

Equipartition Principle for Internal Coordinate Molecular Dynamics

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S Supporting Information

ABSTRACT: The principle of equipartition of (kinetic) energy for all-atom Cartesian molecular dynamics states that each momentum phase space coordinate on the average has $kT/2$ of kinetic energy in a canonical ensemble. This principle is used in molecular dynamics simulations to initialize velocities, and to calculate statistical properties such as entropy. Internal coordinate molecular dynamics (ICMD) models differ from Cartesian models in that the overall kinetic energy depends on the generalized coordinates and includes cross-terms. Due to this coupled structure, no such equipartition principle holds for ICMD models. In this paper, we introduce noncanonical *modal coordinates* to recover some of the structural simplicity of Cartesian models and develop a new equipartition principle for ICMD models. We derive low-order recursive computational algorithms for transforming between the modal and physical coordinates. The equipartition principle in modal coordinates provides a rigorous method for initializing velocities in ICMD simulations, thus replacing the *ad hoc* methods used until now. It also sets the basis for calculating conformational entropy using internal coordinates.

1. INTRODUCTION

The equipartition theorem¹ for canonical ensembles is one of the fundamental principles used in the statistical mechanics theory for molecular systems. This theorem can be used to show that the principle of equipartition of energy holds for Cartesian molecular models.^{1,2} For the kinetic energy, this principle states that each momentum coordinate in the canonical phase space has $kT/2$ of thermal energy on the average (where k is the Boltzmann constant and T is the thermodynamic temperature). This equipartition principle is used for initializing atomic velocities in Cartesian molecular dynamics simulations with a Boltzmann distribution of thermal energy. The equipartition theorem has also been used to connect the classical variance to the quantum harmonic oscillator to derive the equations for calculating absolute entropies using internal coordinates.³

In contrast with Cartesian models, *internal-coordinate molecular dynamics (ICMD)* models utilize relative, instead of absolute, generalized coordinates. A well-known example of ICMD internal coordinates is the *bond length/angle/torsional (BAT)* coordinates,⁴ which, while providing an alternative coordinate representation, retains the full system degrees of freedom. Another example of ICMD models is the *torsion angle molecular dynamics (TAMD)* model. These are BAT models, with additional holonomic constraints that freeze the bond and angle coordinates. Thus, TAMD models have a smaller number of coordinates than the Cartesian or BAT models.^{5–8} While the TAMD models are attractive for tracking the low frequency motion in biomolecules, they give rise to qualitatively different dynamics compared to Cartesian models. Unlike the Cartesian case, the Hamiltonian for ICMD models is not *separable* because the kinetic energy depends not just on the momentum but also on the generalized coordinates. The consequent dynamical cross-coupling among the coordinates makes the ICMD models more complex. This increases the difficulty in

deriving energy conserving integration schemes similar to Velocity Verlet for Cartesian models.

The intuitive presumption that constrained ICMD models behave as the limiting case of increasingly stiff Cartesian models was shown to be incorrect in a series of careful investigations.^{9–11} It was shown that statistical mechanics ensemble averages of conformation dependent quantities from constrained ICMD models differed systematically from those obtained using arbitrarily stiff Cartesian models. The recognition of these differences led Fixman to propose the use of a mass matrix tensor based compensating potential to correct for such discrepancies,¹² and its validity has been verified via numerical experiments.^{13–15} The difficulty in evaluating the compensating potential and its gradient have led researchers to investigate evaluation techniques^{16,17} and to the development of a spatial operators based solution and low-order computational algorithms.^{18,19}

Therefore, it is important to address these differences between ICMD and Cartesian models to make the ICMD simulations more robust and straightforward to use for biomolecular simulations. This work takes a step forward in maturing the understanding and use of ICMD models. We show that the application of the equipartition theorem to the ICMD model does not yield an equipartition principle analogous to that for Cartesian models. Instead, the ensemble averages involve configuration dependent and coupled coordinates that are not easy to interpret or use. We introduce a coordinate transformation to define new ICMD *modal coordinates*. These coordinates transform the system kinetic energy into a decoupled form similar to that for Cartesian models. Moreover, we show that an equipartition principle analogous to that for Cartesian models holds for these modal

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coordinates. This principle holds even though the coordinates are not canonical coordinates in the Hamiltonian sense.

