

Testing Closeness of Discrete Distributions*

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Abstract

Given samples from two distributions over an n -element set, we wish to test whether these distributions are statistically close. We present an algorithm which uses sublinear in n , specifically, $O(n^{2/3}\epsilon^{-8/3}\log n)$, independent samples from each distribution, runs in time linear in the sample size, makes no assumptions about the structure of the distributions, and distinguishes the cases when the distance between the distributions is small (less than $\max\{\epsilon^{4/3}n^{-1/3}/32, \epsilon n^{-1/2}/4\}$) or large (more than ϵ) in ℓ_1 distance. This result can be compared to the lower bound of $\Omega(n^{2/3}\epsilon^{-2/3})$ for this problem given by Valiant [54].

Our algorithm has applications to the problem of testing whether a given Markov process is rapidly mixing. We present sublinear algorithms for several variants of this problem as well.

*A preliminary version of this paper [9] appeared in the 41st Symposium on Foundations of Computer Science, 2000, Redondo Beach, CA.

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[¶]Center for Range Voting, 21 Shore Oaks Drive, Stony Brook, NY, USA. Email: warren.wds@gmail.com. Research done while at NEC Research Institute. Research done while at NEC Research Institute. In the 2000 version of this paper, Smith objected to several things, including (a) the choice of what theorems to include, and (b) the choice of what proofs to present for those theorems. In particular, re the present 2010 paper's upper and lower bound theorems 9 and 20, Smith believed he'd proven an improved result in which the two bounds met. Smith also believed the lower bound proofs presented in the 2000 paper contained lacunae and had wanted those proofs replaced with alternative proofs of his own devising. Those moves were rejected by 4-1 vote. Although Smith created, in whole or part, some of the theorems or lemmas here, he bears zero responsibility for the 2010 paper since he had zero influence, affecting not even a single word, of it – except for this footnote!

1 Introduction

Suppose we have two distributions over the same n -element set, such that we know nothing about their structure and the only access we have to these distributions is the ability to take independent samples from them. Suppose further that we want to know whether these two distributions are close to each other in ℓ_1 norm.¹ A first approach, which we refer to as the *naive approach*, would be to sample enough elements from each distribution so that we can approximate the distribution and then compare the approximations. It is easy to see (see Theorem 23 in Section 3.2) that this naive approach requires the number of samples to be at least linear in n .

In this paper, we develop a method of testing that the distance between two distributions is at most ϵ using considerably fewer samples. If the distributions have ℓ_1 distance at most $\max\{\epsilon^{4/3}n^{-1/3}/32, \epsilon n^{-1/2}/4\}$, then the algorithm will accept with probability at least $1 - \delta$. If the distributions have ℓ_1 distance more than ϵ then the algorithm will accept with probability at most δ . The number of samples used is $O(n^{2/3}\epsilon^{-8/3}\log(n/\delta))$. In contrast, the methods of Valiant [54], fixing the incomplete arguments in the original conference paper (see Section 3), yield an $\Omega(n^{2/3}\epsilon^{-2/3})$ lower bound for testing ℓ_1 distance in this model.

Our test relies on a test for whether two distributions have small ℓ_2 distance, which is considerably easier to test: we give an algorithm with sample complexity independent of n . However, small ℓ_2 distance does not in general give a good measure of the closeness of two distributions according to ℓ_1 distance. For example, two distributions can have disjoint support and still have ℓ_2 distance of $O(1/\sqrt{n})$. Still, we can get a very good estimate of the ℓ_2 distance, say to within $O(1/\sqrt{n})$ additive error, and then use the fact that the ℓ_1 distance is at most \sqrt{n} times the ℓ_2 distance. Unfortunately, the number of queries required by this approach is too large in general. Because of this, our ℓ_1 test is forced to distinguish between two cases.

For distributions with small ℓ_2 norm, we show how to use the ℓ_2 distance to get an efficient test for ℓ_1 distance. For distributions with larger ℓ_2 norm, we use the fact that such distributions must have elements which occur with relatively high probability. We create a filtering test that partitions the domain into those elements with relatively high probability and all the other elements (those with relatively low probability). The test estimates the ℓ_1 distance due to these high-probability elements directly, using the naive approach mentioned above. The test then approximates the ℓ_1 distance due to the low-probability elements using the test for ℓ_2 distance. Optimizing the notion of “high probability” yields our $O(n^{2/3}\epsilon^{-8/3}\log(n/\delta))$ algorithm. The ℓ_2 distance test uses $O(\epsilon^{-4}\log(1/\delta))$ samples.

Applying our techniques to Markov chains, we use the above algorithm as a basis for constructing tests for determining whether a Markov chain is rapidly mixing. We show how to test whether iterating a Markov chain for t steps causes it to reach a distribution close to the stationary distribution. Our testing algorithm works by following $\tilde{O}(tn^{5/3})$ edges in the chain. When the Markov chain is dense enough and represented in a convenient way (such a representation can be computed in linear time and we give an example representation in Section 4), this test remains sublinear in the size of the Markov chain for small t . We then investigate two notions of being *close* to a rapidly mixing Markov chain that fall within the framework of property testing, and show how to test that a given Markov chain is close to a Markov chain that mixes in t steps by following only $\tilde{O}(tn^{2/3})$ edges. In the case of Markov chains that come from directed graphs and pass our test, our theorems show the existence of a directed graph that is both close to the original one and rapidly mixing.

¹Half of ℓ_1 distance between two distributions is also referred to as total variation distance.

1.1 Related Work

Testing Properties of Distributions The use of collision statistics in a sample has been proposed as a technique to test whether a distribution is uniform (see, for example, Knuth [40]). Goldreich and Ron [32] give the first formal analysis that using $O(\sqrt{n})$ samples to estimate the collision probability yields an algorithm which gives a very good estimate of the ℓ_2 distance between the given distribution and the uniform distribution. Their “collision count” idea underlies the present paper. More recently, Paninski [45] presents a test to determine whether a distribution is far from the uniform distribution with respect to ℓ_1 distance using $\Theta(\sqrt{n}/\epsilon^2)$ samples. Ma [42] also uses collisions to measure the entropy of a distribution defined by particle trajectories. After the publication of the preliminary version of this paper, a long line of publications appeared regarding testing properties of distributions including independence, entropy, and monotonicity (see, for example, [8, 10, 7, 12, 5, 54, 49, 48, 51, 1]).

Expansion, Rapid Mixing, and Conductance Goldreich and Ron [32] present a test that they conjecture can be used to give an algorithm with $O(\sqrt{n})$ query complexity which tests whether a regular graph is close to being an expander, where by close they mean that by changing a small fraction of the edges they can turn it into an expander. Their test is based on picking a random node and testing whether random walks from this node reach a distribution that is close to the uniform distribution on the nodes. Our tests for Markov chains are based on similar principles. Mixing and expansion are known to be related [53], but our techniques only apply to the mixing properties of random walks on directed graphs, since the notion of closeness we use does not preserve the symmetry of the adjacency matrix. More recently, a series of papers [22, 37, 43] answer Goldreich and Ron’s conjecture in the affirmative. In a previous work, Goldreich and Ron [31] show that testing that a graph is close to an expander requires $\Omega(n^{1/2})$ queries.

The conductance [53] of a graph is known to be closely related to expansion and rapid-mixing properties of the graph [38, 53]. Frieze and Kannan [27] show, given a graph G with n vertices and α , one can approximate the conductance of G to within additive error α in time $n \cdot 2^{\tilde{O}(1/\alpha^2)}$. Their techniques also yield an $2^{\text{poly}(1/\epsilon)}$ -time test that determines whether the adjacency matrix of a graph can be changed in at most ϵ fraction of the locations to get a graph with high conductance. However, for the purpose of testing whether an n -vertex, m -edge graph is rapid mixing, we would need to approximate its conductance to within $\alpha = O(m/n^2)$; thus, only when $m = \Theta(n^2)$, would the algorithm in [27] run in $O(n)$ time.

We now discuss some other known results for testing of rapid mixing through eigenvalue computations. It is known that mixing [53, 38] is related to the separation between the two largest eigenvalues [4]. Standard techniques for approximating the eigenvalues of a dense $n \times n$ matrix run in $\Theta(n^3)$ floating-point operations and consume $\Theta(n^2)$ words of memory [33]. However, for a sparse $n \times n$ *symmetric* matrix with m nonzero entries, $n \leq m$, “Lanczos algorithms” [46] accomplish the same task in $\Theta(n(m + \log n))$ floating-point operations, consuming $\Theta(n + m)$ storage. Furthermore, it is found in practice that these algorithms can be run for far fewer, even a constant number, of iterations while still obtaining highly accurate values for the outer and inner few eigenvalues.

Streaming There is much work on the problem estimating the distance between distributions in data streaming models where space rather than time is limited (cf., [28, 3, 24, 26]). Another line of work [15] estimates the distance in frequency count distributions on words between various documents, where again space is limited. Guha et al. [35] have extended our result to estimating

the closeness of distribution with respect to a range of f -divergences, which include ℓ_1 distance. Testing distributions in streaming data models has been an active area of research in the recent years (see, for example, [11, 16, 36, 34, 17, 18, 13, 14]).

Other Related Models In an interactive setting, Sahai and Vadhan [52] show that, given distributions \mathbf{p} and \mathbf{q} generated by polynomial-size circuits, the problem of distinguishing whether \mathbf{p} and \mathbf{q} are close or far in ℓ_1 norm is complete for statistical zero knowledge. Kannan and Yao [39] outlines a program checking framework for certifying the randomness of a program’s output. In their model, one does not assume that samples from the input distribution are independent.

Computational Learning Theory There is a vast literature on testing statistical hypotheses. In these works, one is given examples chosen from the same distribution out of two possible choices, say \mathbf{p} and \mathbf{q} . The goal is to decide which of two distributions the examples are coming from. More generally, the goal can be stated as deciding which of two known classes of distributions contains the distribution generating the examples. This can be seen to be a generalization of our model as follows: Let the first class of distributions be the set of distributions of the form $\mathbf{q} \times \mathbf{q}$. Let the second class of distributions be the set of distributions of the form $\mathbf{q}_1 \times \mathbf{q}_2$ where the ℓ_1 difference of \mathbf{q}_1 and \mathbf{q}_2 is at least ϵ . Then, given examples from two distributions $\mathbf{p}_1, \mathbf{p}_2$, create a set of example pairs (x, y) where x is chosen according to \mathbf{p}_1 and y according to \mathbf{p}_2 independently. Bounds and an optimal algorithm for the general problem for various distance measures are given in [19, 44, 20, 21, 41]. None of these give sublinear bounds in the domain size for our problem. The specific model of singleton hypothesis classes is studied by Yamanishi [56].

