical solution (numerical integration)

All numerical solutions are based in some way or other on series expansions.
I.e. (*omitting the vector notation*):
If you know $r_i(t)$ and $\dot{r}_i(t)$ at some time t,
you can find to a good approximation $r_i(t + \delta t)$ as (Taylor series):

$$r_i(t + \delta t) \approx r_i(t) \ + \ \dot{r}_i(t)|_t \cdot \delta t \ + \ \frac{1}{2}\ddot{r}_i(t)|_t \cdot \delta t^2 \ + ...$$

and Newton's equation tells us that

$$\ddot{r}_i(t)|_t = \frac{1}{m_i} \cdot \mathrm{grad}_i V = F_I(t)$$

for a small δt δt is called the time step
The smaller δt, the better your approximation (in principle!)

$\longrightarrow$ We'll have to think how small/big to make our δt in practical cases
How to find 'good' integration methods is studied in
numerical mathematics

Question (c): How to find a suitable $\mathcal{P}(t_0)$?
(*This is the most cumbersome of the 3 questions (a)-(c), which is why we kept it until the end!*)

Problems:

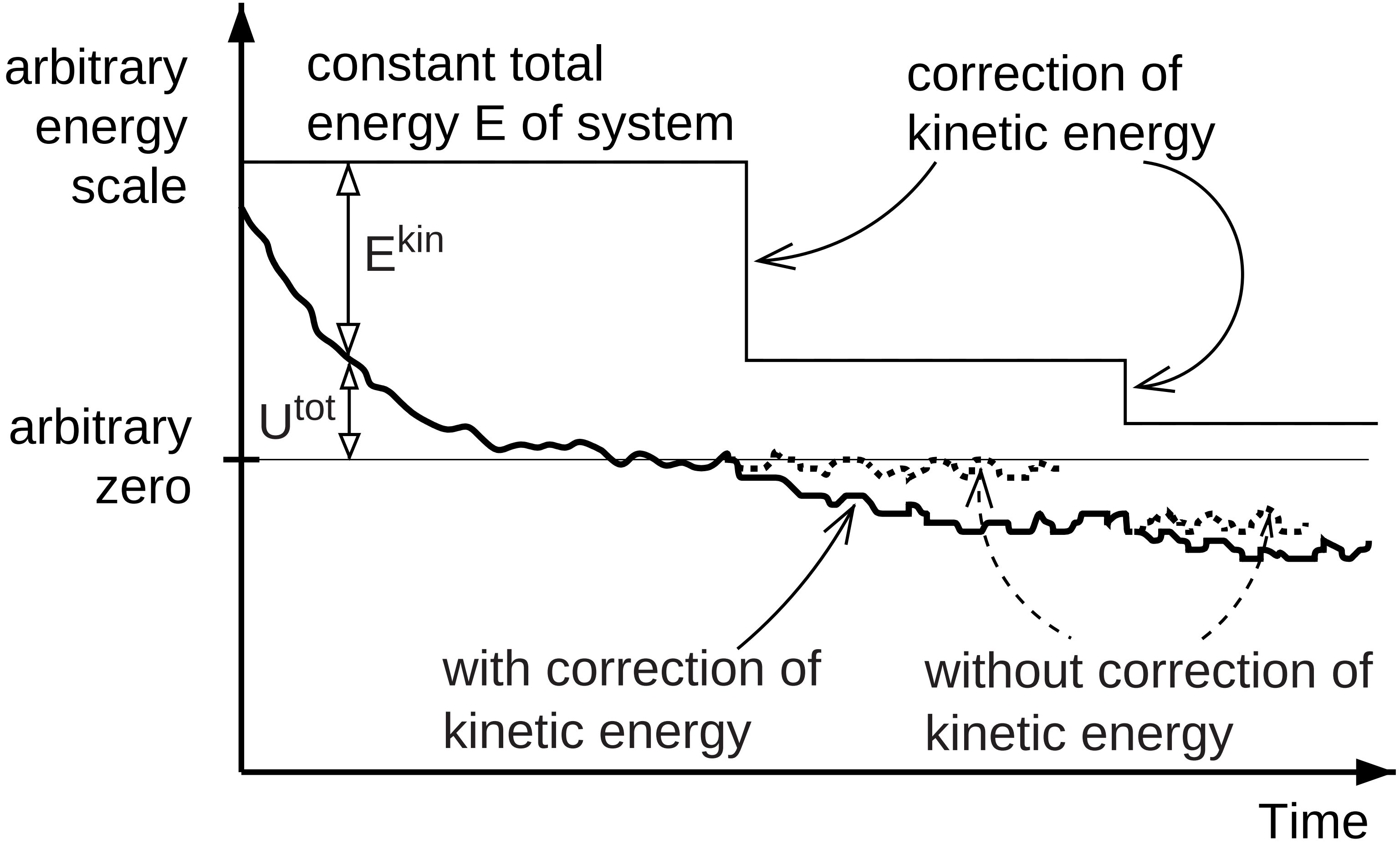
- Our MACROSTATES are characterized by N, V, E being constant
However, we usually do not know E for the system that we want to study.

- Even if we knew E, we don't know how to "make" a $\mathcal{P}$ which has exactly this energy.

- Finally, in a thermodynamic system, at constant composition, we can fix 3 quantities (here N, V, E), all other quantities will fluctuate
(i.e. we should really write $< T >$ for the temperature instead of T etc.)

Note: In the **thermodynamic limit** one can show that the results will not depend on the ensemble if the 'conditions' are the same, e.g.
ensemble: $(NV\mathbf{E})$ with $< T > = \mathbf{T}$ will give the same results as:
ensemble: $(NV\mathbf{T})$ with $< E > = \mathbf{E}$

Answer (c):
The figure shows how to proceed in principle to find a $\mathcal{P}(t_0)$.



1) We "guess" a preliminary $\mathcal{P}(t_0)$ (educated guesses preferred!).
2) We start the simulation (numeric integration).
3) The total energy E will be constant if we integrate correctly.
4) However, almost always, our guessed $\mathcal{P}(t_0)$ will have too much potential energy (interactions) compared to its kinetic energy.
5) The kinetic energy ($\propto$ temperature) will thus increase, the potential energy decrease, first quickly, then more and more slowly.
6) If our system is *well-behaved*, it will approach a steady state. (only fluctuations between kinetic and potential energy, no drift.)
7) Trouble! The MACROSTATE that we have is not at all the one we wanted to study (usually much too much kinetic energy!).
8) We now remove kinetic energy from the system (which is easy: scale the velocities) and use the $\mathcal{P}$ that we have now reached as a new, better guess for $\mathcal{P}(t_0)$
9) We restart the simulation form the new $\mathcal{P}(t_0)$ (GOTO 2) until this $\mathcal{P}(t_0)$ is really the one that we want
In this case, we forget this whole "equilibration procedure" and start the **real simulation**.

Note:

You cannot change the kinetic and potential energies independently

They are linked (Virial Theorem)

So whenever you have changed the kinetic energy (scaled the velocities)
you must wait for the potential energy to relax,
and vice versa

Summary: Making the sample with MD

MD generates (in the simplest case) $\mathcal{P}$s for MACROSTATES characterized by:
- Constant number of particles N,
- constant volume V,
- constant total energy E.

This ensemble is known (surprise! surprise!) as the (N, V, E) ensemble, it is a sub-ensemble of the microcanonic ensemble of statistical mechanics.

Note: MD can be 'doctored' to generate $\mathcal{P}$s representative of other ensembles.

Added value:

MD generates the $\mathcal{P}$s in a meaningful order.
The 'order parameter' is the time t.

MD thus generates $\mathcal{P}(t_1), \mathcal{P}(t_2), \mathcal{P}(t_3), \mathcal{P}(t_4), ...$ for increasing times $t_1, t_2, t_3, ...$

---

in passing, more below after the end of the discussion of MD

MC generates **only** the position-part (the $\vec{R}_I$s) of $\mathcal{P}$, let's call it $\mathcal{C}$,
for MACROSTATES characterized, in the simplest case, by:
- Constant number of particles N,
- constant volume V,
- constant temperature T.

This ensemble is known (even bigger surprise) as the (N, V, T) ensemble, it is a sub-ensemble of the canonic ensemble of statistical mechanics.

MC generates the $\mathcal{C}$s in a random order.

Note:
MC can also be 'doctored' to generate $\mathcal{C}$s representative of other ensembles.

Terminology:

$\mathcal{P}$ (generated by MD) is often called a point in the $6 \cdot N$-dimensional $\mathcal{P}$hase space.

$\mathcal{C}$ (generated by MC) is often called a point in the $3 \cdot N$-dimensional $\mathcal{C}$onfiguration space.

The term **configuration** is used both for $\mathcal{P}$ and $\mathcal{C}$.

The (ordered) $\mathcal{P}$s are (a part of) the system **trajectory**

The list of all $\mathcal{P}$s is often called the **history** of the system.

