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题目：基于马尔可夫链的无偏见选区划分

Impartial Redistricting: A Markov Chain Approach

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Abstract

The gerrymandering problem is a worldwide problem which sets great threat to democracy and justice in district based elections. Thanks to partisan redistricting commissions, district boundaries are often manipulated to benefit incumbents. Since an independent commission is hard to come by, the possibility of impartially generating districts with a computer is explored in this thesis. I have developed an algorithm to randomly produce legal redistricting schemes for Pennsylvania.

A Markov chain random walk model is designed and applied to this problem. Each possible redistricting scheme is treated as a state in the Markov chain. A “flipping” process is designed to move from one state to another through moving a small area from its original district to an adjacent district. Impartial redistricting schemes can be achieved by making many moves in this Markov chain.

I have thoroughly studied into the geographic data of Pennsylvania. Detection and correction of errors in the data allow the model to be built based on it. The data has been simplified and modified to improve efficiency and robustness.

Three criteria are concerned to decide whether a scheme is valid or not: for all districts, they should be 1) simply connected; 2) geographically compact; 3) balanced in population. The whole program is divided into three phases to reach these criteria: 1) initial state formulation (to guarantee simple connection and compactness); 2) preparation phase (to reach population balance); 3) random walk phase (to make the result randomized). The simple connection and compactness features should always be kept throughout the program.

There are four parameters that are for people who use this program to set: 1) the population constraint; 2) the compactness constraint; 3) the random seed; 4) the
number of moves in the random walk phase. The comparison of the former three parameters reveal their influence on the efficiency and outcome of the program. A new parameter is introduced to evaluate whether sufficient moves have been made in the random walk phase.

Default settings are provided based on the analysis. Under the default setting, the outcome is fully randomized after $3 \times 10^8$ random walk moves. It cost 11428.641 seconds (approximately 4 hours), and the average time for every thousand random moves is in the order of magnitude of 40 milliseconds.

**Keywords**

Redistricting, Markov chain, Pennsylvania, Stochastic process
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1. Introduction

Physics phenomena and physics principles embrace the wisdom of nature. People get inspired from them, and models abstracted from physics play brilliant roles in a large number of fields beyond physics. Computer science is one of these fields, and it serves as a bridge to migrate the wisdom of nature to social problems. This paper discusses the use of Markov Chains, which are related to the Brownian motion and the ergodic hypothesis, to solve the gerrymandering problem, a widespread social and political problem.

1.1. The Brownian Motion and the Markov Chain

1.1.1. Introduction to the Markov Chain

A Markov chain is a stochastic process that undergoes transitions from one state to another in a state space. It is named after Andrey Markov. The vital property of a Markov chain is "memorylessness": the probability distribution of the next state depends only on the current state and not on the sequence of events that preceded it. This is also called the Markov property.

In most cases, “Markov Chain” refers to a process with a discrete set of times, i.e. a discrete-time Markov chain (DTMC) \(^1\). (There are also continuous-time Markov chains\(^2\)\(^3\).)

The Markov chain has a strong relationship with the random walk. A random walk is a mathematical formalization of a path that consists of a succession of random steps. The Markov chain is the basic type of the random walk. They have been widely
used in various fields including computer science \textsuperscript{4}, physics \textsuperscript{5,6}, chemistry \textsuperscript{7,8}, ecology\textsuperscript{9}, economics \textsuperscript{10}, psychology \textsuperscript{11}, biology \textsuperscript{12}, etc.

1.1.2. The Brownian Motion in Physics

Brownian motion is the seemingly random movement of particles suspended in a fluid. It was discovered by the English botanist Robert Brown in 1827. When looking through a microscope at particles found in pollen grains in water, Brown noted that the particles moved through the water in a continuous, fast and irregular way.

In 1905, Albert Einstein published a paper \textsuperscript{13} explaining how the Brownian motion was a result of the pollen being moved by individual water molecules. The direction of the force of atomic bombardment is constantly changing, and at different times the particle is hit more on one side than another, leading to the seemingly random nature of the motion.

The Brownian motion has a deep tie with the Markov chain attributing to its underlining stochastic properties. It can be stated more clearly with its abstracted mathematical model.

1.1.3. Mathematical Model of the Brownian Motion

The Brownian motion can be abstracted into a stochastic process with similar behavior, which is called standard Brownian motion or Wiener process in honor of Norbert Wiener. The Wiener process is a continuous-time stochastic process. It plays important roles in pure and applied mathematics, economics, quantitative finance, and physics.

A Wiener process is the scaling limit of random walk in one dimension. In other words, the Brownian motion can be described by the Markov chain. In fact, the Markov chain has been a very important model to study the physical phenomenon of the Brownian motion \textsuperscript{14}.
1.2. The Gerrymandering Problem

The district based election is a world-wide mode of political elections. In America, most of the federal legislators, the House, the Senate and the Congress are all elected from districts.

Elections based on districts reflect the “winner takes all” principle. Take congressional elections in Pennsylvania, the United States as an example: After the 2010 federal Census, Pennsylvania held 18 seats in the Congress, so Pennsylvania needed to be divided into 18 congressional districts. Each district will elect one representative. This means a party can get the seat of a district whether it has gained 51% or 99% of the votes in this district.

Figure 1. Congressional district map of Pennsylvania, spelled out in Act 131 of 2011

According to Article 1, Section 2, of the United States Constitution, a Census must be taken every 10 years, in order to determine the number of congressional seats for each state. Therefore, the boundaries of district need to be redrawn about every 10 years. This is called the redistricting process.

1 The map is cited from http://www.redistricting.state.pa.us/index.cfm.
Such a process is led by a redistricting commission. The incumbents have the chance to manipulate district boundaries to establish a political advantage. Such partisan redistricting is known as “Gerrymandering”. In the 2012 Congressional election of Pennsylvania, Republican got only 48.8% of votes, but 72.2% of representative seats (Act 131 of 2011 in Pennsylvania).

Gerrymandering happens not only in the United States. Australia, Hong Kong, Chile, Greek, Germany and many other countries and regions face the identical problem.

1.3. Attempts to Solve the Gerrymandering Problem

A lot of endeavors have been made towards the gerrymandering problem. However, most of these attempts are from the perspective of politics and laws\(^{[15]}^{[16]}\).

Pang views redistricting as a clustering problem in optimization, and applies optimization and stimulation methods to the gerrymandering problem\(^{[17]}\). Chou Chung-I, uses statistical physics approaches and maps the redistricting problem to a q-state Potts model\(^{[18]}\).

Our group designed a Markov chain to describe the redistricting problem and created a random walk approach to make sure the outcome is utterly randomized and impartial.

Xiaotian Dou worked on this project before me\(^{[19]}\). He tested the random walk method to 50 × 50 grid data, but failed to apply it to the geographical data of Pennsylvania.
My work extends Xiaotian Dou’s work to Pennsylvania geographical data. I analyzed the data carefully, and optimized the connectness, compactness and population balance of districts, and analyzed the statistical features of the Markov chain model.

2. Mathematical Models and Algorithms

2.1. Definition and Properties of the Markov Chain

A sequence of random variables \( X_1, X_2, X_3, \ldots \) can be called a Markov chain, if it has the Markov property, which means that, as stated in Section 1.1.1, the probability distribution of the next state depends only on the current state and not on the sequence of events that preceded it.

All possible values for \( X_i \), \( \forall i \) formulate a countable set \( S \), the state space. Each element \( x \in S \) is called a state. We call \( \lambda = \{ \lambda_x : x \in S \} \) a distribution of \( X_i \), if \( 0 \leq \lambda_x \leq 1, \forall x \in S, And \sum_{x \in S} \lambda_x = 1 \).

\footnote{Figures are cited from [19].}
The formal form of the Markov property is stated as follows:

\[ P(X_{n+1} = x \mid X_1 = x_1, X_2 = x_2, \ldots, X_n = x_n) = P(X_{n+1} = x \mid X_n = x_n) \quad (1) \]

Define the transition probability:

\[ T(x', x) \triangleq P(X_{i+1} = x \mid X_i = x') \quad (2) \]

\( P' (x) \) is a distribution of \( X_i \). It satisfies the detailed balance if:

\[ P' (x) T(x, x') = P' (x') T(x', x) \quad (3) \]

If \( P' (x) \) satisfies the detailed balance, then it is the invariant (stationary) distribution:

\[ P' (x) = \sum_{x'} P' (x') T(x', x) \quad (4) \]

If a chain converges to the invariant distribution, it is ergodic. The property of ergodicity is irrelevant with the initial distribution (state) of the chain.

2.2. Markov Chain Monte Carlo

Markov Chain Monte Carlo (MCMC) is a method for sampling from a probability distribution by means of Markov chains. Applying the accept strategy, it samples from a proposal distribution but reaches a target distribution. There is no necessity for the proposal distribution to be similar to the target distribution.

It maintains a record of \( x^T \), the current state, and the proposal distribution \( q(x \mid x^T) \) depends on it. The sequence of \( x^{(1)}, x^{(2)}, \ldots \) forms the Markov chain.
2.3. The Metropolis–Hastings Algorithm

The Metropolis-Hastings Algorithm can transfer the proposal distribution to the target even if the proposal is not symmetric, which means \( q(x' | x) \neq q(x | x') \).

