QAARM: quasi-anharmonic autoregressive model reveals molecular recognition pathways in ubiquitin

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ABSTRACT

Motivation: Molecular dynamics (MD) simulations have dramatically improved the atomistic understanding of protein motions, energetics and function. These growing datasets have necessitated a corresponding emphasis on trajectory analysis methods for characterizing simulation data, particularly since functional protein motions and transitions are often rare and/or intricate events. Observing that such events give rise to long-tailed spatial distributions, we recently developed a higher-order statistics based dimensionality reduction method, called quasi-anharmonic analysis (QAA), for identifying biophysically-relevant reaction coordinates and substates within MD simulations. Further characterization of conformation space should consider the temporal dynamics specific to each identified substate.

Results: Our model uses hierarchical clustering to learn energetically coherent substates and dynamic modes of motion from a 0.5 μs ubiquitin simulation. Autoregressive (AR) modeling within and between states enables a compact and generative description of the conformational landscape as it relates to functional transitions between binding poses. Lacking a predictive component, QAA is extended here within a general AR model appreciative of the availability of large datasets of protein folding trajectories as well as atomic trajectories that cover the native-state dynamics and folding and unfolding pathways of the entire foldome, called Dynameomics (van der Hagen et al., 2010), has allowed scientists to simulate over 2000 proteins with a combined timescale of 340 ps. Projects such as Folding@home (Beberg et al., 2009) have also accelerated the availability of large datasets of protein folding trajectories as have specialized hardware, such as Anton (Shaw et al., 2007), field-programmable gate-arrays (FPGA; Alam et al., 2007), and GPUs (Harvey et al., 2009).

The availability of such datasets, while useful, has created new challenges in (i) extracting low-dimensional, biophysically-relevant coordinates that elucidate how the protein functions (for example, how a protein recognizes its binding partner), (ii) separating the landscape spanned by the simulations (or even groups of simulations) into a coherent set of conformational substates, (iii) quantifying the intrinsic structural and dynamical properties within a substate and finally, (iv) determining transition rates between these conformational substates. Indeed, important dynamical phenomena within simulated trajectories must be extracted from an enormous quantity of non-specific, ambient fluctuations. Clustering techniques for mining this noisy conformational space often use structural similarity measures, such as root-mean square deviation (RMSD) which quantifies an average value of structural deviation. However, functional motions need not elicit large global RMSD values; indeed, localized protein regions commonly exhibit small but important flexibility. These observations motivated us to examine the statistical nature of atomic fluctuations from long timescale simulations (Ramanathan et al., 2009, 2011b). Our studies across multiple simulations (and

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multiple force-fields) reveal that functionally relevant motions generally occur rarely. These events are reflected in higher-order correlations, manifested in long-tailed spatial (fluctuation) distributions (Mao et al., 1982). Techniques reliant on second-order statistics (variance) are poorly suited to resolve such higher-order correlations in the data, and we have observed that linear orthogonal bases (as in principal component analysis (Amadei et al., 1993)) poorly describe some energy landscapes. Thus, the current frameworks to analyze long timescale trajectories do not guarantee that identified states are correlated with biophysically relevant events.

We recently put forward a low-dimensional representation of protein motions at long timescales using a novel technique, quasi-anharmonic analysis (QAA; Ramanathan et al., 2011a). QAA partitions the conformational landscape using fourth-order spatial-fluctuation statistics and detects substates with energetic coherence. Each region contains conformers that show similarity with respect to biophysically relevant order parameters. The insights gained from QAA were effectively used to resolve higher-order dependencies in spatial fluctuations in the context of molecular recognition and enzyme catalysis.

While QAA effectively captures spatial correlations, it lacks a stochastic model of the underlying dynamics and substrate transitions. To address this shortcoming, we build autoregressive (AR) models to both encode local protein dynamics accessible within energetically coherent substates and permit transitions between connected regions in the landscape. We call this method the quasi-anharmonic autoregressive model (QAARM). Within a QAA-derived subspace, metastable states and their transition rates are extracted using hierarchical Markov clustering which provides parameter sets for the second-order AR model. We show that the learned AR model can be extrapolated to synthesize trajectories of arbitrary length. We exploit the time-invariant statistical regularities within protein motions to investigate equilibrium fluctuations of ubiquitin, a widely studied protein involved in the proteosomal degradation pathway. We show that QAARM can extract and synthesize pathways by which ubiquitin adapts its binding surface to recognize a variety of substrates.

