## Accepted Manuscript

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| PII:          | S0304-3975(16)30612-0                       |
|---------------|---|
| DOI:          | http://dx.doi.org/10.1016/j.tcs.2016.11.017 |
| Reference:    | TCS 10982                                   |
| To appear in: | Theoretical Computer Science                |

Received date:30 April 2016Accepted date:15 November 2016



Please cite this article in press as: T. Shiraga et al., Total Variation Discrepancy of Deterministic Random Walks for Ergodic Markov Chains, *Theoret. Comput. Sci.* (2016), http://dx.doi.org/10.1016/j.tcs.2016.11.017

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### ACCEPTED MANUSCRIPT

# Total Variation Discrepancy of Deterministic Random Walks for Ergodic Markov Chains\*

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November 22, 2016

#### Abstract

Motivated by a derandomization of Markov chain Monte Carlo (MCMC), this paper investigates a *deterministic random walk*, which is a deterministic process analogous to a random walk. There are some recent progress on the analysis of the vertex-wise discrepancy (i.e.,  $L_{\infty}$ -discrepancy), while little is known about the *total variation discrepancy* (i.e.,  $L_1$ -discrepancy), which plays an important role in the analysis of an FPRAS based on MCMC. This paper investigates the  $L_1$ -discrepancy between the expected number of tokens in a Markov chain and the number of tokens in its corresponding deterministic random walk. First, we give a simple but nontrivial upper bound  $O(mt^*)$  of the  $L_1$ -discrepancy for any ergodic Markov chains, where m is the number of edges of the transition diagram and  $t^*$  is the mixing time of the Markov chain. Then, we give a better upper bound  $O(m\sqrt{t^*})$  for *non-oblivious* deterministic random walks, if the corresponding Markov chain is ergodic and lazy. We also present some lower bounds.

Key words: Rotor router model, Propp machine, load balancing, Markov chain Monte Carlo (MCMC), mixing time

#### 1 Introduction

**Background** Markov chain Monte Carlo (MCMC) is a powerful technique of designing randomized approximation algorithms for #P-hard problems. Jerrum et al. [21] showed the equivalence in the sense of the polynomial time computation between *almost* uniform generation and randomized approximate counting for self-reducible problems. A number of fully polynomial-time randomized approximation schemes (FPRAS) based on their technique have been developed for #P-hard problems, such as the volume of a convex body [14, 25, 11], integral of a log-concave function [25], partition function of the Ising model [19], and counting bipartite matchings [20]. When designing an FPRAS based on the technique, it is important that the *total variation distance* of the approximate distribution from the target distribution is sufficiently small, and hence analyses of the mixing times of Markov chains are central issues in a series of works on MCMC for FPRAS to guarantee a small total variation distance. See also Section 2.1 for the terminology of Markov chains.

In contrast, not many results are known about *deterministic* approximation algorithms for #P-hard problems. A remarkable progress is the correlation decay technique, independently devised by Weitz [32] and Bandyopadhyay and Gamarnik [5], and there are several recent developments on the technique. For counting 0-1 knapsack solutions, Gopalan et al. [16], and Stefankovic et al. [30] gave deterministic approximation

<sup>\*</sup>A preliminary version of this paper appeared in the Proceedings of ANALCO '16 [29].

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