Mechanisms for Hiding Sensitive Genotypes with Information-Theoretic Privacy

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Abstract—The growing availability of personal genomics services comes with increasing concerns for genomic privacy. Individuals may wish to withhold sensitive genotypes that contain critical health-related information when sharing their data with such services. A straightforward solution that masks only the sensitive genotypes does not ensure privacy due to the correlation structure within the genome. Here, we develop an information-theoretic mechanism for masking sensitive genotypes, which ensures no information about the sensitive genotypes is leaked. We also propose an efficient algorithmic implementation of our mechanism for genomic data governed by hidden Markov models. Our work is a step towards more rigorous control of privacy in genomic data sharing.

I. INTRODUCTION

A. Motivation

The rise of personal genomics, whereby private individuals are exposed to an increasing range of services for sequencing, sharing, or analyzing their genomes, is leading to growing concerns for genomic privacy [1]–[3]. A personal genome is a rich trove of information about the underlying individual, including predictors for disease risks and other health-related traits, which holds great potential for improving one’s health, yet may cause harm if used against the individual. Unlike other types of personal data like passwords, one’s genetic data cannot be replaced once leaked, and a data breach may even affect the relatives of the individual whose genome is leaked. In order to facilitate the sharing of genomes to improve public health and advance science, we need principled strategies for controlling the privacy risks associated with genomic data sharing.

A key need in this regard is to selectively limit the leakage of information about biological or health-related traits of an individual that can be inferred from the shared genetic data. For example, one may wish to hide certain genotypes (an individual’s genetic information at specific genomic positions) with well-established disease association before sharing his or her data with others (e.g., analytic service providers or researchers). Such a capability would allow individuals to have fine-grained control over their genomic privacy.

Notably, a simple approach to privacy protection, whereby sensitive positions in the genome are masked before sharing the data, does not provide sufficient privacy protection. This is because the correlation structure among different genomic positions can be used to reconstruct the masked data as demonstrated in a number of studies [4], [5].

To prevent such an attack, one could alternatively erase all positions that are highly correlated with the sensitive sites [6], which may be achieved by masking the data within a large window around each sensitive position. Unfortunately, these approaches either provide incomplete privacy protection or require an excessive amount of data to be erased in order to achieve strong privacy, thus limiting the usefulness of the shared data. Here, we aim to design an effective mechanism for sharing a personal genome that provably hides sensitive positions, while introducing a small amount of erasure.

B. Genetics Background

An individual’s genome consists of a pair of sequences, one from each parent, each consisting of around 3 billion nucleotides (A, C, G, and T). Each sequence is referred to as a haplotype. Since most of the genome is identical between different individuals, a common way to compactly represent a personal genome is as a list of positions of variation, paired with the observed nucleotides in the given individual (referred to as a genotype). In this work, we consider the problem of sharing a list of genotypes corresponding to a single haplotype of an individual. Although standard sequencing pipelines produce a genotype at each position that mixes the two haplotypes, well-established methods exist for resolving this ambiguity in order to separate the two haplotypes (a process called phasing), after which our approach could be individually applied to each haplotype.

In our attack scenario, the goal of an adversary is to infer the target individual’s genotypes at specific positions in the genome, given a partially masked genetic sequence of the individual released by our mechanism. In principle, this reconstruction task is equivalent to an extensively studied problem in bioinformatics known as genotype imputation, originally developed for coping with missing data in sequencing experiments, which often cover only a subset of genomic positions. If one were to mask only the sensitive positions before sharing the data, existing imputation algorithms are expected to be effective at revealing the hidden genotypes using other genotypes in their respective neighborhoods.

A state-of-the-art algorithm for genotype imputation, minimac [7], is based on a classical model of genetic sequences.
introduced by Li and Stephens [8]. In this model, a person’s genetic sequence is modelled as a mosaic of a large group of reference sequences from other individuals. This model intuitively captures the underlying biological process of recombination, which describes the interleaving of two haplotypes of each parent when their genetic material is passed onto the child. Formally, these models are expressed as hidden Markov models (HMMs), where a sequence of genotypes of an individual is generated from a sequence of hidden states, representing which reference sequence to copy the genotype for each corresponding position. We adopt this model in our work to capture the underlying distribution of genotypes. Alternative approaches to imputation (e.g. based on matrix factorization [9]) exist. We take the HMM-based approach since it is widely used in genetics for tasks beyond imputation, including phasing [10] and simulation [11]. Further details of this model is provided in Section II.

