I. INTRODUCTION

Soluble proteins are well-packed, and their packing densities may be as high as that of crystalline solids.1–3 Yet there are numerous packing defects or voids in protein structures, whose size distributions are broad.4 The volume \( v \) and area \( a \) of protein does not scale as \( v \approx a^{3/2} \), which would be expected for models of tight packing. Rather, \( v \) and \( a \) scale linearly with each other.5 In addition, the scaling of protein volume and cluster-radius5 is characteristic of random sphere packings. We define voids as topological features and develop a simple algorithm for their detection. For short chains, void geometry is examined by enumerating all conformations. For long chains, the space of void geometry is explored using sequential Monte Carlo importance sampling and resampling techniques. We characterize the relationship of geometric properties of voids with chain length, including probability of void formation, expected number of voids, void size, and wall size of voids. We formalize the concept of packing density for lattice polymers, and further study the relationship between packing density and compactness, two parameters frequently used to describe protein packing. We find that both fully extended and maximally compact polymers have the highest packing density, but polymers with intermediate compactness have low packing density. To study the conformational effects of void formation, we characterize the conformational reduction factor of void formation and found that there are strong end-effect. Voids are more likely to form at the chain end. The critical exponent of end-effect is twice as large as that of self-contacting loop formation when existence of voids is not required. We also briefly discuss the sequential Monte Carlo sampling and resampling techniques used in this study. © 2002 American Institute of Physics.

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void formation, as well as the scaling law of $R$ and wall interval of voids. In the final section, we summarize our results and discuss effective sampling strategy for studying the conformational space of voids.

II. LATTICE MODEL AND VOIDS

Lattice polymers are self-avoiding walks (SAWs), which can be obtained from a chain-growth model. Specifically, an $n$-polymer $P$ on a two-dimensional square lattice $\mathbb{Z}^2$ is formed by monomers $n_i, i \in \{1, \ldots, N\}$. The location $x_i$ of a monomer $n_i$ is defined by its coordinates $x_i = (a_i, b_i)$, where $a_i$ and $b_i$ are integers. The monomers are connected as a chain, and the distance between bonded monomers $x_i$ and $x_{i+1}$ is 1. The chain is self-avoiding: $x_i \neq x_j$ for all $i \neq j$. We consider the beginning and the end of a polymer to be distinct. Only conformations that are not related by translation, rotation, and reflection are considered to be distinct. This is achieved by following the rule that a chain is always grown from the origin, the first step is always to the right, and the chain always goes up at the first time it deviates from the $x$-axis. For a chain polymer, two nonbonded monomers $n_i$ and $n_j$ are in topological contact if they intersect at an edge that they share. If two monomers share a vertex of a square but not an edge, these two monomers are defined as not in contact.

When the number of monomer $n$ is 8 or more, a polymer may contain one or more void [Fig. 1(a)]. We define voids as topological features of the polymer. The complement space $\mathbb{Z}^2 - P$ that is not occupied by the polymer $P$ can be partitioned into disjoint components,

$$\mathbb{Z}^2 - P = V_0 \cup V_1 \cdots \cup V_k.$$ 

Here $V_0$ is the unique component of the complement space that extends to infinity. We call this the outside. The rest of the components that are disjoint or disconnected to each other are voids of the polymer. Because nonbonded monomers intersecting at a vertex are defined as not in contact, they do not break up the complement space. As an example, the unfilled space contained within the polymer in Fig. 1(b) is regarded as one connected void of size 4 rather than two disjoint voids of size 2. This choice is arbitrary, but is consistent with the definition of contact. A simple algorithm for void detection can be found in the Appendix.

III. VOID DISTRIBUTION BY EXACT ENUMERATION

A. Probability of forming voids and expected number of voids

The number of conformations $\omega(n)$ for an $n$-polymer up to $n = 25$ obtained by exhaustive enumeration is shown in Table I. The numbers of conformations for polymers up to

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FIG. 1. Voids of polymers in a square lattice. Unfilled circle represents the first monomer. (a) A void of size 1 is formed in this 17-mer. (b) The two monomers encircled shares a vertex but not an edge of a square and are not in topological contact. The unfilled space contained within the polymer is regarded as one connected void of size 4.
As the chain length grows, it is clear that both $p$ and $\bar{l}$ only by strongly connected unoccupied sites, namely, any voidly, what is the size of the wall of the polymer containing squares that are fully contained within the polymer. Let $v$ be the number of conformations of $n$-polymer with total void size $v$. The expected total void size $\bar{v}$ for the $n$-polymer is

$$\bar{v} = \frac{\sum_v \omega_v(n) \cdot v}{\omega(n)}.$$  

Figure 2(c) shows that the expected void size $\bar{v}$ increases with chain length $n$.

