Testing from *One* Sample: Is the casino really using a riffle shuffle?

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April 25, 2017

Abstract

Classical distribution testing assumes access to i.i.d. samples from the distributions that are being tested. We initiate the study of Markov chain testing, assuming access to a *single sample from the Markov Chains that are being tested*. In particular, we get to observe a single trajectory $X_0, \ldots, X_t, \ldots$ of an unknown Markov Chain $\mathcal{M}$, for which we do not even get to control the distribution of the starting state $X_0$. Our goal is to test whether $\mathcal{M}$ is identical to a model Markov Chain $\mathcal{M}'$.

In the first part of the paper, we propose a measure of difference between two Markov chains, which captures the scaling behavior of the total variation distance between words sampled from the Markov chains as the length of these words grows. We provide efficient and sample near-optimal testers for identity testing under our proposed measure of difference. In the second part of the paper, we study Markov chains whose state space is exponential in their description, providing testers for testing identity of card shuffles. We apply our results to testing the validity of the Gilbert, Shannon, and Reeds model for the riffle shuffle.

∗Supported by a Microsoft Research Faculty Fellowship, and NSF Award CCF-1551875, CCF-1617730 and CCF-1650733.
†Supported by NSF Award CCF-1551875, CCF-1617730 and CCF-1650733.
‡Supported by NSF Award CCF-1551875, CCF-1617730 and CCF-1650733.
1 Introduction

We formulate theories about the laws that govern physical phenomena by making observations and testing them against our hypotheses. A common scenario is when our observations can be reasonably modeled as i.i.d. samples from a distribution that we are trying to understand. This is the setting tackled by most classical work in Statistics. Of course, having access to i.i.d. samples from a distribution is rare and quite commonly a mere approximation of reality. We typically only have access to approximate samples from a stationary distribution, sampled by a Markov chain whose transition matrix/kernel is unknown to us and which can only be observed for some finite time horizon. In fact, to the best of our knowledge, the underlying Markov chain may not even be rapidly mixing, so there is no guarantee that we will ever see samples that are approximately distributed according to the stationary distribution.

These issues are exacerbated in high-dimensional settings, e.g., when observing the configurations of a deck of cards or a weather system, where it may also be completely impractical to work with the high-dimensional stationary distribution itself. Moreover, there are several ways to sample a stationary distribution, so it may be more important to know how it comes to be sampled. For all these considerations, it may be both more interesting and more practical to understand the “mechanics” of the process that generates our observations, namely the transition matrix/kernel of the Markov chain whose evolution we get to observe.

Motivated by these considerations, in this paper we study the problem of testing the identity of Markov chains. We are given access to a single trajectory $X_0, X_1, \ldots, X_t, \ldots$ of some unknown Markov chain $\mathcal{M}$ over some state space $[n]$, and we want to test the identity of $\mathcal{M}$ to some given Markov chain $\mathcal{M}'$. Importantly, we do not get to control the distribution of the starting state $X_0$, and we can only observe a single trajectory of $\mathcal{M}$, i.e. we cannot restart the Markov chain. What could we hope to achieve?

If there is any difference in the transition matrices of $\mathcal{M}$ and $\mathcal{M}'$, one would think that we would ultimately be able to identify it by observing a sufficiently long trajectory. This is certainly true if the transition matrices of the two chains differ at a state that belongs to the strongly connected component of $\mathcal{M}$ absorbing the observed trajectory $(X_t)_t$. For instance, suppose that $\mathcal{M}$ is a chain on states $\{1, 2, \ldots, 7\}$ whose transition matrix is the random walk matrix on a graph that is the disjoint union of a square on nodes $\{1, \ldots, 4\}$ and a triangle on nodes $\{5, 6, 7\}$, while $\mathcal{M}'$’s transition matrix is the random walk matrix on a graph that is the disjoint union of a clique on nodes $\{1, \ldots, 4\}$ and a triangle on nodes $\{5, 6, 7\}$. If our observed trajectory of $\mathcal{M}$ lies in the strong connected component defined by states $\{1, \ldots, 4\}$, we will easily identify its difference to $\mathcal{M}'$. On the other hand, if our observed trajectory of $\mathcal{M}$ lies on the strong component defined by states $\{5, 6, 7\}$, we will not be able to identify that we are not observing a trajectory of $\mathcal{M}'$, no matter how long the trajectory is.

For some notion of difference, $\text{Dist} (\mathcal{M}, \mathcal{M}')$, between Markov chains, we would like to quantify how long a trajectory $X_0, \ldots, X_\ell$ from an unknown chain, $\mathcal{M}$, we need to observe to be able to distinguish, with probability at least $1 - \delta$:

$$\mathcal{M} = \mathcal{M}' \quad \text{versus} \quad \text{Dist} (\mathcal{M}, \mathcal{M}') > \epsilon,$$

(1)

for some given parameters $\delta \in (0, 1)$ and $\epsilon > 0$. Let us call this problem single-sample goodness-of-fit (or identity) testing for Markov chains. We will study it taking $\delta = 1/3$, with the understanding that this probability can be boosted to any small constant at the cost of a $O(\log(1/\delta))$-multiplicative factor in the length $\ell$ of the observed trajectory.
What notion of difference between Markov chains is the right one to use to study the afore-described goodness-of-fit testing problem is not clear. One of our contributions is to identify a meaningful measure of difference in Section 2. What are the desiderata for such a measure? Let us discuss this:

1. First, as our simple example above illustrates, under a worst-case starting state \( X_0 \), we may not be able to identify that \( M \neq M' \) from a single trajectory. So, we would like to identify a notion of difference that takes a value \( \text{Dist}(M, M') = 0 \), whenever chains \( M \) and \( M' \) are indistinguishable from a single trajectory.

2. Whenever \( M \) and \( M' \) are distinguishable from a single trajectory, whose starting state we do not get to control, i.e. from any starting state, we would like that our difference measure quantifies how different the chains are. Clearly, our notion of difference could not just be a combinatorial property of the connectivity of the state space of \( M \) and \( M' \), since the combinatorial structure won’t reflect the magnitude of the differences in the chains.

A natural notion of difference between two chains \( M \) and \( M' \) is the total variation distance between the trajectories (a.k.a. words) \( W^t_M \overset{\text{def}}{=} X_0X_1 \cdots X_t \) and \( W^t_{M'} \overset{\text{def}}{=} Y_0Y_1 \cdots Y_t \) sampled from the two chains in some \( t \) steps and starting at some state \( X_0 = s_0 = Y_0 \). Indeed, this distance captures how different our \( t \)-step observations from the two chains are. As the starting state \( s_0 \) is out of our control, we should rather use the

\[
\min_{s_0} d_{\text{TV}}(W^t_M, W^t_{M'} \mid X_0 = Y_0 = s_0).
\]

In particular, taking the min makes sure that Property 1 above is satisfied.

While there is sometimes a natural \( t \) to use in (2) as we will see in Section 4, where we analyze card shuffles, it is mostly unclear how to set \( t \). Setting \( t \) to infinity will make the above quantity take 0/1 values, which is un-informative about how different the two chains are. Setting \( t \) too small would only capture differences in the proximity of the starting state \( s_0 \). Hence, setting \( t \) to some reasonably large but finite value makes more sense, but how to choose it?

To avoid the conundrum, we propose a notion of difference between Markov chains \( M \) and \( M' \), which captures the scaling behavior, as \( t \to \infty \), of (2). Interestingly, we argue in Section 2 that this scaling behavior is tightly captured by spectral properties of the following matrix:

\[
[P, Q]_f \overset{\text{def}}{=} \left[ \sqrt{P_{ij}} \cdot Q_{ij} \right]_{ij \in [n \times n]},
\]

where \( P \) and \( Q \) are the transition matrices of the two chains, i.e. \( P_{ij} \) and \( Q_{ij} \) denote the probabilities of transitioning from state \( i \) to state \( j \) in the two chains. In Eq. (4), we show a recursive decomposition that allows us to exactly express the square Hellinger similarity, \( 1 - d_{\text{Hel}}^2 \left( W^t_M, W^t_{M'} \right) \) of \( \ell \)-length words sampled from the two chains in terms of the \( \ell \)-th power of the above matrix, and the distribution of the starting states \( X_0 \) and \( Y_0 \) in the two words. Given the relationship between Hellinger and total variation distance (see Eq. (3)), the \( \ell \)-th power of \( [P, Q]_f \) also captures the total variation distance between words sampled from the two chains.

To identify a word-length independent measure of difference between the two chains, we argue that the scaling behavior of the Hellinger distance/total variation distance is captured by the largest eigenvalue \( \lambda_1 = \rho([P, Q]_f) \) of matrix \([P, Q]_f\). We show that always \( \lambda_1 \leq 1 \) (Claim 1), and that \( \lambda_1 = 1 \)
if and only if the two chains have an identical connected component (Claim 1), hence we would be unable to identify the difference between the two chains from a single trajectory and a worst-case starting state, as per our discussion above. Furthermore, the slowest (with respect to the choice of the starting state) that the square Hellinger similarity of the two chains can drop as a function of the length \( \ell \) is \( \lambda_1^2 \ell \), up to factors that do not depend on \( \ell \); this follows from (1) and (6). That is, the slowest that the square Hellinger distance of the two chains can increase is \( 1 - O(\lambda_1) \). Given these, and the intimate relationship between Hellinger and total variation distance (Eq. (3)), we propose the use of \( \text{Dist} (\mathcal{M}, \mathcal{M}') = 1 - \rho([P,Q]_{ij}) \) as a scale-free and meaningful measure of difference between Markov chains. As per our discussion, this notion of distance satisfies Desiderata 1 and 2 outlined above. For symmetric Markov chains, our notion of difference is even more tightly related to the scaling behavior of trajectories sampled from the two chains even for a starting state sampled from the stationary distribution, as per Claim 2. Figure 1 illustrates how \( \text{Dist} (\mathcal{M}, \mathcal{M}') \) behaves for different pairs of Markov chains \( \mathcal{M} \) and \( \mathcal{M}' \).

Our Results. Using our proposed measure of difference between Markov chains we provide algorithms for goodness-of-fit testing of Markov chains, namely Problem (1), targeting two interesting regimes. The first targets applications where the state space is polynomial in the representation of the target Markov chain \( \mathcal{M}' \). The second targets settings where the state space is exponential in the representation of the target chain, but the chain has sparsity and structure. Importantly, this is applicable to testing card shuffles. Our results in the two settings are the following.

In Section 3, we study Problem (1) under \( \text{Dist} (\mathcal{M}, \mathcal{M}') = 1 - \rho([P,Q]_{ij}) \), where \( P \) and \( Q \) are the transition matrices of chains \( \mathcal{M} \) and \( \mathcal{M}' \). We study this problem when \( \mathcal{M} \) and \( \mathcal{M}' \) are both symmetric, and provide near-optimal upper and lower bounds for the minimum length \( \ell \) of a trajectory from the unknown chain \( \mathcal{M} \) that is needed to determine the correct answer with probability at least 2/3. In particular, Theorems 3.1 and 3.2 combined show that the length of the required trajectory from \( \mathcal{M} \) to answer Problem (1) is \( \frac{n}{\epsilon} \), where \( n \) is the size of the state space, up to logarithmic factors and an additive term that does not depend on \( \epsilon \) or \( \mathcal{M} \). Our upper bound is established via an information-efficient reduction from single-sample identity testing for Markov chains with \( n \) states to the classical problem of identity testing of distributions over \( O(n^2) \) elements, from i.i.d. samples. The naive way to obtain such a reduction is to look at every \( \text{MixT}_{\mathcal{M}'} \)-th step of the trajectory of \( \mathcal{M} \), where \( \text{MixT}_{\mathcal{M}'} \) is the mixing time of chain \( \mathcal{M}' \), pretending that these transitions are i.i.d. samples from the distribution \( \{ \frac{1}{n} P_{ij} \}_{ij \in [n^2]} \). This incurs an unnecessary blow-up of a factor of \( \text{MixT}_{\mathcal{M}'} \) in the required length of the observed trajectory, which we show how to avoid, exchanging it with an additive term that is quasi-linear in the hitting time.

In Section 4, we take on the challenge of testing Markov chains whose nominal state-space is exponentially large in their representation, such as shuffles. Often, shuffles have symmetries that allow studying their transitions in a state space of manageable size. For example, the random choices that the riffle shuffle makes in the course of one step do not depend on the permutation of the cards at the beginning of the step, and can be described succinctly. Moreover, viewed appropriately the transitions out of any state are typically sparse. In the riffle shuffle, starting from any permutation there are \( n + 1 \) places to cut the deck. And, starting from a cut, every little step of the riffle has two options (whether to drop a card from the left or the right stack). So breaking down one step of the riffle shuffle into a sequence of simple steps makes the transitions very sparse.

In Definition 2 we provide a model of sparse Markov chains, capturing succinct representations of Markov chains resulting from “breaking up into trivial steps and projecting into a smaller state.
"space" of Markov chains with exponentially large state-spaces such as different variants of the riffle shuffle and other shuffles [BD92]. Roughly speaking a sparse Markov chain in our model performs transitions according to a sequence of transition matrices \( P_1, \ldots, P_n \), over and over again, ad infinitum. We discuss how this model captures the essential mechanics of the riffle shuffle after Definition 2.

Keeping the riffle shuffle as our running application, we develop tools that allow us to perform goodness-of-fit testing of sparse Markov chains according to our model. What difference measure between chains should we use? Given two sparse chains \( P = (P_i)_{i \in [n]} \) and \( Q = (Q_i)_{i \in [n]} \), conforming to our model, we could still define our difference measure between them using spectral properties of matrix \( [P_1, Q_1], [P_2, Q_2], \ldots, [P_n, Q_n] \). However, we find it more natural in this case to use as difference measure the total variation distance between words sampled in one round of sampling transitions from the sequence of matrices \( P_1, \ldots, P_n \) and \( Q_1, \ldots, Q_n \). This total variation distance captures the divergence of the two chains in one iteration through their transitions matrices; in our running application to riffle shuffle, they correspond to the divergence of two riffle shuffles of different parameters in one iteration of the shuffle. With this notion of difference we provide efficient testers, and sample complexity lower bounds; see Theorems 4.1 and 4.4. Our upper bounds imply, in particular, that we can test goodness-of-fit of a given riffle shuffle model, such as the Gilbert-Shannon-Reeds model, against all competing riffle shuffle models at distance \( \geq \epsilon \), from \( O(n^{3/2} / \epsilon^2) \) shuffles. Our tester, applying to testing any sparse Markov chain model, is based on a modified and pruned \( \chi^2 \)-style statistic, inspired by [ADK15], which tracks the number of times a particular transition between two states occured in the observed trajectory of the Markov chain.

Related Work. Testing goodness-of-fit for distributions has a long history in Statistics; for some old and more recent references see, e.g., [Pea00, Fis35, RS81, Agr12]. In this literature the emphasis has been on the asymptotic analysis of tests, pinning down their error exponents as the number of samples tends to infinity [Agr12, TAW10]. In the last two decades or so, distribution testing has also piqued the interest of theoretical computer scientists [BFF+01, Pan08, LRR13, VV14, CDVV14, ADK15, CDGR16, DK16, DDS+13, CRS14], where the emphasis, in contrast, has been on minimizing the number of samples required to test hypotheses with a strong control for both type I and type II errors. A few recent works have identified tight upper and lower bounds on the sample complexity of various testing problems [Pan08, VV14, ADK15, DK16]. All of the papers in this vast body of literature assume access to i.i.d. samples from the underlying distribution.

Some work in Statistics has considered the problem of testing with dependent samples. For instance, [Bar51, M+82, GM+83, MMPV02] and the references therein study goodness-of-fit testing for Markov chains. [TA83], and more recently [BPR16] study the problem of testing the stationary distribution of Markov chains. [Kaz78] studies the problem of detection between two Markov chains. All these works focus on the asymptotic regime where the length of the observed trajectories tends to infinity, as opposed to the non-asymptotic regime that we study here. In the computer science literature [BFR+13] considered the problem of testing the property whether a Markov chain is fast mixing or not. They defined a notion of closeness between two random walks started at different states of the same chain, which is similar in spirit to the distance notion we define in this work.