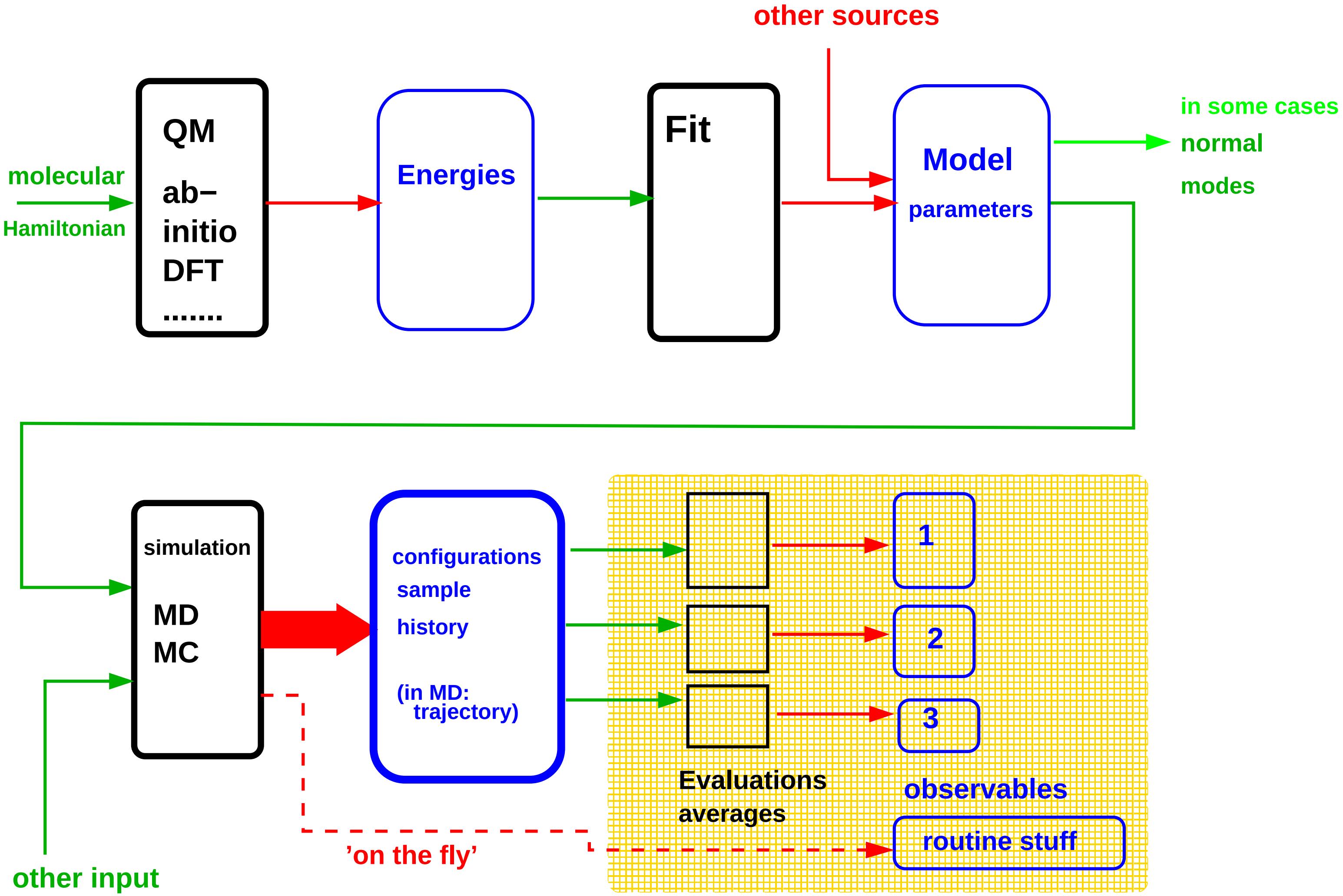
We now know how to generate a large number of microstates $\mathcal{P}$ for the MACROSTATE we are interested in

– How do we know that the steady state that we have reached is "thermal equilibrium"?
– How do we know that we have enough configurations and that they are "representative"?

These are very difficult questions.
There is no way to decide them "a-priori",
they have to be settled "a-posteriori"
by looking at various quantities computed from the simulated sample.

But first we must learn how to compute observables from the simulated sample.

From input to output through a huge amount of intermediate data



This is the most interesting part of molecular simulations

Notes in passing:

–Some people have questioned whether first generating such a huge amount of data and then whittling them down to a few 'observables' qualifies as 'simple'

–Others have called simulation methods 'brute force'

–There is indeed no systematic way to 'improve' (what does it mean?) results (unlike e.g. the variational principle)

–However, simulations usually need fewer, and weaker, assumptions than analytical methods

–In their philosophy, they are akin to experiments
 - computer experiments -
 and thus often allow 'trial and error' approaches

One problem has initially bothered people a lot:

The solution of differential equations (see harmonic oscillator)
depend on the initial conditions

So MD results will depend on initial conditions

– Is this good? Do we want this?

– Are there cases where we want this and others where we do not?

– What can we do to avoid it if we do not like it?

Model 1 $\Longleftrightarrow$ Observable 1

Model 2 $\Longleftrightarrow$ Observable 2

Model 3 $\Longleftrightarrow$ Observable 3

Model 1 $\Longleftrightarrow$ Observable 1

Model 2 $\Longleftrightarrow$ Observable 2

Model 3 $\Longleftrightarrow$ Observable 3

The simulation approach

$$\textbf{One model}\quad\left\{\begin{array}{ll}\Longleftrightarrow & \textbf{Observable 1}\\[1em] \Longleftrightarrow & \textbf{Observable 2}\\[1em] \Longleftrightarrow & \textbf{Observable 3}\end{array}\right.$$

Being able to compute observables **consistently**
is one of the main advancements brought
about by computer simulations

Consistency III: Consistent Coarse Graining

One model

$\Downarrow$

$\Downarrow$

Coarse graining procedure

$\Downarrow$

$\Downarrow$

Coarse grained model

$\Longleftrightarrow$ Observable 1

$\Longleftrightarrow$ Observable 2

$\Longleftrightarrow$ Observable 3

$\Longleftrightarrow$ Observable 4

$\Longleftrightarrow$ Observable 5

$\Longleftrightarrow$ Observable 6

The representative MD sample is thus:

$$\begin{array}{rcll}
\text{Sample} = \{ & & r_1, r_2, r_3, ...r_N, \; v_1, v_2, v_3, ..., v_N & t = 0 \\
& , & r_1, r_2, r_3, ...r_N, \; v_1, v_2, v_3, ..., v_N & t = 1 \\
& , & r_1, r_2, r_3, ...r_N, \; v_1, v_2, v_3, ..., v_N & t = 2 \\
& , & r_1, r_2, r_3, ...r_N, \; v_1, v_2, v_3, ..., v_N & t = 3 \\
& , & \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots & t = \dots \\
& , & r_1, r_2, r_3, ...r_N, \; v_1, v_2, v_3, ..., v_N & t = M \quad \} \\
\hline
= & & q_i \quad , \quad p_i(/m_i) & \\
= & & \{R^{\text{nuclei}}\} \quad , \quad \{\dot{R}^{\text{nuclei}}\} &
\end{array}$$

In the language of differential equations, this is the **system trajectory** (which meanders through (i.e. samples) **phase space**)
we also call this the **configurations**, or the **history**

On the computer: several Mb or Gb of data

(In MC, it is the same <u>except</u>
no velocities and no time, and the $\{r\}$ in random order)

Statistical mechanics: compute thermodynamics averages from the partition function, e.g. some observable A:

From Q (NVT)

$$\langle A \rangle_T = \frac{1}{Q} \int_{\mathrm{all}\ p,q} A(p,q) \cdot \exp \frac{-E(p,q)}{k_\mathrm{B} T} \,\mathrm{d}p\,\mathrm{d}q$$

From Ω (NVE)

$$\langle A \rangle_E = \frac{1}{\Omega} \int_{\mathrm{all}\ p,q} A(p,q) \cdot \delta(E(p,q) - E_0) \,\mathrm{d}p\,\mathrm{d}q$$

where q stands for all positions variables $(x_1, y_1, z_1, x_2.y_2, ..., z_N)$
and p for all velocity variables $(vx_1, vy_1, ..., vz_N)$

So the integrals are $6N$-fold integrals $(\int\int\int ......\int)$ or sums $(\sum\sum\sum\sum..)$ over the (q,p)-space, **phase space**
⇒ not really doable (except in some very simple cases)!

Thermodynamic average from simulations

$$\begin{aligned} \mathrm{MD}: \quad \langle A\rangle_E &= \frac{1}{N}\sum_{i=1}^{N} A(\mathcal{P}_i) \\ \mathrm{MC}: \quad \langle A\rangle_T &= \frac{1}{N}\sum_{i=1}^{N} A(\mathcal{C}_i) \end{aligned}$$

where $\mathcal{P}_i$ is the ith configuration from the sample in phase space
and $\mathcal{C}_i$ is the ith configuration from the sample in **configuration** space
(which contains only the positions, we'll come to this later)

The Metropolis–Hastings algorithm

A Markov chain Monte Carlo method for obtaining a sequence of random samples from a probability distribution for which direct sampling is difficult.
The sequence can be used to approximate the distribution (i.e., to generate a histogram), or to compute an integral (such as an expected value).

