Computer Science and Information Systems 16(1):205–225 https://doi.org/10.2298/CSIS180310015L

On the randomness that generates biased samples: The limited randomness approach

George Lagogiannis[1], Stavros Kontopoulos[2], and Christos Makris[3]

[1] Department of Agricultural Economics and Rural Development,
Agricultural University of Athens,
Iera odos 75, 11855, Athens, Greece
lagogian@aua.gr
[2] Department of Computer Engineering and Informatics, University of Patras,
26500 Patras, Greece
kontopou@ceid.upatras.gr
[3] Department of Computer Engineering and Informatics, University of Patras,
26500 Patras, Greece
makri@ceid.upatras.gr

Abstract. We introduce two new algorithms for creating an exponentially biased sample over a possibly infinite data stream. Such an algorithm exists in the literature and uses $O(\log n)$ random bits per stream element, where n is the number of elements in the sample. In this paper we present algorithms that use $O(1)$ random bits per stream element. In essence, what we achieve is to be able to choose an element at random, out of n elements, by sparing $O(1)$ random bits. Although in general this is not possible, the exact problem we are studying makes it possible. The needed randomness for this task is provided through a random walk. To prove the correctness of our algorithms we use a model also introduced in this paper, the *limited randomness* model. It is based on the fact that survival probabilities are assigned to the stream elements before they start to arrive.

Keywords: Biased reservoir sampling, Markov chain, random walk.

1. Introduction

Let us assume that we want to create a fixed size subset of a data stream of unknown, possibly infinite length. We call this subset a *sample* and let n be the given size of the sample, dictated by the available for this purpose memory. Creating such a sample falls into the general category of *synopsis maintenance* ([3], [6], [7], [10], [12], [14], [16], [17]). The problem of synopsis maintenance has been studied extensively for estimating queries ([4], [7], [17]) in data streams. A survey of stream synopsis construction algorithms can be found in [2].

In this paper we are going to focus on *reservoir sampling* [16], which is an important class of stream synopsis construction methods. Assuming that the length of the stream is known (let N be this length), we can easily create an algorithm to ensure that each stream element has n/N probability of being in the sample when the stream ends. However, the sample of a stream may need to be used before the stream ends, and it is even possible that the stream is endless. When the sample is unbiased and the length of the stream is unknown, the probability for each stream element to enter the sample reduces as the stream progresses (see [16]). This means that as the stream progresses, fewer and fewer elements in the sample belong to the recent history of the stream. Such a sample may be proved useless for answering queries concerning the recent past. To address this problem one needs to create a biased sample. Such a sample is created in [1].

In [1], a bias function $f(r,t)$ is associated with the $r-th$ stream element at the time of arrival of the $t-th$ stream element ($r \leq t$). This function is associated with the probability $p(r,t)$ of the $r-th$ element belonging to the sample at the time of the $t-th$ element. In particular, the function $f(r,t)$ is monotonically decreasing with t (for fixed r) and monotonically increasing with r (for fixed t). For the specific function $e^{-\lambda(t-r)}$, an efficient algorithm is introduced in [1] for creating a sample consistent with that function. The parameter λ defines the bias rate and typically lies in the range [0, 1]. In general, λ is chosen in an application–specific way and it is the inverse of the number of stream elements after which the relative probability of inclusion in the sample reduces by a factor of $1/e$. Throughout this paper, we name this algorithm *Algorithm A*. Also, we assume that $f(r,t)$ is identical to $p(r,t)$.

The introduction of bias results in some upper bounds on the maximum necessary sample size, also called *maximum reservoir requirement*. It is proved in [1] that for the exponential bias function, the maximum reservoir requirement is bounded above by $1/\lambda$, assuming that λ is much smaller than 1, which happens to be the most interesting case. According to Algorithm A, each new stream element takes the place of another element of the sample which is chosen uniformly at random. Given that the size of the sample is n, Algorithm A needs $O(\log n)$ random bits per stream element, in order to choose an element of the sample at random.

In this paper we are going to present algorithms for creating a biased reservoir sample (over a very long, possibly infinite stream of data) consistent with the exponential bias function. The algorithms are based on the unit-cost RAM model, and use $O(1)$ random bits per stream element in the worst-case. Thus, our algorithms outperform Algorithm A in terms of *randomness complexity*.

The issue of reducing the randomness complexity of algorithms is not only of theoretical interest, but of practical as well. The analysis of randomized algorithms is always based on some assumptions concerning the theoretical machine-model used. The most frequently used machine-model is the unit-cost RAM. An interesting assumption concerning the unit-cost RAM, is that it needs $O(1)$ time to uniformly choose an element at random over n elements. This is because $O(\log n)$ random bits are needed for this task and the unit-cost RAM accesses these bits in O(1) time (we assume that w, the word size, is bigger than $\log n$). However this is not realistic, because the actual cost of generating these bits is swept under the carpet, through its assignment to some subroutine that has no cost at all. All the unit-cost RAM needs to do, is to spend $O(1)$ time in order to access $O(w)$ random bits, provided (free of charge) by this subroutine. The issue of the real cost of random bits is addressed in [8]. It is stated there that each random bit can be assumed to cost a constant amount of time "at best". This means that the time complexity of a randomized algorithm is at least equal to the number of random bits it uses. Minimizing the number of random bits is thus a straightforward direction for improving the time complexity of randomized algorithms, in cases where the randomness complexity of the algorithm dominates its overall time complexity. Algorithm A falls into this category as its time complexity is $O(1)$ in the worst-case in a unit-cost RAM, whereas its randomness complexity is $O(\log n)$ (all the time complexities are "per stream element"). Assuming that each random bit costs $O(1)$ time (following the logic of [8]), the random bits in Algorithm A introduce a multiplicative factor of $O(\log n)$ per stream element in the time complexity. Our algorithms avoid this multiplicative factor and the intuition behind this result is given in the following paragraphs.

Let us assume that we have a coin, claimed to be fair. Intuitively, this means that if we toss the coin M times, "heads" or "tails" is supposed to occur at a fraction of M that approaches $1/2$, as M approaches infinity. However, to *evaluate* the coin (i.e. to decide whether the coin is fair or not) we do not need to toss the coin M times, for a big enough M. It suffices to inspect its shape (assume that we have special equipment for this). Clearly, the time of such an inspection is irrelevant (assuming that the shape of the coin remains unchanged over time). Let us now follow the same logic, replacing the coin by an algorithm that creates a sample over a data stream. The coin produces "heads" or "tails", whereas the algorithm produces samples. By setting the sample to be consistent with a bias function $p(r,t)$, we mean that if we execute the algorithm M times on a stream S, the $r-th$ stream element (i.e., $S(r)$) will survive in the sample at time t $(t > r)$ at a fraction of the M produced samples that approaches $p(r,t)$ as M approaches infinity. In order to evaluate such an algorithm (i.e. to decide whether or not the algorithm creates a sample consistent with $p(r,t)$), we need to check its instructions and using these instructions to calculate survival probabilities for the sample elements. If these survival probabilities are consistent with the given bias function, we conclude that the algorithm works as claimed. As with the coin, the time of the evaluation is irrelevant (clearly, the algorithm remains unchanged over time). Although the evaluation can be performed any time, the evaluation at time $t = 0$ (i.e. before the stream elements start to arrive) has a clear advantage, to be explained in the following paragraphs. Evaluating the algorithm at time $t = 0$, means that we have no sample to inspect but we do not actually need an existing sample. It is the "shape of the coin" that matters.

In order to successfully evaluate our algorithms, we must conclude that each time a new stream element arrives, each sample element is equally likely to be deleted from the sample (this is the basic property of the sampling algorithm in [1]). This means that each time a new stream element arrives, we need to perform uniform sampling. For this purpose, our algorithms use a Markov chain whose stationary distribution happens to be the uniform distribution. The random walk corresponding to this Markov chain is composed of *steps*. Each time, one of the elements of the sample is the *position* of the walk. Each step results in a new position of the walk and needs $O(1)$ random bits in the worst-case. Each accessed random bit is used for executing a step of the walk and we choose to delete the element of the sample implied by the position of the walk.