C. Wall size of void

For a void $V$ of size $v$, what is the required minimum length $l(V)$ for a polymer that can form such a void? Equivalently, what is the size of the wall of the polymer containing void $V$? Here we first restrict our discussion to voids formed only by strongly connected unoccupied sites, namely, any neighboring two sites of a void must be sharing at least one edge of the squares. We exclude voids containing weakly connected sites, where two neighboring sites are connected by only one shared vertex [Fig. 1(b)]. For $v = 1, 2, 3$, it is easy from the geometry of the voids to see that $l(V) = 8, 10, 12$, respectively. However, in general $l(V)$ also depends on the shape of the void. A void of size 4 can have five different shapes. If the void is of the shape of a $2 \times 2$ square, $l(4) = 12$. For the other four shapes, $l(4) = 14$.

For any strongly connected void, we find that the following general recurrence relationship for $l(v)$ holds:

$$l(v) = l(v - 1) + \begin{cases} 
2, & \text{if } \Delta \partial V = 3 \\
0, & \text{if } \Delta \partial V = 2 \\
-1, & \text{if } \Delta \partial V = 1 
\end{cases},$$

where $\partial V$ represents the boundary edges of void $V$, and $\Delta \partial V$ represents the net gain in the number of boundary edges introduced by the newly added unoccupied site. Although the number and explicit shapes of strongly connected voids of size up to 5 can be found in Ref. 29, there is no general analytical formula known for the number of shapes of a void of size $v$. This is related to the problem of determining the number of polyominos or animals (as in percolation theory) of a given size.

When weakly connected voids are also considered, there are more possible wall sizes for the void. For 22-mer, the number of different wall sizes observed for a void, strongly or weakly connected, at various size are shown in Fig. 3(a). Voids of size 5 have the largest diversity in wall size. This is of course due to the fixed chain length. A short chain such as the 22-mer has only a small number of ways for forming large voids. Figure 3(b) shows the average wall size for various void sizes in the 22-mer. The expected or average wall size $\bar{w}(n)$ for a void in an $n$-polymer can be calculated as

$$\bar{w}(n) = \sum_v w \cdot \frac{\omega_{v,w}(n)}{\omega_v(n)},$$

where $v$ is the void size, $w$ is the wall size of the void, $\omega_{v,w}(n)$ is the number of $n$-polymers containing a void of size $v$ with wall size $w$, and $\omega_v(n)$ is the total number of $n$-polymers with a void of size $v$. Figure 2(d) shows that $\bar{w}(n)$ increases with chain length. Wall size and void size are analogous to the area and volume of voids in three-dimensional space.

FIG. 2. Geometric properties of chain polymers by exhaustive enumeration. (a) The probability of void formation, (b) the expected number of voids contained in a polymer, (c) the expected void size, and (d) the expected wall size of voids. All these parameters increase with chain length.

FIG. 3. Voids of fixed size in 22-mers can have different shapes and thus sometimes different wall sizes. (a) The distribution of the number of observed different wall sizes for a void depends on the size of the void. Voids of size 5 have the maximum number of different wall sizes. (b) The expected wall size for voids of different size.
packing density 0.92 has the largest number (6756751) of conformations [Fig. 4(b)]. A similar relationship is found among conformations with 2 and 3 voids [Fig. 4(b)].

E. Compactness

Another important parameter that measures the packing of the lattice polymer is the number of nonbonded contacts $t$. It is related to the compactness parameter $\rho$, defined by Chan and Dill $^{12}$ as $\rho = t/t_{\text{max}}$, where $t_{\text{max}}$ is the maximum number of nonbonded contacts possible for an $n$-polymer. Compactness $\rho$ has been studied extensively in seminal works by Chan and Dill $^{12,23,31}$ Although $\rho$ is sometimes correlated with the compactness $c$, these two parameters are distinct. The relationship between compactness and expected packing density for chain polymer of length 14–22 is shown in Fig. 4. For all chain lengths, both maximally compact polymer ($\rho = 1$) and extended polymer ($\rho = 0$) have maximal packing density ($c = 1$), but polymers with low packing densities have intermediate compactness on average. Polymers with $\rho$ between 0.4 and 0.6 have lowest packing density and therefore tend to have larger void size. The explanation is simple. An extended lattice chain polymer has no voids, it therefore achieves maximal packing density of $c = 1$, but its compactness $\rho$ is 0. A maximally compact polymer with $\rho = 1$ also contains no voids, its $c$ is 1. On the other hand, nonmaximally compact polymers can have a range of packing densities.

D. Packing density

An important parameter that describes how effectively atoms fill space is the packing density $p$. In proteins, it is defined by Richards and co-workers as the amount of the space that is occupied within the van der Waals envelope of the molecule, divided by the total volume of space that contains the molecule. $^{3,30}$ It has been widely used by protein chemists as a parameter for characterizing protein folding. $^3$

Following this original definition, the packing density $p$ for the lattice polymer is

$$p = n/(n + v),$$

when a $n$-polymer has a total void size of $v$.