3 APPROACH

An overview of QAARM is shown in Figure 1. MD simulation data is first processed to remove rotational and translational degrees of freedom. QAA is then applied (Section 5) which outputs a reduced dimensional representation of the original MD data. Motivated to detect biophysically relevant energy wells, or highly populated regions, in the low-dimensional QAA space, we next use a simple Markov diffusion model to cluster the conformations into metastable substates (Section 6). Local dynamics within each substate are then captured by a linear, second-order AR model (Section 7) which explicitly models spatial fluctuations. The AR model thus extends the time-insensitive QAA model by considering temporal relationships between successive MD frames.
4 MOLECULAR DYNAMICS SIMULATION OF HUMAN UBIQUITIN

Ubiquitin, a small globular protein, is involved in the proteosomal degradation pathway. It consists of 76 residues and folds into a well defined β-grasp fold. Ubiquitin’s structure is evolutionarily conserved across all eukaryotes, consisting of five anti-parallel β-strands ($\beta_1 - \beta_5$) as well as two α-helices. The primary binding surface (R1 in Fig. 3) of ubiquitin is composed of a small number of residues proximal to the flexible $\beta_1 - \beta_2$ and $\beta_3 - \beta_4$ loops. A secondary binding interface consists of the $\beta_4 - \alpha_2$ region. Ubiquitin binds to over 300 or more targets in the human cell and naturally has been the focus of many experimental and computational efforts to characterize molecular recognition (Meisenberg et al., 2006).

The protocol for simulating ubiquitin in solution has been described in detail in Ramanathan and Agarwal (2009). Briefly, eight crystal structures of ubiquitin (PDB codes: 1UBQ, 1P3Q, 1S1Q, 1TBE, 1YW, 2D3G, 2G45 and 2FCQ) were used for our simulations. Each simulation was carried out using the AMBER suite of tools, and each production run lasted a total of 62.5 ns. Hydrogen atoms were simulated using SHAKE algorithm, while electrostatics were evaluated using the particle mesh-ewald (PME) technique. A cut-off of 10 Å was used for long-range interactions (electrostatic and van der Waals). Conformations were stored every picosecond resulting in a total of 62.5 ns of sampling for the ubiquitin backbone. For analyses only C$\alpha$ atoms were used. All trajectory processing was performed with MATLAB.

5 QUASI-ANHARMONIC REPRESENTATION OF PROTEIN DYNAMICS

QAA is a general, statistically rigorous approach to identify non-Gaussian and rare behavior within extensive atomistic MD trajectories. It utilizes higher-order statistics of protein motions and is not restricted to orthogonal basis directions, a major compromise of existing techniques. QAA identifies energetically coherent substates in the conformational hierarchy and also possible transitions between these substates, consistent with the understanding that proteins sample from a hierarchical, multi-level energy landscape, with minima/maxima separated by energy barriers (Frauenfelder et al., 1988, 1991). Internal protein motions, driven by thermal energy in the solvent, enable proteins to explore this rugged landscape.

Here, we summarize quasi-anharmonic representation of protein motions in long timescale simulation trajectories based on diagonalization of a tensor of fourth-order statistics. This tensor describes positional fluctuations and their couplings. We use an efficient algebraic technique called joint-diagonalization of cumulant matrices (JADE), a well known algorithm in the machine learning literature for analyzing multi-variate data (Cardoso, 1999).

First, we assume that overall rotation/translation degrees of freedom have been removed and hence that positional fluctuations are centered around the origin. Second, second-order correlations are removed from the fluctuation data. In particular, a covariance matrix $G$ is estimated: $G=E(\vec{\alpha}\vec{\alpha}^T)$, which is then diagonalized by orthogonal eigenvectors $B$ and eigenvalues $\Sigma$ using $G=\Sigma B B^T$, followed by elimination of second-order correlations in $\vec{\alpha}$ with $\vec{\alpha}=\Sigma^{-1/2}B^T\vec{\alpha}$, leaving $E(\vec{\alpha}\vec{\alpha}^T)=I$, an identity matrix of size 3N×3N for N atoms under consideration.