Using a Markov chain for performing uniform sampling is not new. Typically, one needs a Markov chain having the uniform distribution as its stationary distribution. In order to extract a random position, the Markov chain must be allowed to "run" for as many steps as necessary in order to reach its stationary distribution. However, when the random position is extracted, the position of the walk is not random any more and in order to retrieve one more random position, one has to let the Markov chain "run" again for as many steps as necessary in order to reach its stationary distribution. In this paper, we simply cancel this fact and instead we extract one random position per step.

The above claim may sound strange. In particular, one may argue that when an element is chosen by our algorithm at any time $t \neq 0$, the position of the walk is deterministically decided. Knowing the position of the walk at time t, how is it possible to choose the next element uniformly at random, by accessing only $O(1)$ random bits? The answer is the following: Accessing the sample at time $t \neq 0$ and calculating survival probabilities for the sample elements, we simply calculate conditional probabilities in regard to time $t = 0$, i.e. probabilities under the condition that the exact accessed sample of time t will occur. In this sense, calculating survival probabilities at any time $t \neq 0$, may be misleading.

To achieve uniform sampling while calculating survival probabilities at time $t = 0$, it suffices to make sure that by the time the stream elements start to arrive, the Markov chain will have reached its stationary distribution (i.e., the uniform distribution). As a result, it will remain in this distribution, which means that in regard to time $t = 0$, all future elements are equally likely to be chosen by our algorithm. More insight on this claim will be given in Section 3, where a more detailed intuitive example is given. We will also use the example of Section 3 for intuitively introducing a new model for evaluating our algorithms, which we call *limited randomness* model.

The structure of the paper is the following: In Section 2, we briefly present Algorithm A. In Section 3 we present the intuition behind the definitions that we present in Section 4. In Section 5, we present the random walk. This way we use this random walk as a black box in Section 6, where we present our new algorithms. We believe that this "black box" usage of the random walk simplifies the description of the algorithms, and helps the reader focus on the rest of the ideas that make our algorithms work.

2. Algorithm A: The exponential bias function

In this section, we will briefly present Algorithm A (i.e., algorithm 2.1 of [1]).

Algorithm A is based on the idea that each new stream element is deterministically inserted into the sample, and replaces one of the old elements of the sample. The old element to be replaced is chosen uniformly at random. Therefore, assuming that the reservoir contains n elements, each element "survives" in the sample with probability $(1 - 1/n)$ every time a new stream element arrives. Then, the element that arrives at time r will exist in the sample at time t with probability $(1 - 1/n)^{t-r} = ((1 - 1/n)^n)^{(t-r)/n}$. For large values of n (and it is reasonable to assume that n is large), the inner $(1 - 1/n)^n$ term is approximately equal to $1/e$, and from substitution, the exponential bias function follows.

It must be noted that Algorithm A is slightly more complicated, because the reservoir is filled gradually, to ensure that the sample is consistent with the exponential bias function from the beginning. We have skipped this part, firstly in order to keep things simple, and secondly because we are going to use the exact methodology, to achieve the same thing.

3. Intuition on the term "limited randomness "

We can use a roulette as an intuitive example. Let us assume that we have a roulette with n numbers (where each number is associated with a different slot), such that in the long run, each number is equally likely to host the ball. However, our roulette has a problem. Assuming that the ball is hosted in a given slot, the nearby slots are more likely than distant ones, to host the ball after the next "throw". This weakness of our roulette comes from the fact that the ball is moved by means of a random walk algorithm (it is an e-roulette). The random walk uses less randomness than what is actually needed in order to guarantee that each time, the ball ends up in a slot that can be assumed to be fully random (it is therefore a *limited randomness roulette*). Although in the long run, one will observe that each number is equally likely to occur, the casino owners have a problem. If the players know the algorithm under which the roulette operates, they will bet their money on slots nearby the most recent winning slot. Even if the players do not know the algorithm under which the roulette operates, they can observe and notice that each time, the ball tends to end-up in a slot that is nearby the previous one. If the casino owners use this roulette in the "traditional" way, their casino is doomed.

To address the issue, the casino owners apply a curtain above the roulette, so that the players cannot see where the ball is before the throw. If the casino owners manage to hide all the information concerning the current position of the ball, so that the players conclude that below the curtain, the ball is equally likely to be in any slot, the problem is solved. This curtain is the basic notion of our mechanism and it will be modeled in the next section. The players now have *limited access* on what is going on.

One might wonder how is it possible to use this roulette instead of the traditional one. In particular, it is clear after a throw, the winning number must be revealed to the players and then the players will bet their money on nearby slots. Even if they cannot see the slots (i.e. they do not know which number corresponds to each slot), they will write down the winning numbers. Each time a winning number x appears, they will check their notes and see what is the most frequent winning number next of x. Then, they will bet their money on this number. It seems that the notion of the curtain did not make this roulette usable after all. Clearly, assuming that the players have no memory of the past, the problem is solved. But is such an assumption reasonable? For casino players, it certainly isn't.

However keep in mind that the central idea behind the algorithms presented in this paper, is that all evaluations (i.e., all probability calculations) are performed at time $t = 0$ (according to the intuition given in Section 1). Assuming that the players have no memory of the past, we simply incorporate into our model the fact that at time $t = 0$, when the evaluation occurs, there is nothing to remember. Thus, our limited randomness roulette can in fact be used, but not with a curtain (the curtain only exists in our evaluation model). The exact use is presented in the next paragraph.

The casino announces that the players are allowed to bet before the game starts, and the game involves N throws. No betting is allowed during the game. Each bet contains an amount of money, a slot where the money is put and the number of throw on which the bet is active. Therefore, each player is allowed to bet on any one of the N throws, before the first throw starts. After all the bets are placed, the roulette is initialized in such a way that the ball is placed in slot chosen uniformly at random among the n slots. Then the throws start. At any time $t \neq 0$, each player may find himself/herself to have an advantage or a disadvantage, based on the position of the ball (i.e. depending on how far from the slot he/she placed a bet, the slot that hosts the ball lies). However, this temporal feeling of stealing the casino, or being stolen by it, is just an illusion (and gambling involves quite a few illusions). The truth is that when the bets are placed, i.e. at time $t = 0$, (it can be derived that) each bet has $1/n$ probability to win and as a result, the game is fair.

4. Definitions

In general, we distinguish in this paper two approaches for a biased reservoir sampling algorithm: According to the *strict* approach, the reservoir is filled gradually and even when it is not full, the sample is consistent with the bias function. According to the *greedy* approach the reservoir is first filled and then the algorithm starts. Therefore it follows that initially, our sample does not comply with the bias function. But as time passes, fewer and fewer of the initial elements continue to exist in the sample, thus the fraction of the sample that was not built according to our function, continuously decreases. By the above definition, Algorithm A is strict.

We distinguish the memory positions used by an algorithm that creates a biased sample, into two parts. The *sample-space*, contains all the memory positions where the elements of the sample are stored. The *surrounding-space* contains all the memory positions used by the algorithm in order to obtain the sample, except the sample-space. The sample-space and the surrounding-space together, correspond to the *entire used-space* of the algorithm. Let us now introduce the concept of the *sample-user*, which informally, is a person able to calculate probabilities and comes in two flavors.

Definition 1. The *sample-user of full access* is an *evaluator* able to access at any time t i) the entire used-space, ii) the algorithm that created the sample and iii) the bias function associated with the algorithm. Based on what he/she can access at time t, the sample-user of full access is able to calculate for each existing or future sample-element x, the probability of x being in the sample for all future (in regard to x) time-points.

Definition 2. The *sample-user of limited access* is an *evaluator* able to access at any time t i) the sample-space, ii) the algorithm that created the sample and iii) the bias function associated with the algorithm. Based on what he/she can access at time t, the sample-user of limited access is able to calculate for each existing or future sample-element x, the probability of x being in the sample for all future (in regard to x) time-points.

