Genome-Wide Association Studies:
Information Theoretic Limits of Reliable Learning

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Abstract

In the problems of Genome-Wide Association Study (GWAS), the objective is to associate subsequences of individuals’ genomes to the observable characteristics called phenotypes. The genome containing the biological information of an individual can be represented by a sequence of length $G$. Many observable characteristics of individuals can be related to a subsequence of a given length $L$ called causal subsequence. The environmental affects make the relation between the causal subsequence and the observable characteristics a stochastic function. Our objective in this paper is to detect the causal subsequence of a specific phenotype using a dataset of $N$ individuals and their observed characteristics.

We introduce an abstract formulation of GWAS which allows us to investigate the problem from an information theoretic perspective. In particular, as the parameters $N, G,$ and $L$ grow, we observe a threshold effect at $\frac{Gh(L/G)}{N}$, where $h(.)$ is the binary entropy function. This effect allows us to define the capacity of recovering the causal subsequence by denoting the rate of the GWAS problem as $\frac{Gh(L/G)}{N}$.

We develop an achievable scheme and a matching converse for this problem, and thus characterize its capacity in two scenarios: the zero-error-rate and the $\epsilon$-error-rate.

Index terms—DNA sequencing, genome-wide association studies, threshold effect.

1 Introduction

DNA sequencing is a modern technology that allows the researchers to access the genomic information of a vast number of individuals. The genome is a high dimensional mathematical object which encodes most of the biological functions of an individual. Finding the relations between the elements of the genome and the individuals’ characteristics is a challenge which requires huge amount of data. Fortunately, DNA sequencing technologies are growing so rapidly that the cost of generating massive genomic datasets is affordable for many research institutes.

In the upstream analysis of DNA sequencing datasets, the target is to recover an individual’s genome from a set of reads produced by a sequencer. The information theoretic aspects of this problem are addressed in [2], where the fundamental limits of reconstructing the genome are characterized. For further studying the problem, please see in [3,5].

In the downstream analysis, after reconstructing the genome, the main challenge is to learn the connections between the genomes and the real world observable characteristics or phenotypes. This problem is known as Genome-Wide Association Studies (GWAS), where given the genomes sequences of a population of individuals and their observed phenotypes, the objective is to learn the sites in the genome that cause or relate to the observed characteristics. In other word, in a genome of length $G$, only a subsequence of length $L$ called causal subsequence is correlated with the observed phenotype.

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Being a fundamental problem in biology and medicine, GWAS has been studied extensively and novel biological results have been discovered (see for instance [6–12]). We note that an important application of GWAS is when the observed phenotype is related to a disease. For instance, there is a number of papers studying the causal factors of diabetes (type I [8] and type II [9]) as well as various types of cancers [10], for example the breast cancer [11] and the prostate cancer [12].

Many algorithms have been proposed to solve the GWAS problem (see for instance [13]). Despite all of these progresses, addressing the problem from an abstract level where reliability in inference is the main objective is missing. We aim at filling this gap by providing the first fundamental limits on this problem. In particular, we study the GWAS problem from an information theoretic perspective.

In this paper an abstract probabilistic model is proposed where it is assumed that a dataset of $N$ individuals’ genomes and their corresponding phenotypes is given. See Figure 1 which shows the proposed model of this paper for studying the problem of learning the causal subsequence. The main properties of this model are as follows.

1. The genomic information of each individual is represented by a sequence of length $G$. This sequence is denoted by $x$ in the figure.
2. The observed phenotype takes two states, which are denoted by 0 and 1.
3. The observed phenotype is related to a specific subsequence of length $L$ of the genome sequence, which is denoted by $x_s$. Here $s$ is the (latent) causal subsequence.
4. The sequence $x_s$ denotes the genomic locations which are correlated to the observed phenotype. The (deterministic) function $f(.)$ maps the genomic information to the label set $\{0, 1\}$. The phenotype is also related to the other effects, such as environmental effects, which are modeled by an additive noise.

To model more closely real-world phenomenon, we note that the phenotypes can come from two different sources: genome and environment. For the modeling of the environmental effects, we assume that the mapping of the genomes to the phenotypes is stochastic, i.e., a susceptible individual based on her genome may show the phenotype with some probability related to her environment. Here we treat these features as an additive noise. Although this assumption may be not realistic in cases that the environmental and genomic effects are dependent, this simplification allows us to analyze the problem in an efficient way and to derive non-trivial results.

A natural way to model the GWAS problem is to consider (latent) patterns from a specific (latent) subsequence of the genome (i.e., the causal subsequence) that cause the observed phenotype. In this paper, the proposed model uses a deterministic function $f(.)$ to take the (latent) patterns into consideration. This assumption allows us to use the results in the theory of machine learning for the analysis of the problem. In particular, we use some bounds based on the VC dimension of the class of functions $f(.)$ to prove the results.

This paper revolves around answering the following question. What is the required sample complexity $N$ that implies the reliable learning of the causal subsequence? Our main contribution is that in a biological plausible model, we characterize the fundamental limits of learning the causal subsequence exactly. We define the rate of GWAS as $\frac{Gh(L/G)}{N}$, where $h(.)$ is the binary entropy function. This definition, as we will see later, is the natural scaling law of the parameters of the problem that allows to define the capacity. Note that we are interested in maximizing the rate for the GWAS problem. A rate is said to be achievable if it is possible to learn the causal subsequence reliably enough, as $N, G$ and $L \to \infty$. The capacity is defined as the supremum of all achievable rates.

1In this paper, we assume that the dataset is drawn from one population, i.e., the population stratification is assumed to be done before. This means that the dataset is homogeneous.

2Vapnik-Chervonenkis dimension.
We define two notions of the zero-error-rate and the $\epsilon$–error-rate estimation of the causal subsequence. In the $\epsilon$–error-rate estimation, we are interested in learning the causal subsequence with an error-rate of at most $\epsilon$, while in the zero-error-rate estimation, no positive error-rate is acceptable. In the zero-error-rate estimation, we fully characterize the capacity region. The capacity is proven to be a finite positive number, which shows that the parameters scaling is correct. In the $\epsilon$–error-rate regime, we show that for small enough $\epsilon$, the capacity is the same as the zero-error-rate case. This shows that, eventually, the problems of estimation of the causal subsequence, with the zero-error-rate and with the $\epsilon$–error-rate are equivalent in the asymptotic regimes.

The rest of the paper is organized as follows. In Section 2, we define the problem in a mathematical model and define the capacity region. In Section 3, we present the main results of the paper. The proofs are in Sections 4 and 5. Finally, Section 6 concludes the paper.

2 Problem Formulation

2.1 Notation

In this paper, random variables are represented by capital letters, such as $X$, and their realizations are represented by lower case letters, such as $x$. But as an exception, we use the capital letters $N$, $G$ and $L$ to denote the problem’s parameters, which are non-random. For a (discrete) random variable $X$, $p_X$ denotes its probability mass function (pmf). Random pmfs are also denoted by capital letters, like $P_X$. We denote the sequences by bold letters, like $\mathbf{x}$, and the capital bold letters represent random sequences, like $\mathbf{X}$. For any positive integer $G$, let $[G] := \{1, 2, \ldots, G\}$. The $\ell_p$ norm of a vector $\mathbf{w} \in \mathbb{R}^n$ for each $p \geq 1$ is defined as

$$\|\mathbf{w}\|_p := \left(\sum_{i=1}^n |w_i|^p\right)^{1/p}. \quad (1)$$

For a sequence of length $G$, like $\mathbf{x} = x_1x_2 \ldots x_G$ and a sequence of length $L$ with entries in $[G]$, like $\mathbf{s} = s_1s_2 \ldots s_L \in [G]^L$, we define $\mathbf{x}_s := x_{s_1}x_{s_2} \ldots x_{s_L}$ as a subsequence of $\mathbf{x}$. Also we denote the length of a sequence $\mathbf{x}$ by $\text{length}(\mathbf{x})$. In this paper, all the logarithms are in the base two and are denoted by $\log(\cdot)$. For any $p \in [0, 1]$, the binary entropy function $h : [0, 1] \to [0, 1]$ is defined as

$$h(p) := p \log\left(\frac{1}{p}\right) + (1-p) \log\left(\frac{1}{1-p}\right). \quad (2)$$
The mutual information of two discrete random variables $X$ and $Y$ is denoted by $I(X;Y)$. The distance of two sequences $s = s_1s_2 \ldots s_L$ and $t = t_1t_2 \ldots t_L$, is defined as

$$\text{dist}(s,t) := \left|\{s_1,s_2, \ldots, s_L\} \triangle \{t_1,t_2, \ldots, t_L\}\right|,$$

where $\triangle$ means the symmetric difference of sets. The set of all strictly increasing sequences of length $L$ with entries in $[G]$ is denoted by $S_{L,G}$. Given a finite set $\mathcal{X}$, we define

$$\mathcal{F}_{L,m} := \\left\{ f: \mathcal{X}^L \to \{0,1\} : \left| f^{-1}(1) \right| = m \right\}. \tag{4}$$

2.2 System Model

We are interested in associating a specific phenotype with the genotype of a population of $N$ individuals. In our problem, each individual’s genotype can be represented by a sequence of length $G$ with elements from a finite set $\mathcal{X}$. Moreover, the phenotype of each individual can take only two states, which can be represented by $\{0,1\}$. There is a stochastic map $\mathcal{F}: y_n = \mathcal{F}(x_n)$, which associates the genotype of the $n^{th}$ individual, denoted by $x_n \in \mathcal{X}^G$, to its phenotype $y_n \in \{0,1\}$. Figure 1 represents the set of biologically plausible functions that we are interested in. In particular, for generating the phenotype $y_n$, first a subsequence of length $L$ of $x_n$, represented by $x_{n,s} = x_{n,s_1}x_{n,s_2} \ldots x_{n,s_L}$ is chosen. Then, $x_{n,s}$ passes through a deterministic binary-valued function $f(.)$ and the result is $f(x_{n,s}) \in \{0,1\}$. Finally, $f(x_{n,s})$ meets an additive noise and makes the label $y_n$. More precisely, $y_n = f(x_{n,s}) \oplus Z_n$, where $Z_n$ is a Bernoulli random variable with parameter $\alpha$. We assume that the additive noises are independent for different individuals and they are also independent from the sequences of the individuals. The existence of this additive noise in the problem setup is due to the effect of the other factors in the observed phenotype, such as environment. Note that this model is robust. In one extreme, the observed phenotype is very correlated with the genome ($\alpha \approx 0$). In the other extreme, the labels are approximately independent from the genome ($\alpha \approx 1/2$). Note that $\alpha \in (0,1/2)$ is given in the problem.