To get the target distribution \( p(x) \), draw sample \( x^* - q_k(x | x') \) and accept it with probability

\[
A_k(x^*, x^\top) = \min(1, \frac{p(x^*)q_k(x^\top | x^*)}{p(x^\top)q_k(x^* | x^\top)}) \tag{5}
\]

By showing the detailed balance, we can show \( p(x) \) is a stable distribution of the Markov chain:

\[
p(x)q_k(x^\top | x)A_k(x^\top | x) \\
= \min(p(x)q_k(x^\top | x), p(x^\top)q_k(x | x^\top)) \\
= \min(p(x^\top)q_k(x | x'), p(x)q_k(x^\top | x)) \\
= p(x^\top)q_k(x | x') \min(1, \frac{p(x)q_k(x^\top | x)}{p(x^\top)q_k(x | x')}) \\
= p(x^\top)q_k(x | x')A_k(x | x') \tag{6}
\]

3. Impartial Redistricting: Definition, Modeling and Method

3.1. Problem Definition

To avoid gerrymandering, our main task is to divide Pennsylvania into 18 districts, and the procedure must be impartial. Being impartial means that the procedure is utterly random, and people cannot manipulate the redistricting outcome through deciding parameters that are open to human to set in this program.

We use “tract” as the smallest geographical unit. Pennsylvania consists of 3150 tracts in total. Each tract has its boundary and population data. They need to be divided into 18 districts.
The primary governing law for House and Senate districts in Pennsylvania is “Constitution of the Commonwealth of Pennsylvania” Article II, Section 16 and Section 17. Lines relevant to redistricting are quoted below:

“The Commonwealth shall be divided into fifty senatorial and two hundred three representative districts, which shall be composed of compact and contiguous territory as nearly equal in population as practicable. Each senatorial district shall elect one Senator, and each representative district one Representative. Unless absolutely necessary no county, city, incorporated town, borough, township or ward shall be divided in forming either a senatorial or representative district.” -- Pa. Const. art. II, §§ 16

The latter two requirements are largely ignored in practice. Although it is not the law for Congressional districts, the overall criteria is the same.

It can be concluded into three standards for a redistricting scheme to be valid according to the law:

1) The area covered by each district should be (simply) connected;
2) The population of each district should be roughly equal;
3) Each district should be geographically compacted.

1) Simply Connected

Simple connection is a topology term. A space is called simply-connected (or 1-connected) if it is path-connected and every path between two points can be continuously transformed, staying within the space, into any other such path while preserving the two endpoints in question. It is required that all the districts to be simply connected.
As a matter of fact, the law only claimed that “districts shall be composed of compact and contiguous territory”, which stands for path-connected. However, all the actual districts are simply connected, and it’s understood that simply connected districts are more reasonable. Besides, requiring simple connection will make the redistricting process much simpler.

2) Population

The law declares that “the difference between the greatest district population and the lowest district population should not exceed the population of one average census tract.”

I set the following criteria to judge whether districts are approximately equal in population:

\[
\left| \frac{P_i}{P_{\text{ave}}} - 1 \right| < \text{popVar}, \forall i = 1, 2, ..., 18
\]  

(7)

Where \( P_i \) is the i-th district’s population, \( P_{\text{ave}} \) is the average population of 18 districts, and \( \text{popVar} \) can be set by people.

Obviously, the smaller \( \text{popVar} \) is, the more justice the redistricting outcome will hold. We can fulfill the law when setting \( \text{popVar} \) smaller than 0.5 – it is a quite
 loose criterion. popVar must be positive, and cannot be too close to zero, because population of tracts varies and we can never make population of each district exactly the same. I set popVar = 0.1 as its default value.

3) Compact

As quoted above, the law mentioned that districts should be compact. This means the shape of a district shall be more similar with a pie than a snake.

![Compactness Illustration]

Figure 4. Illustration for compactness: The district in the left is more compacted than that in the right.

Compactness is a subjective concept. We need a quantitative measure of it. It needs to reflect people’s impression of compactness, to be independent to the size of the district, and to be easy to calculate. I designed the formula below to present the compactness of each district:

\[
CompactnessScore = \frac{\sqrt{\text{area}}}{C} > T
\]  

(8)

Where “area” is the area of the district, C is the simplified perimeter of the district, T is the threshold for Compactness Score. The more compacted a district is, the higher score it may get.

Here we cannot set C as the exact perimeter of the district, because this will cause a fractal problem (See Figure 5).
Figure 5. Illustration for the fractal problem: The district is highly compacted, yet may get a very low compactness Score if we set C as the exact perimeter.

Therefore, we need to simplify the boundary of districts, only to present its overall shape. C is calculated after simplifying the data to prevent complex boundaries from influencing the compactness score.

Figure 6 shows the compactness score for several common graphs. It will help setting the value for threshold. It is open for people to modify T, but the default value is set to 0.14.

Figure 6. Compactness scores for common shapes.
There are numerous legal schemes of redistricting. Our goal is to randomly pick one valid redistricting scheme that fulfills all the criteria, and the process shall be randomized and free from manipulation.

3.2. Markov Chain in the Redistricting Problem

A Markov chain is usually represented by a directed graph. The vertices set stands for the state space of Markov Chain, and the edges represent the probabilities of going from one state to another. We view a scheme of dividing all the tracts into 18 districts as a “state”. We designed the “flipping process” to randomly walk from one state to another.

If we mark all the 18 districts with numbers from 1 to 18, then a state is giving a (reasonable) number (1 ~ 18) to each tract, so that each tract will belong to a district. In different phases of this program, the requirement for the setting varies. It will be further discussed in Section 3.3. The state space of Markov Chain for Gerrymandering Problem is a discrete one, and the number of states in the state space is fairly large yet finite. However, I cannot provide estimation for the size of the state space.

The “flipping process” is a core process in this program. I name it “flipping process” because I transfer from one state to another through flipping a tract that originally belongs to district A to a neighboring district B. It sounds simple, but the problem gets quite complicated when judging whether a tract is “flippable”. Districts modified during a flipping process must satisfy all the criteria which vary for different phases.

Generally speaking, the steps to move from one state of the Markov chain to another are:
1) Randomly pick a tract (name it T) that is on the boundary of at least two districts. (Let’s say District A and B, and Tract T is a part of District A before the flipping begins.)

2) Check whether District A and B may fulfill all the requirements if we do flip T from A to B. If the answer is positive, go on to step 3); otherwise, go back to step 1).

3) Flip T from A to B.

Analyzing these steps, one can realize the complexity of the edges set. The only good news is that this is a finite set, same as the vertices set. However, the size of the edges set might be fairly large, and the approximate size is difficult for estimation.

I build up a Markov chain model for the gerrymandering problem as discussed above. Independence from previous states insures this model to be a Markov chain. Nevertheless, this is a highly complicated Markov chain with hardly any good features to find. We know it is countable, but we don’t know how large it is.

Fortunately, the Metropolis–Hastings Algorithm does not require the whole picture of the directed graph. If we apply the Metropolis–Hastings Algorithm to stochastic picking process, we can make all possible schemes have equal probability to be the final outcome. In other words, probability distribution amongst all possible redistricting schemes may accord to uniform distribution.

To achieve uniform distribution, we need to calculate the probability of moving from State S1 to State S2 when S1 is the current state. It will be influenced by the way to pick a tract, and the requirements for the districts. As a matter of fact, to calculate it, we have to know the marginal probability of the selected move. There is no obvious answer for that because we do not know if a move is valid or not without dedicate calculation. It is achievable, but time consuming.
3.3. Steps to Achieve Impartial Redistricting

This section discusses how to apply the model introduced in Section 3.2 to impartial redistricting.

There are three steps to complete impartial redistricting (see Figure 7): Initial State Formulation, Preparation Phase, and Random Walk Phase.

| Initial State Formulation | Preparation Phase | Random Walk Phase |
|---------------------------|-------------------|-------------------|
| • In the initial state, districts are simply connected and compacted, but not close in population. |
| • We need to reach a valid state before the random walk |
| • Aimed at making populations even for a valid state |
| • Only allow flipping from a district with a larger population to that with a smaller one. |
| • Makes the outcome random through sufficient flips |
| • Any walk (flip) from one valid state to another valid state is approved. |

Figure 7. Three steps for impartial redistricting.

| Features of three steps |
|-------------------------|
| **Simply Connected**    |
| **Compacted**           |
| **Equal Population**    |
| **Initial State**       | √ | √ | × |
| **After Preparation Phase** | √ | √ | √ |
| **After Random Walk Phase** | √ | √ | √ |

There are several ways to construct an initial state that all districts are both simply connected and compacted. See Section 5.2 for more information.

The preparation phase is aimed at reaching a true valid state. It is required to maintain simple-connection and compactness in every flipping in this phase. Besides, approximately equal in population for all the districts should be achieved at the end of
the preparation phase. To fulfill this goal, I only allow moving tracts from districts with a larger population to those with a smaller one in the preparation phase. A few more moves will be made after reaching the first valid state. This is because we do not want the latter phase start with a state that the population restriction will be easily broken. Otherwise, there will not be many choices to make a move at the beginning of the next phase.

The function of the random walk phase is to provide a stochastic result. All three criteria (simple-connection, compactness and equal population) need to be maintained during every move in this phase. No extra conditions are added to the random walk phase, so that the whole process in this phase will be utterly random. The number of “flippings” implemented in this phase is open for people to set.

4. Data Preparation

4.1. The Structure of Pennsylvania’s Geographical Data

Figure 8. Tract data of Pennsylvania. Black lines are boundary of tracts.
The geographical data of Pennsylvania is made up of data of all the tracts. Figure 8 present the original data of the whole state. Table 2 shows the structure of the data of one tract. The data is provided by Professor David Miller, Department of History, Carnegie Mellon University.

Table 2. Example for data of a tract

All the tracts share the same shape tag and LSAD. Each tract has a unique GEO_ID, which contains the information of state, county and tract name. I use the GEO_ID to identify each tract. I never used the CENSUSAREA provided by the original data. Instead I calculate the area of each tract on my own. Besides this table, we also have the population data of each tract.
Following the basic information of the tract is the vertex list. Each line represents a vertex with its x and y coordination. When we connect the vertices in the order they are listed, we draw the boundary of the tract in clock-wise order. To make the boundary enclosed, the last vertex for a tract shall be exactly the same with the first one.