It must be noted that in both definitions, we consider the sample-user to be *memoryless*, in the following sense: At any given time t, the sample-user of full (limited) access is able to calculate probabilities based on what he/she is able to access at time t only. In other words, the sample-user can not keep track of the changes that have occurred to the sample, in order to use the information provided by these changes when calculating probabilities.

The notion of the sample-users is introduced in order to capture the intuition described in the previous section. The different flavors of a sample-user are needed to capture the presence or absence of a curtain that covers all memory positions except the sample-space. According to the above two definitions, the only time-point where a sample-user of full access and a sample-user of limited access have the same “power” is the time before the stream elements start to arrive (i.e., when $t = 0$). This is because at time $t = 0$, the entire used space is empty. We have set the sample-users to be memoryless in order to reflect to the sample-users the fact that all calculations are done at time $t = 0$ because there is nothing to remember at time $t = 0$.

Definition 3. A biased sample *of full randomness* consistent with a function f is a sample where at any time t, a sample-user of full access is not able to find an existing or future element x in the sample, for which at least one time-point decreases the probability of x being in the sample in a way different than the one dictated by f.

Definition 4. A biased sample *of limited randomness* consistent with a function f is a sample where at any time t, a sample-user of limited access is not able to find an existing or future element x in the sample, for which at least one time-point decreases the probability of x being in the sample in a way different than the one dictated by f.

Definition 3 applies to the biased sample created in [1]. In particular, at any time t, the sample-user of full access will conclude by accessing Algorithm A, that each of the n elements in the sample has $1/n$ probability of being deleted from the sample at the next time-point, i.e. each element has $(1 - 1/n)$ probability to survive the next insertion, and this is consistent with the exponential bias function (allowing the substitutions explained in Section 2). Said otherwise, Algorithm A *convinces* a sample-user of full access.

In this paper we present algorithms for creating a biased sample of limited randomness, i.e. algorithms that convince a sample-user of limited access. According to the intuition given so far, convincing a sample-user of limited access suffices for proving that our algorithms produce samples consistent with a given bias function. This is because time $t = 0$ is as good as any for evaluating our algorithms and it turns out that at time $t = 0$, a sample user of limited access and a sample user of full access are identical (they both access the same thing, i.e. the instructions of the algorithm). We believe that this limited access model can be used in order to reduce the randomness complexity of algorithms, in cases where the randomness complexity dominates the overall time complexity.

5. The random walk

5.1. Description of the random walk

In this subsection we present an algorithm for performing a random walk on a list. The list is traversed in left-to-right order, with the leftmost node being the head of the list. Thus, the next node of a node u is the node on the right of u, and we set the next node of the rightmost node of the list to be the head of the list (i.e., we actually have a circle). Similarly, the previous node of u is the node on the left side of u, and the previous node of the head of the list is the rightmost node of the list. We also maintain a pointer called *cursor*, that points to a node of the list which we call *position* of the walk. The walk consists of steps, with each step having an initial, and a final node. The initial node is the position of the walk before the step starts, and the final node is the position of the walk after the step ends. The previous of the final node is called *hit-node*, and thus each step "produces" a hit-node. Initially, before the first step, the position of the walk is the head of the list. A step is briefly described by algorithm Step that follows.

Algorithm Step. We toss a fair coin on the position of the walk. If "tails" occur, the next node of the list becomes the position of the walk, and we repeat the same (i.e. we toss a fair coin again). Otherwise, the position of the walk becomes the hit-node of Step(), we set the cursor to point to the next node (which now becomes the position of the walk) and Step() ends. The maximum number of coins we are allowed to toss, is K. If we toss K coins and no "heads" occur, then we declare the node pointed by the cursor as hit-node, we set the cursor to point to the next node of the list and Step() ends.

A reader unfamiliar to Markov chains should hopefully find Appendix A (where the intuition behind Algorithm Step is given) helpful. An issue that must be discussed is the value of K, the maximum number of coin-tosses we are allowed to have in each step. Obviously, the worst-case time complexity of Step is equal to K. However, as long as $K \geq 2$, observe that since the coin is fair, 2 coin tosses are performed on the average in each step, because this is the average number of tosses until "heads" occur. Thus, the expected number of random bits per step is 2 and Step costs $O(1)$ expected time. By allowing c coin tosses at most, where c is a constant greater than one, we achieve constant worst-case time per step. By allowing only one coin toss, no randomness is inserted into the scheme, and the position of the cursor becomes deterministic for all the future time points.

5.2. Analysis of the random walk

Let n be the length of the list. We will analyze the walk for K such that $2 \leq K \leq n$. Let $m_i = 1/2^i$ and

$$p_i = \begin{cases} m_i, & \text{if } i < K \\ m_{i-1}, & \text{if } i = K \\ 0, & \text{if } i > K \end{cases}$$

We can easily see that the walk can be described by a Markov chain with the following $n * n$ transition matrix.

$$P = \begin{bmatrix} p_n & p_1 & p_2 & p_3 & \cdots & p_{n-1} \\ p_{n-1} & p_n & p_1 & p_2 & \cdots & p_{n-2} \\ \vdots & \vdots & & \vdots & \dots & \vdots \\ p_1 & p_2 & p_3 & p_4 & \cdots & p_n \end{bmatrix}$$

For example, by setting $K = n$ the matrix becomes:

$$P = \begin{bmatrix} 1/2^{n-1} & 1/2 & 1/4 & 1/8 & \dots 1/2^{n-1} \\ 1/2^{n-1} & 1/2^{n-1} & 1/2 & 1/4 & \dots 1/2^{n-2} \\ \vdots & \vdots & \dots & \vdots & \\ 1/2 & 1/4 & 1/8 & 1/16 & \dots 1/2^{n-1} \end{bmatrix}$$

For more details and an extended example see Appendix A. The key observations are that the factors are the same for each row and their sum is equal to 1. The position probability vector at time j is:

$$Pos_j = \left[P_{1,j} P_{2,j} \dots P_{n,j} \right]$$

and can be derived by the initial probability vector at time 0, $\theta = \left[P_{1,0} P_{2,0} \dots P_{n,0} \right]$ as follows: $Pos_j = \theta * P^{(j-1)}$.

Theorem 1 *The random walk described in this subsection simulates a uniform sampling process as time approaches infinity.*

Proof. It is easy to conclude that the Markov chain is irreducible and aperiodic. The states are irreducible because there is a path from any state to all the others. The states are aperiodic because they form one connected component in the graph and anytime the probability of returning to a state is greater than 0, since we can reach any state from any other state with probability greater than 0. The above statements hold for any K. Thus the Markov chain has one limiting distribution π such that $\pi * P = \pi$ and $\sum_{i=1}^{n} \pi_i = 1$, where $\pi_i > 0$. It is straightforward to see that $\pi = [1/n, 1/n, \cdots, 1/n]$. $\square$

5.3. Mixing time of the random walk

Theorem 1 establishes the fact that after "a while", the probability distribution of the Markov chain becomes very close to the uniform distribution. An important issue is how long it is going to take, i.e. what is the *mixing time* of the chain, defined as follows: Let V be the state space of our Markov chain. Let us assume that the chain will ultimately converge to the stationary distribution π which means that for every $i, j \in V$, $lim_{t \to \infty}(P^t)_{ij} = \pi_j$. The L^2 mixing time $r(\epsilon) = \max_{x \in V} min\{t : ||k_t^x - 1||_{2,\pi} \leq \epsilon\}$ is the worst-case time for standard deviation of the density $k_t^x(y) = \frac{(P^t)_{xy}}{\pi_y}$ to drop to ϵ [15]. For reasons of completeness we have calculated this mixing time in Appendix B and it is $O(n^2 \cdot \log n)$ where n is the number of list-nodes.

The mixing time is independent of K. Thus, by increasing K, one expects that the chain will reach the stationary distribution faster, but not asymptotically faster. While asymptotically there is no gain in setting K to be high, there is a gain in setting K to be a constant: The number of random bits per stream element becomes constant in the worst case. This is why in the following of the paper, we set $K = 2$.