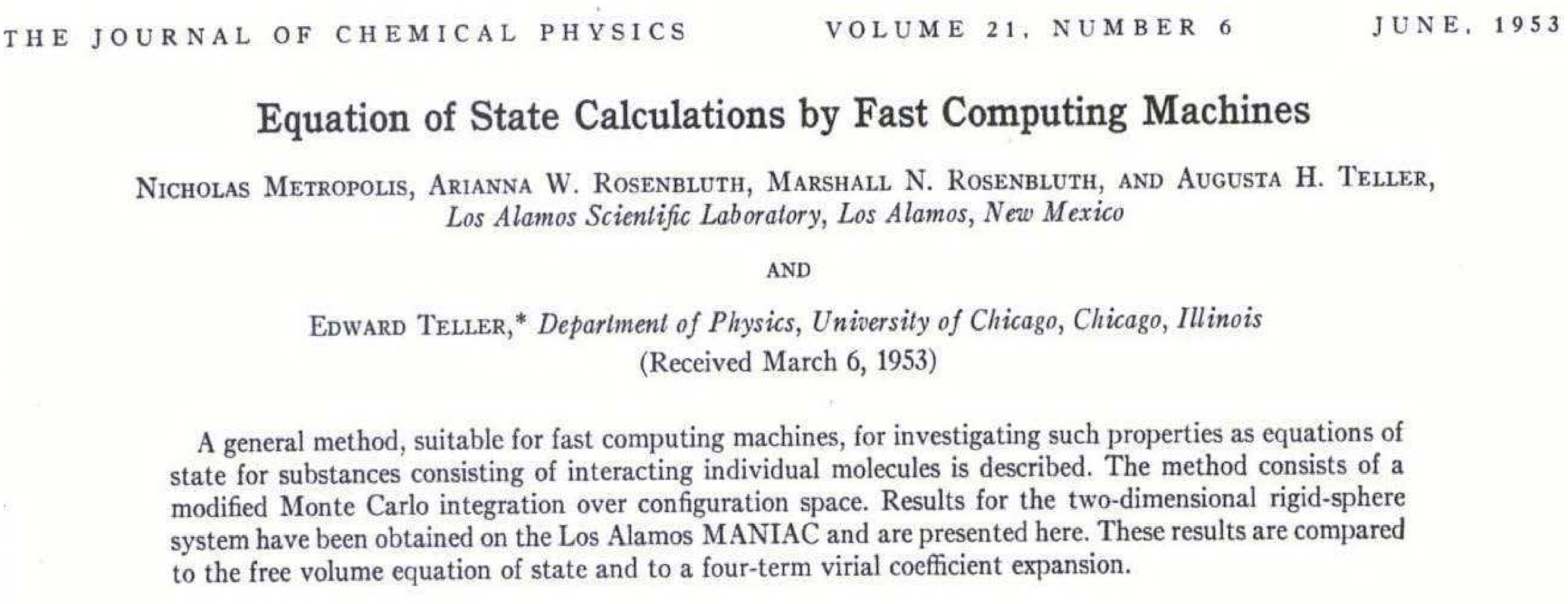
History

Named after
- Nicholas Metropolis, author of
  Equation of State Calculations by Fast Computing Machines (1953)

who proposed the algorithm for the specific case of the Boltzmann distribution

and W. Keith Hastings who extended it to the more general case in 1970.

There is controversy over the credit for discovery of the algorithm. Edward Teller states in his memoirs that the five authors of the 1953 paper worked together for "days (and nights)". M. Rosenbluth, in an oral history recorded shortly before his death credits E. Teller with posing the original problem, himself with solving it, and A.W. Rosenbluth (his wife) with programming the computer. According to M. Rosenbluth, neither Metropolis nor A.H. Teller participated in any way. Rosenbluth's account of events is supported by other contemporary recollections. (from *Wikipedia*)



THE JOURNAL OF CHEMICAL PHYSICS VOLUME 21, NUMBER 6 JUNE, 1953

Equation of State Calculations by Fast Computing Machines

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AND

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(Received March 6, 1953)

A general method, suitable for fast computing machines, for investigating such properties as equations of state for substances consisting of interacting individual molecules is described. The method consists of a modified Monte Carlo integration over configuration space. Results for the two-dimensional rigid-sphere system have been obtained on the Los Alamos MANIAC and are presented here. These results are compared to the free volume equation of state and to a four-term virial coefficient expansion.

- see file metropolis-et-al-1953.pdf (original paper)
- See file

The Metropolis–Hastings algorithm

Use a Markov chain that, at sufficiently long times, generates states that obey the distribution P(x).

The Markov chain must fulfill the conditions **ergodicity** and **balance**.

A Markov chain generates a new state $\mathbf{X}_{t+1}$ that depends only on the previous state $\mathbf{X}_t$.

The algorithm uses a *proposal density* which depends on the current state $\mathbf{X}_t$, to generate a new proposed sample **X’**.

Then **X’** Is accepted as $\mathbf{X}_{t+1}$ if a random number α (uniform between 0 and 1) satisfies:

$$\alpha < P(\mathbf{X}') \, Q(\mathbf{X}_t;\mathbf{X}') \, / \, P(\mathbf{X}_t) \, Q(\mathbf{X}_t;\mathbf{X}')$$

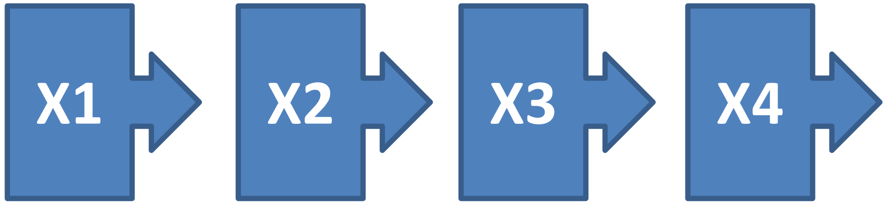
otherwise the new state is the old state: $\mathbf{X}_{t+1} = \mathbf{X}_t$

The procedure is then repeated, $\mathbf{X}_{t+1}$ is renamed to $\mathbf{X}_t$.

The configuration space

A system of particles.
A state of the particles is described by a configuration ω taken from the configuration space Ω (infinite/finite, continuous/discrete)
Example 1 :
N interacting particles described by position and velocity of each in 3D.
Ω is an part of of R^{6N}.
Example 2:Surface with M adsorption sites that are occupied or free.

Markov-chain



dependent random variables

Our circle example:

$X_t = (x_t,y_t)$ in $[0\ 1]^2$
$X' = X_t + \Delta x$
If X' in $[0\ 1]^2$, $X_{t+1}=X'$, else $X_{t+1}=X_t$