The coordinates of vertices are very precise, with 19 significant figures. In the flipping process, only the relative locations of tracts are required. The exact coordinates are only needed when calculating the compactness score (we need the area of a district). The perimeter used in compactness score is the length of the simplified boundary, which is deemed to be inaccurate. Therefore, 19 significant figures are beyond necessity. The redundant digits can be used to identify if two points are meant to be the same one, and we are free to modify some of the redundant digits when necessary. I save these data in the form of “double”, which only holds 15 – 16 digits in Java.

4.2. Error Detection and Correction

4.2.1. Requirements for the Data

The geographical data of Pennsylvania is the basis of this project. Unfortunately, this data contains a lot of errors. As a result, I need to detect and correct errors in the data before I begin the implementation of Markov Chain.

A set of correct data that can be applied to the random walk redistricting method should hold following features:

1) All the tracts should be simple polygons.
2) The tracts should cover the map of the whole state well. That means tracts should not overlap with each other except on their boundaries, and there cannot be holes in the map.
3) For any tract T, there exist two valid redistricting schemes S1 and S2, and S1 and S2 can directly change to each other solely by flipping T from one district to another.

Here I explain why feature 3 is required. If there is a tract T that can never be “flippable”, then T always belongs to the same district D. As a consequence, district D can never leave T and gets stuck in the region near tract T. What’s worse, if two or more “never flippable” tracts that are far away from each other happen to get into one single district, this district gets always stretched.

4.2.2. Step 1: Simple Polygon

In this step, I make sure that all tracts are simple polygons. I write a program to detect tracts that are not simple polygons. I find out five tracts in total, and correct them by hand.

A tract must fulfill three constrains to be a simple polygon:

1) It should be closed. In other words it should start and end at the same vertex.
2) Duplicated vertices except the start and end point are not allowed.
3) All the edges inside a tract shouldn’t intersect with each other.

1) is straightforward to detect.

For 2), I add vertices of one tract to an array one by one. Before adding a new vertex, I check if there are any same vertices already in the array. If so, it means there are duplicated vertices.

For 3), I add edges of one tract to an array one by one. Before adding a new edge, I check if it intersects with any edges in the array. If so, it means there are intersected edges.

Figure 9 shows the five tracts that are not simple polygons. They are all corrected manually.
Figure 9. Five tracts that are not simple polygons (before correction). Green lines represent the problematic tracts; black lines are boundaries of adjacent tracts.

4.2.3. Step 2: Merge the Very Close Points

In this step, if the distance between two points is smaller than a threshold value, they get merged to one point. This step is necessity because most of the edges are stored twice in the data in two tracts, and one point can show up several times in the data. Nevertheless, quite a number of points that are very close to each other and are meant to be the same point turn out to be different, because their last a few digits may be different.

I use buckets to store points, and use Hash Map to store buckets. The overall structure is a Hash Map, which stores a lot of “buckets”. Buckets are in fact Array lists. Each bucket stores points in a certain range of areas. The size of the buckets is 0.1 \times 0.1, which means the whole map is cut into squares of size 0.1 \times 0.1. There are a large number of buckets that are empty, and they do not get initialized and
stored in the Hash Map. This structure is aimed at improve the efficiency of searching a point.

I set the threshold of “very close” to be $10^{-6}$. Insert all the points into the data structure one by one. Before inserting point A, if we can find a point B that is very close to point A and is already inside the Hash Map, then modify A to B.

There are 136,254 points in total (most of them are duplicated, so there are approximately 70,000 different points). But in the original version of data, even after rounding them to the type of double (that is rounding 18-19 digits to 15-16 digits), we only have 18,135 pairs that are exactly the same. After running my program, 53,374 points have been changed to those points very close to them. So in the new version of data, we have $53,374 + 18,135 = 71,509$ pairs of same points. Notice that if three points are the same, they'll be calculated twice in the number "71,509", so 71,509 is a reasonable number for 136,254 points.

I have also worked out some data to show how close these points are. The size of the whole map is about $4.9 \times 10^5 \times 2.9 \times 10^5$. All the 53,374 points I have modified are merged to a point within the distance of $2 \times 10^{-10}$. There is no such pair of points whose distance between each other is in the range of $(2 \times 10^{-10}, 0.01)$, and there are only two pairs whose distance is between 0.1 and 0.01. So the threshold for "very close" can vary from $2 \times 10^{-10}$ to 0.01, and we will get the same outcome. That's a fairly large gap.

4.2.4. The Method to Examine the Data

To test if the data is free of errors or not, I calculate how many times and in which direction all the segments (edges) get passed through.

For example, in tract T1, point A is followed by point B, and in tract T2, point B is followed by point A, and point A, B do not show up in other tracts. Then we can say the segment AB is passed through twice in opposite directions.
All the tracts are already guaranteed to be simple polygons. Based on that, if all the edges on the boundary of the state are passed through once, and all the other edges are passed through twice in opposite directions, then requirement 1 and 2 are reached.

I applied this examination after Step 2. There is no edge which gets passed through more than once in the same direction. And I noticed that the most common type of error is having one or more tracts entirely inside another tract. That leads to Step 3.

4.2.5. Step 3: Tracts inside another Tract

In this step, if tract A is entirely inside tract B, tract A will be deleted and its area will be added to tract B.

Such condition does not violate requirement 1 and 2 described in Section 4.2.1, but conflicts with requirement 3. No tract has a large enough population to stand as a district on its own, so tract B must belong to the same district with tract A. Then tract A can never get flipped to other districts, because flipping tract A would get tract B isolated from its district.

Figure 10. Examples of tracts that are inside another tract from the real data
I put all the tracts into a list one by one. Before putting in a new tract T1, I test its relationship with each tract already in the list. Assume tract T2 is a tract in the list. This is how I test if T1 is inside T2 or T2 inside T1:

If the maximum x coordinate value in T1 is smaller than the minimum x coordinate value in T2, or the minimum x coordinate value in T1 is larger than the maximum x coordinate value in T2, or the maximum y coordinate value in T1 is smaller than the minimum y coordinate value in T2, or the minimum y coordinate value in T1 is larger than the maximum y coordinate value in T2, then T1 and T2 must be separate and we can change T2 to the next tract in the list.

Then I count how many T1's vertices are inside T2, outside T2 and on the boundary of T2 respectively, as inNum, outNum and onNum. If outNum equals zero, T1 is inside T2. So I add T1's area to T2 and move on to next new tract without putting T1 into the list. If outNum and inNum are neither zero, it means T1 and T2 intersect. I record this information and continue to change T2 to the next tract in the list. Otherwise, I pick one vertex P from T2 to see if P is inside or outside T1 (If P is on the boundary of T1, I would pick another vertex and set it to P). If P is outside T1, T1 and T2 do not touch each other; if P is inside T1, T2 is inside T1. T2. So I add T2's area to T1, remove T2 from the list, and change T2 to the next tract in the list.

There are 58 tracts merged into other tract in this step in total. Intersecting situation occurred only once and get corrected in the next step.

4.2.6. Step 4: Last Three Errors to Pass the Examination

I ran the examination again after Step 3, and found there are only three errors remaining in the data.

One error among the three is slight overlap of two tracts, another one is a small hole in the map, and the last one is having two very close points which should be exactly the same.
After correcting these three errors manually, I get a version of data that can pass the examination described in Section 4.2.1.

4.2.7. Step 5: “Nails” on the Boundary

When I ran the program with the data produced at the end of Step 4, the result was as presented in Figure 11:

Figure 11. Results based on data with “nails” on the boundary. Different colors represent different districts.
After only a few moves in the preparation phase, the districts get into a rather unsatisfactory state. The grey district is badly stretched, and the compactness scores are very low, approaching the threshold. (The constraint for compactness is slightly different from Section 3.1; otherwise it will fail to find a valid move much sooner.) As long as it comes to a state like this, it is getting harder and harder to find the next move. This situation is because there are “nails” on the boundary that force the grey district to stretch like this.

“Nails” have a similar influence as tracts that are inside other tracts as stated in Section 4.2.5. It is a violation of property 3 stated in Section 4.2.1.

Figure 12. Illustration of “nails” on the boundary. The red line is the state boundary; the black lines are tract boundaries. The yellow and blue areas are two tracts.

See Figure 12 as an example of “nails”. If Tract Yellow and Tract Blue belong to the same district at some stage, they can never get flipped to other districts. (Tract Blue will never leave Tract Yellow alone as a district with only one tract, because Tract Yellow does not hold a large enough population to be a district alone.) The way to solve this problem is to merge Tract Yellow to Tract Blue.

So, such condition is like a nail, to stick the district at this point and never move away. The grey district must have several nails on it to force it stretching like this.
I select out tracts that touches the state boundary twice. There are five such tracts in total, and I find that they are all “nails” by looking into each of them. Figure 13 shows one example among them.

Figure 13. Example of a “nail” from the real data (tract 42015950500). The red line is the state boundary; the green lines are the tract boundary; The blue area is this tract.

The data correction work is accomplished at the end of this step.

4.3. Data Simplification

Simplification of the tract boundary is needed. I only keep the essential vertices where three or more tract edges join together, and use direct segments to connect them. Other points are neglected.

Figure 14. Illustration for data simplification
There are three reasons why data simplification is a must:

1) **To compute the compactness score**

   As mentioned in Section 3.1.3), we need to simplify the boundary of a district before calculating its compactness score, to avoid the fractal problem. The simplified boundary should represent the overall shape of the district, but ignore unimportant details. The simplification method addressed above simplified the boundaries of tracts rather than districts. By using data modified in this way, boundaries of districts are automatically simplified without additional procedures even when districts are changing over time. And it can well keep the information of tract’s overall shape, and successfully avoid the details of the boundary.