6. New algorithms

Let $S(r)$ be the r-th stream element. Each arriving stream element defines the current time, i.e. the r-th stream element arrives at time-point r. Recall that in [1], it is proved that the reservoir size is bounded above by $1/\lambda$. As a result, initially, we have a list of $1/\lambda$ nodes, which we call *sample-list*. The sample-list is traversed in left-to-right order. The leftmost node is node 1, and the numbers of the nodes increment as we walk rightwards, however the numbers are only implied by the relative order of the nodes in the list and they are not stored in the nodes. The sample-list is the sample-space defined in Section 4.

We are going to present two new algorithms for creating a sample consistent with the exponential bias function. More specifically, we are going to show that according to both algorithms, the probability of $S(r)$ being in the sample at time t (for any $t \geq r$) is $e^{-\lambda(t-r)}$. In order to better state the problem we need to solve, we are going to first introduce a simple but problematic algorithm which we call *Algorithm 0*. In order to make things even simpler, let us assume that each sample element (stored in a node of the sample-list) is accompanied by its arrival time. That is, by accessing a node of the sample-list, we access an element of the sample, and the arrival time of this element.

Algorithm 0. When a new stream element arrives (after the reservoir is filled), we execute algorithm Step(), and replace the element stored in the hit-node by the new stream element.

The problem with Algorithm 0 is that it introduces a (disturbing) certainty for a sample-user of limited access. Let us assume that the user accesses the sample at time t.

Knowing the instructions of our algorithm and accessing the sample-list, the user is able to deterministically decide on the position of the walk: In particular, the cursor points to the next node of the node that contains the most recent element of the sample. This knowledge allows the user to determine for all the elements in the sample, a survival probability for the next time-point different than the one dictated by the exponential bias function. For example, the user will conclude that the element pointed by the cursor has 1/2 probability of being the next to be deleted. If the user starts calculating future probabilities, he/she will conclude that for any time-point more distant into the future than $r(\epsilon)$ time-points, each element can be assumed to be chosen uniformly at random and this is consistent with the given bias function. But for any future time-point between t and $t+r(\epsilon)$, the user will conclude that the instructions of the algorithm do not comply with the given bias function.

An issue that must be discussed, is whether Algorithm 0 manages to convince a sample-user of limited access, if we do not accompany each sample element by its arrival time. Then, the user cannot find the most recent element, therefore cannot decide on the position on the walk. However, this holds only for the elements that already exist in the sample, because the sample-user can obviously connect the future positions of the walk with the positions of the future elements. In particular, after the insertion of $S(t)$ for a future time-point t, the cursor will point to the node next to the one that contains $S(t)$. Therefore, assuming $K = 2$, the probability that $S(t)$ will be deleted at time $t + 1$ is 0 (we assume that the sample-list contains more than two nodes). This probability is not consistent with the exponential bias function, and thus a sample user of limited access is not convinced.

Since our goal is to convince a sample-user of limited access, Algorithm 0 does not solve the problem. In the following section, we are going to present two algorithms that convince a sample-user of limited access. *Algorithm 1* is a *mixing time dependent algorithm* meaning that its space-complexity is proportional to the mixing time of the Markov chain. *Algorithm 2* is a *mixing time independent algorithm* meaning that the mixing time of the Markov chain does not appear in the space-complexity. In both algorithms we do not accompany each sample element by its arrival time, as this is not mentioned in [1]. By adding the arrival times, Algorithm 2 is not affected whereas Algorithm 1 needs some more technical details which we omit for now.

6.1. Algorithm 1: A mixing time dependent solution

Algorithm 1 is based on the walk of Section 5, defined on the sample-list. It follows the greedy approach, i.e. initially we fill up all the nodes of the sample-list with the first $(1/\lambda)$ elements of the stream. We introduce a new list called *cursor-past* of length $r(\epsilon)$ (i.e. the length is equal to the mixing time of the Markov chain, defined in Subsection 5.3). A simple way to perceive the cursor-past list, is the following: A person watches a live program using streaming. There is a time-gap between what is really happening live, and what this person sees. As a result, he/she can only guess what is happening at present time, based on what he/she sees and knowing that what he/she sees happening now has actually happened in the past. In our algorithm, the cursor-past list will create such a time-delay effect on the position of the cursor, revealing to the sample-user the position of the cursor $r(\epsilon)$ time units ago. Based on this position, the user must decide on the current position of the cursor.

Before the stream elements start to arrive, we have the *preprocessing phase*, which includes two tasks. First, we need to set the cursor of the walk to point to one of the nodes of the sample-list, chosen uniformly at random. For this we use $O(\log(1/\lambda))$ random bits and then we need to access the corresponding (by the random bits) node of the sample-list in order to update the cursor, which means that we need to traverse the sample-list. Second, we have to traverse the cursor-past list from left to right. For each node u of the cursor-past list, we execute one step of the walk on the sample-list and store in u a pointer towards the hit-node of the step (keep in mind that the hit-node belongs to the sample-list).

The entire preprocessing phase needs $O(\log(1/\lambda) + r(\epsilon))$ random bits. Assuming that each random bit costs $O(1)$ time, the preprocessing phase needs $O(1/\lambda + r(\epsilon))$ time in the worst-case. One may assume that before the stream elements start to arrive, we have plenty of time to prepare our structures, i.e. the preprocessing time is not a problem.

After the preprocessing phase we have the *fill-up phase*, during which the sample-list is filled with the first $1/\lambda$ elements of the stream. When the sample-list becomes full, Algorithm 1 starts.

Algorithm 1. Let t be the current time and $S(t)$ the newly arrived stream element. We execute Step() and let y be the hit-node. We insert a new rightmost node into the cursor-past list, and store the address of y into this node. Let z be the sample-list node pointed by the leftmost node of the cursor-past list. We exchange the elements between nodes z and y. Then, we store $S(t)$ into z. We delete the leftmost node of the cursor-past list.

Algorithm 1 is graphically depicted in Figure 1 where the sample-list consists of 6 nodes. At time t, $S(t)$ is 60. According to Algorithm 1 we insert the red (rightmost) node in the cursor-past list. The two highlighted nodes of the sample-list will take place in the swap operation. The lower part of the figure visualizes our structures ready for the next insertion, at time $t+1$. Keep in mind that all the sample-user of limited access is allowed to “see”, is the sample-list. Therefore, no node of the sample-list appears highlighted to the sample-user of limited access.

Theorem 2 *Associating Algorithm 1 with the exponential bias function, Algorithm 1 convinces a sample-user of limited access.*

Proof. Let us assume that the user accesses the sample just after $S(t)$ has arrived and let n be the size of the sample-list. In order to calculate the survival probabilities for the elements of the sample-list, the sample-user must decide on the position of the walk. Since the Markov chain has reached its stationary distribution from the preprocessing phase (remember that we have set the cursor to point to each element with equal probability), it remains in the stationary distribution from that point and on, thus the user concludes that any of the nodes of the sample-list can be the position of the walk with equal probability. This means that each element of the sample has $1/n$ probability to be the next we delete, therefore each sample-element will survive the next insertion with probability $1 - 1/n$ and this is consistent with the exponential bias function (see Section 2). In addition, the user cannot decide on the position of the walk for all the future time-points. For example, let t_1 be a future time-point. Let u_j be the node of the sample-list where $S(t_1)$ is going to be placed. In order to calculate the survival probabilities for all the future (in regard to t_1) time-points, the user must decide on the node pointed by the rightmost node of the