The expected packing density $\bar{p}(n)$ for an $n$-polymer can be calculated as

$$\bar{p}(n) = \sum_p p \frac{\omega_p(n)}{\omega(n)},$$

where $\omega(n)$ is the number of all conformations of $n$-mer, $\omega_p(n)$ is the number of $n$-mers with packing density of $p$. The scaling of $\bar{p}(n)$ with the chain length $n$ decreases roughly linearly between $n = 7$ and $n = 22$ [Figure 4(a)]. Because it takes at least two additional monomers to increase the size of a void by one, $\bar{p}(n)$ decreases only when $n$ is an odd number for short chains.

Although voids are packing defects, most conformations with voids have high packing density, namely, the total size of the voids is small. Among all conformations of the 22-mer containing one void, the number of conformations increases monotonically with packing density. The lowest packing density 0.52 has only 11 conformations, whereas the highest

IV. OBTAINING VOID STATISTICS FOR LONG CHAIN POLYMERS VIA IMPORTANCE SAMPLING

Sequential Importance Sampling: Geometrically complex and interesting features emerge only in polymers of sufficient length, which are not accessible for analysis by exhaustive enumeration, due to the fact that the number of possible SAWs increases exponentially with the chain length. Monte Carlo methods are often used to generate samples from all possible conformations and obtain estimates of feature statistics using those samples. However, when chain length becomes large, the direct generation of the SAWs using the rejection method (i.e., generate random walks on the lattice and only accept those that are self-avoiding) from the uniform distribution of all possible SAWs becomes difficult. The success rate $s_N$ of generating SAWs decreases exponentially, $s_N \approx Z_N/(4 \times 3^{N-1})$. For $N = 48$, $s_N$ is only 0.79%. $^{32}$

To overcome this attrition problem, a widely used approach is the Rosenbluth Monte Carlo method of biased sampling. $^{25}$

The task is to grow one more monomer for a $t$-polymer chain that has been successfully grown from 1 monomer after $t-1$ successive steps without self-crossing, until $t = n$, the targeted chain length. In this method, the placement of the $(t+1)$th monomer is determined by the current conformation of the polymer. If there are $n_t$ unoccupied neighbors for the $t$th monomer, we then randomly (with equal probability) set the $(t+1)$th monomer to any one of the $n_t$ sites. However, the resulting sample is biased toward more compact conformations and does not follow the uniform distribution. Hence each sample is assigned a “weight” to adjust for this bias. Any statistic can then be obtained from weighted aver-
age of the samples. In the case of the Rosenbluth chain growth method, the weight is computed recursively as \( w_t = n_p w_{t-1} \).

Liu and Chen\(^{33} \) provided a general framework of Sequential Monte Carlo (SMC) methods which extend the Rosenbluth method to more general setting. Sophisticated but more flexible and effective algorithms can be developed under this framework. In the context of growing polymer, SMC can be formulated as follows. Let \((x_1, \ldots, x_t)\) be the position of the \( t \) monomers in a chain of length \( t \). Let \( \pi_t(x_1), \pi_t(x_1, x_2), \ldots, \pi_t(x_1, \ldots, x_t) \) be a sequence of target distributions, with \( \pi_t(x_1, \ldots, x_t) \) being the final objective distribution from which we wish to draw inference from. Let \( g_{t+1}(x_{t+1}) \) be a sequence of trial distributions which dictates the growing of the polymer. Then we have:

**Procedure SMC (n)**

1. Draw \( x_1^{(j)}, j = 1, \ldots, m \) from \( g_1(x_1) \).
2. Set the incremental weight \( w_1^{(j)} = \pi_1(x_1^{(j)})/g_1(x_1^{(j)}) \) for \( t = 1 \) to \( n-1 \).
3. For \( j = 1 \) to \( m \):
   - Sampling for the \((t+1)\)th monomer for the \( j \)th sample:
     1. Draw position \( x_{t+1}^{(j)} \) from \( g_{t+1}(x_{t+1}) \).
     2. Compute the incremental weight:
        \[
        w_{t+1}^{(j)} = \frac{\pi_{t+1}(x_{t+1}^{(j)}) \cdot g_{t+1}(x_{t+1}^{(j)})}{w_t^{(j)} \cdot \pi_t(x_1^{(j)}, \ldots, x_t^{(j)})}. 
        \]

4. Endfor
5. Resampling
6. Endfor

At the end, the configurations of successfully generated polymers \( \{(x_1^{(j)}, \ldots, x_t^{(j)})\}_{j=1}^m \) and their associated weights \( \{w_n^{(j)}\}_{j=1}^m \) can be used to estimate any properties of the polymers, such as expected void size, compactness, and packing density. That is, the objective inference \( \mu_h = E[\pi(x_1, \ldots, x_n)] \) is estimated with

\[
\hat{\mu}_h = \frac{\sum_{j=1}^m \pi(x_1^{(j)}, \ldots, x_t^{(j)}) \cdot w_n^{(j)}}{\sum_{j=1}^m w_n^{(j)}},
\]

for any integrable function \( h \) of interests.