2) **To reduce space and time consumption**

   The exact boundary information is only useful to calculate the area of districts when calculating the compactness score. I calculate and store each tract’s area before data simplification. After that, the only required data for flipping is relative geographical relationships amongst all the tracts. The modified version of data contains all the information. Therefore, I can abandon the original data and only run my program based on the simplified data. The size of the data is cut down dramatically, and since there are much fewer vertices and edges, it will also reduce time consumption.

3) **To make the sampling process more reasonable**

   In the preparation phase and the random walk phase, the first step of each move is to randomly select the next move. In most cases such selection is made by selecting an edge on the boundary of a district, and then choosing a direction, to flip the tract on the chosen side of the edge to another side of the edge. Before simplifying the data, tracts with curved boundary have a much larger probability to be selected than those with straight boundary. This is unreasonable and may influence the efficiency of
mixing up and making the outcome random. The simplification of data can help solve this problem.

4.4. Data Presentation -- PostScript

It is important to have a unified way to present the data. It is not only required to present the final outcome of the project, but also to help analyzing the problem, programing and debugging. I choose to use PostScript to visualize the data, to draw the tracts, districts and the whole state. Figures quoted above (such as Figure 8, 9, 10 and 11) are all produced by PostScript.

PostScript is a kind of programing language used to produce vector graphs. It is invented by Adobe in 1985, and has been widely used as a page description language.

PostScript is an interpreted, stack-based language inspired by Lisp. The language syntax uses reverse Polish notation, in the form of arguments being followed by operators. Most operators read their argument(s) from the top of the stack, and then place their results back onto the stack. Literals place a copy of themselves on the top of the stack. It has strong abilities in data structures, dynamic typing, scoped memory and garbage collection. Below are examples of basic lines and frequent used lines in my project:

```
4 3 sub 2 1 add mul
Calculate \((4 - 3) \times (2 + 1)\)

/func {2 mul } def
3 func
Define a procedure “func” to be “2 mul”;

“3 func” is equivalent with “3 2 mul”.

1 setlinewidth
0 1 1 setrgbcolor
```
Set the width of the stroke to 1. The unit of length is called “point”, which equals to 1/72 inch, or 127/360 mm.

Set the color to red (in a red/green/blue form).

Move the cursor to coordination (200, 400), and then draw a straight line to (600, 300).

The vital factor leading me to use PostScript is that it provides a way to use java to create vector graphs. Bitmaps made up by pixels cannot present all the information in those complex maps precisely. If Figure 8 were a bitmap, we need an extremely high Image resolution to allow us to see the details of tracts in Pittsburgh directly by zooming in the graph. Vector graphs, on the other hand, lays no constrains for the scale of the graph: we are free to zoom in and out the graph to inspect the whole picture or any tiny tracts.

The syntax of PostScript may not be straightforward for people to read, but it is convenient to write a program to automatically produce PostScript files. I have written programs to produce the whole map of Pennsylvania, a range of the whole map, a single tract, and a tract with all its neighboring tracts, all with various options for coloring of the area and the width and colors of the lines.

5. Details for Implementation

5.1. Data Structure

The parameters that people can set include: popVar, compactness score threshold (T), and the random seed. Please refer to (7) and (8) in Section 3.1 for details of popVar and compactness score threshold. A list of pseudo random numbers is
produced based on the random seed. With different seeds, the list of numbers is also
different, which can lead to a totally different stochastic process.

**Figure 15. Major classes and data structure**

The most important overall data structure includes:

```java
HashMap<String, Tract> tractMap;
ArrayList<District> districtList;
HashMap<Edge, EdgeInfo> edgeMap;
```

The tractMap stores all the tracts. I choose to use HashMap to store them so that I
can find a tract by its ID number quickly. The districtList stores 18 districts in order.
The edgeMap stores all the edges of all tracts and their relevant information.

Here introduces four major classes to present data: Tract, District, Edge and
EdgeInfo. To present vertices I directly used the Point2D.Double class from the
java.awt.geom package.
An instance of the class District contains its list of tracts, set of edges, and set of vertices, as well as basic information (such as population, area, perimeter before and after simplification and so forth). The set of edges and set of vertices stores edges and vertices on the boundary of the district. I choose to use Set to store them because the number of vertices and edges may be large, and it is frequently used to find one edge or vertex from a district.

An instance of the class Tract contains its list of edges and vertices, and other basic information. Different from the class District, I use ArrayList rather than Set to store vertices and edges because they need to stay in a clockwise order.

The class Edge is inherited from Line2D.Double from the java.awt.geom package. I add one variable to it, the length. Line2D uses two points to present a straight line, and the length of the line can be calculated from the two points. However, my edges can be edges after the data simplification introduced in Section 4.3. An edge may come from a curve made up of several old edges. The variable I added is used to store the exact length of the curve, and the direct length from one vertex of the edge to another can be calculated from the points’ coordinates.

In many cases I do not need both the list of vertices and the list of edges. I may only use one of them instead. So there are two Booleans in the Tract class to demonstrate whether the list of vertices and the list of edges have been built. Handling it in this way can save a lot of time and space.

The class EdgeInfo stores a Boolean to demonstrate whether the edge is on the boundary of Pennsylvania, and the adjacent tracts of the edge. There are two reasons why I split such information from the class Edge rather than put them all in one class.

The first reason is that data in EdgeInfo is only used when implementing Markov Chain, but not required when preparing the data. In data preparation I just use the class Edge and there is no need to waste space for EdgeInfo. And when
implementing Markov Chain and random walk, I can still keep the consistency of the definition classes.

The second reason is more important. For the class Edge, \((P1, P2)\) and \((P2, P1)\) are regarded as two different edges, although they are identical in fact. Other than edges on the boundary of Pennsylvania, all the edges get passed through twice in an opposite direction. This means most edges are stored twice in the instances of Tract in different form. However, their values of EdgeInfo are the same. So I modified the equals and hashCode procedure for the class Edge, so that edges in opposite directions are regarded to be the same in the edgeMap. Therefore, I do not waste space to store a giant number of identical instances of EdgeInfo.

5.2. Programing Structure

The class Rmarkovchain

The major class in this program is called “Rmarkovchain”. It contains three most important procedures (and other procedures called by these three). Figure 16 shows its list of procedures.

The initialize() procedure reads data from files and prepares the data structures described in Section 5.1. It also calls the initDistrict() procedure to build the initial state for the Markov chain.

The preWalk() procedure can make one move in the preparation phase, and it may fail and return false. First, it needs to randomly select the next move. Second, it calls the check(…) procedure to test whether the selected move is valid. If the answer is positive, it will implement the flipping and return true; otherwise it will return false.

The ranWalk() procedure is very similar with the preWalk() procedure, but it works for the random walk phase. The way to select the next move and the population check procedure are slightly different. There are some parameters when calling the
check(…) procedure to indicate whether it is in the preparation phase or the random walk phase.

**Figure 16. Major procedures in Rmakovchain**

Apart from these procedures, there are also other auxiliary procedures to produce random numbers in a certain range, to display current condition, to save current condition to files, etc.

*The main procedure*

The main procedure is the entrance of the whole program. It calls the procedures in the Rmarkovchain class.
Pseudo-code 1. The main procedure

create an instance of Rmarkovchain (mc);
mc.initialize();

// preparation phase
EXCEED = 100; //set how many moves to make after reaching a valid state
exceed = 0;
n = 0;
while(exceed < EXCEED){
    if (mc.preWalk())
        n++;
    if (reach a valid state)
        exceed++;
        save current state to file;
}

// random walk phase
RUNNUM = 500000; //set how many moves to make in the random walk phase
m = 0;
while(m < RUNNUM){
    if (mc.ranWalk())
        m++;
        save current state to file;
}

5.3. Initial State Formulation

The requirements for the initial state have been demonstrated in Section 3.3. All the districts in the initial state are required to be simply connected and compacted.

Method 1: Manually Decide the Initial State

The first approach is to set the initial state manually. I cut the map of Pennsylvania into roughly $3 \times 6$ regions. A few steps are applied to make sure every district is connected, and to smooth the boundary of each district. The initial state is shown as Figure 17.
Method 2: Randomly Produce the Initial State

The second option is to produce the initial state in a stochastic way. The simplest method is to randomly select 17 tracts on the boundary of Pennsylvania, and each of them forms a small district containing only one tract. The rest tracts form the 18th district. The last and largest district needs to be guaranteed simply connected, and the 17 small districts need to satisfy the threshold for compactness score.
Comparison and Evaluation

The procedure for method 2 is clearer than that of method 1. Besides, method 2 suits better with the idea of impartial redistricting. Although setting the initial state cannot guarantee to benefit one political party, a different initial state can utterly change the walking path of the program. However, with sufficient moves, the ultimate state will be independent with the initial state. Therefore, letting people to set it is also acceptable.

The benefit for method 1 is that it makes the preparation phase reach its goal faster. In Figure 17, districts are similar in area but vary in population, so the preparation phase is still required. But the difference of population is much smaller than those in Figure 18. Additionally, districts in Figure 17 are already in a district-like shape, while in Figure 18, the largest district should continuously cut land to other districts, which may consume more invalid attempts to keep the largest district compacted. When testing out method 2, it takes only a small number of moves (compared to the number of moves in the random walk phase) to complete the preparation phase and provide a satisfactory intermediate result.

Both method 1 and method 2 are applicable. I choose method 2 in my final version of program (which is tested in Section 6) for its idea of being stochastic.

5.4. Preparation Phase

In the preparation phase, the features of simply connected and compacted should be kept while walking towards balanced population for every district.

The core of this phase is to make sufficient flips until the populations of districts get balanced. After reaching the first valid state, a certain number of extra moves are made so that the random walk phase does not start with a state easy to fall into an invalid one. The default number of extra moves is 100.
For each move, it is accomplished by the procedure “preWalk()”. It mainly contains three parts: randomly selecting the next move, checking if the selected move is a valid one, performing the flip (if valid) and returning the outcome.

