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IMPROVED BOUNDS FOR NOISY GROUP TESTING WITH CONSTANT TESTS PER ITEM

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ABSTRACT. The group testing problem is concerned with identifying a small set of infected individuals in a large population. At our disposal is a testing procedure that allows us to test several individuals together. In an idealized setting, a test is positive if and only if at least one infected individual is included and negative otherwise. Significant progress was made in recent years towards understanding the information-theoretic and algorithmic properties in this noiseless setting. In this paper, we consider a noisy variant of group testing where test results are flipped with certain probability, including the realistic scenario where sensitivity and specificity can take arbitrary values. Using a test design where each individual is assigned to a fixed number of tests, we derive explicit algorithmic bounds for two commonly considered inference algorithms and thereby improve on results by Scarlett & Cevher (SODA 2016) and Scarlett & Johnson (2020) and providing the strongest performance guarantees currently proved for efficient algorithms in these noisy group testing models.

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1. INTRODUCTION

1.1. Motivation and background. Suppose we have a large collection of n people, a small number k of whom are infected by some disease, and where only $m \ll n$ tests are available.

In a landmark paper [15] from 1943, Dorfman introduced the idea of group testing. The basic idea is as follows: rather than screen one person using one test, we could mix samples from individuals in one pool, and use a single test for this whole pool. The task is to recover the infection status of all individuals using the pooled test results.

Dorfman's original work was motivated by a biological application, namely identifying individuals with syphilis. Subsequently, group testing has found a number of related applications, including detection of HIV [51], DNA sequencing [30, 37] and protein interaction experiments [35, 49]. More recently, it has been recognised as an essential tool to moderate pandemic spread [12], where identifying infected individuals fast and at a low cost is indispensable [33]. In particular, group testing has been identified as a testing scheme for the detection of COVID-19 [16, 19].

From a mathematical perspective, group testing is a prime example of an inference problem where one wants to learn a ground truth from (possibly noisy) measurements [1, 2, 9, 21, 22, 28, 42]. Over the last decade, it has regained popularity and today is a field of active research. Results on its information-theoretic and algorithmic properties were recently presented by Scarlett et al. at SODA'16, ISIT'16, ISIT'19 [44, 46, 45], and Baldassini et al. at ISIT'13 [8] and Coja-Oghlan et al. at ICALP'19, COLT'20 [13, 14]. In this paper, we provide improved upper bounds on the number of tests that guarantee successful inference for the noisy variant of group testing.

1.2. Related Work. In the simplest version of group testing, we suppose that a test is positive if and only if the pool contains at least one infected individual. We refer to this as the noiseless case. In this setting, each negative test guarantees that every member of the corresponding pool is not infected, so they can be removed from further consideration. However, a positive test only tells us that at least one item in the test is defective (but not which one), and so requires further investigation.

Dorfman's original work [15] proposed a simple adaptive strategy where a small pool of individuals is tested, and where each positive test is followed up by testing every individual in the corresponding pool individually. Since then it has been an important problem to find the optimal way to recover the population's infection status in the noiseless case. A simple counting argument (see for example [7, Section 1.4]) shows that to ensure recovery with zero error probability, since every possible defective set must give different test outcomes, the following must hold in the noiseless setting:

$$(1.1) \quad 2^m \geq \binom{n}{k} \quad \Rightarrow \quad m \geq m_{\text{inf}}^0 := \frac{1}{\log 2} k \log(n/k)$$

Hwang [24] provided an algorithm based on repeated binary search, which is essentially optimal in terms of the number of tests required in that it requires $m_{\text{inf}}^0 + O(k)$ tests, but may require many stages of testing. As described for example in pandemic plans developed by the EU, US and WHO [18, 38, 39], and in COVID-specific work [36], adaptive strategies may not be suitable for pandemic prevention. For example, if a test takes one day to prepare and for the results to be known, then each stage will require an extra day to perform, meaning that adaptive group testing information can be received too late to be useful.

Hence the need to perform large-scale testing to identify infected individuals fast relative to the doubling time [12, 33, 36] can make adaptive group testing unsuitable to prevent an infectious disease from spreading. Furthermore the preservation of uncharted viruses in a large scale may be challenging due to structural and chemical differences [20]. Due to its automation potential and the fact that tests can be completed in parallel (for example by the use of 96-well PCR plates [17]), the main application of group testing such as DNA screening [11, 30, 37], HIV testing [51] and protein interaction analysis [35, 49] are non-adaptive where all tests are specified upfront and performed in parallel.

The question of whether non-adaptive algorithms (or even adaptive algorithms with a limited number of stages) can attain the bound (1.1) remained open until recently. [4, 14] showed that the answer depends on the prevalence of the disease, for example on the value of $\theta \in (0, 1)$ in a parameterisation where the number of infected individuals $k \sim n^\theta$. Non-adaptive testing schemes can be represented through a binary $(m \times n)$ -matrix that represents which individual participates in which test. Significant research was dedicated to see which design attains the optimal performance. Since deterministic designs were shown to not attain the optimal order [7], research focused on randomized designs. Initial research focused on the case where the matrix entries are iid [3, 5, 45]. Later work considered a constant column design where each individual is assigned to a (near-)constant number of tests [6, 14, 13, 26]. Indeed [14] showed that such a design is information-theoretically optimal in the *noiseless* setting and it is to be expected that this remains true for the noisy case.

To recover the ground truth from the test results and the pooling scheme, this paper focuses on two non-adaptive algorithms, COMP and DD, which are relatively simple to perform and interpret in the noiseless case. We describe them in more detail below, but in brief COMP [10] simply builds a list of all the individuals who ever appear in a negative test and are hence certainly healthy, and assumes that the other individuals are infected. DD [5] uses COMP as a first stage and builds on it by looking for individuals who appear in a positive test that only otherwise contains individuals known to be healthy.

While the noiseless case provides an interesting mathematical abstraction, it is clear that it may not be realistic in practice [40]. In medical applications the two occurring types of noise in a testing procedure are related to sensitivity (positive correct) and specificity (negative correct), and in that language we cannot assume the gold standard of tests with unit specificity and sensitivity. Thus, research attention in recent years has shifted towards the noisy version of group testing [10, 43, 44, 45, 47, 48]. On the one hand, *adaptive* noisy case was considered in [43, 44]. On the other hand [10, 27, 29, 34, 45, 47, 48] looked at the *non-adaptive* noise case from different angles (for instance linear programming, belief propagation, Bernoulli-pooling, Markov-Chain Monte Carlo).

In this paper we focus on the COMP and DD algorithms, since it is possible to deduce explicit performance guarantees for them. The deductions made by the original COMP and DD algorithms are designed for the noiseless case and do not hold in general. However, recent work of Scarlett and Johnson [48] has shown that noisy versions of these algorithms can perform well under certain noise models using Bernoulli i.i.d. test designs, particularly focusing on Z channel and reverse Z channel noise.

As common medical tests have different values for sensitivity and specificity [32] the analysis of a generalized noise model beyond the Z and reverse Z channel is warranted. For example, while group testing strategies appear to be useful to identify individuals infected with COVID-19 (see for example [16, 19]), testing for the presence of the SARS-CoV-19 virus is not perfect [52], and so we need to understand the effect of both false positive and false negative errors in this context, with non-identical error probabilities. For this reason, we consider a general $p - q$ noise model in this paper. Under this model, a truly negative test is flipped with probability p to display a positive test result, while a truly positive test is flipped to negative with probability q (Figure 1). Its formulation is sufficiently general to accommodate the recovery of the noiseless results ($p = q = 0$), Z channel ($p = 0$), reverse Z channel ($q = 0$) and the Binary Symmetric Channel ($p = q$). However, our results include the case of non-zero p and q without having to make the somewhat artificial assumption that false negative and false positive errors are equally likely.

1.3. Contribution. This paper provides a simultaneous extension of [13] and [26, 48], by analysing noisy versions of COMP and DD under more general noise models for constant-column weight designs. We provide explicit bounds on the performance of these algorithms in a generalized noise model. For all typical noise channels (Z , reverse Z and BSC) we compare the constant-column and Bernoulli design and find for all such instances that the former meaningfully outperforms the latter thereby improving on results from [26] and providing the strongest performance guarantees currently proved for efficient algorithms in noisy group testing. As group testing offers an essential tool for pandemic prevention [33] and as the

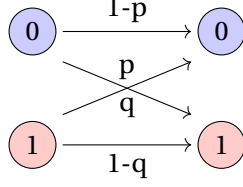


FIGURE 1. The p - q -noise model: the result of each standard noiseless group test is transmitted independently through the given noisy communication channel.

the accuracy of medical testing is limited [32, 40] this paper provides the natural next step in the group testing literature.

1.4. Test design and notation. To formalise our notation, we write n for the number of individuals in the population, σ for a binary vector representing the infection status of each individual, k (the Hamming weight of σ) for the number of infected individuals and m for the number of tests performed. We assume that k is known for purposes of matrix design, though in practice (see [7, Remark 2.3]) it is generally enough to know k up to a constant factor to design a matrix with good properties. In this paper, in line with other work such as [5], we consider a scaling $k \sim n^\theta$ for some fixed $\theta \in (0, 1)$, referred to in [7, Remark 1.1] as the sparse regime. We believe a similar analysis should be possible in the very sparse regime ($k = O(1)$) and linear regime ($k \sim \beta n$ for a fixed β). In addition to the interesting phase transitions observed using this scaling, this sparse regime is particularly relevant as it is the parametrisation to model the early state of a pandemic [50].

Let us next introduce the test design. With $V = (x_i)_{i \in [n]}$ ¹ denoting the set of n individuals and $F = (a_i)_{i \in [m]}$ the set of m tests, the test design can be envisioned as a bipartite factor graph with n variable nodes "on the left" and m factor nodes "on the right". We draw a configuration $\sigma \in \{0, 1\}^V$, encoding the infection status of each individual, uniformly at random from vectors of Hamming weight k . The set of healthy individuals will be denoted by V_0 and the set of infected individuals by V_1 . In symbols,

$$V_0 = \{x \in V : \sigma_x = 0\} \quad \text{and} \quad V_1 = V \setminus V_0 = \{x \in V : \sigma_x = 1\}$$

The lower bound from (1.1) suggests that in the noisy group testing setting it is natural to compare the performance of algorithms and matrix designs in terms of the prefactor of $k \log(n/k)$ in the number of tests required. To be precise, we carry out m tests, and each item is assigned to exactly Δ tests chosen uniformly at random without replacement. We parameterise m and Δ as

$$(1.2) \quad m = ck \log(n/k) \quad \text{and} \quad \Delta = cd \log(n/k)$$

for some suitably chosen constants $c, d \geq 0$.

