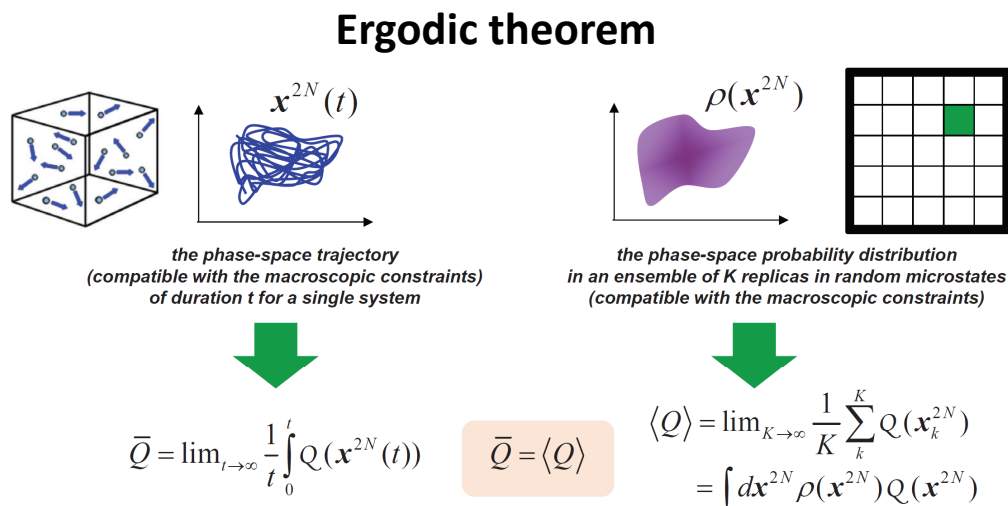


# SAMPLE SOLUTION

# 1 Concepts and Understanding (F2022.1)

Note that the answers given below are more detailed (for didactical purposes!) than what was actually expected from the students during the examination.

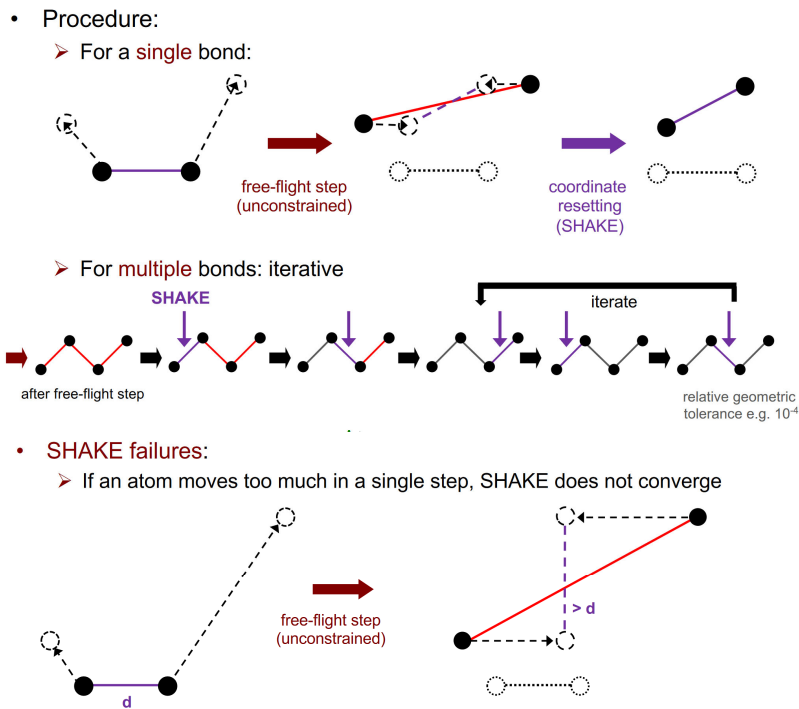
- a. The ergodic theorem states the equivalence between the ensemble averages of statistical mechanics and the time (trajectory) averages of molecular dynamics. See the following summary (in the context of classical mechanics).



