Repetition effects in a Sequential Monte Carlo sampler

Sarah Cannon, Daryl DeFord, and Moon Duchin

August 8, 2024

1 Introduction

In this note, we consider the structure of the SMC (Sequential Monte Carlo) method developed by McCartan–Imai for sampling partitions of a fixed node-weighted graph G into a given number k of connected subgraphs with nearly equal total weight [12]. The main application is to redistricting, where the weight is by population, so we will refer to the partition as a *plan* and its parts as *districts*. SMC operates by fixing a sample size S and a number of districts k, then creating a top generation of partial plans by marking off one connected subset of G with roughly $1/k$ of the total weight in each plan (Figure 1, left). In the next generation, S agents sample with replacement from those partial plans according to a weighting function; continuing the progress in the partial plan, the agents then mark off a second subset of about the same size. This process continues for k generations until the entire graph is marked. We will summarize the salient combinatorial features of this scheme in a *descendancy diagram* D (Figure 1, right), showing only the paths that connect from the bottom layer to the top. The nodes of D involved in these paths are called *active* or *activated*. The final generation consists of S complete partitions. This is the method developed by the SMC authors to generate ensembles of random districting plans, like the four complete plans at the bottom of Figure 1.

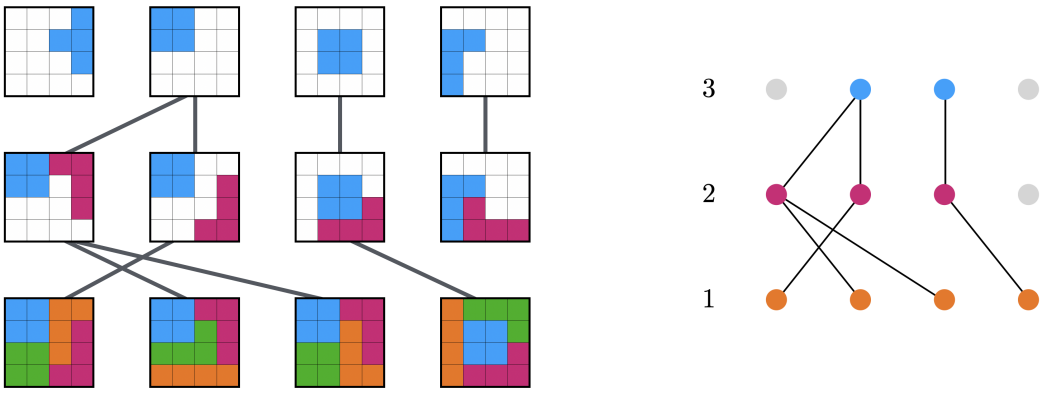


Figure 1: Simple example of partitioning a 4×4 grid into four districts. The adjacency pattern of the grid is the graph G, the number of districts is $k = 4$, and the size of the sample is $S = 4$. At right, the process is abstracted into a *descendancy diagram*. The district marked last (green) does not have a row of the diagram, because it is made up of area left over after the third district (orange) is marked.

SMC samples face a certain amount of characteristic redundancy. As the authors note, "because the SMC algorithm involves repeated resampling with replacement, for a finite number of samples it can suffer from particle system collapse [11], where many of the sampled plans share a small number of common districts (which originate as common ancestor particles in the SMC scheme)." In practical terms, this means that SMC samples can tend to have certain districts or sets of districts repeated many times across plans, like the blue square at the top left of the grid in Figure 1, which appears in 3/4 of the final sample. One aim of this note is to study this concentration of ancestry in combinatorial terms.

The second aim is to understand the tradeoffs faced by users in the choice of sampler. Citing McCartan–Imai again: "Like MCMC algorithms, the SMC algorithm generates samples which approximate the target distribution arbitrarily well as the sample size increases." Our second set of questions explores the convergence guarantees and practical diagnostics available with SMC in relation to the production of various data artifacts used in redistricting analysis, like histograms and boxplots. (See also [4] for more comparison of methods.)

Diagnosing strengths and weaknesses of the method has important real-world value. This is because SMC for redistricting, as implemented by the authors in the open-source package Redist [10], is already in widespread use in courts of law. The repetition of districts has been flagged as a limitation that undermines statistical claims about the sample. For instance, mathematician Kristopher Tapp produced an affidavit in New York state Senate litigation in which he attempted a replication of another expert's SMC ensemble of 5000 maps, and found that a certain set of 31 districts (covering about half of the state) appeared identically in over 64% of the sample.[1] In New Mexico state Senate litigation, a defense brief described the SMC method as being "plagued with duplicate simulations"; as a prophylactic measure to protect against this criticism, a defense expert cosmetically altered his SMC sample by perturbing the boundaries of districts so that he could claim that no districts were duplicated.[2] It is clear that rigorous attention to the issues around duplication and the consequences for statistical interpretation are greatly needed in the field.

1.1 Motivating questions

To understand the SMC algorithm for k districts, we will begin by studying *uniform descendancy diagrams* with levels (also called *layers* or *generations*) labeled $i = 1$ to $k-1$ from bottom to top, each of width S, in which each node chooses a parent uniformly at random from the generation above. Nodes in the top layer (indexed $k-1$) represent partial plans with a single initial district marked, and those at level i represent districting plans with $k-i$ districts marked. At level 1, $k-1$ districts are marked, which determines the kth and final district and amounts to specifying a complete plan. A node in a descendancy diagram is *active* if it has a descendant in the bottom layer, and *surviving ancestors* are active nodes at the top level (so named because they have descendants in the final population). Calculations using descendancy diagrams will omit all non-active nodes, because they have no role in the final sample constructed by SMC.

If we write $D \in \mathcal{D}(S,k)$ for a specific diagram of this form, then let $A(D)$ be the number of surviving ancestors in that diagram, and let $A(S,k)$ be the expected number of surviving ancestors $\mathbb{E}(A(D))$ as D ranges over the uniform distribution on $\mathcal{D}(S,k)$. We consider the following questions.

Question 1 (Ancestor extinction)**.** *As a function of S and k, what is the distribution of the number of surviving ancestors $A(D)$ in a uniform descendancy diagram? Give bounds or asymptotics for the expectation $A(S,k)$.*

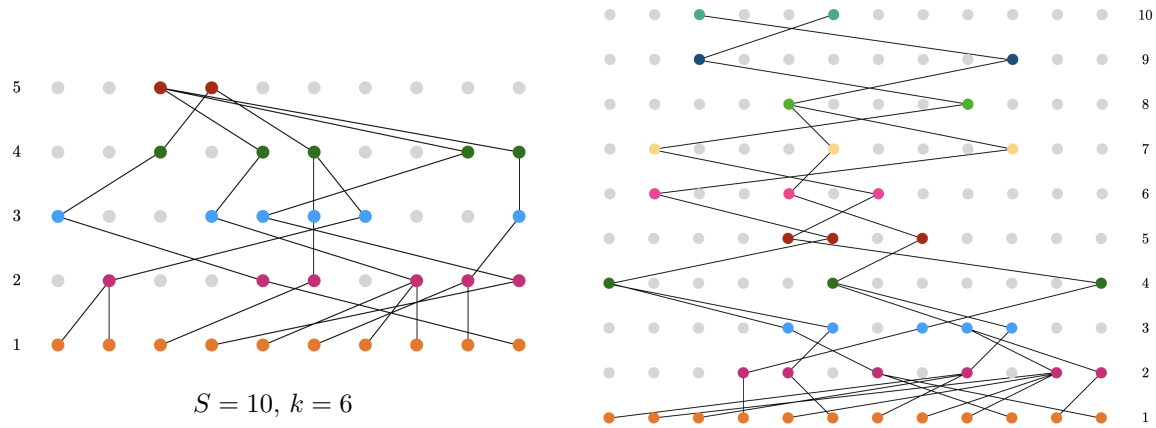
Question 2 (Extent of redundancy)**.** *Define $G(D,j)$ to be the number of final plans with at least j districts in common. How is that G distributed over $\mathcal{D}$ for each j?*

For instance, see Figure 3. Seeing high numbers at low levels is an indicator of repetition. In this case, there is one district that appears in 11 out of 12 final plans (value 11 appearing in top row). Worse than that, it is part of a group of 3 districts that appear identically in those 11 plans (value 11 in row $8 = k-3$). Also, there is a group of 7 districts that appears in 8 out of 12 final plans (value 8 in row $4 = k-7$). So for the sample of plans constructed according to this diagram D, we have $G(D,3) = 11$ and $G(D,7) = 8$.