In our model, the sequence $s$ and the deterministic function $f(.)$ are unknown but they are same for all $N$ individuals. It is assumed that the parameter $L$ is given and also $L/G \in (0,1/2)$. We also assume that the deterministic function $f(.)$ is chosen uniformly and randomly from $\mathcal{F}_{L,m}$, for a given positive integer $m$. Note that the parameter $m$ denotes the number of causal factors of the target phenotype. In the machine learning literature, the parameter $m$ is also related to the Vapnik-Chervonenkis dimension (VC dimension) of the class of functions $f(.)$ in our model. The sequence $s$ is selected randomly and uniformly from the set of all strictly increasing sequences of length $L$ with the entries belong to $[G]$, which is denoted by $S_{L,G}$. The entries of the sequence $s$ represent the sites in the genome that affect the observed labels. The dataset of $N$ individuals sequences is assumed to be sampled uniformly and independently from the set $\mathcal{X}^G$.

We define the parameter $\beta := P(Y_n = 1)$ in the proposed data generation model. It is assumed that $\beta$ is known. Note that $\beta \in (0,1)$. In this paper, our objective is to estimate $s$, given $N$ sampled sequences $\{x_n\}_{n \in [N]}$ and their corresponding observed labels $\{y_n\}_{n \in [N]}$. In the following, we formally define the GWAS algorithms.

**Definition 1.** Algorithm $A_{(G,L,N,\alpha,\beta,m)}$ is a mapping from the set of all possible input datasets, $(\mathcal{X}^G)^N \times \{0,1\}^N$, to the set $S_{L,G}$. When there is no ambiguity, we denote an algorithm by $A_G$ or sometimes by $A$. For a dataset $\{(x_n)_{n \in [N]}, \{y_n\}_{n \in [N]}\}$, $\hat{s} = A(\{x_n\}_{n \in [N]}, \{y_n\}_{n \in [N]})$ denotes the output of the algorithm.

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3 We note that because there is no information about $s$ and $f(.)$ and they are latent in the model, we assume that the prior distribution of them is uniform. It is also worth mentioning that the uniform sampling of $s$ is only needed for the converse proofs. The achievability proofs hold for any prior distribution on the set $S_{L,G}$.

4 Note that $\beta$ is a constant that only depends on $m, L, \alpha$ and $|\mathcal{X}|$. 
Next we formally define the error event and also the probability of error for the algorithms.

**Definition 2.** For a positive \( \epsilon \) and an algorithm \( A_{(G,L,N,\alpha,\beta,m)} \), the error event \( \mathcal{E}_{A,\epsilon} \) is defined as \( \mathcal{E}_{A,\epsilon} := \{ \frac{\text{dist}(\hat{s}, s)}{L} > \epsilon \} \), where \( \hat{s} \) is the output of the algorithm. Also the worst-case probability of error of an algorithm \( A \) is defined as

\[
P^{\text{WC}}_{\epsilon}(A) := \max_{s \in \mathcal{S}_{L,G}} \mathbb{P}(\mathcal{E}_{A,\epsilon}|S = s).
\]

The average probability of error is also defined as \( P^{\text{AVG}}_{\epsilon}(A) := \mathbb{P}(\mathcal{E}_{A,\epsilon}) \).

The parameter \( \epsilon \) is a threshold for the normalized distance between \( s \) and its estimation \( \hat{s} \). Notice that for any algorithm \( A \), \( P^{\text{AVG}}_{\epsilon}(A) \leq P^{\text{WC}}_{\epsilon}(A) \). Also by the definition of the error event, it is obvious that if \( \epsilon_1 \geq \epsilon_2 \) then \( \mathcal{E}_{A,\epsilon_1} \subseteq \mathcal{E}_{A,\epsilon_2} \) and thus \( P^{\text{WC}}_{\epsilon_1}(A) \leq P^{\text{WC}}_{\epsilon_2}(A) \) and \( P^{\text{AVG}}_{\epsilon_1}(A) \leq P^{\text{AVG}}_{\epsilon_2}(A) \).

In this paper, we want to characterize the fundamental limits of the GWAS problem, i.e., the region for the parameters of the problem that the reliable estimation of \( s \) is possible. For this purpose, we derive the fundamental limits in two scenarios. First we study the problem in the case that we want to estimate \( s \) with zero-error-rate, which will be defined formally later. Second, we study the problem of approximating \( s \), where a positive error-rate of \( \epsilon \) is acceptable. In the following definitions, first we define the achievable rates and then we define the capacity region of the problem in two cases.

**Definition 3.** The rate of an algorithm \( A_{(G,L,N,\alpha,\beta,m)} \) is defined as \( R_A := \frac{Gh(L/G)}{N} \), where \( h(.) \) is the binary entropy function.

**Definition 4.** For any positive \( \epsilon \), a positive real \( R \) is said to be \( \epsilon \)-achievable, iff there is a sequence of algorithms \( \{ A_{(G_i,L_i,N_i,\alpha,\beta,m_i)} \}_{i \in \mathbb{F}} \) with rate \( R \), where \( m = o(N^{1/F}) \) such that \( P^{\text{WC}}_{\epsilon}(A_{G_i}) \to 0 \) as \( i \to \infty \).

**Definition 5.** A positive real \( R \) is said to be achievable, iff for any positive \( \epsilon \) is \( \epsilon \)-achievable.

Now we are ready to define the capacity region of the problem.

**Definition 6.** The zero-error-rate capacity is defined as the supremum of all achievable rates and is denoted by \( C(\alpha, \beta) \). Also for any positive \( \epsilon \), the \( \epsilon \)-capacity is defined as the supremum of all \( \epsilon \)-achievable rates and is denoted by \( C_\epsilon(\alpha, \beta) \).

**Remark 1.** Note that the capacity is the inverse of the minimum number of required sampled data, normalized by \( Gh(L/G) \), such that the reliable estimation of \( s \) is asymptotically possible. We notice that in the definition of the zero-error-rate capacity, any positive error-rate must be removed asymptotically, while in the \( \epsilon \)-capacity, an error-rate of at most \( \epsilon \) is acceptable. Also the assumption \( m = o(N) \) means that the size of the given dataset \( N \) is very greater than the number of causal factors. The reliable learning is impossible, when the size of the dataset is in the same order with the number of causal factors.

**Remark 2.** Due to the definitions of the capacities, we have

\[
C(\alpha, \beta) \leq \inf_{\epsilon > 0} C_\epsilon(\alpha, \beta) \leq C_{\epsilon_1}(\alpha, \beta) \leq C_{\epsilon_2}(\alpha, \beta),
\]

for any real positive numbers \( \epsilon_1, \epsilon_2 \), such that \( \epsilon_1 \leq \epsilon_2 \).

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5Assume that \( G_i, N_i \) and \( L_i \) are strictly increasing functions of \( i \).

6By \( m = o(N) \), we mean \( m_i/N_i \to 0 \) as \( i \to \infty \).
3 Main Results

In this section, we state the main results of this paper. In the following theorem, we characterize the capacity $C(\alpha, \beta)$.

**Theorem 1.** The zero-error-rate capacity $C(\alpha, \beta)$ is

$$C(\alpha, \beta) = h(\beta) - h(\alpha),$$  \hspace{1cm} (7)

where $h(.)$ is the binary entropy function.

**Remark 3.** Theorem 1 characterizes the capacity of the zero-error-rate estimation of the causal subsequence. This shows that we have a threshold effect at $Gh(L/G)/N$, in the asymptotic regimes. Note that the capacity is strictly positive because $\beta \in (\alpha, 1 - \alpha)$.

**Remark 4.** For the achievability, we examine all of the subsequences of length $L$ of genome and choose the one for which two binary vectors $(f(x_n, \hat{s}))_{n \in [N]}$ and $(y_n)_{n \in [N]}$ are jointly typical for some $f \in F_{L,m}$. Note that unlike the channel coding, there is no codebook in this setup and the sequences are produced by nature. This changes drastically the proof techniques. However, we prove that the probability of error in the proposed scheme tends to zero, using some approximation methods ignoring the dependency among some events and bounding the effect of this assumption.

**Remark 5.** For the converse, we cannot directly use Fano’s inequality due to the definition of the error. Instead, we develop some inequalities similar to it. The need for this new bound is due to the fact that in our case, if we have an approximation of the causal subsequence with an error rate of at most $\epsilon$, then we can not determine it exactly.

We are also interested in characterizing the minimum number of required samples to find an approximation for the causal subsequence, rather than zero-error-rate learning of it. In the following theorem, we state the result for the $\epsilon$-error-rate capacity.

**Theorem 2.** There is a positive $\epsilon_0 \in (0, 1/2)$, such that for any $\epsilon \in (0, \epsilon_0)$ we have

$$C_\epsilon(\alpha, \beta) = h(\beta) - h(\alpha).$$  \hspace{1cm} (8)

**Remark 6.** It may be surprising that the $\epsilon-$capacity is the same as the zero-error-rate capacity. This shows that there is no difference between the approximation of the causal subsequence and the zero-error-rate learning of it in the asymptotic regimes, from the perspective of the required sample complexity.

**Remark 7.** To prove Theorem 2 we develop a complementary procedure to convert any algorithm that approximates the causal subsequence, according to an error rate of at most $\epsilon$, to another algorithm that learns it with the zero-error-rate condition. Hence using Theorem 1 we conclude the desired result.

The proofs of the main results of this paper can be found in the next two sections.

4 Proof of Theorem 1

4.1 Achievability

Let $R < h(\beta) - h(\alpha)$ be a positive real number. We aim to prove that $R$ is achievable. In particular, for any positive $\epsilon$, we want to show that $R$ is $\epsilon-$achievable. For this purpose, we introduce an algorithm achieving this rate. The algorithm is a jointly typical decoder. First let us have some definitions.
For any positive $\tau$, let $T^N_\tau$ denotes the set of all jointly typical binary sequences of length $N$, with respect to the pmf $p(F(X),Y)$, i.e.,

$$T^N_\tau := \left\{ (u,v) \in \{0,1\}^N \times \{0,1\}^N : \left| - \frac{1}{N} \log \left( \prod_{n=1}^{N} p_F(X_n)(u_n) \right) - H(F(X)) \right| < \tau, \quad \left| - \frac{1}{N} \log \left( \prod_{n=1}^{N} p_Y(v_n) \right) - H(Y) \right| < \tau, \right\}.$$

In other words, $T^N_\tau$ is the set containing all of the pairs of binary sequences of length $N$ with empirical entropies $\tau$–close to the true entropies with respect to the pmf $p(F(X),Y)$.