The theorem holds for  $K \rightarrow \infty$  (which is OK, because the statistical mechanical ensembles are only mathematical constructs) and  $t \rightarrow \infty$  (which is more problematic, since molecular dynamics simulations are always of finite durations). In practice, the theorem will be satisfied for finite simulations provided that all thermodynamically relevant states have been visited during the simulation time, and that each of them has been visited many times.

- b. The three main reasons why the use of constrained bonds is to be preferred over that of flexible bonds are that: (i) bond vibrations are typically uninteresting in condensed-phase (bio)molecular systems, where the relevant motions are related to conformation and solvation, and occur on comparatively slow timescales (with little coupling to the very fast bond oscillations); (ii) in contrast to a classical harmonic oscillation, a constraint is associated with no kinetic energy, heat capacity and entropy, which is a better representation of the quantum-mechanical state for vibrations that are not excited (*i.e.* in the quantum-mechanical ground state) at room temperature (as typical for high-frequency bond vibrations, unless they involve heavy atoms and weak bonds); (iii) the constraining of bonds removes the fastest-frequency motions in the system, which allows for an increase in the molecular dynamics timestep from 0.5 fs to 2 fs. The two simplifications that are made in SHAKE for solving the system of equations involved in constraining all the bonds in a molecule are that: (i) the constraints are uncoupled, *i.e.* they can be reset independently from each other; (ii) it is sufficient to consider the linear term when solving for the Lagrange multipliers, *i.e.* the quadratic term can be neglected. These approximations allow to solve the problem analytically and considering the bonds independently. The price to pay is that the procedure must be iterated to reach the exact solution. The answer to the other questions refers to the illustrations below.

# SHAKE algorithm



The top drawing shows, considering a diatomic molecule (two atoms, one bond), how the SHAKE coordinate resetting operates. The free-flight step is corrected into a constrained step by adding small displacements of the atoms along the bond vector as it was before the step. The displacement is inversely proportional to the mass of each atom (so that the center of mass is not affected by the resetting), with a magnitude calibrated so that the constraint is satisfied after the resetting. The middle drawing explains why the SHAKE procedure is an iterative (rather than one-step) procedure. This comes from the approximations made in SHAKE (neglect of coupling, linearization). Because of coupling between bonds, the resetting of a bond alters the bond distances of all the bonds sharing an atom with this bond, so that bonds that were previously reset may again slightly violate the constraint. Thus, one has to reset all the bonds in sequence, and reiterate the sequence multiple time, until all the constraints are satisfied within a given tolerance. Note that the linearization implies that even for a single bond in a diatomic molecule, SHAKE must be iterated to achieve a high-precision constraining. The bottom drawing explains under which circumstances the algorithm may fail to converge. If the atoms move too much in a single free-flight step (which is generally a sign of something unhealthy going on in the simulation, *e.g.* too large timestep, atom overlap, inconsistent forces), even the largest possible displacement along the bond vector in the previous step cannot result in the satisfaction of the constraint.

c. The statement is ill-formulated. The two bit sequences are the analog of microstates in statistical mechanics, and one cannot ascribe an entropy to a microstate. Instead, one assumes that all microstates are equiprobable, and infers the statistical weight of specified macrostates by the number of microstates they encompass. The Boltzmann entropy is then a logarithmic measure of this weight. For example, if you defined a macrostate A by “all the bits are perfectly separated” and a macrostate B by “t-perfectly-separated bit sequence”, then A would have a much lower statistical weight (realizable by only one microstate), and thus a lower entropy. But you could as well define a macrostate B by “the bits match the incredibly beautiful sequence (0,0,1,1,0,1,1,0,0,1,0,1)” and a macrostate A by “any not-as-beautiful bit sequence”. Now, B would have the lowest statistical weight (realizable by only one microstate), and thus a lower entropy. This is a very common confusion. As a more practical example, comparing two