The questions so far concern the combinatorics of descendancy diagrams, but the combinatorics is only one source of redundancy. It turns out to be compounded by several other factors. One compounding factor is the non-uniformity of weights in the intermediate generations that are used when the each generation picks its parents. A second factor is the graph being partitioned, which can start to have bottlenecks obstructing further district selection if the first few have been marked in an unlucky way.

[1] Tapp further notes that while an ensemble of 5000 63-district maps can have up to 315,000 distinct districts, his replication ensemble had only 12,319, so that each district was repeated an average of 1360 times. He calls this "a head-turning level of redundancy." [2]

[2] "Dr. Chen's implementation of the MCMC version of an SMC algorithm [sic] did not result in any duplicated maps. [Exh. D, Dep. ST 54:17–55:17 (falsely testifying that Dr. Chen's simulations contain duplicates), 136:6–136:20 (correcting his mistaken testimony)]." The opposing expert Sean Trende was no more sophisticated, opining in deposition that "Duplicates happen all the time... So it doesn't bother me, unless it gets extreme to where you end up having, like, 20 maps." [1]



$S = 10,\ k = 6$ $\qquad$ $S = 12,\ k = 11$

Figure 2: These two figures show structures we call *descendancy diagrams*. The bottom row is labeled as generation 1 in each case, increasing in index with each layer until generation $k - 1$ at the top. Each of these two diagrams has $A(D) = 2$, meaning that there are two top-level ancestors from which all members of the bottom generation are descended.

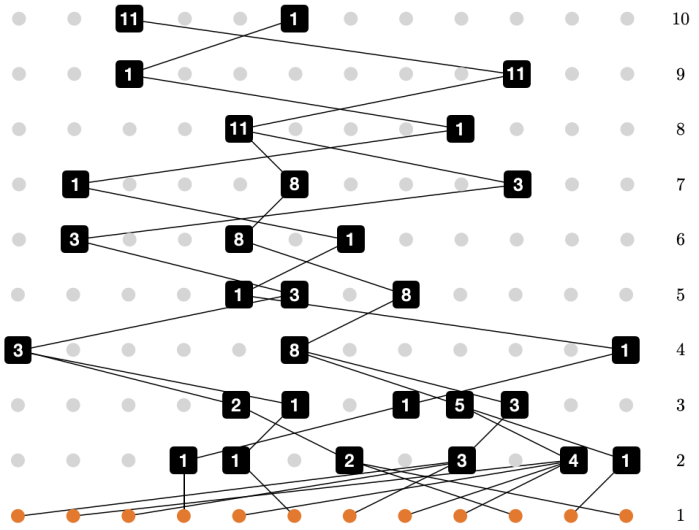


Figure 3: The $S = 12, k = 11$ example is repeated, now with the diagram nodes decorated by their number of final-generation descendants. High numbers appearing on low levels are markers of extreme redundancy.

Question 3 (Weighting and graph topology)**.** *How do ancestry concentration and redundancy get more severe as the weighting factors deviate from uniform, and when realistic graphs are used as the basis for the partition?*

Finally, we broaden the scope and consider the overall quality of the ensemble of S plans that consists of members of the final generation.

Question 4 (Convergence guarantees)**.** *What are the convergence guarantees for the sampling distribution obtained from the weak SMC Central Limit Theorem ([12, Prop 4.2])? How do they limit the extent of redundancy?*

Question 5 (Summary statistics)**.** *How do the convergence guarantees and diagnostics relate to the production of histograms, boxplots, and other percentile summary statistics?*

There are many other elements of the SMC code as implemented in Redist that pull results away from the simplicity of descendancy diagrams, besides those already mentioned (inter-generational weighting factors and bottlenecks in the graph topology). Another example is that SMC creates sequentially labeled districting plans but seeks to sample unlabeled plans; this is addressed with a corrective factor ψ which for $k > 13$ districts requires a second, auxiliary round of Monte Carlo estimation.[3] Another example is a final reweighting step to align the sample more closely with the target distribution.

The validation datasets employed in the article introducing SMC are graphs with 36 and 50 nodes and $k = 3, 4, 6$ districts; it is not at all clear that some of the challenges faced by SMC will become visible at that scale. The New York Senate case, in which the judge gave some credence to SMC ensemble made with default settings, had over 16,000 nodes and $k = 63$ districts.

Finally, it is very important to highlight that most of the SMC samples appearing in expert work, as well as the published work of the SMC authors, use small samples. Typically, sample sizes of 5000 are presented based on a single run at $S = 5000$ or by combining and subsampling multiple runs with $S = 2500$.[4] Thus for practical purposes, SMC sampling is currently intended to be performed with multiple small runs, not with sample sizes in the millions.

Below, we will alternate between trying to isolate the effects of different features of the SMC sampler and simply reporting outcomes when the code is run. This produces both a theoretical and a practical analysis.

Acknowledgments

We thank Peter Winkler and Chris Hoffman for helpful conversations and pointers to the literature. We are grateful to Peter Rock for his excellent work conducting SMC experiments to support this project. We thank Cory McCartan for generously sharing his time to explain SMC for redistricting and the Redist code, as well as for feedback on an earlier draft of this note. This material is based upon work supported by the National Science Foundation under Grant No. DMS-1928930 and by the Alfred P. Sloan Foundation under grant G-2021-16778, while the authors were in residence at the Simons Laufer Mathematical Sciences Institute (formerly MSRI) during the Fall 2023 semester. SC is also supported in part by NSF CCF-2104795; MD by NSF DMS-2005512.

2 Structure of descendancy diagrams

This section presents theoretical results, derived from the combinatorics of the descendancy diagrams, that allow us to bound the $A(S, k)$ values and begin to explain the expected behavior of collisions. We start by providing a Markov chain formulation for calculating exact values of $A(S, k)$ before providing more computationally efficient bounds on asymptotic behavior in terms of two recursive sequences. We conclude by examining the effect of weighting factors at each layer, proving that uniform choices minimize collisions and evaluating how much non-uniformity explains the repetitions found in empirical data.

2.1 Setup

We start with some simple observations about this model. When we take a uniform descendancy diagram with two layers (corresponding to an SMC process with three districts), Question 1 is a rephrasing of the classic birthday problem from probability. As k grows, the generalized birthday problem also has a combinatorial interpretation as a sequential balls-in-bins model (see [14]) or via random coagulations (see

[3] Some district configurations have many more ways of being sequentially labeled than others; this can produce distortion factors of over a million in practice. In SMC/Redist, the corrective factor ψ is described in [12, §4.4.2].