C. Setup and Contributions

In this work, we consider the problem of hiding sensitive genotypes when sharing genomic data. The genotype sequence $X$ of length $n$ is generated by a hidden Markov model as previously described. The user wants to share his or her genotype sequence for genomic services, while keeping private sensitive genotypes in given locations in the sequence. Thus, the problem is to keep the sensitive positions private while introducing minimum number of erasures in the released version of the genotype sequence $X$.

The contribution of this paper is two-fold:

1) For any given underlying distribution $p_X$, we develop an information-theoretic privacy mechanism to hide the sensitive positions. This builds on prior work on ON-OFF privacy [12], [13] and generalize it to general distributions.

2) For the data generative model, i.e., hidden Markov model, considered in this paper, we propose an efficient algorithm to implement the privacy mechanism.

II. REVIEW OF HIDDEN MARKOV MODEL FOR GENOMES

The classical hidden Markov model (HMM) describing the distribution of personal genomes [8] is as follows. First, let $X = (X_1, X_2, \ldots, X_n)$ represent an individual’s (haplotype) genetic sequence of length $n$. Following standard practice in genetics, we adopt a binary alphabet $A = \{0, 1\}$ for each element $X_i$, representing whether the observed nucleotide is identical to the one in the reference human genome (called reference allele) or not (alternative allele).

In addition, we are given a reference dataset of $m$ personal genome sequences $\mathcal{H} = \{h_j : j = 1, \ldots, m\}$, where each sequence $h_j$ is of length $n$. The $i$-th coordinate of $h_j$ is denoted by $h_{i,j}$, which also takes a value in $A$.

In this model, $X$ is viewed as a “mosaic” of reference sequences in $\mathcal{H}$ with potential substitution errors arising from mutations or experimental noise in sequencing. Formally, $X$ depends on a sequence of hidden states $\{S_i\}_{i=1}^{n}$ forming a Markov chain, where each $S_i$ takes an integer in the range $\{1, \ldots, m\}$, representing an index into $\mathcal{H}$. Without loss of generality, we assume that the initial state $S_1$ is uniformly distributed over $\{1, \ldots, m\}$. The transition probability $\pi_{i,j}$ from state $i$ to $j$ is assumed to be $\frac{1}{m}$ and $1 - \epsilon$ for $i \neq j$ and $i = j$ respectively.

Next, each $X_i$ is sampled based on the hidden state $S_i$ by copying the corresponding symbol in the selected reference sequence with a small probability of error. In other words, $X_i$ is equal to the symbol in the $i$-th position of $h_{S_i}$ with probability of error $\theta$. The overall data distribution $p_X$ is fully specified by the tuple $\langle \mathcal{H}, \epsilon, \theta \rangle$. We provide a graphical illustration of $p_X$ in Fig. 1.

In our work, we assume that the parameters of the above model are known. In practice, we expect these parameters to be estimated from a large collection of reference genomes, e.g., including hundreds of thousands of individuals, which are currently available in public data repositories (e.g., UK Biobank [14]). It is worth noting that HMM parameters could be more accurately estimated by using a larger set of reference dataset. However, given the high cost of amassing large-scale genomic data, it would be a significant challenge for an attacker to gain access to a larger dataset than those in the public realm, so our modeling assumption could be thought of as providing privacy protection according to the best knowledge of the field.

![Fig. 1: A graphical illustration of HMM for genomes.](image-url)

III. THE GENOTYPE-HIDING PROBLEM

Let $X = (X_1, \ldots, X_n)$ be the user’s personal genome sequence of length $n$, which is generated by the hidden Markov model described in Section II. In this section, we assume the knowledge of underlying distribution $p_X$, i.e., the personal genome sequence generated by the hidden Markov
model \( (\mathcal{H}, \epsilon, \theta) \), is given. It means that the formulation of the privacy problem is for any given \( p_X \) instead of any particular data generative model such as HMMs.

The user wishes to share \( X \) with others, but is concerned about the information revealed by certain coordinates of \( X \). To hide the data at these sensitive coordinates, the user generates a masked version of the data \( Y = (Y_1, \ldots, Y_n) \), which only partially reveals \( X \). Since we expect substitution errors to be considerably more undesirable than erasures in genetic analyses, we impose a constraint that \( Y_i \) can be either \( X_i \) or the erasure symbol \( * \); we refer to this property as the faithfulness condition. Note that the alphabet of \( Y_i \) is \( \mathcal{A} \cup \{ * \} \).

