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Growing self avoiding walk trees

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Abstract The Growing self avoiding walk model (GSAW) was proposed to explain statistical mechanics of the growth process in polymerization. Close examination of the model reveals that it is suited only for addition polymerization where only one monomer unit is added to the growing polymer chain. In this paper we propose a model for step growth or condensation polymerisation, where all of the monomer is converted first to dimer, all dimers are converted to tetramer etc. In the calculation of probabilities of the walker taking a step in a specified direction in the GSAW model the probability is the reciprocal of the number of steps available if the walker looks one step ahead. It is seen that our model for condensation polymerization GSAW can be generalized to the walker looking a finite number of steps ahead (instead of one only) for the purpose of calculation of probabilities. This is explained in detail in the first section of the paper. In the second section of the paper we explain the use of the Depth first search (DFS) algorithm in the calculation of probabilities and moments for the generalized growing self avoiding walk model. In the third section of the paper we report the exact values of the mean square end to end distances and relevant survival probabilities for the model. When GSAW was first proposed there was a controversy over whether it belonged to the same universality class as the True self avoiding walk $(v = \frac{2}{d+1})$ λ or that of the self avoiding walk $\left(v = \frac{3}{d+2}\right)$. At that time it was conclusively shown that the GSAW model cannot belong to the same universality class as the true self avoiding walk model. However it was never conclusively shown that $v = \frac{3}{d+2}$ for GSAW. In this paper we propose two methods of studying this problem. One method

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is rigorous analysis of the DFS algorithm. We explain how this algorithm can be used to study restricted random walks with finite memory and self avoiding walks. The second method proposed by us is a detailed analysis of the generalised GSAW model proposed by us. This paper is to be viewed as an introductory paper on a new model that should be of interest to both chemists and mathematicians.

Keywords Growing self avoiding walk · Depth first search trees · Condensation polymerization · Growth process in polymerization

1 Introduction

The growing self avoiding walk model (GSAW) was first proposed as a modification of the True self avoiding walk $[1-3]$ $[1-3]$. The modification was as follows: in the True self avoiding walk if the walker is trapped he is allowed to select a previously visited neighbouring site at random, whereas this is disallowed in the Growing self avoiding walk. The model was first proposed by Kremer and Lyklema [\[4](#page-12-2)[–7](#page-12-3)] and Majid et al. [\[8](#page-12-4)]. When the model was first proposed there was a controversy over whether it belonged to the same universality class as the True self avoiding walk $(v = \frac{2}{d+1})$ or that of the self avoiding walk $\left(v = \frac{3}{d+2}\right)$ [\[9\]](#page-12-5). At that time it was conclusively shown that the GSAW model cannot belong to the same universality class as the true self avoiding walk model. Further studies were carried out on other lattices as well [\[10](#page-12-6)[–13](#page-12-7)].

Close examination of the GSAW reveals that it is a model that is ideally suited for addition or chain growth polymerization. If we think of a polymer molecule as a necklace of beads (monomers), then the GSAW model could be thought of as stringing a necklace together bead by bead (single) from an infinitely large collection of beads. On the other hand if one were to construct a similar model for condensation polymerization we could think of all the beads in the collection forming dimer (until no single beads exist). Subsequently all the dimers form tetramers, all the tetramers form octamers etc. This idea is illustrated in Fig. [1.](#page-2-0)

In Fig. [1](#page-2-0) the arrow marked in red refers to the third step of walk. Case 1 refers to GSAW [\[4](#page-12-2)[–7\]](#page-12-3) where one monomer unit is being added at a time. This implies the third step has three possible vacant sites to visit and so the probability of a site being selected is 1/3. Case 2 refers to a condensation reaction wherein a dimer reacts with a dimer. We assume that one of the dimers is $a+X+Y$ as shown on the left side of the figure. Now for the second dimer there are 9 possibilities. All the possibilities are shown in the right side of the Figure. However it is seen that only 8 of these are allowed, the last one being disallowed as it results in a self intersection in the fourth step. As seen if the third step (marked in red) is to take place in the $+X$ direction, then all three possibilities are allowed and the probability of the third step in the +X direction is 3/8. Similarly for the third step in the $+Y$ direction the probability is 3/8. However it is clear from Fig. [1](#page-2-0) that the probability of the third step in $-X$ direction is only 2/8 = 1/4. It is hence seen that the probability of the walker taking the third step in a specified direction is different in the models for addition and condensation polymerization. In the model for condensation polymerization the walker has to look two steps ahead