[4] The largest sample sizes we have found in the SMC 50-state data repository are at $S = 30,000$ [13]. Our independent attempts to produce large runs can reach $S = 100,000$ on certain states, but it is difficult to get past that size using basic professional-level computer resources. This is because the Redist SMC code has significant memory overhead associated with storing partial plans. Even on a medium-sized problem like redistricting Pennsylvania into $k = 18$ districts at the precinct level, a run with $S = 100,000$ consumes over 25 Gb of RAM.

[3]). Even in the language of ancestry, this has been studied in the context of genetic drift as the *Wright-Fisher Model* (see [7]). It is well known that the probability that two individuals' lineages remain distinct for at least i levels is $(1-1/S)^i$ and the probability that ℓ lineages remain (pairwise) distinct for at least i levels is $(1-1/S)^i(1-2/S)^i\dots(1-(\ell-1)/S)^i$. After renormalizing and sending $S\to\infty$, the time of the first (pairwise) coalescence among ℓ distinct lineages approaches an exponential distribution with rate $\ell(\ell-1)/(2S)$. There is a rich literature considering variations of this model, using it to design Markov chains, and extending it to infinite S.

Our setting differs slightly from the Wright-Fisher model by only considering lineages that extend to the bottom layer and discarding the others—in the language developed above, we only track active nodes.

Lemma 1 (One-step probabilities)**.** *If a given generation i has $1\le t\le S$ active nodes, then the expected number of ancestors in the generation immediately above (generation $i+1$) is $S-S(1-\frac{1}{S})^t$. The probability that there are exactly v activated nodes in generation $i+1$ when there are t activated nodes in generation i is $P(v,t,S)=\binom{S}{v}\sum_{i=0}^{v}(-1)^{v-i}\binom{v}{i}\left(\frac{i}{S}\right)^t$.*

Proof. In generation $i+1$, let I_j be an indicator variable representing node j being chosen at least once. For any individual $1\le j\le S$ we have $\mathbb{P}[I_j=1]=1-(1-\frac{1}{S})^t$. Then the number of activated nodes is $\sum_{j=1}^{S}I_j$, and by linearity of expectation its expected value is $S-S(1-\frac{1}{S})^t$, as desired.

The second statement is a birthday problem variant. For each set of $\binom{S}{v}$ parents the probability that all edges end up in that set is $\left(\frac{v}{S}\right)^t$ and applying inclusion/exclusion to account for versions that don't select every element in that set gives the desired result. □

With this lemma we can can compute the expected value across two or more generations exactly, but the formula does not give much insight, so we omit it.

We can reformulate the problem as a Markov chain on the states $1,2,3,\dots,s$ representing the number of activated nodes at a given layer. This is an absorbing Markov chain with absorbing state 1, with transition probabilities given by $M_{i,j}=\begin{cases}P(i,j,s) & i\ge j\\ 0 & i<j\end{cases}$, forming a lower-triangular transition matrix. The expectation we seek is $A(S,k)=\begin{bmatrix}0 & 0 & \cdots & 1\end{bmatrix}M^{k-2}\begin{bmatrix}1\\2\\\vdots\\S\end{bmatrix}$. For example, when $S=3$, we have $M=\begin{bmatrix}1 & 0 & 0\\ 1/3 & 2/3 & 0\\ 1/9 & 6/9 & 2/9\end{bmatrix}$ and for diagrams with two layers ($k=3$) we have that the three nodes have an expected $19/9=2.111...$ parents.

2.2 Limiting behavior

$A(S,k)$ is defined as the expected number of top nodes surviving to the bottom over diagrams $D\in\mathcal{D}(S,k)$. First, observe that for fixed S, we have $\lim_{k\to\infty}A(S,k)=1$. This follows directly from the Markov chain interpretation of the problem, because it is a non-increasing sequence of positive integers with a positive probability of strict decrease at each step while the value is greater than 1.

Given S, construct a sequence of coefficients as follows: $a_{S,0}=1$; and $a_{S,i+1}=1-\left(1-\frac{1}{S}\right)^{(a_{S,i})S}$. Where S is understood to be fixed we will write simply $a_0=1$, $a_{i+1}=1-\left(1-\frac{1}{S}\right)^{a_iS}$. By Lemma 1, these approximate the share of active nodes at a given level of the diagram: $a_iS\approx A(S,i)$. We will get a rigorous upper bound below.

Note that as S gets large, $\left(1-\frac{1}{S}\right)^S$ rapidly converges to $1/e$ from below. With this in mind, we can offer an second approximation with a sequence given by $b_0=1$; and $b_{i+1}=1-\frac{1}{e}^{b_i}$, which is more likely to have a useful generating function, if an analytic description is desired. Table 1 shows the b_i to be good approximations $a_{S,i}$ for large S—and shows that $b_i\le A(S,i)\le a_{S,i}$ in all instances we investigated.

Lemma 2. *For fixed $S>1$ and $a_i=a_{S,i}$, we have $\lim_{i\to\infty}a_i=\frac{1}{S}$.*

i	0	1	2	3	4	5	6	7	8	9	10
$a_{10,i}$	1	0.6513	0.4965	0.4073	0.3490	0.3077	0.2769	0.253	0.234	0.2185	0.2056
$a_{100,i}$	1	0.6340	0.4712	0.3772	0.3155	0.2718	0.2390	0.2135	0.1056	0.1931	0.1625
$a_{1000,i}$	1	0.6323	0.4688	0.3744	0.3124	0.2684	0.2355	0.2099	0.1895	0.1727	0.1587
$a_{5000,i}$	1	0.6322	0.4686	0.3741	0.3121	0.2682	0.2352	0.2096	0.1891	0.1723	0.1583
b_i	1	0.6321	0.4685	0.3741	0.3121	0.2681	0.2352	0.2095	0.1890	0.1723	0.1582

Table 1: Values of $a_{S,i}$ for $S \in \{10, 100, 1000, 5000\}$ and $0 \leq i \leq 10$. As S grows, the $a_{S,i}$ and b_i get close.

Proof. First, we show by induction that $a_i \geq 1/S$ for all i. This is clearly true for $a_0 = 1$. If $a_i \geq 1/S$, then $a_i S \geq 1$ and

$$a_{i+1} = 1 - \left(1 - \frac{1}{S}\right)^{a_i S} \geq 1 - \left(1 - \frac{1}{S}\right)^{1} = \frac{1}{S}.$$

We will also need the following fact, which follows from the inequality $1 + c < e^c$ for $c = 1/(S-1) \neq 0$:

$$-\left(1 - \frac{1}{S}\right) \ln\left(1 - \frac{1}{S}\right)^{S} < 1. \tag{1}$$

As we know $a_{i+1} = 1 - \left(1 - \frac{1}{S}\right)^{a_i S}$, we will focus on the function $f(x) = 1 - \left(1 - \frac{1}{S}\right)^{xS}$. We begin by noting $f(\frac{1}{S}) = \frac{1}{S}$. We also see that

$$f'(x) = -\left(1 - \frac{1}{S}\right)^{Sx} \ln\left(1 - \frac{1}{S}\right)^{S}$$

Equation (1) tells us that $f'(\frac{1}{S}) < 1$. For $x \geq \frac{1}{S}$, the values we are interested in, this slope is always positive (because $\ln\left(1 - \frac{1}{S}\right)^{S}$ is negative) and is strictly decreasing in x. This implies for $x > \frac{1}{S}$, $f(x)$ is strictly bounded above by the line tangent to it at $1/S$:

$$f(x) < f\left(\frac{1}{S}\right) + f'\left(\frac{1}{S}\right)\left(x - \frac{1}{S}\right) = \frac{1}{S} + f'\left(\frac{1}{S}\right)\left(x - \frac{1}{S}\right)$$

First, we will show the sequence of a_i's is decreasing. Using $f'(\frac{1}{S}) < 1$, we see

$$a_{i+1} = f(a_i) < \frac{1}{S} + f'\left(\frac{1}{S}\right)\left(a_i - \frac{1}{S}\right) < \frac{1}{S} + a_i - \frac{1}{S} = a_i$$

As the sequence of a_i's is bounded below by $\frac{1}{S}$ and strictly decreasing, its limit must exist.

