

# Chapter 1

## Introduction

### 1.1 Computational Chemistry and Molecular Modeling

GROMACS is an engine to perform molecular dynamics simulations and energy minimization. These are two of the many techniques that belong to the realm of computational chemistry and molecular modeling. *Computational chemistry* is just a name to indicate the use of computational techniques in chemistry, ranging from quantum mechanics of molecules to dynamics of large complex molecular aggregates. *Molecular modeling* indicates the general process of describing complex chemical systems in terms of a realistic atomic model, with the goal being to understand and predict macroscopic properties based on detailed knowledge on an atomic scale. Often, molecular modeling is used to design new materials, for which the accurate prediction of physical properties of realistic systems is required.

Macroscopic physical properties can be distinguished by (a) *static equilibrium properties*, such as the binding constant of an inhibitor to an enzyme, the average potential energy of a system, or the radial distribution function of a liquid, and (b) *dynamic or non-equilibrium properties*, such as the viscosity of a liquid, diffusion processes in membranes, the dynamics of phase changes, reaction kinetics, or the dynamics of defects in crystals. The choice of technique depends on the question asked and on the feasibility of the method to yield reliable results at the present state of the art. Ideally, the (relativistic) time-dependent Schrödinger equation describes the properties of molecular systems with high accuracy, but anything more complex than the equilibrium state of a few atoms cannot be handled at this *ab initio* level. Thus, approximations are necessary; the higher the complexity of a system and the longer the time span of the processes of interest is, the more severe the required approximations are. At a certain point (reached very much earlier than one would wish), the *ab initio* approach must be augmented or replaced by *empirical* parameterization of the model used. Where simulations based on physical principles of atomic interactions still fail due to the complexity of the system, molecular modeling is based entirely on a similarity analysis of known structural and chemical data. The QSAR methods (Quantitative Structure-Activity Relations) and many homology-based protein structure predictions belong to the latter category.

Macroscopic properties are always ensemble averages over a representative statistical ensemble

(either equilibrium or non-equilibrium) of molecular systems. For molecular modeling, this has two important consequences:

- The knowledge of a single structure, even if it is the structure of the global energy minimum, is not sufficient. It is necessary to generate a representative ensemble at a given temperature, in order to compute macroscopic properties. But this is not enough to compute thermodynamic equilibrium properties that are based on free energies, such as phase equilibria, binding constants, solubilities, relative stability of molecular conformations, etc. The computation of free energies and thermodynamic potentials requires special extensions of molecular simulation techniques.
- While molecular simulations, in principle, provide atomic details of the structures and motions, such details are often not relevant for the macroscopic properties of interest. This opens the way to simplify the description of interactions and average over irrelevant details. The science of statistical mechanics provides the theoretical framework for such simplifications. There is a hierarchy of methods ranging from considering groups of atoms as one unit, describing motion in a reduced number of collective coordinates, averaging over solvent molecules with potentials of mean force combined with stochastic dynamics [7], to *mesoscopic dynamics* describing densities rather than atoms and fluxes as response to thermodynamic gradients rather than velocities or accelerations as response to forces [8].

For the generation of a representative equilibrium ensemble two methods are available: (a) *Monte Carlo simulations* and (b) *Molecular Dynamics simulations*. For the generation of non-equilibrium ensembles and for the analysis of dynamic events, only the second method is appropriate. While Monte Carlo simulations are more simple than MD (they do not require the computation of forces), they do not yield significantly better statistics than MD in a given amount of computer time. Therefore, MD is the more universal technique. If a starting configuration is very far from equilibrium, the forces may be excessively large and the MD simulation may fail. In those cases, a robust *energy minimization* is required. Another reason to perform an energy minimization is the removal of all kinetic energy from the system: if several “snapshots” from dynamic simulations must be compared, energy minimization reduces the thermal noise in the structures and potential energies so that they can be compared better.