There is a large body of statistical literature on estimating properties of Markov chains such as mixing time. The question of estimation is related to but different than the goodness-of-fit testing

\[ \text{We argue, in Section 4, that the spectral and total variation distance approaches to define difference in this model are tightly related, as they are in the symmetric case.} \]
that we perform here. A particularly important parameter is the mixing time of a Markov chain, as it is useful in designing MCMC algorithms. \textsuperscript{[HKS15]} and the references therein study the problem of mixing time estimation in Markov chains.

**Organization** We start with a description of the notational conventions we use and a formal definition of our distance notion between Markov chains in Section \textsuperscript{2}. In Section \textsuperscript{3} we study the problem of testing identity of symmetric Markov chains. We present our tester along with a sample complexity lower bound for this problem in this Section. In Section \textsuperscript{4} we study the identity testing question on riffle shuffles. We present our formulation of this question as a problem of testing identity for sparse Markov chains and present upper and lower bounds for this problem. Finally, in Section \textsuperscript{5} we conclude with some open questions from the framework introduced in this paper.

## 2 Preliminaries

A discrete-time Markov chain is a stochastic process \(\{X_t\}_{t\in\{0,1,\ldots\}}\) over a state space \(S\) which satisfies the Markov property: the probability of being in state \(s\) at time \(t + 1\) depends only on the state at previous time \(t\). In this paper, we only consider Markov chains with a finite state space such that \(|S| = n\). Such Markov chains can be completely specified by a \(n \times n\) transition matrix (kernel) that contains probabilities of transitioning from state \(i\) to state \(j\) in the \(i^{th}\) row and \(j^{th}\) column. The transition matrix has non-negative entries and is a stochastic matrix. We use capital letters \(P,Q,M\) to represent Markov chains as well as their respective transition matrices. The stationary distribution \(\pi\) of a Markov chain \(P\) is a distribution over the state space \(S\) (written as a column vector) such that it satisfies \(\pi^\top \circ P = \pi^\top\). An important parameter in the study of Markov chains is the distribution of the starting state \(s_0\) which we denote by \(\vec{p}\) (for the Markov chain \(P\)). It may or not may not be the stationary distribution. In many cases it will be the distribution with all probability mass at a single state. Two popular notions of distance between distributions will be used heavily in this paper. We state their formal definitions below.

**Definition 1.** The total variation and Hellinger distances between distributions \(p,q\) over \([k]\):

\[
\begin{align*}
d_{TV}(p,q) &\triangleq \frac{1}{2} \sum_{i\in[k]} |p_i - q_i|; \\
d_{Hel}^2(p,q) &\triangleq \frac{1}{2} \sum_{i\in[k]} (\sqrt{p_i} - \sqrt{q_i})^2 = 1 - \sum_{i\in[k]} \sqrt{p_i} \cdot \sqrt{q_i}; \\
\sqrt{2} \cdot d_{Hel}(p,q) &\geq d_{TV}(p,q) \geq d_{Hel}^2(p,q) .
\end{align*}
\]

We now state without proof a well-known result which relates the total variation distance between two distributions to the best achievable distinguishability between the two. This will be useful in understanding our proposed notion of distance between two chains.

**Lemma 2.1.** Given two distributions \(p,q\) and a sample \(x\) drawn from either \(p\) or \(q\), no algorithm can distinguish whether \(x\) was drawn from \(p\) or \(q\) with probability more than \(\frac{1+ d_{TV}(p,q)}{2}\).

## 2.1 Notations

We list the general notational conventions used in this paper. We denote vectors by small letters such as \(\vec{v}\) and matrices by capital letters such as \(A,B,P,Q\). The \(i^{th}\) entry of vector \(\vec{v}\) is denoted by \(v_i\) or \(v[i]\) and the \((ij)^{th}\) entry of matrix \(A\) (\(i^{th}\) row, \(j^{th}\) column) is denoted by \(A_{ij}\) or \(A[i,j]\); \(\vec{e}_i\) denotes the
standard basis vector with 1 in its $i^{th}$ coordinate and 0 elsewhere; $\vec{1}$ denotes the vector of all ones. The “entrywise” $L_1$ and $L_2$ norms of a matrix $A$ are respectfully denoted as $\|A\|_1$ and $\|A\|_2$; $\rho (A)$ denotes the spectral radius of matrix $A$, i.e., the maximum absolute eigenvalue of $A$. The eigenvalues of $A$ are denoted by $\lambda_1, \ldots, \lambda_i, \ldots, \lambda_n$ and the respective right eigenvectors by $\vec{v}_1, \ldots, \vec{v}_i, \ldots, \vec{v}_n$ (left eigenvectors by $\vec{u}_1, \ldots, \vec{u}_n$); for symmetric matrix $A$ we assume that $\lambda_1 \geq \cdots \geq \lambda_i \geq \cdots \geq \lambda_n$.

Before formulating the precise question we study, we need a notion of distance between Markov chains to work with.

### 2.2 Distance between Markov Chains

We begin by considering the following simple question: how close is the behavior of two given Markov chains $P$ and $Q$? A natural notion of distance would tell us how easy it is to distinguish which Markov chain $P$ or $Q$ a word $w = s_0 \rightarrow s_1 \cdots \rightarrow s_\ell$ of certain length $\ell$ was generated from. The answer to this question is precisely captured by the total variation distance $d_{TV} \left( W^\ell_P, W^\ell_Q \right)$ between word distributions $W^\ell_P, W^\ell_Q$ for words of length $\ell$ generated by Markov chains $P$, and respectively $Q$ (see Lemma 2.1). As a proxy for the total variation distance $d_{TV} \left( W^\ell_P, W^\ell_Q \right)$, it is more convenient to use square of the Hellinger distance $d_{Hell}^2 \left( W^\ell_P, W^\ell_Q \right)$ or the closely related Bhattacharya coefficient which is useful for studying divergence of non-stationary and continuous Markov chains as was observed in Kaz78. Similar to Kaz78, we can establish nice recurrence relations for the Bhattacharya coefficient of two word distributions, which is captured by the matrix $[P, Q]_i \overset{\text{def}}{=} \left[ \sqrt{P_{ij} - Q_{ij}} \right]_{i,j \in [n \times n]}$.

$$1 - d_{Hell}^2 \left( W^\ell_P, W^\ell_Q \right) = \sum_{w=s_0 \cdots s_\ell} \sqrt{Pr_P [w] \cdot Pr_Q [w]} = \sum_{w=s_0 \cdots s_\ell} \sqrt{Pr_P [w] \cdot Pr_Q [w]} \circ \vec{1}$$

$$1 - d_{Hell}^2 \left( W^\ell_P, W^\ell_Q \right) = \sum_{w=s_0 \cdots s_\ell} \sqrt{Pr_P [w] \cdot Pr_Q [w]} = \sum_{w=s_0 \cdots s_\ell} \sqrt{Pr_P [w] \cdot Pr_Q [w]} \circ \vec{1}$$

$$= \left [ \sum_{r \in [n]} \sqrt{Pr_P [r \rightarrow s] \cdot Pr_Q [r \rightarrow s]} \sum_{s_{\ell-1}=r} \sqrt{Pr_P [w] \cdot Pr_Q [w]} \circ \vec{1} \right ] \circ \vec{1}$$

$$= \left [ \sum_{w=s_0 \cdots s_{\ell-1}} \sqrt{Pr_P [w] \cdot Pr_Q [w]} \right ] \circ \vec{1}$$

$$= \left [ \sum_{w=s_0 \cdots s_{\ell-1}} \sqrt{Pr_P [w] \cdot Pr_Q [w]} \right ] \circ \vec{1}$$

\[\overset{2}{\text{Hellinger distance is tightly related to the Bhattacharya coefficient between two distributions which is defined as }} BC(p, q) = \sum_{w \in [k]} \sqrt{p_w \cdot q_w}. \text{ It captures similarity of two distributions and lies in } [0, 1].\]
where \( \vec{p} \) and \( \vec{q} \) are vectors of initial distributions of \( s_0 \) over \([n]\), and 
\[
[p, q]_i^\ell \overset{\text{def}}{=} \left[ \sqrt{p_s \cdot q_s} \right]_{s \in [n]}. 
\]

An important observation is that the distance between \( \mathcal{W}_P^\ell \) and \( \mathcal{W}_Q^\ell \) above depends on the initial distribution of the first state in \( w \), and also the length \( \ell \) of the word.

**Assumption on the starting state.** We study two reasonable models for the choice of the starting state: (i) a *worst-case* model where both \( P \) and \( Q \) begin from the same state \( i \), which is chosen in adversarial manner to make \( P \) and \( Q \) look as much alike as possible; (ii) an *average-case* model, where the initial distributions \( \vec{p} = \vec{q} \) for \( P \) and \( Q \) either are given to us, or are related to \( P \) and \( Q \) in some natural way. Given the assumption on the starting state we want to answer the question of what \( \ell \) to pick, so that \( \mathcal{W}_P^\ell \) and \( \mathcal{W}_Q^\ell \) are far apart in squared Hellinger distance (say \( \geq 0.50 \)). For the worst-case and average-case starting state models we respectfully get

\[
\begin{align*}
\min_{\ell \geq 0} \ell : & \forall i \in [n] \quad 0.5 \geq 1 - d_{\text{Hel}}^2 \left( \mathcal{W}_P^\ell, \mathcal{W}_Q^\ell \right) = \epsilon_{i}^\ell \circ \left( [P, Q]_i \right)^\ell \circ \vec{1}. \tag{5} \\
\min_{\ell > 0} \ell : & \quad 0.5 \geq 1 - d_{\text{Hel}}^2 \left( \mathcal{W}_P^\ell, \mathcal{W}_Q^\ell \right) = [\vec{p}, \vec{q}]_i^\ell \circ \left( [P, Q]_i \right)^\ell \circ \vec{1}.
\end{align*}
\]

Due to the relation between Hellinger and total variation distances, the inequality (5) holds for \( 1 - d_{\text{TV}} \left( \mathcal{W}_P^\ell, \mathcal{W}_Q^\ell \right) \) but for a slightly different than 0.5 constant. We call minimal \( \ell \) that satisfies 
\( d_{\text{TV}} \left( \mathcal{W}_P^\ell, \mathcal{W}_Q^\ell \right) \geq \frac{2}{3} \) either for all starting states \( i \in [n] \), or for fixed \( \vec{p}, \vec{q} \) the *minimal distinguishing length*. We note that (5) gives us an estimate on \( \ell \) up to a constant factor.

We note that when \( \ell \) is large, the behavior of RHS of (5) is governed by *the largest eigenvalue* \( \lambda_1 = \rho \left( [P, Q]_i \right) \) of \( [P, Q]_i \). By Perron-Frobenius theorem, we have that the largest eigenvalue of \( [P, Q]_i \) is non-negative and the corresponding left eigenvector \( \vec{u}_1 : \vec{u}_1^\top \circ [P, Q]_i = \lambda_1 \cdot \vec{u}_1^\top \) has non-negative coordinates. In particular, if we choose initial distributions \( \vec{p} = \vec{q} \) proportional to \( \vec{u}_1 \), then

\[
\vec{p}^\top \circ \left( [P, Q]_i \right)^\ell \circ \vec{1} = \lambda_1^\ell \cdot \langle \vec{p}, \vec{1} \rangle = \lambda_1^\ell. \tag{6}
\]

**Claim 1.** It is always true that \( \lambda_1 = \rho \left( [P, Q]_i \right) \leq 1 \). Moreover, \( \lambda_1 = 1 \) iff \( P \) and \( Q \) have an identical connected component\(^4\).

**Proof.** Note that \( \frac{P + Q}{2} \) is a stochastic matrix that entry-wise dominates matrix \( [P, Q]_i \) with non-negative entries. Therefore, \( \lambda_1 \cdot \langle \vec{u}_1, \vec{1} \rangle = \vec{u}_1^\top \circ [P, Q]_i \circ \vec{1} \leq \vec{u}_1^\top \circ \left[ \frac{P + Q}{2} \right] \circ \vec{1} = \vec{u}_1^\top \circ \vec{1} = \langle \vec{u}_1, \vec{1} \rangle \), where \( \vec{1} \) is vector with all 1 entries. We get \( \lambda_1 \leq 1 \), since \( \langle \vec{u}_1, \vec{1} \rangle > 0 \).

For the case of equality, if \( P \) and \( Q \) have the same connected component \( C \), then matrix \( [P, Q]_i \) has the same transition probabilities as Markov chains \( P \) and \( Q \) restricted to the vertices of \( C \). We note that \( C \) is a stochastic matrix and, therefore, its largest positive eigenvalue is one. Hence, 
\( \rho \left( [P, Q]_i \right) \geq \rho \left( C \right) = 1. \)

\(^4\)For example \( \vec{p} \) and \( \vec{q} \) could be respective stationary distributions of \( P \) and \( Q \). However, we still want the assumption that \( \vec{p} = \vec{q} \), as otherwise there might be another strategy to distinguish \( P \) and \( Q \) than observing a long stream of samples \( w \) by making the decision right away based on one initial sample from \( \vec{p} \). Example 1\(^{13} \) illustrates how two Markov chains can produce very similar distributions of words \( \mathcal{W}_P^\ell, \mathcal{W}_Q^\ell \) starting from any state for some large \( \ell \), and yet have vastly different stationary distributions.

\(^{13}\)or *essential communicating class* in the terminology of Book [LPW09].
If $\rho \left( [P, Q]_{ij} \right) = 1$, we apply Perron-Frobenius theorem to $[P, Q]_{ij}$ to get that the largest eigenvalue $\lambda_1 = \rho \left( [P, Q]_{ij} \right) = 1$ has corresponding (left) eigenvector $\vec{u}_1$ with non-negative entries. Similar to the proof of Claim 1 we observe that $\vec{u}_1^\top \circ \left( \frac{P+Q}{2} - [P, Q]_{ij} \right) \circ \mathbf{1} = 0$, and all entries of the matrix in this expression are non-negative. This implies that $P_{ij} = Q_{ij}$ for every strictly positive coordinates $i$ of the eigenvector $\vec{v}_1$ and any $j \in [n]$. Since $\vec{u}_1^\top \circ [P, Q]_{ij} = \vec{u}_1^\top$, we also have $P_{ij} = Q_{ij} = 0$ for any positive coordinate $i$ and zero coordinate $j$ of eigenvector $\vec{u}_1$. Therefore, the set of vertices corresponding to positive coordinates of $\vec{u}_1$ form a component (which might have more than one connected component of $P$ and $Q$) such that $P = Q$ on these vertices. \hfill $\square$

We consider the quantity $\varepsilon \overset{\text{def}}{=} 1 - \rho \left( [P, Q]_{ij} \right)$ as a proxy for the closeness of Markov chains $P$ and $Q$. In particular in (5) if $\vec{p} = \vec{q} = \frac{1}{n} \mathbf{1}$. In this setting of symmetric Markov chains, we can provide sharp bounds on the minimal distinguishing length $\ell$.

**Symmetric Markov Chains.** The stationary distribution for any symmetric Markov chain is the uniform distribution over all states. In this case the starting distributions in the average-case part of equation (5) are $\vec{p} = \vec{q} = \frac{1}{n} \mathbf{1}$. In this setting of symmetric Markov chains, we can provide sharp bounds on the minimal distinguishing length $\ell$.

**Claim 2.** The necessary and sufficient distinguishing length $\ell$, which allows to distinguish $P$ vs. $Q$ with high probability, is $\tilde{\Theta} \left( \frac{1}{\varepsilon} \right)$ (up to a log $n$ factor), where $\varepsilon = 1 - \rho \left( [P, Q]_{ij} \right)$ under both worst-case and average-case assumptions for the starting state.