desks, you cannot objectively ascribe a high entropy to the messy one and a low entropy to the tidy one. What you look at are just two equiprobable desk configurations (and maybe the apparently messy desk results from a very unique form of organization that you are not smart enough to grasp). To ascribe entropies, you have to subjectively define macrostate concepts for “messy” and “tidy” (*e.g.* only nice stacks of papers *vs.* at least one ugly-looking pile of papers). And then you will notice that many more of the equiprobable desk configurations generated at random (*e.g.* by throwing sheets of paper onto a desk) fall in the “messy” as opposed to the “tidy” macrostate. And now you can ascribe entropies to the macrostates “tidy” and “messy”. Summary: entropy only arises when you classify equiprobable microstates into coarser classes called macrostates. And this classification is very much “in the eyes of the beholder”.

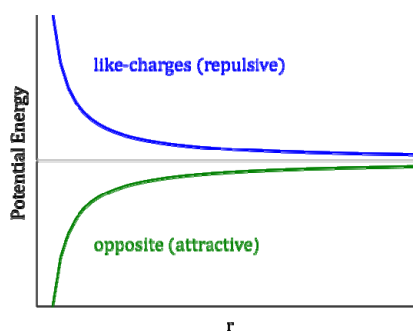
## 2 Fundamental Equations (F2022.2)

Note that the answers given below are more detailed (for didactical purposes!) than what was actually expected from the students during the examination. Watch out not to overlook the requirements “**explain the meaning** of all the involved symbols” and “**state the SI units** of these quantities”.

- a. The equation for the Coulomb interaction between two atoms with partial charges  $q_1$  and  $q_2$  at a distance  $r_{12}$  reads

$$V(r_{12}) = \frac{1}{4\pi\epsilon_0} \frac{q_1 q_2}{r_{12}},$$

where  $V$  is the potential energy (SI unit: J or  $\text{kg}\cdot\text{m}^2\cdot\text{s}^{-2}$ ),  $r_{12}$  the distance (SI unit: m),  $q_1$  and  $q_2$  the charges (SI unit: C or A·s), and  $\epsilon_0$  the permittivity of vacuum (SI unit:  $\text{C}^2\cdot\text{m}^{-1}\cdot\text{J}^{-1}$  or  $\text{A}^2\cdot\text{s}^4\cdot\text{kg}^{-1}\cdot\text{m}^{-3}$ , a basic physical constant). A sketch of the function is shown below, distinguishing the situations  $q_1 \cdot q_2 > 0$  (like-charges, repulsive) and  $q_1 \cdot q_2 < 0$  (opposite-charges, attractive). Formally speaking, there would be a third (trivial) case with  $q_1 \cdot q_2 = 0$  (no interaction).



- b. An expression for the instantaneous observable  $\mathcal{P}$  can be derived from the virial theorem, and reads

$$\mathcal{P}(\mathbf{r}, \mathbf{p}, \mathcal{V}) = \frac{2[\mathcal{K}(\mathbf{p}) - \mathcal{W}(\mathbf{r})]}{3\mathcal{V}},$$

where  $\mathcal{K}$  is the kinetic energy (SI unit: J or  $\text{kg}\cdot\text{m}^2\cdot\text{s}^{-2}$ )

$$\mathcal{K}(\mathbf{p}) = \frac{1}{2} \sum_i^N \frac{\mathbf{p}_i^2}{m_i},$$

$\mathcal{W}$  is the virial (SI unit: J or  $\text{kg}\cdot\text{m}^2\cdot\text{s}^{-2}$ )

$$\mathcal{W}(\mathbf{r}) = -\frac{1}{2} \sum_i^N \mathbf{r}_i \dot{\mathbf{F}}_i,$$

