

Monte Carlo Simulation of the Lennard Jones Fluid in the Canonical Ensemble

The Molecular Sciences Software Institute

Eliseo Marin-Rimoldi and John D. Chodera

I. INTRODUCTION

A. Monte Carlo Integration

In statistical mechanics, we are interested in computing averages of thermodynamic properties as a function of atom positions and momenta¹⁻³. A thermodynamic average depending only on configurational properties can be computed using the following expectation value integral

$$\langle Q \rangle = \int_V Q(\mathbf{r}^N) \rho(\mathbf{r}^N) d\mathbf{r}^N \quad (1)$$

\mathbf{r}^N is a $3N$ dimensional vector containing the positions of the N atoms, where $Q(\mathbf{r}^N)$ is the thermodynamic quantity of interest that depends only on the configuration \mathbf{r}^N , $\rho(\mathbf{r}^N)$ is the probability density whose functional form depends on the statistical mechanical ensemble of interest, and V defines the volume of configuration space over which ρ has support. Note that the integrals over momenta have been factored out, as they can be evaluated analytically. The integral (Eq. 1) is very hard to compute even for small atomic systems. For instance, a monoatomic system of 10 atoms leads to a 30-dimensional integral. Consequently, we need to resort to a numerical integration scheme if we want to study atomic systems.

Monte Carlo methods are numerical techniques frequently used to estimate complex multidimensional integrals which otherwise could not be performed^{4,5}. For instance, the integral of the function $f(\mathbf{x})$, where $\mathbf{x} \in \mathbb{R}^M$, is approximated as

$$I = \int_V f(\mathbf{x}) d\mathbf{x} = \int_V \frac{f(\mathbf{x})}{h(\mathbf{x})} h(\mathbf{x}) d\mathbf{x} = \left\langle \frac{f(\mathbf{x})}{h(\mathbf{x})} \right\rangle_{h(\mathbf{x})} \quad (2)$$

The idea of Monte Carlo integration is to estimate the expectation value $\left\langle \frac{f(\mathbf{x})}{h(\mathbf{x})} \right\rangle_{h(\mathbf{x})}$ by generating random samples of \mathbf{x} from the probability density $h(\mathbf{x})$.

B. Importance Sampling

In Equation 2, we are free to choose the probability distribution $h(\mathbf{x})$. The simplest case is to uniformly generate \mathbf{x} in the volume V . In this way, $h(\mathbf{x})$ becomes constant as

$$h(\mathbf{x}) = \frac{1}{V} \quad (3)$$

Using this sampling density $h(\mathbf{x})$, the integral (Eq. 2) becomes

$$I = \int_V f(\mathbf{x}) d\mathbf{x} \approx \frac{V}{N} \sum_{i=1}^N f(\mathbf{x}_i) \quad (4)$$

where N is the total number of random samples and $f(\mathbf{x}_i)$ is the integrand evaluated using the i^{th} sample. While using a uniform sampling density often works sufficiently well for simple unidimensional cases, it generally fails to produce useful estimates for complex problems.

The problem at hand involves the evaluation of $3N$ -dimensional integral Eq. 1, which is dominated by a small region of configuration space¹⁻³. Using a uniform probability distribution $h(\mathbf{r}^N)$ over the configuration space hypervolume V^{3N} to generate representative samples of this subset is not efficient, as most states generated this way would have a low weight.

A solution to this problem is to sample positions \mathbf{r}^N from the desired equilibrium probability density $\rho(\mathbf{r}^N)$:

$$\mathbf{r}^N \sim \rho(\mathbf{r}^N) \quad (5)$$

This is a way to generate relevant configurations more frequently than configurations that have low probability. Mathematically, we set $h(\mathbf{r}^N) = \rho(\mathbf{r}^N)$. This idea is known as *importance sampling*.

Combining Eqs. 1 and 2 and the condition $h(\mathbf{r}^N) = \rho(\mathbf{r}^N)$, we find that

$$\langle Q \rangle \approx \frac{1}{N} \sum_{i=1}^N Q(\mathbf{r}_i^N). \quad (6)$$

Thus, we can get thermodynamic properties by simply computing an unweighted sample average, given that we perform importance sampling from $h(\mathbf{r}^N) = \rho(\mathbf{r}^N)$.