Let \( K \subset \{ 1, \ldots, n \} \) be the user-provided set of indices of \( X \) containing sensitive information. We require that no information about \( X_K = \{ X_i : i \in K \} \) is revealed when \( Y \) is shared. In other words, we require that

\[
I(X_K; Y) = 0, \tag{1}
\]

which we refer to as the privacy condition. This guarantees that \( X_K \) and \( Y \) are statistically independent, which is stronger than alternative notions of privacy such as local differential privacy [15].

Our goal is to design a privacy mechanism \( p_{Y|X} \) for generating \( Y \) given \( X \) and \( K \) such that both the faithfulness and privacy conditions are satisfied. While doing so, we wish to share as much of \( X \) as possible. Let \( e(Y) \) be the number of erasure symbols in \( Y \). Our goal is to minimize the expected number of erasures \( E[e(Y)] \), where

\[
E[e(Y)] = \sum_{i=1}^{n} p(y_i = *), \tag{2}
\]

and \( 1(\cdot) \) denotes the indicator function. In other words, we are interested in solving the following problem:

\[
\begin{align*}
\text{minimize} & \quad \frac{1}{n} \sum_{i=1}^{n} p(y_i = *) \\
\text{subject to} & \quad I(X_K; Y) = 0 \quad \text{(Privacy)} \\
& \quad Y_i \in \{ X_i, * \}, \forall i \quad \text{(Faithfulness)}
\end{align*}
\]

Although the above problem is an instance of linear programming (LP), the scale of the problem is intractable, given the exponential blowup in the number of variables and constraints as the length of the sequence \( n \) grows. Therefore, we are interested in an analytical characterization of solutions \( p_{Y|X} \) to the above problem.

IV. PRIVACY MECHANISM

In this section, we present a privacy mechanism to generate \( Y \) such that both the faithfulness and privacy conditions are satisfied for any general distribution \( p_X \). Later in Section V, we will focus on \( p_X \) defined by a hidden Markov model and propose an efficient algorithm to implement the privacy mechanism.

As defined, \( Y_i \) can either be \( X_i \) (i.e., no erasure) or * (i.e., erasure), so the problem is to design a proper erasure rate for each coordinate \( i \). Our proposed scheme generates \( Y \) in a sequential manner: Let \( (o_1, \ldots, o_n) \) be any permutation of \( (1, \ldots, n) \). We generate \( Y \) in the order of \( (o_1, \ldots, o_n) \), where each \( Y_{o_i} \) may depend on the preceding variables \( Y_{o_1}, \ldots, Y_{o_{i-1}} \).

**Privacy mechanism:** Given an order \( (o_1, \ldots, o_n) \), generate each \( Y_{o_i} \) according to the following conditional distribution

\[
p \left( y_{o_i} | x_{o_i}, x_K, y_{o_1}, \ldots, y_{o_{i-1}} \right) = \begin{cases} 
\frac{\min_{y \in A|K} \{ \mathbb{P}(x_{o_i} | x_K, y_{o_1}, \ldots, y_{o_{i-1}}) \}}{\mathbb{P}(x_{o_i} | x_K, y_{o_1}, \ldots, y_{o_{i-1}})}, & y_{o_i} = x_{o_i}, \\
1 - \frac{\min_{y \in A|K} \{ \mathbb{P}(x_{o_i} | x_K, y_{o_1}, \ldots, y_{o_{i-1}}) \}}{\mathbb{P}(x_{o_i} | x_K, y_{o_1}, \ldots, y_{o_{i-1}})}, & y_{o_i} = *
\end{cases},
\]

for any \( x_{o_i}, x_K \) and \( y_{o_1}, \ldots, y_{o_{i-1}} \).

**Remark.** One may notice that we do not specify a particular order here, which means that the mechanism works for any given order. However, the choice of the order may affect the performance, i.e., expected number of erasures, of the mechanism. Finding the best order for the sequential mechanism, given \( K \) and \( p_X \), remains an open problem.

**Theorem 1.** The privacy mechanism given in (4) satisfies the privacy and faithfulness conditions.

Note that our privacy mechanism satisfies the faithfulness condition by design. Before verifying the privacy condition, we note the following properties of the privacy mechanism.

1) If \( o_i \in K \), then

\[
\min_{u \in A|K} \mathbb{P}(x_{o_i} | x_K = u, y_{o_1}, \ldots, y_{o_{i-1}}) = 0,
\]

which yields

\[
\mathbb{P}(y_{o_i} = * | x_{o_i}, x_K, y_{o_1}, \ldots, y_{o_{i-1}}) = 1.
\]

This implies that the user needs to always erase \( Y_{o_i} \), if \( X_{o_i} \) is sensitive.