and  $\mathcal{V}$  is the volume (SI unit:  $\text{m}^3$ ). The SI units of  $\mathcal{P}$  are thus the Pa, or  $\text{J}\cdot\text{m}^{-3}$ , often reexpressed as bar, with  $1 \text{ bar} = 10^5 \text{ Pa}$ . In the context of an ideal monoatomic gas, there is no interaction (*i.e.* forces) between the atoms (this is precisely the idealization), so that the virial is zero. In this case, one has  $\mathcal{P}\mathcal{V} = (2/3)\mathcal{K}$ . Due to equipartition  $\mathcal{K} = (3/2)nN_A k_B T = (3/2)nRT$ , where  $n$  is the number of mols,  $T$  the absolute temperature,  $N_A$  the Avogadro constant,  $k_B$  the Boltzmann constant and  $R$  the gas constant. Thus, one finds back the ideal-gas law,  $\mathcal{P}\mathcal{V} = nRT$ . In a real gas, there are interactions. Attractive interactions provide a positive contribution to the virial and thus, tend to decrease the pressure relative to the ideal gas. Conversely, repulsive interactions provide a negative contribution to the virial and

thus, tend to increase the pressure relative to the ideal gas. The instantaneous variable  $\mathcal{P}$  is connected to its canonical ensemble average  $P$  via

$$P = \langle \mathcal{P} \rangle = \frac{\int d\mathbf{r} d\mathbf{p} \mathcal{P}(\mathbf{r}, \mathbf{p}, V) e^{-\beta \mathcal{H}(\mathbf{r}, \mathbf{p}, V)}}{\int d\mathbf{r} d\mathbf{p} e^{-\beta \mathcal{H}(\mathbf{r}, \mathbf{p}, V)}}$$

where  $\langle \dots \rangle$  indicates a canonical ensemble average,  $V$  is the volume (fixed value in the canonical ensemble), and  $\mathcal{H}$  is the Hamiltonian.

### 3 Derivations (F2022.3)

- a. Omitting the zero-point energy (irrelevant here), the equation connecting the Helmholtz free energy  $F$  to the canonical partition function  $Z$  reads

$$F(\lambda) = -\beta^{-1} \ln Z(\lambda) ,$$

where  $\beta \doteq (k_B T)^{-1}$ ,  $k_B$  being the Boltzmann constant and  $T$  the absolute temperature. The equation for the classical partition function  $Z$  (as determined by the Hamiltonian  $\mathcal{H}$ ) reads

$$Z(\lambda) = C \int d\mathbf{r} d\mathbf{p} e^{-\beta\mathcal{H}\lambda}$$

with  $C = (h^{3N} N!)^{-1}$  for indistinguishable particles. Using the previous expressions to formulate  $dF/d\lambda$ , one has

$$\frac{dF(\lambda)}{d\lambda} = -\beta^{-1} Z^{-1} \frac{dZ(\lambda)}{d\lambda} = -\beta^{-1} Z^{-1} C \int d\mathbf{r} d\mathbf{p} \frac{d}{d\lambda} e^{-\beta\mathcal{H}\lambda} = Z^{-1} C \int d\mathbf{r} d\mathbf{p} \frac{\partial \mathcal{H}}{\partial \lambda} e^{-\beta\mathcal{H}\lambda}$$

The expression for a canonical ensemble average  $\langle \dots \rangle$  is

$$\langle A \rangle = Z^{-1} C \int d\mathbf{r} d\mathbf{p} A e^{-\beta\mathcal{H}\lambda} .$$

So we get

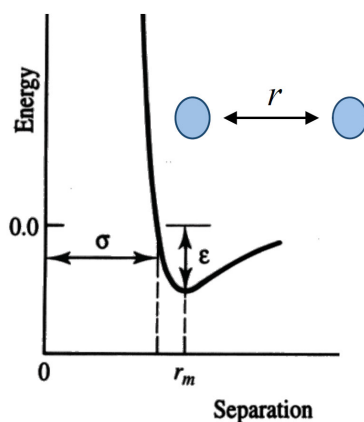
$$\frac{dF(\lambda)}{d\lambda} = \left\langle \frac{\partial \mathcal{H}}{\partial \lambda} \right\rangle ,$$

which is the TI expression.

- b. The number of permutations of an ensemble of  $N$  objects is  $N!$ . In the limit of large  $N$ , we can use the Stirling formula to approximate  $\ln N!$  as  $N \ln N - N$ . In terms of  $N!$ , the approximation becomes  $e^{N \ln N - N} = N^N e^{-N} = (N/e)^N$ .

