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Title: Mixing Time For A 3-Cycle Interacting Particle System: A Coupling Approach

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This thesis examines the mixing times for one-dimensional interacting particle systems. We use the coupling method to study the mixing rates for particle systems on the circle which move according to specific permutations e.g., transpositions and 3-cycles.

Mixing Time For A 3-Cycle Interacting Particle System: A Coupling Approach

by

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Major Professor, representing Mathematics

Chair of the Department of Mathematics

Dean of the Graduate School

I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request.

Matthew Jasper Eves, Author

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Academic

I am greatly indebted to my major advisor Yevgeniy Kovchegov for the time and guidance he has afforded me.

Personal

I wish to thank my wife Laurie for her love and patience as well as my family for their support and encouragement.

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1. INTRODUCTION

1.1. Mixing

The concept of mixing is one that is very intuitive and is something that is encountered on a daily basis. When someone is preparing food from a recipe, they are careful to mix the ingredients together to make a homogenous mixture. Another example that seems particularly apt is that of mixing paint to produce even colors. The different tints are added in small amounts and then mixed thoroughly. Mixing, in the context of a random process, is the point where each value taken by the random variable is equally likely. As a random process begins, some outcomes may not be possible in the short run, but as the process is allowed to unfold all outcomes in the state space become possible. We will be examining how long it takes for a certain process to become mixed.

1.1.1 Coupling

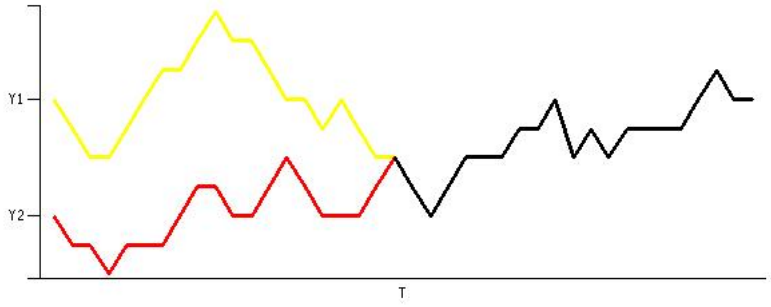
Coupling is a technique used in probability that makes comparisons between probability measures. Coupling is a very useful technique and is often used to simplify problems that would otherwise require many cumbersome calculations. More explicitly,

Definition 1.1.1.1 *A **Coupling** of two random variables X_1 and X_2 defined on probability spaces $(\Omega, \mathcal{F}_1, P_1)$ and $(\Omega, \mathcal{F}_2, P_2)$, respectively, is a new probability space $(\Omega, \mathcal{F}, P)$ over which exist the random variables Y_1 and Y_2 such that Y_1 is equal to X_1 in distribution and Y_2 is equal to X_2 in distribution.*

For two random Processes X_t and Y_t a coupling is a process $(X_t, Y_t)_{t=0}^{\infty}$ with the property that X_t and Y_t are processes with common transition matrix P (The processes may have different starting distributions).

Intuitively, we allow two random processes to take values according to their respective distributions, and the first time the two random variables take the same value at the same time, we cause the two random variables to take values according to a single distribution. That is, the two random variables move together or are "coupled". If we ignore one of the two random processes, we see that the other process takes values as it normally would without consideration for the ignored process. The idea is easily illustrated by Figure 1.1. Consider the random processes Y1 and Y2. At time T, the two processes take the same value and from then onward the processes act as one.

FIGURE 1.1: Coupling of Two Random Processes



1.1.2 Total Variation Distance

When talking about coupling two random processes that are distributed according to their respective probability distributions it is helpful to have a sense of "closeness" of the two probability distributions. We have seen that, with coupling, after a certain time we expect the two processes to continue following a single distribution. In order to determine the "closeness" of two distributions, we employ the total variation distance.

Definition 1.1.2.1 *The **Total Variation Distance** between two probability distributions, μ and ν on Ω is defined as*

$$||\mu - \nu||_{TV} := \max_{A \subset \Omega} |\mu(A) - \nu(A)|$$

Equivalently, for discrete probability distributions we have:

$$||\mu - \nu||_{TV} := \frac{1}{2} \sum_{x} |\mu(x) - \nu(x)|$$

1.1.3 Strong Stationary Times

It is helpful to consider a few definitions relating to mixing and coupling.