2) We notice from (4) that \( x_{o_i} \) is not erased with some nonzero probability, so this mechanism is strictly better than the naive approach of always erasing the positions that may leak sensitive information.

A. Interpretation of the privacy mechanism

Here, we provide some simple intuition behind the proposed privacy mechanism in (4). Given an order \( (o_1, \ldots, o_n) \) of the sequential mechanism, consider a greedy algorithm for solving the problem in (3), which locally minimizes the erasure probability \( p(y_{o_i} = *), \) one coordinate at a time. That is, for each \( i = 1, \ldots, n \), we solve

\[
\min_{p_{Y_{o_i} | x, Y_{o_{1:i-1}}}} \mathbb{P}(y_{o_i} = *) \quad \text{s.t.} \quad I(X_K; Y_{o_i} | Y_{o_{1:i-1}}) = 0 \quad \text{(5)}
\]

\[
Y_{o_i} \in \{ X_{o_i}, * \}
\]

where \( o_{1:i} := \{ o_1, \ldots, o_{i-1} \} \). Note that

\[
I(X_K; Y) = \sum_{i=1}^{n} I(X_K; Y_{o_i} | Y_{o_{1:i-1}}) = 0, \tag{6}
\]
by the chain rule if the first constraint of (5) is satisfied for all \( i \).
It turns out that the privacy mechanism given in (4) is the optimal solution to (5). In other words, if we adopt our sequential mechanism with the ordering \((o_1, \ldots, o_n)\), then the privacy mechanism as given in (4) can be viewed as an optimal greedy optimization algorithm for the given order. We defer the proof to the extended version of this manuscript.

**B. Proof of privacy**

To show the proposed mechanism in (4) satisfies the privacy condition, we know from (6) that it is sufficient to show that
\[
I(Y_{o_1}; X_K|Y_{o_1}, \ldots, Y_{o_{i-1}}) = 0, \tag{7}
\]
for \( i = 1, \ldots, n \).
To establish (7), we will prove that
\[
p(y_{o_i}|x_K, y_{o_{i-1}}) = p(y_{o_i}|y_{o_{i-1}}) \tag{8}
\]
for any \( x_K \) and \( y_{o_{i-1}} \). Since
\[
p(y_{o_i}|x_K, y_{o_{i-1}}) = \sum_{x_{o_i}} p(x_{o_i}|x_K, y_{o_{i-1}}) p(y_{o_i}|x_{o_i}, x_K, y_{o_{i-1}}), \tag{9}
\]
by substituting (4), we have
\[
p(y_{o_i} = x| x_K, y_{o_{i-1}}) = \sum_{x_{o_i}} p(x_{o_i}|x_K, y_{o_{i-1}}) p(y_{o_i} = x| x_{o_i}, x_K, y_{o_{i-1}}) = 1 - \sum_{x_{o_i} \in \mathcal{A}^{|K|-1}} p(x_{o_i}|x_K = u, y_{o_{i-1}}). \tag{10}
\]
Similarly, for \( y_{i} \in \mathcal{A} \), we have
\[
p(y_{o_i}|x_K, y_{o_{i-1}}) = \sum_{x_{o_i}} p(x_{o_i}|x_K, y_{o_{i-1}}) p(y_{o_i} = x| x_{o_i}, x_K, y_{o_{i-1}}) = \sum_{x_{o_i} \in \mathcal{A}^{|K|-1}} \min_{x_{o_i} \in \mathcal{A}^{|K|-1}} p(x_{o_i}|x_K = u, y_{o_{i-1}}). \tag{11}
\]
By combining (10) and (11), we observe that
\[
p(y_{o_i}|x_K, y_{o_{i-1}}) = p(y_{o_i}|y_{o_{i-1}}),
\]
for any \( x_K \) and \( y_{o_1}, \ldots, y_{o_i} \), which finishes the proof of (7).

**V. AN EFFICIENT ALGORITHM FOR HMMs**

In this section, we propose an efficient algorithm to implement the privacy mechanism introduced in Section IV for \( p_X \) based on a hidden Markov model \((\mathcal{H}, \epsilon, \theta)\).