## 1.2 Molecular Dynamics Simulations

MD simulations solve Newton’s equations of motion for a system of  $N$  interacting atoms:

$$m_i \frac{\partial^2 \mathbf{r}_i}{\partial t^2} = \mathbf{F}_i, \quad i = 1 \dots N. \quad (1.1)$$

The forces are the negative derivatives of a potential function  $V(\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N)$ :

$$\mathbf{F}_i = -\frac{\partial V}{\partial \mathbf{r}_i} \quad (1.2)$$

The equations are solved simultaneously in small time steps. The system is followed for some time, taking care that the temperature and pressure remain at the required values, and the coordinates are written to an output file at regular intervals. The coordinates as a function of time

type of bond	type of vibration	wavenumber (cm <sup>-1</sup> )
C-H, O-H, N-H	stretch	3000–3500
C=C, C=O	stretch	1700–2000
HOH	bending	1600
C-C	stretch	1400–1600
H <sub>2</sub> CX	sciss, rock	1000–1500
CCC	bending	800–1000
O-H···O	libration	400– 700
O-H···O	stretch	50– 200

Table 1.1: Typical vibrational frequencies (wavenumbers) in molecules and hydrogen-bonded liquids. Compare  $kT/h = 200 \text{ cm}^{-1}$  at 300 K.

represent a *trajectory* of the system. After initial changes, the system will usually reach an *equilibrium state*. By averaging over an equilibrium trajectory, many macroscopic properties can be extracted from the output file.

It is useful at this point to consider the limitations of MD simulations. The user should be aware of those limitations and always perform checks on known experimental properties to assess the accuracy of the simulation. We list the approximations below.

### The simulations are classical

Using Newton's equation of motion automatically implies the use of *classical mechanics* to describe the motion of atoms. This is all right for most atoms at normal temperatures, but there are exceptions. Hydrogen atoms are quite light and the motion of protons is sometimes of essential quantum mechanical character. For example, a proton may *tunnel* through a potential barrier in the course of a transfer over a hydrogen bond. Such processes cannot be properly treated by classical dynamics! Helium liquid at low temperature is another example where classical mechanics breaks down. While helium may not deeply concern us, the high frequency vibrations of covalent bonds should make us worry! The statistical mechanics of a classical harmonic oscillator differs appreciably from that of a real quantum oscillator when the resonance frequency  $\nu$  approximates or exceeds  $k_B T/h$ . Now at room temperature the wavenumber  $\sigma = 1/\lambda = \nu/c$  at which  $h\nu = k_B T$  is approximately  $200 \text{ cm}^{-1}$ . Thus, all frequencies higher than, say,  $100 \text{ cm}^{-1}$  may misbehave in classical simulations. This means that practically all bond and bond-angle vibrations are suspect, and even hydrogen-bonded motions as translational or librational H-bond vibrations are beyond the classical limit (see Table 1.1). What can we do?

Well, apart from real quantum-dynamical simulations, we can do one of two things:

(a) If we perform MD simulations using harmonic oscillators for bonds, we should make corrections to the total internal energy  $U = E_{kin} + E_{pot}$  and specific heat  $C_V$  (and to entropy  $S$  and free energy  $A$  or  $G$  if those are calculated). The corrections to the energy and specific heat of a one-dimensional oscillator with frequency  $\nu$  are: [9]

$$U^{QM} = U^{cl} + kT \left( \frac{1}{2}x - 1 + \frac{x}{e^x - 1} \right) \quad (1.3)$$

$$C_V^{QM} = C_V^{cl} + k \left( \frac{x^2 e^x}{(e^x - 1)^2} - 1 \right), \quad (1.4)$$

where  $x = h\nu/kT$ . The classical oscillator absorbs too much energy ( $kT$ ), while the high-frequency quantum oscillator is in its ground state at the zero-point energy level of  $\frac{1}{2}h\nu$ .