C. Detailed Balance Condition

The question now becomes how to generate such atomic positions \mathbf{r}^N (or *states*) distributed according to $\rho(\mathbf{r}^N)$. In 1953, Metropolis, Rosenbluth, Rosenbluth, and Teller introduced a solution based on Markov chains⁶. They proposed to use the detailed balance condition in order to ensure

proper configurational sampling from the statistical mechanical distribution of interest. In order to generate a new configuration n from an old configuration m , the detailed balance condition is

$$\rho_m(\mathbf{r}^N) \alpha(m \rightarrow n) P_{acc}(m \rightarrow n) = \rho_n(\mathbf{r}^N) \alpha(n \rightarrow m) P_{acc}(n \rightarrow m) \quad (7)$$

Where $\rho_m(\mathbf{r}^N)$ is the probability of observing state m , $\alpha(m \rightarrow n)$ is the probability of attempting to generate a new state n starting from a state m and $P_{acc}(n \rightarrow m)$ is the probability of accepting such transition. Basically, the condition of detailed balance tells us that the “flux” of transitions from state m to state n equals the flux from state n to state m at equilibrium.

There are many ways to satisfy Eq. 7 by construction of different acceptance probabilities. While Metropolis et. al proposed a choice that both satisfies Eq. 7 and maximizes the average acceptance probability $\langle P_{acc} \rangle$ ⁶, Hastings generalized this to the case where proposal probabilities are not symmetric, such that $\alpha(m \rightarrow n) \neq \alpha(n \rightarrow m)$, producing the *Metropolis-Hastings*⁷ acceptance criteria:

$$P_{acc}(m \rightarrow n) = \min \left[1, \frac{\alpha(n \rightarrow m) \rho_n(\mathbf{r}^N)}{\alpha(m \rightarrow n) \rho_m(\mathbf{r}^N)} \right]. \quad (8)$$

This algorithm is one of a general class of *Markov chain Monte Carlo (MCMC)* algorithms that generate Markov chains to sample a desired target density, and a great deal of the MCMC literature is valuable for molecular simulations⁴.

II. CANONICAL ENSEMBLE MONTE CARLO OF A LENNARD JONES FLUID

Assume we have N monoatomic particles that interact using the Lennard-Jones (LJ) pairwise potential:

$$U(r) = 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right] \quad (9)$$

where r is the interparticle distance, σ is the distance where the interaction energy is zero, and ϵ is the well depth. For simulating argon, for example, a common choice is $\sigma = 3.4 \text{ \AA}$ and $\epsilon/k_B = 120 \text{ K}$.

Our goal is to generate a set of states of N LJ particles distributed according to the canonical (NVT) ensemble

$$\rho_n(\mathbf{r}^N; \beta) = Z(\beta)^{-1} e^{-\beta U(\mathbf{r}^N)} \quad (10)$$

$$Z(\beta) \equiv \int_V e^{-\beta U(\mathbf{r}^N)} d\mathbf{r}^N \quad (11)$$

where $U(\mathbf{r}^N)$ is the potential energy of the system, $\beta = (k_B T)^{-1}$ is the inverse temperature, k_B is the Boltzmann constant, and T is the absolute temperature.

Note that $U(\mathbf{r}^N)$ is given by

$$U(\mathbf{r}^N) = \sum_{i < j} U(r_{ij}) \quad (12)$$

where $r_{ij} \equiv \|\mathbf{r}_j^N - \mathbf{r}_i^N\|_2$ is the interparticle separation distance.

Substituting Eq. 10 into Eq. 8 and assuming $\alpha(n \rightarrow m) = \alpha(m \rightarrow n)$, we obtain

$$P_{acc}(m \rightarrow n) = \min[1, e^{-\beta\Delta U}] \quad (13)$$

where $\Delta U \equiv U(\mathbf{r}_m^N) - U(\mathbf{r}_n^N)$ is the difference in potential energy of the system between the new state n and the old state m . Note that the argument of the energy \mathbf{r}^N has been dropped for clarity.