The transformations between the physical ICMD velocity/momentum coordinates and the modal coordinates involve the square root of the configuration dependent ICMD mass matrix and its inverse. These matrices can be especially expensive to evaluate for constrained ICMD models. We use spatial operators to develop analytical expressions for these coordinate transformation matrices based on closed-form spatial operator factorizations of the ICMD mass matrix and its inverse. Subsequently, these operator expressions lead to recursive, low-order computational algorithms for carrying out the coordinate transformations that entirely avoid the explicit evaluation of the coordinate transformation matrices. The equipartition principle in modal coordinates can now be applied to assigning initial velocities to the internal coordinates according to Boltzmann distribution. We have demonstrated the use of modal coordinate velocities for velocity initialization in the TAMD simulations of protein structure folding and refinement.^{20,21} The theoretical groundwork presented in this paper sets the stage for future calculations of other properties such as conformational entropy from ICMD models.

1.1. Generalized Equipartition Theorem. Let $H(q, p)$ and $\mathcal{L}(q, \dot{q})$ denote the Hamiltonian and the Lagrangian, respectively, for a n -dimensional dynamical system, with $q \in \mathcal{R}^n$ denoting the generalized coordinates and $p \in \mathcal{R}^n$ the conjugate momenta. The elements of p satisfy

$$p_i = \frac{\partial \mathcal{L}(q, \dot{q})}{\partial \dot{q}_i} \quad (1)$$

For a temperature, T , the canonical ensemble partition function, $\mathcal{Z}(T)$, is defined as¹

$$\mathcal{Z}(T) = \frac{1}{h^n} \int_{-\infty}^{\infty} dp_1 \dots \int_{-\infty}^{\infty} dp_n \int_{-\alpha_1}^{\gamma_1} dq_1 \dots \int_{-\alpha_n}^{\gamma_n} dq_n e^{-H(q,p)/kT} \quad (2)$$

where h is Planck's constant and the α_i and γ_i integration limits are determined by the geometry of the problem. The ensemble average of a function $f(q, p)$ is

$$\langle f(q, p) \rangle = \frac{1}{h^n \mathcal{Z}(T)} \int_{-\infty}^{\infty} dp_1 \dots \int_{-\infty}^{\infty} dp_n \int_{-\alpha_1}^{\gamma_1} dq_1 \dots \int_{-\alpha_n}^{\gamma_n} dq_n f(q, p) e^{-H(q,p)/kT} \quad (3)$$

In particular, with y_i and y_j denoting a pair of phase space coordinates, the equipartition theorem^{1,22} states that the ensemble average of the function $f(q, p) = y_i[(\partial H(q, p))/(\partial y_j)]$ is

$$\left\langle y_i \frac{\partial H(q, p)}{\partial y_j} \right\rangle = kT \delta_{i=j} \quad (4)$$

where $\delta_{i=j}$ denotes the Dirac delta function which is unity only when $i = j$ and zero otherwise. A more detailed derivation of this result using integration by parts is included in the Supporting Information.

In this powerful theorem, the y_i and y_j coordinates can be any of the elements of the q or p coordinates. However, the theorem does require that the q and p be canonical phase space

coordinates. Gathering up the ensemble average values in eq 4 for all i and j , we can re-express it in matrix form as

$$\langle y \nabla_y H(q, p) \rangle = \begin{pmatrix} \left\langle y_1 \frac{\partial H(q, p)}{\partial y_1} \right\rangle & \dots & \left\langle y_1 \frac{\partial H(q, p)}{\partial y_{2n}} \right\rangle \\ \vdots & \ddots & \vdots \\ \left\langle y_{2n} \frac{\partial H(q, p)}{\partial y_1} \right\rangle & \dots & \left\langle y_{2n} \frac{\partial H(q, p)}{\partial y_{2n}} \right\rangle \end{pmatrix} = kT I_{2n} \quad (5)$$

where I_{2n} denotes the $2n \times 2n$ identity matrix.

1.2. Cartesian Molecular Dynamics Model. The Hamiltonian for a Cartesian molecular dynamics model with n atoms has the form

$$H(x, p) = \sum_{i=1}^{3n} p_i^2 / 2m_i + \mathcal{U}(x) \quad (6)$$

where $x \in \mathcal{R}^{3n}$ denotes the atom position generalized coordinates, $\mathcal{U}(x)$ denotes the potential energy, and p_i denotes a linear momentum component for an atom with mass m_i . For this Hamiltonian, it follows from the eq 4 equipartition theorem (with $y_i = y_j = p_i$) that

$$\langle p_i^2 / 2m_i \rangle = kT/2 \quad (7)$$

This implies that the average kinetic energy in each conjugate momentum coordinate is $kT/2$. This result is also referred to as the *principle of equipartition of kinetic energy*.^{1,2} This singular principle is a consequence of the following special properties of the Cartesian Hamiltonian in eq 6:

- the quadratic (or harmonic) form of the kinetic energy
- the absence of cross-terms in the kinetic energy expression
- the *separable* nature of the Hamiltonian, i.e., the kinetic energy is independent of the generalized coordinates

2. ICMD MODELS

While Cartesian models use the absolute location of the atoms with respect to a reference frame as generalized coordinates, ICMD models use atom–atom relative coordinates as generalized coordinates. The bond length/angle/torsional (BAT) coordinates are well-known examples of such ICMD coordinates. BAT coordinates provide an alternative representation of the phase space while retaining the dimensionality of the Cartesian model's coordinate space. Torsion angle molecular dynamics (TAMD) ICMD models are BAT models with additional holonomic constraints that freeze the bond and angle degrees of freedom. TAMD models thus have fewer coordinates than the corresponding BAT or Cartesian models.

For an ICMD model with N configuration degrees of freedom, we use $\theta \in \mathcal{R}^N$ to denote its set of generalized coordinates. The ICMD model's kinetic energy depends on a configuration dependent mass matrix $\mathcal{M}(\theta) \in \mathcal{R}^{N \times N}$ and takes the form

$$\mathcal{K}_c(\theta, p) = \frac{1}{2} \dot{\theta}^* \mathcal{M}(\theta) \dot{\theta} = \frac{1}{2} p^* \mathcal{M}^{-1}(\theta) p \quad (8)$$

where the conjugate momenta vector $p \in \mathcal{R}^N$ is given by the expression

$$p = \mathcal{M}(\theta)\dot{\theta} \quad (9)$$

The x^* notation used here denotes the transpose of a vector or a matrix x . The $\mathcal{M}(\theta)$ mass matrix is symmetric and positive definite. Unlike the case of Cartesian models, the ICMD mass matrix is configuration dependent and dense. As a consequence, the system kinetic energy includes cross-terms from the generalized velocity and momentum components (in contrast to eq 6 for Cartesian models). The ICMD Hamiltonian is

$$H(\theta, p) = \frac{1}{2} p^* \mathcal{M}^{-1}(\theta) p + \mathcal{U}(\theta) \quad (10)$$

Observe that the dependency of the kinetic energy on the generalized coordinates implies that the Hamiltonian is *not separable*. The ICMD partition function, $\mathcal{Z}(T)$, is

$$\mathcal{Z}(T) = \frac{1}{h^N} \int_{-\infty}^{\infty} dp_1 \dots \int_{-\infty}^{\infty} dp_N \int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \int_{-\alpha_N}^{\gamma_N} d\theta_N e^{-[\frac{1}{2} p^* \mathcal{M}^{-1}(\theta) p + \mathcal{U}(\theta)]/kT} \quad (11)$$

From eq 10 it follows that

$$\frac{\partial H(\theta, p)}{\partial p_j} = \frac{\partial p^*}{\partial p_j} \mathcal{M}^{-1}(\theta) p = e_j^* \dot{\theta} = \dot{\theta}_j \quad (12)$$

e_j^* above denotes a vector with all zero elements except for the j th element being 1. Using the equipartition theorem eq 4, we thus obtain

$$\left\langle p_i \frac{\partial H(\theta, p)}{\partial p_j} \right\rangle \stackrel{12}{=} \langle p_i \dot{\theta}_j \rangle \stackrel{4}{=} kT \delta_{i=j} \quad (13)$$

The “ $\stackrel{12}{=}$ ” and “ $\stackrel{4}{=}$ ” notation identifies the equation(s) used to establish equalities. While the ensemble average term on the left has the units of energy, it does not lend itself to an interpretation as a principle of equipartition of kinetic energy. This is because p_i depends on multiple velocity coordinates and not just $\dot{\theta}_i$.

Combining eq 13 together for all i and j , the overall ensemble averages can be expressed in matrix form as

$$\langle \dot{\theta} p^* \rangle \stackrel{8}{=} \langle \mathcal{M}^{-1}(\theta) p p^* \rangle \stackrel{13}{=} kT I_N \quad (14)$$

Unlike the Cartesian eq 7, there is no clear way to use this ensemble average relationship to assign the thermal energy across the degrees of freedom in the model with a Boltzmann distribution.