1.2 Notation

We use the following notation. We denote the set $\{1, \dots, n\}$ with $[n]$. The notation $x \in_R [n]$ denotes that x is chosen uniformly at random from the set $[n]$. The ℓ_1 norm of a vector \mathbf{v} is denoted by $\|\mathbf{v}\|_1$ and is equal to $\sum_{i=1}^n |v_i|$. Similarly, the ℓ_2 norm is denoted by $\|\mathbf{v}\|_2$ and is equal to $\sqrt{\sum_{i=1}^n v_i^2}$, and $\|\mathbf{v}\|_\infty = \max_i |v_i|$. We assume our distributions are discrete distributions over n elements, with labels in $[n]$, and will represent such a distribution as a vector $\mathbf{p} = (p_1, \dots, p_n)$, where p_i is the probability of outputting element i .

The *collision probability* of two distributions \mathbf{p} and \mathbf{q} is the probability that a sample from each of \mathbf{p} and \mathbf{q} yields the same element. Note that, for two distributions \mathbf{p}, \mathbf{q} , the collision probability is $\mathbf{p} \cdot \mathbf{q} = \sum_i p_i q_i$. To avoid ambiguity, we refer to the collision probability of \mathbf{p} and \mathbf{p} as the *self-collision probability* of \mathbf{p} . Note that the self-collision probability of \mathbf{p} is $\|\mathbf{p}\|_2^2$.

2 Testing Closeness of Distributions

The main goal of this section is to show how to test whether two distributions \mathbf{p} and \mathbf{q} are close in ℓ_1 norm in sublinear time in the size of the domain of the distributions. We are given access to these distributions via black boxes which upon a query respond with an element of $[n]$ generated according to the respective distribution. Our main theorem is:

Theorem 1 *Given parameters δ and ϵ , and distributions \mathbf{p}, \mathbf{q} over a set of n elements, there is a test which runs in time $O(n^{2/3} \epsilon^{-8/3} \log(n/\delta))$ such that, if $\|\mathbf{p} - \mathbf{q}\|_1 \leq \max(\frac{\epsilon^{4/3}}{32 \sqrt[3]{n}}, \frac{\epsilon}{4\sqrt{n}})$, then the*

test accepts with probability at least $1 - \delta$ and, if $\|\mathbf{p} - \mathbf{q}\|_1 > \epsilon$, then the test rejects with probability at least $1 - \delta$.

In order to prove this theorem, we give a test which determines whether \mathbf{p} and \mathbf{q} are close in ℓ_2 norm. The test is based on estimating the self-collision and collision probabilities of \mathbf{p} and \mathbf{q} . In particular, if \mathbf{p} and \mathbf{q} are close, one would expect that the self-collision probabilities of each are close to the collision probability of the pair. Formalizing this intuition, in Section 2.1, we prove:

Theorem 2 *Given parameter δ and ϵ , and distributions \mathbf{p} and \mathbf{q} over a set of n elements, there exists a test such that, if $\|\mathbf{p} - \mathbf{q}\|_2 \leq \epsilon/2$, then the test accepts with probability at least $1 - \delta$ and, if $\|\mathbf{p} - \mathbf{q}\|_2 > \epsilon$, then the test rejects with probability at least $1 - \delta$. The running time of the test is $O(\epsilon^{-4} \log(1/\delta))$.*

The test used to prove Theorem 2 is given below in Figure 1. The number of pairwise self-collisions in multiset $F \subseteq [n]$ is the count of $i < j$ such that the i th sample in F is same as the j th sample in F . Similarly, the number of collisions between $Q_p \subseteq [n]$ and $Q_q \subseteq [n]$ is the count of (i, j) such that the i th sample in Q_p is same as the j th sample in Q_q .

ℓ_2 -Distance-Test($\mathbf{p}, \mathbf{q}, m, \epsilon, \delta$)

Repeat $O(\log(1/\delta))$ times

1. Let F_p and F_q be multisets of m samples from \mathbf{p} and \mathbf{q} , respectively. Let r_p and r_q be the numbers of pairwise self-collisions in F_p and F_q , respectively.
2. Let Q_p and Q_q be multisets of m samples from \mathbf{p} and \mathbf{q} , respectively. Let s_{pq} be the number of collisions between Q_p and Q_q .
3. Let $r = \frac{2m}{m-1}(r_p + r_q)$. Let $s = 2s_{pq}$.
4. If $r - s > 3m^2\epsilon^2/4$, then reject the current iteration.

Reject if the majority of iterations reject, accept otherwise.

Figure 1: Algorithm ℓ_2 -Distance-Test

We use the parameter m to indicate the number of samples needed by the test to get constant confidence. In order to bound the ℓ_2 distance between \mathbf{p} and \mathbf{q} by ϵ , setting $m = O(\frac{1}{\epsilon^4})$ suffices. By maintaining arrays which count the numbers of times, for example, $N_p(i)$ for F_p , that each element i is sampled and summing $\binom{N_p(i)}{2}$ over all sampled i in the domain, one can achieve the claimed running time bounds for computing an estimate of the collision probability. In this way, essentially m^2 estimations of the collision probability can be performed in $O(m)$ time.

Since $\|v\|_1 \leq \sqrt{n} \cdot \|v\|_2$, a simple way to extend the above test to an L_1 distance test is by setting $\epsilon' = \epsilon/\sqrt{n}$. This would give the correct output behavior for the tester. Unfortunately, due to the order of the dependence on ϵ in the ℓ_2 distance test, the resulting running time is quadratic in n . It is possible, though, to achieve sublinear running times if the input distributions are known to be reasonably evenly distributed. We make this precise by a closer analysis of the variance of the estimator in the test in Lemma 5. In particular, we analyze the dependence of the variances of s and r on the parameter $b = \max(\|\mathbf{p}\|_\infty, \|\mathbf{q}\|_\infty)$. There we show that given \mathbf{p} and \mathbf{q} such that $b = O(n^{-\alpha})$, one can call ℓ_2 -Distance-Test with an error parameter of $\frac{\epsilon}{\sqrt{n}}$ and achieve running time of $O(\epsilon^{-4}(n^{1-\alpha/2} + n^{2-2\alpha}))$. Thus, when the maximum probability of any element is bounded, the ℓ_2 distance test can in fact yield a sublinear-time algorithm for testing closeness in L_1 distance.

In the previous paragraph, we have noted that, for distributions with a bound on the maximum probability of any element, it is possible to test closeness with time and queries sublinear in the domain size. On the other hand, when the *minimum* probability element is quite large, the naive approach that we referred to in the introduction can be significantly more efficient. This suggests a *filtering* algorithm, which separates the domain of the distributions being tested into two parts – the *big* elements, or those elements to which the distributions assign relatively high probability weight, and the *small* elements, which are all other elements. Then, the naive tester is applied to the distributions restricted to the big elements, and the tester that is based on estimating the ℓ_2 distance is applied to the distributions restricted to the small elements.

More specifically, we use the following definition to identify the elements with large weights.

Definition 3 (Big element) *An element i is called big with respect to a distribution \mathbf{p} if $p_i > (\epsilon/n)^{2/3}$.*

The complete test is given below in Figure 2. The proof of Theorem 1 is presented in Section 2.2.

ℓ_1 -Distance-Test($\mathbf{p}, \mathbf{q}, \epsilon, \delta$)

1. Let $b = (\epsilon/n)^{2/3}$.
2. Sample \mathbf{p} and \mathbf{q} for $M = O(\epsilon^{-8/3}n^{2/3} \log(n/\delta))$ times.
3. Let $S^{\mathbf{p}}$ and $S^{\mathbf{q}}$ be the sample sets obtained from \mathbf{p} and \mathbf{q} , respectively, by discarding elements that occur less than $(1 - \epsilon/26)Mb$ times.
4. If $S^{\mathbf{p}}$ and $S^{\mathbf{q}}$ are empty,
 - ℓ_2 -Distance-Test($\mathbf{p}, \mathbf{q}, O(n^{2/3}/\epsilon^{8/3}), \frac{\epsilon}{2\sqrt{n}}, \delta/2$)
 - else
 - i. Let $\ell_i^{\mathbf{p}}$ (resp., $\ell_i^{\mathbf{q}}$) be the times element i appears in $S^{\mathbf{p}}$ (resp., $S^{\mathbf{q}}$).
 - ii. Reject if $\sum_{i \in S^{\mathbf{p}} \cup S^{\mathbf{q}}} |\ell_i^{\mathbf{p}} - \ell_i^{\mathbf{q}}| > \epsilon M/8$.
 - iii. Define \mathbf{p}' as follows: Sample an element from \mathbf{p} . If this sample is not in $S^{\mathbf{p}} \cup S^{\mathbf{q}}$, output it; otherwise, output an $x \in_R [n]$. Define \mathbf{q}' similarly.
 - iv. ℓ_2 -Distance-Test($\mathbf{p}', \mathbf{q}', O(n^{2/3}/\epsilon^{8/3}), \frac{\epsilon}{2\sqrt{n}}, \delta/2$)

Figure 2: Algorithm ℓ_1 -Distance-Test

2.1 Closeness in ℓ_2 Norm

In this section, we analyze Algorithm ℓ_2 -Distance-Test and prove Theorem 2. The statistics r_p , r_q and s in Algorithm ℓ_2 -Distance-Test are estimators for the self-collision probability of \mathbf{p} , of \mathbf{q} , and of the collision probability between \mathbf{p} and \mathbf{q} , respectively. If \mathbf{p} and \mathbf{q} are statistically close, we expect that the self-collision probabilities of each are close to the collision probability of the pair. These probabilities are exactly the inner products of these vectors. In particular, if the set F_p of samples from \mathbf{p} is given by $\{F_p^1, \dots, F_p^m\}$, then, for any pair $i, j \in [m], i \neq j$, we have that $\Pr[F_p^i = F_p^j] = \mathbf{p} \cdot \mathbf{p} = \|\mathbf{p}\|_2^2$. By combining these statistics, we show that $r - s$ is an estimator for the desired value $\|\mathbf{p} - \mathbf{q}\|_2^2$.

In order to analyze the number of samples required to estimate $r - s$ to a high enough accuracy, we must also bound the variance of the variables s and r used in the test. One distinction to

make between self-collisions and collisions between \mathbf{p} and \mathbf{q} is that, for the self-collisions, we only consider samples for which $i \neq j$, but this is not necessary for the collisions between \mathbf{p} and \mathbf{q} . We accommodate this in our algorithm by scaling r_p and r_q appropriately. By this scaling and from the above discussion we see that $\mathbb{E}[s] = 2m^2(\mathbf{p} \cdot \mathbf{q})$ and that $\mathbb{E}[r - s] = m^2(\|\mathbf{p}\|_2^2 + \|\mathbf{q}\|_2^2 - 2(\mathbf{p} \cdot \mathbf{q})) = m^2(\|\mathbf{p} - \mathbf{q}\|_2^2)$.

A complication which arises from this scheme is that the pairwise samples are not independent. We use Chebyshev's inequality (see Appendix A) to bound the quality of the approximation, which in turn requires that we give a bound on the variance, as we do in this section.