The proposed algorithm is as follows.

4.1.1 Algorithm

For a given dataset $(\{x_n\}_{n \in [N]}, \{y_n\}_{n \in [N]})$, the algorithm chooses $\hat{s} \in S_{L,G}$ with the following property: there is a function $f(.) \in \mathcal{F}_{L,m}$, such that the binary vectors $(f(x_n))_{n \in [N]}$ and $(y_n)_{n \in [N]}$ are jointly typical, i.e., $(f(x_n))_{n \in [N]}, (y_n)_{n \in [N]} \in T^N_\tau$. If there are more than one such $\hat{s}$ with this property, the algorithm chooses one of them at random. If there is no such $\hat{s}$, the algorithm chooses an element of $S_{L,G}$ randomly as the output. We denote the proposed algorithm by $A_G$.

4.1.2 Analysis of the algorithm

For any fixed positive $\epsilon$, we aim to prove that any $R < h(\beta) - h(\alpha)$ is $\epsilon$–achievable using the proposed algorithm. In particular, we are interested to show that $P_W^{\text{WC}}(A_G) \to 0$ as $N, G, L \to \infty$. In other words, for any $s \in S_{L,G}$, we want to prove that the probability $\mathbb{P}(\frac{\text{dist}(\hat{s},s)}{L} > \epsilon | s = s)$ tends to zero in the asymptotic regimes.

Fix an arbitrary $s \in S_{L,G}$. Consider two events $\mathcal{E}_1$ and $\mathcal{E}_2$ as follows. $\mathcal{E}_1$ is the event that the causal subsequence $s$ has not the acceptance properties of the algorithm, i.e.,

$$\mathcal{E}_1 := \left\{ \left( (F(X_n),s) \right)_{n \in [N]}, (Y_n)_{n \in [N]} \notin T^N_\tau | s = s \right\}.$$

Also $\mathcal{E}_2$ is the event that there is a $t \in S_{L,G}$ such that $t$ has the acceptance properties of the algorithm and $\text{dist}(s,t) > L\epsilon$. To be more precise, let us define

$$\mathcal{E}_{t,g} := \left\{ \left( (g(X_n,t))_{n \in [N]}, (Y_n)_{n \in [N]} \right) \in T^N_\tau | s = s \right\},$$

and let

$$\mathcal{E}_2 := \bigcup_{\substack{t \in S_{L,G} \\text{dist}(s,t) > L\epsilon}} \mathcal{E}_{t,g}.$$
Lemma 1. [15] Theorem 3.5] (Sauer’s lemma) For any positive integers \( N, m \) and any \( t \in S_{L,G} \),

\[
\max_{\forall n \in \{0, 1\}^N, x_n \in \mathcal{X}^d} \left| \left\{ (g(x_n,t))_{n \in [N]} \in \{0, 1\}^N : g(.) \in \mathcal{F}_{L,m} \right\} \right| \leq \sum_{i=0}^{d} \binom{N}{i},
\]

(15)

where \( d \) is the VC dimension of the class of functions \( \mathcal{F}_{L,m} \).

Corollary 1. For any positive integers \( N \geq m \) and any \( t \in S_{L,G} \), we have

\[
\max_{\forall n \in \{0, 1\}^N, x_n \in \mathcal{X}^d} \left| \left\{ (g(x_n,t))_{n \in [N]} \in \{0, 1\}^N : g(.) \in \mathcal{F}_{L,m} \right\} \right| \leq \left( \frac{eN}{m} \right)^m.
\]

(16)

Proof. First we note that the VC dimension of the class of functions \( \mathcal{F}_{L,m} \) can be upper bounded by \( m^7 \). Hence using Lemma 1 and [15] Corollary 3.3 we can establish the desired result. \( \square \)

Corollary 1 has an important role in our proofs. It establishes a connection between the parameter \( m \) (which is related to the VC dimension of the class of functions considered), and the number of possible observable patterns as the output of \( N \) instances of a function. This bound is very essential for the asymptotic analysis of the algorithm \( A_G \) by the union bound. Note that the condition of Corollary 1 is satisfied asymptotically, since we have assumed that \( m = o(N) \).

Theorem 3. For any positive \( \zeta \) and any \( s \in S_{L,G} \), the following proposition holds with probability \( 1 - o(1) \).

For any \( t \in S_{L,G} \) and any function \( g(.) \in \mathcal{F}_{L,m} \), such that \( \text{dist}(s,t) > L\epsilon \), the probability that \( t \) has the acceptance conditions in the proposed algorithm using the function \( g(.) \) (the probability of the event \( \mathcal{E}_{t,g} \)) is upper bounded by \( 2^{-N(h(\beta)-h(\alpha)-\zeta)} \).

Proof. See appendix A. \( \square \)

Using Corollary 1 for the analysis of the algorithm \( A_G \), it just suffices to check at most \( (eN/m)^m \) functions. Let us denote the event in the statement of Theorem 3 which holds with probability \( 1 - o(1) \), by \( \mathcal{E}_3 \). Now we write

\[
\mathbb{P}(\mathcal{E}_2) = \mathbb{P}(\mathcal{E}_2|\mathcal{E}_3)\mathbb{P}(\mathcal{E}_3) + \mathbb{P}(\mathcal{E}_2|\overline{\mathcal{E}_3})\mathbb{P}(\overline{\mathcal{E}_3})
\]

(17)

\[
\leq \mathbb{P}(\mathcal{E}_2) + \mathbb{P}(\mathcal{E}_2|\overline{\mathcal{E}_3})
\]

(18)

\[
\leq o(1) + \mathbb{P}\left( \bigcup_{t \in S_{L,G}} \mathcal{E}_{t,g} \bigg| \mathcal{E}_3 \right)
\]

(19)

\[
\leq o(1) + \sum_{t \in S_{L,G}, \text{dist}(s,t)>L\epsilon} \left( \frac{eN}{m} \right)^m \times 2^{-N(h(\beta)-h(\alpha)-\zeta)}
\]

(20)

\[
\leq o(1) + \binom{G}{L} \times 2^{m\log\left( \frac{eN}{m} \right) - N(h(\beta)-h(\alpha)-\zeta)},
\]

(21)

where (a) follows by Corollary 1, Theorem 3 and also the union bound. Using [14] Chapter 11, p. 353, we have \( \binom{G}{L} \leq 2^{G h(L/G)} \). Hence

\[
\mathbb{P}(\mathcal{E}_2) \leq o(1) + 2^{G h(L/G) + m \log\left( \frac{eN}{m} \right) - N(h(\beta)-h(\alpha)-\zeta)}
\]

(22)

\[
= o(1) + 2^{N \left( R + \frac{N}{R} \log\left( \frac{eN}{m} \right) - (h(\beta)-h(\alpha)-\zeta) \right)}.
\]

(23)

\(^7\)Actually it can be shown that \( d = \min(m, |\mathcal{X}|^L - m) \).
We note that \( \frac{m}{N} \log \left( \frac{eN}{m} \right) \to 0 \), since \( m = o(N) \). Hence \( \mathbb{P}(\mathcal{E}_2) \) vanishes asymptotically, if

\[
R - h(\beta) - h(\alpha) - \zeta < 0. 
\]

(24)

This shows that by choosing small enough \( \zeta \), any \( R < h(\beta) - h(\alpha) \) is \( \epsilon \)-achievable. This holds for any positive \( \epsilon \) and thus completes the proof.

4.2 Converse

In this section, we prove the converse part of Theorem 1. First we need a lemma.

**Lemma 2.** For any positive \( \epsilon \in (0, 1/2) \), let \( R \) be an \( \epsilon \)-achievable rate. Then, we have

\[
R \leq \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)},
\]

(25)

where \( \delta(.) \) is a function that is defined as \( \delta(\epsilon) := \sup_{x \in (0,1/2)} \frac{h(2\epsilon x)}{h(x)} \).

**Proof.** See appendix B.

It can be shown that \( \delta(\epsilon) = h(\epsilon) \) for any \( \epsilon \in (0, 1/2) \). This follows from the following lemma.

**Lemma 3.** For any \( x, y \in [0, 1/2] \) we have

\[
h(2xy) \leq h(x)h(y),
\]

(26)

where \( h(.) \) is the binary entropy function.

**Proof.** See appendix C.

Using Lemma 3 we conclude that

\[
h(\epsilon) = \left. \frac{h(2\epsilon x)}{h(x)} \right|_{x=1/2} \leq \sup_{x \in (0,1/2)} \frac{h(2\epsilon x)}{h(x)} \leq \sup_{x \in (0,1/2)} h(\epsilon) = h(\epsilon),
\]

(27)

which shows that \( \delta(\epsilon) = h(\epsilon) \).

Now consider an achievable rate \( R \). This implies that for any positive \( \epsilon \), \( R \) is \( \epsilon \)-achievable. Using Lemma 2 we conclude that \( R \leq \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)} \), for any positive \( \epsilon \). Hence,

\[
R \leq \inf_{\epsilon \in (0,1/2)} \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)} = h(\beta) - h(\alpha),
\]

(28)

and this completes the proof.

5 Proof of Theorem 2

The achievability proof of Theorem 2 directly follows from Theorem 1. Hence we need to prove the converse part of the theorem.

Let that \( R \) be an \( \epsilon \)-achievable rate. We prove that \( R \leq h(\beta) - h(\alpha) \). First we note that using Lemma 2, \( R \leq \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)} \). The function \( \delta(.) \) is defined as \( \delta(\epsilon) := \sup_{x \in (0,1/2)} \frac{h(2\epsilon x)}{h(x)} \) and it is proved that \( \delta(\epsilon) = h(\epsilon) \).