5.4.1. Next Movement Selection

Method 1: Simple Randomized Sampling: District -> Edge -> Side

Method 1 demonstrates the most straightforward way of sampling. Specifically there are two ways:

First, randomly select one district from the 18 districts. Second, randomly select one edge from the set of edges on the boundary of the selected district. Third, select the side of the edge on which the district has a larger population than that on the other side.

The selected move is to “flip” the tract on the selected side of the edge to the other side. Since the edge is on the boundary of a district, this means moving this tract from one district to another. In the preparation phase, it is only allowed to flip from districts with larger populations to those with smaller ones.

The edges of districts are saved in Sets rather than Array Lists for the convenience of searching.

Method 2: Simple Randomized Sampling: Edge -> Side

This Method is very similar with Method 1.

Instead of choosing a district and then choosing an edge of it, I can also put all the edges of all districts into one container and randomly select an edge from this container.

Method 3: Buffer All Possible Moves

Method 3 is developed from Method 2.
The “preWalk()” procedure does not promise to make one valid move. If an invalid move is selected, this procedure just returns false, and the procedure will be called again to select the next move again. In the new round of randomly selecting, those invalid moves tested before still have the probability to be selected again. This setting functions well when there are sufficient valid moves. Nonetheless, if there were much fewer valid moves than invalid moves, the program might try a large number of times yet still fail to hit one valid move. Such problem can be solved through buffering. I build a container to hold all possible moves, and delete invalid ones from it once I meet one.

Same as Method 2, the first step is to put all the edges of all districts into one container. This container should be a universal variable rather than a local variable inside “preWalk()”. Then randomly select one edge from the container, and choose a side judging by population. If it turns out to be an invalid move, delete the edge from the container.

After finding a valid move and performing it, the state gets modified, so whether an edge is “flappable” gets changed. It is complex and time consuming to modify the container of possible moves to suit the new state. A more efficient way is to start over with all edges in all districts.

**Comparison and Evaluation**

Method 1 and 2 seems to be similar but performs differently. The first way acts much more efficiently because we do not need to build a new container which is supposed to be fairly large. However, in the second way, the probabilities of each valid flips to be selected are more close to the uniform distribution. This is because in the first way, the probability relies largely on the number of edges a district has, which may vary a lot among districts. The aim of the preparation phase is to reach a valid state. Therefore the distribution is not the major concern in this phase, so it is unnecessary to sacrifice efficiency for the distribution.
Method 3 is more strong and stable than Method 1, but the price for the stableness is high. Method 3 is approximately 10 times slower than Method 1. I tried to combine these two methods: apply Method 1 as default, but if the program tried more than 100 times in one single move, turn to Method 3 and build a buffer. Unfortunately (it can be also addressed fortunately), Method 3 is never used in such a setting. As a result, I adopt solely Method 1 in my final version of program (applied in Section 6).

5.4.2. "Flippability" Check

The check(...) procedure calls three other procedures for three criteria: simply connected, balanced population, and compacted. The checkCompactness(...) procedure can only function correctly when simple-connection is fulfilled, so it is called after passing the other two criteria.

**Pseudo-code 2. check(...)**

```java
boolean check(Tract tract, int indistrict, boolean isPre) {
    if (checkSimpleConnected(tract, indistrict)
        && checkPopulation(tract, indistrict, isPre)) {
        if (checkCompactness(tract, indistrict))
            return true;
    }
    return false;
}
```

**Simply-Connected Check**

First I check the district that the tract is currently in, to check if this district will get cut into two parts. Any edge and point of the tract that is on the boundary of the district is tagged “1”, others tagged “0”. Then we go around the tract. If the tag changed only once from “1” to “0” and once “0” to “1”, it's OK, otherwise it fails in the simple-connected check.
Figure 19. Simply-connected check for the district that the tract is currently in. Brown lines are boundary of districts, and blue lines are tract boundary. The blue tract originally belongs to the light blue district, and is going to move into the yellow district. Former two graphs are invalid moves because the light blue district would get separated. The last graph shows a valid move.

Next I check the district that the tract is going to flip into, to check if this district will become a “ring” and enclose another district inside it. The check method is exactly the same as mentioned above.

Figure 20. Simply-connected check for the district that the tract is going to join in. Brown lines are boundary of districts, and blue lines are tract boundary. The blue tract originally belongs to the light blue district, and is going to move into the yellow district. Former two graphs are invalid moves because the yellow district would get into a ring. The last graph shows a valid move.

A district becoming a ring means that it is no longer simply connected, but still connected. I forbid it for three reasons. First, it is rarely seen in actual redistricting for
districts to be rings, so it goes against people’s impression of the shape of districts. Second, it harms future mobility. The green district in former two graphs of Figure 20 gets enclosed in the yellow district. It is hard for the green district to change and move around unless it breaks out from the yellow district again. The third reason is that it may greatly complicate the simply-connected check procedure and make it time consuming. The formulation and decompose of rings should be considered.

**Population Check**

I only allow moving a tract from a district with larger population to one with smaller population in the preparation phase. It is already guaranteed when choosing the side of the edge to flip, so nothing need to be done in the population check procedure when it is in the preparation phase.

I have tried a more strict way. When flipping tract T from district D1 to district D2, it’s required that \( P_{d1} > P_T + P_{d2} \), where \( P_{d1} \) (\( P_{d2} \) and \( P_T \)) stands for the population of \( D1 \) (\( D2 \) and \( T \)). This makes sure that after each flip, the standard deviation will decrease. However, the program will easily fail to pick a valid move in a short period of time.

**Compactness Check**

I define the compactness score of a district as \( \frac{\sqrt{\text{area}}}{C} > T \), which has been introduced in detail in Section 3.1.

To get the compactness score of new districts, I need to make the flip under test first, calculate the scores of two modified districts and finally flip it back. Therefore simply connected check is needed before checking compactness.

I set the default threshold for each district's score to be 0.15. With this threshold, the program works efficiently. However, if the threshold were set to too high (0.17 as an example), sometimes the program will stuck in the preparation phase and cannot
fulfill both the compactness and the population criteria. The highest threshold that the program permits varies with the random seed. The outcome with the threshold of 0.15 looks compact enough (see more details in Section 6).

I have also tried several kinds of other constraints although they did not appear in the final version of my program.

1) Double thresholds. Other than the threshold for each district, I added a threshold for the sum of 18 districts’ scores.

2) When flipping tract T to district D, if the total length of T's edges that are on D's boundary is less than 5% of T's circumference, I won't allow it to pass the compactness check. This is for avoiding making bad moves and going into bad states. Here “bad states” means states only having a small number of options for the next move, so it might take a long time to pick a valid move afterwards.

For 1), the program can perform well under such constraint as long as the threshold is reasonably set. But I notice not apparent improvement of compactness in the result after adding this constraint. Besides, there is no strong reason why I must add this threshold.

For 2) I designed this constraint hoping that it will guide the walking process to a better direction. However, experiments show me the opposite effect. Such constrain may decline some moves that better to be performed, especially when some district are trying to expand.

5.4.3. “Flipping” Procedure

After making sure the flip is valid, the implementation of the flipping procedure is easy and straightforward. It is accomplished by two steps: removing the tract from its old district, and adding it to the new district. Information stored in the tract also needs to be modified.
The procedure to remove a tract from a district can be summarized as follows:

1) First, decrease the population;
2) Second, delete the common edges both the tract and the District have;
3) Then, add the edges which only the tract has into the district;
4) Finally, refresh the vertexlist based on the edgelist.

Adding a tract to a district is quite similar to the procedure of removing.

5.5. Random Walk Phase

At the beginning of the random walk phase, the features of simple connection, compactness and balanced population are all reached. These three features should always be kept true in every state in the random walk phase.

The core of this phase is to make sufficient flips to randomize the final outcome. To guarantee the result is utterly impartial, no additional influence and constrains are allowed in this phase unless to keep fulfilling the three criteria.

Similar with “preWalk()” in the preparation phase, each move in this phase is accomplished by the procedure “ranWalk()”. It also contains three major parts: randomly selecting the next move, check if the selected move is a valid one, perform the flip (if valid) and return the outcome.

5.5.1. Next Movement Selection

First three methods (simple randomized sampling: district -> edge -> side, simple randomized sampling: edge -> side, and buffering all possible moves) are basically the same with Method 1 and 2 for the preparation phase introduced in Section 5.4.1. The only difference is that in this phase, we need to randomly choose a side of the selected edge to determine the direction of flipping.

*Method 4: Rejecting Sampling Based on Buffering*
In the random walk phase we focus on the probability distribution for possible outcomes and keeping the procedure strictly free from manipulation. We can approach to a target distribution after making sufficient moves. According to the Metropolis-Hastings Algorithm introduced in Section 2.3, the ultimate distribution can be modified as we want.

To demonstrate fairness, I choose to set the target distribution to be uniform. To achieve this goal, it is required to calculate the probability of the following move from the current state and the opposite move to get back to the current state. With buffering it is possible to reach, but have to be quite time consuming (consuming about 50 times of the time of the version tested in Section 6). Therefore it is not adopted in the final version of this project. Same with the preparation phase, I choose to use simple randomized sampling: district -> edge -> side instead.

5.5.2. “Flippability” Check

Simply-connected check and compactness check are exactly the same with the preparation phase.

In Section 3.1 I introduced the constraint for population:

$$\left| \frac{P}{P_{\text{ave}}} - 1 \right| < \text{popVar}, \forall i = 1, 2, ..., 18$$

This means the population of each district $P_i$ should fulfill:

$$P_{\text{ave}} \left( 1 - \text{popVar} \right) < P_i < P_{\text{ave}} \left( 1 + \text{popVar} \right)$$

Function (9) is the criteria for population check in the random walk phase.