2.1. Modal Coordinates. Since the ICMD mass matrix $\mathcal{M}(\theta)$ is symmetric and positive definite, there exists an invertible matrix $m(\theta) \in \mathcal{R}^{N \times N}$ such that

$$\mathcal{M}(\theta) = m(\theta) m^*(\theta) \quad (15)$$

Let $l(\theta) \in \mathcal{R}^{N \times N}$ denote the inverse of $m(\theta)$ so that

$$m^{-1}(\theta) = l(\theta) \text{ and } \mathcal{M}^{-1}(\theta) \stackrel{15}{=} l^*(\theta) l(\theta) \quad (16)$$

Define the *modal coordinates* $v \in \mathcal{R}^N$ as

$$v(\theta, p) \stackrel{\Delta}{=} m^*(\theta) \dot{\theta} \stackrel{9,16}{=} l(\theta) p \quad (17)$$

The “ $\stackrel{\Delta}{=}$ ” notation should be read as “is defined as” and is used within definitional expressions. Using the v modal coordinates, the eq 10 Hamiltonian can be expressed as

$$H(\theta, v) \stackrel{15}{=} \frac{1}{2} v^* v + \mathcal{U}(\theta) \quad (18)$$

In contrast with eq 10, the kinetic energy in this Hamiltonian expression has a decoupled structure without any cross-terms involving the v_i elements. In addition, the kinetic energy no longer explicitly depends on the θ generalized coordinates. These properties are the motivation for referring to these coordinates as “modal” coordinates.

Unlike p , the v coordinates are *not* conjugate momenta of the θ generalized coordinates, and thus the (θ, v) pair is *not* canonical phase space coordinates in the Hamiltonian sense. Now, we change the integration variables from the p_i momentum coordinates to the v_i modal coordinates. Equation 17 implies the following relationship between infinitesimal volumes in the two coordinate spaces:

$$\begin{aligned} dv_1 \dots dv_N &= \det\{l\} dp_1 \dots dp_N \\ &\Rightarrow \det\{\mathcal{M}(\theta)\}^{1/2} dv_1 \dots dv_N \\ &\stackrel{15,16}{=} dp_1 \dots dp_N \end{aligned} \quad (19)$$

Using this in eq 11, the partition function is given by

$$\mathcal{Z}(T) \stackrel{18,19}{=} \frac{1}{h^N} \int_{-\infty}^{\infty} dv_1 \dots \int_{-\infty}^{\infty} dv_N \int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \int_{-\alpha_N}^{\gamma_N} d\theta_N \det\{\mathcal{M}(\theta)\}^{1/2} e^{-[\frac{1}{2} v^* v + \mathcal{U}(\theta)]/kT} \quad (20)$$

The ensemble average of a function $f(\theta, p) \equiv f(\theta, v)$ is given by

$$\begin{aligned} \langle f(\theta, v) \rangle &= \frac{1}{h^N \mathcal{Z}(T)} \int_{-\infty}^{\infty} dv_1 \dots \int_{-\infty}^{\infty} dv_N \int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \\ &\int_{-\alpha_N}^{\gamma_N} d\theta_N f(\theta, v) \det\{\mathcal{M}^{1/2}(\theta)\} \\ &\quad e^{-[\frac{1}{2} v^* v + \mathcal{U}(\theta)]/kT} \end{aligned} \quad (21)$$

Define

$$\mathcal{U}'(\theta) \stackrel{\Delta}{=} \mathcal{U}(\theta) + \mathcal{U}_c(\theta), \text{ where } \mathcal{U}_c(\theta) \stackrel{\Delta}{=} \frac{1}{2} \ln \det\{\mathcal{M}(\theta)\} \quad (22)$$

Using this, eq 21 can be re-expressed as

$$\begin{aligned} \langle f(\theta, v) \rangle &\stackrel{20,11}{=} \frac{1}{h^N \mathcal{Z}(T)} \int_{-\infty}^{\infty} dv_1 \dots \int_{-\infty}^{\infty} dv_N \int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \\ &\int_{-\alpha_N}^{\gamma_N} d\theta_N f(\theta, v) e^{-[\frac{1}{2} v^* v + \mathcal{U}'(\theta)]/kT} \end{aligned} \quad (23)$$