Definition 1.1.3.1 *T is a **stopping time** for the process $\{X_t\}$ if for the occurrence of the predefined event, A, we stop the process if $X_n = A$. Thus by looking at the values of the process up to time n: $X_0, \ldots, X_n$, we can determine that event A has occurred at time $\{T = n\}$*

Definition 1.1.3.2 *A stopping time T of the process $\{X_t\}$ is called a **strong stationary time** if $Prob[T < \infty] = 1$ and X_T has a stationary distribution, π, independent of T.*

Definition 1.1.3.3 *The **coupling time**, τ_{couple}, is the first time that two random processes have the same value at the same time:*

$$\tau_{couple} := \min_{t} \{X_t = Y_t\}$$

Definition 1.1.3.4 *The **mixing time**, τ_{mix}, is the first time that the total variation distance between two distributions is less than a predetermined value, ϵ:*

$$\tau_{mix} := \inf_{t} \{||\mu P^t - \pi||_{TV} \leq \epsilon\}$$

Definition 1.1.3.5 *The **mean hitting time** for a random process $\{X_n\}$ is the average amount of time needed for a process to reach a stopping time.*

From the previous definitions, we see that the coupling time and mixing time are clearly both stopping times. Similar definitions can be found in [2], [3], [6], [7] and [8].

1.1.4 Bounding Mixing Time

It becomes very convenient to know how the coupling time is related to the mixing time.

Theorem 1.1.4.1 *Let the mixing time and coupling time be defined as above. Then*

$$||P^t(x,\cdot) - P^t(y,\cdot)||_{TV} \leq P[\tau_{couple} > t]$$

Proof 1.1.4.1 *Suppose* $X_t \sim \nu_0 P^t$ *and* $Y_t \sim \mu_0 P^t$. *Let* $T = \tau_{couple}$ *for* (X_t, Y_t), *then*

$$\begin{aligned} ||\nu_0 P^t - \mu_0 P^t||_{TV} &= \frac{1}{2}\sum_{x\epsilon S} \big|Prob[X_t = x] - Prob[Y_t = x]\big| \\ &= \frac{1}{2}\sum_{x\epsilon S} \big|Prob[X_t = x, T > t] - Prob[Y_t = x, T > t]\big| \\ &\leq Prob[T > t] \end{aligned}$$

Now, clearly, since the total variation distance is less than the probability that the coupling time has not yet occurred, when the coupling time does occur(i.e. Prob$[T > t] = 0$), the total variation becomes zero, and we are ensured that the mixing time has already occurred for arbitrarily small epsilon. By the Markov inequality we see that the bound is $\tau_{mix} \leq \frac{1}{\epsilon} \max_{x_0} \mathbb{E}[T|X_0 = x_0]$. A sharper estimate can be made if higher moments of T are known.

1.1.5 Martingales

Martingales are also very helpful in finding bounds because they have many nice properties. We introduce a definition and a theorem that will be used.

Definition 1.1.5.1 *Given a random process* $\{X_n\}$ *with* $\mathcal{F}_n$, *the history of the process up to time n. We say the sequence of random variables* $\{M_n\}$ *with* $\mathbb{E}[|M_n|] < \infty$ *is a* ***martingale*** *with respect to* $\mathcal{F}_n$ *if:*

1. *Each M_n is measurable with respect to $X_0, \ldots, X_n$*

   and

2. *For each $m \leq n$;* $\mathbb{E}[M_{n+1}|\mathcal{F}_m] = M_m$

Theorem 1.1.5.1 ***Optional Stopping Theorem***. *Let M_n be a bounded martingale with respect to X_n (i.e., there is a constant C so that $|M_{T\wedge n}| \leq C$), and let T be a stopping time with respect to X_n, with $Prob[T < \infty] = 1$. Then*

$$\mathbb{E}[M_T] = \mathbb{E}[M_0]$$

Proof 1.1.5.1 *(Durrett,[2]) Since $M_{T\wedge n}$ is a martingale with respect to X_n, and from the fact that $\mathbb{E}[M_m] = \mathbb{E}[M_n]$ for $0 \leq m < n$, we have that $\mathbb{E}[M_0] = \mathbb{E}[M_{T\wedge n}]$. Now using the condition $|M_{T\wedge n}| \leq C$ it follows that*

$$\big|\mathbb{E}[M_0] - \mathbb{E}[M_T]\big| = \big|\mathbb{E}[M_{T\wedge n}] - \mathbb{E}[M_T]\big| \leq 2CProb[T > n] \to 0$$

as $n \to \infty$. So we must have $\big|\mathbb{E}[M_0] - \mathbb{E}[M_T]\big| = 0$. Therefore $\mathbb{E}[M_T] = \mathbb{E}[M_0]$

1.2. Statement of Problem

We begin with our model, the circle with n vertices with particle 3-cycles consisting of three adjacent points on the circle which move in the following manner:

$$\begin{aligned} \sigma := &\quad \text{shift particles to the right with wrapping} \\ \sigma^{-1} := &\quad \text{shift particles to the left with wrapping} \end{aligned}$$

Take for example three points with the particles represented by the values 001, here σ and σ^{-1} make the following shifts of the particles:

$$\begin{aligned} \sigma : &\quad 001 \to 100 \\ \sigma^{-1} : &\quad 001 \to 010 \end{aligned}$$

Each vertex on the circle rings with rate 1 according to an exponential waiting time. A vertex represented with the value 1 is considered a particle of interest while vertices with value 0 are considered generic.