Let ∂x denote the set of tests that individual x appears in and ∂a the set of individuals assigned to test a . The resulting (non-constant) collection of test degrees will be denoted by the vector $\Gamma = (\Gamma_a)_{a \in [m]}$. Further, let

$$(1.3) \quad \Gamma_{\min} = \min_{a \in [m]} \Gamma_a \quad \text{and} \quad \Gamma_{\max} = \max_{a \in [m]} \Gamma_a.$$

Throughout, $\mathbf{G} = \mathbf{G}(n, m, \Delta)$ describes the random bipartite factor graph from this construction.

Now consider the outcome of the tests. Recall from above that a standard noiseless group test a gives a positive result if and only if there is at least one defective item contained in the pool, or equivalently if $\sum_{x \in \partial a} \sigma(x) > 0$. Even in the noisy case, this sum is a useful object to consider. Writing $\mathbf{1}$ for the indicator

¹ $_{[n]}$ will be used as an abbreviated notation for the set $\{1, \dots, n\}$.

function, we define

$$(1.4) \quad \sigma^*(a) = \mathbf{1} \left\{ \sum_{x \in \partial a} \sigma(x) > 0 \right\}$$

to be the outcome we would observe in the noiseless case using the test matrix corresponding to \mathbf{G} . We will say that test a is *truly positive* if $\sigma^*(a) = 1$ and truly negative otherwise.

However, we do not observe the values of $\sigma^*(a)$ directly, but rather see what we will refer to as the *displayed* test outcomes $\hat{\sigma}(a)$ – the outcomes of sending the true outcomes $\sigma^*(a)$ independently through the $p - q$ channel of Figure 1. Since in this model a truly positive test remains positive with probability $1 - q$ and a truly negative test is displayed as positive with probability p we can write

$$(1.5) \quad \hat{\sigma}(a) = \mathbf{1} \{ \text{Be}(p) = 1 \} (1 - \sigma^*(a)) + \mathbf{1} \{ \text{Be}(1 - q) = 1 \} \sigma^*(a)$$

where $\text{Be}(r)$ denotes a Bernoulli random variable with parameter r . For models with binary outputs, this is the most general channel satisfying the noisy defective channel property of [7, Definition 3.3], though more general models are possible under the only defects matter property [7, Definition 3.2], where the probability of a test being positive depends on the number of contained infected individuals.

Note that if $p + q > 1$, we can preprocess the outputs from (1.5) by flipping them, i.e. setting $\tilde{p} = 1 - p$ and $\tilde{q} = 1 - q$, where $\tilde{p} + \tilde{q} < 1$. Hence without loss of generality we will assume throughout that $p + q < 1$. In the case $p + q = 1$, the test outcomes are independent of the inputs, and we cannot hope to find the infected individuals – see Theorem 2.3.

With m_0 being the number of truly negative tests, let m_0^f be the number of truly negative tests that are flipped to display a positive test result and m_0^u be the number of truly negative tests that are unflipped. Similarly, define m_1 as the number of truly positive tests, of which m_1^f are flipped to a negative test result and of which m_1^u are unflipped. For reference, for $t \in \{0, 1\}$ we write

$$m_t = |\{a : \sigma^*(a) = t\}|$$

$$m_t^f = |\{a : \sigma^*(a) = t, \hat{\sigma}(a) \neq t\}| \quad \text{and} \quad m_t^u = |\{a : \sigma^*(a) = t, \hat{\sigma}(a) = t\}|$$

Throughout the paper, we use the standard Landau notation $o(\cdot)$, $O(\cdot)$, $\Theta(\cdot)$, $\Omega(\cdot)$, $\omega(\cdot)$ and define $0 \log 0 = 0$. In order to quantify the performance of our algorithms, for any $0 < r \neq s < 1$, we write

$$D_{\text{KL}}(r \| s) := r \log \left(\frac{r}{s} \right) + (1 - r) \log \left(\frac{1 - r}{1 - s} \right),$$

for the relative entropy of a Bernoulli random variable with parameter r to a Bernoulli random variable with parameter s , commonly referred to as the Kullback–Leibler divergence. Here and throughout the paper we use \log to denote the natural logarithm. For r or s equal to 0 or 1 we define the value of $D_{\text{KL}}(\cdot \| \cdot)$ (possibly infinite) on grounds of continuity, so for example $D_{\text{KL}}(0 \| s) = -\log(1 - s)$.

2. MAIN RESULTS

With the test design and notation in place, we are now in a position to state our main results. Theorems 2.1, 2.2 and 2.3 are the centerpiece of this paper featuring improved bounds for the noisy group testing problem for the general $p - q$ model. We follow up with a discussion of the combinatorics underlying both algorithms. Subsequently, we show how the bounds simplify when we consider the special cases of the Z, the reverse Z and Binary Symmetric Channel. Finally, we derive sufficient conditions under which DD provably outperforms the COMP algorithm and compare the bounds of our constant-column design against the Bernoulli design employed in prior literature.

2.1. Bounds for Noisy Group Testing. We will consider two well-known algorithms from the noiseless setting to identify infected individuals in this paper. First, we study a noisy variant of the COMP algorithm, originally introduced in [10].

- 1 Declare every individual that appears in $\alpha\Delta$ or more displayed negative tests as healthy.
- 2 Declare all remaining individuals as infected.

Algorithm 1: The noisy COMP algorithm

Note that for $\alpha = 1/\Delta$ we recover the standard COMP algorithm where an individual is classified as healthy if it appears in at least one displayed negative test which constitutes a sufficient condition in the noiseless case. We now state the first main result of this paper.

Theorem 2.1 (Noisy COMP). *Let $p, q \geq 0, p + q < 1, d \in (0, \infty), \alpha \in (q, e^{-d}(1-p) + (1-e^{-d})q)$. Suppose that $0 < \theta < 1$ and let*

$$m_{\text{COMP}} = m_{\text{COMP}}(n, \theta, p, q) = \min_{\alpha, d} \max \{b_1(\alpha, d), b_2(\beta, d)\} k \log(n/k)$$

$$\text{where } b_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| q)}$$

$$\text{and } b_2(\alpha, d) = \frac{1}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| e^{-d}(1-p) + (1-e^{-d})q)}$$

If $m \geq (1 + \varepsilon)m_{\text{COMP}}$ for some $\varepsilon > 0$, noisy COMP will recover σ w.h.p. given test design \mathbf{G} and test results $\hat{\sigma}$.

The noisy variant of the DD algorithm of [5] was introduced in [48] and reads as follows:

- 1 Declare every individual that appears in $\alpha\Delta$ or more displayed negative tests as healthy and remove such individual from every assigned test.
- 2 Declare every yet unclassified individual who is now the only unclassified individual in $\beta\Delta$ or more displayed positive tests as infected.
- 3 Declare all remaining individuals as healthy.

Algorithm 2: The noisy DD algorithm [48]

This reduces to the noiseless version of DD introduced in [5] by taking $\alpha = \beta = 1/\Delta$. We now state the second main result of the paper.

Theorem 2.2 (Noisy DD). *Let $p, q \geq 0, p + q < 1, d \in (0, \infty), \alpha \in (q, e^{-d}(1-p) + (1-e^{-d})q)$ and $\beta \in (0, e^{-d}(1-q))$ and define $w = e^{-d}p + (1-e^{-d})(1-q)$. Suppose that $0 < \theta < 1$ and let*

$$m_{\text{DD}} = m_{\text{DD}}(n, \theta, p, q) = \min_{\alpha, \beta, d} \max \{c_1(\alpha, d), c_2(\alpha, d), c_3(\beta, d), c_4(\alpha, \beta, d)\} k \log(n/k)$$

$$\text{where } c_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| q)}$$

$$\text{and } c_2(\alpha, d) = \frac{1}{d D_{\text{KL}}(\alpha \| 1-w)}$$

$$\text{and } c_3(\beta, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\beta \| (1-q)e^{-d})}$$

$$\text{and } c_4(\alpha, \beta, d) = \max_{1-\alpha \leq z \leq 1} \left\{ \frac{1}{1-\theta} \frac{1}{d \left(D_{\text{KL}}(z \| w) + \mathbf{1} \left\{ \beta > \frac{ze^{-d}p}{w} \right\} z D_{\text{KL}} \left(\frac{\beta}{z} \left\| \frac{e^{-d}p}{w} \right. \right) \right)} \right\}$$

If $m \geq (1 + \varepsilon)m_{\text{DD}}$ for some $\varepsilon > 0$, then noisy DD will recover σ w.h.p. given test design \mathbf{G} and test results $\hat{\sigma}$.

While the bounds appear cumbersome at first glance due to the numerous optimizations, the optimizations are of finite dimensions and for every specific value of p and q can be efficiently solved to arbitrary precision yielding explicit values for m_{COMP} and m_{DD} . For illustration purposes, we will calculate those bounds for several values of p, q and θ . Motivated by (1.1), we can describe the bounds in terms of rate, in a Shannon-theoretic sense. That is, we define the rate (bits learned per test) of an algorithm in this setting to be

$$R := \frac{\log \binom{n}{k}}{m \log 2} \sim \frac{k \log(n/k)}{m \log 2}.$$

(Recall that we take logarithms to base e throughout this paper). For example the fact that Theorems 2.1 and 2.2 show that noisy COMP and DD respectively can succeed w.h.p. with $m \geq (1 + \epsilon)ck \log(n/k)$ tests for some c is equivalent to the fact that $R = 1/(c \log 2)$ is an achievable rate in a Shannon-theoretic sense.

We now give a counterpart to these two theorems by stating a universal converse for the $p - q$ channel below, improving on the universal counting bound from (1.1). The starting observation (see [7, Theorem 3.1]) is that no group testing algorithm can succeed w.h.p. with rate greater than C_{Chan} – the Shannon capacity of the corresponding noisy communication channel. Thus, we cannot hope to succeed w.h.p. with $m < (1 - \epsilon)ck \log(n/k)$ tests where $c = 1/(C_{\text{Chan}} \log 2)$. Hence as a direct consequence of the value of the channel capacity of the $p - q$ channel given in Lemma F.1 below, we deduce the following theorem.