Suppose, for the sake of contradiction, that the limit of the a_i's is strictly greater than $1/S$, that is, it is $1/S + \alpha$ for some $\alpha > 0$. This means for all $\varepsilon > 0$, there is some sufficiently large i such that $a_i < 1/S + \alpha + \varepsilon$. Choose ε such that $0 < \varepsilon < \alpha(1 - f'(\frac{1}{S}))/f'(\frac{1}{S})$. This is possible to do because $\alpha > 0$ and $f'(\frac{1}{S}) < 1$. Note this choice of ε means $f'(\frac{1}{S})(\alpha + \varepsilon) < \alpha$. It follows that:

$$a_{i+1} = f(a_i) < \frac{1}{S} + f'\left(\frac{1}{S}\right)\left(a_i - \frac{1}{S}\right) < \frac{1}{S} + f'\left(\frac{1}{S}\right)(\alpha + \varepsilon) < \frac{1}{S} + \alpha.$$

As this is a monotone decreasing sequence and we assumed its limit was $\frac{1}{S} + \alpha$, it is impossible to have $a_{i+1} < \frac{1}{S} + \alpha$, giving a contradiction. Therefore it must be the case that the limit of this sequence is $\frac{1}{S}$, as claimed. □

Proposition 3. $A(S, k) \leq a_k S$.

Proof. Let X_i be a random variable denoting the number of active nodes at level i (those that have descendants in level 1). Thus $X_1 \equiv S$. We are trying to get bounds on $\mathbb{E}[X_{k-1}] = A(S, k)$, the expected number of active nodes in the top level of a k-district descendancy diagram, which has $k - 1$ levels.

We will prove by induction that $\mathbb{E}[X_i] \leq a_i S$, which suffices to prove the proposition. When $i = 0$, we have $\mathbb{E}[X_0] = a_0 S = S$, and the statement is true. Fix $i \geq 1$, and suppose $\mathbb{E}[X_i] \leq a_i S$. By Lemma 1 and linearity of expectation, we have

$$\mathbb{E}[X_{i+1} \mid X_i] = S - S\left(1 - \frac{1}{S}\right)^{X_i}.$$

We will use the Law of Total Expectation ($\mathbb{E}[X_{i+1}] = \mathbb{E}[\mathbb{E}[X_{i+1} \mid X_i]]$) and Jensen's Inequality (for $c > 0$, $\mathbb{E}[c^X] \geq c^{\mathbb{E}[X]}$). We get

$$\mathbb{E}[X_{i+1}] = \mathbb{E}[\mathbb{E}[X_{i+1} \mid X_i]] = \mathbb{E}\left[S - S\left(1 - \frac{1}{S}\right)^{X_i}\right] = S - S\mathbb{E}\left[\left(1 - \frac{1}{S}\right)^{X_i}\right] \leq S - S\left(1 - \frac{1}{S}\right)^{\mathbb{E}[X_i]}$$
$$\leq S - S\left(1 - \frac{1}{S}\right)^{a_i S} = a_{i+1} S. \qquad \square$$

Remark 4. *While we only show $a_k S$ is an upper bound, for large k it is tight: in the limit as $k \to \infty$, it matches the trivial lower bound $\mathbb{E}[X_k] \geq 1$, which holds because there is at least one active node at each level. The empirical results, such as those presented in Figure 4, suggest the much stronger asymptotic $A(S, k) \sim a_k S$ as $S, k \to \infty$.*

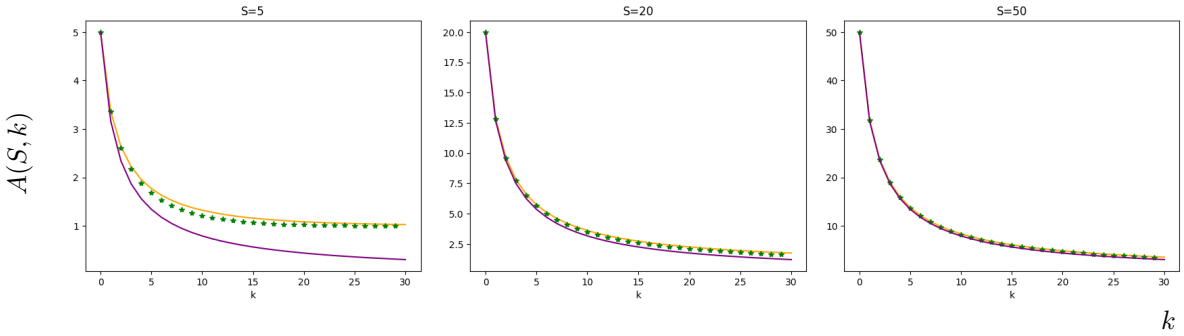


Figure 4: If the distribution of weights is uniform, these plots show the expected number of surviving ancestors (districts drawn in the initial generation that appear in the final sample of plans) as k grows, for $S = 5, 20, 50$. The horizontal axis is k in each plot and the vertical axis is the expected number of top-level ancestors. Green stars are precise outputs from the Markov chain expression, compared to the $a_k S$ values in orange and the $b_k S$ values in purple (each interpolated by a curve). In these small experiments, it is always true that $b_k S \leq A(S, k) \leq a_k S$, and that $a_k S \approx A(S, k)$ is a very good approximation.

Table 2 shows that the predicted repetition (due to combinatorial collision expected under uniform weighting) is already pronounced. However, the empirical runs on real-world geography show far greater redundancy. We include $k = 18$ (PA Congress 2010), $k = 42$ (NM state House), $k = 52$ (CA Congress 2020), $k = 63$ (NY State House), and $k = 203$ (PA State House).

Remark 5. *The case of square diagrams is a natural one to consider. Numerical results suggest that $A(S, S)$ limits to a constant slightly greater than 2. Subsequently, once there are two active nodes in a population of S, it takes an expected S more steps for those to collide, leaving a single common ancestor. This suggests that when $k \approx 2S$, we expect the ancestry to collapse to a single node—one initial district will appear in every plan. This will be further discussed below in Table 3.*

	PA Congress $k = 18$	NM House $k = 42$	CA Congress $k = 52$	NY House $k = 63$	PA House $k = 203$
$a_{5000,k}$	0.1066	0.0466	0.0377	0.0313	0.0099
b_k	0.1065	0.0464	0.0376	0.0312	0.0098
predicted average repetition $1/a \approx S/A$	9.4	21.6	26.6	32.1	102.0
average district repetition (averaged over trials)	18.2	121.6	518.6	785.1	4905.0
max district repetition (averaged over trials)	499.2	1896.9	3104.8	3350.8	4977.1
max district repetition (max over trials)	4515	4951	5000	5000	5000

Table 2: For several realistic-sized problems, we consider the expected repetition of the initial districts that survive to the final sample. We report $1/a$ as predicted average repetition because it is a known bound that is quite tight already for small S. We conduct 1000 trials with $S = 5000$ for each column; completing one trial with $k = 203$ can take up to five days. The fact that the observed average repetition is appreciably more severe than predicted points to the impact of other causes of redundancy, like non-uniform weights, graph bottlenecks, and final reweighting—these have a snowballing impact as the number of districts grows. These will be explored below.