The critical choices that affect the effectiveness of the SMC method are (1) the approximating target distribution \( \pi_t(x_1, \ldots, x_t) \), (2) the sampling distribution \( g_{t+1}(x_{t+1}) \), and (3) the resampling scheme. In this study, we are interested in sampling from the uniform distribution \( \pi_t(x_1, \ldots, x_n) \) of all geometrically feasible conformations of length \( n \), which we call the final objective distribution. It can also be chosen to be the Boltzmann distribution when energy function such as the HP model\(^{11,34,35} \) is introduced.

The Rosenbluth method\(^{26} \) is a special case of SMC. Its target distributions \( \pi_t(x_1, \ldots, x_t) \) is the uniform distribution of all SAWs of length \( t \). Its sampling distribution \( g_{t+1}(x_{t+1}) \) is the uniform distribution among all \( n_p(x_1, \ldots, x_t) \) unoccupied neighboring sites of the last monomer \( x_t \), and the weight function is

\[
w(x_1, \ldots, x_t, x_{t+1}) = w(x_1, \ldots, x_t) n_p(x_1, \ldots, x_t).
\]

When there is no unoccupied neighboring sites (\( n_1(x_1, \ldots, x_t) = 0 \)), there is no place to place the \((t+1)\)th monomer. In this case, the chain runs into a dead end and we declare the conformation dead, with weight assigned to be 0.

In the case of Rosenbluth method, no resampling is used.

Similarly, the \( k \)-step look ahead algorithm\(^{32,36} \) chooses \( \pi_{t+1}(x_1, \ldots, x_{t+1}) \) being the marginal distribution of \( \pi_t(x_1, \ldots, x_{t+k}) \), the uniform distribution of all SAWs of length \( t+k \). Hence \( \pi_{t+1} \) is closer to the final objective distribution—the uniform distribution of all SAWs of length \( n \). Specifically,

\[
\pi_{t+1}(x_1, \ldots, x_{t+1}) = \sum_{x_{t+2} \ldots x_{t+k}} \pi_t(x_1, \ldots, x_{t+k}) \sim n_k(x_1, \ldots, x_{t+1}),
\]

where \( n_k(x_1, \ldots, x_{t+1}) \) is the total number of SAWs of length \( t+k \) \("grown" from \( x_1, \ldots, x_{t+1} \) \) \( i.e., \) with the first \( (t+1) \) positions at \( (x_1, \ldots, x_{t+1}) \). In the \( k \)-step look-ahead algorithm, the sampling distribution is

\[
g_{t+1}(x_{t+1}) = \frac{n_k(x_1 \ldots x_{t+1})}{n_{k+1}(x_1 \ldots, x_t)}.
\]

It chooses the next position according to what will happen \( k \) steps later. Namely, the probability of placing the \( t+1 \)th monomer at \( x \) is determined by the ratio of the total number of SAWs of length \( t+k \) grown from \( (x_1, \ldots, x_{t+1}) \) and the total number of SAWs of the same length \( t+k \) grown from one step earlier \( (x_1, \ldots, x_t) \). The corresponding weight function is

\[
w(x_1, \ldots, x_t, x_{t+1}) = \frac{n_k(x_1, \ldots, x_{t+1})}{n_k(x_1, \ldots, x_t)} \cdot \frac{n_{k+1}(x_1 \ldots x_{t+1})}{n_{k+1}(x_1 \ldots, x_t)} = \frac{n_{k+1}(x_1 \ldots, x_t)}{n_{k+1}^{*}(x_1 \ldots, x_t)}.
\]

Although it has higher computational cost, it usually produces better inference on the final objective distribution, with less \"dead\" conformations. The standard Rosenbluth algorithm is a 1-step look ahead algorithm.

To compare geometric properties estimated from sequential Monte Carlo method and those obtained by exhaust enumeration, we examine the expected number of voids and expected void size for polymer of chain length 14–22. Figure 5 shows that sequential Monte Carlo can provide very accurate estimation of these geometric properties of voids. Here 2-step look ahead is used, with Monte Carlo sample size of 100,000 and no resampling is applied.

The resampling step is one of the key ingredients of the SMC method.\(^{33,37} \) There are many cases where resampling is beneficial. First, note that it is unavoidable to have some
dead conformations during the growth. These chains need to
be replaced to maintain sufficient Monte Carlo sample size.
Second, the weight of some chains may become so relatively
small that their contribution in the weighted average [Eq.
(1)] is negligible. When the variance of the weights is large,
the effective Monte Carlo sample size becomes small.33,37,38
Third, for a specific function $h$, its value may become too
small (even zero) for some sampled conformations. In all
these cases, efficiency can be gained by replacing those con-
formations with “better” ones. This procedure is called “re-
sampling.” There are many different ways to do resampling.
One approach is rejection control,39 which regenerates the
replacement conformations from scratch. An easier approach
is to duplicate the existing and good conformations.33  
Specifically,

**Procedure** **RESAMPLING**

$m$: number of original samples.