5.5.3. “Flipping” Procedure

Exactly the same with the preparation phase.
6. Result and Discussion

6.1. Evaluation of Randomness

There needs an approach to measure if the outcome has been fully randomized in the random walk phase. After sufficient moves, the result state should be independent with the first state. I compare the current state with the first valid state to testify if sufficient moves have been made. There should be approximately 1/18 of all the tracts that start and end in the same district.

6.2. How Districts Change Over Time

First I test the program with default settings: popVar = 0.1; compactness score threshold = 0.14. The random seed is fixed to be 12455. I applied $3 \times 10^8$ moves in the random walk phase. The first valid state occurred after 14675 preparation moves, so there have been 14774 moves in the preparation phase in total. The preparation phase cost 1.255 seconds, and the sum of running time for both phases is 11428.641 seconds (approximately 4 hours). Figure 21 shows the states after each phases.

![Figure 21-1. Initial state. Seed = 12455; popVar = 0.1; compactness score threshold = 0.14.](image-url)
Figure 21-2. After the preparation phase (after 14774 preparation moves).

Figure 21-3. After the random walk phase (after 14774 preparation moves and $3 \times 10^8$ random walk moves).
Comparing Figure 21-1 and Figure 21-2, we can see that the locations of districts in Figure 21-2 share some similarity of those in Figure 21-1. For example, the two pink districts are on the left boundary of Pennsylvania, and the two green ones on the right.

On the other hand, Figure 21-3 is fairly different from Figure 21-2. In the final state, the ratio of tracts that stay in the identical districts with the first valid state (RI) is 0.132. Figure 21 shows the transition of RI throughout the random walk phase.

**Figure 22. RI – Moves curve for the random walk phase. Seed = 12455; popVar = 0.1; compactness score threshold = 0.14. Total random move times: 3 × 10^8.**

There is a rapid decline of RI at the beginning, which roughly follows the shape of a logarithmic function. When the RI gets close to 1/18 (0.56), it vibrates in the range of (0, 0.20). It takes approximately 1 × 10^8 random walk moves to decline to 0.56, which indicates 1 × 10^8 is the order of magnitudes for the number of moves to be sufficient.
Figure 23. District Compactness Score – Moves curve for the random walk phase.

Seed = 12455; popVar = 0.1; compactness score threshold = 0.14.

Figure 23 presents the average and the minimum of compactness score during the random walk phase. The average of the minimum score over all the moves is 0.1403, very close to the threshold (0.14). However, there does not show an overall tendency of decline in compactness score, which guarantees the program to keep moving around in the Markov chain.

Figure 24. District Population – Moves curve for the random walk phase. Seed = 12455; popVar = 0.1; compactness score threshold = 0.14.
The valid range of population with popVar = 0.1 is [638406, 780273]. The maximum and minimum population gets very close to these two thresholds.

![Graph showing Time (ms) vs. Moves (1 x 10^3)]

\[ y = 38.042x + 1225 \]
\[ R^2 = 0.9999 \]

Figure 25. Time – Moves curve for the random walk phase. Seed = 12455; popVar = 0.1; compactness score threshold = 0.14.

Through linear fitting, I calculated the average time for every thousand moves is 38.042 milli-seconds.

**6.3. Outcomes with Different Population Standards**

I set the compactness score threshold to be fixed at 0.14, random seed fixed at 12455, and compare the outcomes with popVar = 0.05/0.10/0.15/0.20. \( 1 \times 10^7 \) random walk moves are implemented.

Comparing popVar = 0.05/0.10/0.15/0.20 in Figure 26, we can conclude that the larger popVar is, the fewer preparation moves we need. Time consumption is relevant with the environment, and it do not present a clear relationship with popVar.
Figure 26. Cumulative Time – Moves curve for the preparation phase with different popVars. Seed = 12455; compactness score threshold = 0.14.

Figure 27. District Population – Moves curve for the random walk phase with different popVars. Seed = 12455; compactness score threshold = 0.14.
From Figure 27, we see that the minimums and maximums of district population always keep very close to the thresholds. Besides, district population varies more with a larger popVar.

Figure 28. RI – Moves curve for the random walk phase with different popVars.

Seed = 12455; compactness score threshold = 0.14.

Figure 29. Time – Moves curve for the random walk phase with different popVar.
When the popVar grows from 0.10 to 0.20, the average time for every thousand moves grows from 37.6 ms to 41.1 ms.

Figure 26, 28 and 29 all prove that the situation of popVar = 0.015 follows different pattern from those with popVar = 0.10/0.15/0.20. The direct influence is the efficiency. Therefore, there should be a minimum value of popVar to guarantee the program can provide a solution in a limited period of time.

### 6.4. Outcomes with Different Compactness Score Thresholds

I set the popVar fixed at 0.10, random seed fixed at 12455, and compare the outcomes with compactness score threshold (CT) = 0.13/0.14/0.15. $1 \times 10^7$ random walk moves are implemented.

![Figure 30. Cumulative Time – Moves curve for the preparation phase with different CTs. Seed = 12455; popVar = 0.10.](image)

It can be concluded from Figure 30 that fewer moves are needed in the preparation phase with lower compactness score threshold.
Figure 31. RI – Moves curve for the random walk phase with different CTs. Seed = 12455; popVar = 0.10.

From Figure 31, we can see that the RI drops faster when CT = 0.13, but the difference between CT = 0.14 and 0.15 is not obvious.

Figure 32. Compactness Score – Moves curve for the random walk phase with different CTs. Seed = 12455; popVar = 0.10.
The minimum compactness score among the 18 districts keeps close to the threshold. The average for 18 districts’ scores is about 0.05 points higher than the minimum value. The variation range for both minimum and average is similar with CT = 0.13/0.14/0.15.

Figure 33. Time – Moves curve for the random walk phase with different CTs.

Seed = 12455; popVar = 0.10.

Setting higher compactness score threshold, we can get better result with more compacted districts. However, a high CT decrease the efficiency of the program, and when CT is set too high, the program may fail to accomplish the preparation phase in a limited time. I find CT = 0.14 a good tradeoff: for satisfying compactness and acceptable moving speed.

### 6.5. Outcomes with Different Random Seeds

This program can operate under any random seeds. I tested it with other seeds (seed = 1 and 201506). The popVar is set to 0.10, and the compactness score threshold is set to 0.14. $1 \times 10^7$ random walk moves are implemented.

Table 3 compares the efficiency of the program when choosing different seeds.
Table 3. Efficiency comparison among different random seeds. popVar = 0.10; Compactness Score Threshold = 0.14.

| Random Seed | 12455 | 1 | 201506 |
|-------------|-------|---|--------|
| Moves in Preparation Phase | 14774 | 28652 | 18468 |
| Total Time of Preparation Phase (ms) | 1225 | 2848 | 1412 |
| Average Time for 1000 Preparation Moves (ms) | 82.58 | 99.12 | 76.35 |
| Average Time for 1000 Random Walk Moves (ms) | 37.619 | 36.862 | 33.685 |

The speed of moving is similar for different random seeds, but the number of moves needed in the preparation phase can vary a lot.

7. Conclusion

My program is successful to produce a randomized redistricting scheme, which proves it to be a feasible approach to avoid the gerrymandering problem with the Markov chain random walk model.

The districts in my redistricting schemes are all simple connected, well compacted with balanced population, especially compared to the actual districts (see Figure 1) and Xiaotian Dou’s result (Figure 2).

People can set the “popVar”, and compact score threshold to customize how strict the restrictions regarding population and compactness should be. Experiments show that the program functions well with popVar = 0.05 and compactness score threshold (CT) = 0.15. However, popVar below 0.05 and CT above 0.15 may result in failure of completing the preparation phase.

A new parameter “RI” is introduced to evaluate to what extent the outcome is randomized through comparing the current state with the first valid state. Experiments show that $3 \times 10^8$ random moves are well enough to produce a randomized result.
under default settings (Figure 22). It takes about 4 hours to complete the whole process.

Different random outcomes can be attained through setting different random seeds. However, changing the random seed will also change the tolerance of popVar and CT, as well as the number of moves required.

There remain several aspects having the potential to be improved in the future in my program:

First, more factors can be added into consideration in the process of redistricting. When setting the boundaries of districts, there are many other factors that are important to emphasize justice, such as the distribution of races and people’s incomes in different areas. As long as there are relevant data and a reasonable method for quantification, they can all be plugged into this program in the similar way of population balance.

Second, comparison between my scheme and the actual districts with the voting data would produce valuable information. Comparing the electing outcome based on my map and the actual outcome can indicate to what extent the redistricting process is gerrymandered. Voting data in every tract is required to perform this.
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基于马尔可夫链的无偏见选区划分——中文概述

摘要

由于基于选区的选举的广泛存在，选区规划成为一个影响到民主和公平的全球性问题。确定选区边界的组织往往带有自己的政治立场与偏见，他们可以通过操纵选区的边界来满足自己的利益，而建立一个完全独立和没有偏见的组织是极其困难的。由此，本文探讨了用计算机进行无偏见的选区划分的可能性，以美国宾夕法尼亚州为例，设计了一个可以随机产生符合法律要求的选区划分方案的算法。

设计了一个基于马尔可夫链的随机游走模型来完成选区的划分。每一个可能的划分方案作为马尔可夫链中的一个状态。设计了一个“翻转”过程，通过将一个小区域从一个选区移动到另一个选区，实现了状态之间的转移。在马尔可夫链中进行了足够次数的游走之后，即可达到一个完全随机且无偏见的选区划分方案。

为保证给出的划分方案是切实有效的，需要考虑三个条件：1）所有选区都应当是单连通的；2）选区的形状应当是紧凑的；3）各选区的人口应当均衡。整个程序被分成三个阶段来满足上述条件：1）产生初始方案（保证单连通性和紧凑性）；2）准备阶段（使人口达到均衡）；3）随机游走阶段（维持上述条件，使最终结果随机化）。