Theorem 2.3. *Let $p, q \geq 0$, $p + q < 1$ and $\epsilon > 0$, write $h(\cdot)$ for the binary entropy in nats (logarithms taken to base e) and $\phi = \phi(p, q) = (h(p) - h(q))/(1 - p - q)$. If we define*

$$m_{\text{COUNT}} = \left(\frac{1}{D_{\text{KL}}(q \| 1/(1 + e^\phi))} \right) k \log(n/k),$$

then for $m \leq (1 - \epsilon)m_{\text{COUNT}}$ no algorithm can recover σ w.h.p. for any matrix design.

Remark 2.4. *Note that the derivation of this result in Lemma 2.3 suggests a choice of density for the matrix:*

$$d = d_{\text{ch}}^* = \log(1 - p - q) - \log\left(\frac{1}{1 + e^\phi} - q\right).$$

While this is not optimal, it may be regarded as a sensible heuristic that provides good rates for a range of p and q values.

2.2. The combinatorics of the noisy group testing algorithms. In the following, we outline the combinatorial structures that Algorithm 1 and 2 take advantage of.

2.2.1. The noisy COMP algorithm. To get started, let us shed light on the combinatorics of noisy COMP (Algorithm 1). For the *noiseless* case, the COMP algorithm classifies each individual that appears in at least one negative test as healthy and all other individuals as infected, since the participation in a negative test is a sufficient condition for the individual to be healthy.

For the noisy case, the situation is not as straightforward, since an infected individual might appear in *displayed* negative tests that were flipped when sent through the noisy channel. Thus, a single negative test is not definitive evidence that an individual is healthy. Yet, we can use the number of negative tests to tell the infected individuals apart from the healthy individuals.

Clearly, noisy COMP (Algorithm 1) using a threshold $\alpha\Delta$ succeeds if no healthy individual appears in less than $\alpha\Delta$ displayed negative tests and no infected individual appears in more than $\alpha\Delta$ displayed negative tests. To this end, we define

$$(2.1) \quad N_x = |\{a \in \partial x : \hat{\sigma}(a) = 0\}|$$

for the number of displayed negative tests that item x appears in. In terms of Figure 2, the algorithm determines the infection status by counting the number of tests of type I.

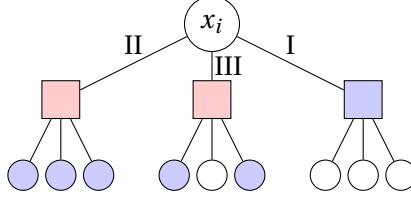


FIGURE 2. Rectangles represent tests (displayed positive in red, displayed negative in blue). Blue circles represent individuals that have been classified as healthy in the first step of DD (or by COMP). White circles represent individuals that are yet unclassified. On the one hand (Type II and III) this can happen before the first round of DD (or by COMP). On the other hand (Type I) it is the case before the algorithms start

2.2.2. *The noisy DD algorithm.* As in the prior section, let us first consider the *noiseless* DD algorithm. The first step is identical to COMP classifying all individuals that are contained in at least one negative test as healthy. In a second step, the algorithm checks each individual to see if they are contained in a positive test as the only yet unclassified individual and thus must be infected.

Again, the situation is more intricate when we add noise, since neither a single negative test gives us confidence that an individual is healthy nor does a positive test where the individual is the single yet unclassified individual inform us that this individual must be infected. Instead we count and compare the number of such tests. The first step of the noisy DD algorithm is identical to noisy COMP, but we are not required to identify all healthy individuals in the first step. Thus, after the first step, we are left with all infected individuals V_1 and a set of yet unclassified healthy individuals which we will denote by $V_{0,PD}$. These are healthy individuals who did not appear in sufficiently many displayed negative tests to be declared healthy with confidence in the first step. In symbols, for some $\alpha \in (0, 1)$

$$V_{0,PD} = \{x \in V_0 : N_x < \alpha \Delta\}$$

To tell V_1 and $V_{0,PD}$ apart, we consider the number of displayed positive tests \mathbf{P}_x where the individual x appears on its own after removing the definitely healthy individuals $V_0 \setminus V_{0,PD}$ from the first step, i.e.

$$(2.2) \quad \mathbf{P}_x = |\{a \in \partial x : \hat{\sigma}(a) = 1 \text{ and } \partial a \setminus \{x\} \subset V_0 \setminus V_{0,PD}\}|$$

Referring to Figure 2, the second step of the algorithm is based on counting tests of type II. Tests of type III contain another yet unclassified individual from $V_{0,PD} \cup V_1$. The noisy DD algorithm takes advantage of the fact that it is less likely for an individual $x \in V_{0,PD}$ to appear as the only yet unclassified individual in a displayed positive test than it is for an individual in $x \in V_1$. For $x \in V_{0,PD}$ such a test would be truly negative and would have been flipped (which occurs with probability p) to display a positive test result. Conversely, an individual $x \in V_1$ renders any of its tests truly positive and thus the only requirement is that the test otherwise contains only definitely healthy individuals and is not flipped (which occurs with probability $1 - q$). For this reason, we will see that the distribution of \mathbf{P}_x differs between $x \in V_1$ and $x \in V_{0,PD}$, and the difference $(1 - q) - p > 0$ helps determine the size of this difference.

2.3. **Applying the results to standard channels.** With Theorem 2.1 and Theorem 2.2 we derived achievable rates for the generalized p - q -model (see Figure 1). prior research considered the Z channel where $p = 0$ and $q > 0$, the Reverse Z channel where $p > 0$ and $q = 0$ and the Binary Symmetric Channel with $p = q > 0$. These channels are the common models in coding theory [41], but are also often considered in medical applications [31, 32] concerned with taking sensitivity ($q > 0$), specificity ($p > 0$) or both ($p > 0$ and $q > 0$) into account. In the following section we will demonstrate how performance guarantees on these channels can directly be obtained from our main theorems.

2.3.1. *Recovery of the noiseless model.* First, we show the noiseless bounds can be simply recovered by setting $p = q = 0$. In the noiseless setting, it is optimal to set both α and β to $1/\Delta$. To see why, observe that in the absence of noise a single negative test is sufficient evidence that an individual is healthy. Conversely, a single positive test where the individual only appears with definitely healthy individuals implies that particular individual must surely be infected. As shown in [13] the optimal parameter choice for d in the constant-column design in the noiseless setting is $\log(2)$. Applying these values to Theorem 2.1 we recover the noiseless bound for COMP.

Corollary 2.5 (COMP in the noiseless setting). *Let $p = q = 0, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{COMP}, \text{noiseless}} = \frac{1}{(1 - \theta) \log^2 2} k \log(n/k).$$

If $m > (1 + \varepsilon) m_{\text{COMP}, \text{noiseless}}$, COMP will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

We also recover the noiseless bounds for the DD algorithm as stated in [26].

Corollary 2.6 (DD in the noiseless setting). *Let $p = q = 0, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{DD}, \text{noiseless}} = \max \left\{ 1, \frac{\theta}{1 - \theta} \right\} \frac{1}{\log^2 2} k \log(n/k).$$

If $m > (1 + \varepsilon) m_{\text{DD}, \text{noiseless}}$, DD will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

2.3.2. *The Z channel.* In the Z channel, we have $p = 0$ and $q > 0$, i.e. no truly negative test displays a positive test result. Thus, we set $\beta = 1/\Delta$ and remain agnostic about α and d . The bounds for COMP and DD thus read.

Corollary 2.7 (Noisy COMP for the Z channel). *Let $p = 0, 0 < q < 1, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{COMP}, Z} = \min_{\alpha, d} \max \{ b_1(\alpha, d), b_2(\alpha, d) \} k \log(n/k)$$

with $b_1(\alpha, d) = \frac{\theta}{1 - \theta} \frac{1}{d D_{\text{KL}}(\alpha \| q)}$ and $b_2(\alpha, d) = \frac{1}{1 - \theta} \frac{1}{d D_{\text{KL}}(\alpha \| e^{-d} + (1 - e^{-d}) q)}$.

If $m > (1 + \varepsilon) m_{\text{COMP}, Z}$, noisy COMP will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Corollary 2.8 (Noisy DD for the Z channel). *Let $p = 0, 0 < q < 1, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{DD}, Z} = \min_{\alpha, d} \max \{ c_1(\alpha, d), c_2(\alpha, d), c_3(d) \} k \log(n/k)$$

with $c_1(\alpha, d) = \frac{\theta}{1 - \theta} \frac{1}{d D_{\text{KL}}(\alpha \| q)}$ and $c_2(\alpha, d) = \frac{1}{d D_{\text{KL}}(\alpha \| e^{-d} + (1 - e^{-d}) q)}$

and $c_3(d) = \frac{\theta}{1 - \theta} \frac{1}{-d \log(1 - e^{-d}(1 - q))}$.

If $m > (1 + \varepsilon) m_{\text{DD}, Z}$, noisy DD will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Proof. The bounds c_1 and c_2 follow directly from Theorem 2.2 by setting $p = 0$. For c_3 we use the fact that $D_{\text{KL}}(1/\Delta \| e^{-d}(1 - q)) = -\log(1 - e^{-d}(1 - q)) + o(1)$. An immediate consequence of $p = 0$ is $c_4 = 0$. \square

An illustration of the bounds from Corollary 2.7 and 2.8 for sample values of q is shown in Figure 5.

2.3.3. *Reverse Z channel.* In the reverse Z channel, we have $q = 0$ and $p > 0$, i.e. no truly positive test displays a negative test result. thus, we set $\alpha = 1/\Delta$ and remain agnostic about β and d . The bounds for the noisy COMP and DD thus read as follows.

Corollary 2.9 (Noisy COMP for the Reverse Z channel). *Let $0 < p < 1, q = 0, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{COMP}, \text{rev} Z} = \frac{1}{1-\theta} \min_d \left\{ \frac{1}{-d \log(1 - e^{-d}(1-p))} \right\} k \log(n/k).$$

If $m > (1 + \varepsilon) m_{\text{COMP}, \text{rev} Z}$, noisy COMP will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Proof. The corollary follows from Theorem 2.1 and the fact that $D_{\text{KL}}(1/\Delta \| 0)$ diverges and $D_{\text{KL}}(1/\Delta \| e^{-d}(1-p)) = -\log(1 - e^{-d}(1-p))$. \square

Note that the optimal d arising from Corollary 2.9 cannot be expressed in terms of standard functions.