With this model, we must find a reasonable estimate of the mixing time. That is, we ask how long we will wait until the probability that a particle of interest is located at a specific vertex is the same for all vertices. The goal is to estimate the mixing time using a coupling argument, and to ensure that the estimate is reasonable. The mixing time should be estimated for a general, large value n, and for a general number of particles of interest k $<$ n.

Previous work has shown by various methods that the bound on the mixing time should be $O(n^2 log(n))$. We seek to obtain such a bound via coupling.

1.3. Previous Work

There are several researchers who have studied mixing times for random processes. Here I only mention the few who's work has most impacted the ideas presented in this thesis. Aldus and Fill [8] have looked at many different models and methods. Ben Morris [5](and references therein) find the bound $O(n^2 log(n))$ for the d-dimensional torus using the chameleon process. Yuval Peres [7] has also worked in this area extensively. It is nearly impossible to talk about this subject without mentioning Persi Diaconis [6].

2. METHODS AND CONSTRUCTIONS

2.1. One Particle Model

Since each vertex on the circle rings with rate 1, according to an exponential waiting time, we wait $\frac{1}{n}$ for a vertex to ring and we wait n for a particular vertex to ring. If we have a single particle denoted by a 1 surrounded by zeros, then there are exactly three 3-cycles that include this specific particle. Within each 3-cycle we have the possibility of shifting by σ or σ^{-1}. Consider 00100 as a representation of this situation. Below we will demonstrate how each of the three 3-cycles moves according to σ and σ^{-1}. For the left most 3-cycle containing the particle of interest (001) we perform the permutations. The whole representation of the model is as follows:

$$\begin{aligned} &\ldots \underline{\mathbf{001}}00\ldots \\ \sigma \quad &\text{gives} \quad \ldots \underline{\mathbf{100}}00\ldots \\ \sigma^{-1} \quad &\text{gives} \quad \ldots \underline{\mathbf{010}}00\ldots \end{aligned} \tag{2.1}$$

Similarly for the center 3-cycle containing the particle of interest (010) we perform the permutations and show how the whole model is affected.

$$\begin{aligned} &\ldots 0\underline{\mathbf{010}}0\ldots \\ \sigma \quad &\text{gives} \quad \ldots 0\underline{\mathbf{001}}0\ldots \\ \sigma^{-1} \quad &\text{gives} \quad \ldots 0\underline{\mathbf{100}}0\ldots \end{aligned} \tag{2.2}$$

Finally, for the right most 3-cycle containing the particle of interest (100) we perform the permutations and show how the whole model is affected.

$$\begin{aligned} &\ldots 00\underline{\mathbf{100}}\ldots \\ \sigma \quad &\text{gives} \quad \ldots 00\underline{\mathbf{010}}\ldots \\ \sigma^{-1} \quad &\text{gives} \quad \ldots 00\underline{\mathbf{001}}\ldots \end{aligned} \tag{2.3}$$

We now notice that in each of the cases (2.1), (2.2), and (2.3) the particle of interest has moved from its original position by a distance of either 1 or 2 vertices. In cases (2.1) and (2.3) we see that one permutation results in a move of two vertices and the other permutation results in a move of only one vertex, while in case (2.2) both permutations result in a move of only one vertex. These observations lead us to think of the movement of the single particle as a random walk with two different step sizes. Since each individual permutation in each case is equiprobable, we can construct the probabilities associated with this random walk by distinguishing between the step sizes and the direction in which the particle moves. The permutations in each of (2.1), (2.2), (2.3) give us six total movements for the particle, two of which move one step right, two others move one step left, one moves two steps right, and the remaining movement moves two steps to the left thus giving Figure 2.1.

FIGURE 2.1: Random Walk Representation of the Single Particle Model

$$\text{Particle moves} = \begin{cases} \text{1 step right} & \text{with probability } \frac{1}{3} \\ \text{1 step left} & \text{with probability } \frac{1}{3} \\ \text{2 steps right} & \text{with probability } \frac{1}{6} \\ \text{2 steps left} & \text{with probability } \frac{1}{6} \end{cases}$$

2.1.1 Coupling With One Particle

In order to find a bound on the mixing time for the single particle model, we employ the concept of coupling. We consider two identical processes of the above described particle system. Each of the processes is allowed to move according to the given permutations individually until the single particle of interest occupies the same vertex in both

processes simultaneously. We then couple the two processes, or allow both processes to make identical permutations causing the two models to become indistinguishable. Consider the two processes A_n and B_n, two individual particle systems, each with a single particle of interest moving according to the permutations σ and σ^{-1} on the circle.

$$A_n : \quad \ldots 010000 \ldots$$

$$B_n : \quad \ldots 000010 \ldots$$

If we ignore the process B_n, it is as if it remains stationary, while A_n is allowed to move as normal, we are in essence finding the mean hitting time for the process A_n. In this case, the mean hitting time would correspond to an upper bound for the coupling time of the processes A_n and B_n.