**Proof.** We first consider the average-case model for the starting state. Note that $[P, Q]_{ij}$ is a symmetric matrix. Let $\vec{v}_1, \ldots, \vec{v}_n$ be normalized orthogonal eigenvectors of $[P, Q]_{ij}$, corresponding to real $\lambda_1 \geq \cdots \geq \lambda_n$ eigenvalues. Then for RHS of (5) we have

\[
\frac{1}{n} \mathbf{1}^\top \circ \left( [P, Q]_{ij} \right)^\ell \circ \mathbf{1} = \frac{1}{n} \mathbf{1}^\top \circ \left( \sum_{i=1}^{n} \lambda_i \cdot \vec{v}_i \circ \vec{v}_i^\top \right)^\ell \circ \mathbf{1} = \sum_{i=1}^{n} \lambda_i^\ell \cdot \frac{1}{n} (\vec{v}_i, \vec{v}_i)^2 = (*)
\]

Now we can write an upper and lower bound on (*) in terms of $\lambda_i^\ell$ (assuming that $\ell$ is even):

\[
\frac{\lambda_1^\ell}{n} = \frac{\lambda_1^\ell}{n} \|\vec{v}_1\|^2 \leq \lambda_i^\ell \cdot \frac{1}{n} \|\vec{v}_1\|^2 \leq (*) \leq \sum_{i=1}^{n} \lambda_i^\ell \cdot \frac{1}{n} \|\vec{v}_i\|^2 \leq \sum_{i=1}^{n} \lambda_i^\ell \cdot \|\vec{v}_i\|_2 = \sum_{i=1}^{n} \lambda_i^\ell \leq n \cdot \lambda_1^\ell,
\]

where in the second inequality we used Perron-Frobenius theorem stating that all coordinates of $\vec{v}_i$ are non negative. Consequently, these bounds imply that $\ell = \Theta \left( \frac{1}{\varepsilon} \right)$ up to a log $n$ factor, if $\rho \left( [P, Q]_{ij} \right) = \lambda_1 = 1 - \varepsilon$. I.e., $\ell = \tilde{\Theta} \left( \frac{1}{\varepsilon} \right)$.

For the worst-case assumption on the starting state, it is sufficient to show an upper bound $\ell = O \left( \frac{\log n}{\varepsilon} \right)$. In this case (7) becomes

\[
\vec{e}_i^\top \circ \left( [P, Q]_{ij} \right)^\ell \circ \mathbf{1} = \sum_{i=1}^{n} \lambda_i^\ell \cdot (\vec{e}_i, \vec{v}_i) \cdot (\mathbf{1}, \vec{v}_i) \leq \sum_{i=1}^{n} |\lambda_i|^\ell \cdot \|\vec{v}_i\|_\infty \cdot \|\vec{v}_i\|_1 \leq \sum_{i=1}^{n} |\lambda_i|^\ell \cdot \sqrt{n} \leq n^{1.5} \cdot \lambda_1^\ell,
\]
since \( \| \vec{v}_i \|_1 \leq \sqrt{n} \| \vec{v}_i \|_2 = \sqrt{n} \), and \( \| \vec{v}_i \|_\infty \leq \| \vec{v}_i \|_2 = 1 \).

We note that, if one could pick the starting state instead of working with average-case or worst-case assumptions of Claim 2, then then \( \ell \) can be much smaller (see Example 1b). Claim 2 gives a strong evidence that \( \operatorname{Dist}(P, Q) \overset{\text{def}}{=} 1 - \rho \left( [P, Q] \sqrt{\frac{1}{n}} \right) \) is a meaningful and important parameter that captures closeness between \( P \) and \( Q \). In the following section we will use it as analytical proxy for the distance between Markov Chains.

**Fixed word length.** In some applications the length \( \ell \) of the observed word might be given a priori. One such example corresponds to card riffle shuffle, where the random choices in the process can be described (see Section 4 for more detail) as a Markov chain over \( O(n^2) \) states (\( n = 52 \) for the card deck), where the process terminates after \( \ell = n \) steps. In this case we can expect a few i.i.d. samples of length-\( \ell \) words. For such examples and more generally for the Markov Chains with a specified number of steps \( T \) it is natural to define \( \operatorname{Dist}(P, Q) \overset{\text{def}}{=} d_{\text{TV}} \left( W_{T P}, W_{T Q} \right) \). Note that now the distance \( \operatorname{Dist}(P, Q) \) satisfies triangle inequality. Moreover, due to the relation between Hellinger and total variation distances we can estimate \( 1 - \frac{\operatorname{Dist}^2(P, Q)}{2} \geq 1 - d^2_{\text{Hel}} \left( W_{T P}, W_{T Q} \right) \), where the RHS term admits a nice analytical expression similar to (4).

\(^5\)In general this notion of distance should be used with care. One thing about parameter \( \operatorname{Dist}(P, Q) = 1 - \rho \left( [P, Q] \sqrt{\frac{1}{n}} \right) \), is that it is not a metric. In particular, \( \operatorname{Dist}(P, Q) \) violates the triangle inequality (\( \operatorname{Dist}(M_1, M_2) = \operatorname{Dist}(M_2, M_3) = 0 \), but \( \operatorname{Dist}(M_1, M_3) > 0 \) for some \( M_1, M_2, M_3 \)) as is illustrated by Example 1a. We note that this problem can only appear for reducible chains, as is shown in Claim 1. Also it is not always possible to extend the sharp bounds on \( \ell \) of Claim 2 from symmetric Markov chains to non-symmetric Markov chains, even if both MC have the uniform distribution as their stationary distribution (see Example 16).
(a) Dist \((M_1, M_2) = 1 - \rho (M_1, M_2)\) is not a metric. Dist \((M_1, M_2) = 0\), but Dist \((M_1, M_3) > 0\).

(b) After one step from state 4, we would know if \(w \sim P\), or \(w \sim Q\). If \(w\) starts from any other state \(s_0 \neq 4\), it would take many steps.

(c) To distinguish \(P\) vs. \(Q\) walking from a random state we need \(\Omega(n)\) steps, but Dist \((P, Q) = 1\).

(d) Dist \((P, Q) = o(1)\), stationary distributions \(\vec{q}_0, \vec{p}_0\) are different: \(d_{TV}(\vec{q}_0, \vec{p}_0) = 1 - o(1)\).

(e) Dist \((P, Q) = 1\). Uniform is stationary for both \(P\) and \(Q\). On average \(\Omega(n)\) steps to tell \(P \neq Q\).

| Example 1a | Two disjoint connected components. |
| Example 1b | \(Q\) – clique \(K_n\); \(P\) – clique \(K_{n-1}\) and disjoint vertex. Eigenvalue of \([P, Q]_{ij}\): \(\lambda_1 = \sqrt{\frac{n-1}{n}} = 1 - o(1), \lambda_2 = \frac{1}{n}; \lambda_3 = \cdots = \lambda_n = 0\) |
| Example 1c | \(P\) – oriented cycle, \(Q\) – cycle with one link substituted by a loop. |
| Example 1d | \(Q\) – oriented cycle with edge \(e = (v_1, v_2)\) substituted by a loop at \(v_1\); \(P\) is almost like \(Q\), but \(e\) has weight \(\frac{1}{\sqrt{n}}\), loop at \(v_1\) has weight \(1 - \frac{1}{\sqrt{n}}\). Stationary distributions: \(\vec{q}_0 = (1, 0, \cdots, 0)^\top\) and \(\vec{p}_0 = (\frac{\sqrt{n}}{n+\sqrt{n-1}}, \frac{1}{n+\sqrt{n-1}}, \cdots, \frac{1}{n+\sqrt{n-1}})^\top\). \(\rho \left([P, Q]_{ij}\right) = \sqrt{1 - \frac{1}{\sqrt{n}}}.\) |
| Example 1e | Two oriented cycles \(P \overset{\text{def}}{=} s_1 \rightarrow s_2 \rightarrow \cdots \rightarrow s_n \rightarrow s_1\) and \(Q \overset{\text{def}}{=} s_1 \rightarrow s_3 \rightarrow s_4 \cdots \rightarrow s_n \rightarrow s_2 \rightarrow s_1\). |

Figure 1: Examples.

3 Identity Testing of Symmetric Markov Chains

As we have formalized a notion of distance between symmetric Markov Chains in the previous section we get a well defined framework from property testing literature \cite{BFF+01, Pan08, LRR13} for testing properties of distributions generated by Markov Chains. Arguably, the next fundamental
question, after deciding one out of two given distributions (we call it A-B testing), is identity testing problem. In this problem the goal is to test from a stream of samples whether the real distribution (which unlike the case of A-B testing is completely unknown to us) coincides with a given hypothesis distribution. We first present a polynomial time algorithm that provides an efficient reduction to the identity testing problem with i.i.d. samples. The algorithm improves on the performance of a naive reduction, which waits for a period of time to get an independent sample and as such suffers a multiplicative loss of mixing time \( \text{MixT}_Q \) of Markov Chain \( Q \). Our algorithm suffers only an additive loss of \( O(\text{HitT}_Q \cdot \log(\text{HitT}_Q)) \) in sampling complexity and allows us to reduce the problem to testing identity with respect to squared Hellinger distance of a distribution supported on a domain of size \( n^2 \) and with access to i.i.d. samples. In the next subsection we provide a nearly matching lower bound for the identity testing problem. We begin by giving a formal statement of the identity testing problem below:

\[
\begin{align*}
\text{Input:} & \quad \varepsilon; \text{ explicit symmetric Markov chain } Q; m \text{ consecutive samples } s_1 \cdots s_m \text{ from a symmetric Markov Chain } P. \\
\text{Output:} & \quad P = Q, \text{ or } P \neq Q \text{ if } 1 - \rho \left( \frac{\|P - Q\|}{\varepsilon} \right) > \varepsilon.
\end{align*}
\]

Our approach. We consider a mapping \( K_{\vec{k}} \) from infinite words \( W_\infty^m \) of an irreducible Markov chain \( M \) to \( \prod_{i=1}^n [n]^{k_i} \), where \( \vec{k} = (k_1, \ldots, k_n) \) is a vector of \( n \) non negative integers, as follows. For each infinite word \( w = s_1s_2 \cdots \) and each state \( i \in [n] \) we look at the first \( k_i \) visits to state \( i \) (i.e., at times \( t = t_1, \ldots, t_{k_i} \) with \( s_t = i \)) and write down the corresponding transitions in the infinite word \( w \), i.e., \( s_{t+1} \). We note that every state is visited almost surely in \( w \), since \( M \) is an irreducible finite-state Markov chain. Therefore, mapping \( K_{\vec{k}} \) defines a probability distribution on \( \prod_{i=1}^n [n]^{k_i} \). We note that this distribution is independent across all different states and/or independent for a particular state \( i \) because of the Markov property of Markov chains. Furthermore, a specific draw for a copy of a state \( i \) is distributed according to the \( i \)-th row of the transition matrix \( M \).

In Lemma 3.1 we show that for a big enough number of samples \( m = \tilde{O}(\text{HitT}_Q \log(\text{HitT}_Q) + \frac{n}{\varepsilon^2}) \) and \( k_i = \tilde{O}(\mathbb{E}(\# \text{ visits to } i)) = O(\frac{n}{\varepsilon^2}) \) the mapping \( K_{\vec{k}} \) is well defined for a finite \( m \) number of samples for all but a small fraction of the words in \( W_\infty^m \). This effectively allows us to generate a large number of independent samples from a discrete distribution corresponding to matrix \( P \): pick uniformly at random a state \( i \in [n] \) and then observe transition from \( i \) according to transition probabilities of \( P \). Indeed, to this end, we first simulate \( m' = \Theta\left(\frac{m}{\log^2(n/\varepsilon)}\right) \) i.i.d. samples from \([n] \). Let \( \vec{k} \) be the histogram of these \( m' \) samples (note that \( \max_i k_i \leq O(m' \log n/n) \) with high probability). We apply \( K_{\vec{k}} \) mapping to our stream of \( m \) consecutive samples of Markov chain \( P \), which is well defined with high probability. Apart from some small probability events (max \( k_i \) is too large, or \( K_{\vec{k}} \) is not defined) we obtain the desired \( m' \) i.i.d. samples.

**Lemma 3.1.** If \( m = \tilde{O}(\log(\text{HitT}_Q) \text{HitT}_Q) \), then \( \Pr[\exists \text{ state } i : |\{t : s_t = w\}| < \frac{m}{8m} \leq \frac{\varepsilon^2}{n}]. \)

**Proof.** To simplify notations we denote by \( \Delta \overset{\text{def}}{=} 2\text{HitT}_Q \). By union bound over all states \( i \) it is enough to show that \( \Pr[|\{t : s_t = w\}| < \frac{m}{8m}] \leq \frac{\varepsilon^2}{n} \) for each fixed state \( i \). We can make sure that in the first \( \frac{m}{2} \) steps state \( i \) is visited at least once with probability at least \( 1 - \frac{\varepsilon^2}{n^2} \). Once

\[\text{in this paper, } \tilde{O} \text{ always hides poly log}(n/\varepsilon) \text{ factors.}\]
we visited state $i$, instead of hitting time for state $i$ we can analyze the **return time** $\text{Return}_i$ for $i$. Note that for symmetric Markov chains $\frac{1}{n} \vec{1}$ (uniform distribution) is a stationary distribution. Therefore, every state appears at average once in every $n$ steps in an infinite word from $W_\infty$. In other terms, the expectation of $\text{Return}_i$ for each state $i$ is exactly $n$. By definition of hitting time we have that in $\frac{n}{2}$ steps the probability of reaching a particular state $i$ from any other state $j$ is greater than $1 - \frac{1}{e}$ (or any other given constant). It implies that $\Pr[\text{Return}_i \geq \frac{n}{2} \cdot C] \leq e^{-C}$ for any $C \in \mathbb{N}$. Indeed, one can show this by induction on parameter $C$. Notice that if the random walk did not return to $i$ after $C - 1$ steps it has stopped at some state $j \neq i$. Then for any choice of $j$ by definition of the hitting time the random walk will return to $i$ with probability at least $1/e$ in the next $\frac{n}{2}$ steps. It is not hard to get a similar bound $\Pr[\text{Return}_i \geq \Delta \cdot C] \leq e^{-C}$ for any $C \geq 1, C \in \mathbb{R}$. To simplify notations we use $X$ to denote the random variable $\text{Return}_i$ and $X_1, \ldots, X_\ell$ to denote $\ell$ i.i.d. samples of $X$. We have

$$X \geq 0 \quad \text{and} \quad \forall C \in \mathbb{R}_{\geq 1}, \Pr[X \geq C] \leq e^{-C} \quad \text{and} \quad \mathbf{E}[X] = n. \quad (8)$$

We only need to show that $\Pr[X_1 + \cdots + X_\ell > m/2] \leq \frac{e^{-\theta}}{\ell^2}$ for $\ell = \frac{m}{8e-n}$. To this end, we use a standard technique for large deviations and apply Markov’s inequality to the moment generating function of $X_1 + \cdots + X_\ell$.

$$\Pr[X_1 + \cdots + X_\ell > m/2] = \Pr[e^{\theta(X_1 + \cdots + X_\ell)} > e^{\theta \cdot m/2}] \leq \frac{\mathbf{E}[e^{\theta(X_1 + \cdots + X_\ell)}]}{e^{\theta \cdot m/2}} = \mathbf{E}[e^{\theta X}]^\ell \quad (9)$$

We note that given restrictions (8) on $X$ maximum of $\mathbf{E}[e^{\theta X}]$ for any fixed $\theta > 0$ is attained at

$$X^* \sim \begin{cases} \Delta \cdot x & x \in [C_0, \infty) \text{ with probability density function } e^{-x} \\ 0 & \text{with remaining probability } 1 - e^{-C_0}, \end{cases}$$

where constant $C_0 > 1$ is such that $\mathbf{E}[X^*] = n$. Indeed, distribution $X^*$ maximizes (9) due to simple variational inequality: $\epsilon \cdot e^{\theta \cdot a} + \epsilon \cdot e^{\theta \cdot b} < \epsilon \cdot e^{\theta \cdot (a-c)} + \epsilon \cdot e^{\theta \cdot (b+c)}$ for any $b \geq a \geq c > 0$, and probability mass $\epsilon > 0$. This inequality allows us to increase $\mathbf{E}[e^{\theta X}]$ and not change $\mathbf{E}[X]$ by tweaking density function $f(x)$ of $X$ $f'(a-c) = f(a-c) + \epsilon$, $f'(a) = f(a) - \epsilon$, $f'(b) = f(b) - \epsilon$, $f'(b+c) = f'(b+c) + \epsilon$, ($f'(x) = f(x)$ for all other $x$), for some $c \leq a$. The only time we cannot apply this incremental change is when $X = X^*$.

