

# A simple method for automated equilibration detection in molecular simulations

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Molecular simulations intended to compute equilibrium properties are often initiated from configurations that are highly atypical of equilibrium samples, a practice which can generate a distinct initial transient in mechanical observables computed from the simulation trajectory. Traditional practice in simulation data analysis recommends this initial portion be discarded to *equilibration*, but no simple, general, and automated procedure for this process exists. Here, we suggest such a conceptually simple automated procedure that does not make strict assumptions about the distribution of the observable of interest, in which the equilibration time is chosen to maximize the number of effectively uncorrelated samples in the production timespan used to compute equilibrium averages. We present a simple Python reference implementation of this procedure, and demonstrate its utility on typical molecular simulation data.

**Keywords:** molecular dynamics (MD); Metropolis-Hastings; Monte Carlo (MC); Markov chain Monte Carlo (MCMC); equilibration; burn-in; timeseries analysis; statistical inefficiency; integrated autocorrelation time

## INTRODUCTION

Molecular simulations use Markov chain Monte Carlo (MCMC) techniques [1] to sample configurations  $x$  from an equilibrium distribution  $\pi(x)$ , either exactly (using Monte Carlo methods such as Metropolis-Hastings) or approximately (using molecular dynamics integrators without Metropolization) [2].

Due to the sensitivity of the equilibrium density  $\pi(x)$  to small perturbations in configuration  $x$  and the difficulty of producing sufficiently good guesses of typical equilibrium configurations  $x \sim \pi(x)$ , these molecular simulations are often started from highly atypical initial conditions. For example, simulations of biopolymers might be initiated from a fully extended conformation unrepresentative of behavior in solution, or a geometry derived from a fit to diffraction data collected from a cryocooled crystal; solvated systems may be prepared by periodically replicating a small solvent box equilibrated under different conditions, yielding atypical densities and solvent structure; liquid mixtures or lipid bilayers may be constructed by using methods that fulfill spatial constraints (e.g. PackMol [3]) but create locally atypical geometries, requiring long simulation times to relax to typical configurations.

As a result, traditional practice in molecular simulation has recommended some initial portion of the trajectory be discarded to *equilibration* (also called *burn-in*<sup>1</sup> in the MCMC literature [4]). While the process of discarding initial samples is strictly unnecessary for the time-average of quantities of interest to eventually converge to the desired expectations [5], and as a result is often not recommended by statisticians [4], the differences in complexity of probability densities typically encountered in statistics and molecular

simulation may explain the difference in historical practice. In the simulation field, discarding initial samples to equilibration nevertheless often allows the practitioner to avoid what may be impractically long run times to eliminate the bias in computed properties in finite-length simulations induced by atypical initial starting conditions.

As an illustrative example, consider the computation of the average density of liquid argon under a given set of reduced temperature and pressure conditions shown in Figure 1. To initiate the simulation, an initial dense liquid geometry at reduced density  $\rho^* \equiv \rho\sigma^3 = 0.960$  was prepared and subjected to local energy minimization. The upper panel of Figure 1 depicts the average relaxation behavior of simulations initiated from the same configuration with different random initial velocities and integrator random number seeds (full simulation details are provided in *Simulation Details*). The average (black line) and standard deviation (shaded grey) of 100 realizations of this process show a characteristic relaxation behavior away from the initial density toward the equilibrium density. The expectation of the running average of the density over many realizations of this procedure (Figure 1, lower panel) significantly deviates from the true expectation (dotted line), leading to significantly biased estimates of the expectation unless simulations are sufficiently long to eliminate this starting point dependent bias—a surprisingly long 30 ns in this case. Note that this bias is present even in the average of many realizations because the *same* atypical starting condition is used for every realization of this simulation process.