## 4 Explicit Calculations (F2022.4)

- a. A sketch of the Lennard-Jones function is shown below. The zero-distance and zero-energy points are indicated, as well as the locations where you can measure  $\sigma$ ,  $r_m$ , and  $\epsilon$ .



For the following tasks, it is useful to calculate the corresponding Lennard-Jones force  $F_{LJ}$ , *i.e.* the negative derivative of  $V_{LJ}$  with respect to  $r$

$$F_{LJ}(r) = 4\epsilon \left[ 12 \left( \frac{\sigma}{r} \right)^{12} - 6 \left( \frac{\sigma}{r} \right)^6 \right] \frac{1}{r} .$$

The sign of  $F_{LJ}$  matches the desired convention, namely it is negative if the force is attractive and positive otherwise. This is easily checked by noting that  $F_{LJ}$  is positive when  $r \rightarrow 0$  (the  $r^{-12}$  term dominates) and negative when  $r \rightarrow \infty$  (the  $r^{-6}$  term dominates). To calculate  $r_m$ , we note that the force should be zero at this point. This leads to the condition

$$12 \left( \frac{\sigma}{r_m} \right)^{12} - 6 \left( \frac{\sigma}{r_m} \right)^6 = 0 ,$$

which is satisfied when  $r_m = 2^{1/6}\sigma$ . Using the approximation  $2^{1/n} \approx 1 + (1/n)\ln 2$  with  $\ln 2 \approx 0.69$ , one has  $2^{1/6} \approx 1.115$ , so that  $r_m = 1.115 \cdot 0.3 \text{ nm}$  which is  $0.3345 \text{ nm}$ . Considering the point  $r = \sigma$ , the Lennard-Jones potential energy is zero. The corresponding force is

$$F_{LJ}(\sigma) = 4\epsilon [12 - 6] \frac{1}{\sigma} .$$

This gives  $4 \cdot 1 \text{ kJ} \cdot \text{mol}^{-1} \cdot 6 \cdot 1/0.3 \text{ nm}^{-1}$ , that is  $80 \text{ kJ} \cdot \text{mol}^{-1} \cdot \text{nm}^{-1}$ . As expected, the value is positive, as we are in the repulsive range. Considering the point  $r = r_m$ , the Lennard-Jones force is zero, and the corresponding potential energy is  $-\epsilon$ , that is  $-1 \text{ kJ} \cdot \text{mol}^{-1}$ .



## 5 Algorithms and Implementation (F2022.5)

a. A possible code for the function `VelAutoCorrel` is given below

```
void VelAutoCorrel ( int N, int kmax, double v[][3*N], double c[] ) {
    int k, kk, i;
    double sum;
    for ( k = 0; k < kmax; k++ ) { // loop over lag times k*dt
        sum = 0;
        for ( kk = 0; kk < kmax - k; kk++ ) { // loop over time origins kk*dt
            for ( n = 0; n < 3*N; n++ ) { // loop over particles and components
                sum += v[k][n] * v[k+kk][n];
            }
        }
        c[k] = sum/(N*(kmax-k));
    }
}
```

Because the number of time origins available to calculate  $c(k\Delta t)$  for a given  $k$  is  $k_{max} - k$ , when  $\tau$  approaches  $t_{sim}$ , the statistics become poor and the curve becomes increasingly “noisy”. According to the Green-Kubo equation, the integral of  $c(\tau)$  is connected to the diffusion constant  $D$  of the system as

$$D = \frac{1}{3} \lim_{\tau \rightarrow \infty} \int_0^\tau d\tau' c(\tau') .$$

The Einstein equation is an alternative to the Green-Kubo equation for calculating  $D$ . It is based on the mean-square-displacement  $s(\tau)$  of the atoms, and reads

$$D = \frac{1}{6} \lim_{\tau \rightarrow \infty} \tau^{-1} s(\tau) .$$