Our techniques extend the work of Goldreich and Ron [32], where self-collision probabilities are used to estimate ℓ_2 norm of a vector, and in turn the deviation of a distribution from uniform. In particular, their work provides an analysis of the statistics r_p and r_q above through the following lemma.

Lemma 4 ([32]) *Consider the random variable r_p in Algorithm ℓ_2 -Distance-Test. Then, $\mathbb{E}[r_p] = \binom{m}{2} \cdot \|\mathbf{p}\|_2^2$ and $\text{Var}(r_p) \leq 2(\mathbb{E}[A])^{3/2}$.*

We next present a tighter variance bound given in terms of the largest weight in \mathbf{p} and \mathbf{q} .

Lemma 5 *There is a constant c such that*

$$\begin{aligned} \text{Var}(r_p) &\leq m^2\|\mathbf{p}\|_2^2 + m^3\|\mathbf{p}\|_2^3 \leq c(m^3b^2 + m^2b), \\ \text{Var}(r_q) &\leq m^2\|\mathbf{q}\|_2^2 + m^3\|\mathbf{q}\|_2^3 \leq c(m^3b^2 + m^2b), \text{ and} \\ \text{Var}(s) &\leq c(m^3b^2 + m^2b), \end{aligned}$$

where $b = \max(\|\mathbf{p}\|_\infty, \|\mathbf{q}\|_\infty)$.

PROOF: Let F be the set $\{1, \dots, m\}$. For $(i, j) \in F \times F$, define the indicator variable $C_{i,j} = 1$ if the i th element of Q_p and the j th element of Q_q are the same. Then, the variable from the algorithm $s_{pq} = \sum_{i,j} C_{i,j}$. Also define the notation $\bar{C}_{i,j} = C_{i,j} - \mathbb{E}[C_{i,j}]$. Given these definitions, we can write

$$\begin{aligned} \text{Var}\left(\sum_{(i,j) \in F \times F} C_{i,j}\right) &= \mathbb{E}\left[\left(\sum_{(i,j) \in F \times F} \bar{C}_{i,j}\right)^2\right] \\ &= \mathbb{E}\left[\sum_{(i,j) \in F \times F} (\bar{C}_{i,j})^2 + 2 \sum_{(i,j) \neq (k,l) \in F \times F} \bar{C}_{i,j} \bar{C}_{k,l}\right] \\ &\leq \mathbb{E}\left[\sum_{(i,j) \in F \times F} C_{i,j}\right] + 2 \cdot \mathbb{E}\left[\sum_{(i,j) \neq (k,l) \in F \times F} \bar{C}_{i,j} \bar{C}_{k,l}\right] \\ &= m^2(\mathbf{p} \cdot \mathbf{q}) + 2 \cdot \mathbb{E}\left[\sum_{(i,j) \neq (k,l) \in F \times F} \bar{C}_{i,j} \bar{C}_{k,l}\right] \end{aligned}$$

To analyze the last expectation, we use two facts. First, it is easy to see, by the definition of covariance, that $\mathbb{E}[\bar{C}_{i,j} \bar{C}_{k,l}] \leq \mathbb{E}[C_{i,j} C_{k,l}]$. Secondly, we note that $C_{i,j}$ and $C_{k,l}$ are not independent

only when $i = k$ or $j = l$. Expanding the sum, we get

$$\begin{aligned}
\mathbb{E} \left[\sum_{\substack{(i,j),(k,l) \in F \times F \\ (i,j) \neq (k,l)}} \bar{C}_{i,j} \bar{C}_{k,l} \right] &= \mathbb{E} \left[\sum_{\substack{(i,j),(i,l) \in F \times F \\ j \neq l}} \bar{C}_{i,j} \bar{C}_{i,l} + \sum_{\substack{(i,j),(k,j) \in F \times F \\ i \neq k}} \bar{C}_{i,j} \bar{C}_{k,j} \right] \\
&\leq \mathbb{E} \left[\sum_{\substack{(i,j),(i,l) \in F \times F \\ j \neq l}} C_{i,j} C_{i,l} + \sum_{\substack{(i,j),(k,j) \in F \times F \\ i \neq k}} C_{i,j} C_{k,j} \right] \\
&\leq cm^3 \sum_{\ell \in [n]} p_\ell q_\ell^2 + p_\ell^2 q_\ell \leq cm^3 b^2 \sum_{\ell \in [n]} q_\ell \leq cm^3 b^2
\end{aligned}$$

for some constant c . Next, we bound $\text{Var}(r)$ similarly to $\text{Var}(s)$ using the argument in the proof of Lemma 4 from [32]. Consider an analogous calculation to the preceding inequality for $\text{Var}(r_p)$ (similarly, for $\text{Var}(r_q)$) where $X_{ij} = 1$ for $1 \leq i < j \leq m$ if the i th and j th samples in F_p are the same. Similarly to above, define $\bar{X}_{ij} = X_{ij} - \mathbb{E}[X_{ij}]$. Then, we get

$$\begin{aligned}
\text{Var}(r_p) &= \mathbb{E} \left[\left(\sum_{1 \leq i < j \leq m} \bar{X}_{ij} \right)^2 \right] \\
&= \sum_{1 \leq i < j \leq m} \mathbb{E}[\bar{X}_{i,j}^2] + 4 \sum_{1 \leq i < j < k \leq m} \mathbb{E}[\bar{X}_{i,j} \bar{X}_{i,k}] \\
&\leq \binom{m}{2} \cdot \sum_{t \in [n]} p_t^2 + 4 \cdot \binom{m}{3} \sum_{t \in [n]} p_t^3 \\
&\leq O(m^2) \cdot b + O(m^3) \cdot b^2.
\end{aligned}$$

Thus, we get the upper bound for both variances. \square

Corollary 6 *There is a constant c such that $\text{Var}(r - s) \leq c(m^3 b^2 + m^2 b)$, where $b = \max(\|\mathbf{p}\|_\infty, \|\mathbf{q}\|_\infty)$.*

PROOF: Since variance is additive for independent random variables, we get $\text{Var}(r - s) \leq c(m^3 b^2 + m^2 b)$. \square

Now using Chebyshev's inequality, it follows that if we choose $m = O(\epsilon^{-4})$, we can achieve an error probability less than $1/3$. It follows from standard techniques that with $O(\log \frac{1}{\delta})$ iterations we can achieve an error probability at most δ .

Finally, we can analyze the behavior of the algorithm.

Theorem 7 *For two distributions \mathbf{p} and \mathbf{q} such that $b = \max(\|\mathbf{p}\|_\infty, \|\mathbf{q}\|_\infty)$ and $m = \Omega((b^2 + \epsilon^2 \sqrt{b})/\epsilon^4)$, if $\|\mathbf{p} - \mathbf{q}\|_2 \leq \epsilon/2$, then ℓ_2 -**Distance-Test**($\mathbf{p}, \mathbf{q}, m, \epsilon, \delta$) accepts with probability at least $1 - \delta$. If $\|\mathbf{p} - \mathbf{q}\|_2 > \epsilon$ then ℓ_2 -**Distance-Test**($\mathbf{p}, \mathbf{q}, m, \epsilon, \delta$) accepts with probability less than δ . The running time is $O(m \log(1/\delta))$.*

PROOF: For our statistic $A = (r - s)$, we can say, using Chebyshev's inequality and Corollary 6, that for some constant c ,

$$\Pr[|A - \mathbb{E}[A]| > \rho] \leq \frac{c(m^3 b^2 + m^2 b)}{\rho^2}.$$

Recalling that $E[A] = m^2(\|\mathbf{p} - \mathbf{q}\|_2^2)$, we observe that the ℓ_2 -**Distance-Test** can distinguish between the cases $\|\mathbf{p} - \mathbf{q}\|_2 \leq \epsilon/2$ and $\|\mathbf{p} - \mathbf{q}\|_2 > \epsilon$ if A is within $m^2\epsilon^2/4$ of its expectation. We can bound the error probability by

$$\Pr [|A - E[A]| > m^2\epsilon^2/4] \leq \frac{16c(m^3b^2 + m^2b)}{m^4\epsilon^4}.$$

Thus, for $m = \Omega((b^2 + \epsilon^2\sqrt{b})/\epsilon^4)$, the probability above is bounded by a constant. This error probability can be reduced to δ by $O(\log(1/\delta))$ repetitions. \square

2.2 Closeness in L_1 Norm

The ℓ_1 -**Distance-Test** proceeds in two phases. The first phase of the algorithm (lines 1–3 and 4(i)–(ii)) determines which elements of the domain are the big elements (as defined in Definition 3) and estimates their contribution to the distance $\|\mathbf{p} - \mathbf{q}\|_1$. The second phase (lines 4(iii)–(iv)) filters out the big elements and invokes the ℓ_2 -**Distance-Test** on the filtered distribution with closeness parameter $\epsilon/(2\sqrt{n})$. The correctness of this subroutine call is given by Theorem 7 with $b = 2\epsilon^{2/3}n^{-2/3}$. With these substitutions, the number of samples m is $O(\epsilon^{-8/3}n^{2/3})$. The choice of threshold b in ℓ_1 -**Distance-Test** for the weight of the big elements arises from optimizing the running-time trade-off between the two phases of the algorithm.

We need to show that by using a sample of size $O(\epsilon^{-8/3}n^{2/3} \log(n/\delta))$, we can estimate the weights of each of the big elements to within a multiplicative factor of $1 + O(\epsilon)$, with probability at least $1 - \delta/2$.

Lemma 8 *Let $b = \epsilon^{2/3}n^{-2/3}$. In ℓ_1 -**Distance-Test**, after taking $M = O(\frac{n^{2/3} \log(n/\delta)}{\epsilon^{8/3}})$ samples from a distribution \mathbf{p} , we define $\bar{p}_i = \ell_i^{\mathbf{p}}/M$. Then, with probability at least $1 - \delta/2$, the following hold for all i : (1) if $p_i \geq (1 - \epsilon/13)b$, then $|\bar{p}_i - p_i| < \frac{\epsilon}{26} \max(p_i, b)$, (2) if $p_i < (1 - \epsilon/13)b$, then $\bar{p}_i < (1 - \epsilon/26)b$.*

PROOF: We analyze two cases; we use Chernoff bounds to show that, for each i , the following holds: If $p_i > b$, then

$$\Pr [|\bar{p}_i - p_i| > \epsilon p_i/26] < \exp(-O(\epsilon^2 M p_i)) < \exp(-O(\epsilon^2 M b)) \leq \frac{\delta}{2n}.$$

If $p_i \leq b$, then

$$\Pr [|\bar{p}_i - p_i| > \epsilon b/26] \leq \Pr \left[|\bar{p}_i - p_i| > \frac{\epsilon b}{26 p_i} p_i \right] < \exp(-O(\epsilon^2 b^2 M/p_i)) \leq \exp(-O(\epsilon^2 M b)) \leq \frac{\delta}{2n}.$$

The lemma follows by the union bound. \square

Now we are ready to prove our main theorem.