2.3 Non-uniform weights

Above we assumed that each active node chooses its parent uniformly at random. In practice, this is not how the SMC code works; the weights depend on graph properties of the partitions. The weight on node j at level i is given by $w_i^{(j)} = \frac{\left(\tau(G_i^{(j)})\right)^{\rho-1}}{\left|\partial G_i^{(j)}\right|}$, where the numerator is τ, the product of the number of spanning trees in the pieces of the partial plan $G_i^{(j)}$, raised to a power $\rho - 1$, and the denominator is the size of the edge cut.

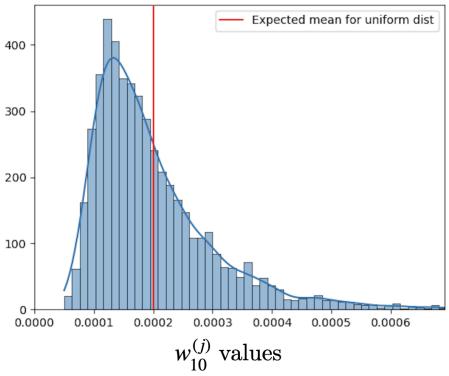


Figure 5: Truncation of a long-tailed histogram of weights in a descendancy diagram on state Senate districts in New Mexico ($k = 42, i = 10, S = 5000$, default settings). If weights were uniform, the distribution of weights would be concentrated at the red line. Instead, when drawing the 33rd district in this SMC process, some 32-district partial plans are over 100 times likelier than others to be chosen.

When $\rho \neq 1$ these weight factors will give wildly different probability of selection to plans based on their compactness, due to τ values for districts that can easily differ by 10^{100} in realistic problems.[5] Even at $\rho = 1$,

[5] In particular, $\tau > e^N$ for many planar graphs on N vertices (for instance $\tau \sim e^{1.6N}$ for triangular lattices), and Congressional

plans with longer boundaries will be weighted down. (See Figure 5 for an empirical example with $\rho = 1$.) These inter-generational weights thus present a compactness-related bias pulling away from uniformity for any choice of parameters.

Next we show that non-uniform weights exacerbate the sample repetition. Recall that X_i was a random variable denoting the number of active nodes at level i, where $X_1 \equiv S$ and parents are chosen uniformly at random at each level. We now set up our second model by fixing some non-uniform distribution over S nodes at each level $1, \ldots, k-2$ for the selection of parents. Fixing those distributions, we initialize $Y_1 \equiv S$, and let Y_i be a random variable denoting the number of active nodes at level i with the specified parent selection probabilities.

Lemma 6 (Uniform descendancy minimizes ancestor collapse)**.** *For $i \geq 2$, let X_i give the count of active nodes at level i randomized over uniform descendancy diagrams, while Y_i is defined instead with the same non-uniform distribution on each level. Then*

$$\mathbb{E}[Y_i \mid Y_{i-1} = a] \leq \mathbb{E}[X_i \mid X_{i-1} = a].$$

Proof. Consider the random variable Y_i. For $j \in \{1, 2, \ldots, S\}$, let p_j denote the probability that an individual at level $i-1$ chooses j as their parent in level i (note the p_j's may also vary with i). We will need Hölder's Inequality, which states that for $p, q \in [1, \infty)$ satisfying $1/p + 1/q = 1$ and any two vectors $\mathbf{u}$ and $\mathbf{v}$, $\|\langle \mathbf{u}, \mathbf{v} \rangle\|_1 \leq \|\mathbf{u}\|_p \|\mathbf{v}\|_q$. We apply this to the vectors $\mathbf{u}$ where $u_j = (1-p_j)/(S-1)$ and $\mathbf{v} = (1, 1, 1, \ldots, 1)$. Note

$$\|\langle \mathbf{u}, \mathbf{v} \rangle\|_1 = \|\mathbf{u}\|_1 = \sum_{j=1}^{S} \frac{1-p_j}{S-1} = 1.$$

Using $p = a$ and $q = a/(a-1)$, we see that

$$\|\mathbf{u}\|_a = \left(\sum_{j=1}^{S} \left(\frac{1-p_j}{S-1} \right)^a \right)^{1/a} = \left(\frac{1}{(S-1)^a} \sum_{j=1}^{S} (1-p_j)^a \right)^{1/a}$$

$$\|\mathbf{v}\|_{a/(a-1)} = \left(\sum_{j=1}^{S} 1^{a/(a-1)} \right)^{(a-1)/a} = S^{(a-1)/a}$$

Putting this together with Hölder's inequality, we see that

$$\left(\frac{1}{(S-1)^a} \sum_{j=1}^{S} (1-p_j)^a \right)^{1/a} S^{(a-1)/a} \geq 1 \qquad \text{and} \qquad \sum_{j=1}^{S} (1-p_j)^a \geq \frac{(S-1)^a}{S^{a-1}} = S \left(1 - \frac{1}{S} \right)^a.$$

We now see that

$$\begin{aligned} \mathbb{E}[Y_i \mid Y_{i-1} = a] = \sum_{j=1}^{S} (1 - (1-p_j)^a) &= S - \sum_{j=1}^{S} (1-p_j)^a \\ &\leq S - S \left(1 - \frac{1}{S} \right)^a = S \left(1 - \left(1 - \frac{1}{s} \right)^a \right) = \mathbb{E}[X_i \mid X_{i-1} = a]. \end{aligned}$$

This completes the proof. □

We find empirically that the weights at each level frequently have a distribution shaped like the one shown in Figure 5, which was drawn from a run on New Mexico state Senate districts. In New Mexico, it was common to see max-to-median weight ratios of 10 within a generation, and max-to-min ratios of 30,

districts might typically contain $N = 500$ precincts. This is one reason that validating on a 6×6 grid with 6 districts is inadequate to see salient effects of scale: in that setting, τ values for individual districts can only differ by a factor of 15. See related discussion in [6, §5.1].

Lowest level with a "mega-ancestor" accounting for φ share of the final outputs
(Low table entries for high φ are signs of extreme redundancy)

F	$S = 10$	100	1000	5000
$\varphi = .01$	—	—	3.8	15.4
.1	—	5.5	51.1	256.3
.25	2.5	18.7	188.3	957.8
.5	5.5	60.2	622.2	3187.3
.75	14.6	144.7	1433.5	7092.4
1	17.9	201.9	2065.2	9966.2

Uniform weights

F	$S = 10$	100	1000	5000
$\varphi = .01$	—	—	2.0	2.0
.1	—	2.0	4.6	78.4
.25	2.0	2.0	19.7	320.1
.5	2.0	2.8	65.8	1032.7
.75	2.0	5.3	151.7	2401.9
1	2.7	11.1	232.3	3533.2

$100 : 1 : 1 \cdots : 1$ weights

F	NM $k = 42$ $S = 5000$	NY $k = 63$ $S = 5000$
$\varphi = .01$	3.2 (100%)	2.9 (100%)
.1	8.8 (100%)	6.9 (100%)
.25	14.9 (71.4%)	11.9 (99%)
.5	17.0 (23.5%)	18.8 (74%)

Actual runs of SMC code

Table 3: Recall that $F(D, \varphi)$ reports the lowest level at which some node is an ancestor to φ share of the bottom generation. (This is vacuous if $\varphi S \leq 1$.) The tables show estimated expectations for $F(D, \varphi)$ with uniform weights and with stylized non-uniform weights—each cell value is obtained by averaging over 1000 trials. Reading across the bottom row in the case of uniform weights (top left) confirms that $A(S, 2S) \approx 1$. Collapse is exacerbated significantly if we use stylized non-uniform weights (top right). However, the actual runs on New Mexico and New York (bottom) show that the empirical repetition can be far greater than what is predicted by the stylized models. For instance, the NM cell at $\varphi = .25$ tells us that 714 out of 1000 trials in New Mexico had a node serving as ancestor to 25% of the final generation, and that node on average occurred at level 14.9 (meaning 25% of the plans had $42 - 15 = 27$ districts in common).

