Gather and Conquer: Region-based Strategies to Accelerate Safe Screening Tests

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Abstract—In this paper, we propose new methodologies to decrease the computational cost of safe screening tests for LASSO. We first introduce a new screening strategy, dubbed “joint screening test”, which allows the rejection of a set of atoms by performing one single test. Our approach enables to find good compromises between complexity of implementation and effectiveness of screening. Second, we propose two new methods to decrease the computational cost inherent to the construction of the (so-called) “safe region”. Our numerical experiments show that the proposed procedures lead to significant computational gains as compared to standard methodologies.

I. INTRODUCTION

In the last decade, sparse representations have proven to be powerful tools to solve many problems in signal processing, machine learning, etc. A standard methodology to find a sparse representation of some \( y \in \mathbb{R}^m \) in a dictionary \( A = [a_1 \ldots a_n] \in \mathbb{R}^{m \times n} \) is the so-called (nonnegative) LASSO problem:

\[
x^*_A \in \text{arg min}_{x \geq 0} P_{\lambda}(y, x),
\]

where \( P_{\lambda}(y, x) = \frac{1}{2} \|y - Ax\|_2^2 + \lambda \|x\|_1 \) and \( x \in \mathbb{R}^n \). We will assume hereafter that \( \|a_i\|_2 = 1 \) for \( i = 1 \ldots n \).

Solving (1) may require a heavy computational load when the dimension of \( x \) becomes large. Therefore, the conception of computationally-efficient techniques to solve (1) has become an active field of research. Among the most popular approaches addressing (1), one can mention interior-point methods [2], proximal gradient algorithms ([3], [4]), homotopy procedures ([5], [6]), splitting methods ([1], [7]) or Frank-Wolfe methodologies [8].

One important contribution in this field is the so-called “safe” screening technique proposed by El Ghaoui et al. in [9]. The idea of safe screening consists in identifying some of the zeros of \( x^*_A \) with a low computational burden. These elements can then be withdrawn from the optimization variables, resulting in a problem of smaller dimension.

The identification of zeros is achieved through the implementation of simple tests. The overall computational gain reached by screening techniques is thus a compromise between their induced computational burden and the number of zeros they can identify. To find a good compromise between these two objectives, the main trend in the current literature has been to improve the definition of the so-called “safe region”, a set of the dual space containing the dual optimal solution of (1). In particular, different geometries for the safe region have been proposed in a series of contributions [10]–[17].

In this paper, we consider another avenue of research. We first note that, in order to implement their screening tests, all contributions mentioned above require to compute (at least) one inner product in \( \mathbb{R}^m \) per atom in the dictionary. Hence, the cost associated to the implementation of the screening test may become prohibitive when the size of the dictionary becomes very large. As a limit case, one can think of the problem of sparse representations in “continuous” dictionaries, where the number of atoms is infinite uncountable, e.g., [18]–[21]. In this context, standard screening methodologies simply become inapplicable.

In this paper, we propose a new screening methodology to deal with this issue. We first introduce a new procedure, dubbed “joint screening”, allowing to safely screen a set of atoms while performing one single test. In particular, we show that a careful design of the proposed method allows to achieve a better compromise between the effectiveness and the efficiency of the screening tests. Following the same lines of thought, we then introduce two methodologies to alleviate the complexity associated to the construction of the safe region. These two approaches aim at identifying efficiently a feasible point of the dual problem of (1). A first strategy is based on the derivation of upper bounds on the maximum inner product between the atoms of the dictionary and the center of the (sphere) safe region. A second strategy, dubbed “dual screening”, allows for an efficient identification of (some of) the atoms of the dictionary not attaining the maximum inner product with the center of the safe region.

This work is an extended version of [22] in which we laid the main foundations of joint screening. The present paper contains all the proofs of our results, extended discussions and developments, as well as extensive simulation results. We also note that the material presented hereafter share some connections with a parallel work [23]. In particular, the authors of [23] came to the same expressions as those presented in Theorems 1 and 2 below in the case of “sphere” regions. Nevertheless, apart from this connection, the two works are distinct since [23] considers the problem of screening with approximate dictionaries (but having the same size as the

1 Let us mention that, although the methodologies proposed in this paper carry over to “continuous” dictionaries, hereafter we restrict our attention to the case of discrete dictionaries. Rigorous derivations in the more-complex formalism of continuous dictionaries is left for future work.
original dictionary) whereas this paper focuses on the problem of screening sets of atoms.

The paper is organized as follows. In Section II, we recall the main principles underlying safe screening methodologies. In Section III we introduce the proposed joint screening tests and discuss the tuning of their parameters. In Section IV, we propose two strategies to construct efficiently safe regions. Finally, in Section V we assess numerically the effectiveness of the proposed methodologies.

II. Standard Procedures for Safe Screening

In this section, we give a brief reminder of the rationale underlying safe screening methods (Sections II-A, II-B and II-C) and emphasize some of their computational bottlenecks (Section II-D). In a last subsection (Section II-E) we motivate the working hypotheses that will be used throughout the paper.