Fourth, the fourth order dependencies denoted by the sum of the cross-cumulant terms are minimized, a procedure equivalent to diagonalizing the tensor $K$. No closed form solution exists for diagonalizing a tensor, however an approximate solution can be found using efficient algebraic techniques, such as Jacobi rotations (Golub and Van Loan, 1996). Just as the eigenbasis $B$ diagonalizes the covariance matrix $G$, a rotation matrix $J$ can be found which approximately diagonalizes the cumulant tensor $K$, leading to: $\hat{\vec{\alpha}}=J\vec{\alpha}.

Substituting for $\hat{\vec{\alpha}}$ from above: $\hat{\vec{\alpha}}=J\Sigma^{-1/2}B^T\vec{\alpha}$, thus $\hat{\vec{\alpha}}=U^{-1}\vec{\alpha}$ implying $U=BS^{-1/2}J^T$.

Thus, $U$ represents anharmonic modes of motion derived by minimizing the fourth-order dependencies in positional fluctuations, in addition to eliminating the second-order correlations (as is the case with quasi-harmonic analysis). Unlike in approaches that use principal component analysis, $U$ can be non-orthogonal and hence intrinsically coupled. The anharmonic modes of motion $U_i$ each a column vector of matrix $U$, are sorted decreasingly by amplitude $|\langle U_i \rangle|$.

Finally, we paint each conformer in the QAA subspace by internal energy, the sum of electrostatic and Van der Waals interactions (computed with NAMDenergy; Phillips et al., 2005) over each conformation. We emphasize that resultant energy coherence within observed substates is an emergent property of the method, that is, conformer internal energies are not considered during the projection onto the QAA subspace.

5.1 Results: organizing ubiquitin conformational landscape into energetically homogenous regions

From the original simulation consisting of nearly 500 000 conformations (0.5 ns), 10 000 equally spaced conformations were collected for training the QAA basis. We performed QAA within a 30-dimensional subspace which covers 95% of the input variance. The anharmonic modes of motion reveal the exquisite ability of ubiquitin to modulate both the primary and secondary binding
We begin hierarchical clustering by constructing a Markov transition matrix using edge weights between conformer pairs. Weights are chosen according to distance within QAA-space between connected conformers.

We then initiate a Markov chain (or random walk) on the weighted undirected network. As Markov transition probabilities homogenize through diffusion, an implicit clustering emerges from the network. First, a set of nodes representing the putative clusters are identified. Then, a Markov transition matrix is newly constructed using this reduced representation. The principle behind this construction is that upon reaching a stationary distribution at the coarsest hierarchy level, the Markov chain has also converged at finer (more local) network levels. This consistency regulates the overall topology of the network and helps build a multi-resolution representation of metastable states.

We expect that fine-grained hierarchy levels will produce many small clusters containing close neighbors in QAA space; that is, most cluster members will be from the same time-window (and single trajectory). As Markov diffusion progresses (fine-grained to coarse), conformers that are more distant neighbors will be connected by edges in the diffused network, and will therefore be assigned to the same cluster. Thus, the hierarchical clustering can highlight dynamical connections between conformers at different timescales.

### 6 Hierarchical Clustering for Metastable Substates

Energy wells in the 30-dimensional QAA-space determine biophysically relevant substates; the structure and dynamics of each can be characterized through clustering. Neighboring conformers in QAA-space have similar internal energies (cf. Fig. 2) and thus are dynamically and kinetically related. To facilitate clustering, we model the MD trajectory as an undirected network where edges connect energetically adjacent conformers in QAA-space. We can then cluster this network using a hierarchical Markov diffusion framework. This approach is an adaptation of our earlier work developing spectral graph partitioning algorithms for segmenting natural images (Chennubhotla and Jepson, 2003, 2005), understanding protein dynamics and allosteric propagation (Chennubhotla and Bahar, 2006, 2007a), and relating signal propagation on a protein structure to its equilibrium dynamics (Chennubhotla and Bahar, 2007b).

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### 6.1 Markov diffusion framework

**Initialization**: the MD simulation is modeled as an undirected graph by placing an edge with weight 1 from each data point to its six nearest Euclidean neighbors in the QAA space. At hierarchy level \( t=0 \) each data point is considered a node. Let \( n_o \) be the number of trajectory frames. The \( n_o \times n_o \) adjacency matrix \( C_0 \) gives the edge weights between each data point pair and the \( n_o \times n_o \) diagonal degree matrix \( D_0 \), \( i \neq j \) gives the weight of the edge between data point \( i \) and \( j \) at hierarchy level \( t \). Nodes with high degrees can be seen as hubs, and nodes with very low degrees can be seen as isolates. The stationary distribution of the Markov chain is given by the normalized degree vector \( \pi_0(i) = \frac{D_0(i,i)}{\sum_j D_0(j,j)} \), and represents the probability of a Markov chain residing in a particular node after infinite iterations.