Now consider a sequence of algorithms \( \{\hat{A}_i\} \), with vanishing probability of error, i.e., \( \mathbb{P}_{\epsilon}^{wc}(\hat{A}_i) \to 0 \). We define a complementary procedure as follows. Assume that the output of the algorithm \( \hat{A}_i \) to a given
dataset is $\tilde{s}$. Let $B_{\tilde{s},\epsilon}$ be a ball with radius $L\epsilon$ in $S_{L,G}$ around $\tilde{s}$, with respect to the distance measure dist(.,.). More precisely, we define

$$B_{\tilde{s},\epsilon} := \left\{ t \in S_{L,G} : \text{dist}(\tilde{s}, t) \leq L\epsilon \right\}. \quad (29)$$

Apply the proposed algorithm in the achievability proof of Theorem 1 to find some $\tilde{s} \in B_{\tilde{s},\epsilon}$ as the estimation of $s$. More precisely, we define

$$\left( (f(x_n, \tilde{s}))_{n \in [N]}, (y_n)_{n \in [N]} \right) \in T^N, \quad (30)$$

for some $f(.,) \in F_{L,m}$. If there is not such $\tilde{s}$, choose one of the elements of $B_{\tilde{s},\epsilon}$ randomly. If there is more than one such element, choose one of them randomly.

We prove that the output of this complementary algorithm is a zero-error-rate estimation of $s$, with high probability. In particular, for any $\epsilon' \in (0, \epsilon)$, we show that the output of the complementary procedure has at most $\epsilon'$—error-rate, with high probability in the asymptotic regimes. More precisely, we prove that $P(\text{dist}(\tilde{s}, s) > \epsilon' | S = s) \to 0$ for any positive $\epsilon' \in (0, \epsilon)$.

Fix a positive $\epsilon' \in (0, \epsilon)$. Define two events $E_1$ and $E_2$ similar to the achievability proof of Theorem 1. More precisely, we define

$$E_1 := \left\{ (F(x_n,s))_{n \in [N]}, (y_n)_{n \in [N]} \right\} \notin T^N \bigg| S = s \bigg\} \cup \left\{ S \notin B_{\tilde{s},\epsilon} \bigg| S = s \right\}. \quad (31)$$

In addition, we define

$$E_{t,g} := \left\{ (g(x_n,t))_{n \in [N]}, (y_n)_{n \in [N]} \right\} \in T^N \bigg| S = s \bigg\} \cap \left\{ t \in B_{\tilde{s},\epsilon} \bigg| S = s \right\}, \quad (32)$$

and

$$E_2 := \bigcup_{t \in S_{L,G}} E_{t,g}. \quad (33)$$

Note that two events $E_1$ and $E_2$ are defined with respect to the parameter $\epsilon'$. Also by the assumption, $\text{dist}(\tilde{s}, s) \leq L\epsilon$, with high probability. In other words, $P(E_{11}) \to 0$. By the law of large numbers, $P(E_{11}) \to 0$. Using the union of events bound, we conclude that $P(E_1)$ vanishes asymptotically.

Now we want to show that $P(E_2)$ tends to zero asymptotically. Similar to the analysis of the proposed algorithm in Theorem 1 using Corollary 1 and Theorem 3, we write

$$P(E_2) = P(E_2|E_3)P(E_3) + P(E_2|E_3)^2 \quad (34)$$

$$\leq P(E_3) + P(E_2|E_3) \quad (35)$$

$$\leq o(1) + P \left( \bigcup_{t \in S_{L,G}} E_{t,g} \bigg| E_3 \right) \quad (36)$$

$$\leq o(1) + \max_{\tilde{s} \in S_{L,G}} [B_{\tilde{s},\epsilon}] \times \left( \frac{eN}{m} \right)^m \times 2^{-N(h(\beta)-h(\alpha)-\zeta)}. \quad (37)$$
Now observe that

\[
\log(|B_{\hat{s}}, \ell|) \leq \log \left( \sum_{\ell=1}^{[L\epsilon]} \left| \left\{ t : S_L, G : \text{dist}(\hat{s}, t) = \ell \right\} \right| \right)
\]

(38)

\[
\leq \log \left( \sum_{\ell=1}^{[L\epsilon]} \left( \frac{L}{\ell} \right) \left( G - L \right) \right)
\]

(39)

\[
\leq \log \left( L \left( \frac{L}{[L\epsilon]} \right) \left( G - L \right) \right)
\]

(40)

\[
(a) \leq \log (L\epsilon) + 2^L h(\epsilon) \times 2^{(G-L)h(\frac{\epsilon L}{G-L})})
\]

(41)

\[
= \log (L\epsilon) + Lh(\epsilon) + (G - L)h(\frac{L\epsilon}{G - L})
\]

(42)

\[
(b) \leq \log (L\epsilon) + Gh(\frac{2\epsilon L}{G}),
\]

(43)

where (a) follows from [14, Chapter 11, p. 353] and (b) follows from the concavity of the function $h(.)$. Therefore, using [37] and [43], we write

\[
\mathbb{P}(\mathcal{E}_2) \leq o(1) + \max_{\hat{s} \in S_{L, G}} |B_{\hat{s}, \epsilon}| \times 2^m \log \left( \frac{mN}{2m} \right) - N(h(\beta) - h(\alpha) - \zeta)
\]

(44)

\[
\leq o(1) + L\epsilon \times 2^{Gh(\frac{2\epsilon L}{G}) + m \log \left( \frac{mN}{2m} \right) - N(h(\beta) - h(\alpha) - \zeta)}
\]

(45)

\[
= o(1) + L\epsilon \times 2^N \left( R \times \frac{h(\beta) - h(\alpha)}{h(\beta) - h(\alpha)} + \frac{mN}{2m} \log \left( \frac{mN}{2m} \right) - (h(\beta) - h(\alpha) - \zeta) \right)
\]

(46)

\[
\leq o(1) + L\epsilon \times 2^N \left( R \times \delta(\epsilon) + \frac{mN}{2m} \log \left( \frac{mN}{2m} \right) - (h(\beta) - h(\alpha) - \zeta) \right),
\]

(47)

where (a) follows from the definition of the function $\delta(.)$. Now since $\frac{mN}{2m} \log \left( \frac{mN}{2m} \right) \to 0$, we conclude that $\mathbb{P}(\mathcal{E}_2)$ vanishes asymptotically\textsuperscript{8} if

\[
R \leq \frac{h(\beta) - h(\alpha) - \zeta}{\delta(\epsilon)},
\]

(48)

for some positive $\zeta$. Let us assume $\delta(\epsilon) < 1/2$. Using Lemma [2] we have

\[
R \leq \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)} < \frac{h(\beta) - h(\alpha) - \zeta}{\delta(\epsilon)},
\]

(49)

for small enough $\zeta$. Hence we conclude that if $R$ is $\epsilon$–achievable, then it is $\epsilon'$–achievable for any $\epsilon' \in (0, \epsilon)$. This means that $R$ is achievable. Hence, using Theorem [1] we conclude that $R \leq h(\beta) - h(\alpha)$ and this completes the proof. Note that based on the fact that $\delta(\epsilon) = h(\epsilon)$, there is a positive $\epsilon_0$ such that for any $\epsilon < \epsilon_0$, we have $\delta(\epsilon) < 1/2$. We are done.

**Remark 8.** Numerical calculation shows that $\epsilon_0 \approx 0.1$ works for the converse of Theorem [2]. However, we do not claim that this is the optimum threshold.

## 6 Conclusion

In this paper a biological data analysis problem known as Genome-Wide Association Study (GWAS) has been studied from an information theoretic view. In the proposed probabilistic model, we fully

\textsuperscript{8}The multiplicative factor $L\epsilon$ does not make any problem, noting that $\frac{\log(L)}{N} \to 0$ asymptotically. This is due to the fact that $N \gg m = \Theta(|X'|)$.
characterized the fundamental limits of learning the causal subsequence. It is shown that two problems of the $\epsilon$-error-rate and the zero-error-rate estimation of the causal subsequence are equivalent. For the future of this work, some extensions of the problem can be considered. The first one is to assume that the environmental effects are not like additive noises in labeling and to explore the capacity in a more general framework. Another extension is to consider the GWAS problem in the case that the labels or phenotypes are not binary-valued. Also modeling the genome sequence by a more realistic probabilistic model is of the future of this work.

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A Proof of Theorem 3

To prove Theorem 3, we need some preliminaries which are available in the following two subsections.

A.1 Preliminaries

In this subsection, we first review some definitions about the divergence measures on probability distributions, as well as their main properties.

**Definition 7.** Let \( f : \mathbb{R}^+ \to \mathbb{R} \) be a convex function, such that \( f(1) = 0 \) and \( f(t) \) is strictly convex at \( t = 1 \). Then, the \( f \)-divergence of any (finite) probability measures \( p_U \) and \( q_U \) on a finite set \( U \) is defined as

\[
D_f(p_U||q_U) = \sum_{u \in U} q_U(u) f\left(\frac{p_U(u)}{q_U(u)}\right).
\]

We notice that the \( f \)-divergences satisfy the data processing inequality.

**Theorem 4.** \([16]\) (Data processing inequality for \( f \)-divergences). For any (finite) probability measures \( p_X, q_X \) and any channel \( p_V|U \), the following inequality holds.

\[
D_f(p_U||q_U) \geq D_f(p_U;p_V|U||q_UP_V|U).
\]

Note that the function \( f(t) = \frac{1}{2}|1-t| \) satisfies the required conditions in Definition 7. It can be shown that in this case, the \( f \)-divergence reduces to the total variation distance of two probability measures.

In the following definition, we define the \( f \)-information between two arbitrary (discrete) random variables.

**Definition 8.** For any (discrete) random variables \( U \) and \( V \), we define

\[
I_f(U;V) := D_f(p_{U,V}||p_U p_V).
\]

Specifically, for the case of \( f(t) = \frac{1}{2}|1-t| \), we can write

\[
I_f(U;V) = \frac{1}{2}\|p_{U,V} - p_U p_V\|_1.
\]

**Lemma 4.** Consider three random variables \( U, V, W \), such that \( U - V - W \) forms a Markov chain. Then, for each \( f \)-divergence we have

\[
I_f(U;V) \geq I_f(U;W).
\]
Proof. First we define the following channel

$$q_{T,W|U,V} := p_{W|V} p_{T|U},$$

(55)

where $p_{T|U}$ is the identity channel, i.e., $T = U$ with probability one. Note that

$$I_f(U;V) = D_f(p_{U,V}||p_U p_V)$$

(56)

$$\geq D_f(p_{U,V} q_{T,W|U,W} || p_U p_V q_{T,W|U,V})$$

(57)

$$= D_f(p_{U,V} p_{T|U} p_{V|T|U} || p_U p_V p_{V|T|U})$$

(58)

$$= D_f(p_{T,W} || p_{T|W} p_{W|V})$$

(59)

$$= D_f(p_{T,W} || p_{T|W} p_{W|V})$$

(60)

$$= I_f(U;W),$$

(61)

which completes the proof. Note that (a) follows from Theorem 4 and (b) follows from the fact that $p_{W|U,V} = p_{W|V}$, which is due to the Markov property.