We have

$$\mathbf{E}[X^*] = \Delta(C_0 + 1)e^{-C_0} = n. \quad (10)$$

We set $\theta \overset{\text{def}}{=} \frac{1}{2\Delta \log \Delta}$ in (9). Now we are ready to estimate $\mathbf{E}[e^{\theta X}]$. To simplify notations we denote $\gamma \overset{\text{def}}{=} \frac{1}{2 \log \Delta}$. We have

$$\mathbf{E}[e^{\theta X}] = 1 - e^{-C_0} + \int_{C_0}^{\infty} e^{\theta \cdot \Delta x} \cdot e^{-x} \, dx = 1 - e^{-C_0} + \int_{C_0}^{\infty} e^{-x(1 - \frac{\Delta}{2\Delta \log \Delta})} \, dx$$

$$= 1 - e^{-C_0} + e^{-C_0(1-\gamma)} = 1 + e^{-C_0} \left(\frac{e^{C_0 \gamma}}{1-\gamma} - 1\right). \quad (11)$$

We notice that $\gamma C_0 < 1$, since from (10) we can conclude that $\frac{e^{C_0}}{C_0 + 1} = \frac{\Delta}{n} \implies C_0 < 2 \log \Delta = 1/\gamma$. The last implication can be obtained as follows: for $C_0 > 2.52$, we have $C_0 - \frac{C_0}{2} \leq C_0 - \ln(1+C_0) = 12$.
ln(Δ/η). Now, we can estimate \( e^{\gamma C_0} \leq 1 + e \cdot \gamma C_0 \) in (11). Furthermore, since \( \gamma < 1/2 \) we have the term \( e^{\gamma C_0} \leq 1 + 2e^\gamma (C_0 + 1) \). With this estimate we continue (11)

\[
\mathbb{E}[e^{\theta \cdot X}] \leq 1 + e^{-C_0} 2e^\gamma (C_0 + 1) = 1 + \frac{e \cdot n}{\Delta \log \Delta}.
\]

(12)

We apply estimate (12) and formula \( \theta = \frac{1}{2\Delta \log \Delta} \) to (9) to obtain

\[
\Pr[X_1 + \cdots + X_\ell > m/2] \leq \left(1 + \frac{e \cdot n}{\Delta \log \Delta}\right)^\ell \leq \frac{e^{-m/8\Delta \log \Delta}}{e^{m/4\Delta \log \Delta}} = e^{\frac{m}{3\Delta \log \Delta}} < \frac{e^2}{n^2},
\]

where in the second inequality we used the fact \( (1 + \frac{e \cdot n}{\Delta \log \Delta}) < e \), and to get the last inequality we used \( m = \tilde{\Omega} (\Delta \log \Delta) \) (where in \( \tilde{\Omega} \) the hidden dependency is only on \( \log \varepsilon \) and \( \log n \)).

1. \( \vec{k} \leftarrow \text{Histogram } (\Theta \left( \frac{m}{\log^2 (n/\varepsilon)} \right) \text{ i.i.d. Uniform } [n] \text{ samples);} \)
2. for \( t \leftarrow 1 \) to \( m - 1 \) do
3. if \(|\text{Samples}[s_t]| < \vec{k}[s_t]| \) then Add \((s_t \rightarrow s_{t+1})\) to \(\text{Samples}[s_t]\);
4. end
5. if \( \exists i, \text{ s.t., } |\text{Samples}[i]| < \vec{k}[i]\) then
6. return \( \text{REJECT}\);
7. else
8. \( \text{Samples } \leftarrow \text{Samples}[1] \cup \cdots \cup \text{Samples}[n]; \)
9. return \( \text{IdentityTestIID } (\varepsilon, \{q_{ij} = \frac{1}{n} \cdot Q_{ij}\}_{i,j \in [n]}, \text{Samples}); \)
10. end

Algorithm 1: Independent Edges Sampler.

We use as a black-box the following recently proposed identity test under the Hellinger distance\(^7\).

Lemma 3.2. Given a discrete distribution \( q \) supported on \([n]\) and access to i.i.d. samples from a discrete distribution \( p \) on the same support, there is an algorithm which can distinguish whether \( p = q \) or \( d_{\text{Hel}} (p, q) \geq \varepsilon \) with probability \( \geq 2/3 \) using \( O \left( \frac{\sqrt{n}}{\varepsilon^2} \right) \) samples.

As a corollary of the lemma, we get a test that can distinguish whether \( P = Q \), or \( d_{\text{Hel}} ^2 (\frac{1}{n} P, \frac{1}{n} Q) \geq \varepsilon \) using \( m = O \left( \frac{n}{\varepsilon} \right) \) i.i.d samples from \( \frac{1}{n} P \), which can be viewed as a distribution on a support of size \( n^2 \). Lemma 3.3 shows that the required distance condition for the i.i.d. sampler is implied by our input guarantee.

Lemma 3.3. \[ \frac{1}{2} \sum_{i,j \in [n]} \left( \sqrt{P_{ij} \frac{1}{n}} - \sqrt{Q_{ij} \frac{1}{n}} \right)^2 = d_{\text{Hel}} ^2 (\frac{1}{n} P, \frac{1}{n} Q) \geq \varepsilon. \]

Proof. We note that, as \( P \) and \( Q \) are symmetric matrices, so is \([P, Q]_f\). Thus we have

\[
1 - \varepsilon = \rho ([P, Q]_f) = \max \| \vec{u} \|_2 = 1 \vec{v}^{\top} \circ [P, Q]_f \circ \vec{u}.
\]

(13)

\(^7\)this result uses a test similar to [ADK15] and is based on private communication with an author on that paper.
If we use a particular \( \vec{v} = \frac{1}{\sqrt{n}} \mathbb{I} \) in (13), then we get the following inequality.

\[
1 - \varepsilon \geq \frac{1}{\sqrt{n}} \mathbb{I}^T \circ [P, Q] \circ \frac{1}{\sqrt{n}} \mathbb{I} = \frac{1}{n} \sum_{i,j} \sqrt{P_{ij} \cdot Q_{ij}} = 1 - d_{\text{Hel}}^2 \left( \frac{1}{n} P, \frac{1}{n} Q \right),
\]

which implies \( d_{\text{Hel}}^2 \left( \frac{1}{n} P, \frac{1}{n} Q \right) \geq \varepsilon. \)

Next we get a bound on sampling complexity of Algorithm 1.

**Theorem 3.1.** Algorithm 1 provides correct output with probability at least 2/3, with a single sample stream of length \( m = \tilde{O} \left( \text{Hit}_Q \cdot \log \text{Hit}_Q + \frac{n}{\varepsilon} \right) \) from \( P \).

**Proof.** In the case \( P = Q \), the probability that Algorithm 1 proceeds to IID tester, i.e., it does not reject \( P \), because of small number of visits to a state, is at least \( \Pr \left[ \forall i : |\{ t \in w : s_t = i \}| > \frac{m}{8 \varepsilon n} \right] \cdot \Pr \left[ \forall i : \frac{m}{8 \varepsilon n} > k_i \right] \geq \left( 1 - \frac{\varepsilon}{n} \right) \cdot \left( 1 - \frac{2 \varepsilon}{n} \right) \geq 1 - \frac{2 \varepsilon^2}{n} \). In the previous estimate, we used Lemma 3.1 to bound \( \Pr \left[ \forall i : |\{ t \in w : s_t = i \}| > \frac{m}{8 \varepsilon n} \right] \), the fact that \( \Pr \left[ \frac{m}{8 \varepsilon n} \leq k_i \right] \leq \frac{\varepsilon^2}{n^2} \) (follows from a Chernoff bound), and a union bound. IID tester then correctly accepts \( P = Q \) with probability at least 4/5. Hence, the error probability is at most \( 1/5 + 2 \varepsilon^2/n < 1/3 \).

For the case \( P \neq Q \), Lemma 3.3 says that if \( 1 - \rho \left( \frac{[P, Q]}{\varepsilon} \right) > \varepsilon \), then distributions passed down to the IID tester \( \{ p : p_{ij} = \frac{1}{n} P_{ij} \} \) and \( \{ q : q_{ij} = \frac{1}{n} Q_{ij} \} \) are at least \( \varepsilon \) far in Hellinger-squared distance. Classic results on identity testing with independent samples give sharp bounds of \( O(\frac{n}{\varepsilon^2}) \) on sampling complexity with respect to total variation distance for distributions with support size \( n^2 \). This estimate can be improved to work for Hellinger distance (Lemma 3.2). In our case this implies a \( O(\frac{n}{\varepsilon}) \) sampling complexity for the IID tester. Furthermore, random mapping \( \mathcal{K}_{\tilde{k}} : \mathcal{W}_P^\infty \rightarrow p \) (where \( \tilde{k} \) is a histogram of \( m' = \Theta \left( \frac{m}{\log^2 (n/\varepsilon)} \right) \) i.i.d. uniform samples from \([n]\)) produces \( m' \) i.i.d. samples from \( p \). Hence, if Algorithm 1 has sufficient samples from \( P \) to define the mapping \( \mathcal{K}_{\tilde{k}} \), it would be able to distinguish \( p \) and \( q \) with probability at least 2/3. On the other hand, if Algorithm 1 gets finite number of samples which are not sufficient to define the mapping \( \mathcal{K}_{\tilde{k}} \), then it correctly rejects \( P \) before even running the IID tester.

Thus in both cases the probability of error is at most 1/3. \( \square \)

**3.1 Lower Bound.**

In this section we provide nearly matching lower bound to our result in Theorem 3.1.

**Theorem 3.2.** There is an instance of Identity testing problem for symmetric Markov chain \( Q \) that requires a word of length at least \( \Omega(\frac{n}{\varepsilon}) \) to check identity of \( Q \) with 99% confidence.

**Proof.** We use Le Cam’s two point method and construct a class of Markov chains \( \mathcal{P} \) s.t. (i) every \( P \in \mathcal{P} \) is at least \( \varepsilon \) far from \( Q \) for a given constant \( \varepsilon \). That is \( 1 - \rho \left( \frac{[P, Q]}{\varepsilon} \right) \geq \varepsilon \) for any \( P \in \mathcal{P} \); (ii) there is a constant \( c > 0 \), s.t. it is impossible to distinguish a word of length \( m \) generated by a randomly chosen Markov chain \( \tilde{P} \sim \mathcal{P} \), from a word of length \( m \) produced by \( Q \) with probability equal to or greater than \( \frac{99}{100} \) for \( m \leq \frac{cn}{\varepsilon} \). To prove (ii) we show that the total variation distance between the \( m \)-word distributions obtained from the two processes, \( Q \) and \( P \), is small when \( m < \frac{cn}{\varepsilon} \) for some constant \( c \). We denote distribution of length \( m \) words obtained from \( Q \) by \( \mathcal{W}_Q^m \), and from
MC $\tilde{P} \sim P$ by $W_m^n$. We represent symmetric MC as undirected weighted graphs $G = (V,E)$. We allow graph to have multi-edges (this is helpful to provide an intuitive understanding of the lower bound construction and is not essential). We can ultimately remove all multi-edges and give a construction with only simple edges by doubling the number of states.

**Markov Chain $Q$:** complete double graph on $n$ vertices with uniform weights, i.e.,

$$\forall \ i \neq j \ (ij)_1, (ij)_2 \in E \quad Q_{(ij)_1} = Q_{(ij)_2} = \frac{1}{2(n-1)}.$$  

**Family $\mathcal{P}$:** for any pair of vertices $i \neq j$ there are two bidirectional edges $(ij)_1, (ij)_2$ with weights randomly (and independently for each pair of $(i,j)$) chosen to be either

$$P_{(ij)_1}, P_{(ij)_2} = \frac{1 \pm \sqrt{8\varepsilon}}{2(n-1)}, \quad \text{or} \quad P_{(ij)_1}, P_{(ij)_2} = \frac{1 \mp \sqrt{8\varepsilon}}{2(n-1)}.$$

To make this instance a simple graph with at most one bidirectional edge between any pair of vertices we apply a standard graph theoretic transformation: we make a copy $i'$ for each vertex $i$; for each pair of double edges $e_1 = (ij)_1, e_2 = (ij)_2$ construct 4 edges $(ij), (ij'), (i'j), (i'j')$ with weights $w(ij) = w(i'j') = w(e_1)$ and $w(i'j) = w(ij) = w(e_2)$.

As all Markov chains $Q$ and $P \in \mathcal{P}$ are symmetric with respect to the starting state, we can assume without loss of generality that word $w$ starts from the state $i = 1$. First, we observe that for the simple graph $2n$-state representation

**Lemma 3.4.** Every Markov chain $P \in \mathcal{P}$ is at least $\varepsilon$-far from $Q$.

**Proof.** For any $P \in \mathcal{P}$, it can be seen that

$$[P, Q]_i \circ \mathbf{I} = \left(\frac{\sqrt{1+\sqrt{8\varepsilon}} + \sqrt{1-\sqrt{8\varepsilon}}}{2}\right) \cdot \mathbf{I}.$$  

By Perron-Frobenius theorem $\mathbf{I}$ is the unique eigenvector corresponding to the largest absolute value eigenvalue. Hence, $\rho\left([P, Q]_i\right) = \frac{\sqrt{1+\sqrt{8\varepsilon}} + \sqrt{1-\sqrt{8\varepsilon}}}{2}$ which by Taylor series expansion implies

$$1 - \rho\left([P, Q]_i\right) \geq \varepsilon + \frac{5}{2} \varepsilon^2 + o(\varepsilon^2) \geq \varepsilon \text{ for any } \varepsilon < \frac{1}{8}.$$

We say that a given word $w = s_1 \ldots s_m$ from a Markov chain $P$ represented as a multi-edge graph on $n$ states has a $(ij)$ collision, if any state transition between states $i$ and $j$ (in any direction along any of the edges $(ij)_1, (ij)_2$) occurs more than once in $w$. We now state and prove the following claims about the Markov chain family $\mathcal{P}$.

**Lemma 3.5.** Consider a word $w$ of length $m$ drawn from $Q$. The expected number of collisions in $w$ is at most $O\left(\frac{m^2}{n^2}\right) = O\left(\frac{1}{\varepsilon^2}\right)$.

**Proof of Lemma 3.5.** Let $I_w(t_1, t_2, (ij))$ indicate the event that in the multi-edge interpretation of the Markov chain $\tilde{P}$, the transition along $(ij)$ edge occurs at times $t_1 < t_2$ in $w$. First, we observe that $\Pr[s_{t_1} = s|s_{t_1-1} = x] \leq \frac{1}{n-1}$ and $\Pr[s_{t_2} = s|s_{t_1-1} = x] \leq \frac{1}{n-1}$ for all $x$ and both $s = i$ or $s = j$. 