A. Flow of Calculations in a Metropolis Monte Carlo simulation

The following workflow can be used to implement the Metropolis algorithm to sample the canonical ensemble of configurations of LJ particles^{8,9}:

1. Generate an initial system state m .
2. Choose an atom with uniform probability from $\{1, \dots, N\}$ from old state m .
3. Propose a new state n by translating a LJ particle by a uniform random displacement $\Delta r \sim U(-\Delta x, +\Delta x)$ in each dimension. The displacement scale Δx should not be too large as this would likely result in particle overlaps, but should not be too small as this would result in a slow sampling of configurational space. More on this below.
4. The difference in energy between the new and old states is computed. Note that you do not need to compute the *total* system energy difference, as all particles but one remain at the same position. It is enough to get difference in energy of the selected molecule in the new and old states.
5. The new state is accepted or rejected using the Metropolis criterion. Practically, this can be implemented as follows. If a move from m to n is “downhill”, $\beta\Delta U \leq 0$, the move is always accepted. For “uphill” moves, a random number ζ is generated uniformly on $(0,1)$. If $\zeta < \exp[-\beta\Delta U]$, the move is accepted. Otherwise, the move is rejected. If a non-symmetric proposal is used, this acceptance scheme will have to be modified to implement Eq. 8.

B. Technical considerations

Initial configuration. To start the simulation, we have to generate an initial configuration. We will provide two options: start using a random configuration or start using a previously

equilibrated state. During the Metropolis Monte Carlo simulation, particle translations will help to create configurations consistent with the temperatures and box volumes that we set and will remove any overlap that might exist in the initial random configuration. In the second option, we will use a pre-equilibrated NIST configuration that will help us benchmark the energy calculations of our code.

Random number generation. Computers cannot generate truly random numbers. Instead, they rely on *pseudorandom number generators* (PRNGs) that aim to produce random numbers with the desired statistical properties and long recurrence times between repeats of the same random number sequence. Using a low-quality random number generator can lead to simulation artifacts that can lead to incorrect physical behavior^{10,11}. We recommend you avoid writing your own PRNGs, as this can lead to inadvertent implementation of an ill-conceived algorithm¹². Instead, rely on high-quality, well-understood PRNGs and implementations that have are well-supported, such as the Mersenne Twister^{13,14} implementation provided by `numpy.random`.

Equilibration. When the initial configuration is highly atypical compared to true samples from the equilibrium density—such as the initial 3D lattice conditions compared to a true disordered liquid state—it may require very long simulation times for the bias in equilibrium averages computed over the entire trajectory to become small compared to the statistical error¹⁵. It is therefore common practice to discard some initial part of the simulation to *equilibration* and to average over the subsequent *production* region to minimize this bias at the cost of potentially increasing statistical error by including less data in the average. While common practice traditionally had selected an arbitrary initial portion of the simulation to equilibrium, modern best practice recommends the use of an automated approach for selecting the optimal equilibration/production split point in a manner that maximizes the number of statistically uncorrelated samples in the production part of the trajectory¹⁵. To do this, you can use the `pymbar.timeseries.detectEquilibration` function from the `pymbar` module to analyze an array containing timeseries data for your observable (such as energies, box volumes, or densities)¹⁵.

System size and periodic boundary conditions. A typical simulation of a Lennard-Jones fluid is carried out anywhere from 216 to 10,000 particles. This amount of particles is far away of being representative of a bulk liquid. To get around this problem, we employ a trick called periodic boundary conditions. The primary simulation box is surrounded by copy images of itself. For a cubic simulation, there would be 26 images around the central box. This trick has two implications

1. If the position of a particle (i.e. Cartesian coordinates) is outside the simulation box after a particle translation, an identical particle should enter the box through the opposite face of

