# Knot Probability for Self-Avoiding Loops on a Cubic Lattice 

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#### Abstract

We investigate the probability for appearance of knots in self-avoiding loops (SALs) on a cubic lattice. A set of $N$-step loops is generated by attempting to combine pairs of $N / 2$-step self-avoiding walks constructed by a dimerization method. We demonstrate that our method produces unbiased samples of SALs, and study the knot formation probability as a function of loop size. Our results corroborate the conclusions of Yao et. al. with loops generated by a Monte Carlo method [1].


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Knots and links naturally appear in long polymers [2], and play a prominent role in biological systems and processes [3]. Examples include chromosomes during cell division [4], knots in bacterial DNA [5], or knots in the native states of proteins [6]. It can be shown rigorously that very long self-avoiding loops are always knotted [7]. However, the theoretical proofs do not provide the frequency of the knots, or the functional dependence of their frequency on loop size. Quantitative insight into this question was first provided by a numerical study of random walks on a lattice [8]. Excluded volume effects, or self-avoiding (SA) interactions, are certainly crucial for correct description of polymers [9]; however, their incorporation into numerical studies is not simple. Earlier studies considered continuum models of selfavoiding loop (SAL) polymers with varying degrees of self-repulsion [10, 11], and demonstrated that with increasing number of monomers $N$, the fraction of unknotted loops decreases as $\mathrm{e}^{-N / N_{o}}$. The characteristic size at which knots appear is surprisingly large: It increases from several hundred steps in the absence of self-avoidance, to hundreds of thousands for strongly SA polymers. Since the value of $N$ used in typical simulations does not exceed several thousands, for SAL one can assume that the probability of an unknotted configuration simply decays exponentially. The value of $N_{o}$ can then be extracted by noting that for $N \ll N_{o}$ the probability of the knotted configurations is $P_{N} \approx N / N_{o}$. A recent study by Yao et al. [1] investigated the knotting probability of SALs on a cubic lattice with $N \leq 3000$ and found $N_{o} \approx 2.5 \times 10^{5}$. Our results corroborate the above study using a different approach to generating SALs.

Generating sufficiently large numbers of SALs has been the main obstacle to the study of statistics of knots in polymers. Static methods for creating SA polymers one at a time have the advantage of producing configurations that are independent of each other. If we do not require the two ends of a polymer to meet, several methods generate samples of "properly weighted" configurations: For lattice or for continuum models with

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FIG. 1: The probability that two $N / 2$-step SAWs with the same origin terminate at the same point (full circles), and the probability of their forming a proper SAL (open circles). (These results were obtained in our simulations by including a 48-fold symmetry factor enhancement, as explained in the text.) The ratio between the latter and the former, i.e. the probability that the loop formed by the $N / 2$-step pairs is selfavoiding (diamonds) as a function of $N$.
"hard" potentials, this means that every configuration has the same weight. In the dimerization algorithm 12, an $N$-step SA walk (SAW) is created by generating two ( $N / 2$ )-step SAWs and attempting to concatenate them. (If the concatenated walk is self-intersecting, it is discarded and the pair creation process is restarted.) The resulting SAWs are properly weighted, i.e. each has the same weight. While this method is very efficient 13], it is not well suited for generating SALs: To produce a properly weighted $2 N$-step SAL, we could first generate two $N$-step SAWs, assume that they both start at the origin, and check whether they do not intersect and end at the same point creating a loop, discarding the pair if they do not form a proper $S A L$. However, the probability of two


FIG. 2: The solid line depicts the probability distribution for the end to end distance of a single self-avoiding walk of length 256. The dashed line corresponds to the "correct ensemble" in which two such walks accidentally meet at the same position. In Ref. [16], the former ensemble is used to generate instances of the latter, weighting the resulting configurations with the appropriate bias. The full circles are the distribution of the end-to-midpoint distance of actual, successfully generated, 512 -step SALs in our dimerization procedure.

SAWs in $d$ dimensions accidentally terminating at the same point is proportional to $R^{-d} \sim N^{-d \nu}$, where $R^{2}$ is the mean squared end-to-end distance of $N$-step SAWs, and in $d=3$ the swelling exponent is $\nu=0.588$ 14. Full circles in the Fig. 1 depict this decay with $N$. In addition, the probability that two such walks do not intersect each other decays as $N^{2(1-\gamma)}$, where $\gamma=1.158$ in $d=3$ 15], as demonstrated by the diamonds in Fig. Thus, successful formation of a three-dimensional SAL using this direct method is proportional to $N^{-2.08}$, as depicted by open circles in Fig. 1

To circumvent the problem of the rarity of cases where two SAWs starting from the origin terminate at the same point, Chen suggested 16] accumulating lists of SAWs. Whenever two SAWs in the list have the same end-toend distance, they are rotated to make their endpoints coincide, thus producing a loop. Keeping the information on large numbers of SAWs is computationally memoryintensive. A more serious concern is that the ensemble of generated loops is biased: The solid line in Fig. 2 depicts the probability distribution of the end-to-end distance $r$ for 256-step SAWs; the dashed line corresponds to the subset of cases where a pair of SAWs has the same endpoint. The latter is the correct ensemble for loops, while the former is the ensemble produced when accumulated SAWs are rotated and linked. This distinction in weight (bias) is well-known, and is properly corrected in Chen's algorithm. However, as in all bias-corrected methods, while the expectation value of a desired quantity is correctly reproduced, the variance of this quantity increases with system size. Essentially, bias-corrected methods at-