**Corollary 2.** Consider random variables $U, V, W, T$, such that $U - V - W - T$ forms a Markov chain. Then, we have

$$\|p_{U,T} - p_U p_T\|_1 \leq \|p_{V,W} - p_V p_W\|_1.$$  

(62)

Proof. Consider $f(t) = \frac{1}{2} |1 - t|$ and use Lemma 3 twice.

We need a result on the equivalency of $\ell_1$ and $\ell_\infty$ norms which is stated in the following lemma.

**Lemma 5.** For any $w \in \mathbb{R}^n$ we have

$$\|w\|_\infty \leq \|w\|_1 \leq n \|w\|_\infty \tag{63}$$

In what follows, we present some definitions about the dependency of (discrete) random variables.

**Definition 9.** For any (discrete) random variables $U, V$ and any $\mu \in [1, \infty)$, we write $U \mu \perp V$ iff $p_{U,V}(u,v) \leq \mu \times p_U(u)p_V(v)$ for each $u, v$.

Note that for any independent random variables $U, V$, we have $U \frac{1}{2} \perp V$. Also if we have $U \mu \perp V$, then we conclude $U \mu' \perp V$ for any $\mu' \geq \mu$.

The following lemma relates the above definition to the total variation distance.

**Lemma 6.** Assume that we have $\|p_{U,V} - p_U p_V\|_1 \leq \epsilon$ for some positive $\epsilon$. Then, for

$$\mu = 1 + \frac{\epsilon}{\min_u p_U(u) \times \min_v p_V(v)},$$

(64)

we have $U \mu \perp V$.

Proof. First we note that using Lemma 5 we have

$$\|p_{U,V} - p_U p_V\|_\infty \leq \|p_{U,V} - p_U p_V\|_1 \leq \epsilon.$$ 

(65)
Hence for any $u, v$ we have

\begin{align*}
  p_{U,V}(u,v) & \leq p_U(u)p_V(v) + \epsilon \\
  & = p_U(u)p_V(v)\left(1 + \frac{\epsilon}{p_U(u)p_V(v)}\right) \\
  & \leq p_U(u)p_V(v)\left(1 + \frac{\epsilon}{\min_u p_U(u) \times \min_v p_V(v)}\right) \\
  & = \mu \times p_U(u)p_V(v),
\end{align*}

which completes the proof.

We need the following lemma in some parts of proofs which are presented later.

**Lemma 7.** For any (discrete) random variables $U, V$ such that $V$ takes values in the set $\{0, 1\}$ we have

\[ \|p_{U,V} - p_Up_V\|_1 \leq 2 \times \max_u \left| p_{V|U}(1, u) - p_V(1) \right|. \]

**Proof.** Note that we have

\begin{align*}
  \|p_{U,V} - p_Up_V\|_1 &= \sum_{u,v} \left| p_{U,V}(u,v) - p_U(u)p_V(v) \right| \\
  &= \sum_{u,v} \left| p_U(u)p_{V|U}(v,u) - p_U(u)p_V(v) \right| \\
  &= \sum_{u,v} p_U(u) \left| p_{V|U}(v,u) - p_V(v) \right| \\
  &= \sum_u p_U(u) \left| p_{V|U}(1, u) - p_V(1) \right| + \sum_u p_U(u) \left| p_{V|U}(0, u) - p_V(0) \right| \\
  &= \sum_u p_U(u) \left| p_{V|U}(1, u) - p_V(1) \right| + \sum_u p_U(u) \left| (1 - p_{V|U}(1, u)) - (1 - p_V(1)) \right| \\
  &= 2 \times \sum_u p_U(u) \left| p_{V|U}(1, u) - p_V(1) \right| \\
  & \leq 2 \times \max_u \left| p_{V|U}(v,u) - p_V(v) \right| \times \sum_u p_U(u) \\
  &= 2 \times \max_u \left| p_{V|U}(1, u) - p_V(1) \right|. 
\end{align*}

Concentration inequalities play an important role in the proofs of this paper. Specifically, we use the Hoeffding’s inequality, which is described as follows.

**Lemma 8.** [15, Theorem D.1] (Hoeffding’s inequality) Let $U_i, i \in [n]$, be $n$ i.i.d. random variables taking values in $[a,b]$. Then, for any positive $\epsilon$, we have

\[ \Pr\left( \left| \frac{U - \mathbb{E}[U]}{n} \right| \geq \epsilon \right) \leq 2 \exp\left( -\frac{2\epsilon^2}{(b-a)^2} \right), \]

where $U = \sum_{i=1}^{n} U_i$.

In what follows, we propose a lemma about the approximation of probabilities.
Lemma 9. Consider $n$ random variables $U_i$, $i \in [n]$ which are distributed according a probability measure $p_{U_1:n}$, each over a finite set $U$. Also consider a discrete random variables $W$ that take values over a finite set $W$. Let $w^* := \arg\max_{w \in W} P(W = w)$. Consider $n$ random variables $V_i$, $i \in [n]$, each takes values over a finite set $V = U$, such that $p_{V_1:n} = p_{U_1:n}|W=w^*$. All in all, the probability low governing the above random variables factors as

$$p_{U_1:n,V_1:n,W} = p_{U_1:n}p_{V_1:n}p_{W|U_1:n} \tag{80}$$

In addition, consider an arbitrary deterministic function $\psi : U^n \to \{0, 1\}$, and define the events $E_1 := \{\psi(U_{1:n}) = 1\}$, and $E_2 := \{\psi(V_{1:n}) = 1\}$. We claim that the following inequality holds.

$$P(E_2) \leq |W| \times P(E_1). \tag{81}$$

Proof. We write

$$P(E_1) = E_{U_{1:n}}[\psi(U_{1:n})] \tag{82}$$

$$\overset{(a)}{=} E_{W} E_{U_{1:n}}[\psi(U_{1:n})|W] \tag{83}$$

$$\geq P(W = w^*) \times E_{U_{1:n}}[\psi(U_{1:n})|W = w^*] \tag{84}$$

$$= P(W = w^*) \times E[\psi(V_{1:n})] \tag{85}$$

$$\geq \frac{1}{|W|} \times E[\psi(V_{1:n})] \tag{86}$$

$$= \frac{1}{|W|} \times P(E_2), \tag{87}$$

where (a) follows from the law of iterated expectation and (b) follows from the definition of $w^*$.

Let us state the following lemma.

Lemma 10. For given positive integers $n, m$ such that $n \geq m$, define

$$Q_m := \left\{ (v_1, v_2, \ldots, v_n) \in \{0, 1\}^n : \sum_{i=1}^n v_i = m \right\}. \tag{88}$$

Consider $n$ binary random variables $V_i \in \{0, 1\}$, $i \in [n]$ which are distributed as

$$p_{V_1:n}(v_{1:n}) = \frac{1}{|Q_m|} \times 1_{\{v_{1:n} \in Q_m\}}. \tag{89}$$

Then, for any positive $\epsilon$ and any (non-empty) $T \subseteq [n]$, we have

$$P\left(\left| V - E[V] \right| \geq \epsilon \right) \leq 2(n + 1) \exp \left( -2|T|\epsilon^2 \right), \tag{90}$$

where $V = \sum_{i \in T} V_i$.

Proof. The proof is based on the combining the results of Lemma 8 and Lemma 9. Consider $n$ i.i.d. binary random variables $U_i \in \{0, 1\}$, $i \in [n]$, such that $p := P(U_i = 1) = m/n$. Let us define a random
variable \( W := \sum_{i \in [n]} U_i \). Note that \( W \) takes values from the set \( W = \{0, 1, \ldots, n\} \). Note that \( W \) is distributed according to a binomial distribution with parameters \( n, p \). Notice that

\[
W^* = \arg\max_{w \in \{0, 1, \ldots, n\}} P(W = w) = \arg\max_{w \in \{0, 1, \ldots, n\}} \binom{n}{w} \times p^w \times (1 - p)^{n-w}
\]

where (a) follows since \( m = np \) is a positive integer and so it is equal to the mode of \( W \).

Now observe that for any \( v_{1:n} \in \{0, 1\}^n \) we have

\[
p_{U_{1:n}|W=m}(v_{1:n}) = \frac{P(W = m|U_{1:n} = v_{1:n}) \times P(U_{1:n} = v_{1:n})}{P(W = m)} = \frac{\mathbb{1}\{v_{1:n} \in \mathcal{Q}_m\} \times p^m \times (1 - p)^{n-m}}{\binom{n}{m} \times p^m \times (1 - p)^{n-m}}
\]

where (a) follows from the fact that \( |\mathcal{Q}_m| = \binom{n}{m} \). Let us define a function \( \psi : \{0, 1\}^n \to \{0, 1\} \) as follows.

\[
\psi(x_1, x_2, \ldots, x_n) = \mathbb{1}\left\{ \left| \sum_{i \in T} x_i \right| - p \left| T \right| \geq \epsilon \right\}.
\]

Now observe that the random variables \( U_{1:n}, V_{1:n} \) and \( W \) and the function \( \psi(.) \) satisfy the required conditions of Lemma 9. Hence we conclude that

\[
P\left( \left| \frac{V - \mathbb{E}[V]}{|T|} \right| \geq \epsilon \right) \leq |W| \times P\left( \left| \frac{U - \mathbb{E}[U]}{|T|} \right| \geq \epsilon \right) \]

\[
\leq |W| \times 2 \exp\left( -2|T|\epsilon^2 \right)
\]

where (a) follows from Lemma \( \text{S} \) and (b) follows the fact that \( W = \{0, 1, \ldots, n\} \). We are done.

The following definitions are about the intersection of the subsequences.

**Definition 10.** For any \( s, t \in \mathcal{S}_{L,G} \), we define a sequence

\[
\text{int}(s, t) := w_1 w_2 \ldots w_k \in [G]^k
\]

such that

1. \( \{w_1, w_2, \ldots, w_k\} = \{s_\ell : \ell \in [L]\} \cap \{t_\ell : \ell \in [L]\} \),
2. \( w_1 < w_2 < \ldots < w_k \).