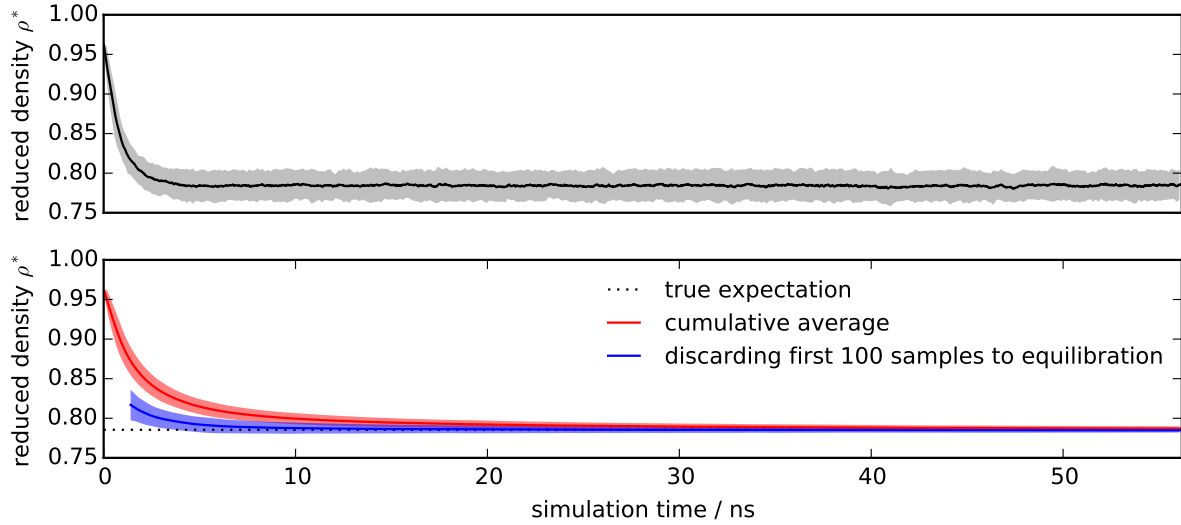
## STATEMENT OF THE PROBLEM

Consider successively sampled configurations  $x_t$  from a molecular simulation, with  $t = 1, \dots, T$ . We presume we are interested in computing the expectation

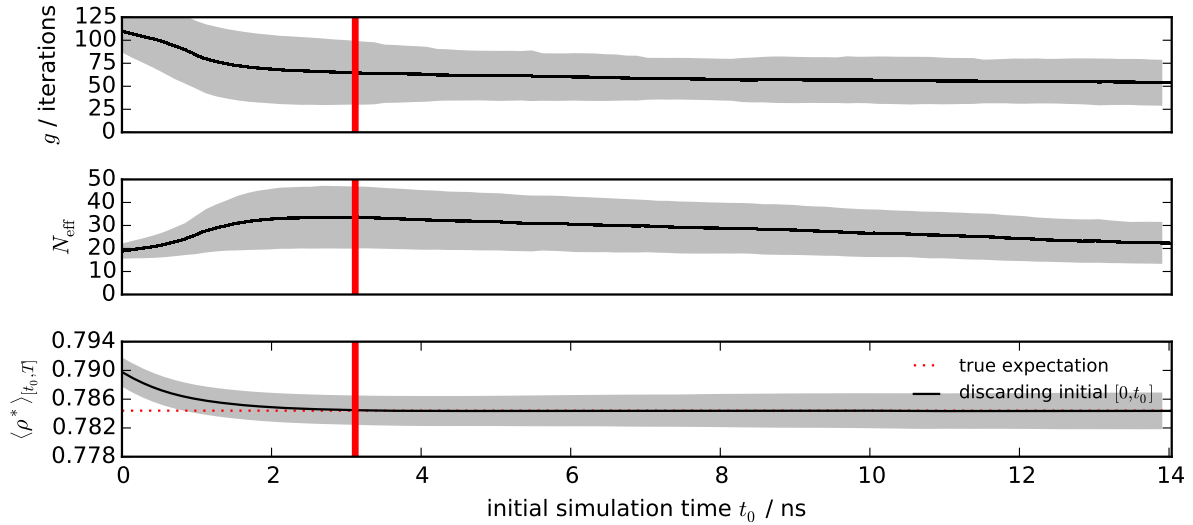
$$\langle A \rangle \equiv \int dx A(x) \pi(x) \quad (1)$$

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<sup>1</sup> The term *burn-in* comes from the field of electronics, in which a short “burn-in” period is used to ensure that a device is free of faulty components—which often fail quickly—and is operating normally [4].