Corollary 2.10 (Noisy DD in the Reverse Z channel). *Let $0 < p < 1, q = 0, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{DD}, \text{rev} Z} = \min_{\beta, d} \max \{c_2(d), c_3(\beta, d), c_4(\beta, d)\} k \log(n/k)$$

with $c_2(d) = \frac{1}{-d \log(1 - e^{-d}(1-p))}$ *and* $c_3(\beta, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\beta \| e^{-d})}$

and $c_4(\beta, d) = \frac{1}{1-\theta} \frac{1}{d \left(-\log(1 - e^{-d}(1-p)) + D_{\text{KL}}\left(\beta \| \frac{e^{-d}p}{e^{-d}p + (1-e^{-d})}\right) \right)}$

If $m > (1 + \varepsilon) m_{\text{DD}, \text{rev} Z}$, noisy DD will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Proof. The bounds $c_1 = 0, c_2, c_3$ follow from Theorem 2.2 and the same manipulations as above. For c_4 , note that z needs to take the value 1 since $1 - \alpha = 1 - 1/\Delta$, whence the simplification follows immediately. \square

An illustration of the bounds of Corollary 2.9 and 2.10 for sample values of p is shown in Figure 6.

2.3.4. *Binary Symmetric Channel.* In the Binary Symmetric Channel (BSC), we set $p = q > 0$. Even though information-theoretic arguments would suggest setting $d = \log 2$, we formulate the expression below with general d . We also keep the threshold parameters α and β . The bounds for the noisy DD and COMP only simplify slightly.

Corollary 2.11 (Noisy COMP in the Binary Symmetric Channel). *Let $0 < p = q < 1/2, 0 < \theta < 1$ and $\varepsilon > 0$. Further, let*

$$m_{\text{COMP}, \text{BSC}} = \min_{\alpha, d} \max \{b_1(\alpha, d), b_2(\alpha, d)\} k \log(n/k)$$

with $b_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| p)}$ *and* $b_2(\alpha, d) = \frac{1}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| e^{-d} + p - 2e^{-d}p)}$.

If $m > (1 + \varepsilon) m_{\text{COMP}, \text{BSC}}$, noisy COMP will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Corollary 2.12 (Noisy DD in the Binary Symmetric Channel). *Let $0 < p = q < 1/2, 0 < \theta < 1$ and $\varepsilon > 0$ and define $v = 1 - e^{-d} - p + 2e^{-d}p$. Further, let*

$$m_{\text{DD}, \text{BSC}} = \min_{\alpha, \beta, d} \max \{c_1(\alpha, d), c_2(\alpha, d), c_3(\beta, d), c_4(\alpha, \beta, d)\} k \log(n/k)$$

with $c_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\alpha \| p)}$ *and* $c_2(\alpha, d) = \frac{1}{d D_{\text{KL}}(\alpha \| e^{-d} + p - 2e^{-d}p)}$

and $c_3(\beta, d) = \frac{\theta}{1-\theta} \frac{1}{d D_{\text{KL}}(\beta \| (1-p)e^{-d})}$

and $c_4(\alpha, \beta, d) = \max_{1-\alpha \leq z \leq 1} \left\{ \frac{1}{1-\theta} \frac{1}{d \left(D_{\text{KL}}(z \| v) + \mathbf{1} \left\{ \beta > \frac{ze^{-d}p}{v} \right\} z D_{\text{KL}}\left(\frac{\beta}{z} \| \frac{e^{-d}p}{v}\right) \right)} \right\}$.

If $m > (1 + \varepsilon) m_{\text{DD}, \text{BSC}}$, noisy DD will recover σ w.h.p. given $\mathbf{G}, \hat{\sigma}$.

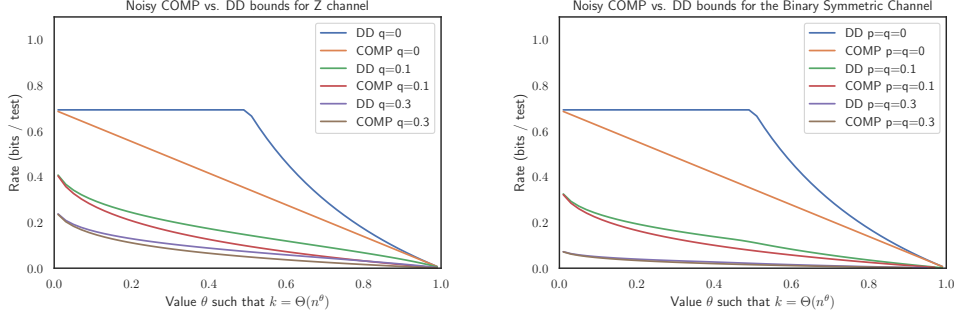


FIGURE 3. Comparison of the bound for noisy DD and noisy COMP in the Z-channel and the Binary Symmetric Channel for different noise level.

An illustration of the bounds of Corollary 2.11 and 2.12 is shown in Figure 7.

2.4. Comparison of noisy COMP and DD. An obvious next question is to find conditions under which the noisy DD algorithm outperforms noisy COMP. For the noiseless setting, it can be easily shown that DD provably outperforms COMP for all $\theta \in (0, 1)$. For the noisy case, matters are slightly more complicated.

Recall that noisy COMP classifies all individuals appearing in less than $\alpha\Delta$ displayed negative tests as infected while noisy DD additionally requires such individuals to appear in more than $\beta\Delta$ displayed positive tests as the only yet unclassified individual. Thus, it might well be that an infected individual is classified correctly by noisy COMP, while it is missed by the noisy DD algorithm.

That being said, our simulations indicate that noisy DD generally outperforms noisy COMP, but for the reason mentioned above we can only prove that noisy DD outperforms noisy COMP for the reverse Z channel while remaining agnostic about the Z channel and the Binary Symmetric Channel, as the next proposition evinces.

Proposition 2.13. *For all $p, q \geq 0$ with $p + q < 1$ there exists a $d^* \in (0, \infty)$ such that $m_{COMP} \geq m_{DD}$ as long as $e^{-d^*} p \geq q$.*

In terms of the common noise channels Proposition 2.13 gives the following corollary.

Corollary 2.14. *In the reverse Z channel, $m_{COMP} \geq m_{DD}$.*

Our simulations suggest that this superior performance of noisy DD holds as well for the Z channel and Binary Symmetric Channel. Please refer to Figure 3 for an illustration.

2.5. Relation to Bernoulli testing. [26] derived sufficient bounds for noisy group testing and a Bernoulli test design where each individual joins every test with some fixed probability. Thus, the variable degrees fluctuate and we end up with some individuals assigned only to few tests. In contrast, we work under a model in this paper where each individual joins an equal number of tests Δ chosen uniformly at random without replacement. For the noiseless case, it is by now clear that the constant-column design better facilitates inference than the Bernoulli test design [13, 26]. We find that the same holds true for the noisy variant of the COMP algorithm. Let us denote by m_{COMP}^{Ber} the number of tests required for the noisy COMP to succeed under a Bernoulli test design.

Proposition 2.15. *For all $p + q < 1$, we have*

$$m_{COMP}^{Ber} \geq m_{COMP}$$

We see the same effect for the noisy variant of the DD algorithm for all simulations, but for technical reasons only prove it for the Z channel.

Proposition 2.16. For the Z channel where $p = 0$ and $0 < q < 1$, we have

$$m_{DD}^{Ber} > m_{DD}$$

For an illustration on the magnitude of the difference, we refer to Figure 4 and Figure 8.

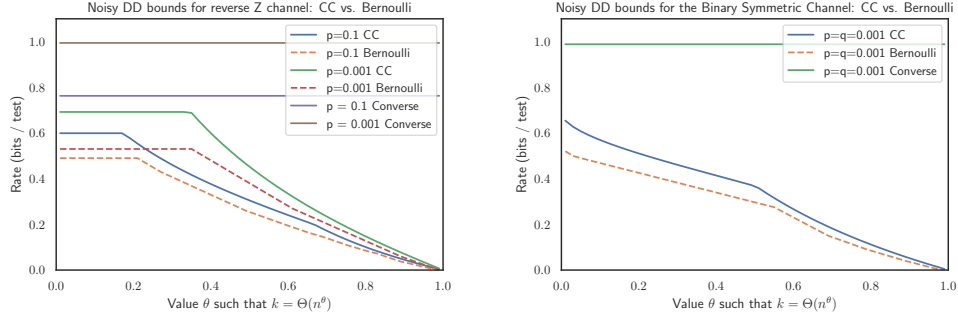


FIGURE 4. Comparison of DD bounds under a Bernoulli test design ([48]) and constant column test design (present paper) for the reverse Z and Binary Symmetric Channel

APPENDIX

The core of the technical sections is the proof of Theorems 2.1 and Theorem 2.2. Some groundwork with standard concentration bounds and group testing properties can be found in Section A. We continue with the proof of Theorems 2.1 and 2.2 in Sections B and C, respectively. The structure of the proofs follows a similar logic. First, we derive the distributions for the number of displayed positive and negative tests for infected and healthy individuals. Second, we threshold these distributions using sharp Chernoff concentration bounds to deduce the bounds stated in Theorem 2.1 and Theorem 2.2. Thereafter, we proceed to the proof of Proposition 2.13 in Section D, while the proofs of Propositions 2.15 and 2.16 follow in Section E. We conclude with the proof of the converse result from Theorem 2.3 in Section F.

APPENDIX A. GROUNDWORK

For starters, let us recall the Chernoff bound for binomial and hypergeometric distributions.

Lemma A.1 (Chernoff bound for the binomial distribution [25]). *Let $p < q < r \in (0, 1)$ and $X \sim \text{Bin}(n, q)$ be a binomially distributed random variable. Then*

$$\begin{aligned}\mathbb{P}(X \leq \lceil pn \rceil) &= \exp\left(-\left(1 + n^{-\Omega(1)}\right) nD_{\text{KL}}(p \parallel q)\right) \\ \mathbb{P}(X \geq \lceil rn \rceil) &= \exp\left(-\left(1 + n^{-\Omega(1)}\right) nD_{\text{KL}}(r \parallel q)\right)\end{aligned}$$

Lemma A.2 (Chernoff bound for the hypergeometric distribution [23]). *Let $p < q < r \in (0, 1)$ and $Y \sim H(N, Q, n)$ be a hypergeometrically distributed random variable. Further, let $q = Q/N$. Then*

$$\begin{aligned}\mathbb{P}(H(N, Q, n) \leq \lceil pn \rceil) &= \exp\left(-\left(1 + n^{-\Omega(1)}\right) nD_{\text{KL}}(p \parallel q)\right) \\ \mathbb{P}(H(N, Q, n) \geq \lceil rn \rceil) &= \exp\left(-\left(1 + n^{-\Omega(1)}\right) nD_{\text{KL}}(r \parallel q)\right)\end{aligned}$$

The next lemma provides that the test degrees, as defined in (1.3) above, are tightly concentrated. Recall from (1.2) that the number of tests $m = ck \log(n/k)$ and each item appears in $\Delta = cd \log(n/k)$ tests.