As seen in (4), the privacy mechanism determines the probability of erasing \( X_{o_i} \) mainly based on the probability \( p(x_{o_i}|x_K, y_{o_{i-1}}) \). By employing a belief propagation approach akin to the well-known forward-backward algorithm [16], we develop an efficient algorithm to track the computation of \( p(x_{o_i}|x_K = u, y_{o_{i-1}}) \) for all \( u \in \mathcal{A}^{|K|} \). The novelty of our algorithm is that it incorporates the stochasticity of the privacy mechanism in addition to that of the HMM.

In the following, we present the details of our algorithm for \( |K| = 1 \) for simplicity. A brief discussion on \( |K| > 1 \) is included at the end of this section, and we defer the details to the extended version of this manuscript. Without loss of generality, we assume that \( K = \{1\} \). In addition, we set the order \((o_1, o_2, \ldots, o_n)\) to \((1, 2, \ldots, n)\); such a linear order enables our algorithm to be computationally efficient.

First, note that it is sufficient to describe how to compute \( p(x_i|x_1, y_{[i-1]}) \) for all \( u \in \mathcal{A} \) and \( i \in [n] \), which fully determines the distribution of \( y_1, \ldots, y_n \) specified by our privacy mechanism, i.e.,
\[
p(y_{i}|x_i, x_1 = u, y_{[i-1]}) = \frac{1 - \min_{u \in \mathcal{A}} \mathbb{P}(x_i|x_1 = u, y_{[i-1]})}{\mathbb{P}(x_i|x_1 = u, y_{[i-1]})} \tag{12}
\]
where \([i] := \{1, \ldots, i\}\).
We begin by expressing \( p(x_i|x_1, y_{[i-1]}) \) as
\[
p(x_i|x_1, y_{[i-1]}) = \sum_{s_i} p(s_i|x_1, y_{[i-1]}) p(x_i|s_i, x_1, y_{[i-1]}).
\]
Similarly, for \( p(s_i|x_1) \) and \( p(s_i|y_{[i-1]}) \) are both specified by the HMM, we need to compute only the term \( p(s_i|x_1 = u, y_{[i-1]}) \). To simplify our notation, we introduce the following variable to represent this term:
\[
\psi^{(i)}(u) = p(s_i|x_1 = u, y_1, \ldots, y_i). \tag{14}
\]
Note that, if we have \( \psi^{(i-1)}(u) \) for all \( u \in \mathcal{A} \) for a given position \( i \), then we can calculate (13) as
\[
p(x_i|x_1, y_{[i-1]}) = \sum_{s_i} p(x_i|s_i) \sum_{s_{i-1}} p(s_i|s_{i-1}) \psi^{(i-1)}(x_1). \tag{15}
\]
To efficiently compute \( \psi^{(i)}(u) \) for all \( u \in \mathcal{A} \) and \( i \in [n] \), we use the following iterative algorithm.

**Initialization:** Since \( x_1 \) is a sensitive position, we know that \( y_1 = * \) regardless of \( x_1 \). Thus,
\[
\psi^{(1)}(u) = p(s_1|x_1 = u), \tag{16}
\]
where \( p(s_1|x_1 = u) \) is easily determined based on the HMM.

**Iterations:** Using Bayes’ rule, we can express \( \psi^{(i)}(u) \) as
\[
\psi^{(i)}(u) = p(s_i|x_1 = u, y_{[i-1]}) \propto p(s_i|x_1 = u, y_{[i-1]}) p(y_i|s_i, x_1 = u, y_{[i-1]}), \tag{17}
\]
where
\[
p(s_i|x_1, y_{[i-1]}) = \sum_{s_{i-1}} \psi^{(i-1)}(x_1) p(s_i|s_{i-1}),
\]
\[
p(y_i|s_i, x_1, y_{[i-1]}) = \sum_{x_i} p(x_i|s_i) p(y_i|x_i, x_1, y_{[i-1]}).
\]

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Therefore, \( \psi^{(i)}(u) \) can be computed given \( \psi^{(i-1)}(u') \) for all \( u' \in A \). Note that the terms \( p(s_i | s_{i-1}) \) and \( p(x_i | s_i) \) are given by the HMM, and \( p(y_i | x_i, x_{1:i-1}) \) is given by our mechanism as shown in (12). Using this recurrence relation, \( \psi^{(i)}(u) \) for all \( i \in [n] \) can be computed.