In particular, the ensemble average of $f(v) = v_i v_j$ is

$$\begin{aligned} \langle v_i v_j \rangle &\stackrel{23}{=} \frac{1}{h^N \mathcal{Z}(T)} \int_{-\infty}^{\infty} dv_1 \dots \int_{-\infty}^{\infty} dv_N \int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \\ &\int_{-\alpha_N}^{\gamma_N} d\theta_N v_i v_j e^{-[\frac{1}{2} v^* v + \mathcal{U}'(\theta)]/kT} \\ &= \frac{1}{h^N \mathcal{Z}(T)} \int_{-\infty}^{\infty} dv_1 \dots \int_{-\infty}^{\infty} dv_N v_i v_j e^{-v^* v / 2kT} \\ &\int_{-\alpha_1}^{\gamma_1} d\theta_1 \dots \int_{-\alpha_N}^{\gamma_N} d\theta_N e^{-\mathcal{U}'(\theta)/kT} \end{aligned} \quad (24)$$

Integrating over the generalized and modal coordinates, we obtain

$$\langle v_i v_j \rangle \stackrel{24}{=} kT \delta_{i=j} \quad (25)$$

Recalling from eq 18 that $v_i^2/2$ is the kinetic energy for the v_i modal coordinate, this result implies that the v_i modal coordinate components are uncorrelated with each other, and moreover, the average kinetic energy in each of these coordinate elements is $kT/2$. The v_i coordinates are decoupled in a manner similar to that of the velocity and momentum coordinates for the Cartesian model. Thus, eq 25 represents an equipartition principle for ICMD models that is the analog of the principle for Cartesian models in eq 7.

Unlike the case for Cartesian models, this equipartition principle holds even though (θ, v) are noncanonical coordinates. Indeed, no such principle holds for the (θ, p) canonical coordinates. Together with the decoupled (no cross-terms) nature of the eq 18 kinetic energy expression, the “modal” properties of v coordinates are seen to disentangle the dynamical cross-coupling between the canonical momentum coordinates for ICMD models. Combining eq 25 for all i and j elements, we obtain the matrix expression

$$\langle v v^* \rangle = kT I_N \quad (26)$$

Equation 26 is the matrix version of the equipartition principle for ICMD models.

Having established the theory and nature of the equipartition principle for constrained and unconstrained ICMD models, we now turn to further exploring the properties of the $m(\theta)$ transformation matrix needed for defining the v modal coordinates. In the following sections, we derive closed-form analytical expressions that hold for general ICMD models for these quantities. These analytical expressions form the basis of low-order computational algorithms for working with coordinates and consider the tractable use of our theoretical results in practical applications.

3. PHYSICAL TO MODAL COORDINATE TRANSFORMATIONS

When working with multiple coordinate representations, as a practical matter (e.g., during molecular dynamics simulations), there is a need to be able to transform between the physical and modal coordinates. In our case, we need to be able to go between the v modal and the $\dot{\theta}$ physical velocities. From eq 17, we observe that the $m(\theta)$ and $l(\theta)$ matrices are needed to carry out these coordinate transformations so that

$$v = m^*(\theta)\dot{\theta} \text{ and } \dot{\theta} = l^*(\theta)v \quad (27)$$

We now look into the issue of obtaining these coordinate transformation matrices. The configuration dependent $J(\theta) \in \mathcal{R}^{3n \times N}$ Jacobian matrix relates Cartesian generalized velocities \dot{x} to the ICMD $\dot{\theta}$ velocities via the expression

$$\dot{x} = J(\theta)\dot{\theta}, \text{ where } J(\theta) \triangleq \begin{pmatrix} \frac{\partial x_1}{\partial \theta_1} & \dots & \frac{\partial x_N}{\partial \theta_N} \\ \vdots & \vdots & \vdots \\ \frac{\partial x_{3n}}{\partial \theta_1} & \dots & \frac{\partial x_{3n}}{\partial \theta_N} \end{pmatrix} \quad (28)$$

This Jacobian can be used to obtain the following expression for the ICMD mass matrix:

$$\mathcal{M}(\theta) = J^*(\theta) M J(\theta) \quad (29)$$

where $M \in \mathcal{R}^{3n \times 3n}$ denotes the constant, diagonal matrix with the atom masses along the diagonal. \mathcal{M} is in fact the mass matrix for the Cartesian model.

For BAT models, $N = 3n$, and $J(\theta)$ is square and invertible. The structure of the BAT system Jacobian and its determinant play an important role in entropy studies for molecular systems.^{10,23} Indeed, for BAT models $m(\theta)$ is simply

$$m(\theta) = J^*(\theta) M^{1/2} \quad (30)$$

This expression for $m(\theta)$ is both square and invertible and together with its inverse provides the desired coordinate transformation matrices for BAT ICMD models.