Theorem 9 *For $\epsilon \geq 1/\sqrt{n}$, ℓ_1 -**Distance-Test** accepts distributions \mathbf{p}, \mathbf{q} such that $\|\mathbf{p} - \mathbf{q}\|_1 \leq \max(\frac{\epsilon^{4/3}}{32\sqrt[3]{n}}, \frac{\epsilon}{4\sqrt{n}})$, and rejects when $\|\mathbf{p} - \mathbf{q}\|_1 > \epsilon$, with probability at least $1 - \delta$. The running time of the test is $O(\epsilon^{-8/3}n^{2/3} \log(n/\delta))$.*

PROOF: Suppose items (1) and (2) from Lemma 8 hold for all i , and for both \mathbf{p} and \mathbf{q} . By Lemma 8, this event happens with probability at least $1 - \delta/2$.

Let $S = S^{\mathbf{p}} \cup S^{\mathbf{q}}$. By our assumption, all the big elements of both \mathbf{p} and \mathbf{q} are in S , and no element that has weight less than $(1 - \epsilon/13)b$ in both distributions is in S . Let Δ_1 be the ℓ_1 distance attributed to the elements in S ; that is, $\sum_{i \in S} |p_i - q_i|$. Let $\Delta_2 = \|\mathbf{p}' - \mathbf{q}'\|_1$ (in the case that S is empty, $\Delta_1 = 0$, $\mathbf{p} = \mathbf{p}'$ and $\mathbf{q} = \mathbf{q}'$). Note that $\Delta_1 \leq \|\mathbf{p} - \mathbf{q}\|_1$. We can show that $\Delta_2 \leq \|\mathbf{p} - \mathbf{q}\|_1$, and $\|\mathbf{p} - \mathbf{q}\|_1 \leq 2\Delta_1 + \Delta_2$.

Next, we show that the algorithm estimates Δ_1 in a brute-force manner to within an additive error of $\epsilon/9$. By Lemma 8, the error on the i th term of the sum is bounded by

$$\frac{\epsilon}{26}(\max(p_i, b) + \max(q_i, b)) \leq \frac{\epsilon}{26}(p_i + q_i + 2\epsilon b/13),$$

where the last inequality follows from that p_i and q_i are at least $(1 - \epsilon/13)b$. Consider the sum over i of these error terms. Notice that this sum is over at most $2/((1 - \epsilon/13)b)$ elements in S . Hence, the total additive error is bounded by

$$\sum_{i \in S} \frac{\epsilon}{26}(p_i + q_i + 2\epsilon b/13) \leq \frac{\epsilon}{26}(2 + 4\epsilon/(13 - \epsilon)) \leq \epsilon/9$$

since $\epsilon \leq 2$.

Note that $\max(\|\mathbf{p}'\|_\infty, \|\mathbf{q}'\|_\infty) \leq b + n^{-1} \leq 2b$ for $\epsilon \geq 1/\sqrt{n}$. So, we can use the ℓ_2 -**Distance-Test** on \mathbf{p}' and \mathbf{q}' with $m = O(\epsilon^{-8/3}n^{2/3})$ as shown by Theorem 7.

If $\|\mathbf{p} - \mathbf{q}\|_1 < \frac{\epsilon^{4/3}}{32\sqrt[3]{n}}$, then so are Δ_1 and Δ_2 . The first phase of the algorithm clearly accepts. Using the fact that, for any vector v , $\|v\|_2^2 \leq \|v\|_1 \cdot \|v\|_\infty$, we get $\|\mathbf{p}' - \mathbf{q}'\|_2 \leq \frac{\epsilon}{4\sqrt{n}}$. Therefore, the ℓ_2 -**Distance-Test** accepts with probability at least $1 - \delta/2$. Similarly, if $\|\mathbf{p} - \mathbf{q}\|_1 > \epsilon$, then either $\Delta_1 > \epsilon/4$ or $\Delta_2 > \epsilon/2$. Either the first phase of the algorithm or the ℓ_2 -**Distance-Test** will reject.

To see the running time bound, note that the time for the first phase is $O(n^{2/3}\epsilon^{-8/3} \log(n/\delta))$ and that the time for ℓ_2 -**Distance-Test** is $O(n^{2/3}\epsilon^{-8/3} \log \frac{1}{\delta})$. It is easy to see that our algorithm makes an error either when it makes a bad estimation of Δ_1 or when ℓ_2 -**Distance-Test** makes an error. So, the probability of error is bounded by δ . \square

The next theorem improves this result by looking at the dependence of the variance calculation in Section 2.1 on L_∞ norms of the distributions separately.

Theorem 10 *Given two black-box distributions \mathbf{p}, \mathbf{q} over $[n]$, with $\|\mathbf{p}\|_\infty \leq \|\mathbf{q}\|_\infty$, there is a test requiring $O((n^2\|\mathbf{p}\|_\infty\|\mathbf{q}\|_\infty\epsilon^{-4} + n\sqrt{\|\mathbf{q}\|_\infty\epsilon^{-2}}) \log(1/\delta))$ samples that (1) if $\|\mathbf{p} - \mathbf{q}\|_1 \leq \frac{\epsilon^2}{\sqrt[3]{n}}$, it accepts with probability at least $1 - \delta$ and (2) if $\|\mathbf{p} - \mathbf{q}\|_1 > \epsilon$, it rejects with probability at least $1 - \delta$.*

2.3 Testing ℓ_1 Distance from Uniformity

A special case of Theorem 2 gives a constant-time algorithm which provides an additive approximation of the ℓ_2 distance of a distribution from the uniform distribution. For the problem of testing that \mathbf{p} is close to the uniform distribution in ℓ_1 distance (i.e., testing closeness when \mathbf{q} is the uniform distribution), one can get a better sample complexity dependence on n .

Theorem 11 *Given $\epsilon \leq 1$ and a black-box distribution \mathbf{p} over $[n]$, there is a test that takes $O(\epsilon^{-4} \cdot \sqrt{n} \cdot \log(1/\delta))$ samples, accepts with probability at least $1 - \delta$ if $\|\mathbf{p} - U_{[n]}\|_1 \leq \epsilon/\sqrt{3n}$, and rejects with probability at least $1 - \delta$ if $\|\mathbf{p} - U_{[n]}\|_1 > \epsilon$.*

The proof of Theorem 11 relies on the following lemma, which can be proven using techniques from Goldreich and Ron [32] (see also Lemma 5 in this paper).

Lemma 12 *Given a black-box distribution \mathbf{p} over $[n]$, there is an algorithm that takes $O(\epsilon^{-2} \cdot \sqrt{n} \cdot \log(1/\delta))$ samples and estimates $\|\mathbf{p}\|_2^2$ within an error of $\epsilon\|\mathbf{p}\|_2^2$, with probability at least $1 - \delta$.*

PROOF: [of Lemma 12] Consider the random variable r_p from the ℓ_2 -Distance-Test. Since $\mathbb{E}[r_p] = \binom{m}{2} \cdot \|\mathbf{p}\|_2^2$, we only need to show that it does not deviate from its expectation too much with high probability. Again, using Chebyshev's inequality and Lemma 5,

$$\Pr[|r_p - \mathbb{E}[r_p]| > \epsilon \mathbb{E}[r_p]] \leq \frac{O(m^2 \|\mathbf{p}\|_2^2 + m^3 \|\mathbf{p}\|_2^3)}{\epsilon^2 m^4 \|\mathbf{p}\|_2^4} \leq \frac{1}{4},$$

where the last inequality follows for $m = O(\epsilon^{-2} \sqrt{n})$ from the fact that $\|\mathbf{p}\|_2 \geq n^{-1/2}$. The confidence can be boosted to $1 - \delta$ using $O(\log(1/\delta))$ repetitions. \square

We note that, for an additive approximation of $\|\mathbf{p}\|_2$, an analogous argument to the proof above will yield an algorithm that uses $O(\epsilon^{-4})$ samples.

PROOF: [of Theorem 11] The algorithm, given in Figure 3, estimates $\|\mathbf{p}\|_2^2$ within $\epsilon^2 \|\mathbf{p}\|_2^2/5$ using the algorithm from Lemma 12 and accepts only if the estimate is below $(1 + 3\epsilon^2/5)/n$.

Uniformity-Distance-Test($\mathbf{p}, m, \epsilon, \delta$)

1. Accept if GR-Uniformity- ℓ_2 -Distance-Test($\mathbf{p}, \epsilon^2/5$) returns an estimate at most $(1 + 3\epsilon^2/5)/n$.
2. Otherwise, reject.

Figure 3: Algorithm Uniformity-Distance-Test

First, observe the following relationship between the ℓ_2 distance to the uniform distribution and the collision probability.

$$\|\mathbf{p} - U_{[n]}\|_2^2 = \sum_i (p_i - \frac{1}{n})^2 = \sum p_i^2 - \frac{2}{n} \cdot \sum p_i + \frac{1}{n} = \|\mathbf{p}\|_2^2 - \frac{1}{n} \quad (1)$$

If $\|\mathbf{p} - U_{[n]}\|_1 \leq \epsilon/\sqrt{3n}$, then $\|\mathbf{p} - U_{[n]}\|_2^2 \leq \epsilon^2/3n$. Using (1), we see that $\|\mathbf{p}\|_2^2 \leq (1 + \epsilon^2/3)/n$. Hence, for $\epsilon \leq 1$, the estimate will be below $(1 + \epsilon^2/5)(1 + \epsilon^2/3)/n \leq (1 + 3\epsilon^2/5)/n$ with probability at least $1 - \delta$.

Conversely, suppose the estimate of $\|\mathbf{p}\|_2^2$ is below $(1 + 3\epsilon^2/5)/n$. By Lemma 12, $\|\mathbf{p}\|_2^2 \leq (1 + 3\epsilon^2/5)/((1 - \epsilon^2/5)n) \leq (1 + \epsilon^2)/n$ for $\epsilon \leq 1$. Therefore, by (1), we can write

$$\|\mathbf{p} - U_{[n]}\|_2^2 = \|\mathbf{p}\|_2^2 - \frac{1}{n} \leq \epsilon^2/n.$$

So, we have $\|\mathbf{p} - U_{[n]}\|_2 \leq \epsilon/\sqrt{n}$. Finally, by the relation between ℓ_1 and ℓ_2 norms, $\|\mathbf{p} - U_{[n]}\|_1 \leq \epsilon$.