$n = \{x_1^{(j)},...,x_m^{(j)}\}_{j=1}^m$: original properly weighted

samples for $j=1$ to $m$

Set resampling probability of $j$th conformation $\propto \alpha^{(j)}$

endfor

for $*=1$ to $m$

Draw $*j$th sample from original samples

$\{x_1^{(j)},...,x_m^{(j)}\}_{j=1}^m$ with probabilities $\{\alpha^{(j)}\}_{j=1}^m$

//Each sample in the newly formed sample is assigned a new weight.

//*$j$-th chain in new sample is a copy of $k$-th chain in original sample.

$w^{(*)j} = w^{(k)}/\alpha^{(k)}$

endfor

In the resampling step, the $m$ new samples

$\{x_1^{(*)j},...,x_m^{(*)j}\}_{j=1}^m$ can be obtained either by residual
sampling or by simple random sampling. In residual
sampling, we first obtain the normalized probability

$\tilde{\alpha}^{(j)} = \alpha^{(j)}/\Sigma \alpha^{(j)}$. Then $m\tilde{\alpha}^{(j)}$ copies of the $j$th sample are
made deterministically for $j=1,...,m$. For the remaining $m
- \Sigma m\tilde{\alpha}^{(j)}$ samples to be made, we randomly sample from
the original set with probability proportional to $m\tilde{\alpha}^{(j)}$

The choice of resampling probability proportional to $\alpha^{(j)}$
is problem specific. For general function $h$, such as the end-
to-end extension $\|x_n-x_1\|$, it is common to use

$\alpha^{(j)} = w^{(j)}$. In this case, all the samples in the new set have equal weight.

When the function is irregular, a carefully chosen set of $\alpha^{(j)}$
will increase the efficiency significantly.

The method of pruning and enriching of Grassberger40 is
a special case of the residual sampling, with $\alpha^{(j)} = 0$ for the
$k$ chains with zero weight (dead conformations), $\alpha^{(j)} = 2$ for
the top $k$ chains with largest weights, and $\alpha^{(j)} = 1$ for the rest
of the chains. Residual sampling on this set of $\alpha$ is com-
tpletely deterministic. The resulting sample consists of two
copies of the top $k$ conformations (each of them having half
of their original weight) and one copy of the middle $n-2k$
chains with their original weight. The $k$ dead conformations
are removed.

In our study of the relationship between compactness and
packing density, we use a more flexible resampling
method. Our focus is on the packing density among all con-
formations within certain range of compactness. In this case,
our object target distribution is the uniform distribution
among all possible SAW’s with compactness measure falling
within a certain interval, i.e., a truncated distribution. Al-
though compactness changes slowly as the chain grows, to
grow into a long chain it is possible that the compactness of
a chain evolve and cover a wide range during growth. Hence
we choose the uniform distribution of all possible SAWs of
length $t$ as our target distribution at $t$, and only select those
with the desired compactness at the end for our estimation of
the packing density. In order to have a larger number of usable
samples (i.e., to achieve better acceptance rate) at the end,
we encourage growth of chains with desirable compactness
through resampling. Specifically,

**Procedure** **RESAMPLING** ($m,d,c,$)

$m$: Monte Carlo sample size, $d$: steps of looking-back.

c: targeting compactness.

$k$: number of dead conformations.

Divide $m-k$ samples randomly into $k$ groups.

for group $i=1$ to $k$

Find conformations not picked in previous $d$ steps,

//Pick the best conformation $P_j$, for example

$P_j$—polymer with min$|c-c_j|$

Replace one of $k$ dead conformations with $P_j$

Assign both copies of $P_j$ half its original weight.

endfor

Here $d$ is used to maintain higher diversity for resampled
conformations.

Most polymers sampled by sequential Monte Carlo with
two step look-ahead but no resampling are well-extended
with few voids, as shown in Figs. 6(a) and 6(b). In Fig. 6(b),
the majority of the conformations have a higher packing den-
sity. They have small compactness ($<0.5$) and large packing
density. There are not enough compact conformations. As a
result, a small number of samples are accepted at the end
whose compactness falls within the desired interval of higher
than 0.5. By using the resampling step described above, we
were able to generate more samples near the desired compact-
ness value of 0.6 [Fig. 6(c)]. Figure 6(c) is a pure histogram
of compactness in the observed samples, without regard-
ing the weight of the samples. Here resampling is
applied at each sequential Monte Carlo growth step. Figure
6(d) shows that the resampling technique is also very effective
in shifting the samples to small packing density values,
the subject of several studies. 12,41 The asymptotic value of 