The situation is quite different once holonomic constraints are present such as for TAMD ICMD models. Due to the constraints, $N < 3n$, while eqs 28 and 29 still hold, the $J(\theta)$ matrix for constrained ICMD models is neither square nor invertible. Thus, eq 30 is no longer usable since it yields a nonsquare (and thus noninvertible) $m(\theta)$ matrix. An option then is to use eq 29 to explicitly evaluate the mass matrix followed by a numerical factorization step to obtain a square and invertible $m(\theta)$ matrix.

3.1. Analytical Expressions for $m(\theta)$ and $l(\theta)$. In this section, we use spatial operators to develop analytical expressions that lead to recursive, low-order computational algorithms for transforming between the v and $\dot{\theta}$ coordinates. The end result will be an algorithm that implements the eq 27 transformations without requiring the explicit evaluation of the $m(\theta)$ and $l(\theta)$ matrices. While these procedures are valid with or without holonomic constraints, they are essential when holonomic constraints are present. The developments we describe assume that the ICMD model has a tree topology (such as for BAT and TAMD models). The extensions for closed-chain topology models are possible using constraint embedding techniques¹⁹ but are not discussed here.

Spatial operators are a valuable technique for analyzing the dynamics of ICMD models and developing computational dynamics algorithms.¹⁹ They have been used to develop the $O(N)$ algorithms for solving the ICMD equations of motion⁶ that have been applied to study molecular dynamics problems.^{20,21} The following describes key analytical spatial operator expressions for the square factorization and inversion of the mass matrix:¹⁹

$$\begin{aligned} \mathcal{M} &= \mathcal{H}\phi M \phi^* \mathcal{H}^* \\ \mathcal{M} &= [I + \mathcal{H}\phi \mathcal{K}] \mathcal{D} [I + \mathcal{H}\phi \mathcal{K}]^* \\ [I + \mathcal{H}\phi \mathcal{K}]^{-1} &= [I - \mathcal{H}\psi \mathcal{K}] \\ \mathcal{M}^{-1} &= [I - \mathcal{H}\psi \mathcal{K}]^* \mathcal{D}^{-1} [I - \mathcal{H}\psi \mathcal{K}] \end{aligned} \quad (31)$$

The first expression defines the Newton–Euler operator factorization of the mass matrix \mathcal{M} in terms of the \mathcal{H} hinge articulation, the ϕ rigid body propagation, and the M link spatial inertia operators. While this factorization has nonsquare factors, the second expression describes an alternative factorization involving only square factors with block diagonal \mathcal{D} and block lower-triangular $[I + \mathcal{H}\phi \mathcal{K}]$ matrices. This factorization involves new spatial operators that are associated with the articulated body (AB) forward dynamics algorithm^{24,25}

Table 1. Recursive, Base-to-Tip Algorithms for Converting between the $\dot{\theta}$ and ν Coordinates Using eq 33 for Serial-Topology Systems

$\nu = \mathcal{D}^{1/2}[I + \mathcal{H}\phi\mathcal{K}]^*\dot{\theta}$	$\dot{\theta} = [I - \mathcal{H}\psi\mathcal{K}]^*\mathcal{D}^{-1/2}\nu$
$\mathcal{V}(N+1) = 0$	$\mathcal{V}(N+1) = 0$
for $k = N \dots 1$	for $k = N \dots 1$
$\mathcal{V}^+(k) = \phi^*(k+1, k)\mathcal{V}(k+1)$	$\mathcal{V}^+(k) = \phi^*(k+1, k)\mathcal{V}(k+1)$
$\nu(k) = \mathcal{D}^{1/2}(k)[\dot{\theta}(k) + \mathcal{G}^*(k)\mathcal{V}^+(k)]$	$\dot{\theta}(k) = \mathcal{D}^{-1/2}(k)\nu(k) - \mathcal{G}^*(k)\mathcal{V}^+(k)$
$\mathcal{V}(k) = \mathcal{V}^+(k) + \mathcal{H}^*(k)\dot{\theta}(k)$	$\mathcal{V}(k) = \mathcal{V}^+(k) + \mathcal{H}^*(k)\dot{\theta}(k)$
end loop	end loop

for the system. The next expression describes an analytical expression for the inverse of the $[I + \mathcal{H}\phi\mathcal{K}]$ operator. Using this leads to the final analytical expression for the inverse of the mass matrix. These operator expressions hold generally for tree-topology systems irrespective of the number of bodies, the types of hinges, the specific topological structure, and even for the case of nonrigid links.¹⁹