The sample complexity of the procedure will be $O(\epsilon^{-4} \cdot \sqrt{n} \cdot \log(1/\delta))$, arising from the estimation of $\|\mathbf{p}\|_2^2$ within $\epsilon^2 \|\mathbf{p}\|_2^2/5$. \square

3 Lower Bounding the Sample Complexity

In this section we consider lower bounds on the sample complexity of testing closeness of distributions. In a previous version of this paper [9], we claimed an almost matching $\Omega(n^{2/3})$ lower bound on the sample complexity for testing the closeness of two arbitrary distributions. Although it was later determined that there were gaps in the proofs, recent results of [54] have shown that in fact the almost matching lower bounds do hold. Although new proof techniques were needed, certain technical ideas such as “Poissonization” and the characterization of “canonical forms of testing algorithms” that first appeared in the earlier version of this work did in fact turn out to be useful in the correct lower bound proof of [54]. We will outline those ideas in this section.

We begin by discussing a characterization of canonical algorithms for testing properties of distributions. Then we describe a pair of families of distributions that were suggested in the earlier version of this work, and were in fact used by Valiant [54] in showing the correct lower bound. Next, we investigate the required dependence on ϵ . Finally, we briefly consider naive learning algorithms, which can be defined as algorithms that, given samples from a distribution, output a distribution with small distance to the input distribution. We show that naive learning algorithms require $\Omega(n)$ samples. We also note that, more recently, the dependency of testing uniformity on distance parameter ϵ and n has been tightly characterized to be $\Theta(\sqrt{n}/\epsilon^2)$ by Paninski [45].

3.1 Characterization of Canonical Algorithms for Testing Properties of Distributions

In this section, we characterize canonical algorithms for testing properties of distributions defined by permutation-invariant functions. The argument hinges on the irrelevance of the labels of the domain elements for such a function. We obtain this canonical form in two steps, corresponding to the two lemmas below. The first step makes explicit the intuition that such an algorithm should be symmetric, that is, the algorithm would not benefit from discriminating among the labels. In the second step, we remove the use of labels altogether, and show that we can present the sample to the algorithm in an aggregate fashion. Raskhodnikova et al. [48] use this characterization of canonical algorithms for proving lower bounds on the sample complexity of distribution support size and element distinctness problems.

Characterizations of property testing algorithms have been studied in other settings. For example, using similar techniques, Alon et al. [2] show a canonical form for algorithms for testing graph properties. Later, Goldreich and Trevisan [29] formally prove the result by Alon et al. In a different setting, Bar-Yossef et al. [6] show a canonical form for sampling algorithms that approximate symmetric functions of the form $f : A^n \rightarrow B$ where A and B are arbitrary sets. In the latter setting, the algorithm is given oracle access to the input vector and takes samples from the coordinate values of this vector.

Next, we give the definitions of basic concepts on which we build a characterization of canonical algorithms for testing properties of distributions. Then, we describe and prove our characterization.

Definition 13 (Permutation of a distribution) *For a distribution \mathbf{p} over $[n]$ and a permutation π on $[n]$, define $\pi(\mathbf{p})$ to be the distribution such that for all i , $\pi(\mathbf{p})_{\pi(i)} = p_i$.*

Definition 14 (Symmetric Algorithm) *Let \mathcal{A} be an algorithm that takes samples from k discrete black-box distributions over $[n]$ as input. We say that \mathcal{A} is symmetric if, once the distributions are fixed, the output distribution of \mathcal{A} is identical for any permutation of the distributions.*

Definition 15 (Permutation-invariant function) A k -ary function f on distributions over $[n]$ is permutation-invariant if for any permutation π on $[n]$, and all distributions $(\mathbf{p}^{(1)}, \dots, \mathbf{p}^{(k)})$,

$$f(\mathbf{p}^{(1)}, \dots, \mathbf{p}^{(k)}) = f(\pi(\mathbf{p}^{(1)}), \dots, \pi(\mathbf{p}^{(k)})).$$

Lemma 16 Let \mathcal{A} be an arbitrary testing algorithm for a k -ary property \mathcal{P} defined by a permutation-invariant function. Suppose \mathcal{A} has sample complexity $s(n)$, where n is the domain size of the distributions. Then, there exists a symmetric algorithm that tests the same property of distributions with sample complexity $s(n)$.

PROOF: Given the algorithm \mathcal{A} , construct a symmetric algorithm \mathcal{A}' as follows: Choose a random permutation of the domain elements. Upon taking $s(n)$ samples, apply this permutation to each sample. Pass this (renamed) sample set to \mathcal{A} and output according to \mathcal{A} .

It is clear that the sample complexity of the algorithm does not change. We need to show that the new algorithm also maintains the testing features of \mathcal{A} . Suppose that the input distributions $(\mathbf{p}^{(1)}, \dots, \mathbf{p}^{(k)})$ have the property \mathcal{P} . Since the property is defined by a permutation-invariant function, any permutation of the distributions maintains this property. Therefore, the permutation of the distributions should be accepted as well. Let S_n denote the set of all permutations on $[n]$. Then,

$$\Pr \left[\mathcal{A}' \text{ accepts } (\mathbf{p}^{(1)}, \dots, \mathbf{p}^{(k)}) \right] = \sum_{\pi \in S_n} \frac{1}{n!} \Pr \left[\mathcal{A} \text{ accepts } (\pi(\mathbf{p}^{(1)}), \dots, \pi(\mathbf{p}^{(k)})) \right],$$

which is at least $2/3$ by the accepting probability of \mathcal{A} .

An analogous argument on the failure probability for the case of the distributions $(\mathbf{p}^{(1)}, \dots, \mathbf{p}^{(k)})$ that should be rejected completes the proof. \square

In order to avoid introducing additional randomness in \mathcal{A}' , we can try \mathcal{A} on all possible permutations and output the majority vote. This change would not affect the sample complexity, and it can be shown that it maintains correctness.

Definition 17 (Fingerprint of a sample) Let S_1 and S_2 be multisets of at most s samples taken from two black-box distributions over $[n]$, \mathbf{p} and \mathbf{q} , respectively. Let the random variable C_{ij} , for $0 \leq i, j \leq s$, denote the number of elements that appear exactly i times in S_1 and exactly j times in S_2 . The collection of values that the random variables $\{C_{ij}\}_{0 \leq i, j \leq s}$ take is called the fingerprint of the sample.

For example, let sample sets be $S_1 = \{5, 7, 3, 3, 4\}$ and $S_2 = \{2, 4, 3, 2, 6\}$. Then, $C_{10} = 2$ (elements 5 and 7), $C_{01} = 1$ (element 6), $C_{11} = 1$ (element 4), $C_{02} = 1$ (element 2), $C_{21} = 1$ (element 3), and for remaining i, j 's, $C_{ij} = 0$.

Lemma 18 If there exists a symmetric algorithm \mathcal{A} for testing a binary property of distributions defined by a permutation-invariant function, then there exist an algorithm for the same task that gets as input only the fingerprint of the sample that \mathcal{A} takes.

PROOF: Fix a canonical order for C_{ij} 's in the fingerprint of a sample. Let us define the following transformation on the sample: Relabel the elements such that the elements that appear exactly the same number of times from each distribution (i.e., the ones that contribute to a single C_{ij} in

the fingerprint) have consecutive labels and the labels are grouped to conform to the canonical order of C_{ij} 's. Let us call this transformed sample the standard form of the sample. Since the algorithm \mathcal{A} is symmetric and the property is defined by a permutation-invariant function, such a transformation does not affect the output of \mathcal{A} . So, we can further assume that we always present the sample to the algorithm in the standard form.

It is clear that given a sample, we can easily write down the fingerprint of the sample. Moreover, given the fingerprint of a sample, we can always construct a sample (S_1, S_2) in the standard form using the following algorithm: (1) Initialize S_1 and S_2 to be empty, and $e = 1$, (2) for every C_{ij} in the canonical order, and for $C_{ij} = k_{ij}$ times, include i and j copies of the element e in S_1 and S_2 , respectively, then increment e . This algorithm shows a one-to-one and onto correspondence between all possible sample sets in the standard form and all possible $\{C_{ij}\}_{0 \leq i, j \leq s}$ values.

Consider the algorithm \mathcal{A}' that takes the fingerprint of a sample as input. Next, by using algorithm from above, algorithm \mathcal{A}' constructs the sample in the standard form. Finally, \mathcal{A}' outputs what \mathcal{A} outputs on this sample. \square

Remark 19 *Note that the definition of the fingerprint from Definition 17 can be generalized for a collection of k sample sets from k distributions for any k . An analogous lemma to Lemma 18 can be proven for testing algorithms for k -ary properties of distributions defined by a permutation-invariant function. We fixed $k = 2$ for ease of notation.*

3.2 Towards a Lower Bound on the Sample Complexity of Testing Closeness

In this section, we present techniques that were later used by Valiant [54] to prove a lower bound on the sample complexity of testing closeness in ℓ_1 distance as a function of the size n of the domain of the distributions. We give a high-level description of the proof, indicate where our reasoning breaks down and where Valiant [54] comes in.

Theorem 20 ([54]) *Given any algorithm using only $o(n^{2/3})$ samples from two discrete black-box distributions over $[n]$, for all sufficiently large n , there exist distributions \mathbf{p} and \mathbf{q} with ℓ_1 distance 1 such that the algorithm will be unable to distinguish the case where one distribution is \mathbf{p} and the other is \mathbf{q} from the case where both distributions are \mathbf{p} .*

By Lemma 16, we may restrict our attention to symmetric algorithms. Fix a testing algorithm \mathcal{A} that uses $o(n^{2/3})$ samples from each of the input distributions.

Let us assume, without loss of generality, that n is a multiple of four and $n^{2/3}$ is an integer. We define the distributions \mathbf{p} and \mathbf{q} as follows: (1) For $1 \leq i \leq n^{2/3}$, $p_i = q_i = \frac{1}{2n^{2/3}}$. We call these elements the *heavy* elements. (2) For $n/2 < i \leq 3n/4$, $p_i = \frac{2}{n}$ and $q_i = 0$. We call these element the *light* elements of \mathbf{p} . (3) For $3n/4 < i \leq n$, $q_i = \frac{2}{n}$ and $p_i = 0$. We call these elements the *light* elements of \mathbf{q} . (4) For the remaining i 's, $p_i = q_i = 0$. Note that these distributions do not depend on \mathcal{A} .

The ℓ_1 distance of \mathbf{p} and \mathbf{q} is 1. Now, consider the following two cases:

- Case 1: The algorithm is given access to two black-box distributions: both of which output samples according to the distribution \mathbf{p} .
- Case 2: The algorithm is given access to two black-box distributions: the first one outputs samples according to the distribution \mathbf{p} and the second one outputs samples according to the distribution \mathbf{q} .

To get a sense of why these distributions should be hard for any distance testing algorithm, note that when restricted to the heavy elements, both distributions are identical. The only difference between \mathbf{p} and \mathbf{q} comes from the light elements, and the crux of the proof is to show that this difference will not change the relevant statistics in a statistically significant way. For example, consider the statistic which counts the number of elements that occur exactly once from each distribution. One would like to show that this statistic has a very similar distribution when generated by Case 1 and Case 2, because the expected number of such elements that are light is much less than the standard deviation of the number of such elements that are heavy.