In what follows, we define a set containing the subsequences of a specific sequence with some properties.

**Definition 11.** For any \( s \in \mathcal{S}_{L,G} \), define

\[
\mathcal{I}_\epsilon(s) := \left\{ \text{int}(s, t) \left| t \in \mathcal{S}_{L,G}, \text{dist}(s, t) \geq L\epsilon \right. \right\}.
\]
Note that we have $|\mathcal{I}_s(s)| \leq 2^L$.

**Lemma 11.** For any $s, t \in \mathcal{S}_{L,G}$, the following statements are equivalent.

1. $\text{dist}(s, t) \geq L\epsilon$,
2. $\text{length}(\text{int}(s, t)) \leq L(1 - \epsilon/2)$.

**Proof.** Let $\mathcal{S} := \{s_1, s_2, \ldots, s_L\}$ and $\mathcal{T} := \{t_1, t_2, \ldots, t_L\}$. Note that

$$\text{dist}(s, t) \geq L\epsilon \iff |\mathcal{S} \cup \mathcal{T}| - |\mathcal{S} \cap \mathcal{T}| \geq L\epsilon \quad (104)$$

$$\iff |\mathcal{S}| + |\mathcal{T}| - 2|\mathcal{S} \cap \mathcal{T}| \geq L\epsilon \quad (105)$$

$$\iff 2L - 2|\mathcal{S} \cap \mathcal{T}| \geq L\epsilon \quad (106)$$

$$\iff |\mathcal{S} \cap \mathcal{T}| \leq L(1 - \epsilon/2) \quad (107)$$

$$\iff \text{length}(\text{int}(s, t)) \leq L(1 - \epsilon/2). \quad (108)$$

\[ \square \]

### A.2 Preliminaries for Theorem 3

In this subsection, we present some lemmas and definitions related to the proof of Theorem 3.

**Definition 12.** For any $g(.) \in \mathcal{F}_{L,m}$ and any $t \in \mathcal{S}_{L,G}$ define a random variable $J_{t,g} := g(X_t)$. Here $X$ is a random sequence distributed uniformly over $X^G$.

We note that the probability distribution of $J_{t,g}$ for any $g(.)$ and $t$ is like follows.

$$p_{J_{t,g}}(u) = \begin{cases} \gamma & u = 1 \\ 1 - \gamma & u = 0, \end{cases} \quad (109)$$

where $\gamma := m/|X|^L$ is a parameter. Also for any function $F(.)$ which is chosen randomly and uniformly from the set $\mathcal{F}_{L,m}$ and any sequence $S$ which is chosen randomly and uniformly from the set $\mathcal{S}_{L,G}$, we have the following identity.

$$p_{J_{t,g}} = p_{J_{S,g}} = p_{J_{t,F}} = p_{J_{S,F}}. \quad (110)$$

We note that throughout this section, we have fixed an arbitrary $s \in \mathcal{S}_{L,G}$ (see Theorem 3 again).

In the following lemma, we aim to show that with probability tending one, $J_{t,g}$ and $Y$ are (approximately) independent, if $\text{dist}(s, t) \geq L\epsilon$. In other words, we want to show that $J_{t,g} \overset{\mu}{\perp} Y$ for some $\mu \to 1$. Let us clarify this statement in the following lemma.

**Lemma 12.** For any $g(.) \in \mathcal{F}_{L,m}$, any $t \in \mathcal{S}_{L,G}$ and also any $\mu \in (1, \infty)$ define the following event

$$\mathcal{E}_{t,g}^\mu := \left\{ J_{t,g} \overset{\mu}{\perp} Y \right\} \quad (111)$$

Note that $Y = J_{s,F} \oplus Z$, where $Z$ is the additive noise in the model (see Figure 1). Let us define

$$\mathcal{E}^\mu := \bigcap_{\text{dist}(s, t) \geq L\epsilon} \mathcal{E}_{t,g}^\mu \quad (112)$$

Then, $P(\mathcal{E}^\mu) \to 1$ for any $\mu \in (1, \infty)$.

\[ ^9 \text{Note that the joint distribution } P_{Y,J_{t,g}} \text{ depends on the random function } F(.). \text{ Hence it is a random pmf and is denoted by capital letters. Notice that } F(.) \text{ is uniformly distributed over } \mathcal{F}_{L,m}. \]
Proof. Let us define the parameter
\[
\kappa := \frac{\mu - 1}{2 \times \min(\beta, 1 - \beta) \times \min(\gamma, 1 - \gamma)}.
\] (113)
Assume that \(X\) is chosen randomly and uniformly from the set \(\mathcal{X}^L\). Let us define the event\(^{10}\)
\[
\mathcal{E}^\kappa_{w, x'} := \left\{ \left| P_{J_{s,F}} X_w = x' (1) - P_{J_{s,F}} (1) \right| \leq \kappa \right\},
\] (114)
for any \(w \in \mathcal{I}_s(s)\) and any \(x' \in \mathcal{X}^{\text{length}(w)}\). Now we need the following two lemmas.

Lemma 13.
\[
\mathcal{E}^\kappa_{\text{int}} := \bigcap_{t \in S_{L,G}} \bigcap_{\begin{subarray}{c} \text{dist}(s,t) \geq L \epsilon \\
\text{x'} \in \mathcal{X}^{\text{length}(\text{int}(s,t))}
\end{subarray}} \mathcal{E}^\kappa_{\text{int}(s,t), x'} \subseteq \mathcal{E}^\mu = \bigcap_{t \in S_{L,G}} \bigcap_{\begin{subarray}{c} \text{dist}(s,t) \geq L \epsilon \\
g(.) \in F_{L,m}
\end{subarray}} \mathcal{E}^\mu_{t,g}
\] (115)

Proof. See appendix. \(\square\)

Lemma 14. For any \(t \in S_{L,G}\), such that \(\text{dist}(s,t) \geq L \epsilon\), any \(g(.) \in F_{L,m}\), and any \(x' \in \mathcal{X}^{\text{length}(\text{int}(s,t))}\) we have
\[
\mathbb{P}(\overline{\mathcal{E}^\kappa_{\text{int}(s,t), x'}}) \leq 2 \times (|\mathcal{X}|^L + 1) \times \exp \left( -2 |\mathcal{X}|^{\frac{1}{2} L \epsilon \kappa^2} \right).
\] (116)

Proof. See appendix. \(\square\)

Now we note by the union of events bound we have
\[
\mathbb{P}(\mathcal{E}^\mu) \geq \mathbb{P}(\overline{\mathcal{E}^\kappa_{\text{int}}}) \geq 1 - \mathbb{P}\left( \bigcup_{t \in S_{L,G}} \bigcup_{\begin{subarray}{c} \text{dist}(s,t) \geq L \epsilon \\
x' \in \mathcal{X}^{\text{length}(\text{int}(s,t))}
\end{subarray}} \mathcal{E}^\kappa_{\text{int}(s,t), x'} \right) \geq 1 - \mathbb{P}\left( \bigcup_{w \in \mathcal{I}_s(s)} \bigcup_{x' \in \mathcal{X}^{\text{length}(w)}} \mathcal{E}^\kappa_{w, x'} \right) \geq 1 - \sum_{w \in \mathcal{I}_s(s)} \mathbb{P}(\mathcal{E}^\kappa_{w, x'}) \geq 1 - \sum_{w \in \mathcal{I}_s(s)} 2 (|\mathcal{X}|^L + 1) \exp \left( -2 |\mathcal{X}|^{\frac{1}{2} L \epsilon \kappa^2} \right) \geq 1 - \left( \sum_{t=1}^{L} |\mathcal{X}|^t \right) \times 2^{L+1} (|\mathcal{X}|^L + 1) \exp \left( -2 |\mathcal{X}|^{\frac{1}{2} L \epsilon \kappa^2} \right) \geq 1 - L |\mathcal{X}|^L \times 2^{L+1} (|\mathcal{X}|^L + 1) \exp \left( -2 |\mathcal{X}|^{\frac{1}{2} L \epsilon \kappa^2} \right) = 1 - o(1),
\] (122)
where (a) follows from Lemma 13, (b) follows from Lemma 14, and (c) follows from the fact that \(|\mathcal{I}_s(s)| \leq 2^L\). We are done.

\(^{10}\)Note that the random choice of the function \(F(.)\) has no effect on the distribution of \(J_{s,F}\), i.e., \(p_{J_{s,F}} = p_{J_{s,F}}\).
A.3 Proof of Theorem 3

Now we are ready to start the proof. Fix an arbitrary \( s \in S_{L,G} \) throughout the proof. Note that

\[
I(F(X_s);Y) = I(J_{s,F};Y) = H(Y) - H(Y|F(X_s)) = h(\beta) - h(\alpha).
\]  

(126)

Notice that based on the joint AEP theorem [14 Theorem 7.6.1], if \( f(X_s) \) is independent from \( g(X_t) \), for any \( f(.) \), \( g(.) \) \( \in F_{L,m} \) and also any \( t \in S_{L,G} \) with a normalized distance of at least \( \epsilon \) with \( s \), then the desired result is established. However, in the theorem, this condition does not hold. In particular, if two sequences \( s, t \) have an intersection, then this independence criterion may not be true in general. This phenomenon means that we can not immediately use the AEP theorem for the proof. However, we showed that if we choose the function \( F(.) \) \( \in F_{L,m} \) uniformly at random, then for sequences like \( t \) that have at least a normalized distance of \( \epsilon \) with \( s \), this independence criterion holds approximately. We proved this statement in Lemma 12.

Now we use similar steps to [14 Theorem 7.6.1] to prove the theorem. Fix an arbitrary \( \mu \in (1, \infty) \). Consider the event \( E^\mu \) which is defined in Lemma 12. Fix a sequence \( t \in S_{L,G} \) satisfying \( \text{dist}(s,t) > L\epsilon \), and a function \( g(.) \) \( \in F_{L,m} \). Define the random variable \( U_n := g(X_{n,t}) \) for each \( n \in [N] \).