**FIG. 1. Illustration of the motivation for discarding data to equilibration.** To illustrate the bias in expectations induced by relaxation away from initial conditions, 100 replicates of a simulation of liquid argon were initiated from the same energy-minimized initial configuration constructed with initial reduced density  $\rho^* \equiv \rho\sigma^3 = 0.960$  but different random number seeds for stochastic integration. **Top:** The average of the reduced density (black line) over the replicates relaxes to the region of typical equilibrium densities over the first few ns of simulation time. **Bottom:** If the average density is estimated by a cumulative average from the beginning of the simulation (red line), the estimate will be heavily biased by the atypical starting density even beyond 10 ns. Discarding even a small amount of initial data—in this case 100 initial samples ( $\sim 1.4$  ns, blue line)—results in a cumulative average estimate that converges to the true average (black dotted line) much more rapidly. Shaded regions denote 95% confidence intervals.



**FIG. 2. Statistical inefficiency, number of uncorrelated samples, and bias for different equilibration times.** Trajectories of length  $T = 2\,000$  iterations ( $\sim 28$  ns) for the Lennard-Jones system described in Fig. 1 were analyzed as a function of equilibration time choice  $t_0$ . Averages over all 100 replicate simulations (all starting from the same initial conditions) are shown as dark lines, with shaded lines showing standard deviation of estimates among replicates. **Top:** The statistical inefficiency  $g$  as a function of equilibration time choice  $t_0$  is initially very large, but diminishes rapidly after the system has relaxed to equilibrium. **Middle:** The number of effectively uncorrelated samples  $N_{\text{eff}} = (T - t_0 + 1)/g$  shows a maximum at  $t_0 = 222$  iterations ( $\sim 3.1$  ns), suggesting the system has equilibrated by this time. The red vertical line in all plots marks this choice of  $t_0 = 222$  iterations. **Bottom:** The cumulative density average  $\langle \rho^* \rangle$  computed over the span  $[t_0, T]$  shows that the bias (deviation from the true estimate, shown as red dashed lines) is minimized for choices of  $t_0 \geq 222$  iterations. The standard deviation among replicates (shaded region) grows with  $t_0$  because fewer data are included in the estimate. The choice of optimal  $t_0$  that maximizes  $N_{\text{eff}}$  (red vertical line) strikes a good balance between bias and variance. The true estimate (red dashed lines) is computed from averaging over the range  $[5\,000, 10\,000]$  iterations over all 100 replicates.

of a mechanical property  $A(x)$ . For convenience, we will refer to the timeseries  $a_t \equiv A(x_t)$ , with  $t = 0$ . The estimator  $\hat{A} \approx \langle A \rangle$  constructed from the entire dataset is given by

$$\hat{A}_{[1,T]} \equiv \frac{1}{T} \sum_{t=1}^T a_t. \quad (2)$$

While  $\lim_{T \rightarrow \infty} \hat{A}_{[1,T]} = \langle A \rangle$  for an infinitely long simulation<sup>2</sup>, the bias in  $\hat{A}_{[1,T]}$  may be significant in a simulation of finite length  $T$ .

By discarding samples  $t < t_0$  to equilibration, we hope to eliminate the initial transient and provide a less biased estimate of  $\langle A \rangle$ ,

$$\hat{A}_{[t_0,T]} \equiv \frac{1}{T - t_0 + 1} \sum_{t=t_0}^T a_t. \quad (3)$$

We can quantify the overall error in an estimator  $\hat{A}$  by the expected error  $\delta^2 \hat{A}$ ,

$$\begin{aligned} \delta^2 \hat{A} &\equiv E_{x_0} \left[ \left( \hat{A} - \langle A \rangle \right)^2 \right] \\ &= E_{x_0} \left[ \left( \hat{A} - E_{x_0}[\hat{A}] \right)^2 \right] + \left( E_{x_0}[\hat{A}] - \langle A \rangle \right)^2 \end{aligned} \quad (4)$$

where  $E_{x_0}[\cdot]$  denotes the expectation over independent realizations of the simulation initiated from the same configuration  $x_0$  but with different initial velocities and random number seeds. The first term, denotes the variance in the estimator  $\hat{A}$  where the trajectory is initiated from  $x_0$ :

$$\text{var}_{x_0}(\hat{A}) \equiv \left( \hat{A} - E_{x_0}[\hat{A}] \right)^2 \quad (6)$$

while the second term denotes the contribution from the squared bias,

$$\text{bias}_{x_0}^2(\hat{A}) \equiv \left( E_{x_0}[\hat{A}] - \langle A \rangle \right)^2 \quad (7)$$