Our initial attempts at formalizing the intuition above were incomplete. However, completely formalizing this intuition, Valiant [54] subsequently showed that a symmetric algorithm with sample complexity $o(n^{2/3})$ can not distinguish between these two cases. By Lemma 16, the theorem follows.

Poissonization For simplifying the proof, it would be useful to have the frequency of each element be independent of the frequencies of the other elements. To achieve this, we assume that algorithm \mathcal{A} first chooses two integers s_1 and s_2 independently from a Poisson distribution with the parameter $\lambda = s = o(n^{2/3})$. The Poisson distribution with the positive parameter λ has the probability mass function $p(k) = \exp(-\lambda)\lambda^k/k!$. Then, after taking s_1 samples from the first distribution and s_2 samples from the second distribution, \mathcal{A} decides whether to accept or reject the distributions. In the following, we give an overview of the proof that \mathcal{A} cannot distinguish between Case 1 and Case 2 with success probability at least $2/3$. Since both s_1 and s_2 will have values larger than $s/2$ with probability at least $1 - o(1)$ and the statistical distance of the distributions of two random variables (i.e., the distributions on the samples) is bounded, it will follow that no symmetric algorithm with sample complexity $s/2$ can.

Let F_i be the random variable corresponding to the number of times the element i appears in the sample from the first distribution. Define G_i analogously for the second distribution. It is well known that F_i is distributed identically to the Poisson distribution with parameter $\lambda = sr$, where r is the probability of element i (cf., Feller ([25], p. 216)). Furthermore, it can also be shown that all F_i 's are mutually independent. Thus, the total number of samples from the heavy elements and the total number of samples from the light elements are independent.

Canonical Testing Algorithms Recall the definition of the fingerprint of a sample from Section 3.1. The random variable C_{ij} , denotes the number of elements that appear exactly i times in the sample from the first distribution and exactly j times in the sample from the second distribution. We can then assume that the algorithm is only given the fingerprint of the sample, and apply Lemma 18.

Arguing in this way can lead to several subtle pitfalls, which Valiant's proof [54] circumvents by developing a body of additional, very nontrivial, technical machinery to show that the distributions on the fingerprint when the samples come from Case 1 or Case 2 are indistinguishable.

3.3 Other Lower Bounds

In this section, we first give two lower bounds for the sample complexity of testing closeness in terms of the distance parameter ϵ . Then, we show that a naive learning algorithm for distributions require $\Omega(n)$ samples.

By appropriately modifying the distributions \mathbf{p} and \mathbf{q} from the proof, we can give a stronger version of Theorem 20 with a dependence on ϵ .

Corollary 21 *Given any test using only $o(n^{2/3}/\epsilon^{2/3})$ samples, there exist distributions \mathbf{a} and \mathbf{b} of ℓ_1 distance ϵ such that the test will be unable to distinguish the case where one distribution is \mathbf{a} and the other is \mathbf{b} from the case where both distributions are \mathbf{a} .*

We can get a lower bound of $\Omega(\epsilon^{-2})$ for testing the ℓ_2 distance with a rather simple proof.

Theorem 22 *Given any test using only $o(\epsilon^{-2})$ samples, there exist distributions \mathbf{a} and \mathbf{b} of ℓ_2 distance ϵ such that the test will be unable to distinguish the case where one distribution is \mathbf{a} and the other is \mathbf{b} from the case where both distributions are \mathbf{a} .*

PROOF: Let $n = 2$, $a_1 = a_2 = 1/2$ and $b_1 = 1/2 - \epsilon/\sqrt{2}$ and $b_2 = 1/2 + \epsilon/\sqrt{2}$. Distinguishing these distributions is exactly the question of distinguishing a fair coin from a coin of bias $\Theta(\epsilon)$ which is well known to require $\Theta(\epsilon^{-2})$ coin flips. \square

The next theorem shows that learning a distribution using sublinear number of samples is not possible.

Theorem 23 *Suppose we have an algorithm that draws $o(n)$ samples from some unknown distribution \mathbf{b} and outputs a distribution \mathbf{c} . There is some distribution \mathbf{b} for which the output \mathbf{c} is such that \mathbf{b} and \mathbf{c} have ℓ_1 distance close to one.*

PROOF: (Sketch) Let A_S be the distribution that is uniform over $S \subseteq \{1, \dots, n\}$. Pick S at random among sets of size $n/2$ and run the algorithm on A_S . The algorithm only learns $o(n)$ elements from S . So with high probability the ℓ_1 distance of whatever distribution the algorithm output will have ℓ_1 distance from A_S of nearly one. \square

4 Applications to Markov Chains

Random walks on Markov chains generate probability distributions over the states of the chain, induced by the endpoints of the random walks. We employ ℓ_1 -**Distance-Test**, described in Section 2, to test mixing properties of Markov Chains.

This application of ℓ_1 -**Distance-Test** is initially inspired by the work of Goldreich and Ron [32], which conjectured an algorithm for testing expansion of bounded-degree graphs. Their algorithm is based on comparing the distribution of the endpoints of random walks on a graph to the uniform distribution via collisions. Subsequently to this work, Czumaj and Sohler [22], Kale and Seshadri [37], and Nachmias and Shapira [43] have independently concluded that the algorithm of Goldreich and Ron is provably a test for expansion property of graphs.

4.1 Preliminaries and Notation

Let \mathbf{M} be a Markov chain represented by the transition probability matrix \mathbf{M} . The point distribution u th state of \mathbf{M} corresponds to an n -vector $\mathbf{e}_u = (0, \dots, 1, \dots, 0)$, with a one in only the u th location and zeroes elsewhere. The distribution generated by t -step random walks starting at state u is denoted as a vector-matrix product $\mathbf{e}_u \mathbf{M}^t$.

Instead of computing such products in our algorithms, we assume that our ℓ_1 -**Distance-Test** has access to an oracle, `next_node` which on input of the state u responds with the state v with probability $\mathbf{M}(u, v)$. Given such an oracle, the distribution $\mathbf{e}_u^T \mathbf{M}^t$ can be generated in $O(t)$ steps.

Furthermore, the oracle itself can be realized in $O(\log n)$ time per query, given linear preprocessing time to compute the cumulative sums $\mathbf{M}_c(j, k) = \sum_{i=1}^k \mathbf{M}(j, i)$. The oracle can be simulated on input u by producing a random number α in $[0, 1]$ and performing binary search over the u th row of \mathbf{M}_c to find v such that $\mathbf{M}_c(u, v) \leq \alpha \leq \mathbf{M}_c(u, v + 1)$. It then outputs state v . Note that when \mathbf{M} is such that every row has at most d nonzero terms, slight modifications of this yield an $O(\log d)$ implementation consuming $O(n + m)$ words of memory if \mathbf{M} is $n \times n$ and has m nonzero entries. Improvements of the work given in [55] can be used to prove that in fact constant query time is achievable with space consumption $O(n + m)$ for implementing `next_node`, given linear preprocessing time.

We define a notion of closeness between states u and v , based on the distributions of endpoints of t step random walks starting at u and v respectively.

Definition 24 We say that two states u and v are (ϵ, t) -close if the distribution generated by t -step random walks starting at u and v are within ϵ in the L_1 norm, i.e. $\|\mathbf{e}_u \mathbf{M}^t - \mathbf{e}_v \mathbf{M}^t\|_1 < \epsilon$. Similarly we say that a state u and a distribution \mathbf{s} are (ϵ, t) -close if $\|\mathbf{e}_u \mathbf{M}^t - \mathbf{s}\|_1 < \epsilon$.

We say \mathbf{M} is (ϵ, t) -mixing if all states are (ϵ, t) -close to the same distribution:

Definition 25 A Markov chain \mathbf{M} is (ϵ, t) -mixing if a distribution \mathbf{s} exists such that for all states u , $\|\mathbf{e}_u \mathbf{M}^t - \mathbf{s}\|_1 \leq \epsilon$.

For example, if \mathbf{M} is $(\epsilon, O(\log n \log 1/\epsilon))$ -mixing, then \mathbf{M} is *rapidly-mixing* [53]. It can be easily seen that if \mathbf{M} is (ϵ, t_0) -mixing then it is (ϵ, t) mixing for all $t > t_0$.

We now make the following definition:

Definition 26 The average t -step distribution, $\mathbf{s}_{\mathbf{M}, t}$ of a Markov chain \mathbf{M} with n states is the distribution

$$\mathbf{s}_{\mathbf{M}, t} = \frac{1}{n} \sum_u \mathbf{e}_u \mathbf{M}^t.$$

This distribution can be easily generated by picking u uniformly from $[n]$ and walking t steps from state u . In an (ϵ, t) -mixing Markov chain, the average t -step distribution is ϵ -close to the stationary distribution. In a Markov chain that is not (ϵ, t) -mixing, this is not necessarily the case.

Each test given below assumes access to an ℓ_1 distance tester ℓ_1 -**Distance-Test** (u, v, ϵ, δ) which given oracle access to distributions $\mathbf{e}_u, \mathbf{e}_v$ over the same n element set decides whether $\|\mathbf{e}_u - \mathbf{e}_v\|_1 \leq f(\epsilon)$ or if $\|\mathbf{e}_u - \mathbf{e}_v\|_1 > \epsilon$ with confidence $1 - \delta$. The time complexity of L_1 -**test** is $T(n, \epsilon, \delta)$, and f is the *gap* of the tester. The implementation of ℓ_1 -**Distance-Test** given earlier in Section 2 has gap $f(\epsilon) = \epsilon/(4\sqrt{n})$, and time complexity $T = O(\epsilon^{-8/3} n^{2/3} \log \frac{n}{\delta})$.

4.2 A Test for Mixing and a Test for Almost-Mixing

We show how to decide if a Markov chain is (ϵ, t) -mixing; then, we define and solve a natural relaxation of that problem.

In order to test whether \mathbf{M} is (ϵ, t) -mixing, one can use ℓ_1 -**Distance-Test** to compare each distribution $\mathbf{e}_u \mathbf{M}^t$ with $\mathbf{s}_{\mathbf{M}, t}$, with error parameter ϵ and confidence δ/n . The running time is $O(nt \cdot T(n, \epsilon, \delta/n))$. The algorithm is given in Figure 4.

The behavior of the test is as follows: If every state is $(f(\epsilon)/2, t)$ -close to some distribution \mathbf{s} , then $\mathbf{s}_{\mathbf{M}, t}$ is $f(\epsilon)/2$ -close to \mathbf{s} . Therefore every state is (ϵ, t) -close to $\mathbf{s}_{\mathbf{M}, t}$ and the tester passes. On

Mixing($\mathbf{M}, t, \epsilon, \delta$)

1. For each state u in \mathbf{M}
 Reject if ℓ_1 -**Distance-Test**($\mathbf{e}_u \mathbf{M}^t, \mathbf{s}_{\mathbf{M},t}, \epsilon, \delta/n$) rejects.
2. Otherwise, accept.