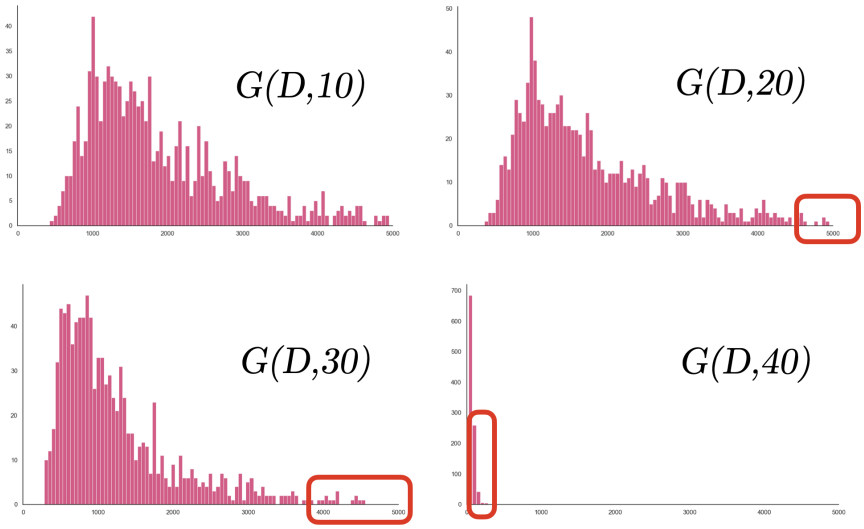
even with $\rho = 1$. In New York's Senate districts, these ratios were commonly 30 and 2000, respectively. As we will see, skews of this kind will tend to significantly increase the collision rate.

Recall that one goal (Question 2) is to measure the distribution of statistics $G(D, j)$ defined as the number of final plans in D with j districts exactly in common. A mathematically more natural expression that contains the needed information but is a bit harder to phrase in English is $F(D, \varphi)$, the lowest level at which there is a "mega-ancestor" accounting for φ share of the final generation:

$$F(D, \varphi) := \min\{i : \exists\ j \text{ with } d(i, j) > \varphi \cdot S\}.$$

Table 3 shows an simulated comparison of $F(D, \varphi)$ between the case of uniform weights and a simple non-uniform setup where one node at each layer is 100 times more likely to be selected than each of the others (that is, the weights are $100 : 1 : 1 \cdots : 1$). Each are run 1000 times. As we would expect given Lemma 6, the ancestor collapse is accelerated in the non-uniform case. But even this significantly understates the actual repetition in 1000 runs to make SMC samples from New Mexico and New York; we can compare this as well to Tapp's expert affidavit finding roughly that $F(D, .6) < 31$ for a $S = 5000$ sample in New York. The excess degeneracy in real-world samples is partly because the graph partition step itself can boost repetition; if partial progress has created a hard-to-split remainder, this creates yet another scenario in which a generation may be filled out with repeats. (This is referred to as graph "bottlenecks" elsewhere in this note.)

Figure 6 turns this around and shows the distribution of $G(D, j)$, the number of plans with j districts in common, for the same 1000 SMC runs on the New Mexico Senate. Though the redundancy is striking in New Mexico, it is even worse in New York, the other real-world example we track throughout this note.



Observed $G(D, j)$ for New Mexico runs

Figure 6: We now recast the information from the same 1000 SMC runs to spell out the redundancy. The histograms show how many plans have a set of j districts exactly in common. A few observations are visible in the marked areas. On several runs, more than 98% of outputs shared 20 districts out of 42 exactly in common. On several runs, more than 90% of outputs shared 30 districts exactly in common. And finally, more than 1/4 of the runs have 50 or more plans in their outputs that are nearly identical statewide, sharing 40 out of 42 districts. These plots are from New Mexico; the effects in New York are still more extreme.

3 Convergence guarantees and diagnostics

In [12], the main convergence result is a weak central limit theorem stated as follows.

Proposition 7 (McCartan–Imai Prop 4.2). *Let $\pi_S = \sum_{j=1}^{S} w^{(j)} \delta_{[\xi(j)]}$ be the weighted particle approximation generated by [their SMC Algorithm]. Then for all measurable h on unlabeled plans, as $S \to \infty$,*

$$\sqrt{S}\left(\mathbb{E}_{\pi_S}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \xrightarrow{d} \mathcal{N}(0, V_{\mathrm{SMC}}(h))$$

for some asymptotic variance $V_{\mathrm{SMC}}(h)$.

As the authors note, this is convergence in probability rather than almost sure convergence. This style of convergence result does not rule out significant sample repetition. To understand the guarantees better, consider the following construction.

Example 8 (Controlled repetition sampler (CRS)). *Fix a parameter $0 < \alpha < 1/2$. Given a distribution π on a state space Ω, let the* controlled repetition sampler with parameter α *be defined as follows: a sample of size S is constructed by taking one draw $x \sim \pi$ and adding x to the sample $\lceil S^{\alpha} \rceil$ times, each with weight $1/S$. Next, create a smaller SMC sample of $S' = S - \lceil S^{\alpha} \rceil$ plans. If a plan in this smaller sample is assigned weight $w^{(j)}$ by SMC, we add it to our CRS sample with normalized weight $w^{(j)} S'/S$.*

Despite the amount of repetition present, where up to $\sqrt{S}$ plans in the sample of S are fully identical, this CRS method still satisfies the conclusions of Proposition 7. (This is proved in Appendix A.) Note that the power S^{α} could be replaced with any function of S such that $f(S)/\sqrt{S - f(S)} \to 0$.

To compensate for the repetition from SMC or CRS and attempt to recover the shape of a distribution when large samples are computationally expensive, one may be tempted to combine multiple separate samples rather than enlarging a single sample. Indeed, even for a small validation example (dividing the 6×6 grid

into $k = 6$ districts, [12, Fig 4]) the SMC authors have averaged 24 independent runs to obtain their estimates rather than enlarging the size of a single sample. In other published work [13], the same authors and collaborators present ensembles of 5000 maps for all 50 states, and do so in most cases by combining subsamples from multiple SMC runs. But we know of no theory for this: it is not clear what balance of the sample size S and the number of separate runs would constitute best practices for users of SMC.[6]

In SMC/Redist, the main convergence diagnostic is the Gelman–Rubin $\hat{R}$ statistic, which compares within-sample variance to between-sample variance, typically applied to batches of 2500 or 5000 plans.[7] Discussing related issues for MCMC, Charles Geyer [9] wrote of several popular techniques for using many short runs in place of one long run as "worse than useless": they raise your confidence and produce cosmetically better samples while giving no reason to believe the outputs are close to the target. For now, the computational costs of SMC/Redist lock users in to a many-short-runs framework.