Lemma A.3. *With probability $1 - o(n^{-2})$ we have*

$$dn/k - \sqrt{dn/k} \log n \leq \Gamma_{\min} \leq \Gamma_{\max} \leq dn/k + \sqrt{dn/k} \log n$$

Proof. The probability that an individual x is assigned to test a is given by

$$(A.1) \quad \mathbb{P}(x \in \partial a) = 1 - \mathbb{P}(x \notin \partial a) = 1 - \binom{m-1}{\Delta} \binom{m}{\Delta}^{-1} = \Delta/m = d/k$$

Since each individual is assigned to tests independently, the total number of individuals in a given test follows the binomial distribution $\text{Bin}(n, d/k)$. The assertion now follows from the Chernoff bound for binomial distributions (Lemma A.1). \square

Next, we show that the number of truly negative tests \mathbf{m}_0 (and thus the number of truly positive tests \mathbf{m}_1) are tightly concentrated.

Lemma A.4. *With probability $1 - o(n^{-2})$ we have $\mathbf{m}_0 = e^{-d} m + O(\sqrt{m} \log^3 n)$.*

Proof. Recall from (A.1) that

$$\mathbb{P}(x \in \partial a) = d/k$$

Since infected individuals are assigned to tests mutually independently, we find for a test a that

$$\mathbb{P}(V_1 \cap \partial a = \emptyset) = \mathbb{P}(\text{Bin}(k, d/k) = 0) = (1 - d/k)^k = (1 + n^{-\Omega(1)}) e^{-d}.$$

Consequently, $\mathbb{E}[\mathbf{m}_0] = (1 + n^{-\Omega(1)})e^{-d}m$. Finally, changing the set of tests for a specific infected individual shifts the total number of negative tests by at most Δ . Therefore, the Azuma-Hoeffding inequality yields

$$\mathbb{P}(|\mathbf{m}_0 - \mathbb{E}[\mathbf{m}_0]| \geq t) \leq 2 \exp\left(-\frac{t^2}{4k\Delta^2}\right).$$

The lemma follows from setting $t = \sqrt{m} \log^3 n$. \square

With the concentration of \mathbf{m}_0 and \mathbf{m}_1 at hand, we readily obtain estimates for $\mathbf{m}_0^f, \mathbf{m}_0^u, \mathbf{m}_1^f$ and \mathbf{m}_1^u .

Corollary A.5. *With probability $1 - o(n^{-2})$ we have*

- (i) $\mathbf{m}_0^f = e^{-d}pm + O(\sqrt{m} \log^4 n)$
- (ii) $\mathbf{m}_0^u = e^{-d}(1-p)m + O(\sqrt{m} \log^4 n)$
- (iii) $\mathbf{m}_1^f = (1 - e^{-d})qm + O(\sqrt{m} \log^4 n)$
- (iv) $\mathbf{m}_1^u = (1 - e^{-d})(1-q)m + O(\sqrt{m} \log^4 n)$

Proof. Since each test is flipped with probability p and q independently, the claims follow from Lemma A.4 and the Chernoff bound for the binomial distribution (Lemma A.1). \square

In the following, let \mathcal{E} be the event that the bounds from Lemma A.4 and A.5 hold.

APPENDIX B. PROOF OF COMP BOUND, THEOREM 2.1

Recall from (2.1) that we write N_x for the number of displayed negative tests that item x appears in (as illustrated by the right branch of Fig. 2). The proof of Theorem 2.1 is based on two pillars. First, Lemmas B.1 and B.2 provide the distribution of N_x for healthy and infected individuals, respectively. We will see that these distributions differ according to the infection status of the individual. Second, we will derive a suitable threshold $\alpha\Delta$ via Lemma B.3 and B.4 to tell healthy and infected individuals apart w.h.p. We start by analysing individuals in the infected set V_1 . Throughout the section, we assume $\alpha \in (q, e^{-d}(1-p) + (1 - e^{-d})q)$.

Lemma B.1. *Given $x \in V_1$, its number of displayed negative tests N_x is distributed as $\text{Bin}(\Delta, q)$.*

Proof. Any test containing an infected individual is truly positive because of the presence of the infected individual. Since an infected individual is assigned to Δ different tests and each such test is flipped with probability q independently, the lemma follows immediately. \square

Next, we consider the distribution for healthy individuals. Recall that \mathcal{E} denotes the event that the bounds from Lemma A.4 and Corollary A.5 hold.

Lemma B.2. *Given $x \in V_0$ and \mathcal{E} , N_x is distributed as $H(m, m(e^{-d}(1-p) + (1 - e^{-d})q) + n^{-\Omega(1)}), \Delta)$.*

Proof. Since x is healthy, the outcome of all the tests remains the same if it is removed from consideration (if we perform group testing with $n - 1$ items and the corresponding reduced matrix).

Thus, given \mathcal{E} , we find that with x removed the $\mathbf{m}_0^f, \mathbf{m}_0^u, \mathbf{m}_1^f, \mathbf{m}_1^u$ still satisfy the bounds from Corollary A.5. As a result the number of displayed negative tests (which consist of unflipped truly negative tests and flipped truly positive tests) is given by

$$(B.1) \quad \mathbf{m}_0^u + \mathbf{m}_1^f = \left(e^{-d}(1-p) + (1 - e^{-d})q\right)m + O(\sqrt{m} \log^4 n)$$

Now, adding x back into consideration: $x \in V_0$ chooses Δ tests without replacement independently of this. Hence the number of displayed negative tests it appears in N_x is distributed as $H(m, \mathbf{m}_0^u + \mathbf{m}_1^f, \Delta)$ and the lemma follows. \square

Moving to the second pillar of the proof, we need to demonstrate that no infected individual is assigned to more than $\alpha\Delta$ displayed negative tests as shown by the following lemma.

Lemma B.3. *If $c > (1 + \eta) \frac{\theta}{1-\theta} \frac{1}{dD_{\text{KL}}(\alpha\|q)}$ for some small $\eta > 0$, $N_x < \alpha\Delta$ for all $x \in V_1$ w.h.p.*

Proof. We have to ensure that $\mathbb{P}(\exists x \in V_1 : N_x \geq \alpha\Delta) = o(1)$. By Lemma B.1 and the union bound, we thus need to have

$$o(1) = k \cdot \mathbb{P}(N_x \geq \alpha\Delta : x \in V_1) = k \cdot \mathbb{P}(\text{Bin}(\Delta, q) \geq \alpha\Delta) = k \cdot \exp\left(-\left(1 + \Delta^{-\Omega(1)}\right) \Delta D_{\text{KL}}(\alpha\|q)\right),$$

by the Chernoff bound for the binomial distribution (Lemma A.1). Since $k \sim n^\theta$ and $\Delta = cd(1-\theta)\log n$ this implies

$$\theta - cd(1-\theta)D_{\text{KL}}(\alpha\|q) < 0$$

The lemma follows from rearranging terms. \square

We proceed to show that no healthy individual is assigned to less than $\alpha\Delta$ displayed negative tests.

Lemma B.4. *If $c > (1 + \eta) \frac{1}{1-\theta} \frac{1}{dD_{\text{KL}}(\alpha\|e^{-d}(1-p) + (1-e^{-d})q)}$ for some small $\eta > 0$, $N_x > \alpha\Delta$ for all $x \in V_0$ w.h.p.*

Proof. We need to ensure that $\mathbb{P}(\exists x \in V_0 : N_x < \alpha\Delta) = o(1)$. Since \mathcal{E} occurs w.h.p. by Lemma A.4 and Corollary A.5, we need to have by Lemma B.2 and the union bound that

$$(B.2) \quad (n-k) \cdot \mathbb{P}(N_x \leq \alpha\Delta | x \in V_0, \mathcal{E}) \leq n \cdot \mathbb{P}\left(H\left(m, m\left(e^{-d}(1-p) + (1-e^{-d})q + n^{-\Omega(1)}\right), \Delta\right) \leq \alpha\Delta\right) = o(1).$$

Together with the Chernoff bound for the hypergeometric distribution (Lemma A.2) this implies

$$1 - cd(1-\theta)D_{\text{KL}}\left(\alpha\|(1-pe^{-d} + (1-e^{-d})q)\right) < 0$$

in a similar way to the proof of Lemma B.3. The lemma follows from rearranging terms. \square

Proof of Theorem 2.1. The theorem is now an immediate consequence of Lemma B.3 and B.4 which guarantee that w.h.p. classifying individuals according to the threshold $\alpha\Delta$ for negative displayed tests recovers σ , and the fact that the choice of α and d is at our disposal. \square

APPENDIX C. PROOF OF DD BOUND, THEOREM 2.2

The proof of Theorem 2.2 follows a similar two-step approach as the proof of Theorem 2.1 by first finding the distribution of \mathbf{P}_x (the number of displayed positive tests where individual x appears on its own after removing the definitely healthy individuals $V_0 \setminus V_{0,\text{PD}}$, illustrated by the left branch of Fig. 2). We then threshold the distributions for healthy and infected individuals. To get started, we revise the second bound from Theorem 2.1 to allow $kn^{-\Omega(1)}$ healthy individuals to not be classified yet after the first step of DD. Throughout the section, we assume $\alpha \in (q, e^{-d}(1-p) + (1-e^{-d})q)$ and $\beta \in (0, e^{-d}(1-q))$.

Lemma C.1. *If*

$$c > (1 + \eta) \frac{1}{dD_{\text{KL}}(\alpha\|e^{-d}(1-p) + (1-e^{-d})q)}$$

for some small $\eta > 0$, we have $|V_{0,\text{PD}}| = kn^{-\Omega(1)}$ w.h.p.