A. Some convex considerations

Problem (1) is convex and always admits (at least) one solution. The dual problem associated to (1) can be written as (see for example [24])

\[ z^\star_\lambda = \arg \max_{z \in Z} D_\lambda (y, z), \] (2)

where

\[ D_\lambda (y, z) = \frac{1}{2} \| y \|^2 - \frac{\lambda^2}{2} \| y - z \|^2, \] (3)

\[ Z = \{ z \in \mathbb{R}^m : \langle a_i, z \rangle \leq 1, \ i = 1 \ldots n \}, \] (4)

and \( \langle \cdot, \cdot \rangle \) denotes the inner product in \( \mathbb{R}^m \). Since \( D_\lambda (y, z) \) is a strictly concave coercive function and \( Z \) is a closed set, problem (2) admits a unique solution \( z^\star_\lambda \), see [25, Proposition A.8].

The primal and dual solutions \( (x^\star_i, z^\star_\lambda) \) are related through the well-known Karush-Kuhn-Tucker (KKT) conditions [25, Proposition 5.1.5]:

\[ x^\star_i \geq 0, \ \langle a_i, z^\star_\lambda \rangle \leq 1 \text{ for all } i, \] (5)

\[ \langle a_i, z^\star_\lambda \rangle - 1 \cdot x^\star_i(i) = 0 \text{ for all } i, \] (6)

\[ y = \lambda z^\star_\lambda + A x^\star, \] (7)

where \( x^\star_i(i) \) denotes the \( i \)th component of \( x^\star_i \). The KKT conditions are necessary and sufficient optimality conditions for \( (x^\star_i, z^\star_\lambda) \). We will see in the next section that safe screening methods exploit the necessity of these conditions to identify some zeros of \( x^\star \).

B. Safe screening: standard methodologies

Safe screening procedures, first proposed in [9], leverage the following observation: if \( S \subset \mathbb{R}^m \) is a region such that \( z^\star_\lambda \in S \), then the following inequality trivially holds

\[ \langle a_i, z^\star_\lambda \rangle \leq \max_{z \in S} \langle a_i, z \rangle, \]

and from (6), we thus have

\[ \max_{z \in S} \langle a_i, z \rangle < 1 \Rightarrow x^\star_i(i) = 0. \] (8)

In other words, if the inequality in the left-hand side of (8) is satisfied, one is ensured that the \( i \)th component of the solution \( x^\star_i \) is equal to zero.

Since the seminal work [9] by El Ghaoui and co-authors, different screening tests, based on different choices of \( S \), have been proposed in the literature, see [10]–[15]. The most popular ones are probably the tests based on “sphere” regions, that is

\[ S = B(c, 1 - \tau) \triangleq \{ z : \| z - c \|^2 \leq 1 - \tau \}, \] (9)

for some parameters \( c \in \mathbb{R}^m \) and \( \tau \leq 1 \). Interestingly, for this particular choice, the general screening test (8) takes the following simple form:

\[ \langle a_i, c \rangle < \tau \Rightarrow x^\star_i(i) = 0. \] (10)

Other geometries for \( S \) (e.g., domes), leading to slightly more involved screening tests, have also been considered in [16], [17]. In this paper, we exclusively focus on spherical safe regions, although the material presented hereafter can also be extended to more complex definitions of \( S \).

C. Finding a safe region

A crucial step in the design of a safe screening test is the identification of a safe region \( S \), that is a region such that \( z^\star_\lambda \in S \). Many methods addressing this task have been proposed in the literature, see e.g., [9]–[17]. As far as spherical regions are concerned, we can for example mention the “ST1” sphere introduced in [9], whose center \( c \) and radius \( 1 - \tau \) are defined as:

\[ c = \frac{x}{\sqrt{\| x \|^2}}, \quad 1 - \tau = \frac{\sqrt{\| x \|^2}}{\| x \|^2}, \] (11)

where \( z \in Z \) is some dual feasible point. Another (more recent) example is the so-called “GAP” sphere [14] for which

\[ c = z, \quad 1 - \tau = \sqrt{2 \frac{D_\lambda (y, z) - D_\lambda (y, x)}{\lambda}}, \] (12)

where \( x \geq 0 \) and \( z \in Z \) can be any primal-dual feasible points.

A common ingredient to all the methodologies proposed so far to define a safe region \( S \), is the identification of a dual feasible point \( z \in Z \), that is

\[ \langle a_i, z \rangle \leq 1 \text{ for all } i = 1 \ldots n. \] (13)

Unfortunately, in the vast majority of cases, such a dual feasible point is not directly available and its identification must therefore be part of the construction of the safe region. In [9], El Ghaoui et al. suggested a simple procedure, dubbed “dual scaling”, to build a dual feasible point from any vector \( \tilde{z} \in \mathbb{R}^m \). Their method is based on the following simple observation: given any \( \tilde{z} \in \mathbb{R}^m \), we have that

\[ z = \left( \max_{1 \leq i \leq n} \langle a_i, \tilde{z} \rangle \right)^{-1} \tilde{z}. \] (14)
is dual feasible. In other words, as long as the inner products between \( s \in \mathbb{R}^m \) and the atoms of the dictionary can be evaluated, one can always compute a dual feasible point via (14). To the best of our knowledge, dual scaling is the standard procedure used in all the contributions of the literature to identify a dual feasible point.