Fig. 1 Calculation of probabilities for GSAW (0) and GSAW (1)

and enumerate the number of vacant sites. The probability of him taking a step in a particular direction then depends on ratio of the number of vacant sites after that step has been taken to the total number of vacant sites after two steps have been taken. This idea can then be generalized to the walker taking any finite number of steps ahead and it forms the basis for our model for condensation polymerization. In Fig. [2](#page-4-0) we illustrate the case of a four step walk in two dimensions, where the walker looks 1 and 2 steps ahead. We use the notation $GSAW(m-1)$ for the walker looking *m* steps ahead. Here we illustrate the case of the walker taking a step only in the $+X$ direction. The sum of the probabilities is 1/4. Symmetry dictated the sum of the probabilities is the same if the first step is taken along the $+Y$, $-X$, and $-Y$ directions. On the left column of the figure we display 4 step self avoiding walk as a figure and on the right side we report the probabilities of each step and the probability of the walk as a whole. For example in the first figure of *GSAW* (0) the probability of the first step is 1/4, the second step is 1/3, the third step is 1/3 and the final step is 1/2 and the total probability for the walk is computed as 1/72. Subsequently we provide a general definition for the probabilities based on these ideas.

Exact enumeration of the expectation of the square of the end to end distance and the survival probabilities calculated using the Depth first search (DFS) algorithm in two dimensions ($m = 1$ to 10) and three dimensions ($m = 1$ to 8) are reported in the third section of this paper.

1.1 Definition of probabilities for GSAW (*m* − 1) walks

Let S_{n+m} be the set of self avoiding walks of $n+m$ steps starting at the origin [\[14](#page-12-8)]. Let $P_n = (p(0), \ldots, p(n))$ be the sites of an *n* step self avoiding walk starting at the origin. Let $F_{n+m}(P_n)$ denote the subset of walks in S_{n+m} for which $P_n =$ $(p(0),..., p(n))$ are the first $n + 1$ sites and $|F_{n+m}(P_n)|$ is the cardinality of this subset. Let $P'_{n+1} = (p(0),..., p(n), p(n+1))$ be the sites of an $n+1$ step self avoiding walk starting at the origin whose first *n* sites are $p(0), \ldots, p(n)$.

We now define the probability of the $n + 1$ step being along sites p_n and p_{n+1} in $GSAW(m-1)$ as:

$$
pr (n + 1) = \frac{|F_{n+m}(P'_{n+1})|}{|F_{n+m}(P_n)|}, |F_{n+m}(P_n)| > 0.
$$
 (1)

 $pr(n + 1)$ is a conditional probability. It is the probability of the n+1th step being along sites p_n and p_{n+1} given that the walk has survived up to n steps. The probability of the walk $P'_{n+1} = (p(0), ..., p(n), p(n+1))$ in GSAW $(m-1)$ is given by:

$$
Prob\left(P'_{n+1}\right) = \prod_{i=1}^{n+1} pr(i) \text{ where } pr(i) \text{ is given by (1)}.
$$

Note: $|F_{n+m}I(P'_{n+1})| = 0$ for GSAW (0) if P'_{n+1} is a trap. Similarly if P_{n+1} leads into a trap and say the walker is trapped after *M* steps then $|F_{n+m}I(P'_{n+1})|$ is not equal to 0 for $m < M$ but $|F_{n+m}I(P'_{n+1})| = 0$ for m greater than or equal to M .