## BIAS-VARIANCE TRADEOFF

With increasing equilibration time  $t_0$ , bias is reduced, but the variance—the contribution to error due to random variation from having a finite number of uncorrelated samples—will increase because less data is included in the estimate. This can be seen in the bottom panel of Figure 2, where the shaded region (denoting the standard deviation among sample estimates) increases in width with increasing equilibration time  $t_0$ .

<sup>2</sup> We note that this equality only holds for simulation schemes that sample from the true equilibrium distribution  $\pi(x)$ , such as Metropolis-Hastings Monte Carlo or Metropolized integration schemes. Molecular dynamics simulations utilizing finite timestep integration without Metropolization will produce averages that may deviate from the true expectation  $\langle A \rangle$  [?].

To examine the tradeoff between bias and variance explicitly, Figure 3 plots the bias and variance (here, shown as standard error) contributions against each other as a function of  $t_0$  (denoted by color). At  $t_0 = 0$ , the bias is large but variance is minimized. With increasing  $t_0$ , bias is eventually eliminated but then variance rapidly grows as fewer uncorrelated samples are included in the estimate. There is a clear optimal choice at  $t_0 \sim 222$  iterations that minimizes variance while also effectively eliminating bias.

## SELECTING THE EQUILIBRATION TIME

Here, we concern ourselves with this question: Is there a simple approach to choosing an optimal equilibration time  $t_0$  that provides a significantly improved estimate  $\hat{A}_{[t_0,T]}$ , such that  $\delta^2 \hat{A}_{[t_0,T]} < \delta^2 \hat{A}_{[1,T]}$ ? We note that, for cases in which the simulation is not long enough to reach equilibrium, no choice of  $t_0$  will eliminate bias completely; the best we can hope for is to minimize this bias.

While several automated methods for selecting the equilibration time  $t_0$  have been proposed, these approaches have shortcomings that have greatly limited their use. The reverse cumulative averaging method [6], for example, uses a statistical test for normality to determine the point before which the observable timeseries deviates from normality. While this concept may be reasonable for experimental data, where measurements often represent the sum of many random variables such that the central limit theorem's guarantee of asymptotic normality ensures the distribution of the observable will be approximately normal, there is no such guarantee that instantaneous measurements of a simulation property of interest will be normally distributed. In fact, many properties will be decidedly *non-normal*. For a biomolecule such as a protein, for example, the radius of gyration, end-to-end distance, and torsion angles sampled during a simulation will all be highly non-normal. Instead, we require a method that makes no assumptions about the nature of the distribution of the property under study.

## AUTOCORRELATION ANALYSIS

The set of successively sampled configurations  $\{x_t\}$  and their corresponding observables  $\{a_t\}$  compose a correlated timeseries of observations. To estimate the statistical error or uncertainty in a stationary timeseries free of bias, we must be able to quantify the *effective number of uncorrelated samples* present in the dataset. This is usually accomplished through computation of the *statistical inefficiency*  $g$ , which quantifies the number of correlated timeseries samples needed to produce a single effectively uncorrelated sample of the observable of interest. While these concepts are well-established for the analysis of both Monte Carlo and molecular dynamics simulations [7–10], we review it here for the sake of clarity.