Proof. The lemma follows immediately by replacing the r.h.s. of (B.2) with $kn^{-\delta}$ for some small $\delta = \delta(\eta)$, rearranging terms and applying Markov's inequality. \square

For the next lemmas, we need an auxiliary notation denoting the number of tests $\mathbf{m}_{0,\text{nd}}$ that only contain individuals from $V_0 \setminus V_{0,\text{PD}}$. In symbols,

$$\mathbf{m}_{0,\text{nd}} = \left| \{a \in F : \partial a \subset V_0 \setminus V_{0,\text{PD}}\} \right|.$$

Lemma C.2. *If*

$$c > (1 + \eta) \frac{1}{dD_{\text{KL}}(\alpha \| e^{-d}(1-p) + (1-e^{-d})q)}$$

for some small $\eta > 0$, we have $\mathbf{m}_{0,nd} = (1 - n^{-\Omega(1)}) e^{-d} m$ with probability $1 - o(n^{-2})$.

Proof. As in the proof of Lemma B.2 above, we consider the graph in two rounds: first we consider the tests containing infected individuals. Since each healthy individual $x \in V_0$ does not impact the number of positive and negative tests, we know by Lemma A.4 that with probability $1 - o(n^{-2})$ we have $\mathbf{m}_0 = e^{-d} m + O(\sqrt{m} \log^4 n)$ after the first round.

Now consider some particular negative test a . The probability that a healthy individual x is assigned to this test is d/k by (A.1). By Lemma C.1, we know that $|V_{0,\text{PD}}| = kn^{-\Omega(1)}$. Since each such individual is assigned to tests mutually independently, we find for the truly negative test a that

$$\mathbb{P}(V_{0,\text{PD}} \cap \partial a = \emptyset) = \mathbb{P}(\text{Bin}(|V_{0,\text{PD}}|, d/k) = 0) = (1 - d/k)^{kn^{-\Omega(1)}} = 1 - n^{-\Omega(1)}$$

We therefore have $\mathbb{E}[\mathbf{m}_{0,nd}] = (1 - n^{-\Omega(1)}) e^{-d} m$. Finally, changing the set of tests for a specific individual $x \in V_1 \cup V_{0,\text{PD}}$ shifts $\mathbf{m}_{0,nd}$ by at most Δ . The lemma follows by a similar application of the Azuma-Hoeffding inequality as used in the proof of Lemma A.4. \square

Let \mathcal{F} be the event that $\mathbf{m}_{0,nd} = (1 - n^{-\Omega(1)}) e^{-d} m$ indeed. By Lemma C.2, $\mathbb{P}(\mathcal{F}) = 1 - o(n^{-2})$ if

$$c > (1 + \eta) \frac{1}{dD_{\text{KL}}(\alpha \| e^{-d}(1-p) + (1-e^{-d})q)}$$

for some small $\eta > 0$. With Lemma C.2 at hand, we are in a position to describe the distribution of \mathbf{P}_x for healthy and infected individuals. Let us start with infected individuals.

Lemma C.3. *Given an infected individual $x \in V_1$ and assuming \mathcal{F} holds, \mathbf{P}_x is distributed as $H(m, m(e^{-d}(1-q) + n^{-\Omega(1)}), \Delta)$.*

Proof. Consider an infected individual $x \in V_1$. As before, if we remove x from tests, this will change $\mathbf{m}_{0,nd}$ by at most Δ .

Thus, by Lemma C.2 the number of tests that x is assigned to that contain neither infected individuals nor individuals from $V_{0,\text{PD}}$ is distributed as $H(m, m(e^{-d} + n^{-\Omega(1)}), \Delta)$ given \mathcal{F} . Since each test featuring x will truly be positive and will be displayed positive with probability $1 - q$ independently, the lemma follows immediately. \square

To describe the distribution of \mathbf{P}_x for healthy individuals, let us introduce the random variable $\mathbf{P}_x(P)$, which is \mathbf{P}_x conditioned on the individual appearing in P displayed positive tests, as follows:

$$\mathbb{P}(\mathbf{P}_x(P) = t) = \mathbb{P}(\mathbf{P}_x = t | N_x = \Delta - P)$$

Then, we find for healthy individuals the following conditional distribution.

Lemma C.4. *Given $x \in V_0$ and \mathcal{F} , $\mathbf{P}_x(P)$ is distributed as*

$$H\left(m\left(e^{-d}p + (1 - e^{-d})(1 - q) + n^{-\Omega(1)}\right), m\left(e^{-d}p + n^{-\Omega(1)}\right), P\right).$$

Proof. We proceed with the same exposition as in the proof of Lemma C.3. Since individual $x \in V_0$ is assigned to exactly P displayed positive, $\mathbf{P}_x(P)$ is distributed as $H(\mathbf{m}_0^f + \mathbf{m}_1^u, \mathbf{m}_{0,nd}, P)$. The lemma follows from Corollary A.5 and Lemma C.2. \square

Having derived the distributions for \mathbf{P}_x for $x \in V_1$ and $\mathbf{P}_x(P)$ for $x \in V_0$ we can now determine a threshold $\beta\Delta$ of displayed positive tests where the individual appears only with individuals from the set $V_0 \setminus V_{0,\text{PD}}$ such that we can tell V_1 and $V_{0,\text{PD}}$ apart and thus recover σ . Let us start with infected individuals.

Lemma C.5. *As long as*

$$c > (1 + \eta) \max \left\{ \frac{1}{dD_{\text{KL}}(\alpha \| e^{-d}(1-p) + (1-e^{-d})q)}, \frac{\theta}{1-\theta} \frac{1}{dD_{\text{KL}}(\beta \| (1-q)e^{-d})} \right\}$$

for some small $\eta > 0$, we have $\mathbf{P}_x > \beta\Delta$ for all $x \in V_1$ w.h.p.

Proof. We need to ensure that $\mathbb{P}(\exists x \in V_1 : \mathbf{P}_x < \beta\Delta) = o(1)$. For the bound on c from the lemma, we know that \mathcal{F} occurs w.h.p. by Lemma C.2. In combination with Lemma C.3 and the union bound we need to ensure

$$(C.1) \quad k \cdot \mathbb{P}(\mathbf{P}_x \leq \beta\Delta | x \in V_1, \mathcal{F}) = k \cdot \mathbb{P}\left(H\left(m, m\left(e^{-d}(1-q) + n^{-\Omega(1)}\right), \Delta\right) \leq \beta\Delta\right) = o(1)$$

Using the Chernoff bound for the hypergeometric distribution (Lemma A.2), (C.1) holds if

$$(C.2) \quad \theta - cd(1-\theta)D_{\text{KL}}\left(\beta \| (1-q)e^{-d}\right) < 0$$

The lemma follows from rearranging terms in (C.2). □

We proceed with the set of individuals $V_{0,\text{PD}}$.

Lemma C.6. *As long as*

$$c > (1 + \eta) \max \left\{ \frac{1}{dD_{\text{KL}}(\alpha \| e^{-d}(1-p) + (1-e^{-d})q)}, \max_{1-\alpha \leq z \leq 1} \left\{ \frac{1}{1-\theta} \frac{1}{d\left(D_{\text{KL}}(z \| e^{-d}p + (1-e^{-d})(1-q)) + zD_{\text{KL}}\left(\frac{\beta}{z} \| \frac{e^{-d}p}{e^{-d}p + (1-e^{-d})(1-q)}\right)\right)} \right\} \right\}$$

for some small $\eta > 0$, we have $\mathbf{P}_x < \beta\Delta$ for all $x \in V_{0,\text{PD}}$ w.h.p.

Proof. We need to ensure that $\mathbb{P}(\exists x \in V_{0,\text{PD}} : \mathbf{P}_x > \beta\Delta) = o(1)$. For the bound on c from the lemma, we know that \mathcal{F} occurs w.h.p. by Lemma C.2. Moreover, \mathcal{E} occurs w.h.p. by Lemma A.4 and Corollary A.5. We write $w = e^{-d}p + (1-e^{-d})(1-q)$ for brevity. Combining this fact with Lemma B.2 and C.4 we need to ensure

$$(C.3) \quad (n-k) \sum_{P=(1-\alpha)\Delta}^{\Delta} \mathbb{P}(\mathbf{N}_x = \Delta - P | x \in V_{0,\text{PD}}, \mathcal{E}) \mathbb{P}(\mathbf{P}_x(P) \geq \beta\Delta | x \in V_{0,\text{PD}}, \mathcal{F}) \\ = (1 - n^{-\Omega(1)}) n \sum_{P=(1-\alpha)\Delta}^{\Delta} \mathbb{P}(H(m, m(w + n^{-\Omega(1)}), \Delta) = P)$$

$$(C.4) \quad \mathbb{P}\left(H\left(m(w + n^{-\Omega(1)}), m\left(e^{-d}p + n^{-\Omega(1)}\right), P\right) \geq \beta\Delta\right) = o(1)$$

By the Chernoff bound for the hypergeometric distribution (Lemma A.2) and setting $z = P/\Delta$, we reformulate the left-hand-side of (C.4) to

$$n \sum_{P=(1-\alpha)\Delta}^{\Delta} \exp\left(- (1 + o(1))\Delta \left(D_{\text{KL}}(z \| w) + \mathbf{1}\left\{ \beta > \frac{ze^{-d}p}{w} \right\} zD_{\text{KL}}\left(\frac{\beta}{z} \| \frac{e^{-d}p}{w}\right) \right)\right) \\ = (1 + n^{-\Omega(1)}) n \max_{1-\alpha \leq z \leq 1} \left\{ \exp\left(- (1 + o(1))\Delta \left(D_{\text{KL}}(z \| w) + \mathbf{1}\left\{ \beta > \frac{ze^{-d}p}{w} \right\} zD_{\text{KL}}\left(\frac{\beta}{z} \| \frac{e^{-d}p}{w}\right) \right)\right) \right\}$$

where the second equality follows since the sum consists of $\Theta(\Delta) = \Theta(\log n)$ many summands. Since $\mathbb{P}(\mathcal{F}) = 1 - n^{-\Omega(1)}$ for our choice of c by Lemma C.2 rearranging terms readily yields that the expression in (C.3) is indeed of order $o(1)$. □

Proof of Theorem 2.2. The theorem is now immediate from Lemma B.3, C.1, C.5 and C.6 and the fact that the choice of α, β and d is at our disposal. □

APPENDIX D. COMPARISON OF THE NOISY DD AND COMP BOUNDS

The following section is intended to prove sufficient conditions under which the DD algorithm is guaranteed to outperform COMP. However, these conditions are not necessary and DD might (and for all performed simulations does) outperform COMP for even wider settings.