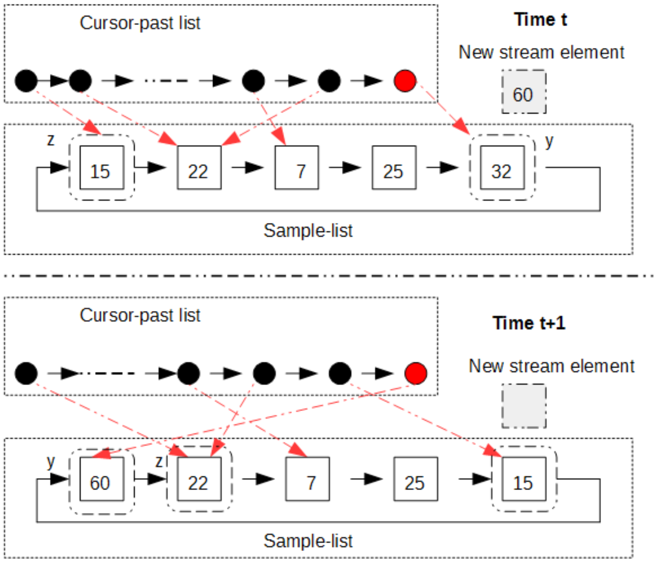


Fig. 1. Graphical representation of Algorithm 1.

cursor-past list. Being certain on the position of the walk implied by the leftmost node of the cursor-past list (it is the node next of u_j) does not help the sample-user. The length of the cursor-past list ensures that given a node pointed by the leftmost node of the cursor-past list, the node pointed by the rightmost node of the cursor-past list is fully random, i.e. the rightmost node may point to each node of the sample-list with probability $1/n$. Therefore each sample-element has $1/n$ probability not to survive at $t_1 + 1$, i.e. each element will survive the next insertion with probability $1 - 1/n$. □

Algorithm 1 uses O(1) random bits per stream element in the worst-case (remember that we have set $K = 2$ in Step). The rest of the actions need $O(1)$ time in the worst-case. The space-complexity is $O(r(\epsilon) + 1/\lambda)$, dominated by the size of the two lists (sample-list and cursor-past list). The space-complexity is critical. As long as it is dominated by the sample-list, Algorithm 1 is space-efficient. Although in our case this is not true, we believe that Algorithm 1 is interesting from a theoretical point of view, and as a “tool” that can be used elsewhere. To get rid of the mixing time in the space-complexity, we need to find another way (i.e. other than the cursor-past list) for disconnecting the position of the cursor from the most recent element of the sample. Such an algorithm is presented in the next subsection.

6.2. Algorithm 2: A mixing time independent solution

Algorithm 2 is presented in both the strict and the greedy approach and let us start from the strict one. We name *left(i)*, the part of the sample-list from node 1 to node i. It follows that left($1/\lambda$) is the entire sample-list. For each i ($1 \leq i \leq 1/\lambda$), we associate a random walk on left(i) (we call it i-*walk*) based on algorithm Step. Thus we have $1/\lambda$ walks. We allocate another list of $1/\lambda$ memory positions called *cursor-list*. As with the sample-list, a number (between 1 and $1/\lambda$) is implied for each node of the cursor-list, according to the order (from left to right) of the nodes in the list. $\forall\ i$ ($1 \leq i \leq 1/\lambda$), the i-th node of the cursor-list is going to host the cursor of the i-walk.

If i elements of the stream have been inserted into the sample-list, they occupy $left(i)$ and the i-walk is the *active-walk*. Initially, since no stream element exists in the sample, all walks are *inactive* and clearly, if the i-walk is active, then all the j-walks $(1 \leq j < i)$ have been active in the past. When the i-walk becomes inactive, the $(i + 1)$-walk will become active. Keep in mind that although we have defined $1/\lambda$ walks, we need to keep track of only two walks: the active-walk and the $(1/\lambda)$-walk.

When a walk becomes inactive, we free the node of the cursor-list corresponding to the cursor of this walk. As a result, the nodes of the cursor-list are set free in left to right order and at all times, the leftmost node of the cursor-list contains the cursor of the active walk (we call this pointer *active-cursor*). This means that we are able to access the active-cursor in constant time. It is also clear that the rightmost node of the cursor-list contains the cursor of the $(1/\lambda)$-walk (we call this cursor *final-cursor*). Thus, by maintaining a pointer towards this node, we are able to access the final-cursor in constant time. Finally, we maintain a pointer called *active-limit*, towards the rightmost node of the active walk (i.e. if the i-walk is the active walk, we maintain a pointer towards the i-th node of the sample-list).

Before the elements of the stream start to arrive we have the *preprocessing phase* where we traverse the cursor-list from left to right and store in the i-th node, a pointer to a position of the sample-list, chosen uniformly at random among all sample-list positions between 1 and i. After this task is completed, $\forall\ i$ ($1 \leq i \leq 1/\lambda$), the i-th node of the cursor-list contains the cursor of the i-walk. For the preprocessing phase we use $O(1/\lambda \cdot \log(1/\lambda))$ random bits. Assuming that each random bit costs $O(1)$ time, the worst-case time complexity for the preprocessing phase is $O((1/\lambda)^2 \cdot \log(1/\lambda))$ because for each i we need to traverse the sample-list from node 1 to node i in order to access the node chosen uniformly at random among all the nodes from node 1 to node i.

The above description is depicted graphically in Figure 2. According to the figure, the active walk is the 5-walk, the filled nodes of the sample-list are represented through rectangles and the empty ones through circles. Above the sample-list, we illustrate the cursor-list. The shaded nodes on the left part of the cursor-list have been deleted in the past, and the leftmost (black) node contains the cursor of the active-walk. The highlighted node of the sample-list is pointed by the active-limit pointer. The sample-user of limited access can only see the sample-list and since the active-limit pointer is “out of sight”, no node of the sample-list appears highlighted to the sample-user of limited access.

Assume that at the time of (just after) the arrival of $S(t)$, the fraction of the reservoir filled is $F(t) = i \cdot \lambda$, which means that i elements have been inserted into the reservoir and they occupy left(i). It follows that the i-walk is the active-walk. Let w be the node pointed by the active-limit pointer, and z be the node next to w. We are now ready to proceed to the description of Algorithm 2.

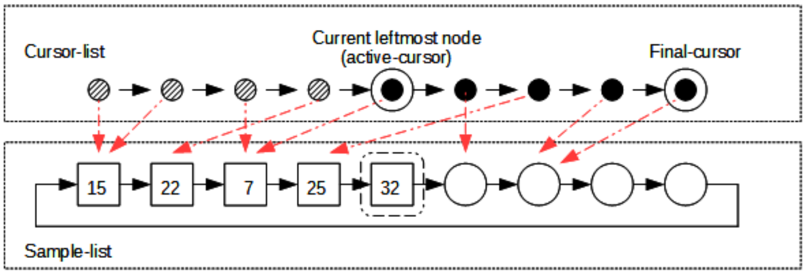


Fig. 2. The background for introducing Algorithm 2.

Algorithm 2. When $S(t+1)$ arrives, we deterministically add it to the sample. **If** the final-cursor points to a non-empty position of the sample-list, the new stream element is going to replace an existing element of the sample i.e. the number of elements in the sample will remain the same. We execute a step for the i-walk and appropriately update the active-cursor. Let g be the node pointed by the active-cursor. The previous node of g is the hit-node of the step, and let x be that node. We delete x from the sample-list by connecting the previous node of x to g. Then, we insert x between w and z. We store $S(t+1)$ in x. We set the *active-limit* pointer to point to x. **Else** the number of elements in the sample will increment and the $(i+1)$-walk will become the active-walk. We insert $S(t+1)$ in z. We delete and free the leftmost node of the cursor-list, making the $(i+1)$-th walk to be the active walk. We update the active-limit pointer to point to z. **End-If**. We execute a step for the $(1/\lambda)$-walk.

A first observation is that the elements are stored in increasing arrival order, from left to right. Clearly, the space-complexity is $O(1/\lambda)$ dominated by the length of the two lists. In practical terms, the entire used-space is initially twice the space of the sample-list. However, each time the number of elements inside the sample increases, we free the leftmost node of the cursor-list and as a result, the entire used-space decreases over time. When the entire sample-list is filled with elements, only one node from the cursor-list remains. It is the node that contains the cursor of the $(1/\lambda)$-walk. This means that in regard to Algorithm A, the only memory overhead that remains is the one due to the pointers that support the sample-list. Concerning the time complexity, Algorithm 2 clearly uses $O(1)$ random bits per stream element and beyond that, all the other actions cost $O(1)$ time. Assuming that each random bit costs $O(1)$ time, our algorithm needs constant time per stream element in the worst-case.