(b) We can treat the bonds (and bond angles) as *constraints* in the equations of motion. The rationale behind this is that a quantum oscillator in its ground state resembles a constrained bond more closely than a classical oscillator. A good practical reason for this choice is that the algorithm can use larger time steps when the highest frequencies are removed. In practice the time step can be made four times as large when bonds are constrained than when they are oscillators [10]. GROMACS has this option for the bonds and bond angles. The flexibility of the latter is rather essential to allow for the realistic motion and coverage of configurational space [11].

### Electrons are in the ground state

In MD we use a *conservative* force field that is a function of the positions of atoms only. This means that the electronic motions are not considered: the electrons are supposed to adjust their dynamics instantly when the atomic positions change (the *Born-Oppenheimer* approximation), and remain in their ground state. This is really all right, almost always. But of course, electron transfer processes and electronically excited states can not be treated. Neither can chemical reactions be treated properly, but there are other reasons to shy away from reactions for the time being.

### Force fields are approximate

Force fields provide the forces. They are not really a part of the simulation method and their parameters can be modified by the user as the need arises or knowledge improves. But the form of the forces that can be used in a particular program is subject to limitations. The force field that is incorporated in GROMACS is described in Chapter 4. In the present version the force field is pair-additive (apart from long-range Coulomb forces), it cannot incorporate polarizabilities, and it does not contain fine-tuning of bonded interactions. This urges the inclusion of some limitations in this list below. For the rest it is quite useful and fairly reliable for biologically-relevant macromolecules in aqueous solution!

### The force field is pair-additive

This means that all *non-bonded* forces result from the sum of non-bonded pair interactions. Non pair-additive interactions, the most important example of which is interaction through atomic polarizability, are represented by *effective pair potentials*. Only average non pair-additive contributions are incorporated. This also means that the pair interactions are not pure, *i.e.*, they are not valid for isolated pairs or for situations that differ appreciably from the test systems on which the models were parameterized. In fact, the effective pair potentials are not that bad in practice. But the omission of polarizability also means that electrons in atoms do not provide a dielectric constant as they should. For example, real liquid alkanes have a dielectric constant of slightly more than 2, which reduce the long-range electrostatic interaction between (partial) charges. Thus, the simulations will exaggerate the long-range Coulomb terms. Luckily, the next item compensates this effect a bit.

### Long-range interactions are cut off

In this version, GROMACS always uses a cut-off radius for the Lennard-Jones interactions

and sometimes for the Coulomb interactions as well. The “minimum-image convention” used by GROMACS requires that only one image of each particle in the periodic boundary conditions is considered for a pair interaction, so the cut-off radius cannot exceed half the box size. That is still pretty big for large systems, and trouble is only expected for systems containing charged particles. But then truly bad things can happen, like accumulation of charges at the cut-off boundary or very wrong energies! For such systems, you should consider using one of the implemented long-range electrostatic algorithms, such as particle-mesh Ewald [12, 13].

#### Boundary conditions are unnatural

Since system size is small (even 10,000 particles is small), a cluster of particles will have a lot of unwanted boundary with its environment (vacuum). We must avoid this condition if we wish to simulate a bulk system. As such, we use periodic boundary conditions to avoid real phase boundaries. Since liquids are not crystals, something unnatural remains. This item is mentioned last because it is the least of the evils. For large systems, the errors are small, but for small systems with a lot of internal spatial correlation, the periodic boundaries may enhance internal correlation. In that case, beware of, and test, the influence of system size. This is especially important when using lattice sums for long-range electrostatics, since these are known to sometimes introduce extra ordering.

## 1.3 Energy Minimization and Search Methods

As mentioned in sec. 1.1, in many cases energy minimization is required. GROMACS provides a number of methods for local energy minimization, as detailed in sec. 3.10.