Note that we have

\[
\begin{align*}
\Pr(E_{L,G}|E^\mu) &= \Pr\left\{ \left( (U_n)_{n \in [N]}, (Y_n)_{n \in [N]} \right) \in T^N | E^\mu, S = s \right\} \\
&= \sum_{(u^{N},y^{N}) \in T^N} p_{U^{N},Y^{N}|E^\mu,S=s}(u^{N},y^{N}).
\end{align*}
\]

(127)

Using Lemma 12 we conclude that

\[
\begin{align*}
\Pr(E_{L,G}|E^\mu) &= \sum_{(u^{N},y^{N}) \in T^N} p_{U^{N},Y^{N}|E^\mu,S=s}(u^{N},y^{N}) \\
&\leq \mu^N \sum_{(u^{N},y^{N}) \in T^N} p_{U^{N}|E^\mu,S=s}(u^{N}) \times p_{Y^{N}|E^\mu,S=s}(y^{N}) \\
&\leq \mu^N \sum_{(u^{N},y^{N}) \in T^N} 2^{-N\text{H}(g(X_t)) - N\text{H}(Y) - 2\tau} \\
&\leq \mu^N \times 2^{-N\text{H}(g(X_t)) - N\text{H}(Y) - 3\tau} \\
&= 2^{-N(h(\beta) - h(\alpha) - \log(\mu)) - 3\tau}
\end{align*}
\]

(129)

which completes the proof, if \( \mu \in (1, \infty) \) is set to be small enough.

B Proof of Lemma 2

By the assumption of the lemma, there is a sequence of algorithms \( \{A_{(G_i,L_i,N_i,\alpha,\beta,m_i)}\}_{i \in \mathbb{N}} \) with rate \( R \) such that we have \( \lim_{i \to \infty} P^\text{WC}_i(A_{G_i}) = 0 \). This implies that \( \lim_{i \to \infty} P^\text{AVG}_i(A_{G_i}) = 0 \). For a fixed positive integer \( i \), let \( S \) be a random sequence that is distributed uniformly over the set \( S_{L,G} \). Also let \( F(.) \) be a random function that is distributed uniformly over the set \( S_{L,G} \). There are \( N_i \) samples \( X^{N_i} \), which are sampled uniformly and independently from the set \( |\mathcal{X}|^G \), and their corresponding labels \( Y^{N_i} \), which are generated based on the parameters \( \alpha \) and \( \beta \). We denote the output of the algorithm \( A_{(G_i,L_i,N_i,\alpha,\beta,m_i)} \) to the dataset \( (X^{N_i},Y^{N_i}) \) by \( \hat{S} \). Let us define the event \( E_i := E_{A_{G_i},\epsilon} = \{ \text{dist}(\hat{S},S) \leq \epsilon \} \) and also let \( E := 1\{ E_i \} \). Note that \( \Pr(E_i) = P^\text{AVG}_i(A_{G_i}) \). Hence, we have \( \lim_{i \to \infty} \Pr(E_i) = 0 \).

The proof consists of the following steps.
(i) First we claim that
\[
H(S|\hat{S}) \leq 1 + \mathbb{P}(\mathcal{E}_i) \log \left( \frac{G_i}{L_i} \right) + \log(L_i\epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{L_i\epsilon}{G_i - L_i} \right). \tag{134}
\]

(ii) Then, we notice that
\[
\log\left( \frac{G_i}{L_i} \right) = H(S) = H(S|\hat{S}) + I(S;\hat{S}) \tag{135}
\]
\[
\leq 1 + \mathbb{P}(\mathcal{E}_i) \log\left( \frac{G_i}{L_i} \right) + \log(L_i\epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{L_i\epsilon}{G_i - L_i} \right) + I(S;\hat{S}). \tag{137}
\]

(iii) The third step of the proof is to show that we have
\[
I(S;\hat{S}) \leq N_i h(\beta) - N_i h(\alpha). \tag{138}
\]

(iv) Combining the above arguments shows that
\[
\log\left( \frac{G_i}{L_i} \right) \leq 1 + \mathbb{P}(\mathcal{E}_i) \log\left( \frac{G_i}{L_i} \right) + \log(L_i\epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{L_i\epsilon}{G_i - L_i} \right) + N_i h(\beta) - N_i h(\alpha). \tag{139}
\]

(v) Then, from \cite[Chapter 11, p. 353]{14}, we establish that
\[
\frac{1}{G_i + 1} 2^{G_i h(L_i/G_i)} \leq \left( \frac{G_i}{L_i} \right) \leq 2^{G_i h(L_i/G_i)}. \tag{140}
\]

By taking the logarithm from two sides, we conclude
\[
G_i h(L_i/G_i) - \log(G_i + 1) \leq \log\left( \frac{G_i}{L_i} \right) \leq G_i h(G_i/L_i). \tag{141}
\]

(vi) The proof continues as follows. Using (141) and (139), we have
\[
G_i h(L_i/G_i) - \log(G_i + 1) \leq 1 + \mathbb{P}(\mathcal{E}_i) G_i h(L_i/G_i) + \log(L_i\epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{\epsilon L_i}{G_i - L_i} \right) + N_i h(\beta) - N_i h(\alpha). \tag{142}
\]

Dividing two sides of (142) by \(G_i h(L_i/G_i)\) results
\[
1 - \frac{\log(G_i + 1)}{G_i h(L_i/G_i)} \leq \frac{1}{G_i h(L_i/G_i)} + \mathbb{P}(\mathcal{E}_i) + \frac{\log(L_i\epsilon)}{G_i h(L_i/G_i)} + \frac{L_i}{G_i h(L_i/G_i)} h(\epsilon) + \frac{(G_i - L_i) h\left( \frac{\epsilon L_i}{G_i - L_i} \right)}{G_i h(L_i/G_i)} h(\frac{\epsilon L_i}{G_i - L_i}) + \frac{h(\beta) - h(\alpha)}{R}. \tag{143}
\]

Using the concavity of the function \(h(\cdot)\), we have that
\[
\frac{L_i}{G_i} h(\epsilon) + \frac{(G_i - L_i)}{G_i} h\left( \frac{\epsilon L_i}{G_i - L_i} \right) \leq h(2\epsilon L_i/G_i). \tag{145}
\]
Hence, we conclude that

$$1 - \frac{\log(G_i + 1)}{G_i h(L_i/G_i)} \leq \frac{1}{G_i h(L_i/G_i)} + \mathbb{P}(\mathcal{E}_i) + \frac{\log(L_i \epsilon)}{G_i h(L_i/G_i)} + \frac{h(2\epsilon L_i/G_i)}{h(L_i/G_i)} \leq \frac{h(\beta) - h(\alpha)}{R}. \quad (146)$$

Applying the inequality $G_i h(L_i/G_i) \geq L_i \log(G_i/L_i)$ shows that we have

$$1 - \frac{\log(G_i + 1)}{L_i \log(G_i/L_i)} \leq \frac{1}{G_i h(L_i/G_i)} + \mathbb{P}(\mathcal{E}_i) + \frac{\log(L_i \epsilon)}{L_i \log(G_i/L_i)} + \frac{h(2\epsilon L_i/G_i)}{h(L_i/G_i)} \leq \frac{h(\beta) - h(\alpha)}{R} (a) \quad (147)$$

$$(1 - \frac{\log(G_i + 1)}{L_i \log(G_i/L_i)}) + \mathbb{P}(\mathcal{E}_i) + \frac{\log(L_i \epsilon)}{L_i \log(G_i/L_i)} + \frac{h(2\epsilon L_i/G_i)}{h(L_i/G_i)} + \frac{\delta(\epsilon)}{1 - \delta(\epsilon)} \leq \frac{h(\beta) - h(\alpha)}{R}. \quad (148)$$

where $(a)$ follows by the definition of the function $\delta(.)$.

(vii) Finally, we claim that at the limit of $i \to \infty$, two terms $\frac{\log(G_i + 1)}{L_i \log(G_i/L_i)}$ and $\frac{\log(L_i \epsilon)}{L_i \log(G_i/L_i)}$ vanish. Using this claim and by letting $i \to \infty$ in (148), we conclude that

$$1 \leq \delta(\epsilon) + \frac{h(\beta) - h(\alpha)}{R}, \quad (149)$$

or

$$R \leq \frac{h(\beta) - h(\alpha)}{1 - \delta(\epsilon)}, \quad (150)$$

which completes the proof of the lemma.

In what follows, we prove the above stated claims. In particular, the claims in steps (i),(ii) and (vii) need to be proved.

### B.1 Proof of (i)

Note that we have

$$H(E_i, S|\hat{S}) = H(S|\hat{S}) + H(E_i|S, \hat{S}) \quad (151)$$

$$= H(E_i|S) + H(S|\hat{S}, E_i). \quad (152)$$

We note that $H(E_i|S, \hat{S}) = 0$ and $H(E_i|\hat{S}) \leq 1$. Hence we have

$$H(S|\hat{S}) \leq 1 + H(S|\hat{S}, E_i) \quad (153)$$

$$= 1 + \mathbb{P}(\mathcal{E}_i)H(S|\hat{S}, E_i = 1) + \mathbb{P}(\mathcal{E}_i)H(S|\hat{S}, E_i = 0) \quad (154)$$

$$\leq 1 + \mathbb{P}(\mathcal{E}_i)H(S|\hat{S}, E_i = 1) + H(S|\hat{S}, E_i = 0) \quad (155)$$

$$(a) \leq 1 + \mathbb{P}(\mathcal{E}_i)H(S) + H(S|\hat{S}, E_i = 0) \quad (156)$$

$$= 1 + \mathbb{P}(\mathcal{E}_i) \log\left(\frac{G_i}{L_i}\right) + H(S|\hat{S}, E_i = 0) \quad (157)$$

$$= 1 + \mathbb{P}(\mathcal{E}_i) \log\left(\frac{G_i}{L_i}\right) + H(S|\hat{S}, E_i = 0), \quad (158)$$

22
where (a) follows from the fact that conditioning reduces the entropy. Note that

\[ H(S|\hat{S}, E_i = 0) \leq \max_{\hat{s} \in S_{L_i, G_i}} \log(|\{ t \in S_{L_i, G_i} : \frac{\text{dist}(\hat{s}, t)}{L_i} \leq \epsilon \}|) \]  

(159)

\[ = \max_{\hat{s} \in S_{L_i, G_i}} \log(\sum_{\ell=1}^{[L_i \epsilon]} |\{ t \in S_{L_i, G_i} : \text{dist}(\hat{s}, t) = \ell \}|) \]  

(160)

\[ = \max_{\hat{s} \in S_{L_i, G_i}} \log(\sum_{\ell=1}^{[L_i \epsilon]} \left( \frac{L_i}{\ell} \right) \left( G_i - L_i \right) ) \]  

(161)

\[ \leq \log(L_i \epsilon) \left( \frac{L_i}{[L_i \epsilon]} \right) \left( G_i - L_i \right), \]  

(162)

where (a) follows from the fact that \( \epsilon \in (0, 1/2) \). Using (141) and (162) we conclude

\[ H(S|\hat{S}, E_i = 0) \leq \log(L_i \epsilon) \left( \frac{L_i}{[L_i \epsilon]} \right) \left( G_i - L_i \right), \]  

(163)

\[ \leq \log(L_i \epsilon \times 2^{L_i h(\epsilon)} \times 2^{(G_i - L_i) h(L_i \epsilon)} ) \]  

(164)

\[ = \log(L_i \epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{L_i \epsilon}{G_i - L_i} \right), \]  

(165)

Combining (158) and (165) results

\[ H(S|\hat{S}) \leq 1 + P(\mathcal{E}_i) \log\left( \frac{G_i}{L_i} \right) + \log(L_i \epsilon) + L_i h(\epsilon) + (G_i - L_i) h\left( \frac{L_i \epsilon}{G_i - L_i} \right), \]  

(166)

which completes the proof.