12-05-11

Reminder: Accept uphill moves

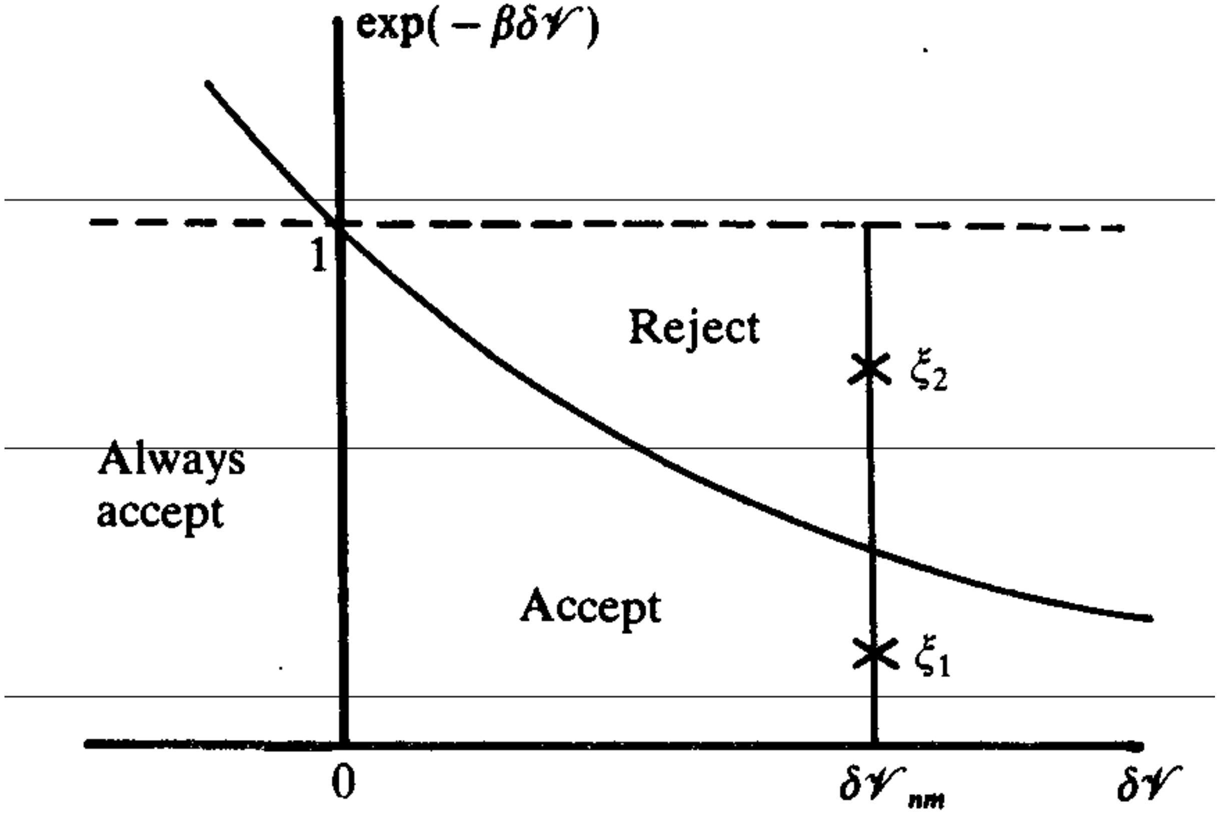


Fig. 4.5 Accepting uphill moves in the MC simulation.

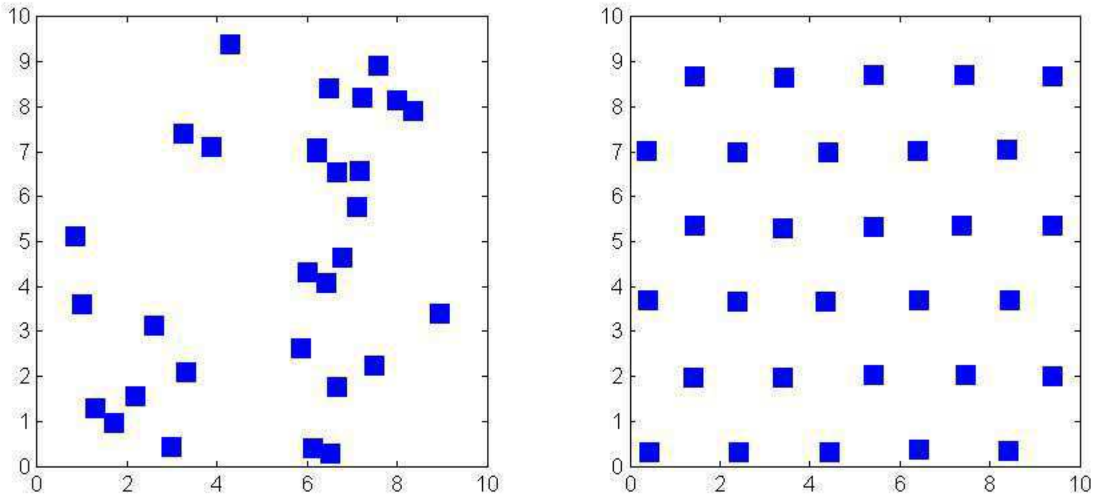
Example:2D-particles

We discuss in detail the program ‘metro1_surf_esimple_v1.m’
(Distributed in the word-document ‘Metropolis_mc_handout.docx’)
Technical details:

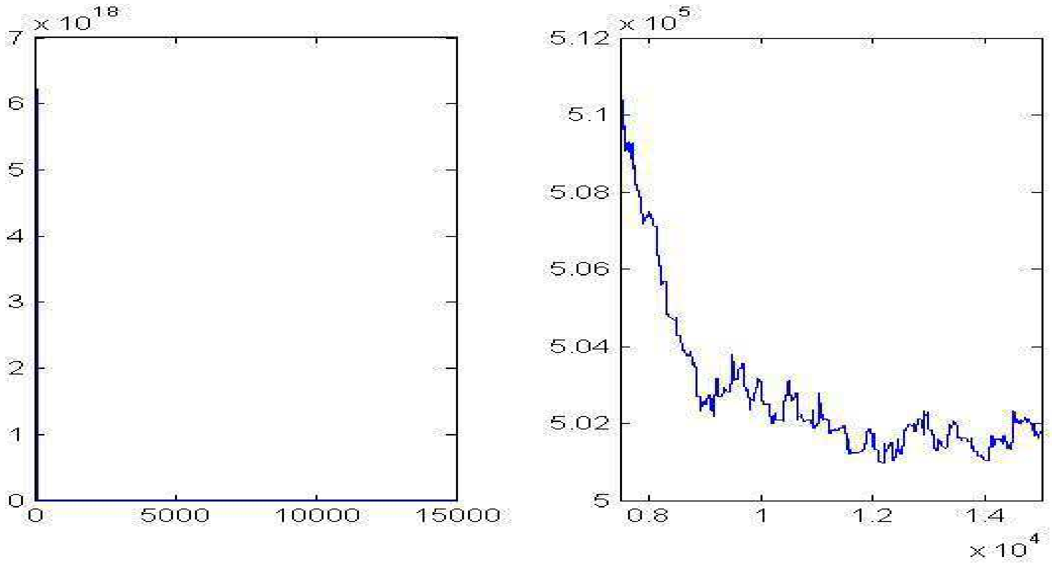
- Application: Atoms/molecules adsorbed on surfaces
- Equilibration
- Behaviour in dependence of T, system size, E^{pot}, …
- causes different equilibrium situations !
- Analysis of trajectories (next page)

Scenario of a 'crystal' :

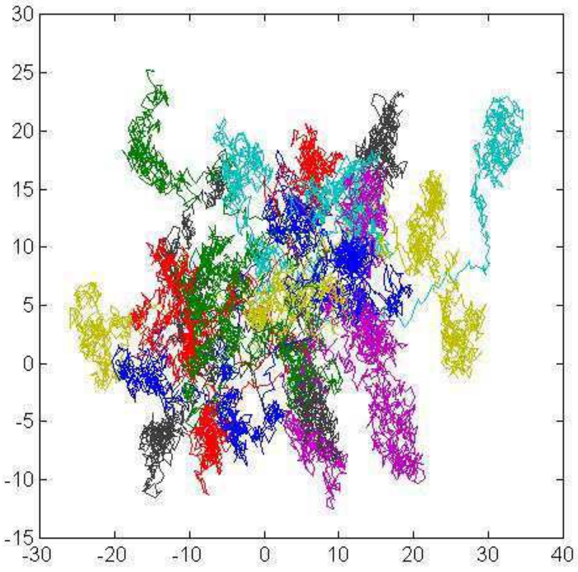
Random starting coordinates equilibrated after 15000 steps



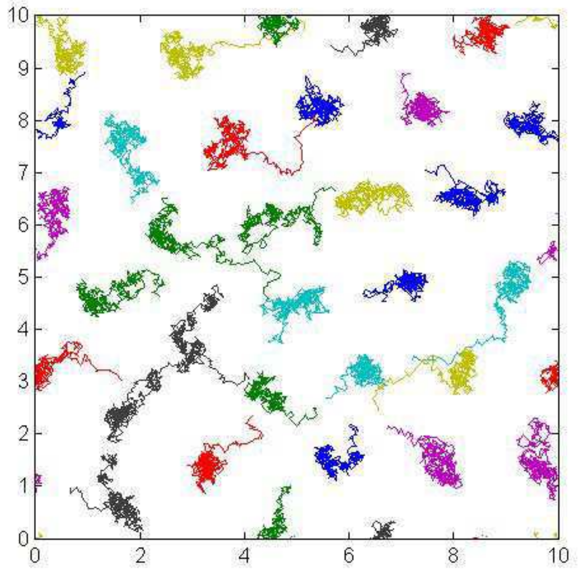
Energy (very high at start) Energy (nearly) equilibrated after 15k steps