15
Thus for any $t_2 \geq t_1 + 2$ by a union bound for all four possible cases of $s_{t_1}, s_{t_1+1}, s_{t_2}, s_{t_2+1} \in \{i, j\}$ we have
\[
\mathbb{E}[I_w(t_1, t_2, (ij))] \leq \frac{4}{(n-1)^4}.
\]
Similarly, for the case $t_2 = t_1 + 1$ we can obtain
\[
\mathbb{E}[I_w(t_1, t_2, (ij))] \leq \frac{2}{(n-1)^3}.
\]
Let $X$ denote the random variable which is equal to the total number of collisions in the word $w$. Then,
\[
\mathbb{E}[X] = \sum_{t_2 \geq t_1 + 2} \sum_{i \neq j} \mathbb{E}[I_w(t_1, t_2, (ij))] + \sum_{t_1} \sum_{i \neq j} \mathbb{E}[I_w(t_1, t_1 + 1, (ij))]
\leq \frac{4}{(n-1)^4} \cdot \frac{m^2}{2} \cdot \frac{n(n-1)}{2} + 2 \cdot \frac{1}{(n-1)^3} \cdot m \cdot \frac{n(n-1)}{2} = O\left(\frac{m^2}{n^2}\right).
\]

We also consider 3-way collisions which are collisions where there was at least 3 different transitions between a pair of states $i$ and $j$ in the word $w$.

**Lemma 3.6.** Consider a word $w$ of length $m$ drawn from $Q$. The probability of $w$ having a 3-way collision is at most $O\left(\frac{m^3}{n^3}\right) = o(1)$.

**Proof of Lemma 3.6.** Similar to the proof of Lemma 3.5 we can give a sharp upper bound on the expected number of 3-way collisions with the most significant term being $\frac{8m^3}{6(n-1)^6} \cdot \frac{n(n-1)}{2}$, i.e., the expected number of 3-way collisions is $O\left(\frac{m^3}{n^3}\right)$. By Markov inequality we obtain the required bound on the probability of a 3-way collision.

Now consider a typical word $w$ generated by $Q$. As we know from Lemma 3.6 it has no 3-way collisions and by Markov inequality and Lemma 3.5 has at most $O\left(\frac{1}{n^3}\right)$ collisions with high probability. As we show next a typical word $w$ has similar probabilities under $Q$ or $\bar{P} \sim P$ models.

**Lemma 3.7.** For $m = O\left(\frac{n}{\varepsilon}\right)$ at least $\frac{1}{2}$ fraction of words $w = s_1 \cdots s_m$ generated by $Q$ satisfy
\[
\frac{1}{2} \cdot \Pr_Q[w] < \Pr_{\bar{P} \sim P}[w] < 2 \cdot \Pr_Q[w]
\]

**Proof of Lemma 3.7.** For each feasible word $w$ in $Q$, i.e., $w$ such that $\Pr_Q[w] > 0$
\[
\Pr_Q[w] = \left(\frac{1}{2(n-1)}\right)^{m-1}, \quad \Pr_{\bar{P} \sim P}[w] = \prod_{j > i} P_{(ij)} \sum_{\frac{1+\sqrt{8\varepsilon}}{2(n-1)}}^{1} \bar{P}_{(ij)}[\{(ij)_{1} \in w\}] \cdot \bar{P}_{(ij)}[\{(ij)_{2} \in w\}]
\]

First, if $w$ has only one transition along edge $(ij)$, then the corresponding term in $\Pr_{\bar{P} \sim P}[w]$
\[
\sum_{P_{(ij)} \leq \frac{1+\sqrt{8\varepsilon}}{2(n-1)}} \bar{P}_{(ij)}[\{(ij)_{1} \in w\}] \cdot \bar{P}_{(ij)}[\{(ij)_{2} \in w\}] = \frac{1}{2} \left(\frac{1 + \sqrt{8\varepsilon}}{2(n-1)} + \frac{1 - \sqrt{8\varepsilon}}{2(n-1)}\right) = \frac{1}{2(n-1)}.
\]
From Lemma 3.6, we know that probability of a 3-way collision in \( w \) is \( o(1) \) under \( Q \) model. We observe that for a 2-way collision \( (ij) \) (a collision which is not a 3-way collision), the corresponding term in \( \Pr_{P \sim P}[w] \) for the case of transition along two different edges \( (ij)_1 \) and \( (ij)_2 \) is

\[
\sum_{P((ij)_1)} \Pr[\{(ij)_1 \in w\}] \cdot \Pr[\{(ij)_2 \in w\}] = \frac{1 + \sqrt{8\varepsilon}}{2(n - 1)} \cdot \frac{1 - \sqrt{8\varepsilon}}{2(n - 1)} = \frac{(1 - 8\varepsilon)}{4(n - 1)^2}.
\]

We call this type of collision type I collision. For the other case (type II collisions) of transition along the same edges the respective probability is \( \frac{(1 + 8\varepsilon)}{4(n - 1)^2} \). By Lemma 3.5 and by Markov inequality the total number of collisions is \( O(\frac{1}{\varepsilon^2}) \) with probability \( \frac{3}{4} \). We can also make sure that out of these collisions number of type I and type II collisions is roughly the same. More precisely, the difference between numbers of type I and type II collisions is at most \( O(\frac{1}{\varepsilon}) \) with probability of at least \( \frac{3}{4} \). Indeed, the choice of edge collision type in \( w \) is uniform between type I and type II, and is independent across all collision edges. Now, for small enough \( m \) we can make sure that at least \( \frac{1}{2} \) fraction of words \( w \) has number of collisions at most \( \frac{c_1}{2} \varepsilon^2 \) and the difference between number of type I and II collisions is at most \( \frac{c_2}{2} \varepsilon^2 \), for some small constants \( c_1, c_2 > 0 \). Thus the corresponding density functions can be related as follows.

\[
2 > (1 + 8\varepsilon)^{c_2 \varepsilon^2} \cdot \Pr_{P \sim P}[w] > (1 - 64\varepsilon^2)^{c_1 / 2} \cdot (1 - 8\varepsilon)^{c_2 / 2} > 1/2
\]

Lemma 3.7 shows that \( d_{TV}(W^m_{P}, W^m_{Q}) \leq \frac{3}{4} \), which implies that no algorithm can successfully distinguish \( Q \) from the family \( P \) with probability greater than \( \frac{3}{4} \) for some \( m = \Omega(\frac{\varepsilon^2}{\varepsilon}) \).

\[\square\]

4 Card Shuffling

A commonly used technique to shuffle decks of \( n = 52 \) cards is the riffle shuffle: first, the dealer cuts the deck into two piles. Then, the piles are “riffled” together: the shuffler successively drops cards from the bottom of each pile to form a new pile. There are two variable aspects in this procedure. First, the numbers of cards in each pile after the initial cut can vary. Second, each time the dealer drops a card she needs to choose the pile from which the card is dropped.

The most well studied mathematical model for riffle shuffle is due to Gilbert, Shannon, and Reeds (GSR-model for short): first, the deck is cut into two packs according to a \((n, 0.5)\)-binomial random variable where \( n \) is the number of cards in the deck; next, cards are dropped one by one from the bottom of one or the other pile with probability proportional to the relative sizes of the piles (i.e., if the left pile contains \( a \) cards and the right pile \( b \) cards, the next card drops from the left pile with probability \( \frac{a}{a + b} \)). A well known result in this model is due to Bayer and Diaconis [BD92] who gave a sharp mathematical analysis of the mixing time of the riffle shuffle Markov chain showing that “seven shuffles are necessary and sufficient to approximately randomize 52 cards,” which actually convinced Las Vegas casinos to increase the number of shuffles in their shuffling procedures.

There have been some statistical studies validating the accuracy of the GSR model for riffle shuffles in practice. For example Diaconis and Reeds (see [Dia88]) did empirical analysis of about
a hundred riffle shuffles performed by each of them. They looked at a few different statistics including the count of consecutive cards dropped from each of the piles. In other work (see \cite{Dia02} open problem 5), Chakraborty and Diaconis pointed out that some shuffling machines performing riffle shuffles do not conform to the GSR model. Instead they proposed another model to capture this observed phenomenon (we call it \textit{CD-model}), where, in contrast to the GSR model, cards are dropped with probability $\frac{a}{a+b}$ from the pile containing $b$ cards and $\frac{b}{a+b}$ from the pile containing $a$ cards.

Despite a large interest in card shuffling and all the existing work mentioned above, there has not been much theoretical statistical analysis on the question of testing whether a particular shuffling model is accurate. In this section we propose a new theoretical framework for the statistical analysis of riffle shuffles. We aim to address the following question:

How many trials are needed to test that shuffles are performed according to a specified probabilistic model?

It is natural to parametrize a riffle shuffle by (i) the distribution of possible cuts, and (ii) the probability $p_{ab}$ of choosing the next card to be dropped from the left pile for each profile $(a,b)$ of the number of cards left in the two piles. In this description each riffle shuffle can be represented as a random walk on a 2-dimensional grid $(a,b) \in \mathbb{Z}^2$ that starts at a position chosen from a specified distribution on the diagonal $a + b = n$ and decreases the sum of the coordinates $a + b$ by one at each move. In fact, we get an almost one-to-one correspondence between riffle shuffles and the aforementioned random walks on the $n \times n$ grid (the only shuffle that corresponds to more than one path on the grid is the identical permutation). Therefore, by knowing the initial permutation of cards at the beginning of the shuffle, and by scanning the permutation of cards obtained after one riffle shuffle we can reconstruct (except for the unimportant case of void shuffle) the random walk of $n$ steps taken by our grid Markov Chain. We note that this grid representation might not be enough to accurately model the behavior of a dealer. For example, shufflers often tend to drop chunks of consecutive cards from left or right pile regardless of the pile sizes. To address this issue one might want to introduce an extra parameter – which pile the last card was taken from – to our grid parameterization, which can be done by doubling the number of states in the Markov chain. To capture this and other potential extensions of the Markov chain model for a riffle shuffle we introduce the following general theoretical framework.

**Definition 2** (Sparse MC). Consider a Markov chain defined by transition matrices $P = \{P_t\}_{t=1}^{n_1}$ over $n_2$ states that proceeds in $n_1$-step rounds, as follows. Starting from some state $X_0 = s_0$ it follows a transition according to $P_1$, then $P_2$, etc, then $P_{n_1}$ to arrive at some state $X_1$. Starting from $X_1$ it repeats transitions according to $P_1, \ldots, P_{n_1}$, in sequence, and so on, ad infinitum. The transition matrices are assumed \textit{sparse} having $O(n_3)$ non-zero entries.

To relate the above definition to the riffle shuffle, we should think of the state space as the set $\{(a,b) | 0 \leq a + b \leq n\}$, where $n = 52$. So in particular, there are $n_2 = O(n^2)$ states. There are $n_1 = n + 1$ transition matrices. $P_1$ takes us from an uncut deck of cards, corresponding to the state $(0,0)$, to a cut deck corresponding to a state in set $\{(a,b) | a + b = n\}$. Then each other transition matrix $P_t$, $t > 1$, maps a state in $\{(a,b) | a + b = n - t + 2\}$ to states in $\{(a,b) | a + b = n - t + 1\}$. All transition matrices have $O(n)$ non-zero entries. Note that this way of modeling the riffle shuffle, while forgetting the specific ordering of cards, maintains the essential information that we need to test a riffle shuffle model, and in particular saves exponentially in the size of the state space.
Testing sparse Markov chains. We develop tools for goodness-of-fit testing of sparse Markov chain models.

Simplification: To avoid carrying around several parameters, we will henceforth take \(n_1 = n_3 = n\) and \(n_2 = O(n^2)\), which is what we would need for the riffle shuffle. Our results, namely the use and analysis of our edge tester, extend to the general case. We will also assume that \(P_{n_1}\) is the trivial matrix taking all states into a fixed state \(s_0\), which is also what we would need for the riffle shuffle, namely \(s_0 = (0, 0)\). Again, our results easily extend to the general case.

With these simplifications in place, we can break an observed trajectory from a sparse Markov shuffle, namely \(s\). One sample is a word \(w = s_0 \cdots s_n\), whose transitions \(s_{t-1} \rightarrow s_t\) are performed according to transition matrix \(P_t\).

As described in Section 2.2, a natural measure of distance between two Markov chains \(Q = \{Q_t\}_{t=1}^n\) and \(P = \{P_t\}_{t=1}^n\) is the total variation distance between words of certain length sampled from these chains. As we have a natural length \(n\) to use here, we can take our distance between chains to be \(\operatorname{Dist}(P, Q) \overset{\text{def}}{=} d_{\text{TV}}(W^n_P, W^n_Q)\).

We note that \(\frac{\operatorname{Dist}(P, Q)}{2} = \frac{d_{\text{TV}}^2(W^n_P, W^n_Q)}{2} \leq d_{\text{Hel}}^2(W^n_P, W^n_Q)\) and for Hellinger-squared distance we can derive a formula similar to (1): \(1 - d_{\text{Hel}}^2(W^n_P, W^n_Q) = \overrightarrow{e}_1^\top \circ [P_1, Q_1] \circ \cdots \circ [P_t, Q_t] \circ \cdots \circ [P_n, Q_n] \circ \overrightarrow{1}\). In particular, we could alternatively define our distance using the spectral approach we took in Section 3. To this end we can define a large matrix \(Q^*\) for Markov chain \(Q\) that acts on \(n(n+1)\) states \((n+1)\) distinct copies \(n_t\) of \(n\) states for each \(t \in \{0, \cdots, n\}\), such that \(Q^*\) behaves exactly like matrix \(Q_t\) on states \(n_{t-1}\) transitioning them to states \(n_t\), and for \(t = n\) states \(n_t\) are transitioned to the initial state \(s_1\) with \(t = 0\). We similarly define large matrix \(P^*\) for the Markov chain \(P\).

Then it turns out that the spectral radius \(\rho\left([Q^*, P^*]_n\right)^{n+1} = 1 - d_{\text{Hel}}^2(W^n_P, W^n_Q)\).

With these definitions we are interested in the following testing problem:

**Input:** \(Q = \{Q_t\}_{t=1}^n\), s.t. each \(Q_t\) is sparse, i.e., it has only \(O(n)\) non zero entries in total; \(m\) samples of \(w = s_0 \cdots s_n\) from a sparse Markov chain \(P = \{P_t\}_{t=1}^n\).

**Output:** \(P = Q\), or \(P \neq Q\) if \(\operatorname{Dist}(P, Q) \geq \varepsilon\).

### 4.1 Upper Bound

For the upper bound, one might consider an appropriately defined statistic on the number of visits to a particular state \(s_{i,t}\) to distinguish between the two cases. Such statistics however can be mathematically difficult to deal with and we obtain worse bounds on the moments. In this paper, instead, we consider a different statistic. We look at all one-step transitions that can have positive probability in the Markov chain \(Q\) or \(P\), we call these one-step transitions as edges. We denote a generic edge from a state \(s_{i,t-1}\) to a state \(s_{j,t}\) by \(e\); the set of all possible edges by \(E\); the set of transitions in \(E\) between states at time \(t-1\) and time \(t\) by \(E(t)\) for each \(t \in \{n\}\). For each edge \(e\), let \(q_e\) and \(p_e\) be the probabilities that there was a transition along edge \(e\) in one sample \(s_1 \cdots s_n\) from \(Q\), or from \(P\), respectively. Our statistic is defined on these edges. From a high level perspective, it consists of two steps:

**Pruning.** We remove all rare edges, i.e., edges that are traversed with probability less than \(O(\frac{\varepsilon^2}{n^2})\) in \(Q\). We show that the Markov chain obtained post pruning and renormalization is still close to
the original chain (Lemma 4.5). This step is necessary as rare instances of such transitions along rare edges could potentially shift the value of the statistic by a lot and we want to avoid that. Let $E^*$ be the resulting pruned set of edges. We reject all samples from $P$ that go along any removed edge $e \notin E^*$. We return $P \neq Q$ if there are too many rejected samples. Otherwise, we continue to the next step. In Lemma 4.6 we show that returning $P \neq Q$ in this step doesn’t affect the success probability by too much.