From the second equation in eq 31, we can identify a square $m(\theta)$ that satisfies eq 15's $\mathcal{M}(\theta) = m(\theta) m^*(\theta)$ relationship to obtain the following analytical expressions for the desired coordinate transformation matrices for ICMD models:

$$m(\theta) = [I + \mathcal{H}\phi\mathcal{K}]\mathcal{D}^{1/2}, \quad l(\theta) = \mathcal{D}^{-1/2}[I - \mathcal{H}\psi\mathcal{K}] \quad (32)$$

We have thus obtained explicit expressions for the transformation matrices needed to go between the ν and the $\dot{\theta}$ coordinates, and which lead to the following version of the transformation expressions in eq 27:

$$\nu(\theta) = \mathcal{D}^{1/2}[I + \mathcal{H}\phi\mathcal{K}]^*\dot{\theta}, \quad \dot{\theta} = [I - \mathcal{H}\psi\mathcal{K}]^*\mathcal{D}^{-1/2}\nu \quad (33)$$

Evaluation of either of the above expressions in principle requires $O(N^2)$ computations for the evaluation of the matrices and the matrix/vector products.

However, the special internal structure of the spatial operators allows us to entirely avoid evaluating these matrices and instead carry out the required matrix/vector products recursively with just $O(N)$ cost,^{19,25} and the recursive algorithms corresponding to the eq 33 transformations are shown in Table 1. Each of these recursions proceeds from the ICMD base toward the tips of the ICMD tree. The algorithm on the left transforms the physical $\dot{\theta}$ velocities into the ν modal coordinates, while the algorithm on the right does the converse. The intermediate $\mathcal{V}(k) \in \mathbb{R}^6$ quantity in the recursions is the combined angular and linear velocity of the k th coordinate frame. The computational cost of these algorithms scales linearly with the number of degrees of freedom. For notational simplicity, the algorithms in the table are for serial topology systems, and the more general tree topology versions are described in ref 19.

In summary, the spatial operator results in this section provide a way to carry out the coordinate transformations with $O(N)$ cost, and without requiring the expensive evaluation of any of the configuration dependent \mathcal{M} , m , or l matrices.

4. THEORETICAL IMPLICATIONS FOR VELOCITY INITIALIZATION

At the start of a molecular dynamics simulation, initial velocities need to be assigned to the generalized velocity coordinates in a manner that is consistent with the Boltzmann distribution of thermal energy. The simulation temperature for the simulation

determines the overall kinetic energy to be assigned to the system.

4.1. Cartesian Models. For Cartesian simulations, the equipartition principle in eq 7 implies that the kinetic energy can be independently assigned to each of the $\dot{x}(i)$ velocity coordinates using a Boltzmann distribution with mean of $kT/2$ such that

$$\langle M^{1/2}\dot{x} \dot{x}^* M^{1/2} \rangle = kT I_{3n} \quad (34)$$

4.2. Unconstrained ICMD Models. Since the equipartition principle does not hold for the physical (θ, p) coordinates in an ICMD model, such a procedure cannot be directly used to initialize the $\dot{\theta}$ generalized velocities to properly distribute the thermal energy. Since the equipartition principle is available for Cartesian models, a commonly used option is to begin by assigning the \dot{x} Cartesian atom velocities using the above-described Cartesian equipartition principle and then transition to the $\dot{\theta}$ ICMD generalized velocities. For the full-dimensional BAT ICMD models, such a transition to $\dot{\theta}$ is easily carried out using the relationship

$$\dot{\theta} = J^{-1}(\theta)\dot{x} \quad (35)$$

We can check that this procedure is correct by verifying that the ICMD equipartition principle in eq 26 holds. Toward this, observe that

$$\langle \nu \nu^* \rangle \stackrel{30}{=} \langle M^{1/2} J \dot{\theta} \dot{\theta}^* J^* M^{1/2} \rangle \stackrel{35}{=} \langle M^{1/2} \dot{x} \dot{x}^* M^{1/2} \rangle \stackrel{34}{=} kT I_{3n} \quad (36)$$

Thus, as we might intuitively expect, we can conclude that for BAT coordinates, the procedure of initializing the Cartesian velocities, followed by a transformation to the BAT velocities via eq 35, is statistically correct.