B.2 Proof of (iii)

Note that

\[ I(S; \hat{S}) \overset{(a)}{=} I(S; X^{N_i}, Y^{N_i}) \]  

(167)

\[ = I(S; X^{N_i}) + I(S; Y^{N_i}|X^{N_i}) \]  

(168)

\[ \overset{(b)}{=} I(S; Y^{N_i}|X^{N_i}) \]  

(169)

\[ = H(Y^{N_i}|X^{N_i}) - H(Y^{N_i}|X^{N_i}, S) \]  

(170)

\[ \overset{(c)}{\leq} N_i h(\beta) - H(Y^{N_i}|X^{N_i}, S), \]  

(171)

where (a) follows from the data processing inequality and the fact that \( S \to (X^{N_i}, Y^{N_i}) \to \hat{S} \) form a Markov Chain, (b) follows from the fact that \( S \) and \( X^{N_i} \) are independent random variables and thus \( I(S; X^{N_i}) = 0 \) and (c) follows from the fact that we have

\[ H(Y^{N_i}|X^{N_i}) \leq H(Y^{N_i}) = N_i H(Y) = N_i h(P(Y = 1)) = N_i h(\beta). \]  

(172)
We note that

\[ H(Y^N|X^N_s, S) \overset{(a)}{=} H(Y^N|X^N_s, F(\cdot)) \overset{(b)}{=} H(Y^N|(F(X_n, S))_{n \in [N_i]}, Y^{n-1}) \]

\[ \overset{(c)}{=} N_i H(Y|F(X_s)) = N_i h(\alpha), \]

where (a) follows by the fact that conditioning reduces the entropy, (b) follows by the telescopic property of the joint entropy and (c) holds because of the memoryless property of the additive noise in our model. Combining [171] and [177] results

\[ I(S; \tilde{S}) \leq N_i h(\beta) - N_i h(\alpha), \]

which completes the proof.

### B.3 Proof of (vii)

We note that for the proof of the claim, it suffices to only show that \( \frac{\log(G_i + 1)}{L_i \log(G_i / L_i)} \) vanishes asymptotically, since we have \( \log(G_i + 1) \geq \log(L_i \epsilon) \). Hence we focus on the proof of this statement. We write

\[ \frac{\log(G_i + 1)}{L_i \log(G_i / L_i)} = \frac{\log(G_i + 1)}{L_i \log(G_i) - L_i \log(L_i)} = \frac{1}{L_i \left( \frac{\log(G_i)}{\log(G_i + 1)} - \frac{\log(L_i)}{\log(G_i + 1)} \right)}. \]

Note that

\[ L_i \left( \frac{\log(G_i)}{\log(G_i + 1)} - \frac{\log(L_i)}{\log(G_i + 1)} \right) \geq L_i \left( \frac{\log(G_i)}{\log(G_i + 1)} - \frac{\log(L_i)}{\log(2L_i + 1)} \right) \]

\[ = L_i \left( \frac{\log(G_i)}{\log(G_i + 1)} - \frac{\log(2L_i + 1)}{\log(2L_i + 1)} + \frac{\log(L_i)}{\log(2L_i + 1)} \right) \]

\[ = -L_i \log((G_i + 1)/G_i) + \Theta \left( \frac{L_i}{\log(L_i)} \right). \]

We note that \( L_i \log((G_i + 1)/G_i) \approx \frac{L_i}{G_i \log(G_i + 1)} \) and it vanishes asymptotically. Hence, at the limit of \( i \to \infty \), the R.H.S of [182] is \( \Theta(L_i / \log(L_i)) \) and so we have \( L_i \left( \frac{\log(G_i)}{\log(G_i + 1)} - \frac{\log(L_i)}{\log(G_i + 1)} \right) \to \infty \) as \( i \to \infty \).

Hence, using [179], we conclude that \( \frac{\log(G_i + 1)}{L_i \log(G_i / L_i)} \to 0 \) as \( i \to \infty \) and so the claim is proved.

### C Proof of Lemma 3

Let us define \( f_y(x) := h(x)h(y) - h(2xy) \) for any \( y \in [0, 1/2] \). Note that \( f_y(0) = f_y(1/2) = 0 \). We aim to prove that \( f_y(\cdot) \) is a non-negative function over the interval \([0, 1/2]\). We notice that for completing the proof, it suffices to show that for each \( y \), the function \( f_y(\cdot) \) is concave over the interval \([0, 1/2]\).

Note that

\[ \frac{d}{dx} f_y(x) = \frac{h(y)}{\ln(2)} \ln \left( \frac{1-x}{x} \right) - \frac{2y}{\ln(2)} \ln \left( \frac{1-2xy}{2xy} \right). \]

\( ^{11} \)Note that for any constant \( c \in (0, 1) \), we have \( c/G_i \leq \ln(1 + 1/G_i) \leq 1/G_i \) for any large enough \( G_i \).
Now we write

\[
\frac{d^2}{dx^2} f_y(x) = h(y) \frac{-1}{\ln(2) x(1 - x)} + \frac{4y^2}{\ln(2) 2xy(1 - 2xy)} - \frac{1}{x \ln(2) \left(1 - x\right)} \left(-h(y) + 2y\right)
\]

which completes the proof, since we have \(h(y) \geq 2y\) for any \(y \in [0, 1/2]\).

D Proof of Lemma 13

Assume that any event in the L.H.S. of (115) occurs. We aim to prove that for any \(t \in S_{L,G}\), such that \(\text{dist}(s, t) \geq L\epsilon\), and any \(g(.) \in F_{L,m}\), the event \(E_{t,g}^\mu\) occurs. We write

\[
E_{t,g}^\mu = \{ J_{t,g} \perp Y \} 
\]

(a) follows from Lemma 6, (b) follows from Corollary 2 and the fact that we have the following Markov chain

\[
J_{t,g} - X_t - \text{int}(s, t) - X_s - J_{s,F} - Y, \quad (196)
\]

and also, (c) follows from Lemma 7. We are done.

E Proof of Lemma 14

Let \(X \in \mathcal{X}^G\) be a random sequence which is distributed uniformly over \(\mathcal{X}^G\). Note that

\[
P_{J_{s,F} | \text{int}(s, t) = x'}(1) = \mathbb{E}_X \left[ F(X_s) \mid \text{int}(s, t) = x' \right] \quad (197)
\]

(a) follows from Lemma 6}

\[
\frac{1}{|\mathcal{X}^{(L - \text{length}(\text{int}(s, t)))}|} \sum_{x \in \mathcal{X}^G \mid \text{int}(s, t) = x'} F(x_s). \quad (198)
\]

We are done.
where (a) follows from the fact that
\[
\left| \{ x \in \mathcal{X}^G : x_{\text{int}(s,t)} = x' \} \right| = |\mathcal{X}|(L - \text{length}(\text{int}(s,t))) .
\] (199)

Now we write
\[
P(\mathcal{E}_{\text{int}(s,t),x'}) = P\left( \left| P_{J_s,F}x_{\text{int}(s,t)} = x' \right| - P_{J_s,F}(1) \right| \geq \kappa \right)
\] (200)
\[
= P\left( \left| P_{J_s,F}x_{\text{int}(s,t)} = x' \right| - \gamma \right| \geq \kappa \right)
\] (201)
\[
= P\left( \frac{1}{|\mathcal{X}|(L - \text{length}(\text{int}(s,t)))} \sum_{x \in \mathcal{X}^G} F(x_s) - \gamma \right| \geq \kappa \right),
\] (202)

Now let \( \phi : \mathcal{X}^L \rightarrow [|X|^L] \) be a bijection mapping and \( n = |\mathcal{X}|^L \). Define \( n \) random variables \( V_i = F(\phi^{-1}(i)) \), \( i \in [n] \). Let
\[
\mathcal{T} := \left\{ \phi(x) \mid x \in \mathcal{X}^G, x_{\text{int}(s,t)} = x' \right\} .
\] (203)

Note that \( |\mathcal{T}| = |\mathcal{X}|(L - \text{length}(\text{int}(s,t))) \). Define \( V = \sum_{i \in \mathcal{T}} V_i \). Note that \( E[V_i] = \gamma \) for any \( i \).

Now notice that the random variables \( V_i \), \( i \in [n] \), and the set \( \mathcal{T} \subseteq [n] \) satisfy the required conditions of Lemma \[10\]. Hence using Lemma \[10\] we conclude that
\[
P(\mathcal{E}_{\text{int}(s,t),x'}) = P\left( \left| \frac{V - E[V]}{|\mathcal{T}|} \right| \geq \kappa \right)
\] (204)
\[
\leq 2(n + 1) \exp \left( -2|\mathcal{T}|\kappa^2 \right) \tag{205}
\]
\[
= 2(|\mathcal{X}|^L + 1) \exp \left( -2|\mathcal{X}|(L - \text{length}(\text{int}(s,t)))\kappa^2 \right) \tag{206}
\]
\[
\leq 2(|\mathcal{X}|^L + 1) \exp \left( -2\sqrt{\frac{1}{2}L}\kappa^2 \right), \tag{207}
\]

where (a) follows from Lemma \[11\]. We are done.