For a given equilibration time choice  $t_0$ , the statistical uncertainty in our estimator  $\hat{A}_{[t_0, T]}$  can be written as,

$$\begin{aligned} \delta^2 \hat{A}_{[t_0, T]} &\equiv E_{x_0} \left[ \left( \hat{A}_{[t_0, T]} - \langle \hat{A} \rangle \right)^2 \right] \\ &= E_{x_0} \left[ \hat{A}_{[t_0, T]}^2 \right] - E_{x_0} \left[ \hat{A}_{[t_0, T]} \right]^2 \\ &= \frac{1}{T_{t_0}^2} \sum_{t, t'=t_0}^T [\langle a_t a_{t'} \rangle - \langle a_t \rangle \langle a_{t'} \rangle] \\ &= \frac{1}{T_{t_0}^2} \sum_{t=t_0}^T [\langle x_t^2 \rangle - \langle x_t \rangle^2] \\ &\quad + \frac{1}{T_{t_0}^2} \sum_{t \neq t'=t_0}^T [\langle a_t a_{t'} \rangle - \langle a_t \rangle \langle a_{t'} \rangle]. \end{aligned} \quad (8)$$

where  $T_{t_0} \equiv T - t_0 + 1$ , the number of correlated samples in the timeseries  $\{a_t\}_{t_0}^T$ . In the last step, we have split the double-sum into two separate sums—a term capturing the variance in the observations  $a_t$ , and a remaining term capturing the correlation between observations.

If  $t_0$  is sufficiently large for the initial bias to be eliminated, the remaining timeseries  $\{a_t\}_{t_0}^T$  will obey the properties of both *stationarity* and *time-reversibility*, allowing us to write,

$$\begin{aligned} \delta^2 \hat{A}_{[t_0, T]}^{\text{equil}} &= \frac{1}{T_{t_0}} [\langle a_t^2 \rangle - \langle a_t \rangle^2] \\ &\quad + \frac{2}{T_{t_0}} \sum_{n=1}^{T-t_0} \left( \frac{T_{t_0} - n}{T_{t_0}} \right) [\langle a_t a_{t+n} \rangle - \langle a_t \rangle \langle a_{t+n} \rangle] \\ &\equiv \frac{\sigma_{t_0}^2}{T_{t_0}} (1 + 2\tau_{t_0}) \\ &= \frac{\sigma_{t_0}^2}{T_{t_0}/g_{t_0}} \end{aligned} \quad (9)$$

where the variance  $\sigma^2$ , statistical inefficiency  $g$ , and integrated autocorrelation time  $\tau$  (in units of the sampling interval) are given by

$$\sigma^2 \equiv \langle a_t^2 \rangle - \langle a_t \rangle^2 \quad (10)$$

$$\tau \equiv \sum_{t=1}^{T-1} \left( 1 - \frac{t}{T} \right) C_t \quad (11)$$

$$g \equiv 1 + 2\tau \quad (12)$$

with the discrete-time normalized fluctuation autocorrelation function  $C_t$  defined as

$$C_t \equiv \frac{\langle a_n a_{n+t} \rangle - \langle a_n \rangle^2}{\langle a_n^2 \rangle - \langle a_n \rangle^2}. \quad (13)$$

In practice, it is difficult to estimate  $C_t$  for  $t \sim T$ , due to growth in the statistical error, so common estimators of  $g$  make use of several additional properties of  $C_t$  to provide useful estimates [4].

The  $t_0$  subscript for the variance  $\sigma^2$ , the integrated autocorrelation time  $\tau$ , and the statistical inefficiency  $t_0$  mean that these quantities are only estimated over the production

portion of the timeseries,  $\{a_t\}_{t=t_0}^T$ . Since we assumed that the bias was eliminated by judicious choice of the equilibration time  $t_0$ , this estimate of the statistical error will be poor for choices of  $t_0$  that are too small.

## THE ESSENTIAL IDEA

Suppose we choose some arbitrary time  $t_0$  and discard all samples  $t \in [0, t_0)$  to equilibration, keeping  $[t_0, T]$  as the dataset to analyze. How much data remains? We can determine this by computing the statistical inefficiency  $g_{t_0}$  for the interval  $[t_0, T]$ , and computing the effective number of uncorrelated samples  $N_{\text{eff}}(t_0) \equiv (T - t_0 + 1)/g_{t_0}$ . If we start at  $t_0 \equiv T$  and move  $t_0$  to earlier and earlier points in time, we expect that the effective number of uncorrelated samples  $N_{\text{eff}}(t_0)$  will continue to grow until we start to include the highly atypical initial data. At that point, the integrated autocorrelation time  $\tau$  (and hence the statistical inefficiency  $g$ ) will greatly increase, and the effective number of samples  $N_{\text{eff}}$  will start to plummet.