V. VOID DISTRIBUTION OF LONG CHAINS

We apply the techniques of sequential Monte Carlo with resampling to study the statistical geometry of voids in long chain polymers. Each Monte Carlo simulation starts with a sample size of 200,000, and we take the averaged values of 20 simulations. Resampling is carried out every 5 steps in the process of the chain growth. Figure 7(a) shows that the probability of void formation increases with the chain length. At chain length 105–110, about half of the conformations contain voids. At chain length 200, the standard deviation (8.5 \times 10^{-3}) is maximum. The expected number of voids [Fig. 7(b)] increases linearly with chain length. Similar linear scaling behavior is also observed in proteins.4 The expected wall size of void and void size also increase with chain length [Figs. 7(c) and Fig. 7(d)]. The expected packing density is found to decrease with chain length, which is consistent with the scaling relationship of void size and chain length shown in Fig. 7(d). The compactness \( \rho \) of chain polymer has been the subject of several studies.12,41 The asymptotic value of \( \rho \) we found is 0.18, slightly different from that reported in Ref. 41 (\( \rho = 0.16 \)), and is within the range of 0.16–0.24 reported in Ref. 12. Different resampling strategies are applied where dead conformations are removed and other conformations with the targeted property is duplicated. Resampling favors conformations with small radius-of-gyration in Figs. 7(a)–7(e), and conformations with large weight in Fig. 7(f).

To explore the relationship of packing density \( p \) and compactness \( \rho \), we use sequential Monte Carlo with 2-step look-ahead to sample 200,000 conformations, each with an appropriate weight assigned. This is repeated 20 times, and the weighted average values of the packing density at various compactness for chains with 60–100 monomers are plotted (Fig. 8). The compactness value corresponding to the minimum packing density seems to have shifted from 0.462 for the 22-mer by enumeration to above 0.5 for the 100-mer as obtained by sampling. However, the overall pattern of \( \rho \) and \( p \) found by Monte Carlo is very similar to the pattern found by enumeration for polymers with \( N \approx 22 \) [Fig. 4(d)]. Data shown in Figs. 8 and 4(d) are not redundant. Rather, they complement each other and together provide a full picture of the relationship of \( \rho \) and \( p \) for chain length between \( N = 14 \)–22 and \( N = 30 \)–100. The lowest packing density \( p_{\text{min}} \) of these lattice polymers occur at compactness \( \rho = 0.525 \). However, an accurate estimation of the value of asymptotic \( p_{\text{min}} \) as \( N \to \infty \) requires simulation of longer chains.
The accuracy of geometric properties of long chain polymers estimated by Monte Carlo can be assessed by the standard deviation obtained from multiple Monte Carlo runs.

VI. END EFFECTS OF VOID FORMATION

What is the effect of void formation on the size of conformational space? We consider the conformational reduction factor of voids. Following Refs. 12, 23, 31, we define the conformational reduction factor due to the constraint of a void as

$$R(n; i, j) = \frac{\omega(n; i, j)}{\omega(n)},$$

where $\omega(n; i, j)$ is the number of conformations that contains a void beginning at monomer $(i)$ and ending at monomer $(j)$, and $\omega(n)$ is the total number of conformations of $n$-polymers. $R(n; i, j)$ reflects the restriction of conformational space due to the formation of a void with wall interval of $k = |i - j|$. Figure 9(a) shows a 24-mer with one void that starts at $i = 4$ and $j = 23$. Its wall size is $k = 19$. Unlike self-contacts or self-loops, which was subject of detailed studies by Chan and Dill,12,23,31 all conformations analyzed here must contain a void. The polymer shown in Fig. 9(b) with a large loop has no void, and such polymers do not contribute to the numerator of $R$.

Figure 10(a) shows the reduction factor $R$ calculated by enumeration for voids at different starting positions with wall intervals $k = 7, 9, 11$. There are clearly strong end-effects: The reduction factor of voids of the same wall interval depends on where the void is located. $R$ decreases rapidly as the void moves from the end of chain towards the middle. Void formation is much more preferred at the end of chain.

Similar end effects of void formation are also observed for the 50-mer sampled by sequential Monte Carlo [Fig. 10(b)]. Because the exact total number of conformations of the 50-mer $\omega(50)$ is unknown, we plot the value of $R \times$ constant, where constant is common to all data points at different starting positions and wall intervals. Our interest is how $R$ changes its relative values.

The end-effect of voids has the same origin as the end-effect of self-contact, which has been extensively studied by Chan and Dill.12,23,31 Because of the effect of excluded volume, sterically it is less hindering to form a void at the end of a polymer. When a void is formed, the conformational...
space of the $k+1$ monomers between monomer $i$ and $j$, as well as the two tails become restricted. When the void is formed at the chain end, only one tail is subject to conformational restriction.