Figure 4: Algorithm Mixing

the other hand, if there is no distribution that is (ϵ, t) -close to all states, then, in particular, $\mathbf{s}_{\mathbf{M},t}$ is not (ϵ, t) -close to at least one state and so the tester fails. Thus, we have shown the following theorem.

Theorem 27 *Let \mathbf{M} be a Markov chain. Given ℓ_1 -**Distance-Test** with time complexity $T(n, \epsilon, \delta)$ and gap f and an oracle for `next_node`, there exists a test with time complexity $O(nt \cdot T(n, \epsilon, \delta/n))$ with the following behavior: If \mathbf{M} is $(f(\epsilon)/2, t)$ -mixing then $\Pr[\mathbf{M} \text{ is accepted}] > 1 - \delta$; if \mathbf{M} is not (ϵ, t) -mixing then $\Pr[\mathbf{M} \text{ is accepted}] < \delta$.*

For the implementation of ℓ_1 -**Distance-Test** given in Section 2, the running time of **Mixing** algorithm is $O(\epsilon^{-8/3} n^{5/3} t \log \frac{n}{\delta})$. It distinguishes between chains which are $\epsilon/(4\sqrt{n})$ mixing and those which are not ϵ -mixing. The running time is sublinear in the size of \mathbf{M} if $t \in o(n^{1/3}/\log(n))$.

A relaxation of this procedure is testing that *most* starting states reach the same distribution after t steps. If $(1 - \rho)$ fraction of the states u of a given \mathbf{M} satisfy $\|\vec{s} - \mathbf{e}_u \mathbf{M}^t\|_1 \leq \epsilon$, then we say that \mathbf{M} is (ρ, ϵ, t) -almost mixing. The algorithm in Figure 5 tests whether a Markov chain is (ρ, ϵ, t) -almost mixing.

AlmostMixing($\mathbf{M}, t, \epsilon, \delta, \rho$)

Repeat $O(1/\rho \cdot \ln(1/\delta))$ times

1. Pick a state u in \mathbf{M} uniformly at random.
2. Reject if ℓ_1 -**Distance-Test**($\mathbf{e}_u \mathbf{M}^t, \mathbf{s}_{\mathbf{M},t}, \epsilon, \delta\rho$) rejects.

Accept if none of the tests above rejected.

Figure 5: Algorithm AlmostMixing

Thus, we obtain the following theorem.

Theorem 28 *Let \mathbf{M} be a Markov chain. Given ℓ_1 -**Distance-Test** with time complexity $T(n, \epsilon, \delta)$ and gap f and an oracle for `next_node`, there exists a test with time complexity $O(\frac{t}{\rho} T(n, \epsilon, \delta\rho) \log \frac{1}{\delta})$ with the following behavior: If \mathbf{M} is $(\rho, f(\epsilon)/2, t)$ -almost mixing then $\Pr[\mathbf{M} \text{ is accepted}] > 1 - \delta$; If \mathbf{M} is not (ρ, ϵ, t) -almost mixing then $\Pr[\mathbf{M} \text{ is accepted}] < \delta$.*

4.3 A Property Tester for Mixing

The main result of this section is a test that determines if a Markov chain's matrix representation can be changed in an ϵ fraction of the non-zero entries to turn it into a $(4\epsilon, 2t)$ -mixing Markov chain. This notion falls within the scope of property testing [50, 30, 31, 23, 47], which in general takes a set S with distance function Δ and a subset $P \subseteq S$ and decides if an elements $x \in S$ is in

P or if it is far from every element in P , according to Δ . For the Markov chain problem, we take as our set S all matrices \mathbf{M} of size $n \times n$ with at most d non-zero entries in each row. The distance function is given by the fraction of non-zero entries in which two matrices differ, and the difference in their average t -step distributions.

4.3.1 Preliminaries

We start with defining a distance function on a pair of Markov chains on the same state space.

Definition 29 Let \mathbf{M}_1 and \mathbf{M}_2 be n -state Markov chains with at most d non-zero entries in each row. Define distance function $\Delta(\mathbf{M}_1, \mathbf{M}_2) = (\epsilon_1, \epsilon_2)$ if and only if \mathbf{M}_1 and \mathbf{M}_2 differ on $\epsilon_1 dn$ entries and $\|\mathbf{s}_{\mathbf{M}_1, t} - \mathbf{s}_{\mathbf{M}_2, t}\|_1 = \epsilon_2$. We say that \mathbf{M}_1 and \mathbf{M}_2 are (ϵ_1, ϵ_2) -close if $\Delta(\mathbf{M}_1, \mathbf{M}_2) \leq (\epsilon_1, \epsilon_2)$.²

A natural question is whether all Markov chains are ϵ -close to an (ϵ, t) -mixing Markov chain, for certain parameters of ϵ . For example, given a strongly connected and dense enough Markov chain, adding the edges of a constant-degree expander graph and choosing $t = \Theta(\log n)$ yields a Markov chain which (ϵ, t) -mixes. However, for sparse Markov chains or small ϵ , such a transformation does not work. Furthermore, the situation changes when asking whether there is an (ϵ, t) -mixing Markov chain that is close both in the matrix representation and in the average t -step distribution: specifically, it can be shown that there exist constants $\epsilon, \epsilon_1, \epsilon_2 < 1$ and Markov chain \mathbf{M} for which no Markov chain is both (ϵ_1, ϵ_2) -close to \mathbf{M} and $(\epsilon, \log n)$ -mixing. In fact, when ϵ_1 is small enough, the problem becomes nontrivial even for $\epsilon_2 = 1$. The Markov chain corresponding to random walks on the n -cycle provides an example which is not $(t^{-1/2}, 1)$ -close to any (ϵ, t) -mixing Markov chain.

Overview As before, our algorithm proceeds by taking random walks on the Markov chain and comparing final distributions by using the ℓ_1 -Distance-Test. We define three types of states. First, a *normal* state is one from which a random walk arrives at nearly the average t -step distribution. In the discussion which follows, t and ϵ denote constant parameters fixed as input to the algorithm.

Definition 30 Given a Markov Chain \mathbf{M} , a state u of the chain is *normal* if it is (ϵ, t) -close to $\mathbf{s}_{\mathbf{M}, t}$. That is if $\|\mathbf{e}_u \mathbf{M}^t - \mathbf{s}_{\mathbf{M}, t}\|_1 \leq \epsilon$. A state is *bad* if it is not normal.

Testing normality requires time $O(t \cdot T(n, \epsilon, \delta))$. Using this definition, the first two algorithms given in this section can be described as testing whether all (*resp.* most) states in \mathbf{M} are *normal*. Additionally, we need to distinguish states which not only produce random walks which arrive near $\mathbf{s}_{\mathbf{M}, t}$ but which have low probability of visiting a bad state. We call such states *smooth* states.

Definition 31 A state \mathbf{e}_u in a Markov chain \mathbf{M} is *smooth* if (a) u is (ϵ, τ) -close to $\mathbf{s}_{\mathbf{M}, t}$ for $\tau = t, \dots, 2t$ and (b) the probability that a $2t$ -step random walk starting at \mathbf{e}_u visits a bad state is at most ϵ .

Testing smoothness of a state requires $O(t^2 \cdot T(n, \epsilon, \delta))$ time. Our property test merely verifies by random sampling that most states are smooth.

²We say $(x, y) \leq (a, b)$ if $x \leq a$ and $y \leq b$.

4.3.2 The Test

We present below algorithm **TestMixing** in Figure 6, which on input Markov chain \mathbf{M} and parameter ϵ determines whether at least $(1 - \epsilon)$ fraction of the states of \mathbf{M} are smooth according to two distributions: uniform and the average t -step distribution. Assuming access to ℓ_1 -**Distance-Test** with complexity $T(n, \epsilon, \delta)$, this test runs in time $O(\epsilon^{-2}t^2T(n, \epsilon, \frac{1}{6t}))$.

TestMixing(\mathbf{M}, t, ϵ)

1. Let $k = \Theta(1/\epsilon)$.
2. Choose k states u_1, \dots, u_k uniformly at random.
3. Choose k states u_{k+1}, \dots, u_{2k} independently according to $\mathbf{s}_{\mathbf{M},t}$.
4. For $i = 1$ to $2k$
 - (a) $u = \vec{e}_{u_i}$.
 - (b) For $w = 1$ to $O(1/\epsilon)$ and $j = 1$ to $2t$
 - i. $u = \text{next_node}(\mathbf{M}, u)$
 - ii. ℓ_1 -**Distance-Test**($\mathbf{e}_u \mathbf{M}^t, \mathbf{s}_{\mathbf{M},t}, \epsilon, \frac{1}{6t}$)
 - (c) For $\tau = t$ to $2t$, ℓ_1 -**Distance-Test**($\vec{e}_{u_i} \mathbf{M}^\tau, \mathbf{s}_{\mathbf{M},t}, \epsilon, \frac{1}{3t}$)
5. Pass if all tests pass.

Figure 6: Algorithm TestMixing

The main lemma of this section says that any Markov chain that is accepted by our test is $(2\epsilon, 1.01\epsilon)$ -close to a $(4\epsilon, 2t)$ -mixing Markov chain. First, we describe the modification of M that we later show is $(4\epsilon, 2t)$ -mixing.

Definition 32 F is a function from $n \times n$ matrices to $n \times n$ matrices such that $F(\mathbf{M})$ returns $\widetilde{\mathbf{M}}$ by modifying the rows corresponding to bad states of \mathbf{M} to \mathbf{e}_u , where u is any smooth state.

An important feature of the transformation F is that it does not affect the distribution of random walks originating from smooth states very much.

Lemma 33 Given a Markov chain \mathbf{M} and any state $u \in M$ which is smooth. If $\widetilde{\mathbf{M}} = F(\mathbf{M})$, then, for any time $t \leq \tau \leq 2t$, $\|\mathbf{e}_u \mathbf{M}^\tau - \mathbf{e}_u \widetilde{\mathbf{M}}^\tau\|_1 \leq \epsilon$ and $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \widetilde{\mathbf{M}}^\tau\|_1 \leq 2\epsilon$.

PROOF: Define Γ as the set of all walks of length τ from u in \mathbf{M} . Partition Γ into Γ_B and $\bar{\Gamma}_B$ where Γ_B is the subset of walks which visit a bad state. Let $\chi_{w,i}$ be an indicator function which equals 1 if walk w ends at state i , and 0 otherwise. Let weight function $W(w)$ be defined as the probability that walk w occurs. Finally, define the primed counterparts Γ' , etc. for the Markov chain $\widetilde{\mathbf{M}}$. Now the i th element of $\mathbf{e}_u \mathbf{M}^\tau$ is $\sum_{w \in \Gamma_B} \chi_{w,i} \cdot W(w) + \sum_{w \in \bar{\Gamma}_B} \chi_{w,i} \cdot W(w)$. A similar expression can be written for each element of $\mathbf{e}_u \widetilde{\mathbf{M}}^\tau$. Since $W(w) = W'(w)$ whenever $w \in \bar{\Gamma}_B$ it follows that $\|\mathbf{e}_u \mathbf{M}^\tau - \mathbf{e}_u \widetilde{\mathbf{M}}^\tau\|_1 \leq \sum_i \sum_{w \in \Gamma_B} \chi_{w,i} |W(w) - W'(w)| \leq \sum_i \sum_{w \in \Gamma_B} \chi_{w,i} W(w) \leq \epsilon$.