**χ²-statistic on edges.** For each non rare edge $e \in E^*$ we count the number of transitions $n_e$ along $e$. We define $\chi^2$ edge statistic $Z_e = \frac{(n_e - q_e \cdot m)^2 - n_e}{q_e \cdot m}$. Our main statistic is

$$Z = \sum_{e \in E^*} Z_e = \sum_{e \in E^*} \frac{(n_e - q_e \cdot m)^2 - n_e}{q_e \cdot m}.$$  

We accept or reject $P = Q$ depending on $Z$ being smaller or larger than a certain threshold. This test is similar in spirit to that of [ADK15] but requires much more involved analysis. Indeed, in our setting it is not clear which statistic to use: one can attempt to count frequencies of state visits in the MC, or employ other state dependent statistics. After many trials and errors we figured out that doing the analysis across separate edges was the best approach. Indeed, since we are dealing with non i.i.d. but dependent samples, obtaining a non-trivial variance bound for our edge statistic proves to be a challenging task. Similar to the classical i.i.d. setting, poissonisation helps to ease the analysis in our setting too. However, we rely on it in a more subtle way: the effects of poissonisation at the top layer of $n$ states percolate nicely through to the bottom layers of the chain as shown in Lemma 4.1. We show that $\text{Var}[Z] = O\left(kn^3\right)$ in Lemmas 4.3 and 4.4. Another challenge for us was to relate the new definition of distance between two non stationary Markov chains with the parameters in the description of their kernels, as e.g. in our Lemma 4.2. Our $\chi^2$ test yields the following guarantee on the number of samples

**Theorem 4.1.** There is an algorithm that can tell whether $P = Q$, or $P \neq Q$, when $\text{Dist}(P, Q) \geq \varepsilon$, with probability at least $\frac{2}{3}$ using $O\left(\frac{n^{3/2}}{\varepsilon^2}\right)$ samples.

Note that, while we state the above theorem in terms of the number of samples, we really mean that we observe a single trajectory from the sparse Markov chain which we have partitioned into segments of length $n$. In particular, the length of the required trajectory for the above statements is a factor of $n$ larger than the stated number of samples. Additionally note that to properly compare to our results from Section 3, we should note that the number of states here is $O(n^2)$. All details are provided in Section 4.2. We also have a complementary lower bound which is presented in Section 4.3.

### 4.2 More Details on the Tester for Sparse Markov Chains

We consider all one-step transitions that can have positive probability in the Markov chain $Q$ or $P$, we call these one-step transitions as edges. We denote a generic edge from a state $s_{i,t-1}$ to a state $s_{j,t}$ by $e$; the set of all possible edges by $E$; the set of transitions in $E$ between states at time $t-1$ and time $t$ by $E(t)$ for each $t \in [n]$. For each edge $e$, let $q_e$ and $p_e$ be the probabilities that there was a transition along edge $e$ in one sample $s_1 \cdots s_n$ from $Q$, or from $P$, respectively. Our test, from a high level perspective, consists of two steps:
**Pruning.** We remove all rare edges, i.e., edges that are traversed with probability less than \(O(\frac{1}{n^2})\) in \(Q\). Let \(E^*\) be the resulting pruned set of edges. We reject all samples from \(P\) that go along any removed edge \(e \notin E^*\). We return \(P \neq Q\) if there are too many rejected samples. Otherwise, we continue to the next step.

**\(\chi^2\)-statistic on edges.** For each non rare edge \(e \in E^*\) we count the number of transitions \(n_e\) along \(e\). We define \(\chi^2\) edge statistic \(Z_e = \frac{(n_e - q_e \cdot m)^2 - n_e}{q_e \cdot m}\). Our main statistic is

\[
Z = \sum_{e \in E^*} Z_e = \sum_{e \in E^*} \frac{(n_e - q_e \cdot m)^2 - n_e}{q_e \cdot m}.
\]

We accept or reject \(P = Q\) depending on \(Z\) being smaller or larger than a certain threshold.

In the remainder of this section we mostly focus on the latter step. Specifically, we analyze the \(\chi^2\) edge statistic in the case when \(q_e \geq \Omega(\frac{2}{n})\) for all \(e \in E\) and \(p_e = 0\) for all \(e \notin E\). At the end of the section we explain why after the pruning step these conditions are satisfied.

**Poisson Sampling.** Throughout the analysis of \(\chi^2\) statistic, we use the standard Poissonization approach. Instead of drawing exactly \(m\) samples from \(P\), we first draw \(m' \sim \text{Poisson}(m)\), and then draw \(m'\) samples from \(P\). The benefit of this is that the number of times different elements in the support of the cut distribution occur in the sample become independent, giving simpler analysis. Moreover, the number of transitions observed along the edge \(e \in E(t)\), \(n_e\), for a fixed \(t\) will be distributed as \(\text{Poisson}(m \cdot p_e)\), independently for all \(e \in E(t)\) (see Lemma 4.1). As \(\text{Poisson}(m)\) is tightly concentrated around \(m\), this additional flexibility comes only at a sub-constant cost in the sample complexity with an inversely exponential in \(m\), additive increase in the error probability.

We note that as in equations (1 – 2) from [ADK15] the expectation and variance of our \(\chi^2\) statistic are as follows.

\[
\mathbb{E}[Z_e] = m \cdot \frac{(p_e - q_e)^2}{q_e} \quad \text{and} \quad \mathbb{V}[Z_e] = 2 \frac{p_e^2}{q_e} + m \cdot \frac{p_e(p_e - q_e)^2}{q_e^2}.
\]

**Lemma 4.1.** The number of transitions \(n_e\) along an edge \(e\) is distributed as \(\text{Poisson}(m \cdot p_e)\) and all \(n_e\) are independent for \(e \in E(t)\), for any \(t \in [n]\).

**Proof.** The proof proceeds by induction on \(t\) and is based on the following two standard observations on Poisson random variables:

- (Observation I) for any discrete distribution \(D\), \(k \sim \text{Poisson}(\lambda)\) i.i.d. samples from \(D\) form a collection of jointly independent Poisson random variables for the occurrences of each element in the support of \(D\), i.e., distribution \(\prod_i \text{Poisson}(\lambda \cdot \Pr_{x \sim D}[x = i])\);

- (Observation II) the sum of two independent Poisson random variables with distributions \(\text{Poisson}(\lambda_1)\) and \(\text{Poisson}(\lambda_2)\) is a Poisson random variable with the distribution \(\text{Poisson}(\lambda_1 + \lambda_2)\).

For \(t = 1\) as we start with \(\text{Poisson}(m)\) samples, Observation I gives us the desired result. For the induction step (from \(t = k\) to \(t = k + 1\)), we observe that counts of visits to each particular state \(i\) at time \(t\) are independent Poisson random variables by Observation II. Now, Observation I applied to the states at time \(t\) yields the desired result. \(\square\)
The following procedure correctly distinguishes between the case $P = Q$, or $\text{Dist}(P, Q) \geq \varepsilon$, in the regime when $q_e \geq \Omega(\frac{\varepsilon^2}{m^2})$ for all $e \in E(Q)$ and $p_e = 0$ for all $e \notin E$.

**Input:** $\varepsilon$; an explicit $k$-sparse Markov Chain $Q = \{Q_i\}_{i=1}^n$; (Poisson) $m$ samples from a Markov Chain $P = \{P_i\}_{i=1}^n$, where $n_e$ denotes the number of transitions along the edge $e$.

**Output:** Accept if $P = Q$, or reject if $\text{Dist}(P, Q) \geq \varepsilon$

```
1 E ← \{e : q_e > 0\};
2 Z ← \sum_{e \in E} \frac{(n_e - q_e \cdot m)^2 - q_e \cdot m}{q_e \cdot m};
3 if $Z \leq 2\sqrt{k} n^{3/2}$ then
4     return ACCEPT;
5 else
6     return REJECT;
7 end
```

**Algorithm 2:** \( \chi^2 \) Edge Test

**Theorem 4.2.** Algorithm 2 is correct with probability at least $4/5$, if $m \geq \frac{C n^{3/2}}{\varepsilon^2}$ for some $C = O(1)$, $q_e \geq \frac{\varepsilon^2}{kn^2}$ for all $e \in E$, and $p_e = 0$ for all $e \notin E$.

**Proof.** To get the desired result we analyze expectation and variance of $Z$. First, we relate the expected value of $Z$ with the distance $\text{Dist}(P, Q)$ between $P$ and $Q$.

**Lemma 4.2.** $\mathbb{E}[Z] \geq \frac{m}{4} \cdot \text{Dist}^2(P, Q)$.

**Proof.** We recall that

$$
\begin{align*}
d_{\text{ite}}^2(P, Q) &= 1 - e_1^T \circ \left[ P_1, Q_1 \right]_f \circ \cdots \circ \left[ P_t, Q_t \right]_f \circ \cdots \circ \left[ P_n, Q_n \right]_f \circ \mathbb{I} \\
&= e_1^T \circ \left( \frac{P_1 + Q_1}{2} \right) \circ \cdots \circ \left( \frac{P_n + Q_n}{2} \right) \circ \mathbb{I} - e_1^T \circ \left[ P_1, Q_1 \right]_f \circ \cdots \circ \left[ P_n, Q_n \right]_f \circ \mathbb{I} \\
&= \frac{1}{2} \sum_{t=1}^{n} \left( \frac{P_t + Q_t}{2} - \left[ P_t, Q_t \right]_f \right) \circ \left( \frac{P_{t+1} + Q_{t+1}}{2} \right) \cdots \left( \frac{P_n + Q_n}{2} \right) \circ \mathbb{I}
\end{align*}
$$

where in the last line $\left[ P_t, Q_t \right]_{(i',j')^2} = \left( \sqrt{P_t(ij)} - \sqrt{Q_t(ij)} \right)^2$.

Indeed, the first equality holds true as $P_t \circ \mathbb{I} = Q_t \circ \mathbb{I} = \mathbb{I}$ for any $t \in [n]$; the second equality is a telescopic sum; the last equality is simply the formula for the complete square. Let $q_t$ and $p_t$ be the respective distribution vectors over the states $s_{i,t}$, $i \in [n]$ in $Q$ and $P$ Markov chains. We also define distributions $p_0 = q_0 = e_1$.

By applying Cauchy-Schwarz inequality to the corresponding Bhattacharya coefficient of $P$ and
Q at a fixed state $i$ and time $t$ we obtain

$$
\sum_{E} \frac{p_t(i) - q_t(i)}{q_t(i)} = \sum_{j:(ij) \in E(t)} \frac{(p_{t-1}(i)Q_t(ij) - q_{t-1}(i)Q_t(ij))^2}{q_{t-1}(i)Q_t(ij)}
$$

We show that corresponding terms in $E[Z] = \sum_{i,t} \sum_{e:(ij) \in E(t)} E[Z_e]$ give an upper bound on (15) for each fixed state $i$.

$$
\frac{1}{m} \sum_{e:(ij) \in E(t)} E[Z_e] = \sum_{e:(ij) \in E(t)} \frac{(p_e - q_e)^2}{q_e} = \sum_{j:(ij) \in E(t)} \frac{(p_{t-1}(i)P_t(ij) - q_{t-1}(i)Q_t(ij))^2}{q_{t-1}(i)Q_t(ij)}
$$

where the third and forth equalities hold true as $\sum_{j:(ij) \in E(t)} P_t(ij) = \sum_{j:(ij) \in E(t)} Q_t(ij) = 1$, and to get the last inequality one can simply use identity $(a-b)^2 = (\sqrt{a} - \sqrt{b})^2 \left(\frac{\sqrt{a} + \sqrt{b}}{\sqrt{b}}\right)^2$. Now, we claim that the expression in RHS of (16) is at least RHS of (15) for a given $i$, i.e., we need to show that

$$
\sum_{j:(ij) \in E(t)} \left(\sqrt{P_t(ij)} - \sqrt{Q_t(ij)}\right)^2 + \frac{(p_{t-1}(i) - q_{t-1}(i))^2}{q_{t-1}(i)} \geq 0.
$$

The inequality is obviously true, if $\frac{p_{t-1}(i)}{q_{t-1}(i)} \geq \frac{p_{t-1}(i)q_{t-1}(i)}{2}$. Otherwise, without loss of generality, we can substitute the term

$$
\sum_{j:(ij) \in E(t)} \left(\sqrt{P_t(ij)} - \sqrt{Q_t(ij)}\right)^2
$$
with an upper bound of 2. Furthermore, by denoting \( x = \sqrt{\frac{m-1(t)}{q_{e-1}(t)}} \) the inequality \([17]\) can be rewritten as \( q_{e-1}(i) \cdot (2x^4 - x + (x^2 - 1)^2) \geq 0 \), and, indeed, one can verify that this fourth degree polynomial is always positive.

Now we estimate the variance of random variable \( Z \)

**Lemma 4.3.** \( \mathbb{E}[Z] \geq \left( \frac{12\sqrt{k}}{e} + \frac{2\sqrt{2} + \sqrt{k}}{\sqrt{e}} \right) \cdot \sqrt{\text{Var}[Z]} \), when \( m \geq Cn^{3/2} \) and \( \text{Dist}(P, Q) \geq \varepsilon. \)

**Proof.** We recall that \( Z = \sum_{e \in E} Z_e \) and by Lemma 4.1 all \( Z_e \) for a fixed \( t \) and \( e \in E(t) \) are independent. For any random variables \( X_1, \ldots, X_n \) it is true that

\[
\text{Var}[X_1 + \cdots + X_n] \leq \left( \sqrt{\text{Var}[X_1]} + \cdots + \sqrt{\text{Var}[X_n]} \right)^2.
\]

We use this estimate for \( X_t = \sum_{e \in E(t)} Z_e \) to obtain

\[
\sqrt{\text{Var}[Z]} \leq \sum_{t=1}^{n} \sqrt{\sum_{e \in E(t)} \text{Var}[Z_e]} = \sum_{t=1}^{n} \sqrt{\sum_{e \in E(t)} 2 \frac{p_e^2}{q_e^2} + m \cdot \frac{p_e(p_e - q_e)^2}{q_e^2}}.
\]

We further simplify the above expression by using the fact that \( \sqrt{x + y} \leq \sqrt{x} + \sqrt{y} \).

\[
\sqrt{\text{Var}[Z]} \leq \sum_{t=1}^{n} \left[ \sqrt{\sum_{e \in E(t)} 2 \frac{p_e^2}{q_e^2}} + \sqrt{m} \sum_{e \in E(t)} \frac{p_e(p_e - q_e)^2}{q_e^2} \right]. \tag{18}
\]

On the other hand, by Lemma 4.2

\[
\mathbb{E}[Z] \geq \frac{1}{2} \mathbb{E}[Z] + \frac{m}{8} \text{Dist}^2(P, Q) = m \cdot \left( \frac{1}{2} \sum_{e \in E} \frac{(p_e - q_e)^2}{q_e} + \frac{\varepsilon^2}{8} \right). \tag{19}
\]

In the following we use \([19]\) to give separate upper bounds on each of the two summation terms in the RHS of \([18]\).