Analogous to the forward-backward algorithm, our algorithm has polynomial computational complexity of \( O(nm^2) \), with respect to the sequence length \( n \) and the number of reference sequences \( m \). Clearly, \( \min_{u \in A^{[K]}} p(x_o, x_K = u, y_{o:i-1}) \) can be easily obtained once \( p(x_i | x_K = u, y_{o:i-1}) \) for all \( u \) have been computed. This overhead involves a factor of \( |A|^{|K|} \) in the computational complexity, but we expect \( |K| \) to be a small constant in practice (e.g., less than 10); since genotype correlation is predominantly local, the user may apply our mechanism to local regions of the genome of a permissible length, each of which including only a few sensitive positions.

Algorithm 1 Mechanism for hiding a genotype in \( x \)

Input: Genome sequence \( x = (x_1, \ldots, x_n) \) from an HMM with parameters \((H, \epsilon, \theta)\), where \( x_1 \) is sensitive

Output: Masked genome sequence \( y = (y_1, \ldots, y_n) \), s.t. \( I(x_1; y) = 0 \) and \( y_i \in \{x_i, \ast\} \) for all \( i \in [n] \)

1: Initialize \( \psi^{(1)}(u) = p(s_1 | x_1 = u) \) based on \((H, \epsilon, \theta)\)
2: for \( i = 2, \ldots, n \) do
3: \( u \in A \) do
4: Compute \( p(x_i | x_1 = u, y_{i-1}) \) according to (15)
5: end for
6: Calculate the erasure probability for \( y_i \) using (12)
7: Generate \( y_i \in \{x_i, \ast\} \) according to the erasure probability
8: for \( u \in A \) do
9: Compute \( \psi^{(i)}(u) \) according to (17)
10: end for
11: end for

For multiple sensitive positions, i.e., \( |K| > 1 \), the term \( p(s_i | s_{i-1}) \) in (13) will be replaced by \( p(s_i | s_{i-1}, x_K) \), so we need to additionally track this term, which can be done in the same manner as calculating the backward probabilities in the forward-backward algorithm.

VI. TOWARDS AN UNDERSTANDING OF OPTIMALITY

As we described in Section IV-A, our mechanism can be viewed as a greedy algorithm for minimizing the number of erasures of a mechanism that perfectly hides the sensitive genotypes. However, the optimality of the greedy algorithm remains incompletely understood.

As discussed previously, it may depend on the order of generating positions. Furthermore, a sequential mechanism may not be optimal in general, that is to say, generating multiple positions jointly (in contrast to a sequential mechanism that generates one position at a time) may lead to a better solution.

Nevertheless, one can show that an upper bound on the (non-erasure) rate of any feasible solution to this genotype hiding problem (3) is given by

\[
\frac{1}{n} \sum_{i=1}^{n} p(y_i \neq \ast) \leq \frac{1}{n} \sum_{i=1}^{n} \sum_{x_i \in A} \min_{u \in A^{[K]}} p(x_i | x_K = u) .
\]

In addition, our proposed mechanism attains this upper bound for \( X \) that forms a Markov chain (not HMM) with a single sensitive position. We defer the proof details of these results to the extended version of this work. Interestingly, our preliminary simulation study for the HMM case, shown in Fig. 2, suggests that the performance of our mechanism is sometimes very close to the upper bound, while in certain settings, the gap between the our mechanism and the upper bound is considerably large. Closing the gap between the mechanism and the upper bound is our ongoing work.

Fig. 2: Comparison of our mechanism and the upper bound on simulated HMM data, with \( m = 10, n = 100, \theta = 0.01, K = \{1\} \). Transition probability \( \epsilon \) refers to the probability of leaving the current state in each step of the HMM, where the next state is chosen uniformly at random.

VII. CONCLUSION AND FUTURE WORK

In this paper, we developed an information-theoretically private mechanism to hide sensitive genotypes, and proposed an efficient algorithmic implementation of this mechanism for hidden Markov models.

There are several key directions for future work. First, although we focused on achieving information-theoretic privacy, it may be useful in practice to consider a relaxed notion such as differential privacy [17]. This may give the user the ability to determine the desired tradeoff between the level of privacy and the amount of data to be erased. Second, our work could be further integrated with existing strategies for mitigating re-identification risk by embedding the genome in a larger collection of genomes [18]. Lastly, it would be interesting to explore the generalization of our mechanism to a broader class of data generative models, which may allow similar mechanisms to be developed for protecting sensitive data in other domains.

ACKNOWLEDGMENT

The work of F. Ye and S. E. Rouayheb was supported in part by NSF Grant CCF 1817635. H. Cho is funded by Eric and Wendy Schmidt through the Schmidt Fellows program at Broad Institute.
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