程序中共有四个可以人为设定的参数：1）人口的限制；2）紧凑性的限制；3）随机种子；4）随机游走阶段的游走次数。通过控制变量地比较前三个参数，揭示了它们对程序效率和结果的影响。引入了一个新的参数来反映最终方案的随机程度，从而评估游走阶段的游走次数是否充足。在默认设定下，经历 $3 \times 10^8$ 次随机游走之后得到了充分随机化的结果。总耗时为 11428.641 秒（约合 4 小时），平均每千次游走的时间在 40 毫秒的数量级。

关键词

选区划分；马尔可夫链；宾夕法尼亚州；随机过程
第一章 前言

物理学的现象和原理蕴含着自然的智慧。人们从中汲取灵感，从物理中抽象出的模型在许多物理以外的学科扮演着重要的角色。计算机科学就是这样的学科之一，它起到连接物理学智慧和社会生活问题的桥梁作用。本文探讨了应用马尔可夫模型——一个与物理中的布朗运动和遍历性假设由深刻联系的模型——解决选区划分问题——一个具有普遍性意义的社会政治问题——的方法。

1.1 布朗运动与马尔可夫链

马尔可夫链是指一种在状态空间中进行状态转移的随机过程。其核心特性是“无记忆性”：下一个状态的概率分布仅取决于当前状态，与如何达到当前状态的历史无关。马尔可夫链既包括离散型也包括连续型。

马尔可夫链与随机游走是相近的两个概念。随机游走是指一条包含了一系列随机步骤的路径。马尔可夫链是随机游走中最基本的一种形态。马尔可夫链随机游走在众多领域有重要的应用，包括物理、计算机、化学、经济、心理学等等。

物理学中的布朗运动是指小颗粒在流体中的无规律运动。由于其潜在的随机性特征，布朗运动与马尔可夫链有深刻的联系。布朗运动可以被抽象成一个数学上的随机模型，称为维纳过程。维纳过程是一个时间连续的随机过程，随机游走取极限后即可得到维纳过程。换言之，可以用马尔可夫链描述物理学上的布朗运动。马尔可夫链是研究布朗运动物理现象的重要工具之一[1]。

1.2 杰利蝾螈：选区划分的操纵问题

基于选区的选举是一种全球性的政治选举模式。一个选区中的胜者可以获得该选区中的所有选票，无论其在该选区中的支持率是51%还是99%。

根据美国法律规定，在每10年一次的人口普查之后，需要重新分配每个州的国会议员席位，也要重新确定选区的边界。选区的划分由一个专门的委员会完成，这给执政党操纵选区边界从而营造政治上的优势的机会。
在 2012 年的选举中，宾夕法尼亚州共有 18 个国会议员席位，因此需要将整个州划分为 18 个选区，每个选区选出一位议员。共和党只赢得了全州 48.8% 的选票，却获得了 72.2% 的议员席位。图 1 是 2012 年宾夕法尼亚州的选区图。

![选区划分图](http://www.redistricting.state.pa.us/index.cfm)

图 1. 宾夕法尼亚国会选区划分图（宾夕法尼亚州 2011 年第 131 条例）

选区划分的操纵问题不仅存在于美国。澳大利亚、香港、智利、希腊、德国等大量的其他国家和地区都面临着同样的问题。

### 1.3 选区划分操纵问题的研究现状

大多数针对选区划分问题的研究均是从政治和法律的角度出发的[2][3]，也有少数其他的尝试。庞善臣从聚类问题的角度，将优化和模拟方法应用于选区划分[4]；吴仲义使用统计物理的方法，将选区划分问题映射为 Q 态 Potts 模型[5]。

本小组设计了一个马尔可夫链来描述选区划分问题，用随机游走的方法保证结果是完全随机，从而无偏见的。在我之前，窦晓添在 $50 \times 50$ 的网格上测试了该模型，但没有成功地将模型应用于宾夕法尼亚州的实际数据上[6]。
图 2. 窦晓添在网格上和实际数据上的测试结果

我的工作将窦晓添的工作延伸到了实际地图数据上。我深入分析了宾夕法尼亚州的地图数据，优化了对选区单连通性、紧湊性和人口均衡性的控制，并分析了不同参数在此马尔可夫链中发挥的作用。

第二章 数学模型与算法

2.1 马尔可夫链

一个随机变量序列 $X_1, X_2, X_3,...$ 可以被称为马尔可夫链，当其满足马尔可夫性质，即下一个状态的概率分布仅与当前状态相关，与当前状态之前的序列无关。

所有可能的取值 $X_i, \forall i$ 组成一个可数集 $S$，称为状态空间。$S$ 的任意元素 $x \in S$ 称为一个状态。$\lambda = \{\lambda_x : x \in S\}$ 称为 $X_i$ 的一个分布，当其满足 $0 \leq \lambda_x \leq 1 \ \forall x \in S$, 且 $\sum_{x \in S} \lambda_x = 1$。

马尔可夫性质的规范化表示如下:

$$P(X_{n+1} = x \mid X_1 = x_1, X_2 = x_2, ..., X_n = x_n) = P(X_{n+1} = x \mid X_n = x_n)$$

(1)

定义转移概率为:

$$T(x', x) \triangleq P(X_{n+1} = x \mid X_n = x')$$

(2)

\[\text{该图片引自参考文献[6]}\]
$P'(x)$ 是 $X_i$ 的一个分布。当其满足如下条件时，称其满足细致平衡:

$$P'(x)T(x, x') = P'(x')T(x', x)$$

(3)

若 $P'(x)$ 满足细致平衡，则其为该马尔可夫链的稳定分布:

$$P'(x) = \sum_x P'(x')T(x', x)$$

(4)

如果一个马尔可夫链收敛到一个稳定分布，则称其为遍历的。遍历性与马尔可夫链的初始状态无关。

2.2 马尔可夫链蒙特卡罗方法

马尔可夫链蒙特卡罗方法是一种基于马尔可夫链的随机取样方法。利用接受策略，可以从一个原始分布出发，达到服从目标分布的取样。原始分布可以和目标分布具有完全不同的形态特征。

这一方法需要记录当前的状态 $x^T$，原始分布 $q(x | x^T)$ 是基于当前状态的。序列 $x^{(1)}, x^{(2)}, ...$ 组成了马尔可夫链。

2.3 Metropolis–Hastings 算法

当原始分布是非对称，即 $q(x | x') \neq q(x' | x)$ 时，可以利用 Metropolis-Hastings 算法将原始分布转化成目标分布。

为获得目标分布 $p(x)$，取样 $x^* \sim q_k(x | x^T)$ 并以如下的概率接受之:

$$A_k(x^*, x^T) = \min(1, \frac{p(x^*)q_k(x^T | x^*)}{p(x^T)q_k(x^* | x^T)})$$

(5)

通过证明细致平衡，我们可以证明 $p(x)$ 是该马尔可夫链的稳定分布:
本科生毕业论文——中文概述

第三章 无偏见选区划分：定义、模型与方法

3.1 问题定义

我们的任务是将宾夕法尼亚州无偏见地划分成 18 个选区。无偏见意味着整个过程是完全随机的，且不能通过设定参数而人为地操纵选区划分结果。

我们将最小的地理单元称为“区块（Tract）”。宾夕法尼亚州一共有 3150 个区块，每个区块有其地理边界和人口。需要将所有的区块划分为 18 个选区。

为使选区划分的结果符合法律要求，需要满足三条标准：

1) 每个选区所覆盖的地域应当是单连通的；

2) 每个选区的总人口应当大致相等；

3) 每个选区的地理形状应当是紧凑的。

1) 单连通

单连通是一个几何学概念。对于一个单连通区域，任意选定区域中的两点，在此区域内，所有连接这两点的路径可以连续地变化到其它路径而不离开此区域。

图 3. 非单连通区域（左）和单连通区域（右）举例
2) 人口

法律规定人口最大的选区和人口最小的选区人口之差不得超过每个选区的平均人口。

我设定的人口标准如下:

\[
\left| \frac{P_i}{P_{ave}} - 1 \right| < \text{popVar}, \forall i = 1, 2, ..., 18
\] (7)

其中\(P_i\)是第\(i\)个选区的人口, \(P_{ave}\)是18个选区的平均人口, \(\text{popVar}\)可以人为设定。

\(\text{popVar}\)越小,划分方案在人口意义上越公平。为满足法律要求, \(\text{popVar}\)必须小于0.5,同时\(\text{popVar}\)必须为正,但不能太接近0,因为每个区块有不同的人口,不可能使所有选区的人口完全相等。\(\text{popVar}\)的默认值设为0.1。

3) 紧凑性

紧凑性是指选区的形状应更接近一个圆而不是像蛇一样伸展开来。

![图4. 紧凑性的说明：图左的形状比图右更紧凑](image)

为定量地表达紧凑性,我设计了一下公式来衡量一个选区的紧凑程度:

\[
\text{CompactnessScore} = \frac{\sqrt{\text{area}}}{C} > T
\] (8)
area 是该选区的面积，C 是简化后的选区周长，T 是紧凑性得分（CS）的阈值。CS 越高，选区越紧凑。

这里 C 不能使用选区的精确周长，否则会导致分形问题（见图 5）。因此，需要对选区边界数据进行简化，只表征选区的大致形状。CS 的阈值 T 的默认值设为 0.14。

图 5. 分形问题举例。此选区是紧凑的，但其精确的周长很长，若在 CS 计算中使用精确周长，会使其得分很低

3.2 选区划分中的马尔可夫链

马尔可夫链通常可以用有向图表示。图的顶点集表示马尔可夫链的状态空间，图的边表示从一个状态转移到另一个状态的概率。将任意一个符合要求的选区划分方案视为一个状态：设计了一个“翻转”过程，通过将一个区块移至其相邻的选区，实现了不同状态之间的随机游走。