2.2. Model For More Than One Particle

The two particle model follows the same process as the one particle model, the only difference is the presence of two particles of interest which will force us to devise a new coupling strategy.

2.2.1 Coupling With Multiple Particles

To create a coupling scheme that will allow us to find a bound on the coupling time, we consider two processes A_n and B_n. We define the manner in which each of the processes reacts depending on the location of the particles of interest. As a result, the two processes have the potential to become coupled. The situations we will be considering are those in which two particles are in the same 3-cycle when its exponential clock rings. Consider the following situation:

$$\begin{array}{lccccccc} A_n: & \ldots & 0 & \boxed{1} & \boxed{1} & \boxed{0} & 0 & \ldots \\ B_n: & \ldots & 0 & \boxed{0} & \boxed{1} & \boxed{1} & 0 & \ldots \end{array}$$

Here to ensure coupling we allow the two processes to move only in one of three ways. The particular permutations for each of the processes are the same permutations σ, σ^{-1} that we saw in the single particle case, but we also add here a "lazy" permutation, id, where id represents no change in the 3-cycle. Thus to define how each of the processes will move, we will write $\begin{pmatrix} p_1 \\ p_2 \end{pmatrix}$ meaning that the top 3-cycle will move according to permutation p_1 and the bottom 3-cycle will move according to permutation p_2. Thus for the above example each of the pairs of permutations $\begin{pmatrix} \sigma \\ id \end{pmatrix}$, $\begin{pmatrix} \sigma^{-1} \\ \sigma \end{pmatrix}$, and $\begin{pmatrix} id \\ \sigma^{-1} \end{pmatrix}$ ensure that the upper and lower 3-cycles will be completely coupled. Notice that if one looks only at the permutations applied to the top process or the bottom process, the two processes proceed as they normally would with each individual permutation occurring with probability $\frac{1}{3}$.

The representation of the two processes can be simplified by representing the differences in the two processes as discrepancies [4]. If the top process has a one at a given vertex and the bottom process has a zero, then the discrepancy is denoted d^+. If the top process has a zero at a given vertex and the bottom process has a one, then the discrepancy is denoted d^-. All other vertices will be marked with zeroes since no discrepancies exist at those vertices. With this notation, the above example is now represented as:

$$\ldots \quad 0 \quad \boxed{d^+ \quad 0 \quad d^-} \quad 0 \quad \ldots$$

We can now classify each possible particle interaction using the discrepancy notation and also determine which sets of permutations ensure coupling. Table 2.1 lists the permutations that ensure coupling for each specific configuration of discrepancies within a 3-cycle. This information will allow us to devise a strategy for a successful coupling. The strategy

TABLE 2.1: Coupling Strategy

Permutations	Situations Where Coupling is Ensured
$\begin{pmatrix} id \\ \sigma \end{pmatrix}, \begin{pmatrix} \sigma \\ \sigma^{-1} \end{pmatrix}, \begin{pmatrix} \sigma^{-1} \\ id \end{pmatrix}$	$d^+\ 0\ d^-$, $d^-\ d^+\ 0$, $0\ d^-\ d^+$ $d^+\ d^+\ d^-$, $d^+\ d^-\ d^+$, $d^-\ d^+\ d^+$ $d^+\ d^-\ d^-$, $d^-\ d^+\ d^-$, $d^-\ d^-\ d^+$
$\begin{pmatrix} \sigma \\ id \end{pmatrix}, \begin{pmatrix} \sigma^{-1} \\ \sigma \end{pmatrix}, \begin{pmatrix} id \\ \sigma^{-1} \end{pmatrix}$	$d^-\ 0\ d^+$, $0\ d^+\ d^-$, $d^+\ d^-\ 0$
	No Additional Coupling
$\begin{pmatrix} \sigma \\ \sigma \end{pmatrix}, \begin{pmatrix} \sigma^{-1} \\ \sigma^{-1} \end{pmatrix}, \begin{pmatrix} id \\ id \end{pmatrix}$	Otherwise

is to simply choose one of the three effective pairs of permutations when a corresponding group of discrepancies within a 3-cycle is encountered, otherwise we perform the same