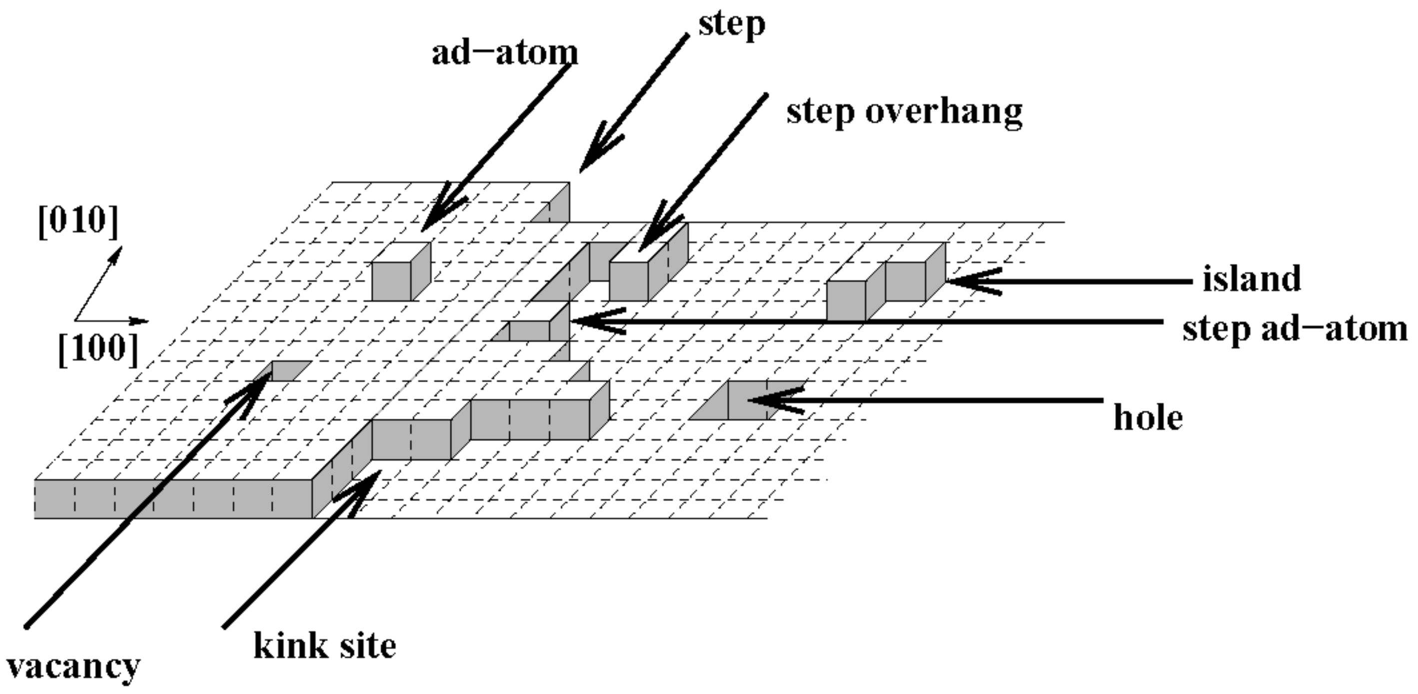
Trajectory during equilibration
(useless to evaluate)



Trajectory after equilibration
(for property calculation)



Another application:
Crystal growth – discrete MC

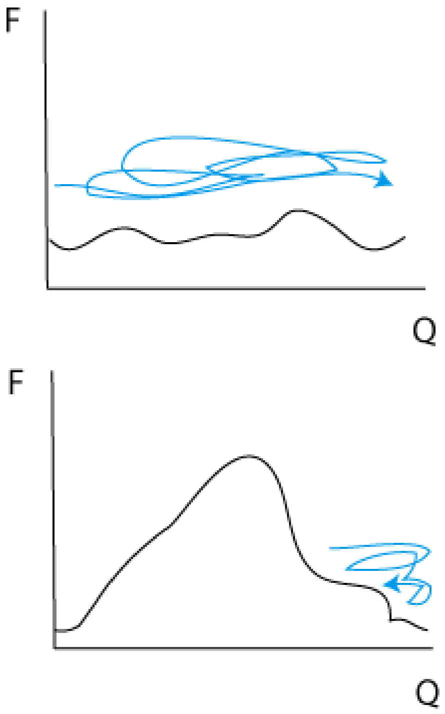


Umbrella sampling

Improve sampling of a where ergodicity is hindered by the form of the system's energy landscape.

Example:

- Solid at its melting point:
- Order parameter *Q*,
    liquid (low *Q*)
    solid (high *Q*)
- Both are low in energy, but separated by a gy barrier
- Prevents the simulation from adequately sampling both phases.



Diffusion MC

See slides in file ‘Judy_chow_DMC’
(nicht Stoff der LV)
…

Umbrella sampling

- $w(\mathbf{r}^N)$ is a function chosen to promote configurations that would otherwise be inaccessible to a Boltzmann-weighted Monte Carlo run.
- $w(\mathbf{r}^N)$ may be chosen such that $w = w(Q)$, taking high values at intermediate Q.
- Boltzmann weighting is replaced by a potential chosen to cancel the influence of the energy barrier present.

Markov chain distribution :

$$\pi(\mathbf{r}^N) = \frac{w(\mathbf{r}^N)\exp\left(-U(\mathbf{r}^N)/k_B T\right)}{\int w(\mathbf{r}'^N)\exp\left(-U(\mathbf{r}'^N)/k_B T\right) d\mathbf{r}'^N}$$

Of course one must 'calculate back' (*w s*ubscript indicates values from the umbrella-sampled simulation :

$$\langle A\rangle = \frac{\langle A/w\rangle_w}{\langle 1/w\rangle_w}$$

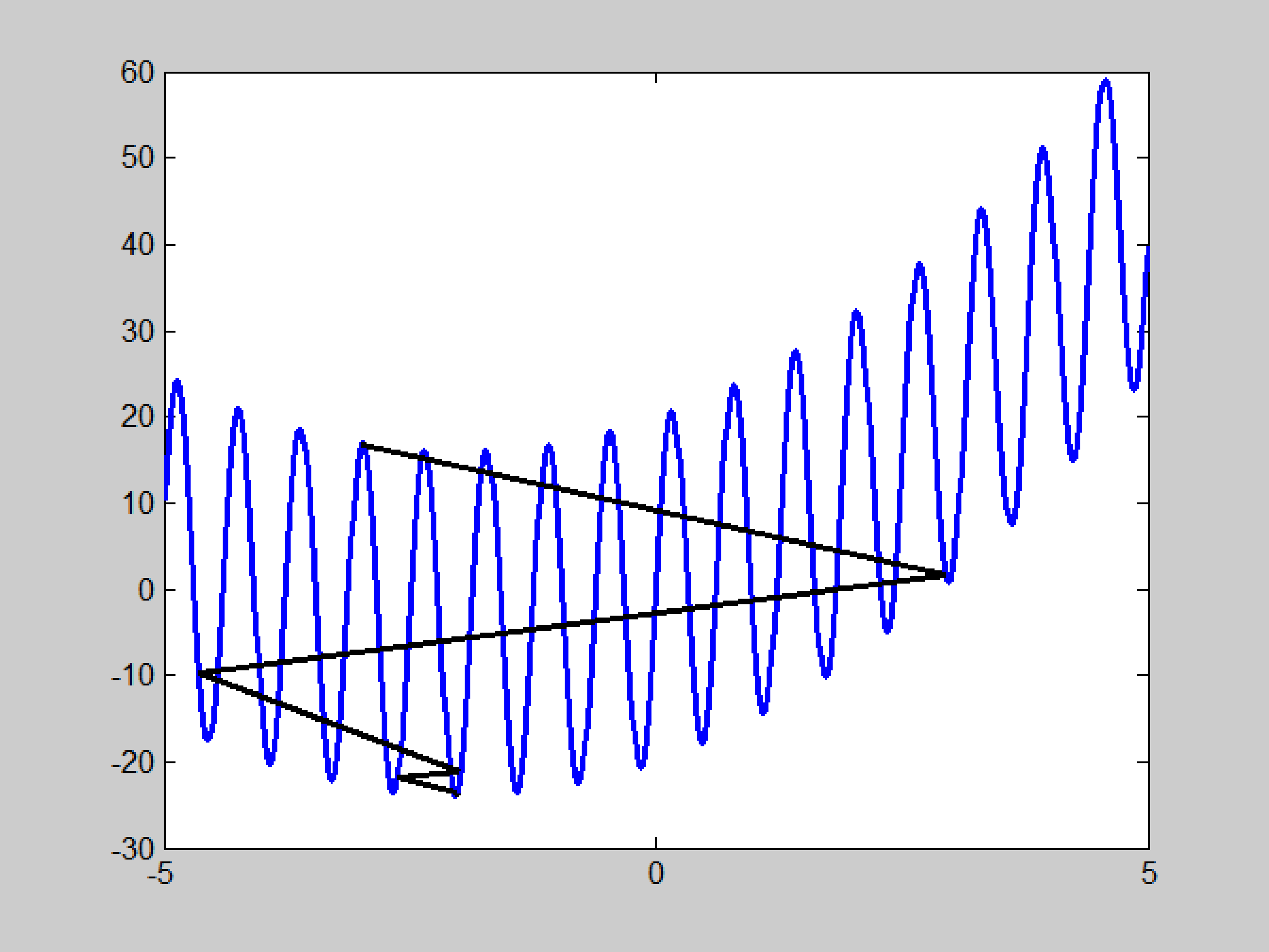
Simulated Annealing

Idea: Global optimization (avoiding local minima) by slowly lowering T !
Useful but sometimes the low efficiency is a problem.
A very rudimentary program: ‘siman.m’:

```
function siman
% demonstrating simulated annealing:
%
y=inline('x.^2+20*sin(x*10)+4*x');                         % function
clf; xax=[-5:0.02:5]; p=plot(xax,y(xax),'blue');
set(p,'linewidth',2); hold on;
T=10; naccept=0; xold=-3; yold=y(xold);
for nmove=1:1000,                                          % annealing loop
   r=T*randn;                                              % random number
   xnew=xold+r; ynew=y(xnew);
   if yold-ynew > rand*T,                                  % accept or reject
      p=plot([xold xnew],[yold ynew],'k'); set(p,'linewidth',2);
      xold=xnew; yold=ynew; naccept=naccept+1;
      xold=xnew;   yold=ynew;                              % keep old, calculate new x,y
   end%if
   T=T*0.99;                                               % reduce 'Temperature'
   if mod(nmove,100)==1; disp([nmove naccept xold yold]); end
end%for
```