**First term of** \([18]\). To estimate the first term, we split \( E \) into two sets

\[
E_1 \overset{\text{def}}{=} \{ e \in E : p_e \leq 2q_e \} \quad \text{and} \quad E_2 \overset{\text{def}}{=} \{ e \in E : p_e > 2q_e \}
\]

We define accordingly the sets \( E_1(t) \) and \( E_2(t) \) for each \( t \in [n] \). Again we have

\[
\sum_{t=1}^{n} \sqrt{\sum_{e \in E(t)} 2 \frac{p_e^2}{q_e^2}} \leq \sum_{t=1}^{n} \sqrt{\sum_{e \in E_1(t)} 2 \frac{p_e^2}{q_e^2}} + \sum_{t=1}^{n} \sqrt{\sum_{e \in E_2(t)} 2 \frac{p_e^2}{q_e^2}}.
\]

**Estimate for** \( E_1 \). We have \( 2 \frac{p_e^2}{q_e^2} \leq 8 \) for any edge \( e \in E_1 \). Therefore, by the sparsity condition \( \sum_{e \in E_1(t)} 2 \frac{p_e^2}{q_e^2} \leq 8n \cdot k \), where \( k = O(1) \). Thus,

\[
\sum_{t=1}^{n} \sqrt{\sum_{e \in E_1(t)} 2 \frac{p_e^2}{q_e^2}} \leq \sqrt{8k} \cdot n^{3/2} \leq \frac{\sqrt{8k}}{C} \cdot m \cdot \varepsilon^2 \leq \frac{4\sqrt{8k}}{C} \cdot \mathbb{E}[Z]. \tag{20}
\]
Estimate for $E_2$. We have \( \frac{(p_e - q_e)^2}{q_e} \geq \frac{p_e^2}{4q_e} \) for any $e \in E_2$. Therefore,

\[
\frac{\sqrt{32k}}{C} \cdot E[Z] \geq \frac{\sqrt{32km}}{C} \cdot \sum_{t=1}^{n} \left( \frac{1}{16} \sum_{e \in E_2(t)} \frac{2p_e^2}{q_e} + \varepsilon^2 \right) \geq \frac{\sqrt{32km}}{C} \sqrt{\frac{4\varepsilon^2}{16 \cdot 8n}} \sum_{t=1}^{n} \left\{ \sum_{e \in E_2(t)} \frac{2p_e^2}{q_e} \right\} \\
\geq \frac{\sqrt{32km}}{C} \sqrt{\frac{\varepsilon^2}{32n}} \cdot \sqrt{\frac{\varepsilon^2}{kn^2}} \sum_{t=1}^{n} \left\{ \sum_{e \in E_2(t)} \frac{2p_e^2}{q_e} \right\} \geq \sum_{t=1}^{n} \left\{ \sum_{e \in E_2(t)} \frac{2p_e^2}{q_e} \right\}, \tag{21}
\]

where the first inequality holds by (19); the second inequality is simply AM-GM inequality; and to get the third inequality we used the bound $q_e \geq \frac{\varepsilon^2}{kn\pi}$.

Second term of (18). We split $E$ into another two sets $E_3, E_4$ (similarly define $E_3(t)$ and $E_4(t)$):

- $E_3 \overset{\text{def}}{=} \{ e \in E : p_e \leq 2\sqrt{nq_e} \}$ and $E_4 \overset{\text{def}}{=} \{ e \in E : p_e > 2\sqrt{nq_e} \}$

Again

\[
\sum_{t=1}^{n} \sqrt{\sum_{e \in E(t)} \frac{p_e(p_e - q_e)^2}{q_e^2}} \leq \sum_{t=1}^{n} \sqrt{\sum_{e \in E_3(t)} \frac{p_e(p_e - q_e)^2}{q_e^2}} + \sum_{t=1}^{n} \sqrt{\sum_{e \in E_4(t)} \frac{p_e(p_e - q_e)^2}{q_e^2}}
\]

Estimate for $E_3$. We have

\[
2 \sqrt{\frac{2}{C}} \cdot E[Z] \geq \sqrt{\frac{2}{C}} m \cdot \sum_{t=1}^{n} \left( \sum_{e \in E_3(t)} \frac{(p_e - q_e)^2}{q_e} + \frac{\varepsilon^2}{4n} \right) \geq \sqrt{\frac{2}{C}} m \sqrt{\frac{\varepsilon^2}{n}} \sum_{t=1}^{n} \left\{ \sum_{e \in E_3(t)} \frac{(p_e - q_e)^2}{q_e} \right\} \\
\geq m \sqrt{\frac{2\varepsilon^2}{Cn}} \cdot \sqrt{\frac{1}{2n^{1/2}}} \sum_{t=1}^{n} \left\{ \sum_{e \in E_3(t)} \frac{p_e(p_e - q_e)^2}{q_e^2} \right\} = \sqrt{m} \sum_{t=1}^{n} \left\{ \sum_{e \in E_3(t)} \frac{p_e(p_e - q_e)^2}{q_e^2} \right\}, \tag{22}
\]

where the first inequality holds by (19), the second inequality is AM-GM inequality, to get the third inequality we use definition of $E_3$ that $\frac{p_e}{q_e} \leq 2\sqrt{n}$.

Estimate for $E_4$. We have $p_e - q_e \geq \left( 1 - \frac{1}{2\sqrt{n}} \right) p_e$ for any $e \in E_4$. Therefore,

\[
\frac{\sqrt{k}}{\sqrt{2C} \left( 1 - \frac{1}{2\sqrt{n}} \right)} \cdot E[Z] \geq m \frac{\sqrt{k}}{\sqrt{2C}} \sum_{e \in E_4} \frac{p_e(p_e - q_e)}{q_e} \geq \sqrt{m} \frac{km \cdot 2\varepsilon^2}{2C \cdot kn^3/2} \sum_{e \in E_4} \frac{p_e^{1/2}(p_e - q_e)}{q_e} \\
\geq \sqrt{m} \sum_{t=1}^{n} \left\{ \sum_{e \in E_4(t)} \frac{p_e^{1/2}(p_e - q_e)}{q_e} \right\}, \tag{23}
\]

where the first inequality follows from (19), to get the second inequality we estimate $\sqrt{p_e} \geq \sqrt{2n^{1/2}q_e} \geq \sqrt{\frac{2\varepsilon^2}{kn\pi/2}}$, to get the last inequality we simply use that $\sqrt{x} + \sqrt{y} \geq \sqrt{x + y}$.

Finally, combining estimates (20), (21), (22), (23) we obtain the desired bound on the variance.

\[\square\]

Lemma 4.4. If $P = Q$, then $\text{Var}[Z] \leq \sqrt{k} n^{3/2}$.  

25
Proof. Using similar estimate as in the proof of Lemma 4.3 we get
\[
\sqrt{\operatorname{Var}[Z]} \leq \sum_{t=1}^{n} \sqrt{\sum_{e \in E(t)} \operatorname{Var}[Z_e]} = \sum_{t=1}^{n} \left( \sum_{e \in E(t)} 2E^2 q_e^2 \right) \leq n \cdot \sqrt{kn}.
\]

To conclude the proof of Theorem 4.2 it remains to notice that in case \( P = Q \) the error probability (Algorithm 2 returns “reject”) is at most
\[
\Pr \left[ Z > 2\sqrt{kn}^{3/2} \right] \leq \Pr \left[ Z > 2\sqrt{\operatorname{Var}[Z]} \right] \leq \frac{1}{5},
\]
where the first inequality follows from Lemma 4.4, the last is Cantelli’s inequality, since \( \mathbb{E}[Z] = 0 \). On the other hand, when \( \operatorname{Dist}(P,Q) \geq \varepsilon \), then \( \mathbb{E}[Z] \geq m \cdot \varepsilon^2 \). If Algorithm 2 makes an error by returning “accept”, then \( Z \leq 2\sqrt{\mathbb{E}[Z]} \leq \frac{2n \varepsilon^2}{C \sqrt{k}} \). Thus \( Z - \mathbb{E}[Z] \leq \left( \frac{2n \varepsilon^2}{C \sqrt{k}} - 1 \right) \mathbb{E}[Z] \). Now if \( C \) is such that \( 1 - \frac{2n \varepsilon^2}{C \sqrt{k}} \geq 2 \cdot \left( 12\sqrt{\frac{2 \varepsilon^2}{C}} + 2\sqrt{2 + \sqrt{3}} \right) \) (any constant \( C \geq \max \left( \sqrt{2}(42\sqrt{2} + 4), (8\sqrt{2} + 4\sqrt{3})^2 \right) \) would work), then \( Z - \mathbb{E}[Z] \leq -2\sqrt{\operatorname{Var}[Z]} \) by Lemma 4.3. Furthermore, by Cantelli’s inequality
\[
\Pr \left[ Z \geq 2\sqrt{kn}^{3/2} \right] \leq \Pr \left[ Z \geq -2\sqrt{\operatorname{Var}[Z]} \right] \leq \frac{1}{5},
\]
i.e., probability of Algorithm 2’s error in the case \( P \neq Q \) is at most \( \frac{1}{5} \). \( \square \)

Analysis of pruning step. Here we slightly modify Markov Chains \( Q \) and \( P \) so that probability of traversing any edge in \( Q \) is \( \Omega(\varepsilon^2) \) and that \( P \) only uses these edges. To this end, we sequentially remove edges from \( Q \) that have too low probability of traversal in \( Q \). Effectively, in the pruning process we are sampling from \( Q \), but rejecting all the samples that use a “rare” edge. We choose the threshold for the “rare” edges in such a way that we would reject at most \( \varepsilon^2 \) fraction of samples from \( Q \). Recall that the Markov chain obtained by pruning \( Q \) is denoted as \( Q^* \). After pruning of \( Q \), we do the corresponding empirical rejection sampling for \( P \) (see Algorithm 3) which is equivalent to obtaining samples from the modified Markov chain \( P^* \). If there are too many rejected samples, we conclude that \( \operatorname{Dist}(P,P^*) > \operatorname{Dist}(Q,Q^*) \) with high probability, and thus \( P \neq Q \). Otherwise we proceed to Algorithm 2 for the modified \( Q \) and pruned samples from \( P \).

Let \( Q^* \) be a modified Markov Chain \( Q \) that sample \( w \sim Q \) and reject any \( w \) with \( e \notin E^* \).

Lemma 4.5. \( \operatorname{Dist}(Q,Q^*) \leq 2\varepsilon^2 \)

Proof. By definition of the set of pruned edges \( E^* \), by removing each new edge we lose at most \( \varepsilon^2 / \sqrt{kn} \) fraction of samples. As there are only at most \( kn^2 \) edges in \( Q \), the probability of avoiding removed edges is at least \( (1 - \frac{\varepsilon^2}{\sqrt{kn}})^{kn^2} \geq 1 - \varepsilon^2 \). Thus at most \( \varepsilon^2 \) fraction of words \( W^m_Q \) are rejected in \( W^m_{Q^*} \), which implies that \( 2\varepsilon^2 \leq d_{TV} \left( W^m_Q, W^m_{Q^*} \right) = \operatorname{Dist}(Q,Q^*) \). \( \square \)

We need to argue about probability of error in Algorithm 3. First, in the case \( P = Q \) Algorithm 3 could incorrectly return “reject”. Our next Lemma 4.6 provides the necessary bound. On the other hand, when \( P \neq Q \) and Algorithm 3 does not return “reject”, we want Algorithm 2 to be able to distinguish \( P^* \) and \( Q^* \). To this end, Lemma 4.6 shows that \( \operatorname{Dist}(P^*,Q^*) = \Omega(\varepsilon) \) with high probability.

26
Lemma 4.6.

where the first inequality holds because \(2m \epsilon E_0\) probability at least \(\frac{\epsilon^2}{k \alpha^2}\).

Proof.

and \(x\) probability that if \(\text{Dist}(\cdot)\) is Cantelli’s inequality. 

\[
\begin{aligned}
\text{Input: } \epsilon; \text{ an explicit } k\text{-sparse Markov Chain } & Q = \{Q_t\}_{t=1}^n; m \text{ samples from a Markov Chain } \\
P = \{P_t\}_{t=1}^n \\
\text{Output: } m \cdot (1 - 2\epsilon^2) \text{ i.i.d. samples from pruned } P^* \text{ and pruned } Q^* \text{ s.t., each } q_e = \Omega(\frac{\epsilon^2}{n^2}); \text{ reject } P \text{ if there are not enough samples. }
\end{aligned}
\]

Let \(E^* = \{e: q_e > 0\} \cap \sum e \leq \frac{\epsilon^2}{k \alpha^2}\) do 

\[
\begin{aligned}
E^* & \leftarrow E^* \setminus e; \quad \text{ /* } e = (ij), e \in E(t) */ \\
\text{Delete } (e, Q); \quad \text{ /* set } Q_t(ij) = 0, \text{ re-normalize row } i \text{ in } Q_t */ \\
\text{foreach edge } e \in E^* \text{ do Recompute}(q_e); \\
\text{end}
\end{aligned}
\]

\[
\begin{aligned}
\text{for } w = s_1 \cdots s_n \sim P \text{ do } \\
\text{if } \forall t \ (s_t s_{t+1}) \in E^* \text{ then Add } w \text{ to PrunedSamples; } \\
\text{else increase RejectCount; } \\
\text{end}
\end{aligned}
\]

\[
\begin{aligned}
\text{if } \text{RejectCount} > 2m \epsilon^2 \text{ then } \\
\text{return REJECT; } \\
\text{else } \\
\text{return PrunedSamples; } \\
\text{end}
\end{aligned}
\]

Algorithm 3: Pruning Test. In the pruned Markov Chain \(Q^*\) all edges with \(q_e > 0\) satisfy \(q_e \geq \frac{\epsilon^2}{k \alpha^2}\); samples from Markov Chain \(P^*\) can only go along these edges.

Lemma 4.6.

1. If \(P = Q\), then Algorithm 3’s error of rejecting \(P\) is at most 0.1.

2. If \(\text{Dist}(P, Q) \geq \epsilon\), then either \(\text{Dist}(P^*, Q^*) = \Omega(\epsilon)\), or Algorithm 3 correctly rejects \(P\) with probability at least 0.9.

Proof. Let \(X_\ell\) be Bernoulli random variables for \(\ell \in [m]\) denoting \((X_\ell = 1)\) whether \(\ell\)-th sample from \(P\) was rejected, or accepted to \(P^*\) \((X_\ell = 0)\). Then the number of rejected samples \(X = \sum_{\ell=1}^m X_\ell\). Variables \(X_\ell\) are i.i.d. Let \(x = \Pr[X = 1]\).

1. If \(P = Q\), then probability of rejecting a sample from \(P\) is not more than \(\epsilon^2\), i.e., \(x \leq \epsilon^2\). \(\mathbb{E}[X] = m \cdot x, \mathbb{V}[X] = m \cdot (x - x^2)\). Then

\[
\Pr[X \geq 2m \epsilon^2] \leq \Pr[X \geq \mathbb{E}[X] + 3\sqrt{\mathbb{V}[X]}] \leq \frac{1}{10},
\]

where the first inequality holds because \(2m \epsilon^2 > m \cdot \epsilon^2 + 3\sqrt{m \epsilon^2} > \mathbb{E}[X] + 3\sqrt{\mathbb{V}[X]}\); the second is Cantelli’s inequality.

2. We first observe that \(\text{Dist}(P^*, Q^*) \geq \epsilon - \text{Dist}(Q, Q^*) - \text{Dist}(P, P^*)\). We want to argue that if \(\text{Dist}(P, P^*) \geq 6\epsilon^2\), then Algorithm 3 rejects \(P\) with probability at least 9/10. Indeed, then probability \(x\) of rejecting a sample from \(P\) must be at least \(\frac{1}{2}\)Dist \((P, P^*) \geq 3\epsilon^2\), then \(\mathbb{E}[X] \geq 3m \epsilon^2\) and

\[
\Pr[X \leq 2m \epsilon^2] \leq \Pr[X - \mathbb{E}[X] \leq -\frac{\mathbb{E}[X]}{3}] \leq \Pr[X - \mathbb{E}[X] \leq -3\sqrt{\mathbb{V}[X]}] \leq \frac{1}{10},
\]
Thus we get $\text{Dist}(P^*, Q^*) \geq \varepsilon - \text{Dist}(Q, Q^*) - \text{Dist}(P, P^*) \geq \varepsilon - 2\varepsilon^2 - 6\varepsilon^2 \geq \frac{\varepsilon}{2}$ if $\varepsilon$ is small enough constant.

\textbf{Theorem 4.3.} Together, Algorithm 3 and Algorithm 2 tell whether $P = Q$, or $P \neq Q$, when $\text{Dist}(P, Q) \geq \varepsilon$, with probability at least $\frac{2}{3}$ using $O(n^{3/2}/\varepsilon^2)$ samples.