permutations for both processes simultaneously. For example, if a 3-cycle with vertex discrepancies d^+ 0 d^- rings, we will then choose from the pairs of permutations $\begin{pmatrix} \sigma \\ id \end{pmatrix}$, $\begin{pmatrix} \sigma^{-1} \\ \sigma \end{pmatrix}$, $\begin{pmatrix} id \\ \sigma^{-1} \end{pmatrix}$ with probability $\frac{1}{3}$ each. By proceeding in this manner, we provide ourselves with the best opportunity to couple the two processes while at the same time ensuring that the two processes, when considered individually, proceed as they would if they weren't dependent upon one another. If a 3-cycle with vertex discrepancies 0 0 d^+ rings, then we will choose from the pairs of permutations $\begin{pmatrix} \sigma \\ \sigma \end{pmatrix}$, $\begin{pmatrix} \sigma^{-1} \\ \sigma^{-1} \end{pmatrix}$, $\begin{pmatrix} id \\ id \end{pmatrix}$ with probability $\frac{1}{3}$ each. It becomes immediately clear, upon studying the multiple particle model, that the only possible particle interactions are considered in sections 2.1 and 2.2. The particle interactions are occurring within 3-cycles and so if all three vertices have the same value, the permutations become trivial. The non trivial cases then consist of having at least one particle of interest but not more than two in a 3-cycle. Table 2.1 therefore becomes very important in identifying the nontrivial cases and in determining the best course of action to ensure coupling in all models with k particles of interest.

Although the 3-cycle permutations are described by examining the one and two particle cases, it still remains to make an argument for the mixing time of the model containing k particles of interest. It is our belief that the solution to this case can be generalized from the previous cases.

3. RESULTS

3.1. Result for One Particle

3.1.1 One Particle Transpositions

To help in our understanding of the problem it is beneficial to simplify the movement of particle to simple adjacent transpositions. That is when a vertex on the circle rings, the particle of interest moves to an adjacent vertex. Thus the particle moves one vertex to the right or to the left with probability $\frac{1}{2}$. This model can be easily recognized as a simple random walk on the circle. For a coupling argument, we consider two processes S_1 and S_2 representing two copies of the simple random walk with corresponding discrepancies d_1^+ and d_2^-. If we fix the position of d_1^+ at certain vertex, say 0, and think of d_2^- as moving twice as fast as normal, we have not changed the overall nature of the model. The benefit of doing this is that we can now let the event that d_2^- arrives at vertex 0 be a stopping time. This allows us to say that the mean hitting time ensures that a coupling has occurred. We need only calculate the mean hitting time for a simple random walk on a finite graph with n vertices. The solution to this problem is well known. The mean hitting time here is simply the product of the distances of d_2^- from the endpoints of the graph. In this construction, d_2^- can approach the vertex 0 from the left or from the right. An upper bound is found by considering the worst case. The farthest that d_2^- can be from 0 is $\frac{n}{2}$ in either direction so this will be the worst case scenario. Therefore the mean hitting time in the case of a simple random walk would be bounded by $\frac{n^2}{4}$.

3.1.2 One Particle 3-Cycle Solution

As described in Section 3.1.1 finding a bound on the mean hitting time, T, will allow us to find a bound on the coupling time for our model on the circle, which in turn will give a bound on the mixing time. In the single particle case, we found that the movement of the

particles in the 3-cycle is equivalent to a random walk with two different step sizes. The random walk is described in Figure 2.1. With this random walk we must devise a clever way to handle the two different step sizes. If we record the steps made in this random walk as R (meaning right) and L (meaning left) and then give these steps a subscript of 1 or 2 corresponding to the step size, then we will be able to decompose the process into the two step sizes. Consider a sequence of steps:

$$L_1L_2R_2R_2L_1R_1R_2R_1R_1L_1R_2....$$

We first consider only the steps of size 1, that is consider only the subsequence of L's and R's with subscript 1.

$$L_1L_1R_1R_1L_1...$$

Here we have a simple random walk on the circle. The mean hitting time, T, for such a random walk is bounded by $\frac{n^2}{4}$. We must now relate the frequency of steps of size 1 to steps of size 2. The probability that a step of size 1 has occurred is $\frac{2}{3}$ and so we consider a geometric random variable with parameter $p_1 = \frac{2}{3}$, marking the event that a step of size 1 has occurred. This means we wait on average $\frac{3}{2}$ for a step of size 1 to occur. Thus for our model the mean hitting time, considering only steps of size 1, is bounded by $\frac{3}{2} * \frac{n^2}{4}$. Now at this point we consider the steps of size two which may have quickened or slowed the mean hitting time. That is, due to the steps of size two we may or may not have achieved the hitting time. Since the probability of going two steps right is equal to the probability of going two steps left, we find that with probability greater than $\frac{1}{2}$ the mean hitting time has arrived. The event that the mean hitting time has arrived then becomes another geometric random variable with parameter $p_2 = \frac{1}{2}$ and thus the expected wait for the mean hitting time to occur is $\frac{1}{p} = 2$. This gives us the bound

$$E[T] \leq 2 * (\frac{3}{2} * \frac{n^2}{4}) = \frac{3n^2}{4}$$

Therefore for one particle, $\tau_{mix} \leq \frac{3n^2}{4}$.