Additionally, since $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \mathbf{M}^\tau\|_1 \leq \epsilon$ by the definition of smooth, it follows that $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \widetilde{\mathbf{M}}^\tau\|_1 \leq \|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \mathbf{M}^\tau\|_1 + \|\mathbf{e}_u \mathbf{M}^\tau - \mathbf{e}_u \widetilde{\mathbf{M}}^\tau\|_1 \leq 2\epsilon$. \square

We can now prove the main lemma.

Lemma 34 *If according to both the uniform distribution and the distribution $\mathbf{s}_{\mathbf{M},t}$, $(1 - \epsilon)$ fraction of the states of a Markov chain \mathbf{M} are smooth, then the matrix \mathbf{M} is $(2\epsilon, 1.01\epsilon)$ -close to a matrix $\widetilde{\mathbf{M}}$ which is $(4\epsilon, 2t)$ -mixing.*

PROOF: Let $\widetilde{\mathbf{M}} = F(\mathbf{M})$. $\widetilde{\mathbf{M}}$ and \mathbf{M} differ on at most $\epsilon n(d + 1)$ entries. This gives the first part of our distance bound. For the second we analyze $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{s}_{\widetilde{\mathbf{M}},t}\|_1 = \frac{1}{n} \sum_u \|\mathbf{e}_u \mathbf{M}^t - \mathbf{e}_u \widetilde{\mathbf{M}}^t\|_1$ as follows. The sum is split into two parts, over the nodes which are smooth and those nodes which are not. For each of the smooth nodes u , Lemma 33 says that $\|\mathbf{e}_u \mathbf{M}^t - \mathbf{e}_u \widetilde{\mathbf{M}}^t\|_1 \leq \epsilon$. Nodes which are not smooth account for at most ϵ fraction of the nodes in the sum, and thus can contribute no more than ϵ absolute weight to the distribution $\mathbf{s}_{\widetilde{\mathbf{M}},t}$. The sum can be bounded now by $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{s}_{\widetilde{\mathbf{M}},t}\|_1 \leq \frac{1}{n}((1 - \epsilon)n\epsilon + \epsilon n) \leq 2\epsilon$.

In order to show that $\widetilde{\mathbf{M}}$ is $(4\epsilon, 2t)$ -mixing, we prove that for every state u , $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \mathbf{M}^{2t}\|_1 \leq 4\epsilon$. The proof considers three cases: u smooth, u bad, and u normal. The last case is the most involved.

If u is smooth in the Markov chain \mathbf{M} , then Lemma 33 immediately tells us that $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_u \widetilde{\mathbf{M}}^{2t}\|_1 \leq 2\epsilon$. Similarly if u is bad in the Markov chain \mathbf{M} , then in the chain $\widetilde{\mathbf{M}}$ any path starting at u transitions to a smooth state v in one step. Since $\|\mathbf{s}_{\mathbf{M},t} - \mathbf{e}_v \widetilde{\mathbf{M}}^{2t-1}\|_1 \leq 2\epsilon$ by Lemma 33, the desired bound follows.

If \mathbf{e}_u is a normal state which is not smooth, then we need a more involved analysis of the distribution $\mathbf{e}_u \widetilde{\mathbf{M}}^{2t}$. We divide Γ , the set of all $2t$ -step walks in \mathbf{M} starting at u , into three sets, which we consider separately.

For the first set take $\Gamma_B \subseteq \Gamma$ to be the set of walks which visit a bad node before time t . Let \mathbf{d}_b be the distribution over endpoints of these walks, that is, let \mathbf{d}_b assign to state i the probability that any walk $w \in \Gamma_B$ ends at state i . Let $w \in \Gamma_B$ be any such walk. If w visits a bad state at time $\tau < t$, then in the new Markov chain $\widetilde{\mathbf{M}}$, w visits a smooth state v at time $\tau + 1$. Another application of Lemma 33 implies that $\|\mathbf{e}_v \widetilde{\mathbf{M}}^{2t-\tau-1} - \mathbf{s}_{\mathbf{M},t}\|_1 \leq 2\epsilon$. Since this is true for all walks $w \in \Gamma_B$, we find $\|\mathbf{d}_b - \mathbf{s}_{\mathbf{M},t}\|_1 \leq 2\epsilon$.

For the second set, let $\Gamma_S \subseteq \Gamma \setminus \Gamma_B$ be the set of walks not in Γ_B which visit a smooth state at time t . Let \mathbf{d}_s be the distribution over endpoints of these walks. Any walk $w \in \Gamma_S$ is identical in the chains \mathbf{M} and $\widetilde{\mathbf{M}}$ up to time t , and then in the chain $\widetilde{\mathbf{M}}$ visits a smooth state v at time t . Thus since $\|\mathbf{e}_v \widetilde{\mathbf{M}}^t - \mathbf{s}_{\mathbf{M},t}\|_1 \leq 2\epsilon$, we have $\|\mathbf{d}_s - \mathbf{s}_{\mathbf{M},t}\|_1 \leq 2\epsilon$.

Finally, let $\Gamma_N = \Gamma \setminus (\Gamma_B \cup \Gamma_S)$, and let \mathbf{d}_n be the distribution over endpoints of walks in Γ_N . Γ_N consists of a subset of the walks from a normal node u which do not visit a smooth node at time t . By the definition of normal, u is (ϵ, t) -close to $\mathbf{s}_{\mathbf{M},t}$ in the Markov chain \mathbf{M} . By assumption at most ϵ weight of $\mathbf{s}_{\mathbf{M},t}$ is assigned to nodes which are not smooth. Therefore $|\Gamma_N|/|\Gamma|$ is at most $\epsilon + \epsilon = 2\epsilon$.

Now define the weights of these distributions as ω_b, ω_s and ω_n . That is ω_b is the probability that a walk from u in \mathbf{M} visits a bad state before time t . Similarly ω_s is the probability that a walk does not visit a bad state before time t , but visits a smooth state at time t , and ω_n is the probability that a walk does not visit a bad state but visits a normal, non-smooth state at time t . Then, $\omega_b + \omega_s + \omega_n = 1$. Finally, $\|\mathbf{e}_u \widetilde{\mathbf{M}}^{2t} - \mathbf{s}_{\mathbf{M},t}\|_1 = \|\omega_b \mathbf{d}_b + \omega_s \mathbf{d}_s + \omega_n \mathbf{d}_n - \mathbf{s}_{\mathbf{M},t}\|_1 \leq \omega_b \|\mathbf{d}_b - \mathbf{s}_{\mathbf{M},t}\|_1 + \omega_s \|\mathbf{d}_s - \mathbf{s}_{\mathbf{M},t}\|_1 + \omega_n \|\mathbf{d}_n - \mathbf{s}_{\mathbf{M},t}\|_1 \leq (\omega_b + \omega_s) \max\{\|\mathbf{d}_b - \mathbf{s}_{\mathbf{M},t}\|_1, \|\mathbf{d}_s - \mathbf{s}_{\mathbf{M},t}\|_1\} + \omega_n \|\mathbf{d}_n - \mathbf{s}_{\mathbf{M},t}\|_1 \leq 4\epsilon$. \square

Given this, we finally can show our main theorem.

Theorem 35 *Let \mathbf{M} be a Markov chain. Given ℓ_1 -Distance-Test with time complexity $T(n, \epsilon, \delta)$ and gap f and an oracle for `next_node`, there exists a test such that if \mathbf{M} is $(f(\epsilon), t)$ -mixing then the test accepts with probability at least $2/3$. If \mathbf{M} is not $(2\epsilon, 1.01\epsilon)$ -close to any $\widetilde{\mathbf{M}}$ which is $(4\epsilon, 2t)$ -mixing then the test rejects with probability at least $2/3$. The runtime of the test is $O(\frac{1}{\epsilon^2} \cdot t^2 \cdot T(n, \epsilon, \frac{1}{6t}))$.*

PROOF: Since in any Markov chain \mathbf{M} which is (ϵ, t) -mixing all states are smooth, \mathbf{M} accepts this test with probability at least $(1-\delta)$. Furthermore, any Markov chain with at least $(1-\epsilon)$ fraction of smooth states is $(2\epsilon, 1.01\epsilon)$ -close to a Markov chain which is $(4\epsilon, 2t)$ -mixing, by Lemma 34. \square

4.4 Extension to Sparse Graphs and Uniform Distributions

The property test can also be made to work for general sparse Markov chains by a simple modification to the testing algorithms. Consider Markov chains with at most $m \ll n^2$ nonzero entries, but with no nontrivial bound on the number of nonzero entries per row. Then, the definition of the distance should be modified to $\Delta(M_1, M_2) = (\epsilon_1, \epsilon_2)$ if M_1 and M_2 differ on $\epsilon_1 \cdot m$ entries and the $\|\mathbf{s}_{M_1, t} - \mathbf{s}_{M_2, t}\|_1 = \epsilon_2$. The above test does not suffice for testing that \mathbf{M} is (ϵ_1, ϵ_2) -close to an (ϵ, t) -mixing Markov chain $\widetilde{\mathbf{M}}$, since in our proof, the rows corresponding to bad states may have many nonzero entries and thus \mathbf{M} and $\widetilde{\mathbf{M}}$ may differ in a large fraction of the nonzero entries. However, let D be a distribution on states in which the probability of each state is proportional to cardinality of the support set of its row. Natural ways of encoding this Markov chain allow constant time generation of states according to D . By modifying the algorithm to also test whether most states according to D are smooth, one can show that \mathbf{M} is close to an (ϵ, t) -mixing Markov chain $\widetilde{\mathbf{M}}$.

Because of our ability to test ϵ -closeness to the *uniform* distribution in $O(n^{1/2}\epsilon^{-2})$ steps [32], it is possible to speed up our test for mixing for those Markov chains known to have uniform stationary distribution, such as Markov chains corresponding to random walks on regular graphs. An ergodic random walk on the vertices of an undirected graph instead may be regarded (by looking at it “at times $t + 1/2$ ”) as a random walk on the *edge-midpoints* of that graph. The stationary distribution on edge-midpoints always exists and is uniform. So, for undirected graphs we can speed up mixing testing by using a tester for closeness to the uniform distribution.

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A Chebyshev’s Inequality

Chebyshev’s inequality states that for any random variable A , and $\rho > 0$,

$$\Pr [|A - E[A]| \geq \rho] \leq \frac{\text{Var}(A)}{\rho^2}.$$