Theorem 3 *Associating Algorithm 2 with the exponential bias function, Algorithm 2 convinces a sample-user of limited access.*

Proof. Let us assume that the active-walk is the i-walk. The user concludes that the i-walk is the active-walk because the sample has i elements. To calculate future probabilities, the user must decide on the position of the active-walk. When the i-walk became the active-walk, the active-cursor was set to point to a node of the i-walk chosen uniformly at random. Not being able to access the active-cursor, the user concludes that it may point to any node of the i-walk with probability $1/i$, because the Markov chain associated with this walk has reached its stationary distribution and obviously, each step from that point and on cannot change the distribution. Let us now assume that the current time is t, the length of the sample-list is n and the fraction of the sample-list occupied by elements is $F(t)$ (note that at this point, the proof of Theorem 2.2. in [1] starts). Then, according to the algorithm, when $S(t+1)$ arrives, an element of the sample is going to be deleted with probability $F(t)$ and if such a deletion is decided, each of the $n \cdot F(t)$ elements of the sample have equal probability $1/(n \cdot F(t))$ of being deleted (because, as stated above, the cursor may point to each position with equal chances). As a result, the probability of an element being deleted is $F(t)(1/(n \cdot F(t))) = 1/n$. It follows that the probability of a stream element to survive at $t+1$ is $1 - 1/n$. Thus, the element that arrives at time r will survive in the sample at time t with probability $(1 - 1/n)^{t-r} = ((1 - 1/n)^n)^{(t-r)/n}$. For large values of n, the inner $(1 - 1/n)^n$ term is approximately equal to $1/e$, and from substitution, the exponential bias function follows (note that at this point, the proof of Theorem 2.2. in [1] ends). In advance, the user cannot decide on the position of the walk for any future time-point and as a result, whatever holds for the existing sample-elements also holds for the future sample-elements. □

One issue of interest to be discussed is the following: The walk of Section 5 is defined on a static list. According to Algorithm 2, we are able to delete an internal node of the list and re-insert it as the new rightmost node of the active walk. This results in the position of the active-walk moving one node to the left. The same holds for the position of the $(1/\lambda)$-walk. This is not the walk we presented in Section 4. In particular it now follows that in each step the probability of doing nothing i.e. going one position forward and then one position backwards (thus ending up at the starting point) is 1/2, the probability to move one node to the right is 1/4 and so on. This is a lazy version of our walk and it is trivial to see that in this lazy version the stationary distribution remains the same. Thus, Algorithm 2 is not affected.

Going to the greedy approach is trivial. It turns out that we do not need the cursor-list, but instead only the cursor for the $(1/\lambda)$-walk. Therefore, the space remains the same and equal to the final space consumed by the strict approach. The time complexity remains identical to that of the strict approach.

7. Discussion

Let us now summarize the main issue introduced in this paper, which is derived by the comparison between the algorithm (and methodology) in [1] and the algorithms (and methodology) we present in this paper. In both cases, a bias function $f(r,t)$ is associated with the $r-th$ stream element at the time of arrival of the $t-th$ stream element ($r \leq t$). This function is associated with the probability $p(r,t)$ of the $r-th$ element belonging to the reservoir at the time of the $t-th$ element. However, the issue here is the time of the association. In [1], the association can be done at any time t. In our paper, the function is associated at time $t=0$, for all the future elements of the sample. This is a logical choice since the probability is implied by the algorithm, in the sense that we have manufactured our algorithms to create samples consistent with the exponential bias function. In other words, survival probabilities are decided when the algorithm is created. It then follows that the randomness used in [1] is more than the randomness we really need in order to obtain a biased sample. It is a sample-user of limited access that we actually have to convince, and not a sample-user of full access. This observation has led to optimal randomness complexity for the problem we are studying and we believe that the technique we use for introducing randomness to our algorithms (i.e. the notion of limited access) may be useful in other problems.

References

1. Aggarwal C. C.: On biased reservoir sampling in the presence of stream evolution. In proceedings of the 32nd international conference on Very large data bases , pp. 607–618. Seoul, Korea (2006).
2. Aggarwal C. C. and Yu P. S.: A Survey of Synopsis Construction in Data Streams. Data Streams - Models and Algorithms, pp. 169–207 (2007)
3. Babcock B., Datar M. and Motwani R.: Sampling from a Moving Window over Streaming Data. In proceedings of ACM-SIAM Symposium of Discrete Algorithms, pp. 633–634, San Francisco, USA (2002).
4. Babu S. and Widom J.: Continuous queries over data streams. ACM SIGMOD Record Archives, Volume 30, Issue 3, pp 109–120 (2001).
5. Chung F. R. K. , Graham R. L. and Yau S.-T.: On Sampling with Markov Chains. In proceedings of the seventh international conference on Random structures and algorithms, pp. 55–77, Atlanta, USA (1996).
6. Gibbons P. and Mattias Y.: New Sampling-Based Summary Statistics for Improving Approximate Query Answers. In proceedings of ACM SIGMOD, pp. 331–342, Seattle, USA (1998).
7. Gibbons P.: Distinct sampling for highly accurate answers to distinct value queries and event reports. In Proceedings of 27th International Conference on Very Large Data Bases, pp. 541–550, Rome, Italy (2001).
8. Goldreich O.: Another Motivation for Reducing the Randomness Complexity of Algorithms. Studies in Complexity and Cryptography. Miscellanea on the Interplay between Randomness and Computation, pp. 555–560, (2011).
9. Jerrum M. and Sinclair A.: Conductance and the rapid mixing property for Markov chains: the approximation of permanent resolved. In proceedings of the twentieth annual ACM Symposium on Theory of Computing, pp. 235–244. Chicago, USA (1988).
10. Hellerstein J., Haas P. and Wang H.: Online Aggregation. In proceedings of ACM SIGMOD, pp. 171–182, Tucson, USA (1997).
11. Lawler G. F. and Sokal A. D.: Bounds on the L^2 Spectrum for Markov Chains and Markov Processes: A Generalization of Cheeger's Inequality. Transactions of the American Mathematical Society Vol. 309, No. 2, pp. 557–580 (1988).
12. Manku G. and Motwani R.: Approximate Frequency Counts over Data Streams. In proceedings of the 28th International Conference on Very Large Data Bases, pp. 346–357, Hong Kong, China (2002).
13. Manku G., Rajagopalan S. and Lindsay B.: Random Sampling for Space Efficient Computation of order statistics in large datasets. In proceedings of ACM SIGMOD, pp. 251–262, Philadelphia, USA (1999).
14. Matias Y., Vitter J. S. and Wang M.: Wavelet-Based Histograms for Selectivity Estimation. In proceedings of ACM SIGMOD, pp. 448–459, Seattle, USA (1998).

15. Montenegro R.: Intersection Conductance and Canonical Alternating Paths: Methods for General Finite Markov Chains. Combinatorics, Probability and Computing, Volume 23, Issue 4, pp. 585–606 (2014).
16. Vitter J. S.: Random sampling with a Reservoir. ACM Transactions on Mathematical Software, Volume 11 Issue 1, pp. 37–57 (1985).
17. Wu Y., Agrawal D. and Abbadi A.: Applying the Golden Rule of Sampling for Query Estimation. In proceedings of ACM SIGMOD, pp. 449–460, Santa Barbara, USA (2001).