“翻转”的基本流程如下：

1) 随机选取一个与其它选区接壤的区块 T，称其原来属于的选区为 A，一个与 T 相邻的选区为 B;

2) 检查假设把 T 划分给选区 B，A 和 B 是否满足要求，若满足，进行步骤 3，否则回到步骤 1;

3) 把 T 划分给选区 B（称之为将 T 从 A 翻转至 B）。
由于“翻转”过程仅和当前状态有关，和状态历史无关，所以这是一个马尔可夫链。此马尔可夫链是非对称的，可以利用 Metropolis-Hastings 算法来使所有符合要求的划分方案有相同的概率被取到，即达到均一分布。

为达到均一分布，需要计算当前状态为 $S_1$ 时，从状态 $S_1$ 到状态 $S_2$ 的概率，及当前状态为 $S_2$，从 $S_2$ 到 $S_1$ 的概率。这是可以计算但十分复杂的。

### 3.3 无偏见选区划分方法

如图 6，选区划分的过程分为三个阶段：初始状态的生成，准备阶段，随机游走阶段。

![图 6. 选区划分的三个阶段](image)

**初始状态生成**
- 在初始状态中，选区是单连通的且紧凑的，但人口不均衡
- 需要在随机游走前先到达一个满足条件的状态

**准备阶段**
- 在保持单连通和紧凑的同时追求人口均衡，从而达到一个满足所有条件的状态
- 只允许将区块从人口大的选区移动到人口小的选区

**随机游走阶段**
- 通过充分的游走使输出结果完全随机
- 时刻保持单连通、紧凑和人口均衡，任何满足所有条件的状态之间的“翻转”过程均是被允许的

第四章 地图数据准备

### 4.1 数据格式

宾夕法尼亚州的地图数据是由所有区块的数据构成的。图 7 是原始数据，表 1 是一个区块的数据示例。除了如表 1 所示的数据外，我们还拥有每个区块的人口数据。
区块数据由基本信息和边界信息组成。基本信息中，GEO_ID 是区分不同区块的标志。边界信息是区块的顶点列表，每一行是一个顶点的 x 坐标和 y 坐标。把这些顶点依次连接起来，就顺时针绘制除了该区块的边界。区块顶点列表的第一个顶点和最后一个顶点应当是完全相同的。

表 1. 区块数据示例

| _SHAPE_TAG_ = Area |
|-------------------|
| GEO_ID=42003417200 |
| STATE=42          |
| COUNTY=003        |
| TRACT=417200      |
| NAME=4172         |
| LSAD=Tract        |
| CENSUSAREA=0.509000000000000 |
| (-184392.8318613689000; -48105.4997117861640) |
| (-184286.7000800712000; -48099.0085129352660) |
| (-183800.1752343245000; -48016.7707332467330) |
| (-183530.1332642245400; -47791.3872410956900) |
| (-182939.7449407636000; -47793.5470193865690) |
| (-183112.0001321420700; -48183.9252565298670) |
| ...... (省略若干行) |
| (-185189.5858982463300; -48085.5522457489500) |
| (-184392.8318613689000; -48105.4997117861640) |

图 7. 宾夕法尼亚州原始区块数据。黑色线条为区块的边界。
4.2 数据更正

原始数据中含有大量的错误。通过编程自动检测，手动和自动相结合修改的方式，使得修改后的数据满足以下条件:

1) 所有的区块均为简单多边形；

2) 区块恰好覆盖整个州的地图，区块之间既没有空隙，也没有重叠；

3) 对任意的区块 $T$，均存在状态 $S_1$ 和 $S_2$，使得 $S_1$ 和 $S_2$ 之间可以仅通过翻转区块 $T$ 而直接转化。

4.3 数据简化

为了计算紧凑性评分 $CS$，提升程序效率和健壮性，需要对数据进行简化。如图 8，仅保留有三条或以上边交汇的顶点，忽略其它的点，把保留下来的顶点直接用线段连接，即得到简化后的数据。

![图8 数据简化的说明](image_url)

4.4 数据展示

我选择使用 PostScript 进行数据的可视化展示。PostScript 是一种用于产生向量图的编程语言，其作为页面描述语言得到了广泛的应用。我通过编写 Java 程序，自动从数据产生 PostScript 文件。由于 PostScript 采用向量图的表示方法，可以对图像进行高倍数的放大，方便查看地图的细节。前述图 7 就是用 PostScript 生成的。
第五章 马尔可夫链的实践细节

5.1 数据结构

用户可以设置的主要参数包括：人口的约束 popVar，紧凑性评分阈值 CT，及随机种子。基于随机种子，Java 的内置算法可以产生一系列的伪随机数。选取不同的种子将导致完全不同的随机过程。

图 9 展示了程序的主要数据结构。

![主要的类和数据结构](image.png)

图 9. 主要的类和数据结构

5.2 程序结构

程序的核心的类称为 Rmarkovchain，它包含了三个主要方法，分别为 initialize(), preWalk(), ranWalk(), 结构如图 10 所示。Inititalize()负责数据结构的搭建及初始状态的生成。preWalk()和 ranWalk()分别负责完成准备阶段和随机游走阶段中的一次游走。若发现随机选择的翻转是不符合要求的，会直接返回 false 而不是继续尝试。

在主方法中调用 Rmarkovchain 的方法，从而实现选区的划分。
5.3 初始状态的生成

随机生成初始状态，同时要保证每个选区的单连通性和紧凑性。随机选择 17 个处于州边界上的区块，每个区块作为一个独立的选区，剩余的区块作为第 18 个选区。需要检测是否所有选区均满足紧凑性，以及最大的选区是否满足单连通性。

5.4 游走过程

准备阶段和随机游走阶段是类似的，由多次游走组成。首先选取待执行的翻转，然后检测此翻转是否满足要求，若满足，则执行此翻转，否则，重新选取翻转。准备阶段的终止条件是达到符合所有要求（包括人口均衡）的状态，之后再进行确定次数的游走（默认次数是 100 次）；随机游走阶段则直接规定游走次数。
选取待执行的翻转的过程必须是随机的。首先随机选择一个选区，再随机选择选区边界上的一条边，最后选择这条边两侧中的一侧，选定的翻转即为将这条边选定侧的区块翻转到另一侧的选区。在最后一步，选定边的一侧时，准备阶段一定选择选区人口较多的一侧，而在随机游走阶段中，这一选择是随机的。

在准备阶段，只检测选定的翻转是否维持受影响的两个选区的单连通性和紧凑性。在随机游走阶段，需要检测单连通性、紧凑性和人口的均衡。

第六章 结果与讨论

6.1 评估结果的随机性

需要有一个定量的方式来研究结果是否是随机的。如果游走的次数足够多，最终的状态应当与初始状态无关，因此可以通过比较最终状态和第一个满足条件的状态来衡量游走次数是否充足。设 \( m \) 为在最终状态和第一个满足条件状态中属于同一个选区的区块数，\( N \) 为总区块数，引入 \( RI = m / N \) 描述结果的随机性。

6.2 划分方案产生的过程

在默认设置下进行测试，\( \text{popVar} = 0.1, \text{CT} = 0.14 \)，随机种子 = 12455，共进行 \( 3 \times 10^8 \) 次随机游走。图 11 给出了不同阶段的状态图。

图 11-1. 初始状态
图 11-2. 准备阶段结束。共经历 14774 次准备阶段的游走

图 11-3. 最终结果。共经历 $3 \times 10^8$ 次随机游走

图 12–15 给出了各变量随游走步数的变化规律。
图 12. 随机游走阶段中，RI 随游走步数的变化规律

可见 RI 首先以大致对数函数的形式迅速下降，然后在 0.1 左右震荡，一般保持在 0.1 以下，最高时可以震荡至超过 0.2。

图 13. 随机游走阶段中，CS 随游走步数的变化规律

CS 一直在大致相同的范围内震荡，最小值非常逼近阈值。
6.3 不同参数的作用与影响

保持随机种子和 CT 不变，改变 popVar，可以发现当 popVar 不太小（≥0.1）时，popVar 越大，准备阶段所需步数越少，但所需时间反而更长；人口最大和最小的选区的人口始终非常贴近人口阀值，且 popVar 越大，人口波动的范围越大；popVar 不太小（≥0.1）时，popVar 越大，每千步随机游走所需时间越长。
但当 popVar 很小（=0.05）时，每次游走所需时间明显增长，且准备阶段步数明显增多。

保持随机种子和 popVar 不变，改变 CT，可以发现 CT 越大，准备阶段所需步数越多；对不同 CT 取值，CT 最小的选区的 CT 值均很接近阈值，浮动范围类似，CT 均值比最小值高 0.05 左右；CT 越大，每千步随机游走的时间越长。

对于不同的随机种子，游走的速度较为接近，但准备阶段所需的游走步数相差很大。

### 第七章    结论与展望

我设计的程序达到了目标的效果，可以在较短的时间内完全随机地产生符合要求的选区划分方案，无偏见性得到了保证。与实际的选区和窦晓添的结果相比，选区的单连通性、紧凑性和人口均衡得到了更好的控制。可以通过设置参数来控制紧凑性和人口均衡的严格程度，可以通过设置不同的随机种子来获得完全不同的随机结果。

此项目还有很多方面有改进的空间：

第一，更多的因素可以纳入到选区划分的考量。有很多超出人口和选区的地理形状的因素会影响一个选区划分方案的公平性，如种族的分布，不同收入阶层的分布等。只要有合理的定量化描述方法，这些因素都能以类似人口均衡的限制条件的模式添加到该程序中。

第二，结合选票数据的分析可以提供更有价值的结果。如果能够获取每个区块的选票数据，可以模拟在此程序给出的选区划分方案上的选举结果，与实际的选举结果进行对比，从而体现实际的选举结果在多大程度上受到了操纵选区边界的影响。
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