Simulated Annealing

Starting from any position the global minimum is located in less than 1000 steps:



Thermodynamic average from simulations

$$\begin{aligned} \mathrm{MD:} \quad \langle A \rangle_E &= \frac{1}{N} \sum_{i=1}^{N} A(\mathcal{P}_i) \\ \mathrm{MC:} \quad \langle A \rangle_T &= \frac{1}{N} \sum_{i=1}^{N} A(\mathcal{C}_i) \end{aligned}$$

where $\mathcal{P}_i$ is the ith configuration from the sample in phase space
and $\mathcal{C}_i$ is the ith configuration from the sample in **configuration** space
(which contains only the positions, we'll come to this later)

Part 3: results, results, results

Examples of thermodynamic averages routinely computed from MD-simulations (all masses assumed to be equal to simplify the equations)

$$\frac{3}{2}\,k_{\mathrm{B}}T = \frac{3}{2}\,m\,\left(\frac{1}{N}\sum_{i=1}^{N} v_i^2\,\right) = \frac{3}{2}\,m\langle v^2\rangle_N$$

We can compute this for all particles,
for selected particles (to check e.g. whether the system is in equilibrium),
for selected degrees of freedom (e.g. using only the v_xs, v_θs, $v_{....}$s),
also combinations thereof, etc.etc.

An important technique used here is **binning** (histograms)

Here one does several averages at the same time:

$$\langle n(A(x+\Delta x)\rangle_E \propto \sum_{\text{all configurations}} \delta(A_i \text{ between } A(x) \text{ and } A(x+\Delta x))$$

i.e. a 1 is added to the counter $n(A(x+\Delta x)$ every time a value of A_i between $A(x)$ and $A(x+\Delta x)$ is found in the configurations

We decide on a Δx (the resolution) and study $\langle n_A(x)\rangle$, which, suitably normalized, is the probability distribution (of A): $p_A(x)$

How to code this:

```
REAL A
INTEGER INDEX
REAL or INTEGER histogram(....), total_number_of_A

A = ...........
index = convert_to_integer ( A / resolution + shift)
histogram(index) = histogram(index) + 1
total_number_of_A = total_number_of_A + 1
```

You have to make sure that your histogram does not overflow,
i.e. that no `index` larger or smaller than the array boundaries
of `histogram` appears during the computations
(Compilers can generate code to do this automatically, but then it runs much more slowly)
You can then normalize the histogram to one:

```
LOOP OVER index
histogram(index) = histogram(index) / total_number_of_A
```

Histograms often computed in the equilibrium system:

Binning v_x $(v_y,\ v_z)$: we get a Gaussian
(width depending on the mass and the temperature)

Binning v^2: we get the Maxwell-Boltzmann distribution

Binning interparticle distances $r_{\alpha\beta}(= r_{\beta\alpha})$
(and normalizing correctly):
we get the radial pair distribution functions (rdf, $g(r)$),
which are important in many statistical mechanics theories,
(more about this later)
and can also be obtained (not so easily, but still)
from X-ray scattering, neutron scattering, electron scattering ....

Note

$$n_{\alpha\beta}(R_{\alpha\beta}) = 4\pi \cdot \frac{N_\beta}{V} \cdot \int_0^{R_{\alpha\beta}} r^2_{\alpha\beta} \; g_{\alpha\beta}(r_{\alpha\beta}) \; \mathrm{d}r_{\alpha\beta}$$

is the average number of neighbors of type β around a particle
of type α in a sphere of radius $R_{\alpha\beta}$ (upper limit of integral).

$$\textbf{Thus}: \quad g_{\alpha\beta} = g_{\beta\alpha} \quad \text{(from the definition)} \;, \; \text{but} \quad n_{\alpha\beta} \neq n_{\beta\alpha}$$

So often it is more instructive to plot the n rather than the g.
Example:
The average number of water molecules around an ion is meaningful
(the hydration number)
The average number of ions around a water molecule is much less intuitive

As an aside

The $g(r)$s are so important
(many properties e.g. of liquids can be approximated
'in the 2-body approximation' if one knows them)
People have tried, and in many cases succeeded,
in computing them without taking the detour through the
huge simulation ensemble (see above)

On thus tries to go straight from the pair potentials to the $g(r)$s

The methods are usually called 'integral equation theory'
more later (may be)

The g-functions are related through Fourier transforms (FT)
to the experimental X-ray–, neutron– (elastic),
electron–scattering functions:

$$S(Q) \propto \sum x_\alpha x_\beta \; f_\alpha \; f_\beta \; \big(\mathrm{FT}(g_{\alpha,\beta}(r) - 1)\big)$$

Q scattering vector, also often called k
α, β types of atom in the system
x mole fractions
f factors that depend on the type of scattering and type of atom

As we have seen, when we use **MD** to construct (a sample of) the 'microcannonical (NVE)' ensemble, we get, quasi 'for free', information about the time evolution of the system.

This can be studied 'in equilibrium' and 'out of equilibrium'

The way to explore the evolution of things in the equilibrium ensemble* is to compute time-correlation functions

* Equilibrium does not mean that 'nothing moves', it is just that for macroscopic observables one has $\frac{\partial}{\partial t} = 0$

So we extend the equation

$$\langle A \rangle_E = \frac{1}{N} \sum_{i=1}^{N} A(\mathcal{P}_i)$$

to become

$$\langle A(0)A(t) \rangle_E = \frac{1}{M_j} \frac{1}{N} \sum_{i=1}^{N} \sum_{j=1}^{M_j} A(\mathcal{P}(t_j)_i) \otimes A(\mathcal{P}(t_j + t)_i) = c_{AA}(t)$$

<u>auto</u>correlation, or more generally

$$\langle A(0)B(t) \rangle_E = \frac{1}{M_j} \frac{1}{N} \sum_{i=1}^{N} \sum_{j=1}^{M_j} A(\mathcal{P}(t_j)_i) \otimes B(\mathcal{P}(t_j + t)_i) = c_{AB}(t)$$

<u>cross</u>correlation
$\otimes$ is some operation, often a scalar product.
Like previously, the i-sum can be over all or only over selected particles

Example: velocity autocorrelation function $C_{vv}(t)$

$\otimes$ will be a scalar product
So I can regroup all the $A_i(t_j)$ in a big vector $\mathcal{V}$
for the time t:

$$\begin{aligned}\mathcal{V}(t) \quad = \quad & (\ vx_1(t), vy_1(t), vz_1(t), vx_2(t), vy_2(t), vz_2(t), vx_3(t), \\ & vy_3(t), vz_3(t), ..., vx_N(t), vy_N(t), vz_N(t)\ )\end{aligned}$$

a big $3N$-dimensional vector, and one gets

$$\langle v(0)v(t)\rangle_E = \frac{1}{M_j}\sum_{j=1}^{M_j}(\mathcal{V}(t_j))\cdot(\mathcal{V}(t_j+t)) = c_{vv}(t)$$

(the i-sum is already in the scalar product)

The Fourier Transforms (FT) of correlation functions are called ’spectra’:

$$c_{vv}(\omega) = f \cdot \int_0^\infty c_{vv}(t) \cdot \cos(\omega\ t)\ \mathrm{d}t = \mathrm{FT}(c_{vv}(t))$$

(It is enough to take the cosine since the (classical) correlation function is even in time: $c_{vv}(t) = c_{vv}(-t)$)
f is some factor that people chose differently.

A time-correlation function (time domain)
and a spectrum (frequency domain)
thus contain exactly the same information
(*experimentally one may be much harder to get than the other*)

Molecular graphics

There are many (free and commercial) graphics programs that can 'read' the configurations from MD (and MC) simulations and:

– draw graphic symbols of various kinds (colored spheres etc.) to show the particle positions

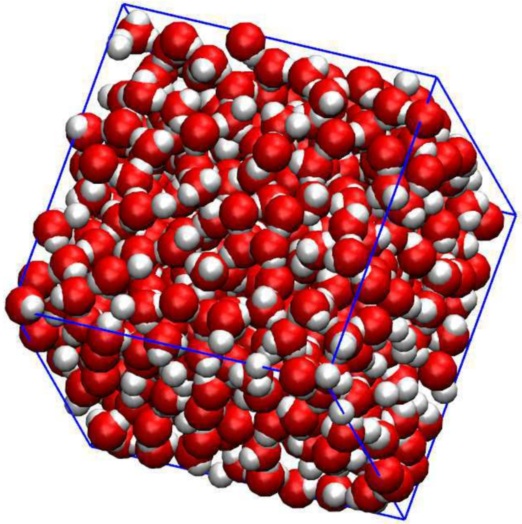
– draw other symbols (e.g. lines) based on geometric criteria (which it computes from the positions

– do some statistics

– make animations

– ...