This suggests an alluringly simple algorithm for identifying the optimal equilibration time—pick the  $t_0$  which maximizes the number of uncorrelated samples  $N_{\text{eff}}$ . In mathematical terms,

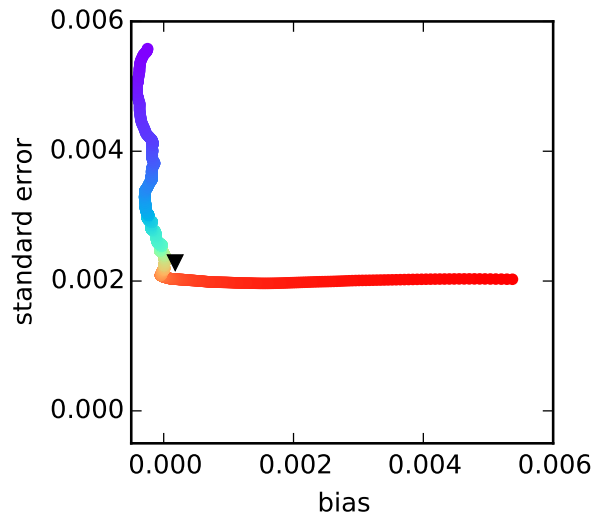
$$t_0^{\text{opt}} = \underset{t_0}{\text{argmax}} N_{\text{eff}}(t_0) \quad (14)$$

$$= \underset{t_0}{\text{argmax}} \frac{T - t_0 + 1}{g_{t_0}} \quad (15)$$

Figure 2 demonstrates the application of this concept to the liquid argon system described above, using averages of the statistical inefficiency  $g_{t_0}$  and  $N_{\text{eff}}(t_0)$  computed over 100 independent replicate trajectories. At short  $t_0$ , the average statistical inefficiency  $g$  (Figure 2, top panel) is large due to the contribution from slow relaxation from atypical initial conditions, while at long  $t_0$  the statistical inefficiency estimate is much shorter and nearly constant of a large span of time origins. As a result, the average effective number of uncorrelated samples  $N_{\text{eff}}$  (Figure 2, middle panel) has a peak at  $t_0 \sim 222$  iterations (Figure 2, vertical red lines). The effect on bias in the estimated average reduced density  $\langle \rho^* \rangle$  (Figure 2, bottom panel) is striking—the bias is essentially eliminated for the choice of equilibration time  $t_0$  that maximizes the number of uncorrelated samples  $N_{\text{eff}}$ .

But how will this strategy work for cases where we do not know the statistical inefficiency  $g$  as a function of the equilibration time  $t_0$  precisely? When all that is available is a single simulation, our best estimate of  $g_{t_0}$  is estimated from that simulation alone over the span  $[t_0, T]$ —will this affect the quality of our estimate of equilibration time? Empirically, this does not appear to be the case—the black triangle in Figure 3 shows the bias and variance for estimates computed over the 100 replicates where  $t_0$  is individually determined from each simulation.

[JDC: Add discussion about RMS error to body text.]



**FIG. 3. Bias-variance tradeoff for fixed equilibration time versus automatic equilibration time selection.** Trajectories of length  $T = 2\,000$  iterations ( $\sim 28$  ns) for the Lennard-Jones system described in Fig. 1 were analyzed as a function of equilibration time choice  $t_0$ . Using 100 replicate simulations, the average bias (average deviation from true expectation) and standard deviation (random variation from replicate to replicate) were computed as a function of a prespecified fixed equilibration time  $t_0$ , with colors running from  $t_0 = 0$  (red) to  $t_0 = 1\,800$  iterations (blue). As is readily discerned, the bias for small  $t_0$  is initially large, but minimized for larger  $t_0$ . By contrast, the standard error (a measure of variance, estimated here by standard deviation among replicates) grows as  $t_0$  grows above a certain critical time (here,  $\sim 222$  iterations). If the  $t_0$  that maximizes  $N_{\text{eff}}$  is instead chosen *individually* for each trajectory based on that trajectory’s estimated statistical inefficiency  $g_{[t_0, T]}$ , the resulting bias-variance tradeoff (black triangle) does an excellent job minimizing bias and variance simultaneously, comparable to what is possible for a choice of equilibration time  $t_0$  based on knowledge of the true bias and variance among many replicate estimates. [JDC: Add colorbar and uncertainties to plotted points.]