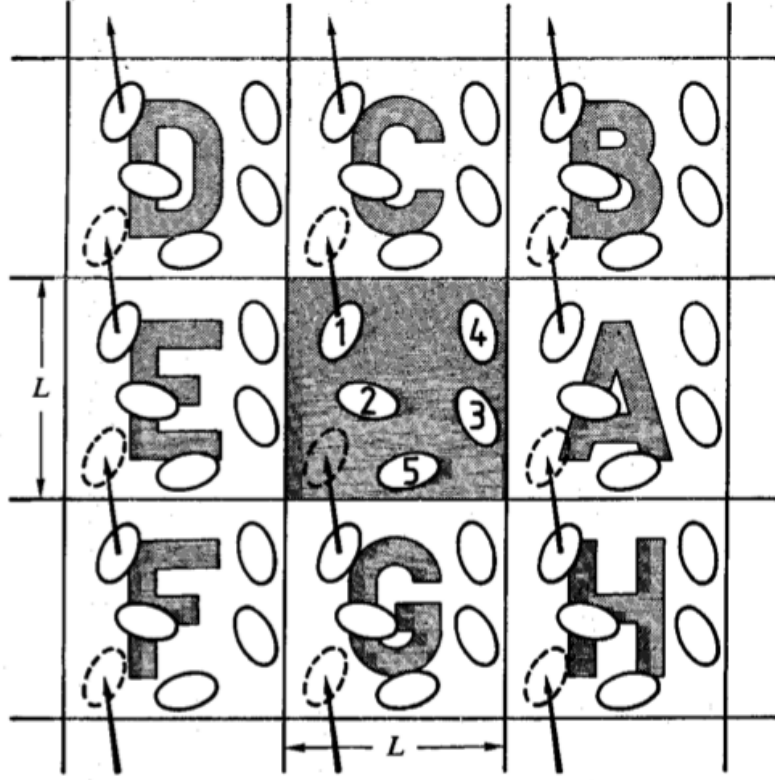


FIG. 1. Molecule one is displaced outside the bounds of the central box and placed back in through the opposite side of the box. Image from Allen and Tildesley. ¹⁶

the box, as shown in Figure 1

2. When computing distances r_{ij} used in the evaluation of the LJ potential (Eq. 12), we use the *minimum image distance*. See Figure 2.

Maximum displacement Δx . As noted above, the Metropolis Monte Carlo algorithm requires translating a selected LJ particle by a random perturbation. This displacement should not be too large as this would result in particle overlaps and low acceptance rates; on the other hand, it should not be so small as to result in inefficient sampling of configuration space. A common practice is to adjust the maximum particle displacement Δx during an explicit equilibration phase in order to achieve $\sim 50\%$ acceptance translation rates over a recent window of $\sim N$ Monte Carlo trial moves.

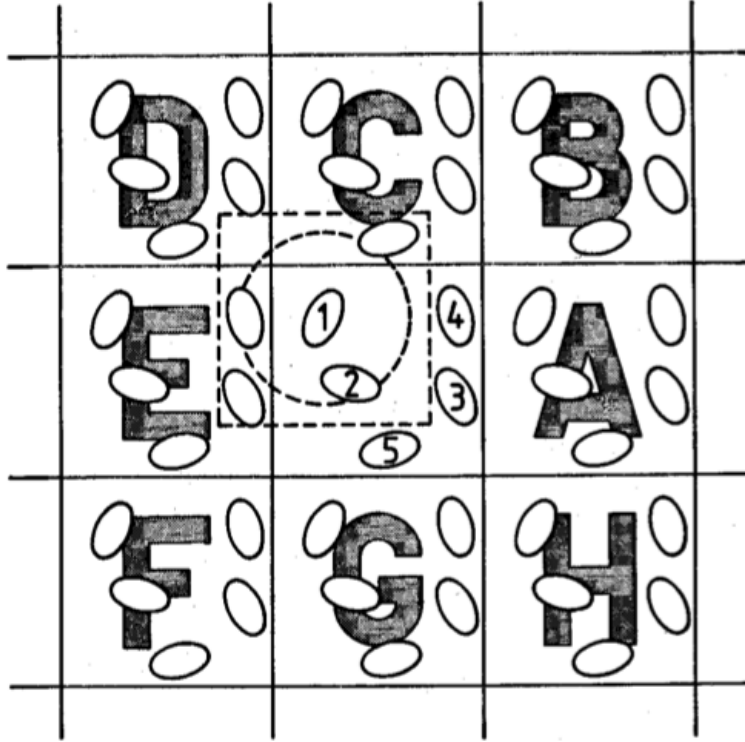


FIG. 2. Representation of the minimum image distance. Molecule 1 does not interact with molecule 4 located in the simulation box because the distance between particles is greater than the cutoff. However, molecule 1 does interact with the image of molecule 4 located in box E. Image from Allen and Tildesley [16](#)