**Iteration**: for \( t = 1 \) until done:

1. Compute the diagonal degree matrix \( D_{t-1} \), with entries
   \[
   D_{t-1}(i,j) = \begin{cases} 
   \sum_{j=1}^{n_o} C_{t-1}(i,j) & i = j \\
   0 & i \neq j 
   \end{cases}
   \]

   and the Markov transition matrix \( M_{t-1} = C_{t-1} D_{t-1}^{-1} \).

2. Diffuse the Markov transition matrix by repeated multiplication \( M_{t-1}^t = M_{t-1} \times M_{t-1} \) to reveal distant connectivity.

3. Determine the \((n_o-1) \times n_o \) kernel matrix \( K_t \) to carry network information from hierarchy level \((t−1)\) to level \(t\). The kernel matrix is made up of a subset of \(n_o \times n_o \) columns of \( M_{t-1}^t \), which are selected so that all \(n_o\) points have some probability.

4. Solve \( \tilde{\pi}_t = K_t \tilde{\pi}_t \) for \( \tilde{\pi}_t \) with an expectation-maximization algorithm to find a low-dimensional representation \( \tilde{\pi}_t \) of the stationary distribution \( \pi_{t-1} \).
(5) Compute $C_t$ using $ar{\pi}_t$:

$$C_t = \text{diag}(\bar{\pi}_t) K_t \text{diag}(K_t \bar{\pi}_t)^{-1} K_t \text{diag}(\bar{\pi}_t)$$

where $K_t^T$ denotes the transpose of $K_t$ and $\text{diag}(\bar{\pi}_t)$ indicates the diagonal matrix formed from the vector $\bar{\pi}_t$.

(6) $t \rightarrow t+1$.

Termination: end if $m \leq 2$. At this point, the network has been divided into one or two clusters.

Backwards iteration along the hierarchy allows computation of an $(m_{t-1} \times m_t)$ ownership matrix $O_t$ for each hierarchy level $t$, in which $O_t(i,j)$ gives the probability that data point $i$ belongs to cluster $j$ at level $t$ of the hierarchy:

$$O_t(i,j) = \frac{K_t(i,j) \bar{\pi}_t(j)}{\sum_{k=1}^{m_t} K_t(i,k) \bar{\pi}_t(k)}$$

where $\sum_{j=1}^{m_t} O_t(i,j) = 1$. The ownership matrix gives the probability distribution for the likelihood that a data point belongs to any metastable state of the trajectory, providing a soft partitioning of the data. A hard partitioning is determined by assigning each data point to the cluster to which it has maximal ownership probability.

6.2 Results: characterizing metastable substrates in the ubiquitin landscape

The connectivity matrix $C_0$ at clustering initialization is shown in Figure 3. The connectivity matrix shows several regions of high cross-talk. Iterative diffusion of the Markov chain derived from this connectivity matrix, followed by kernel selection, results in six hierarchy levels with 10 000, 4486, 978, 78, 11, and 2 clusters at each respective level.

To provide parameters for the AR model (Section 7), a membership threshold must be chosen that is fine enough to capture local dynamics, but still coarse enough to allow flexibility. We chose a membership threshold such that all cluster members were reachable from the cluster center within 50 ps, where a subsate’s center is defined as the closest conformer to the mean of that subsate. The mean QAA-space distance between conformers in successive frames is $\bar{d}$, and the standard deviation is $\sigma_d$. The hierarchy level at which 99.7% of the conformers are within $\bar{d} + 3\sigma_d$ of their subsate center is selected for further processing. Following this criterion, AR analysis was pursued using statistics from level 4 of the hierarchy.