Fig. 2 Method of calculation of one step probabilities for GSAW (0) and GSAW (1) for a four step walk in two dimensions. The first step is in the +X direction. Since there is a symmetry factor of 4 for each such walk, the sum of the probabilities is 1/4. Likewise there are $+Y$, $-X$ and −Y directions and so the total probability is 1

There are 21 such walks whose probability is equal to 1/108 and 4 walks whose probability is 1/72

Thus, the sum of the probabilities of all walks in +X direction

is

$$
(4 * 1/72) + (21 * 1/108) = 1/4
$$

The sum of the probabilities of all walks in $+X$ direction = $1/4$

2 Depth first search trees

The DFS method in combination with the pivot algorithm has been used to estimate the connective constant of self avoiding walks $[15–17]$ $[15–17]$ The author along with a fellow worker has recently used the DFS tree to derive the generating function for a memory four walk [\[18](#page-12-11)]. The method used is to trace the search and keep track of the vertices in the DFS tree where self intersection occurs. The vertex in the tree at which this occurs is thereby deleted along with all its descendants. This information in then used to derive recursion formulae using the inclusion exclusion criteria followed by the search along the DFS tree. The algorithm used by us has been reported in Ref. [\[17\]](#page-12-10) and is being repeated here verbatim for the sake of continuity in discussion.

We first define the terms used in the algorithm (Graph theory terms commonly used such as vertex, level of a vertex, first visit to a vertex, last visit to a vertex are used without definition and are the same as in Bondy and Murthy [\[19](#page-12-12)]):

If $-\varepsilon_1, \varepsilon_1, -\varepsilon_2, \varepsilon_2, \ldots, -\varepsilon_d, \varepsilon_d$ are the 2*d* unit vectors in *d* dimensional Euclidean space.

F refers to the set $(-\varepsilon_1, \varepsilon_1, -\varepsilon_2, \varepsilon_2, \ldots, -\varepsilon_d, \varepsilon_d)$, accessible in that order. *l* (*v*) refers to the level of the vertex v_{n} , $t(v)$ refers to the time of visit to a vertex v_{n} , *first* (v) refers to the time of the first visit to v , *last*(v) refers to the time of the second (last) visit to *v*.

C refers to the family of *n* step self avoiding walks. This might refer to the co ordinates of the entire walk, or the moments of the end to end distance, radius of gyration or any such relevant parameter.

St refers to the Stack used in the algorithm.

Set the vertex $v := u$ refers to the co ordinates of the self avoiding walk resulting from appending the vector u to the self avoiding walk at the previous level.

Algorithm 1

INPUT: Number of steps n , dimension d , Family of unit vectors in d dimension \vec{F} .

OUTPUT: Family of self avoiding walks of *n* steps \mathbb{C} , $\sum_{i=0}^{n} C_i$, time of visit of each vertex of the DFS tree, time of first visit to each vertex of the DFS tree, time of second (last) visit to each vertex of the DFS tree.

- 1: Set $i := 0$ and $St := \varphi$.
- 2: Set the origin as the root of the tree r and set $v:=r$.
- 3: increment i by 1.
- 4: Set $t(v) := 1$, first(v) := $t(v)$, and $l(v) := 0$.
- 5: Place v at the top of the stack St .
- 6: for $j:=1$ to $j:=N$ do set $E(j):=F$
- 7: while St is non empty do
- 8: if $I(v) \le n$ do

9: set $k:=1$

 $10:$ if $E(k)$ is non empty do

2.1 Structure of the DFS tree for self avoiding walks of four steps in two dimensions

In the Figure given below we display a branch of DFS tree for 4 step self avoiding walks in two dimensions. The first number in the box represents the chronological order in which a vertex appears, 1 represents $(0,0)$, 2 represents $(-1,0)$, 3 represents (−2,0) etc. The second number represents the time of first visit to a vertex and the third number the time of last (second) visit to a vertex. To explain further the first walk to be stored is $[(0,0), (-1,0), (-2,0), (-3,0), (-4,0)]$ and this is given by the left most branch:

1 1 306, 2 2 77, 3 3 28, 4 4 11, 5 5 6 The second walk to be stored is $[(0,0), (-1,0), (-2,0), (-3,0), (-3,-1)]$ and this is given by the branch:

1 1 306, 2 2 77, 3 3 28, 4 4 11, 6 7 8

3 Exact enumeration

In Table [1](#page-8-0) we report the exact enumeration values of the conditional expectation of the square of the end to end distance of *n* step walks, given that the walk has survived up to that many steps in two dimension for *GSAW*(*m* − 1) for *m* from 1 to 10. The second number reported is $\sum_{\Omega} p_{\omega \varepsilon \Omega}$ and is equal to the sum of the probabilities of walks that survive up to the given number steps, reported up to 3 decimal places. This number is usually referred to as the partition function in the physics and chemistry literature. For example second number 0.997 in the GSAW (0) column for 8 steps means that the sum of the probabilities that survive up to 8 steps is 0.997 (some walks are trapped after 7 steps). When no second number is reported the sum of the probabilities is greater than 0.999. The first column refers to the Uniform distribution i.e. the probability of a walk of *n* steps is the reciprocal of the number of such walks. Values reported in all cases (including the first column) are calculated using the DFS algorithm. Values reported in the first column have been reported by other authors (for a much larger number of steps) [\[14\]](#page-12-8). Values in the second column have also been reported by other authors before [\[4](#page-12-2)[–6\]](#page-12-13).

In Table [2](#page-9-0) we report the exact enumeration values of the conditional expectation of the square of the end to end distance of n step walks, given that the walk has survived up to that many steps, in three dimension for $GSAW(m-1)$ for *m* from 1 to 8. No second number is reported as the sum of the probabilities (partition function in the physics and chemistry literature) is greater than 0.999 in all cases. The first column refers to the Uniform distribution i.e. the probability of a walk of *n* steps is the reciprocal of the number of such walks. Values reported in all cases are calculated using the DFS algorithm. Values reported in the first column have been reported by other authors (for a much larger number of steps) [\[14\]](#page-12-8). Values in the second column have also been reported by other authors before $[4-6]$ $[4-6]$ (Fig. [3\)](#page-10-0).

4 Discussion

Examination of Fig. [3](#page-10-0) will help in understanding the inclusion exclusion followed in the DFS tree. This then can be stated formally as a theorem for restricted random walks of finite memory with the uniform distribution.

First we explain some notation that is used:

All standard definition of Self avoiding walks apply [\[19](#page-12-12)].

Let C_n^{τ} be the number of memory τ restricted random walks of *n* steps in *d* dimension.

Forn $> 2\tau$, $2 < \lambda \leq \tau$, *let* $P_n^{\tau}(\lambda)$ be the number of restricted random walks of *n* steps in *d* dimension whose first $n - 1$ steps obey the memory τ condition, and whose *n*th step results in a λ step reversal. In other words $P_n^{\tau}(\lambda)$ is the number of

Table 1 Mean square end to end distance for GSAW (*m* −1) in two dimension The number in italics represents the probability that the walk has survived up to the given number of steps

Table Mean square end to end distance for GSAW (*m* 1) in three dimension

Fig. 3 Branch of DFS tree for 4 step SAW in 2D

*n*step restricted random walks of memory τ but whose head has a λ step self avoiding polygon.

For n > 2 τ , 2 < $\beta \leq \tau$, *let* $Q_n^{\tau}(\beta, \lambda)$ be the number of restricted random walks of *n* steps in *d* dimension whose first $\beta - 1$ steps obey the memory τ condition, whose βth step results in a β step reversal, whose next $n - 1 - β$ steps obey the τ memory condition, but whose last step results in a λ step reversal. In other words $Q_n^{\tau}(\beta, \lambda)$ is the number of *n*step restricted random walks of memory τ but whose tail has a β step self avoiding polygon and whose head has a λ step self avoiding polygon.