4 Discussion

Since spanning tree methods were introduced in redistricting around 2018, many authors who need a single exemplar of a plan (such as to serve as the starting point for a Markov chain) obtain one by recursively partitioning a tree down to districts. One way to view SMC for redistricting is that it constructs the whole sample by running this seeding process many times. Employing the structure of a descendancy diagram allows the use of weights that help control the properties of the sample, but at the cost of introducing significant combinatorial redundancy.

Repetition undermines statistical conclusions and data visualization. SMC is sometimes claimed to produce nearly independent samples from arbitrary distributions.[8] However, district repetition can create massive dependencies, with many plans being identical on large regions, for the sample sizes currently possible with SMC/Redist. Numerous factors that are present in real use cases—non-uniform weights stemming from compactness terms, and restricted choices in the decision tree caused by the connection topology of the state, among others—can contribute to very severe repetition, which is visible in plots. A highly redundant sample does not allow for reliable outlier analysis because its percentile statistics will often be far from those of the target distribution. To put the same point in visual terms: significant repetition undermines the use of an SMC ensemble to infer the shape of a distribution of summary statistics, such as in histograms and boxplots. If statistics such as $\hat{R}$ are used as diagnostics on a histogram, they should be applied to the height of each bar. A box-and-whiskers plot on Pennsylvania, as shown in [12, Fig 7], would need 90 $\hat{R}$ calculations (top whisker, third quartile, median, first quartile, bottom whisker for each district), which would require many runs of SMC.[9]

Final reweighting cannot compensate for small samples. The SMC process leverages importance sampling by constructing an initial sample through a descendancy diagram and then reweighting according to the target distribution π only when the sample is complete. Before the final reweighting, the sample is approximately distributed by the spanning tree distribution τ on partitions—but somewhat distorted by repetition, labeling bias, and other artifacts of the construction. The authors intend to use this method to target arbitrary distributions $\pi(\xi) \propto e^{-J(\xi)}\tau(\xi)^{\rho}$, but, in particular, the energy functional J is never used until the descendancy diagram is complete; partitions that are never encountered by the tree-based generation process cannot be rescued by reweighting. Thus attempts to target a general π with SMC will fare no better than applying one-shot reweighting to previously known methods to sample from τ, such as MCMC. The accuracy depends on emitting a large and diverse sample from the descendancy process. The Redist implementation of SMC struggles to produce sample sizes beyond the tens of thousands on practical problems, which means that many legally relevant events will never be observed—whereas current Markov chain methods for sampling from τ can be run to billions of steps.

[6] For the illustrative example CRS, the ideal structure would be many samples of size 1. For SMC, this would fail, because a large S is already needed for the reweighting of the final sample to take the target distribution into account at all.

[7] Information on the $\hat{R}$ diagnostic can be found at [8, 15].

[8] For instance, this is explicit in the Redist documentation at https://perma.cc/YV37-JZNR.

[9] See [5] for an example where a diagnostic metric, in that case the Kolmogorov–Smirnov statistic, is used in this way to support a box-and-whiskers plot.

All-purpose SMC ensembles are unsuited for novel measurements. Courts have often expressed an interest in the presence of individual districts with particular properties. For instance, in the litigation challenging the Pennsylvania Congressional plan, the court strongly discouraged the division of Pittsburgh across two districts (and the special master was said to treat it as a "disqualifying feature" of a plan).[10] This preference emerged long after the initial expert work had been conducted. In the New Mexico legal challenge, the parties to litigation debated whether it was disqualifying if any district "contains more than 60% of the state's active oil wells."[11] These examples illustrate that it will frequently be legally relevant to know if some district-level property is common in a neutrally constructed ensemble. If the most-repeated district in some Pennsylvania SMC run happens to divide Pittsburgh, say, the ensemble can give a highly misleading answer. Ensembles constructed with current methodology, including the ALARM ensembles published in *Scientific Data* [13], are unsuited for estimating the frequency with which district-level properties occur, beyond those properties tested at the time of data generation.[12]

All issues compound with large numbers of districts. Large numbers of districts (large k) exacerbate all of the problems described here.[13] The published validation efforts only go up to $k \leq 6$ districts, and the authors themselves have used subdivision to make the problem more tractable—the ALARM 50-state project breaks up Texas ($k = 38$), Florida ($k = 27$), and California ($k = 52$) into three or more ad hoc pieces, redistricts them separately with SMC runs, and combines the outputs to make statewide Congressional plans.[14] Ensembles that have been modularized in this way have an unknown relationship to the target distribution on the full state.

SMC for redistricting is a highly valuable addition to the literature on sampling methods for graph partitioning. In addition to the theoretical contribution, the Redist package that implements SMC is commendably well-documented and user-friendly, and its authors have chosen default settings that allow beginners to run to completion on many full-sized problems. Also notably, the main code faced by users of Redist is in R, a programming language that is popular in social science graduate training. This has created the conditions for even first-time users of graph algorithms to generate materials for expert reports in court cases across the United States, but without a deep understanding of diagnostics and limitations.[15]

In this note, we show that the combinatorics of descendancy diagrams combines with a host of other factors to create potentially severe district repetition in SMC samples. In most cases at the full problem scale of a U.S. state, minimizing the effects of repetition would call for far larger sample sizes than is currently possible. Issues compound when attempting to target distributions that differ from the spanning tree distribution τ or when the plans have more than about a dozen districts. All of these observations counsel caution in using SMC on full-scale redistricting problems.

[10] *Carter v. Chapman* (2022), see https://www.pacourts.us/assets/opinions/Supreme/out/J-20-2022mo.pdf?cb=1.

[11] *Republican Party vs. Oliver* (2023), see nmlegis.gov links, particularly *Plaintiff's Opposed Motion to Exclude Expert Report & Expert Testimony of Dr. Jowei Chen* [1].

[12] In [13], the $\hat{R}$ statistic is used on a preset list of metrics: "Finally, we evaluate the convergence of the algorithm for the specific set of summary statistics described above that are of interest to practitioners." It does not seem that $\hat{R}$ is being applied to each histogram bin or boxplot element, but rather to means of one-dimensional statistics.

[13] Even with small numbers of districts, there can be issues: if few districts have many units, then the inter-generational weights can be highly non-uniform, which will likewise boost repetition. We suspect this is a real but less severe worry.

[14] See Texas, Florida, and California README files from the ALARM 50-state project.

[15] Experts indicating that SMC/Redist was their first exposure to graph algorithms, and sometimes even to algorithmic sampling methods more broadly, filed reports not only in New Mexico and New York, but also North Carolina, Pennsylvania, Louisiana, and Texas, and possibly more.

References

[1] Legislative defendants' response to plaintiffs' proposed motion to exclude. Fifth Judicial District of New Mexico. *Republican Party of New Mexico v. Maggie Toulouse Oliver* (2022). https://www.nmlegis.gov/Redistricting2021/Litigation%20Docs/292%20-%20September%2025,%202023%20Plaintiff's%20Opposed%20Motion%20to%20Exclude%20Expert%20Report%20&%20Expert%20Testimony%20of%20Dr.%20Jowei%20Chen.pdf.

[2] Second Affidavit of Dr. Kristopher R. Tapp, PhD. Supreme Court of the State of New York. *Harkenrider v. Hochul* (2022). https://perma.cc/29X3-59CX.