Four cluster centers from the connectivity matrix are shown for example clusters in Figure 3. Clusters can be mapped from QAA-space onto the connectivity matrix to visualize accessibility between substrates. As an example, dynamically distant clusters are illustrated in Figure 3 by the red and green enclosed regions. The metastable substrates identified share significant similarities in both conformational and energetic space, however, they do not interact directly in QAA-space. This produces a partitioning of the landscape that is quite unique from the perspective of understanding ubiquitin’s equilibrium fluctuations: the landscape’s extremia represent distinct conformations of ubiquitin’s binding regions. Note that while $\beta_1 - \beta_2$ and $\beta_1 - \beta_4$ adapt an ‘open’ conformation in the structure shown in green (average separation of over 18 Å), the red structure shows the binding regions ‘close’ to each other (average separation of 13.5 Å). Thus, the inherent motions of ubiquitin involve sampling the two metastable states with almost exclusively no cross-talk. However, note that both the red and green structures can interconvert between the metastable states highlighted in gray. These metastable states represent the so-called intermediates which are necessarily visited before sampling either open or close conformations. Intermediate metastable states also highlight the importance of ancillary structural changes that ubiquitin might have to undergo in order to sample either the open or close conformations. These changes are predominantly located along $\beta_2 - \alpha_1$ and the C-terminal tip of $\alpha_1$ helix. Thus, for the opening and closing of the binding region in ubiquitin, our pathways deduced from the Markov transition matrices reveal that it is energetically more favorable to undergo conformational changes along the two regions highlighted in gray.

7 BUILDING AR MODELS

Motivated by the need for a compact, linear and generative model of ubiquitin’s dynamics, we extend our findings from QAA and hierarchical clustering with a stochastic AR model inspired by problems in control theory and signal processing (Blake and Isard, 1998). Understood as a second-order stochastic differential equation that has been sampled at regular intervals, the model relates each successive protein conformation to the previous two. It consists of an appearance model and a dynamic model, which can be conceptualized, respectively, as encoding the protein in a meaningful low-dimensional (embedded) space and modeling characteristic motions within that subspace. Because we learn summarizing parameters for the protein’s dynamics in the model, we can synthesize extrapolated trajectories of arbitrary length. As a contrast to molecular dynamics methods, where the system and environment are simulated and dynamics result, the approach here models dynamics explicitly and exploits the statistical regularities intrinsic to a natively fluctuating protein. Within this approach, time-evolution of the protein’s conformation $\bar{\pi}_t$ results from coupling the
The dynamical model, Equation (7), exploits our knowledge of past states \( \vec{\overline{\omega}_t} = U \vec{\tilde{\omega}}_t + \vec{\varepsilon}_t \) where weights \( \vec{\omega}_t \) spanned by \( \vec{\varepsilon}_t \) upon mapping each embedded state back to full conformational space. The basis chosen here, \( U \), is the first 30 anharmonic modes which are extracted using QAA and which span the conformational subspace available to the dynamic model. Both deterministic and stochastic elements are contained in the model’s dynamic component [Equation (7)]. The deterministic element is a second order Markov model in which the state at time \( t \), \( \vec{\omega}_t \), is a linear combination of states \( \vec{\omega}_{t-1} \) and \( \vec{\omega}_{t-2} \). Stochasticity is introduced by the Gaussian driving distribution \( \vec{\varepsilon}_t \), which quantifies motions that are not fully captured by the linear model. More temporal information is available to this model than to a first order model; we show that this permits characterization of complex motion patterns that extend over several timeframes (or MD conformations during training). Distinct from the connectivity matrix in Section 4, the transition matrices \( A_1 \) and \( A_2 \) here constitute the second-order transition matrices of the stochastic process and must be learned from training simulation data. In the following subsections we address learning these dynamical model parameters and generating synthetic trajectories.

### 7.1 Learning the dynamical model

The dynamical model, Equation (7), exploits our knowledge of past states (conformations) to propose a future state. Before we can compute transition matrices \( A_1 \) and \( A_2 \) from training data, we first project the ubiquitin simulation into the embedded 30-dimensional QAA-space to yield training states \( \vec{\omega}_t \):

\[
\vec{\omega}_t \equiv U^T \vec{x}_t, \tag{8}
\]

where columns of \( X \), \( x_1 \ldots x_F \), are \( 3N \) vectors carrying the protein’s coordinates (for \( N \) residues). Following the derivation put forward in Hyndman (2007), the AR model is defined sequentially over the weights:

\[
\vec{\omega}_3 \approx A_1 \vec{\omega}_2 + A_2 \vec{\omega}_1
\]