Then the following theorem holds:

Theorem 4.1

$$
C_n^{\tau} = [2d - 1] \left[C_{n-1}^{\tau} - \sum_{k=2}^{\frac{\tau}{2}} P_{n-1}^{\tau}(2k) \right] + \sum_{k=2}^{\frac{\tau}{2}} \sum_{j=2}^{\frac{\tau}{2}} Q_n^{\tau}(2k, 2j) \text{ for all } n \ge 2\tau.
$$

Proof First we note that:

$$
C_n^{\tau} = [2d - 1] C_{n-1}^{\tau} - \sum_{k=2}^{\frac{\tau}{2}} P_n^{\tau} (2k)
$$

Next using the reasoning on the comparison of $n - 1$ and *n* step DFS trees we find that: τ

$$
P_n^{\tau}(2k) = [2d - 1] \left[P_{n-1}^{\tau}(2k) \right] + \sum_{j=2}^{2} Q_n^{\tau}(2k, 2j)
$$

This theorem has been used to evaluate $\chi^4(z) = \sum_{n=0}^{\infty} C_n^4 z^n$ [\[17\]](#page-12-10) and work is in progress to evaluate this function for restricted random walks of higher memory. The method to be followed is to express $Q_n^{\tau}(\beta, \lambda)$ in terms of $P_i^{\tau}(\lambda)$ *f or i* < *n* and $P_i^{\tau}(\lambda)$ in terms of C_l^{τ} *f or l* < *i*.

Rigorous mathematical analysis of $GSAW(m - 1)$ walks is different from the analysis of self avoiding walks with uniform distribution in one very important respect, viz., the probabilities and expectation of the moments of the end to end distance are conditional probabilities and expectations in $GSAW(m - 1)$, the condition being that the walk survives attrition due to traps up to the given number of steps. In other words the conditional probability assigned to a walk of *n* steps given that the walk has survived up to *n* steps is equal to $\frac{\bar{p}_{\omega}}{\sum_{\omega \in \Omega} p_{\omega}}$ and the conditional expectation of the end to end distance is given by:

$$
\frac{\sum_{\Omega} r_{\omega \varepsilon \Omega}^2 p_{\omega \varepsilon \Omega}}{\sum_{\Omega} p_{\omega \varepsilon \Omega}}
$$

This quantity [\[4](#page-12-2)[–9](#page-12-5)] along with $\frac{\sum_{\Omega} r_{\omega\epsilon\Omega}^4 p_{\omega\epsilon\Omega}}{\sum_{\Omega} p_{\omega\epsilon\Omega}}$ and $\frac{\sum_{\Omega} r_{\omega\epsilon\Omega}^6 p_{\omega\epsilon\Omega}}{\sum_{\Omega} p_{\omega\epsilon\Omega}}$ have been studied [\[5\]](#page-12-14) by earlier authors.

In an earlier work the author and co worker had explained an Algorithm based on the Breadth first search tree [\[18](#page-12-11)] (BFS) and showed that the BFS and DFS trees are isomorphic. Both trees contain and enormous amount of information about SAW and GSAW (*m* − 1). The number of vertices at each level of the tree gives the number of self avoiding walks for the number of steps equal to the level. Also to borrow terms from genealogy (family tree) the probability of a vertex in the tree being selected in

 \Box

GSAW(0) is equal to the reciprocal of the number of siblings the vertex has plus one (for the vertex itself). In GSAW (1) it is equal to the ratio of the number of children the vertex has to the total number of children he and his siblings have and in GSAW (2) it is equal to the ratio of the number of grand children the vertex has to the total number of grand children he and his siblings have, and so on. So on a single run of a computer program that uses Algorithm 1 all the data in Tables [1](#page-8-0) or [2](#page-9-0) can be obtained. This explains the reason for deriving Theorem [4.1](#page-10-1) in an introductory paper on a model for condensation polymerization.

5 Conclusion

In this paper we:

- (1) Introduced a new model for condensation polymerization and showed how this can incorporated into a general model for polymerization based on a model for addition polymerization developed many years ago [\[4](#page-12-2)[–9\]](#page-12-5).
- (2) Showed how models for equilibrium and non equilibrium properties of polymers in good solvent can be studied rigorously using the Breadth first search and DFS techniques commonly used in computer science.

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