Proof of Proposition 2.13. In order to prove the proposition, we need to find conditions under which

$$\min_{\alpha, d} \max \{b_1(\alpha, d), b_2(\alpha, d)\} \geq \min_{\alpha, \beta, d} \max \{c_1(\alpha, d), c_2(\alpha, d), c_3(\beta, d), c_4(\alpha, \beta, d)\}$$

We write α^* and d^* for the values that minimise the maximum of the two terms at the LHS, at which point we know that $b_1(\alpha^*, d^*) = b_2(\alpha^*, d^*)$. Then it is sufficient to show that there exists β^* such that

$$b_1(\alpha^*, d^*) = b_2(\alpha^*, d^*) \geq \max \{c_1(\alpha^*, d^*), c_2(\alpha^*, d^*), c_3(\beta^*, d^*), c_4(\alpha^*, \beta^*, d^*)\}$$

By inspection for any α and d $b_1(\alpha, d) = c_1(\alpha, d)$ and $b_2(\alpha, d) \geq c_2(\alpha, d)$ since $\theta \in (0, 1)$.

Next, we will show that $b_2(\alpha, d) \geq c_4(\alpha, \beta, d)$ for any α, β in the respective bounds and $d \in (0, \infty)$. Writing $w = e^{-d}p + (1 - e^{-d})(1 - q)$, and recalling that by assumption that $\alpha \leq 1 - w$ (or $w \leq 1 - \alpha$) we readily find that

$$(D.1) \quad D_{\text{KL}}(\alpha \| 1 - w) = \min_{1 - \alpha \leq z \leq 1} (D_{\text{KL}}(z \| w)) \leq \min_{1 - \alpha \leq z \leq 1} \left(D_{\text{KL}}(z \| w) + z \mathbf{1} \left\{ \beta > \frac{ze^{-d}p}{w} \right\} D_{\text{KL}} \left(\frac{\beta}{z} \parallel \frac{e^{-d}p}{w} \right) \right)$$

where the first equality follows since $D_{\text{KL}}(\alpha \| 1 - w) = D_{\text{KL}}(1 - \alpha \| w)$ and $D_{\text{KL}}(z \| w) > D_{\text{KL}}(1 - \alpha \| w)$ for any $z > 1 - \alpha$. The bound follows. Note that (D.1) indeed holds for any choice of α, β and d in the respective bounds stated in the theorem.

Finally, we need to demonstrate that $c_3(\beta^*, d^*) \leq b_2(\alpha^*, d^*)$. Since β is not an optimisation parameter in $b_2(\alpha^*, d^*)$ and the bound in (D.1) holds for any value of β , we can simply set it to the value that minimizes $c_3(\beta^*, d^*)$ which is $\beta = 1/\Delta$ and for which we find

$$c_3(\beta^*, d^*) = \frac{\theta}{1 - \theta} \frac{1}{d^* \log(1 - e^{-d^*}(1 - q))}.$$

Thus, to obtain the desired inequality we need to ensure that for the optimal choice α^* from COMP

$$\theta D_{\text{KL}}(\alpha^* \| e^{-d^*}(1 - p) + (1 - e^{-d^*})q) \leq -\log(1 - e^{-d^*}(1 - q))$$

Using the bound

$$\theta D_{\text{KL}}(\alpha \| e^{-d}(1 - p) + (1 - e^{-d})q) \leq -\theta \log(1 - (e^{-d}(1 - p) + (1 - e^{-d})q)) \leq -\log(1 - (e^{-d}(1 - p) + (1 - e^{-d})q))$$

which is obtained by setting $\alpha = 1/\Delta$, we find that $c_3(\beta^*, d^*) \leq b_2(\alpha^*, d^*)$ if

$$-\log(1 - e^{-d^*}(1 - q)) \geq -\log(1 - e^{-d^*}(1 - p) + (1 - e^{-d^*})q) \Leftrightarrow e^{-d^*}p \geq q$$

□

As mentioned before, due to bounding $b_2(\alpha^*, d^*)$ the result is not sharp. However, one immediate consequence of Proposition 2.13 is that DD is guaranteed to outperform COMP for the reverse Z channel.

APPENDIX E. RELATION TO BERNOULLI TESTING

In the noiseless case [26] shows that the constant column weight design (where each individual joins exactly Δ different tests) requires fewer tests to recover σ than the Bernoulli design (where each individual is included in each test with a certain probability independently). In this section we show that in the noisy case, the COMP algorithm requires fewer tests for the constant column weight design than for the Bernoulli design, and derive sufficient conditions under which the same is true for the noisy DD algorithm.

To get started, let us state the relevant bounds for the Bernoulli design. [48] derived these bounds for the Z channel, reverse Z channel and Binary Symmetric Channel. Building on this work, let us extend these bounds for the general $p - q$ -model. The test design and notation is identical to the constant column design employed so far with the key difference that individuals are not assigned to Δ tests uniformly at random without replacement, but that each individual is included in each test with probability $\Delta/m = d/k$ independently. Our first observation is the size of $\mathbf{m}_0, \mathbf{m}_0^f, \mathbf{m}_0^u, \mathbf{m}_1^f$ and \mathbf{m}_1^u carry over without further ado.

Lemma E.1. *The bounds from Lemma A.4 and Corollary A.5 hold for the Bernoulli test design.*

Proof. The crucial observation is that (A.1) now becomes $\mathbb{P}(x \in \partial a) = \Delta/m$ for any individual $x \in V$ and test $a \in F$ where we avoid any dependencies between tests that we encountered before. The rest of the proof follows exactly the proof of Lemma A.4 and Corollary A.5. \square

Proposition E.2 (Noisy COMP under Bernoulli). *Let $p, q \geq 0, p + q < 1, d \in (0, \infty), \alpha \in (q, e^{-d}(1-p) + (1-e^{-d})q)$. Suppose that $0 < \theta < 1$ and $\varepsilon > 0$ and let*

$$m_{\text{COMP}}^{\text{Ber}} = m_{\text{COMP}}^{\text{Ber}}(n, \theta, p, q) = \min_{\alpha, d} \max\{b_1(\alpha, d), b_2(\alpha, d)\} k \log(n/k)$$

$$\text{where } b_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{k D_{\text{KL}}(\alpha d/k \| qd/k)}$$

$$\text{and } b_2(\alpha, d) = \frac{1}{1-\theta} \frac{1}{k D_{\text{KL}}(\alpha d/k \| (e^{-d}(1-p) + (1-e^{-d})q)d/k)}$$

If $m > (1 + \varepsilon) m_{\text{COMP}}^{\text{Ber}}$, COMP will recover σ under the Bernoulli test design w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Proof. Using the same two-round exposition of the graph as in prior proofs and again denoting by N_x the number of displayed negative tests for an individual x , we readily find

$$N_x \sim \text{Bin}(m, qd/k) \quad \text{for } x \in V_1$$

$$N_x \sim \text{Bin}(\mathbf{m}_0^u + \mathbf{m}_1^f, d/k) \quad \text{for } x \in V_0$$

Using the union bound, we thus have

$$(E.1) \quad k \cdot \mathbb{P}(N_x > \alpha \Delta | x \in V_1) = o(1) \Leftrightarrow c > b_1(\alpha, d)$$

$$(E.2) \quad (n-k) \cdot \mathbb{P}(N_x < \alpha \Delta | x \in V_0) = o(1) \Leftrightarrow c > b_2(\alpha, d)$$

closing the proof of the proposition. \square

Along the same lines, we obtain the bounds of the DD algorithm under the Bernoulli design.

Proposition E.3 (Noisy DD under Bernoulli). *Let $p, q \geq 0, p + q < 1, d \in (0, \infty), \alpha \in (q, e^{-d}(1-p) + (1-e^{-d})q)$ and $\beta \in (e^{-d}p, e^{-d}(1-q))$. Suppose that $0 < \theta < 1, \zeta \in (0, \theta)$ and $\varepsilon > 0$ and let*

$$m_{\text{DD}}^{\text{Ber}} = m_{\text{DD}}^{\text{Ber}}(n, \theta, p, q) = \min_{\alpha, \beta, d} \max\{c_1(\alpha, d), c_2(\alpha, d), c_3(\beta, d), c_4(\beta, d)\} k \log(n/k)$$

$$\text{where } c_1(\alpha, d) = \frac{\theta}{1-\theta} \frac{1}{k D_{\text{KL}}(\alpha d/k \| qd/k)}$$

$$\text{and } c_2(\alpha, d) = \frac{1-\zeta}{1-\theta} \frac{1}{k D_{\text{KL}}(\alpha d/k \| (e^{-d}(1-p) + (1-e^{-d})q)d/k)}$$

$$\text{and } c_3(\beta, d) = \frac{\theta}{1-\theta} \frac{1}{k \cdot D_{\text{KL}}(\beta d/k \| e^{-d}(1-q)d/k)}$$

$$\text{and } c_4(\beta, d) = \frac{\zeta}{1-\theta} \frac{1}{k \cdot D_{\text{KL}}(\beta d/k \| e^{-d}pd/k)}$$

If $m > (1 + \varepsilon)m_{DD}^{Ber}$, DD will recover σ under the Bernoulli test design w.h.p. given $\mathbf{G}, \hat{\sigma}$.

Proof. The bounds for $c_1(\alpha, d)$ and $c_2(\alpha, d)$ follow as in the proof of Proposition E.2 by replacing the right-hand side of (E.2) with n^ζ for some $\zeta \in (0, \theta)$. Next, we note that the bound for $m_{0,nd}$ of Lemma C.2 still holds as long as $\zeta \in (0, \theta)$. Using the same two-round exposition of the graph as in prior proofs and denoting by \mathbf{P}_x the number of displayed positive tests for an individual x such that the remaining neighbourhood of the test is a subset of $V_0 \setminus V_{0,PD}$, we readily find

$$\begin{aligned} k \cdot \mathbb{P}(\mathbf{P}_x < \beta\Delta | x \in V_1) &= o(1) \Leftrightarrow c > c_3(\beta, d) \\ (n - k) \cdot \mathbb{P}(\mathbf{P}_x > \beta\Delta | x \in V_0) &= o(1) \Leftrightarrow c > c_4(\beta, d) \end{aligned}$$

concluding the proof of the proposition. \square

To compare the bounds of the Bernoulli and constant-column test design we employ the following handy observation.