$\Longrightarrow$ exercises



Configuration from MD-simulation

544 water molecules
ρ=1 g cm^{-3}
→ PBC, box-edge= 25.34Å
(T = 300 K)

Part 4

’Other’ simulation (and other) methods

Sometimes molecular simulations either
- provide much more information than we need
- cannot be carried out meaningfully because of
  - lack of information (model)
  - lack of computational resources
  - costs (industry)
  - .....

This can be addressed by:

- Applying different levels of theory to different parts of the problem
  e.g. in QM/MM approaches
  by coupling to 'cheaper' methods
  (normal modes, field equations on grids,....)
- Coarse graining
  e.g. by removing (integrating over) the solvent
  and treating only the solute
- Computing (with approximations) only certain quantities,
  e.g. rdfs in integral theory approaches

We'll look briefly at these things in the reverse order

Let's look at the basic ideas of **integral equation theory**

We define a 'total' pair **correlation** function as:

$$h(r_{ij}) = g(r_{ij}) - 1$$

which goes to 0 for r large, as a correlation function should

which we divide up into a 'direct' and and 'indirect' part:

$$h(r_{13}) = c(r_{12}) + \rho \cdot \int\limits_{\text{all particles 3}} c(r_{13}) \cdot h(r_{23})\, \mathrm{d}r_3$$

where the integral describes the 'indirect' influence of particle 1 on particle 2 via particle 3.
(The g_{12}-function results not only from the interaction of 1 with 2, but also from **all** interactions between 1 and 3, and 3 and 2)

This is called the Ornstein Zernike (OZ) equation

$c(r_{ij})$ is called the 'direct correlation' (ρ is the density)

Since we know neither h nor c
we need one more equation for any attempt to solve this.

This additional equation, an approximation, is called
the **closure relation**

There are several in the literature, among which:
the Percus Yevick approximation
the Hypernetted-chain equation

This is a very specialized field of statistical mechanics, and we shall not dwell much on this here.

See the Wikipedia articles on these topics

See also prof. Wim Briels lecture:
`http://cbp.tnw.utwente.nl/PolymeerDictaat/index.html`

The relation with the pair potential is made in the closure relation, e,g, in HNC via the 'potential of mean force' (PMF, $\mathcal{W}$)

If one thinks of $g(r)$ as a probability (distribution), one can write some sort of 'Boltzmann factor' $(N_1/N_2 = \exp(-\Delta E/(k_\mathrm{B}T))$

$$g_{ij}(r_{ij}) = \exp(\frac{-\mathcal{W}_{ij}(r_{ij})}{k_\mathrm{B}T})$$

We note in passing
The PMF is often used in other contexts too.
When one has the g-functions, like in MD, it is simply
(beware the error bars)
computed by taking the logarithm of $g(r)$
Several thermodynamic quantities can be computed from $\mathcal{W}$

We assume (see above, no ijs written))

$$c = g^{\text{total}} - g^{\text{indirect}} = \exp(\frac{-\mathcal{W}}{k_{\text{B}}T}) - \exp(\frac{-(\mathcal{W} - V)}{k_{\text{B}}T})$$

and V is the pair potential

Fourier transform techniques are used to solve this
ONE DIMENSIONAL integral
→ So even if the math is complected,
at the end it is fast on the computer
(i.e. get g-functions in minutes, not hours)

'Removing' the solvent: **Brownian** (and similar) **Dynamics**

This is of interest if we are interested in some *'big'* solute
(i.e. much bulkier, much heavier than the solvent molecules)
in a solutions

In this case, we are often not interested in the (fast) motions of the *'little'* solvent molecules
and it would thus be nice if they could somehow be removed from the simulation
(there are usually many more solvent than solute molecules)

Idea:
Solve equations of motion only for the solute particles,
describe the influence of the solvent by:

– and 'effective' solute-solute potential (cf. PMF $\mathcal{W}(r)$)
– a friction term in the equations of motion
– an additional (stochastic, random)- force that balances the friction

So the equation of motion becomes for a solute particle i

$$M_i \cdot \frac{\partial^2 r_i}{\partial t^2} + \gamma \cdot \frac{\partial r_i}{\partial t} = -\mathrm{grad}_i\ \mathcal{V} + \mathcal{F}_i$$

In red the new terms:
– velocity dependent: friction
– additional force $\mathcal{F}$ to compensate the friction

The various methods
(Brownian Dynamics (BD), Dissipative Particle Dynamics (DPD) etc.)
differ in what they postulate for $\mathcal{V}$, the friction and the compensating forces.

$\mathcal{V}$ is a suitable solute-solute effective potential
(e.g. the PMF obtained from MD or MC simulations)

If the $\mathcal{V}$, γ and $\mathcal{F}$ are taken from molecular simulations,
this would be real 'coarse graining'

Hybrid methods

See e.g.
Hybrid Particle-Continuum Methods in Computational Materials Physics
edited by M.H. Müser, G. Sutmann, and R.G. Winkler
Publication Series of the John von Neumann Institute for Computing NIC
Series Volume 46
available for free on the Internet

From the preface:
,,, It [*the book*] covers subjects from modeling of hydrodynamic interactions between particles in complex fluids or environments, through coarse-grained descriptions of biological systems, to the coupling of atomically represented regions with various continuum-based theories for fluids and solids. Special aspects are long-time-scale properties of systems with slow collective dynamics, ...

Example:

Molecular Dynamics Meets Finite Elements:
An Approach for Coupled Simulations of Nanocomposites
S.Pfaller, G.Possart, P.Steinmann, M.Rahimi , M.C. Böhm, F. Müller-Plathe

Hybrid techniques bring together the **advantages** of particle-based and continuum- based tools by coupling the different domains. In our approach, we aim to combine the efficiency of continuum mechanics with the accuracy of MD simulations by applying the particle-based approach only in regions of interest, e.g. in the vicinity of solid-polymer interfaces. The remaining parts are treated by continuum mechanics at a much coarser resolution. Thus, a spatial decomposition into a particle region and into a continuum is necessary.

However as Hans Ågren (Stockholm) famously said:

QM-MM methods combine the **disadvantages** of QM
with the **disadvantages** of MM

In the 'hybrid' methods, where one uses a spatial decomposition,
e.g. QM 'inside' and MM (i.e. mainly MD) 'outside' (as in QM-MM),
or
MD 'inside' and continuum mechanics (e,g Navier-Stokes)) 'outside',
or
MD 'inside' and BD 'outside',
the main problems arise in the intermediate region:

How to couple the 'inside' with the 'outside'

This is an active area of current research

summary

– Molecular simulations allow to link molecular properties with macroscopic observables at **finite temperatures**
In most cases this cannot be treated by conventional theory
(i.e. analytical methods)

– Molecular simulations allow the **consistent** determination of many observables from from one model

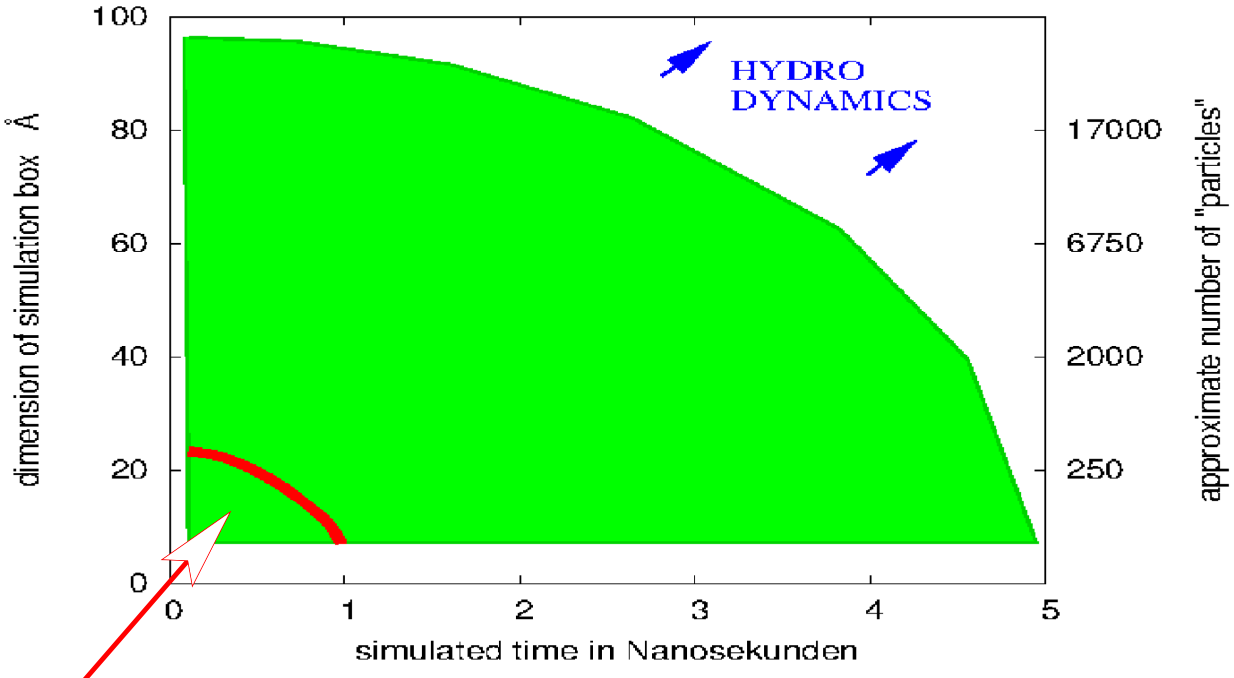
– Molecular simulations are part of a well defined hierarchy of methods, making thus **coarse graining** possible (if not easy!)