## DISCUSSION

The scheme described here—in which the equilibration time  $t_0$  is computed using Eq. 14 as the time origin that maximizes the number of uncorrelated samples in the production region  $[t_0, T]$ —is both conceptually and computationally straightforward. It provides an approach to determining the optimal amount of initial data to discard to equilibrate in order to minimize variance while also minimizing initial bias, and does this without employing statistical tests that require unsatisfiable assumptions of normality of the observable of interest. As we have seen, this scheme empirically appears to select a practical compromise between bias and variance even when the statistical inefficiency  $g$  is estimated directly from the trajectory using Eq. 12.

A word of caution is necessary. One can certainly envision pathological scenarios where this algorithm for selecting an optimal equilibration time will break down. In cases where the simulation is not long enough to reach equilibrium—let alone collect many uncorrelated samples from it—no choice of equilibration time will bestow upon the data the ability to produce an unbiased estimate of the true expectation. Similarly, in cases where insufficient data is available for the statistical inefficiency to be estimated well, this algorithm is expected to perform poorly. However, in these cases, the data itself should be suspect if the trajectory is not at least an order of magnitude longer than the minimum estimated autocorrelation time.

## SIMULATION DETAILS

All molecular dynamics simulations described here were performed with OpenMM 6.2 [11] (available at [openmm.org](http://openmm.org)) using the Python API. All scripts used to run simulations, analyze data, and generate plots—along with the simulation data itself and scripts for generating figures—are available on GitHub<sup>3</sup>.

The argon model system comes from the [openmmtools](https://github.com/choderalab/openmmtools) package<sup>4</sup>. [JDC: Note details of switching function, cut-off, and long-range isotropic dispersion correction.] Simulations were performed using a box of  $N = 500$  argon atoms at reduced temperature  $T^* \equiv k_B T / \epsilon = 0.850$  and reduced pressure  $p^* \equiv p \sigma^3 / \epsilon = 1.266$  using a Langevin integrator [12] with timestep  $\Delta t = 0.01 \tau$ , where characteristic oscillation timescale  $\tau = \sqrt{m r_0^2 / 72 \epsilon}$ , with  $r_0 = 2^{1/6} \sigma$  [13]. A Metropolis Monte Carlo barostat was used with box volume moves attempted every 25 timesteps. [JDC: Note how volume proposal size was determined.] Densities were recorded every 25 timesteps.

The automated equilibration detection scheme is also available in the [timeseries](https://github.com/choderalab/pybar) module of the [pybar](https://github.com/choderalab/pybar) package as `detectEquilibration()`, and can be accessed using the following code:

```
from pybar.timeseries import detectEquilibration
# determine equilibrated region
[t0, g, Neff_max] = detectEquilibration(A_t)
# discard initial samples to equilibration
A_t = A_t[t0:]
```