Energy truncation and tail corrections. If two particles are separated by more than a certain distance, we typically truncate their interaction energy if $r > r_c$, where r_c denotes the *cutoff distance*. Truncating interactions removes contribution to the potential energy that might be non negligible and can lead to significant artifacts, such as significantly perturbed densities when a barostat is used to sample the NPT ensemble due to neglected long-range dispersion interactions. We can estimate the truncated interactions by incorporating an energy correction, known as the tail or long range correction. For the Lennard-Jones fluid, we assume that we have an homogeneous liquid at $r > r_c$ to obtain the correction for neglecting this contribution for all

Quantity	Expression
Length	$L^* = L/\sigma$
Density	$\rho^* = N\sigma^3/V$
Energy	$U^* = U/\epsilon$
Pressure	$P^* = P\sigma^3/\epsilon$
Temperature	$T^* = k_B T/\epsilon$
Volume	$V^* = V/\sigma^3$
Time	$t^* = t\sqrt{\frac{\epsilon}{m\sigma^2}}$

TABLE I. Conversion factors between real and reduced units.

interacting pairs of particles¹⁷:

$$U_{\text{correction}} = \frac{8\pi N^2}{3V} \epsilon \sigma^3 \left[\frac{1}{3} \left(\frac{\sigma}{r_c} \right)^9 - \left(\frac{\sigma}{r_c} \right)^3 \right] \quad (14)$$

For a Lennard-Jones fluid, it is common to set $r_c \sim 3\sigma$, since the pair interaction at this separation is small, $U(3\sigma) \approx 4[(3)^{-12} - (3)^{-6}] \approx -0.0055\epsilon$, or about 0.5% of the well depth ϵ . You will want to verify that your computed properties are relatively insensitive to the choice of cutoff r_c so that a too-short cutoff does not induce artifacts in computed physical properties.

Reduced units. Lennard-Jones fluids have the surprisingly pleasant behavior of possessing universal behavior when expressed in terms of *reduced units* as

$$U^*(r_{ij}) = 4 \left[\left(\frac{1}{r_{ij}^*} \right)^{12} - \left(\frac{1}{r_{ij}^*} \right)^6 \right] \quad (15)$$

where

$$U^* = \frac{U}{\epsilon} \quad (16)$$

and

$$r^* = \frac{r}{\sigma} \quad (17)$$

That is, when plotted in reduced units, all Lennard-Jones fluids exhibit the same universal behavior despite the exact choices of ϵ and σ used in the simulation. See Table I for a list of variables in reduced units. Using reduced units for input and output will allow you to compare your results with others.

C. Reference calculations

See the following resources for NIST Lennard-Jones fluid reference data:

- [Reference thermodynamic data \(\$N = 500\$, \$T^* = 0.90\$ and \$0.90\$, \$r_c = 3\sigma\$ \)](#)
- [Reference snapshot potential energies and virials](#)

III. CONCRETE TASKS

Implement one (or more) methods to generate initial configurations. You will want to implement more than one method to generate an initial configuration. This will allow you to test if your code produces the same final answers with different initial conditions. We will provide the options of randomly generating an initial set of coordinates or starting from a previously equilibrated state.

Implement the pairwise and long tail correction equations. These are the LJ potential energy and its long tail correction expression. Use reduced units, as in Equation 15 to facilitate comparison with others.

Implement a function that computes the total energy of the system. Compare to the NIST reference snapshot potential energies and virials.

Implement the Metropolis algorithm and compare to the NIST benchmark. See Section II A as a reference. This is the part of the code where you will implement features such as periodic boundary conditions, minimum image distance, particle translation and the acceptance criteria. You can use the state point $T^* = 0.9$, $\rho^* = 0.9$, and $r_c = 3\sigma$ and compare to the NIST benchmark for thermodynamic data.

Check if your energies are consistent with the NIST benchmark.

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