3.2. Result for Two Particles

3.2.1 Transpositions With Two Particles

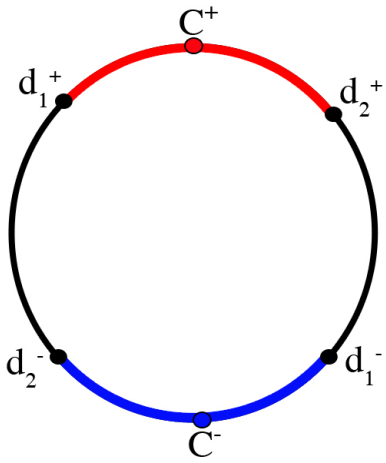
Since we already have the bound of $\frac{n^2}{4}$ for the coupling time for a single particle moving according to transpositions, we now investigate the speed at which the first coupling occurs when two particles are concerned.

Again we initially consider the less complex case of adjacent particle transpositions to simplify the problem. As was seen in the single particle case, a reformulation of the model can aid in bounding the mixing time. For the two particle case we seek such a reformulation. Consider a model with the following configuration of discrepancies:

$$\ldots 00 d_1^+ 0 \ldots 0 d_2^+ 0 \ldots 0 d_1^- 0 \ldots 0 d_2^- 0 \ldots$$

This model is also well represented by Figure 3.1.

FIGURE 3.1: Representation of the Two Particle Model



Let $L_+ := d(d_1^+, d_2^+)$ where $d(\cdot, \cdot)$ is the distance between the two vertices. Similarly let $L_- := d(d_1^-, d_2^-)$. Define C_+ as the center of mass of the positive discrepancies and

define C_- as the center of mass of the negative discrepancies. We notice that for

$$|C_+ - C_-| \leq \frac{L_+ + L_-}{2} \tag{3.1}$$

at least one discrepancy is canceled.

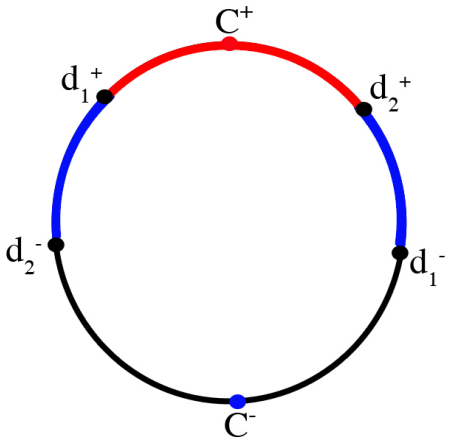
The model can be simplified once more by first noting that the movement of the center of mass is independent of the movement of its two corresponding discrepancies. More precisely, the movement of the center of mass is independent of whether distance between the corresponding discrepancies increases or decreases. Let $L(t)$ denote the distance between the d_i^+'s at time t, $i = 1, 2$ (similarly for d_i^-). Let $C(t)$ denote the position of C^+ at time t (similarly for C^-). Then consider:

$$\begin{aligned} Prob[C(t) \rightarrow \text{right} | L(t) \text{ decreases at time t}] &= Prob(d_1(t) \rightarrow \text{right }) = \frac{1}{2} \\ &= Prob(d_2(t) \rightarrow \text{left}) \\ &= Prob[C(t) \rightarrow \text{left} | L(t) \text{ decreases at time t}] \\ &= Prob[C(t) \rightarrow \text{left}] = Prob[C(t) \rightarrow \text{right}] \end{aligned}$$

Therefore, the movement of the center of mass is independent of the change in the distance between its corresponding discrepancies. It should be clear that this is true for both centers of mass. As a result of this finding, we notice that the center of mass $C(t)$ is a martingale. Because the movements to the right and left have the same probability, each of the discrepancies is also a martingale. This allows us to again simplify the model. If we let the lengths of the discrepancies be "glued" together, the resulting model gives us one center of mass buffered by the lengths of the discrepancies on either side (we call these "wings"), and the other center of mass is left as a single vertex. Then from (3.1) we see that when the lone center of mass hits either one of the wings, the process is coupled. Figure 3.2 gives a good representation.