A. The intuition on Algorithm Step

In order to give the intuition behind this algorithm, let us name the list L. Let us set $length(L) = 5$ and $K = length(L)$ i.e., the maximum number of coin-tosses per step is 5. We assume that time increments (starting from 0) with each step, and suppose that someone is trying to guess the node pointed by the cursor, without accessing the cursor. At time 0, the node pointed by the cursor can be deterministically determined because the cursor points to the head of the list. Now, let us "travel" into the future and make our first stop at time-point 1. The probabilities for the cursor to point to each node at time 1 are shown in the following table (where "T" stands for "tails" and "H" stands for "heads") and let us be a bit more detailed on how these probabilities are derived: Let us focus on the probability that the cursor points to Node 1 at time-point 1. It follows that the execution of Step() that moved the cursor (starting from Node 1) back to Node 1 contains as many coin-tosses as necessary for the cursor to complete the circle. This means that the first coin-toss cannot cannot result to "heads" because then, the cursor will stop at Node 2 (keep in mind that a step ends when the coin-toss results to "heads" or when 5 coin-tosses have occurred). Given that the first coin-toss results to "tails" the second coin-toss cannot result to "heads" because then the cursor will stop at Node 3 (therefore the event "TH" leads to Node 3). Following this logic we conclude that in order for the cursor to complete a full circle, either the event "TTTTT" or the event "TTTTH" must occur during the first execution of Step(). The probability of each of these two events to occur is $1/32$. We conclude that the probability for the cursor to return to Node 1 at time-point 1 is $1/16$.

Node 1	Node 2	Node 3	Node 4	Node 5
$P_{1,1} = 1/16$ (event TTTTT OR TTTTH)	$P_{2,1} = 1/2$ (event H)	$P_{3,1} = 1/4$ (event TH)	$P_{4,1} = 1/8$ (event TTH)	$P_{5,1} = 1/16$ (event TTTH)

As time passes i.e. as more steps are performed, coin tosses gradually insert randomness into the scheme, introducing an increasing uncertainty on the position of the cursor. The probabilities at time-point 2 are shown below.

$P_{1,2} = P_{1,1} * 1/16 + P_{2,1} * 1/16 + P_{3,1} * 1/8 + P_{4,1} * 1/4 + P_{5,1} * 1/2$
$P_{2,2} = P_{2,1} * 1/16 + P_{3,1} * 1/16 + P_{4,1} * 1/8 + P_{5,1} * 1/4 + P_{1,1} * 1/2$
$P_{3,2} = P_{3,1} * 1/16 + P_{4,1} * 1/16 + P_{5,1} * 1/8 + P_{1,1} * 1/4 + P_{2,1} * 1/2$
$P_{4,2} = P_{4,1} * 1/16 + P_{5,1} * 1/16 + P_{1,1} * 1/8 + P_{2,1} * 1/4 + P_{3,1} * 1/2$
$P_{5,2} = P_{5,1} * 1/16 + P_{1,1} * 1/16 + P_{2,1} * 1/8 + P_{3,1} * 1/4 + P_{4,1} * 1/2$

In general, for time-point i, we have:

$P_{1,i} = P_{1,i-1} * 1/16 + P_{2,i-1} * 1/16 + P_{3,i-1} * 1/8 + P_{4,i-1} * 1/4 + P_{5,i-1} * 1/2$
$P_{2,i} = P_{2,i-1} * 1/16 + P_{3,i-1} * 1/16 + P_{4,i-1} * 1/8 + P_{5,i-1} * 1/4 + P_{1,i-1} * 1/2$

$P_{3,i} = P_{3,i-1} * 1/16 + P_{4,i-1} * 1/16 + P_{5,i-1} * 1/8 + P_{1,i-1} * 1/4 + P_{2,i-1} * 1/2$
$P_{4,i} = P_{4,i-1} * 1/16 + P_{5,i-1} * 1/16 + P_{1,i-1} * 1/8 + P_{2,i-1} * 1/4 + P_{3,i-1} * 1/2$
$P_{5,i} = P_{5,i-1} * 1/16 + P_{1,i-1} * 1/16 + P_{2,i-1} * 1/8 + P_{3,i-1} * 1/4 + P_{4,i-1} * 1/2$

It is not difficult to write a simple program and see that these probabilities converge to 1/5, as time progresses. Thus, after "a while", enough randomness has been inserted, for the cursor to be in each position with equal chances.

B. Bounding the mixing time

Bounding the mixing time of a Markov chain can be difficult. Here, we will use the conductance method ([9], [11]), according to which the ergodic flow between two subsets $S, T \subset V$ is defined to be

$$Q(S,T) = \sum_{i \in S, j \in T} \pi_i P_{ij}$$

The method could bound the mixing time for lazy reversible Markov chains, but it was extended in [15] in order to apply to general finite ergodic Markov chains. According to [15], the *intersection conductance* $\hat{\Phi}(A)$ of $A \subset V$ (and $\bar{A}$, the complement of A) is given by

$$\hat{\Phi}(A) = \hat{\Phi}(A, \bar{A}) = \frac{\sum_{u \in V} min\{Q(A,u), Q(\bar{A},u\})}{2\pi(A)\pi(\bar{A})}$$

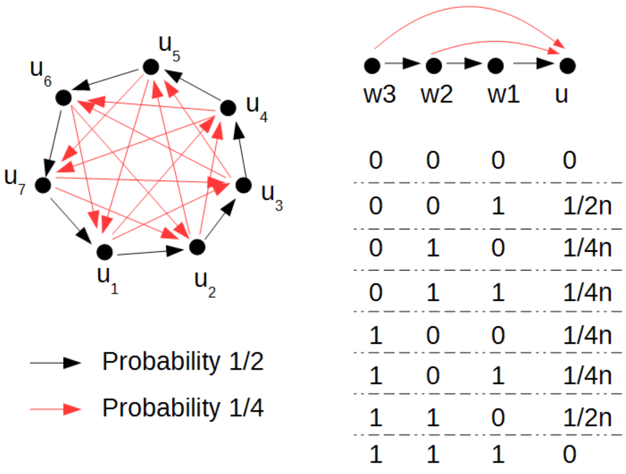
Then, the intersection conductance is $\hat{\Phi} = \min_{\emptyset \subsetneq A \subsetneq V} \hat{\Phi}(A)$. In [15] it is proved that the mixing time of a finite ergodic Markov chain is

$$r(\epsilon) \leq \frac{12}{\hat{\Phi}^2} log \frac{1}{\epsilon\sqrt{\pi_0}}$$

where $\pi_0 = \min_{u \in V} \pi_u$.
We are first going to bound the mixing time for $K = 2$, i.e. if at most 2 coin tosses are allowed in algorithm Step. For every $i, j \in V$, if $p_{ij} = 1/2$, we say that state j is the *next* of i. The left part of Figure B.1 visualizes the walk on 7 nodes. The black arrows correspond to probabilities of 1/2 and the red ones to probabilities of 1/4. The "contribution" of a node u in the numerator of $\hat{\Phi}(A)$, depends on the status of the three "preceding" nodes (according to the order defined by the black arrows). We distinguish 8 cases, depending on whether each of the 3 nodes belongs to A, or to $\bar{A}$. We name each case through the corresponding 3-bit number (each node corresponds to a 1, if it belongs to A, or to a 0, otherwise).

Let us introduce the following terminology: Set A *outperforms* set B, if $\hat{\Phi}(A) \leq \hat{\Phi}(B)$. Let $A \subset V$. Then, if all the states of A are connected through probabilities of 1/2, we call the set, *tight*. We are now ready to bound the mixing time of the Markov chain assuming that $K = 2$.

Theorem B 1 *Setting $K = 2$, $r(\epsilon) = O(n^2 \log n)$, where n is the number of states and $n \geq 8$.*



w3	w2	w1	u
0	0	0	0
0	0	1	1/2n
0	1	0	1/4n
0	1	1	1/4n
1	0	0	1/4n
1	0	1	1/4n
1	1	0	1/2n
1	1	1	0

Fig. B.1. The random walk for 2 coin tosses. On the right, we show all the possible additives in the nominator of $\hat{\Phi}(A)$, because of node u.