Void formation is different from self-contact. When monomer $i$ and $j$ form self-contact, it may involve the formation of a void, but it is also possible that there will be no unfilled space between $i$ and $j$. When a void is formed beginning at monomer $i$ and ending at monomer $j$, some monomers between $i$ and $j$ will have unsatisfied contact interactions. Self-contacting loops have been analyzed in previous theoretical studies$^{32,43}$ which have been confirmed by exhaustive enumeration.$^{23,31}$ An important study of the role of loop formation in understanding the disulfide bond and protein folding can be found in Ref. 44. Compared to non-bonded self-contact, the effect of conformational reduction is more pronounced for void formation. For the two-dimensional lattice, the ratios between reduction factors of self-contact at chain end and mid-chain of a sufficiently long polymer are 1.3, 1.4, 1.5, and 1.6 for $k=3, 5, 7,$ and 9, respectively,$^{23}$ whereas the ratios for voids at the chain end and the symmetric midpoint of the $N=22$ polymer are 3.4, 4.0, and 4.4, for $k=7$, 9, and 11.

We now consider the power-law dependence of $R(N;i,j)$ on the wall interval $k=[i−j]$. In the study by Chan and Dill,$^{31}$ the scaling exponent $\nu$ of the reduction factor $R$ and loop length $k=[i−j]$ for $R(N;i,j)\approx k^{-\nu}$ is found to be dependent both on $k$ and the location of the cycle in the chain. The values of $\nu$ for self-contact range from 1.6 when $k=N$ to 2.4 when the loop is in the middle of a long chain with two long tails. Because void formation involves at least 8 monomers, its scaling behavior is less amenable to exhaust enumeration, and application of Monte Carlo sampling is essential. Based on estimations from Monte Carlo simulation of void formation in the 50-mer, the value of $\nu$ depends on the void initiation position $l_0$ from the end of the polymer chain. $\nu$ ranges from $1.4 \pm 0.2$ for $l_0=1$ to $3.0 \pm 0.2$ for $l_0=8$ [Fig. 10(c)]. Our results show that the scaling exponent of $R$ with $k=[i−j]$ for void formation is similar to that of the self-contacting loop. This scaling exponent also depends on the location of the void. The exponent $\nu$ is estimated from the nonlinear least square regression fit of the data using the Gauss–Newton algorithm as implemented in the GNU package R. A cautionary note is that the estimation of standard error of $\nu$ is accurate asymptotically only for large samples,$^{45}$ and therefore maybe overly optimistic in our case, where the number of data points is very small. An accurate estimation of confidence interval of $\nu$ for small sample nonlinear regression is beyond the scope of this work.

VII. CONCLUSION

In this work, we have studied the statistical geometry of voids as topological features in two-dimensional lattice chain polymers. We define voids as unfilled space fully contained within the polymer, and have developed a simple algorithm for its detection. We have explored the relationship of various statistical geometric properties with the chain length of the polymer, including the probability of void formation $\pi_v$, the expected number of voids $\bar{n}_v$, the expected void size $\bar{v}$, the expected wall size of voids $\bar{w}$, packing density $\rho$, and the expected compactness $\rho$. Our results show that for chains of $>105–110$ monomers, at least half of the conformations contain a void. At about 150 monomers, there will be at least one void expected in a polymer. The expected wall size scale linearly with the chain length, and about 10% of the monomers participate in the formation of voids. We formalize the concept of the packing density for lattice polymers. We found that both the packing density and compactness decrease with chain length. The asymptotic value of compactness $\rho$ is estimated to be 0.18.

We have also characterized the relationship of packing density and compactness, which are two parameters that have been used frequently for studying protein packing. Our results indicate that packing density reaches minimum values between compactness 0.4–0.6. The effects of voids are studied by analyzing the conformational reduction factor $R$ of void formation. We found that there is a significant end-effect for void formation; the ratio of $R$ at chain end and at mid-chain may be twice as large as that of the $R$ factor for contact loops, where the formation of voids is not required.

In this study, we have applied sequential Monte Carlo sampling and resampling (SMC) techniques to study the statistical geometry of voids. SMC is essential for exploring the geometry of long chain polymers. The origin of SMC can be traced back to the work of Rosenbluth and Rosenbluth,$^{26}$ where the idea of placing the current monomer with probability dictated by the outcome of future steps was first formulated. Grassberger was the first to apply the technique of resampling by weight to grow the chain polymer.$^{33}$ Independently, Liu and Chen provided the general framework of Sequential Monte Carlo, which unifies for the first time the techniques of delayed sampling (look-ahead of future steps) and resampling by arbitrary statistical property. Although SMC has had many applications in science and engineering,$^{46}$ we report in this paper the first application of SMC for sampling a variety of rare events in growing polymers. Specifically, we make concrete novel applications of SMC in sampling rare conformations with the prescribed value of radius of gyration and compactness. Because the general framework of the SMC has not been described before for growing chain polymer, we also provide in this publication details of the validation of the method.