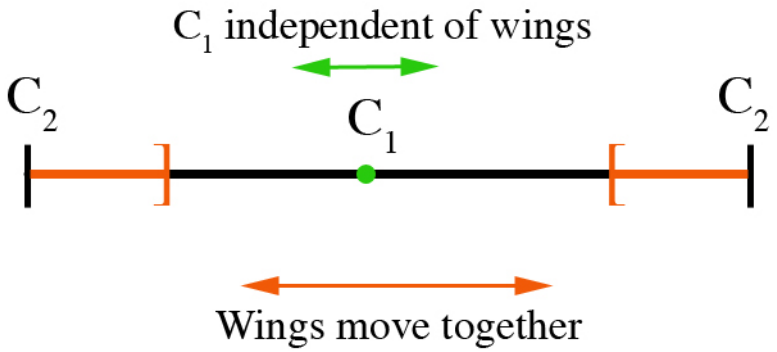
The purpose of reformulating the representation of the model is to provide every

FIGURE 3.2: Representation with Wings



opportunity to find a solution. This is often better achieved by looking at the same problem in as many different ways as possible. By representing the model with wings we are able to see that the problem here reduces to a problem that has been considered before. We can now think of the model as that of a random walk with moving boundaries. The wings act as the boundaries that move together, and the center of mass that is buffered by the wings, say C_2, can be thought of as the endpoints of an interval. This is a result of the circular structure of our model. Finally, the other center of mass, C_1, moves as a random walk independently of the wings. We can now clearly identify a stopping time for

FIGURE 3.3: Random Walk with Moving Boundary



the model. The first time that C_1 hits one of the boundaries, we have our first coupling.

This formulation has provided the most intuitive representation of the model. We

have not yet effectively been able to calculate the speed at which the first coupling occurs. Work on this problem is ongoing.

3.2.2 3-Cycles With Two Particles

A solution for the 3-cycle case is believed to be directly related to adjacent transpositions as was demonstrated in the single particle case. The fact that a speed for the first coupling was not calculated for the adjacent transpositions has impeded the overall progress, but we include a description of how the two particle case is similar and can be bounded once a bound is found for transpositions.

All models and reformulations made in the case of transpositions apply to the 3-cycle permutations. We must simply remember that in the case of a random walk, the 3-cycles have two different step sizes. The different step sizes can be dealt with by using the same method described in Section 3.1.2.

Here we show that the 3-cycle model has similar properties to the adjacent transposition model. Specifically we show that the center of mass for a given type of discrepancy moves independently of the distance between discrepancies.

$$
\begin{aligned}
&Prob[C(t) \rightarrow \text{right} | L(t) \text{ decreases at time t}] = \\
&\qquad = Prob(d_1(t) \rightarrow 1 \text{ to the right }) + Prob(d_1(t) \rightarrow 2 \text{ to the right }) = \frac{1}{2} \\
&\qquad = Prob(d_2(t) \rightarrow 1 \text{ to the left}) + Prob(d_2(t) \rightarrow 2 \text{ to the left }) \\
&\qquad = Prob[C(t) \rightarrow \text{left} | L(t) \text{ decreases at time t}] \\
&\qquad = Prob[C(t) \rightarrow \text{left}] = Prob[C(t) \rightarrow \text{right}]
\end{aligned}
$$

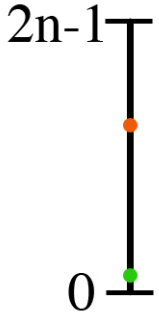
Again, the centers of mass are martingales as well as the discrepancies themselves. This leads to the formulation of a random walk with moving boundary. We then consider the step sizes separately and combine the results by creating geometric random variables that mark whether a given step size has achieved a stopping time. This argument follows the same logic as the argument made for 3-cycles as described in Section 3.1.1.

3.3. Other Helpful Formulations

Another technique that may offer a possible solution to the above two formulations is that of considering this random walk in terms of Brownian motion. Brownian motion is the scaling limit of a random walk. That is as the step sizes become smaller the random walk approximates Brownian motion. Our random walk clearly has mean $\mu = 0$ and finite variance σ^2. If we consider our process$\{X_n\}$ after N steps. Let $S_n = X_0 + X_1 + \cdots + X_{N-1}$. We can apply the Donsker's Theorem[9] to our random walk by scaling S_n by $\sigma\sqrt{n}$ and scaling time by N. With this scaling, we have $Y_n = \frac{S_n}{\sigma\sqrt{n}} \to N(0,1)$ in distribution.

If we also consider another reformulation of the model we can give another possibly effective method of solving the two particle system. The reformulation is as follows. We recognize that the formulation described in Figure 3.3 has symmetry since the wings have the same length and move together, if we simply cut the model in half and consider twice as many vertices (since the center of mass only takes half steps), the model reformulates to two independent random walks on the same set of vertices as depicted in Figure 3.4.