4.3. Constrained ICMD Models. For constrained ICMD models, this procedure for transforming Cartesian velocities to ICMD velocities breaks down. For the constrained case, $N < 3n$ and the $J(\theta)$ Jacobian is nonsquare and noninvertible, and eq 35 cannot be used. Instead, the Cartesian velocities need to be mapped to the lower-dimensional ICMD velocities space. Let $P \in \mathbb{R}^{N \times 3n}$ denote such a mapping matrix so that

$$\dot{\theta} = P\dot{x} \quad (37)$$

We again evaluate $\langle \nu \nu^* \rangle$ along the lines of eq 36 to obtain

$$\langle \nu \nu^* \rangle = m^* P P^* m kT \quad (38)$$

For this expression to be consistent with the ICMD equipartition principle in eq 26 requires that the P mapping matrix be such that $m^* P P^* m$ is the identity matrix. One value of P that satisfies this requirement is

$$P = \mathcal{M}^{-1} \mathcal{H} \phi \mathcal{M}^{1/2} \quad (39)$$

because then

$$m^* P P^* m = m^* M^{-1} M M^{-1} m = m^* M^{-1} m = I_N^{15,16}$$

This P is indeed the correct mapping matrix that ensures that the Cartesian model procedure for distributing thermal energy does so correctly for the ICMD model as well. Unlike the *ad hoc* projection techniques used in practice,²⁶ this procedure provides a thermodynamically rigorous method for initializing the velocities in ICMD models from Cartesian velocity assignments. While theoretically correct, a practical disadvantage is that the P matrix in eq 39 requires the expensive computation of the mass matrix inverse.

Instead of this expensive Cartesian velocities based initialization technique, we can exploit the ICMD equipartition principle to develop a much simpler and direct procedure for correctly initializing (constrained and unconstrained) ICMD simulations where the kinetic energy assignment obeys the required Boltzmann distribution. The procedure makes use of the modal coordinates equipartition principle in eq 26 to initialize the v_i ICMD velocity variables with mean $kT/2$ energy distributed in accordance with the Boltzmann distribution. Once all the modal coordinates have been initialized, we convert them to $\hat{\theta}$, ICMD physical velocities, using the $O(N)$ recursive algorithm on the right of Table 1 as was discussed in section 3.1. Observe that in contrast with eq 39, this procedure does not require the explicit computation of the mass matrix inverse.

5. CONCLUSIONS

Cartesian MD models are widely used, and a rich body of accompanying theory has evolved that addresses a broad range of topics including statistical mechanics, free energy computations, canonical models, numerical integration techniques, etc. to guide their correct use. In contrast, the use of ICMD models, especially constrained ICMD models, is not common. This stems from their added complexity as well as a lack of theoretical understanding of their behavior given the fundamentally different nature of such models. We have begun addressing several issues related to ICMD models to improve the effective use of ICMD simulations. In this paper, we have derived the equipartition principle for ICMD models, by introducing a new set of noncanonical modal coordinates. This principle applies to both the unconstrained and constrained types of ICMD models. This sets the stage for rigorous velocity initialization and the calculation of torsional entropy from ICMD trajectories.^{5,6,9–11,18,27} We have implemented and tested the use of modal coordinate velocities in ICMD simulations and applied it to study protein folding and protein homology model refinement.^{20,21} Much still remains to be done in developing, validating, and maturing ICMD techniques in areas such as the choice of constraints, structure preserving numerical integrators, entropy analysis, and their application to problems such as studying protein domain motion, protein structure refinement, etc.

Turning our attention to computational issues, we use spatial operators to obtain analytical expressions for the transformations needed to go between the modal and physical velocity coordinates. Additionally, we show that the transformations can be carried out via low-order recursive algorithms that entirely avoid the expensive need for computing the transformation matrices. The availability of such low-order computational algorithms allows us to consider ideas beyond

theory and explore the use of modal coordinates for other ICMD dynamics problems.

Such modal coordinates were originally identified as a set of diagonalizing coordinates that decoupled the ICMD (non-Hamiltonian) equations of motion.^{19,28} A remarkable property of the modal coordinates is the orthogonality to the Coriolis forces term in the equations of motion—a property that does not hold for equations of motion based on physical velocity coordinates. This orthogonality property has been shown to simplify control and stability analysis for constrained ICMD like systems. We believe that modal coordinates hold promise for the development of model reduction and numerical integration techniques for ICMD dynamics that we plan to address in future research.

■ ASSOCIATED CONTENT

§ Supporting Information

The detailed steps in Tolman's derivation²² of the equipartition relationship in eq 4. This information is available free of charge via the Internet at <http://pubs.acs.org>.

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Notes

The authors declare no competing financial interest.

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