Lemma E.4. Let $0 < x, y < 1$ and $d > 0$ be constants independent of k . As $k \rightarrow \infty$

$$kD_{\text{KL}}\left(\frac{xd}{k} \parallel \frac{yd}{k}\right) = d(D_{\text{KL}}(x \parallel y) + v(x, y)) + o(1/k)$$

with

$$(E.3) \quad v(x, y) = y - x + (1 - x) \log\left(\frac{1 - y}{1 - x}\right) \leq 0$$

Proof. Applying the definition of the Kullback-Leibler divergence and Taylor expanding the logarithm we obtain

$$\begin{aligned} k \cdot D_{\text{KL}}\left(\frac{xd}{k} \parallel \frac{yd}{k}\right) &= xd \cdot \log\left(\frac{x}{y}\right) + (k - xd) \left(\log\left(1 - \frac{xd}{k}\right) - \log\left(1 - \frac{yd}{k}\right)\right) \\ &= xd \cdot \log\left(\frac{x}{y}\right) + (k - xd) \left(-\frac{xd}{k} + \frac{yd}{k} + o\left(\frac{1}{k^2}\right)\right) \\ &= d \left(x \cdot \log\left(\frac{x}{y}\right) - x + y\right) + o(1/k) \\ &= d \left(D_{\text{KL}}(x \parallel y) + y - x - (1 - x) \log\left(\frac{1 - x}{1 - y}\right)\right) + o(1/k). \end{aligned}$$

We can bound $v(x, y)$ from above by writing the final term as $(1 - x) \log\left(1 + \frac{x - y}{1 - x}\right) \leq (1 - x) \frac{x - y}{1 - x} = x - y$, using the standard linearisation of the logarithm. \square

We are now in a position to prove Proposition 2.15 and 2.16.

Proof of Proposition 2.15. The lemma follows by comparing the bounds from Theorem 2.1 and Proposition E.2 and applying Lemma E.4. \square

Proof of Proposition 2.16. As evident from Corollary 2.8, the fourth bound $c_4(\alpha, \beta, d)$ vanishes under the Z channel. Now comparing the bounds from Theorem 2.2 and Proposition E.3, observing that $(1 - \zeta)/(1 - \theta) > 1$ for $\zeta < \theta$ and applying Lemma E.4 immediately implies the lemma. \square

APPENDIX F. CONVERSE BOUND

We can give some sense of the sharpness of these results by considering the $p - q$ communication channel. That is, we write X for the channel input and Y for the output of a noisy channel with error probabilities given exactly by Figure 1. Recall that [7, Theorem 3.1] shows that the capacity of a particular noisy group testing problem is bounded above by the Shannon capacity of the corresponding channel. For completeness we derive the capacity and optimal signalling strategy of the $p - q$ channel in terms of $h(\cdot)$, the binary entropy in nats (logarithms taken to base e):

Lemma F.1. If $p + q < 1$ the Shannon capacity of the $p - q$ channel of Figure 1 measured in nats is

$$(F.1) \quad C_{Chan} = D_{\text{KL}}\left(q \parallel \frac{1}{1 + e^\phi}\right) = D_{\text{KL}}\left(p \parallel \frac{1}{1 + e^{-\phi}}\right),$$

where $\phi = (h(p) - h(q))/(1 - p - q)$. This is achieved by taking

$$(F.2) \quad \mathbb{P}(X = 0) = \frac{1}{1 - p - q} \left(\frac{1}{1 + e^\phi} - q \right).$$

Proof. Write $\mathbb{P}(X = 0) = \gamma$ and $\mathbb{P}(Y = 0) = T(\gamma) := (1 - p)\gamma + q(1 - \gamma)$. Then since the mutual information

$$(F.3) \quad I(X; Y) = h(Y) - h(Y|X) = h(T(\gamma)) - (\gamma h(p) + (1 - \gamma)h(q)),$$

we can find the optimal T by solving

$$0 = \frac{\partial}{\partial \gamma} I(X; Y) = (1 - p - q) \log\left(\frac{1 - T(\gamma)}{T(\gamma)}\right) - (h(p) - h(q)),$$

which implies that the optimal $T^* = 1/(1 + e^\phi)$. We can solve for this for $\gamma^* = (T^* - q)/(1 - p - q)$ to find the expression above. As $\frac{\partial}{\partial^2 \gamma} I(X; Y) < 0$ it is indeed a maximum. Substituting this in (F.3) we obtain that the capacity is given by

$$(F.4) \quad \begin{aligned} h(T^*) - (\gamma^* h(p) + (1 - \gamma^*)h(q)) &= h\left(\frac{1}{1 + e^\phi}\right) - ((T^* - q)\phi + h(q)) \\ &= \log(1 + e^\phi) - \phi(1 - q) - h(q) \\ &= D_{\text{KL}}(q \parallel 1/(1 + e^\phi)) \end{aligned}$$

as claimed in the first expression in (F.1) above. We can see that the second expression in (F.1) matches the first by writing the corresponding expression as $D_{\text{KL}}(1 - p \parallel 1/(1 + e^\phi)) = \log(1 + e^\phi) - \phi p - h(p)$, which is equal to (F.4) by the definition of ϕ . \square

Note that this result suggests a choice of density for the matrix: since each test is negative with probability e^{-d} , equating this with (F.2) suggests that we take

$$d = d_{\text{ch}}^* = \log(1 - p - q) - \log\left(\frac{1}{1 + e^\phi} - q\right).$$

This is unlikely to be optimal in a group testing sense, since we make different inferences from positive and negative tests, but gives a closed form expression that may perform well in practice. For the noiseless and BSC case observe that $\phi = 0$, and we obtain $d_{\text{ch}}^* = \log 2$.

APPENDIX G. ILLUSTRATION OF BOUNDS FOR Z, REVERSE Z CHANNEL AND THE BSC

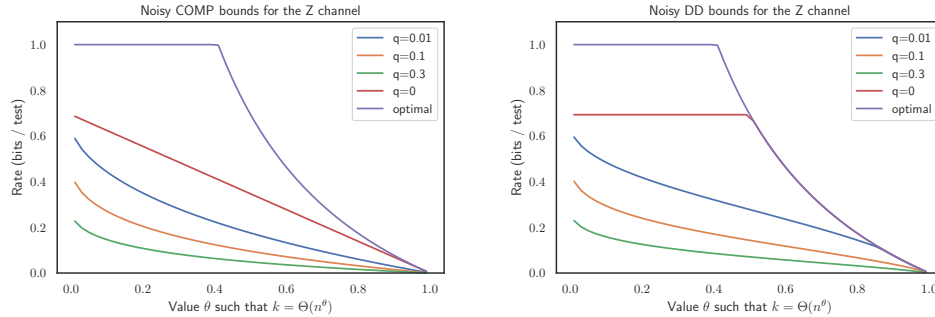


FIGURE 5. Illustration of achievability bounds for noisy COMP and DD under the Z channel. The *optimal* curve refers to the information-theoretic non-adaptive lower bound in the *noiseless* setting

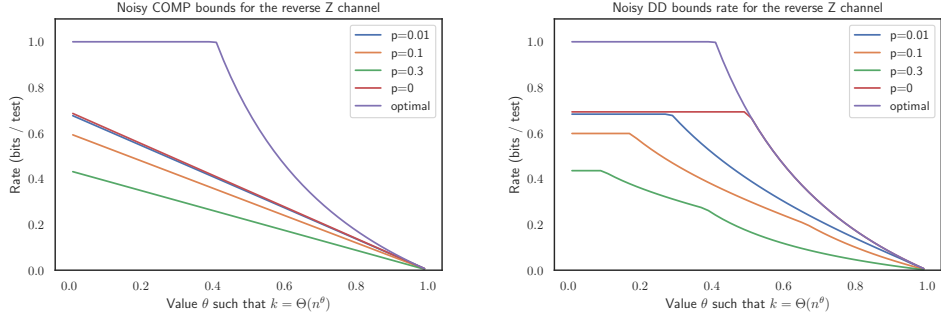


FIGURE 6. Illustration of achievability bounds for noisy COMP and DD under the reverse Z channel. The *optimal* curve refers to the information-theoretic non-adaptive lower bound in the *noiseless* setting

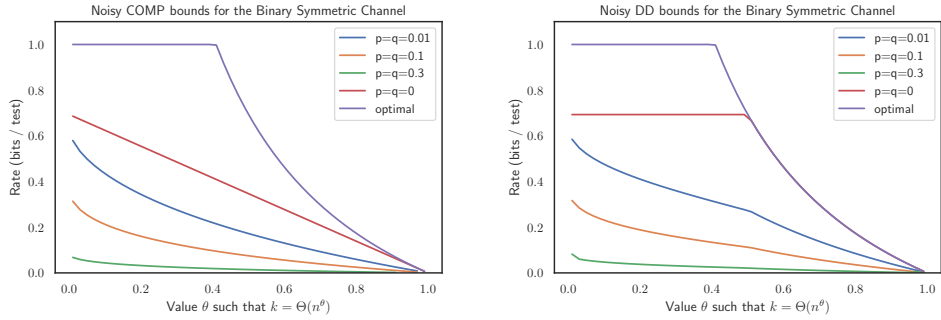


FIGURE 7. Illustration of achievability bounds for noisy COMP and DD under the Binary Symmetric Channel. The *optimal* curve refers to the information-theoretic non-adaptive lower bound in the *noiseless* setting

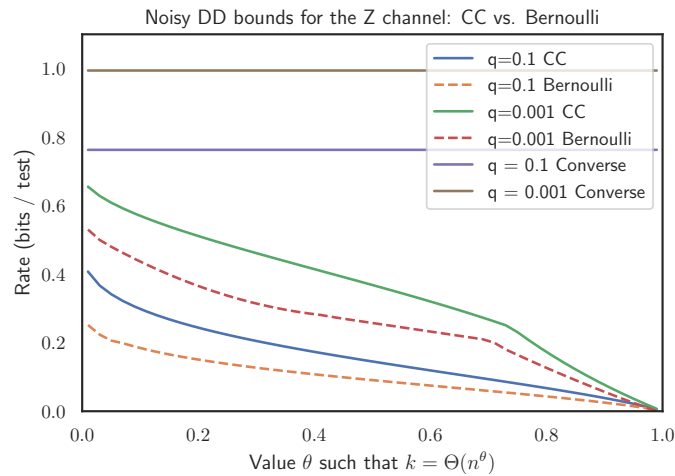


FIGURE 8. Comparison of the noisy DD rates under Bernoulli pooling ([48]) with the DD bounds and converse with constant-column design as provided in the paper at hand within the Z-Channel

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