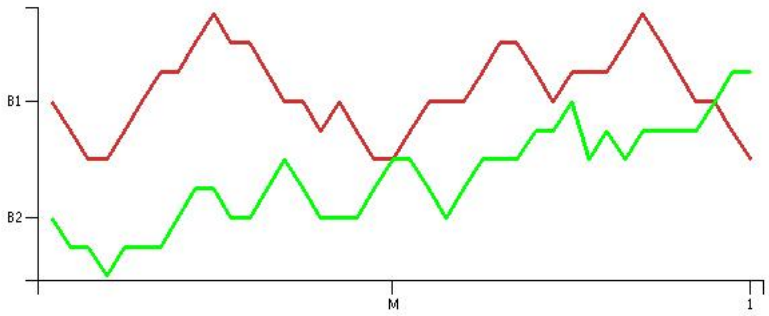
FIGURE 3.4: Symmetric Reformulation



We now apply Donsker's Theorem to each of these independent random walks effectively re-scaling time to the interval [0,1] and giving two independent instances of Brownian motion. If we let $N = n^2$, we have allowed the processes to run long enough to

achieve the first coupling which corresponds to the first meeting of the two independent processes. If we can calculate this first meeting time, the time coordinate of the meeting of the processes would correspond to the coefficient for the first coupling (by our assertions a multiple of n^2). The idea is expressed in Figure 3.5.

FIGURE 3.5: First Meeting Time for Scaled Brownian Motion



The constant M in the figure marks the first meeting time which would correspond to the first coupling time for the two particle case. The speed of the first coupling in the case of adjacent transpositions would then be bounded by $M \cdot \frac{n^2}{4}$.

This method seems to be the most viable for calculating the actual value for the speed of the first coupling. It definitely warrants more detailed examination.

4. CONCLUSIONS

4.1. One Particle Model

The coupling argument presented for the one particle case was a successful one. By considering adjacent transpositions first, we were able to find a the mean hitting time for a random walk with a single step size. Making use of the coupling construction, the mean hitting time provided an upper bound on the coupling time. The coupling time then gives a reasonable upper bound for the mixing time.

Taking the result from transpositions and translating it to the 3-cycle case included a short argument using geometric random variables marking the arrival of stopping times. This technique seems to be particularly useful for dealing with a random walk with two different step sizes.

The overall bound on the mixing time for a 3-cycle with one particle was successfully calculated and agrees with intuition and previous work. The bound calculated was:

$$\tau_{mix} \leq \frac{3n^2}{4}$$

4.1.1 Fixed Number of Particles

A bound of $O(n^2)$ can be immediately devised from the single particle case. That is, for a fixed number of particles we can bound the mixing time by simply considering each particle separately. For example, if we have 25 particles of interest on a circle with n vertices (here n is quite large), then a bound on the mixing time would be:

$$\tau_{mix(25)} \leq 25 \cdot \frac{3n^2}{4} = \frac{75n^2}{4}$$

This type of bound is reasonable as long as the number of particles of interest, k, is substantially smaller than the number of vertices, n.

4.2. Multiple Particles

The many reformulations of the problem, in the case of two particles, have helped in reducing the problem to its simplest form and also to a form that has been studied before. The problem comes in calculating an exact constant coefficient for the speed of the first coupling. It seems that, in most cases, the work previously done has not focused on a specific constant, but the more general case.

While this thesis does not provide a bound beyond $O(n^3)$(a result of Section 4.1.1 for $k = \lfloor \epsilon n \rfloor$), we believe that with the construction and methods described herein a bound of $O(n^2 log(n))$ can be proved. The coupling construction is a successful one and a reasonable bound on the mixing time is a workable problem. With more time and a more in-depth study of the techniques employed here a solution is assured.

No specific work on models with more than two particles is given in this thesis, however, it is clear that subsequent cases will be related to the two particle case. If an efficient method for calculating the speed of the first coupling in the two particle case can be developed, the method should then lend itself to many particles.

Again, being led by previous results, we expect the overall bound on the mixing time to be $O(n^2 log(n))$. This leads us to conclude that for each subsequent particle added to the model, the speed of the first coupling should increase at least proportionately similar to the coupon collector problem. The idea here is that for two particles, the first coupling occurs at least two times faster than a single particle, for three particles the first coupling occurs at least three times faster than a single particle, etc.. The bound on the mixing time for a model with $k = \lfloor \epsilon n \rfloor$, $0 < \epsilon < 1$, particles (where n is large) would be:

$$\tau_{mix} \leq \frac{3n^2}{4}(1 + \frac{1}{2} + \frac{1}{3} + \frac{1}{4} + \cdots + \frac{1}{k} + o(1)) \approx \frac{3n^2}{4} log(n)$$

giving a bound of $O(n^2 log(n))$. The work here is ongoing.

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