FIG. 3: A trefoil knot in a 64 -step SAL on a cubic lattice.
tempt to reconstruct one distribution from a tail of another distribution; the distributions moving further apart with size. Fortunately, as can be seen from Fig. 2] for moderate values of $N$ the distributions are not very different, and good results were obtained in Refs. 10, 11] by this method. Alternatively, Yao et al. 1] used a Monte Carlo pivoting method 17 to generate many SAL configurations starting from an initial loop on a cubic lattice. While this method produces correctly weighted configurations, they may be statistically dependent. Cognizant of this difficulty, Yao et al. sampled the system at time intervals significantly exceeding the decay time of geometrical correlations, and verified that the times of appearance of knots behave like in a Poisson process.

In this work we employ a direct unbiased approach to generating ( $2 N$ )-step SALs. We first use successive dimerizations to generate two $N$-step SAWs, and then check whether (if starting from the same origin) they form a SAL. As discussed before, the probability of successful pairing of two SAWs decays as $\sim N^{-2.08}$; this includes the rejection probability that two segments of a formed loop intersect. We find that the latter probability has only a weak dependence on the size of the loop. Indeed, the distribution of the distance between the origin and the 128th monomer in 256-step SALs, depicted by full circles in Fig. 2 practically coincides with the probability distribution (dashed line) of generating loops from two SAW segments, irrespective of their mutual intersections.

The small probability of two SAWs forming a loop can be enhanced 48 -fold, by taking advantage of symmetries of the lattice to consider only SAWs whose end-point coordinates $\vec{r}=(x, y, z)$ satisfy the relations $x \geq y \geq z \geq 0$. This is achieved by generating a regular $N$-step SAW,


FIG. 4: Full circles depict the probability that an $N$-step SAL forms a knot. Error bars indicate one standard deviation. For comparison, open circles show the results of Ref. [1].
and then performing the following transformations: If the coordinate $x$ of the end-point is negative, the walk is reflected with respect to $y-z$ plane; and similarly for the other end-point coordinates. If the end-point has $x<y$ then $x$ and $y$ coordinates are interchanged along the whole walk; with corresponding interchanges for other pairs of axes. As a result of these transformations, we reduce the space in which the end-point can be located by a factor of 48 , and thus increase the probability of forming a loop. In continuum, such reduction of space does not introduce any bias, since each SAW in the allowed subspace corresponds to 48 SAWs in the original space. This is, however, not true for SAWs ending on the boundaries of the allowed subspace; e.g. there are only 24 SAWs with $x=y>z>0$, and consequently loops created by SAWs ending at such points are underrepresented by a factor of 2 . In continuum, configurations with $x=y$ have zero measure, but on discrete lattices a finite fraction of loops have this property, thus, creating a slightly biased sample. Since this is a boundary effect, it decreases with the inverse linear size of the space considered, i.e. it will be proportional to $1 / R$.

The direct method is quite efficient for generating small loops. The minimal (trefoil) on a cubic lattice consists
of 24 steps [18], and the probability of its occurrence is extremely small. For $N=64$, we had to examine 510 million pairs of $32-$ step SAWs in order to find 1.4 million SALs, out of which 27 formed a trefoil knot of the type depicted in Fig. 3 At this point the probability to have a knot is $0.000022 \pm 0.000004$. We used the Alexander polynomial [19, 20] (at the value of its argument equal to -1 ) to determine the presence and type of a knot. Since almost all observed knots were trefoils, and very few more complicated knots were encountered, this invariant sufficed for our purposes. The limiting factor in our simulations was computer time, and we could not go beyond $N=1024$, for which several months of CPU on a multiple processor computer were necessary to reach sufficient accuracy. At this value of $N$, the probability to form SALs dropped to $10^{-5}$, even after the 48 -fold enhancement of the sampling. While the correction to bias in sampling symmetric configurations was important for $N=64$, it became negligible for $N=1024$.

Figure 4 depicts our results for the probability $p_{N}$ of having a knot in a SAL of length $N$. The curvature in the results for this range of values of $N$ prevents a reliable extraction of $N_{o}$ by a linear fit. Our two highest data points compare well with the lowest data points of Yao et al. 1] that are included for comparison. While our results give a slightly larger probability than in Ref. [1], the difference is only one standard deviation, and is not significant at this level of accuracy. We also note that out of the 59 knots detected for $N=512$, only two were not trefoils, consistent with the results of Ref. 1].

In conclusion, we used the most direct method for generating an unbiased ensemble of SALs on a cubic lattice (up to symmetry factors). The method does not require large memory, but is very time consuming. While quite efficient for small and moderate sized SALs, it is limited to loops of around 1000 steps, at which the probability of forming a knot is around half a percent. Our results are consistent with those of Ref. 1], and provide an independent support of the conclusions from Monte Carlo sampling.

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