– Limitations are the **space** (MC and MD) and **time** (MD) **domains** that can be explored.

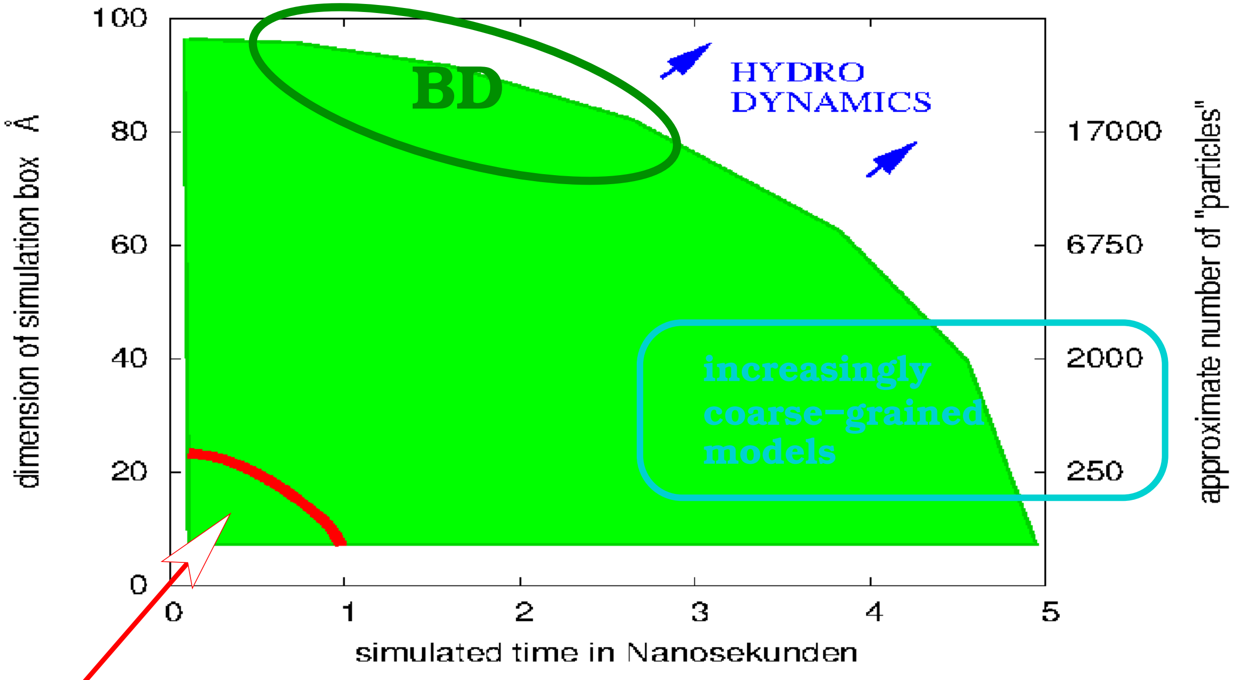
– Computer time (and storage) still is, and always will be, a limitation
$\Longrightarrow$ **pure brute force does not work, smart approaches are required**

Space-time window

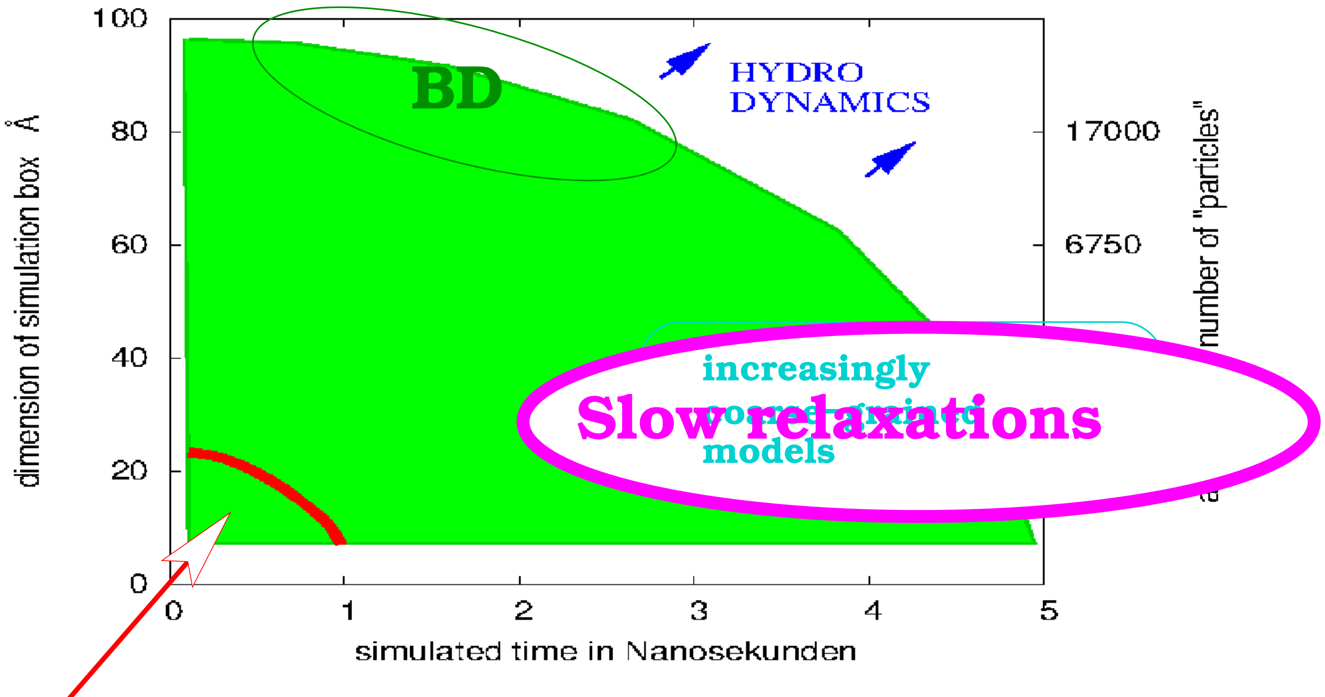
accessible to molecular (MD) simulations



'almost' instantaneaous measurements (X−ray, spectroscopy)
IR, Raman, NMR



'almost' instantaneaous measurements (X-ray, spectroscopy)
IR, Raman, NMR



Slow relaxations

’almost’ instantaneaous measurements (X–ray, spectroscopy)
IR, Raman, NMR

analytical vs. predictive usage

A referee recently stressed in a comment:

".. the importance of carefully validating models before their applications .."

However, this is more easily said than done:
– using simulations as an analytical tool → possible (*and often done*)
– using simulations as a predictive tool → difficult at best
(if you do not want your result just
to reflect your prejudice)

Books

P.W. Atkins, Physical Chemistry, *XY*th Edition, Oxford University Press
for general physical chemistry

D.A. McQuarrie, Statistical Mechanics, Harper & Row
for molecular partition function, equilibria, and everything on liquids

E. B. Wilson, J. C. Decius and P. C., Cross Molecular Vibrations
The Theory of Infrared and Raman Vibrational Spectra, Dover Books
THE classic on normal modes and vibrational spectra

C. Kittel, Introcuction to Solid State Physics, Wiley
The title says it all

R.K. Pathria (and P.D. Beale in later editions)
Statistical Mechanics, Elsevier
http://home.basu.ac.ir/~psu/Books/[Pathria_R.K.,_Beale_P.D.]_Statistical_mechanics.pdf
for the introduction to the 'partition function'

M.P. Allen, D.J. Tildesley,
Computer Simulation of Liquids, Oxford Science
detailed explanations of the fundamentals, with FORTRAN codes
`http://www.ccl.net/cca/software/SOURCES/FORTRAN/allen-tildesley-book/f.00.shtml`

I.R. Levine, Quantum chemistry, Prentise Hall
one of my favorite QC books
`http://www.slideshare.net/diegogarciadossantos/0835quantum-chemistry-5th-edition-by-ira-n-levine`

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