\[
\vec{\omega}_4 \approx A_1 \vec{\omega}_3 + A_2 \vec{\omega}_2
\]

\[
\vdots
\]

\[
\vec{\omega}_F \approx A_1 \vec{\omega}_{F-1} + A_2 \vec{\omega}_{F-2} \tag{9}
\]

with unknowns \( A_1 \) and \( A_2 \). We concatenate state vectors and transition matrices with the notation \( W_{ij} \equiv [\vec{\omega}_i \, \vec{\omega}_{i+1} \ldots \vec{\omega}_j] \) and \( \mathbf{A} \equiv [A_1 \, A_2] \) to express the system in matrix form:

\[
W_{3 \ldots F} = \mathbf{A} W_{1 \ldots 2}^2 \quad \text{where} \quad W_{1 \ldots 2}^2 \equiv \begin{bmatrix} W_{1,2} & W_{1,2-1} \\ W_{1,2-1} & W_{1,2-2} \end{bmatrix} \tag{10}
\]

The total squared error between the true states and the predicted states is minimized with the Frobenius norm

\[
\mathbf{A} = \arg \min_{\mathbf{A}} \| A W_{1 \ldots 2}^2 - W_{3 \ldots F} \|_F. \tag{11}
\]

Generally the state subspace is much smaller than the number of observations (training simulation frames), so \( W_{ij} \) is rarely square. The solution to (11) then follows:

\[
\mathbf{A} = W_{3 \ldots F} W_{1 \ldots 2}^{-2}, \tag{12}
\]

where \( F^* = F \left( F F^T \right)^{-1} \) denotes the pseudo-inverse of a matrix \( F \). Representative \( A_1 \) and \( A_2 \) matrices are shown in Figure 4A. The stochastic term, \( \vec{\varepsilon}_t \), represents those dynamics that are inadequately captured by the second-order linear model, and is drawn from a Gaussian distribution with covariance equal to that of the prediction error.
We can conceptualize each substate's transition matrices as linearly
The learned transition matrices
frames compares with approximately 25 ns of MD simulation.
time step found in the training data; the 25 000 synthetic trajectory
to propagate the AR-derived dynamics than with conventional
Equations (6) and (7). Starting from a randomly selected frame
embedded to full conformational space is carried in the QAA basis
ubiquitin’s dynamics. Additionally, it should be noted that the
data (cluster membership for 10 000 training and testing frames is
the protein visited 76 of the 78 clusters present in the training
error averaged over the training sequence. That is,
\[ R = \frac{1}{\hat{w}_2} \sum_{x \in \mathcal{S}} \left[ P^{\hat{A}_1} \right] 
\]
where the prediction error is
\[ P = W_{1, T - 1} (A_1 W_{2, T - 1} + A_2 W_{1, T - 1})^{-1}. \]
(13)
Interpreted physically, each \( A_1 \) and \( A_2 \) pair encodes the local, time
invariant dynamics. The eigen-decomposition of \( [A_1 \ A_2] \) yields the
exponential decay constants \( \beta_m = \frac{1}{\lambda_m} \log \frac{1}{2} \) for these local dynamics,
where \( \lambda_m < 1 \) denotes any positive eigenvalue (Fig. 4B).

7.2 Synthesizing new motion sequences
The learned transition matrices \( A_1 \) and \( A_2 \), unique to each cluster,
can be used to generate novel structure sequences of arbitrary
length. That is, \( \hat{w}_2 \) and \( \hat{w}_1 \) now constitute the unknowns in Equations (6) and (7). Starting from a randomly selected frame
from our training trajectory, we propagate the model using only
the learned transition matrices. Within the QAA space defined by
the column vectors of \( U \), we compare each generated conformer
to the mean structure of every cluster. At every step, the nascent
trajectory is assigned to the cluster center with nearest Euclidean
distance, and permitted to evolve according to that cluster’s \( A_1 \),
\( A_2 \), and \( \hat{w}_1 \) until it moves closer to a different cluster center. We
generated a synthetic trajectory of 25 000 frames, during which the protein visited 76 of the 78 clusters present in the training
data (cluster membership for 10 000 training and testing frames is
shown in Fig. 4). Other than error/transition parameters and the
determined local mean of each cluster, no temporal information
from the training data was necessary for the time-evolution of
ubiquitin’s dynamics. Additionally, it should be noted that the
entirety of the generative process is carried out in the embedded
QAA subspace, and the appearance model, Equation (6), is only
used in post processing to return to full, 3N conformation space.
We can conceptualize each substate’s transition matrices as linearly
encoding local dynamics, whereas reconstruction information from
embedded to full conformational space is carried in the QAA basis
vectors \( U \). For less storage and computing resources are required to
propagate the AR-derived dynamics than with conventional
sampling. Temporally, the synthetic trajectory employs the same
time step found in the training data; the 25 000 synthetic trajectory
frames compares with approximately 25 ns of MD simulation.