[3] Jean Bertoin. *Random Fragmentation and Coagulation Processes.* Cambridge University Press, 2006.

[4] Sarah Cannon, Moon Duchin, Dana Randall, and Parker Rule. Spanning tree methods for sampling graph partitions, 2022.

[5] Jeanne Clelland, Haley Colgate, Daryl DeFord, Beth Malmskog, and Flavia Sancier-Barbosa. Colorado in Context: Congressional Redistricting and Competing Fairness Criteria in Colorado. *Journal of Computational Social Science*, 5:180–226, May 2021.

[6] Daryl DeFord, Moon Duchin, and Justin Solomon. Recombination: A Family of Markov Chains for Redistricting. *Harvard Data Science Review*, 3(1), March 2021. https://hdsr.mitpress.mit.edu/pub/1ds8ptxu.

[7] Rick Durrett. *Probability Models for DNA Sequence Evolution.* Springer, second edition, 2008.

[8] Andrew Gelman and Donald B. Rubin. Inference from iterative simulation using multiple sequences. *Statistical Science*, 7(4):457–472, 1992.

[9] Charles J. Geyer. Introduction to Markov chain Monte Carlo. In *Handbook of Markov chain Monte Carlo*, Chapman & Hall/CRC Handb. Mod. Stat. Methods, pages 3–48. CRC Press, Boca Raton, FL, 2011.

[10] C. T. Kenny, C. McCartan, B. Fifield, and K. Imai. Redist: Computational algorithms for redistricting simulation. R Package. https://CRAN.R-project.org/package=redist.

[11] Jun S. Liu, Rong Chen, and Tanya Logvinenko. A theoretical framework for sequential importance sampling with resampling. In *Sequential Monte Carlo methods in practice*, Stat. Eng. Inf. Sci., pages 225–246. Springer, New York, 2001.

[12] Cory McCartan and Kosuke Imai. Sequential Monte Carlo for sampling balanced and compact redistricting plans. *The Annals of Applied Statistics*, 17(4):3300 – 3323, 2023.

[13] Cory McCartan, Christopher T. Kenny, Tyler Simko, George Garcia III, Kevin Wang, Melissa Wu, Shiro Kuriwaki, and Kosuke Imai. Simulated redistricting plans for the analysis and evaluation of redistricting in the United States. *Scientific Data*, 9:689, 2022.

[14] Martin Raab and Angelika Steger. "Balls into Bins" — A simple and tight analysis. In Michael Luby, José D. P. Rolim, and Maria Serna, editors, *Randomization and Approximation Techniques in Computer Science*, pages 159–170, Berlin, Heidelberg, 1998. Springer Berlin Heidelberg.

[15] Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner. Rank-normalization, folding, and localization: An improved $\hat{R}$ for assessing convergence of MCMC (with discussion). *Bayesian Analysis*, 16(2), June 2021.

A Weak CLT for controlled repetition sampler

Proposition 9. *For any $0 < \alpha < 1/2$, the controlled repetition sampler with parameter α satisfies*

$$\sqrt{S}\left(\mathbb{E}_{\pi_S}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \xrightarrow{d} \mathcal{N}(0, V_\alpha(h))$$

for any measurable function h, where V_α is an asymptotic variance.

Proof. We will use $\pi_{S'}$ to denote the distribution for the SMC sample of size S' used above (before it is reweighted by S'/S), and π_S to denote our complete sample of size S, where

$$\pi_S = \frac{\lceil S^{1/3} \rceil}{S}\delta_{[\xi_0]} + \frac{S'}{S}\pi_{S'} = \frac{\lceil S^{1/3} \rceil}{S}\delta_{[\xi_0]} + \sum_{j=1}^{S'} \frac{S'}{S} w^{(j)} \delta_{[\xi(j)]}.$$

Let h be any measurable function on unlabelled plans. We know, from Proposition 7 applied to $\pi_{S'}$, that as $S \to \infty$ (which also implies $S' \to \infty$),

$$\sqrt{S'}\left(\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \xrightarrow{d} \mathcal{N}(0, V_{\mathrm{SMC}}(h))$$

We define a random variables $Y'_S := \sqrt{S'}\left(\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right)$, and let $Z \sim \mathcal{N}(0, V_{SMC})$. We know for any a,

$$\lim_{S\to\infty} \Pr(Y'_S \leq a) = \Pr(Z \leq a).$$

Because Z is a continuous random variable and thus $\Pr(Z = a) = 0$, it's also true that for any sequence b_S with $\lim_{S\to\infty} b_S = a$,

$$\lim_{S\to\infty} \Pr(Y'_S \leq b_S) = \Pr(Z \leq a).$$

Let $Y_S := \sqrt{S}\left(\mathbb{E}_{\pi_S}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right)$, and note that we are trying to show the sequence Y_S converges in distribution to $\mathcal{N}(0, V_{SMC})$. We see that

$$\mathbb{E}_{\pi_S}\left[h\left([\xi]\right)\right] = \frac{\lceil S^{1/3} \rceil}{S} h([\xi_0]) + \frac{S'}{S}\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right].$$

Using that we can rewrite $\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right] = \frac{\lceil S^{1/3} \rceil}{S}\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right] + \frac{S'}{S}\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]$, it follows that

$$\begin{aligned}
Y_S &= \sqrt{S}\left(\frac{\lceil S^{1/3} \rceil}{S} h([\xi_0]) + \frac{S'}{S}\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \\
&= \frac{\lceil S^{1/3} \rceil}{\sqrt{S}} h([\xi_0]) - \frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right] + \frac{S'}{\sqrt{S}}\left(\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \\
&= \frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\left(h([\xi_0]) - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) + \sqrt{\frac{S'}{S}} \cdot \sqrt{S'}\left(\mathbb{E}_{\pi_{S'}}\left[h\left([\xi]\right)\right] - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) \\
&= \frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\left(h([\xi_0]) - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) + \sqrt{\frac{S'}{S}} Y'_S
\end{aligned}$$

If we consider $\Pr(Y_S \leq a)$ for any a, we see that

$$\begin{aligned}
\Pr\left(Y_S \leq a\right) &= \Pr\left(\frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\left(h([\xi_0]) - \mathbb{E}_{\pi}\left[h\left([\xi]\right)\right]\right) + \sqrt{\frac{S'}{S}} Y'_{S'} \leq a\right) \\
&= \Pr\left(Y'_S \leq \sqrt{\frac{S}{S'}}\left(a + \frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\left(\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right] - h([\xi_0])\right)\right)\right)
\end{aligned}$$

Note for $b_S := \frac{\sqrt{S}}{\sqrt{S'}}\left(a + \frac{\lceil S^{1/3} \rceil}{\sqrt{S}}\left(\mathbb{E}_{\pi}\left[h\left([\xi]\right)\right] - h([\xi_0])\right)\right)$, we see that $\lim_{S\to\infty} b_S = a$, as $\sqrt{S/S'}$ goes to one and $\frac{\lceil S^{1/3} \rceil}{\sqrt{S'}}$ goes to 0. We conclude that for all a,

$$\lim_{S\to\infty} \Pr(Y_S \leq a) = \lim_{S\to\infty} \Pr(Y'_S \leq b_S) = \Pr(Z \leq a),$$

and so Y_S converges in distribution to $\mathcal{N}(0, V_\alpha)$, as claimed. Note this result would hold with $S^{1/3}$ replaced by S^α for any $\alpha < 1/2$.

□