Proof. We need to find the set A that outperforms all other sets. Let us first consider all the sets that contain d states, for a given d such that $1 < d \leq n/2$ (by allowing A to contain more nodes, $\bar{A}$ contains less than $n/2$ nodes and by renaming A to $\bar{A}$ and $\bar{A}$ to A, we fall into the same case). Thus, let A be such a set of cardinality d. Then, the denominator in $\hat{\Phi}(A)$ is $2 \cdot \frac{d}{n} \cdot \frac{n-d}{n}$. Since all the sets of cardinality d produce the same denominator, the one that results to the smallest numerator outperforms all the others. Observe, that in Figure B.1, the contribution of a node to the numerator of $\hat{\Phi}(A)$ is 0 if the three preceding states either all belong to A, or all belong to $\bar{A}$. As a result, among all the sets of cardinality d, the ones that outperform all the others are the tight ones. This is because in this case, the number of states for which the three preceding states either belong to A or not, maximizes and thus the numerator is minimized. For example, in Figure B.2 the states represented by squares belong to A, and the states represented by circles belong to $\bar{A}$. It follows that only u_2, u_3, w_2 and w_3 will contribute to the numerator. In particular, for u_2 we have the case 001 (see Figure B.1), for u_3 we have the case 011, for w_2 we have case 110 and for w_3 we have case 100. Observe that if A, B are tight sets (of states) of the same cardinality, then $\hat{\Phi}(A) = \hat{\Phi}(B)$.

We have now concluded that among all the sets of states having the same cardinality, anyone that is tight outperforms all the others. As a result, instead of trying to find the set A that minimizes $\hat{\Phi}(A)$ among all possible sets, we need to examine only the tight ones. Observe now that all the tight sets of more than two states produce the same numerator. As a result, among all the tight sets with more than two states, we must find the ones that result to the maximum denominator in order to minimize the fraction. The denominator is maximized for any set having $n/2$ states. We have now concluded that if A is tight and contains $n/2$ states and B is any other set of states that contains more than two states, $\hat{\Phi}(A) \leq \hat{\Phi}(B)$. For any tight set A of $n/2$ states we have the following:

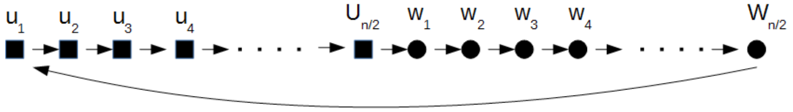


Fig. B.2. The rectangles correspond to the states of A. The arrows corresponding to probabilities with value less than 1/2 are omitted.

$$\hat{\Phi}(A) = \frac{\frac{1}{4n}+\frac{1}{2n}+\frac{1}{2n}+\frac{1}{4n}}{2\frac{1}{2}\frac{1}{2}} = \frac{3}{n}.$$

It remains to see if there is a tight set of cardinality 1 or 2 that outperforms the tight sets of cardinality $n/2$. For any tight set B of cardinality 2, only four nodes will contribute to the numerator of $\hat{\Phi}(B)$. In particular, the second (according to the order of the black arrows) node of B will fall into case 001, and the next three nodes (that belong to $\bar{B}$) will fall into cases 011, 110 and 100, respectively. It follows that for any tight set B of cardinality 2:

$$\hat{\Phi}(B) = \frac{3n}{8(n-2)}.$$

Similarly, for any single state set C, only the three states after the one that belongs to C are going to contribute to the numerator and they are going to fall into cases 001, 010 and 100 (according to the order defined by the black arrows). Thus, for any single state set C we have:

$$\hat{\Phi}(C) = \frac{\frac{1}{2n}+\frac{1}{4n}+\frac{1}{4n}}{2\frac{1}{n}\frac{n-1}{n}} = \frac{n}{2(n-1)}.$$

It follows that any tight set A of cardinality $n/2$ outperforms all tight sets of cardinality 1 and 2 for all $n \geq 8$, and as a result, it outperforms any other set of states. We have now concluded that by allowing at most two coin tosses, $\hat{\Phi} = \frac{3}{n}$. This means that setting $\epsilon = 1/n^c$ for some constant c, we get $r(\epsilon) \in O(n^2 \log n)$. $\square$

It remains to find the mixing time for $K > 2$. Clearly, by increasing K we increase the area that each step can cover, and thus it is a fact that the mixing time is going to improve. However, asymptotically things remain the same, as the next theorem states.

Theorem B 2 *Setting* $K = n$, $r(\epsilon) \in O(n^2 \log n)$, *where* n *is the number of states and* $n \geq 8$.

Proof. Since we know that the chain with $K > 2$ reaches the stationary distribution faster than the one with $K = 2$, it suffices to find a set A such that $\hat{\Phi}(A)$ is small enough to imply $O(n^2 \log n)$ mixing time. Then, even if there exists another set B that outperforms A, it follows $\hat{\Phi}(B)$ can only imply $O(n^2 \log n)$ mixing time. We choose A to be a tight set of $n/2$ states, and we will prove that by setting $\epsilon = 1/n^c$ for some constant

c, $\frac{12}{(\hat{\Phi}(A))^2} \log \frac{1}{\epsilon\sqrt{\pi_0}} = O(n^2 \log n)$. For the description we are going to use Figure B.2, where the states of A appear as rectangles, and the states of $\bar{A}$ appear as circles. Keep in mind that the arrows corresponding to probabilities with value less than 1/2 are omitted, however since $K = n$, each state is actually connected to all the other states. For states from w_2 until u_1 (following the arrows of probability 1/2), it is the set A that contributes to the numerator of $\hat{\Phi}(A)$. For states from u_2 until w_1 it is the set $\bar{A}$ that contributes to the numerator of $\hat{\Phi}(A)$. In particular:

Node w_2 contributes $\frac{1}{n}(\frac{1}{4} + \frac{1}{8} + \cdots + \frac{1}{2^{\frac{n}{2}+1}}) < \frac{1}{2n}$
Node w_3 contributes $\frac{1}{n}(\frac{1}{8} + \frac{1}{16} + \cdots + \frac{1}{2^{\frac{n}{2}+2}}) < \frac{1}{4n}$
....
Node u_1 contributes $\frac{1}{n}(\frac{1}{\frac{n}{2}+1} + \frac{1}{\frac{n}{2}+1} + \cdots + \frac{1}{2^n}) < \frac{1}{n2^{\frac{n}{2}}}$

It follows that the total contribution of all the states from w_2 to u_1 is smaller than $\frac{1}{n}$. Examining the remaining states (i.e. from u_2 to w_1), the results are identical. It follows that when set A is a tight set of $n/2$ edges we have the following:

$\hat{\Phi}(A) < \frac{\frac{2}{n}}{2\frac{1}{2}\frac{1}{2}} = \frac{4}{n}$. Observe that the following also holds: $\hat{\Phi}(A) = O(\frac{4}{n})$

As a result, by setting $\epsilon = 1/n^c$ for some constant c, we get $\frac{12}{(\hat{\Phi}(A))^2} \log \frac{1}{\epsilon\sqrt{\pi_0}} = O(n^2 \log n)$. ☐

George Lagogiannis was born in Xylokastro, a small town located in the north-east coast of Peloponnisos, Greece. He is an assistant professor at the department of Agricultural Economics and Rural Development in the Agricultural University of Athens. His research is focused on the field of data structures and algorithms.

Stavros Kontopoulos is a Phd student in the area of distributed indexing structures. His interests among others are: distributed system design, data streaming technologies, and NoSql databases. He is also a software engineer with more than 10 years of experience in various industries. His current focus is on machine learning and data streaming.

Christos Makris is an Associate Professor in the University of Patras, Department of Computer Engineering and Informatics, from September 2017. Since 2004 he served as an Assistant Professor in CEID, UoP, tenured inthat position from 2008. His research interests include Data Structures,Information Retrieval, Data Mining, String Processing Algorithms, Computational Geometry, Internet Technologies, Bioinformatics, and Multimedia Databases. He has published over 100 papers in refereed scientific journals and conferences and has more than 600 citations excluding self-citations (h-index:16).

Received: March 10, 2018; Accepted: July 25, 2018.