7.3 Results: predicted pathways of molecular
recognition in ubiquitin
The underlying stochastic dynamical model allows us to synthesize
new conformations of arbitrary length. This is particularly useful
when one has to predict the binding mode of ubiquitin with another
protein. Note that in our simulations, ubiquitin was simulated in its
substrate-free form. However, when we synthesize 25 000
conformers from QAARM, its utility becomes quite evident. The
conformers show remarkable fluctuations along the flexible regions
of ubiquitin (highlighted in Fig. 5A). Further, these motions are
largely similar to the fluctuations in the ubiquitin simulations, as
evidenced by projecting the synthesized conformations back onto
the QAA basis space.

It is also interesting to note that the projection of the synthesized
conformers onto the QAA basis space reveals novel pathways of
ubiquitin binding. To illustrate this, we chose the PDB id: 2FIF
where ubiquitin interacts with Rabex-5 along the secondary binding
site of ubiquitin (\( \beta_2 - \alpha_1 \) and \( \beta_3 - \alpha_4 \) interface). We computed the estimated number of contacts each synthesized conformer would
form if it were to be superimposed onto the crystal structure. Since
we use only Cα atoms to generate the conformers, we consider
two atoms to be in contact whenever they are separated by less
than 7.3 Å (a standard practice in coarse-graining literature (Bahar
and Cui, 2003)). The results of this computation are illustrated
in Figure 5B. By projecting the synthesized conformers onto the
QAA basis space, we discover that a small number of conformers
(highlighted by the ellipse) form a large number of contacts with the
substrate. Furthermore, the other parts of the landscape (in QAA)
show meager contacts with the substrate. This allows us to pin-point
a specific mechanism by which only a small number of the generated
conformers can bind to ubiquitin in a specific manner. Although it
remains to be seen if these conformations are also energetically
favorable, we believe that QAARM has allowed one to predict
complex formation by exploiting the statistical regularities in the
substrate-free simulations of ubiquitin. Thus, in line with previous
studies that proposed conformational selection to be a predominant
pathway for recognizing binding partners in ubiquitin (Lange et al.,
2008), our studies also predict a similar mechanism (at least at the
Cα resolution).

8 DISCUSSION AND CONCLUSION
Well-sampled conformational space is more useful with
organizational principles which can describe and characterize
it. Methods for extracting meaningful features and events must
cope with longer simulations of increasingly larger and more
complicated systems, and should eventually be used for validating
and error-checking MD simulations themselves. The trajectory
studied here samples many of the unique binding poses ubiquitin
must adopt for specific recognition of diverse ligands, providing
a rich platform for studying functionally relevant structural
transitions. However, ubiquitin’s structural shifts are subtle when compared to those of hinge or multidomain proteins; that these motions and connecting pathways are distinctly resolved with our method speaks to the utility and suitability of higher-order statistics for decomposing conformational space.

We exploited long-tail spatial distributions in former work (QAA), and we extended it in this article with linear stochastic models which account for temporal dependencies. This allows us to explore specific, local dynamics accessible to a protein within energetically homogeneous wells. Clustering to determine substates was performed here within the 30-dimensional QAA subspace, and we plan to compare our identified substates to those from other clustering methods in the future. Additionally, increasingly subtle or energetically local behaviors can be encoded by learning AR models at successive clustering levels; how we couple AR models at potentially disparate hierarchical levels to give a coherent picture of protein fluctuations is a topic of future work. In addition, we plan to apply maximum entropy methods to enable the dynamics of even poorly-sampled energy wells to be incorporated into the AR-model. While we demonstrated our framework on ubiquitin, we have already used QAA on several other protein systems where we expect QAARM to be useful as well.

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REFERENCES


QAARM reveals molecular recognition pathways