The potential energy function of a (macro)molecular system is a very complex landscape (or *hypersurface*) in a large number of dimensions. It has one deepest point, the *global minimum* and a very large number of *local minima*, where all derivatives of the potential energy function with respect to the coordinates are zero and all second derivatives are non-negative. The matrix of second derivatives, which is called the *Hessian matrix*, has non-negative eigenvalues; only the collective coordinates that correspond to translation and rotation (for an isolated molecule) have zero eigenvalues. In between the local minima there are *saddle points*, where the Hessian matrix has only one negative eigenvalue. These points are the mountain passes through which the system can migrate from one local minimum to another.

Knowledge of all local minima, including the global one, and of all saddle points would enable us to describe the relevant structures and conformations and their free energies, as well as the dynamics of structural transitions. Unfortunately, the dimensionality of the configurational space and the number of local minima is so high that it is impossible to sample the space at a sufficient number of points to obtain a complete survey. In particular, no minimization method exists that guarantees the determination of the global minimum in any practical amount of time. Impractical methods exist, some much faster than others [14]. However, given a starting configuration, it is possible to find the *nearest local minimum*. “Nearest” in this context does not always imply “nearest” in a geometrical sense (*i.e.*, the least sum of square coordinate differences), but means the minimum that can be reached by systematically moving down the steepest local gradient. Finding this nearest local minimum is all that GROMACS can do for you, sorry! If you want to find other

minima and hope to discover the global minimum in the process, the best advice is to experiment with temperature-coupled MD: run your system at a high temperature for a while and then quench it slowly down to the required temperature; do this repeatedly! If something as a melting or glass transition temperature exists, it is wise to stay for some time slightly below that temperature and cool down slowly according to some clever scheme, a process called *simulated annealing*. Since no physical truth is required, you can use your imagination to speed up this process. One trick that often works is to make hydrogen atoms heavier (mass 10 or so): although that will slow down the otherwise very rapid motions of hydrogen atoms, it will hardly influence the slower motions in the system, while enabling you to increase the time step by a factor of 3 or 4. You can also modify the potential energy function during the search procedure, *e.g.* by removing barriers (remove dihedral angle functions or replace repulsive potentials by *soft-core* potentials [15]), but always take care to restore the correct functions slowly. The best search method that allows rather drastic structural changes is to allow excursions into four-dimensional space [16], but this requires some extra programming beyond the standard capabilities of GROMACS.

Three possible energy minimization methods are:

- Those that require only function evaluations. Examples are the simplex method and its variants. A step is made on the basis of the results of previous evaluations. If derivative information is available, such methods are inferior to those that use this information.
- Those that use derivative information. Since the partial derivatives of the potential energy with respect to all coordinates are known in MD programs (these are equal to minus the forces) this class of methods is very suitable as modification of MD programs.
- Those that use second derivative information as well. These methods are superior in their convergence properties near the minimum: a quadratic potential function is minimized in one step! The problem is that for  $N$  particles a  $3N \times 3N$  matrix must be computed, stored, and inverted. Apart from the extra programming to obtain second derivatives, for most systems of interest this is beyond the available capacity. There are intermediate methods that build up the Hessian matrix on the fly, but they also suffer from excessive storage requirements. So GROMACS will shy away from this class of methods.

The *steepest descent* method, available in GROMACS, is of the second class. It simply takes a step in the direction of the negative gradient (hence in the direction of the force), without any consideration of the history built up in previous steps. The step size is adjusted such that the search is fast, but the motion is always downhill. This is a simple and sturdy, but somewhat stupid, method: its convergence can be quite slow, especially in the vicinity of the local minimum! The faster-converging *conjugate gradient method* (see *e.g.* [17]) uses gradient information from previous steps. In general, steepest descents will bring you close to the nearest local minimum very quickly, while conjugate gradients brings you *very* close to the local minimum, but performs worse far away from the minimum. GROMACS also supports the L-BFGS minimizer, which is mostly comparable to *conjugate gradient method*, but in some cases converges faster.