Sequential Monte Carlo allows the generation of an increased number of conformations with a variety of interesting characteristics. For example, we can replace dead conformations with existing conformations of highest weight, or conformations with highest compactness, or with the smallest radius of gyration. Figure 6 provided examples where the distribution of conformations of polymers obtained by SMC can be adjusted by resampling. In Fig. 11, we further elaborate on the general flexibility of SMC for sampling that targets on a variety of statistical properties, as well as the important fact that SMC maintains properly weighted samples, which is essential for any statistical inference.

Figure 11(a) shows the histograms of conformations of 100-mer at different packing density generated without resampling. Figure 11(c) shows the histograms of conformations
when resampling by weight and resampling by compactness \( \rho \) are used. To resample by weight, dead conformations are replaced with conformations of the highest weight. To resample by compactness, dead conformations are replaced with conformations of the lowest compactness. Note that the total number of surviving conformations that reach a chain length of 100 is much higher than without resampling. Resampling by compactness generates many more conformations with higher compactness. In Figs. 11(c) and 11(d), resampling is applied to every step of the chain growth process. Unlike Fig. 6(d), where resampling favors the compactness value of \( \rho = 0.6 \), resampling in Fig. 11(c) favors samples with the highest value of compactness \( \rho \). Other resampling schemes are possible, e.g., resampling by radius-of-gyration, by packing density. During resampling, the number \( k \) of dead conformations at each step of growth is identified and these are replaced with conformations of interest from \( k \) randomly divided groups. These conformations must have not been resampled in the previous four steps of the growth process to maintain sample diversity. Both histograms where resampling is used deviate from that of Fig. 11(a). Resampling by weight shifts the peak of the conformations to below 0.2, and resampling by compactness turns the histogram into bimodal. The latter produces a lot more conformations with compactness \( \rho > 0.4 \).

SMC sampling and resampling use biased samples since conformations are generated with a probability different from that of the target distribution. The bias is dictated by the different method of resampling and different choices of the number of steps of look-ahead in sequential Monte Carlo. An essential component of a successful biased Monte Carlo sampling is the appropriate weight assignment to each sample conformation. This is necessary because we need to estimate the expected values of the parameter such as packing density and void size under the target distribution of all geometrically feasible conformations. In Fig. 11(a), where each of the 100,000 starting conformations is generated by a two-step look-ahead without resampling, not every conformation is generated with the same probability and therefore is assigned a different weight accordingly. Figure 11(b) shows the weight-adjusted histogram, which is indicative of the probability density function at different compactness for the population of all geometrically feasible 100-mers. Figure 11(d) shows that when weights are incorporated and the area of the histogram normalized to the final number of surviving conformations, the weighted distributions of conformations using different resampling techniques have excellent agreement with the weighted distribution when no resampling is used [Fig. 11(b)]. All weighted histograms are normalized so the total area equals to the total number of surviving conformations reaching 100-mer. This example shows that by incorporating weights, the target distributions can be faithfully recovered even when the sampling is very biased.

Although sequential Monte Carlo sampling is very effective, the estimation of parameters associated with rare events remain difficult. In Fig. 10 where the conformational reduction factor \( R \) is plotted at various void initiation positions and wall interval lengths, voids starting at position 1 but with odd wall intervals \( (k \in \{1,13,\ldots,25\}) \) are much rarer, and it is unlikely that sequential Monte Carlo sampling with limited sample size can provide a large enough effective sample size for the accurate estimation of scaling parameters \( \nu \), where \( R(N;i,j) \approx k^{-\nu} \).

In this study, we are interested in the statistics of void geometry, and our target distribution is the uniform distribution of all conformations of length \( n \). With the introduction of an appropriate potential function and alphabet of monomers such as the HP model\(^{11,34,35} \) we can study the thermodynamics, kinetics, and sequence degeneracy of chain polymers when voids are formed in polymers. In these cases, our target distributions will be chain polymers under the Boltzmann distribution derived from the corresponding potential functions.

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**APPENDIX: VOIDS DETECTION IN TWO-DIMENSIONAL LATTICE POLYMER**

To detect voids in a polymer, we use a simple search method. For an \( I \times I \) lattice, we start from the lower-left corner. Once we found an unoccupied site \( u \), we use the breath-first-search (BFS) method to identify all other unoccupied sites that are connected to site \( u \). These sites are grouped together and marked as “visited.” Collectively they represent one void in the lattice. We continue this process until all unoccupied sites are marked as visited:
Algorithm VOIDDETECTION (lattice, l)

\( v = 0 \) // Number of voids

for \( i = 1 \) to \( l \)
    for \( j = 1 \) to \( l \)
        if site \((i, j)\) is unoccupied and not visited
            \( v \leftarrow v + 1 \)
            Mark \((i, j)\) as visited.
            BREADTHFIRSTSEARCH(lattice, \((i, j)\))
            Update the size of void \((i, j)\)
    endfor
endfor

Details of BFS can be found in algorithm textbooks such as Ref. 47.