## PRACTICAL COMPUTATION OF STATISTICAL INEFFICIENCY

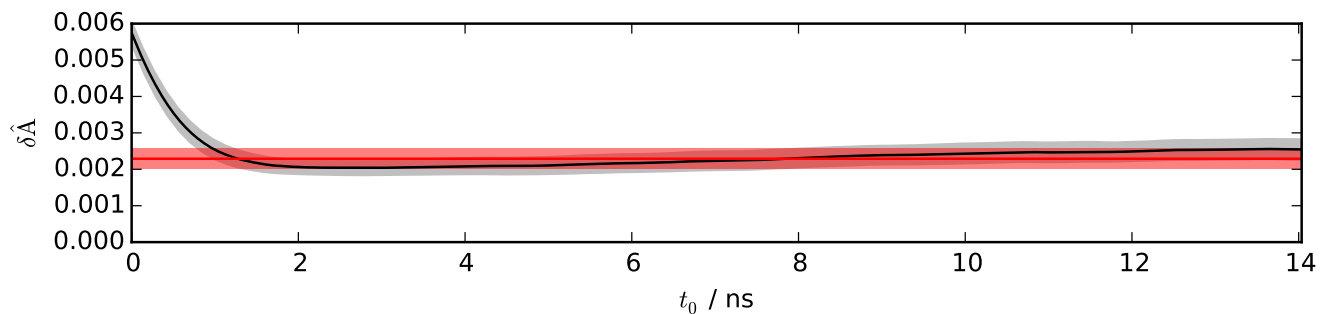
The computation of the statistical inefficiency  $g$  (defined by Eq. 12) for a finite timeseries  $a_t$ ,  $t = 1, \dots, T$  deserves

<sup>3</sup> All scripts and data are available at:

<http://github.com/choderalab/automatic-equilibration-detection>

<sup>4</sup> available at <http://github.com/choderalab/openmmtools>





**FIG. 4. RMS error for fixed equilibration time versus automatic equilibration time selection.** Trajectories of length  $T = 2\,000$  iterations ( $\sim 28$  ns) for the Lennard-Jones system described in Fig. 1 were analyzed as a function of fixed equilibration time choice  $t_0$ . Using 100 replicate simulations, the RMS error (average root mean squared deviation from true expectation, as defined in Eq. 4) was computed (black line) along with 95% confidence interval (gray shading). The RMS error is minimized for fixed equilibration time choices in the range 2–6 ns. If the  $t_0$  that maximizes  $N_{\text{eff}}$  is instead chosen *individually* for each trajectory based on that trajectory’s estimated statistical inefficiency  $g_{[t_0, T]}$  using Eq. 14, the resulting RMS error (red line, 95% confidence interval shown as red shading) is quite close to the minimum RMS error achieved from any particular *fixed* choice of equilibration time  $t_0$ , suggesting that this simple automated approach to selecting  $t_0$  performs reasonably well.

some comment. There are, in fact, a variety of schemes for estimating  $g$  described in the literature, and their behaviors for finite datasets may differ, leading to different estimates of the equilibration time  $t_0$  using the algorithm of Eq. 14.

The main issue is that a straightforward approach to estimating the statistical inefficiency using Eqs. 11–13 in which the expectations are simply replaced with sample estimates causes the statistical error in the estimated correlation function  $C_t$  to grow with  $t$  in a manner that allows this error to quickly overwhelm the sum of Eq. 11. As a result, a number of alternative schemes—generally based on controlling the error in the estimated  $C_t$  or truncating the sum of Eq. 11 when the error grows too large—have been proposed.

For stationary, reversible Markov chains, Geyer observed that a function  $\Gamma_k \equiv \gamma_{2k} + \gamma_{2k+1}$  of the unnormalized fluctuation autocorrelation function  $\gamma_t \equiv \langle a_i a_{i+t} \rangle - \langle a_i \rangle^2$  has a number of pleasant properties (Theorem 3.1 of [14]): It is strictly, positive, strictly decreasing, and strictly convex. [JDC: Check conditions of Geyer proofs.] These properties can be exploited to define a family of estimators called *initial sequence methods* (see Section 3.3 of [14] and Section 1.10.2

of [4]), of which the *initial convex sequence* (ICS) estimator is generally agreed to be optimal, if somewhat complex to implement. [JDC: Give implementation details?]

All computations in this manuscript used the fast multiscale method described in Section 5.2 of [10]. This method is related to a multiscale variant of the *initial positive sequence* (IPS) method of Geyer [15], where contributions are accumulated at increasingly longer lag times and the sum of Eq. 11 is truncated when the terms become negative. We have found this method to be both fast and to provide useful estimates of the statistical inefficiency, but it may not perform well for all problems. [JDC: Give implementation details? Compare with ICS?]

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