\textit{Proof.} In case $P = Q$, Algorithm 3 produces $P^* = Q^*$ and $m(1 - 2\varepsilon^2)$ samples from $P^*$ with probability at least 0.9. Furthermore, Algorithm 2 converts these $m(1 - 2\varepsilon^2)$ samples into Poisson $m' = \Omega(m)$ samples and accepts $P = Q$ with $4/5$ probability. Overall, we have $4/5 \cdot 0.9 > 2/3$ probability of correctly accepting $P = Q$.

When $\text{Dist}(P, Q) \geq \varepsilon$, Algorithm 3 either correctly rejects $P^*$, or produces $P^*$ and $Q^*$ s.t. $\text{Dist}(P^*, Q^*) \geq \frac{\varepsilon}{2}$ with probability at least 0.9. In the latter case Algorithm 2 correctly rejects $P^*$ with probability at least $4/5$. Overall, we get the probability of correctly rejecting $P$ to be at least $4/5 \cdot 0.9 > 2/3$.

\subsection*{4.3 Lower Bound}

In this section we will show that any algorithm that tests identity of a sparse Markov chain representing card riffle shuffling requires at least $\Omega\left(\frac{n}{\varepsilon^2}\right)$ independent trials, where each trial is a $n$-length word generated by a sparse Markov chain. We recall Definition 2 of a sparse Markov chain adapting it slightly for the convenience of lower bound presentation. Sparse Markov chains $P = \{P_t\}_{t=1}^T, Q = \{Q_t\}_{t=1}^T$: each independent run consists of $T = O(n)$ time steps; has $O(n)$ states for each time $t$; Markov chain starts from a single state at $t = 0$; there are only $O(1)$ possible transitions $P_t(ij) \neq 0$ from each state $i$ to other states for all but the very first time step $t > 0$.

\textbf{Theorem 4.4.} There is an instance of Identity testing problem for a sparse Markov chain $Q$ that requires at least $m \geq \Omega\left(\frac{n}{\varepsilon^2}\right)$ i.i.d. samples to check identity of $Q$ with 99\% confidence.

\textit{Proof.} The high-level proof idea is similar to that of Theorem 3.2 but particular details and proofs are more involved. At an abstract level, we construct a sparse Markov chain $Q$, with respect to which we are interested in testing identity, and a class of sparse Markov chains $\mathcal{P}$ such that

1. Every $P \in \mathcal{P}$ is at least $\varepsilon$ far from $Q$, i.e., $d_{TV}\left(W_p^T, W_Q^T\right) \geq \varepsilon$ for any $P \in \mathcal{P}$.

2. There is a constant $c > 0$, such that it is impossible to distinguish $m$ i.i.d. samples of $T$-length words generated by a random Markov chain $\tilde{P} \sim \mathcal{P}$ from the samples produced by $Q$ with probability equal to or greater than $\frac{99}{100}$, for $m \leq \frac{cn}{\varepsilon^2}$.

We denote the joint distribution of $m$ i.i.d. samples from $Q$ by $Q^\otimes m$ and that from $P$ by $P^\otimes m$. To prove the last point we show that $d_{TV}\left(Q^\otimes m, \tilde{P}^\otimes m\right)$ is small for some $m = \Omega\left(\frac{n}{\varepsilon^2}\right)$. We now describe our construction. To simplify presentation, we use multi-edges in the description of sparse Markov chains. We convert this instance into simple edge graph by the same duplicating trick we employed in the lower bound construction of Theorem 3.2.

\textbf{Markov Chain $Q$:} $T = 2n + 1$ time steps; single state at $t = 0$, states $[2n]$ at each $1 \leq t \leq T$. All states are divided into two categories: Frequently visited $(F) \overset{\text{def}}{=}[2i - 1, i \in [n]}$ and

\footnote{We assume $\varepsilon = \omega(n^{-1/6})$ in the requirement $\text{Dist}(P, Q) \geq \varepsilon$, when $P \neq Q$.}
Rare \((R) \defeq \{2i, i \in [n]\}\). Table below describes weighted multi-graph \(Q = \{Q_t\}_{t=1}^T: x \in F, y \in R, x, y \in [2n]\) denote respective generic frequent and rare states. We adopt notational convention: \(0 \defeq 2n, 2n + 1 \defeq 1\).

| \(t=1\) | \(F \rightarrow F\) | \(F \rightarrow R\) | \(R \rightarrow F\) | \(R \rightarrow R\) |
|-------|-----------------|-----------------|-----------------|-----------------|
|       | \((1 \rightarrow x) \in E\)             | \(Q_t(1, x) = \frac{1}{n}\) | \(\emptyset\)   | \(\emptyset\)   |
| \(t=2k\) | \((x \rightarrow x) \in E\)             | \((x \rightarrow x \pm 1) \in E\) | \((y \rightarrow y \pm 1) \in E\) | \(Q_t(y, y \pm 1) = \frac{1}{2}\) | \(\emptyset\)   |
| \(t=2k+1\) | \((x \rightarrow x) \in E\)             | \(Q_t(x, x) = 1\)             | \(\emptyset\)   | \(\emptyset\)   | \((y \rightarrow y)_{1,2} \in E\) | \(Q_t(e_1) = Q_t(e_2) = \frac{1}{2}\) |

**Family \(\mathcal{P}\):** every \(P \in \mathcal{P}\) has the same set of states and edges as \(Q\). Similar to the construction in Section 4.1, we only change weights of the multi-edge pairs (independently and uniformly at random for each pair \((y \rightarrow y)_{1,2}\) and time \(t\)):

\[
P_t(e_{1,2}) = \frac{1 \pm 4\varepsilon}{2} \quad \text{or} \quad P_t(e_{1,2}) = \frac{1 \mp 4\varepsilon}{2}.
\]

The idea of this construction is that a typical trajectory of Markov chain \(Q\) or \(P \in \mathcal{P}\) stays in frequent states almost all the time and very rarely visits one of the rare states. However, a typical trajectory has constant probability of visiting a rare state.

**Lemma 4.7.** Any \(P \in \mathcal{P}\) is at least \(\varepsilon\)-far from \(Q\), i.e., \(\text{Dist}(P, Q) = d_{TV}(\mathcal{W}_P^T, \mathcal{W}_Q^T) \geq \varepsilon\).

**Proof.** Consider a \(P \in \mathcal{P}\). First, we argue that probability of any word \(w\) with only a single visit to a rare state (at even \(t = 2k\)) satisfies \(|\text{Pr}_Q[w] - \text{Pr}_P[w]| = 4\varepsilon \cdot \text{Pr}_Q[w]\). Indeed, let visit to the rare state \(2i\) in \(w\) happen at the time \(t = 2k\), then

\[
\begin{align*}
\text{Pr}_Q[w] &= \text{Pr}_Q[s_1 \ldots s_{2k}] \cdot \frac{1}{2} \cdot \text{Pr}_Q[s_{2k+1} \ldots s_{2n+1}|s_{2k+1}] \\
\text{Pr}_P[w] &= \text{Pr}_P[s_1 \ldots s_{2k}] \cdot \frac{1}{2} (1 \pm 4\varepsilon) \cdot \text{Pr}_P[s_{2k+1} \ldots s_{2n+1}|s_{2k+1}].
\end{align*}
\]

Therefore, as \(Q\) and \(P\) have the same transitional probabilities of \(s_t \rightarrow s_{t+1}\) for \(t \neq 2k\), we get

\[
|\text{Pr}_Q[w] - \text{Pr}_P[w]| = 4\varepsilon \cdot \text{Pr}_Q[w].
\]

Now, the probability of visiting a rare state exactly once (at even \(t\)) in \(Q\) is precisely

\[
\sum_{w \text{ with } 1 \text{ rare visit}} \text{Pr}_Q[w] = n \cdot \frac{2}{n} \cdot \left(1 - \frac{2}{n}\right)^{n-1} > 2 \cdot e^{-2} > \frac{1}{4},
\]

where we used inequality \((1 - \frac{1}{n})^{n-1} > e^{-1}\) to get the estimate in the right hand side. Hence,

\[
d_{TV}(\mathcal{W}_P^T, \mathcal{W}_Q^T) \geq \sum_{w \text{ with } 1 \text{ rare visit}} |\text{Pr}_Q[w] - \text{Pr}_P[w]| = \sum_{w \text{ with } 1 \text{ rare visit}} 4\varepsilon \cdot \text{Pr}_Q[w] \geq 4\varepsilon \cdot \frac{1}{4} = \varepsilon.
\]

\[\square\]
We define collisions and 3-way collisions similar to the proof of Theorem 3.2. Namely, a collision is a transition that occurs in two samples (3-way collision – in at least three samples) of $Q^\otimes m$ or $P^\otimes m$ from the same state and at the same time. Moreover, as $P \sim P$ and $Q$ are the same except for the double edges between rare states, we are only interested in the collisions along multi-edges between rare states.

**Lemma 4.8.** The expected number of collisions in samples $Q^\otimes m$ is $O \left( \frac{m^3}{n^2} \right) = O \left( \frac{1}{\epsilon^4} \right)$.

Proof. Let $I_w(m_1, m_2, y, t)$ indicate the event that either of the transitions along edges $e_{1,2} = y \rightarrow y$ at time $t$, occurred in samples $m_1$ and $m_2$. Note that at each fixed time all of the $n$ frequent states are equally likely to occur in a sample from $Q$. Therefore, the probability of visiting a rare state $y$ at time $t$ in a single run is at most $O(1/n^2)$. This implies $\Pr_Q[I_w(m_1, m_2, y, t) = 1] = O \left( \frac{1}{n^2} \cdot \frac{1}{n^2} \right) = O(1/n^4)$. Let $X$ denote the total number of collisions.

\[ \mathbb{E}[X] = \sum_{m_1 \neq m_2} \sum_{i \neq j} \mathbb{E}[I_w(m_1, m_2, y, t)] = O \left( m^2 n^2 \cdot \frac{1}{n^4} \right) = O \left( \frac{m^2}{n^2} \right) \]

\[ \square \]

**Lemma 4.9.** The probability of a 3-way collision in samples $Q^\otimes m$ is $o(1)$.

Proof. Similar to the proof of Lemma 4.8, we can give an upper bound on the expected number of 3-way collisions being $O \left( \frac{n^3 m^3}{n^2} \cdot \frac{1}{n^2} \right) = O \left( \frac{m^3}{n^4} \right)$. Markov’s inequality concludes the proof. \[ \square \]

Now consider a typical set of $m$ words generated by $Q$ (or equivalently drawn from $Q^\otimes m$). As we know from Lemma 4.9 it has no 3-way collisions and by Markov’s inequality and Lemma 4.8 it has at most $O \left( \frac{1}{\epsilon^2} \right)$ collisions with probability greater than $9/10$ (for sufficiently small $c > 0$ and $m = \frac{cn}{\epsilon^2}$). As we show next a typical set of $m$ words drawn from $Q$ has similar probability under the $\bar{P} \sim \bar{P}$ and $Q$ models.

**Lemma 4.10.** At least $1/2$ of the sets $S = \{w_1, \ldots, w_m\}$ of samples from $Q^\otimes m$ satisfy

\[ \frac{1}{2} \cdot \Pr_{Q^\otimes m}[S] < \Pr_{P^\otimes m}[S] < 2 \cdot \Pr_{Q^\otimes m}[S] \]

Proof. We consider the ratio of the respective probabilities $\left(*\right) \overset{\text{def}}{=} \frac{\Pr_{P^\otimes m}[S]}{\Pr_{Q^\otimes m}[S]}$. As in Lemma 3.7, both probabilities in the numerator and denominator can be expressed in terms of simple statistics for the set $S$, specifically the number of single step transitions between pairs of states. Also similar to the Lemma 3.7, the corresponding multiplicative terms for $P^\otimes m$ and $Q^\otimes m$ are identical except for the collisions along multi-edges between two rare states (at least two transitions between a pair of rare states). Moreover, we also differentiate type I and type II collisions between rare states: (type I) transitions between rare states $y \rightarrow y$ at time $t$ were made along different edges $e_1$ and $e_2$; (type II) two transitions were made along the same edge either $e_1$, or $e_2$. Per type I and II collisions the corresponding terms in $\left(*\right)$ are respectively $(1 - 4\epsilon)(1 + 4\epsilon) = 1 - 16\epsilon^2$ and $1 + 16\epsilon^2$.

We further continue following the proof of the Lemma 3.7 and make sure that with high probability there are only $X = O \left( \frac{1}{\epsilon^2} \right)$ collisions and no 3-way collisions in $S$. We can make sure that the difference between numbers of type I and type II collisions is at most $O(\sqrt{X}) = O \left( \frac{1}{\epsilon^2} \right)$ with probability at least $3/4$, as the choice of collision type in $w$ under $Q$ model is uniform between
type I and type II and independent across different collisions. For small enough \( m = \Omega(\frac{n}{\varepsilon^2}) \) we can make sure that at least \( \frac{1}{2} \) fraction of words \( w \) under \( Q \) model have the number of collisions at most \( \frac{c_1}{\varepsilon^4} \) and also have the difference between number of type I and type II collisions at most \( \frac{c_2}{\varepsilon^2} \), for some small constants \( c_1, c_2 > 0 \). In this case we get the following bounds on (\(*\)).

\[
2 > \left(1 + 16\varepsilon^2\right)^{\frac{c_2}{\varepsilon^2}} > \frac{\Pr_{\bar{P}^\otimes m}[S]}{\Pr_{Q^\otimes m}[S]} > \left(1 - 256\varepsilon^4\right)^{\frac{c_1}{\varepsilon^4}} \cdot (1 - 16\varepsilon^2)^{\frac{c_2}{\varepsilon^2}} > 1/2
\]

Lemma 4.10 shows that \( d_{TV}(Q^\otimes m, \bar{P}^\otimes m) \leq \frac{3}{4} \) for \( m \leq \frac{cn}{\varepsilon^2} \) for some constant \( c \), which implies that no algorithm can successfully distinguish \( Q \) from the family \( P \) with probability greater than \( \frac{3}{4} \). □

5 Open Questions

In this paper, we proposed a new framework for studying property testing questions on Markov chains. There seem to be multiple avenues for future research and abundant number of open problems arising from this framework. We first list some questions which may be of interest here.

1. What is the optimal sample complexity for identity testing on symmetric Markov chains? In this paper, we show an upper bound of \( O\left(\HitT_Q \cdot \log(\HitT_Q) + \frac{n}{\varepsilon}\right) \) samples (Theorem 3.1). We conjecture that \( \Theta\left(\frac{n}{\varepsilon}\right) \) (same as our lower bound) is the right sample complexity for this problem and an explicit dependence on the hitting time of chain \( Q \) may not be necessary. It is implicitly captured to an extent by the guarantee we get from the parameter \( \varepsilon \).

2. What is the optimal sample complexity for identity testing on the sparse Markov chains defined in Section 4? In this paper, we show an upper bound of \( \tilde{O}\left(\frac{n^{3/2}}{\varepsilon^2}\right) \) (Theorem 4.2). We conjecture that \( \Theta\left(\frac{n}{\varepsilon^2}\right) \) (same as our lower bound) is the right sample complexity for this problem.

3. As there is a natural operation of taking a convex combination of Markov chains, it is natural to ask how our spectral definition of distance \( 1 - \rho\left([P, Q]_{[i]}\right) \) between two symmetric chains changes if we substitute either \( P \) or \( Q \) with a convex combination of \( P \) and \( Q \). How does the distance now relate to the original value?

4. How is the distance \( \varepsilon = 1 - \rho\left([P, Q]_{[i]}\right) \) between two Markov chains \( P \) and \( Q \) related to the distance between Markov chains \( P^k \) and \( Q^k \), i.e., states in Markov chains \( P \) and \( Q \) being observed only at intervals of size \( k \)?

5. Given \( \varepsilon_2 \geq \varepsilon_1 \), and access to words from each of two chains, can we distinguish whether the two chains are \( \leq \varepsilon_1 \)-close or \( \geq \varepsilon_2 \)-far? This problem, known as closeness testing in literature, is another interesting direction using our framework.
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