D. Computational cost of standard methodologies

In this section, we comment on the complexity required to implement the safe screening techniques discussed above. Let us first notice that screening can be applied in either a “static” or a “dynamic” way. Static screening means that the screening procedure is applied once before the application of the optimization algorithm addressing (1). Dynamic screening corresponds to the repeated application of a screening technique throughout the iterations of the optimization algorithm. In the latter case, the size of the dictionary can thus be reduced all along the optimization process. In order to address jointly these two cases, we assume in the rest of this paper (with a slight abuse of notation) that \( n \) represents the number of atoms in the dictionary before the application of the screening method. In the static case, \( n \) thus corresponds to the initial number of atoms in the dictionary; in the dynamic case, \( n \) is the number of atoms which have not yet been screened at the current iteration of the optimization process.

With this convention in mind, we have that the computational cost associated to the implementation of safe screening techniques typically evolves linearly with the size \( n \) of the dictionary. This order of complexity stems from two particular steps in the screening process.

First, it can be seen from (8) that the implementation of the standard screening test necessitates the evaluation of the quantity “\( \max_{z \in S}(a_i, z) \)” for each atom of the dictionary. Hence, the computational load required to perform this operation obviously evolves linearly with the total number of atoms. For example, in the case where \( S \) is a sphere region, (10) involves the computation of the inner products between the center of the sphere \( c \) and each atom of the dictionary, leading to a complexity scaling as \( \mathcal{O}(mn) \).

A second computational bottleneck is related to the definition of the safe region \( S \), more specifically the identification of a dual feasible point. As mentioned in Section II-C, the standard technique to construct such a point is “dual scaling”, see (14). Now, the naive application of this method entails the computation of \( n \) inner products \( \langle a_i, z \rangle \), leading to a complexity scaling as \( \mathcal{O}(mn) \).

This linear evolution of the complexity may become prohibitive in some applications, in particular those involving very large dictionaries. In this paper, we propose new procedures to reduce this computational cost. We address the two issues mentioned above separately. In Section III, we introduce new screening tests allowing to jointly identify a set of zeros in \( x^*_\lambda \). In Section IV, we address the problem of computing efficiently a dual feasible point. These methodologies are assessed numerically in Section V.

Before proceeding to the presentation of the proposed methods, let us make two important remarks about our complexity analysis. First, dynamic screening can sometimes benefit from the computation already carried out in the optimization procedure solving the LASSO problem. In such a case, the order of complexity required to implement the screening tests may be much smaller than those mentioned above. An example of such a scenario is safe sphere test with proximal gradient procedures (e.g., [3]) where the inner products needed to implement the screening are already evaluated in the main recursion of the optimization algorithm. Nevertheless, we will show numerically in Section V that, even in such a situation, the proposed methodologies may lead to some computational gain over the standard screening approach.

A second remark concerns the operating regime that will be considered in this paper. More specifically, we will assume that (1) has to be solved for one given dictionary \( A \) and several different instances of \( y \) and \( \lambda \) (as it may appear in many applications, e.g., direction-of-arrival estimation, signal deconvolution, denoising of a sequences of images, etc.). This allows us to distinguish between the concepts of “offline” and “online” complexity. The “offline” complexity refers to all the operations which can be done once for all before the resolution of the different instances of the LASSO problem (these operations only involve the dictionary). The “online” complexity relates to all the operations which have to be repeated for each new instance of the LASSO problem (depending on \( y \) and \( \lambda \)). In the rest of this paper, we will mainly motivate the proposed methods via their online complexity, since the latter tends to dominate the overall computational burden when the number of problem instances becomes large. Some pointers to the offline complexity will also be given although we will not dwell on this subject, as it depends a lot on the LASSO problem under consideration and the design choices made by the practitioners.

E. Working hypotheses

In this section, we introduce two working assumptions that will be considered in the rest of the paper. These two hypotheses will always be assumed verified even when not explicitly mentioned in the statement of our results.

As a first working hypothesis, we suppose that the penalization parameter \( \lambda \) appearing in the LASSO problem (1) satisfies

\[
\lambda < \lambda_{\text{max}}, \tag{15}
\]

where \( \lambda_{\text{max}} \triangleq \max_i \langle a_i, y \rangle \). This assumption makes sense from a practical point of view since \( x^*_\lambda \neq 0 \) if and only if (15) is satisfied. In other words, considering (1) with \( \lambda \geq \lambda_{\text{max}} \) always leads to the all-zero solution.

Our second working hypothesis reads

\[
\tau > -\|c\|_2, \tag{16}
\]

where \( c \) and \( \tau \) are respectively the center and the radius parameters of the safe sphere considered in the screening test. In order to motivate our assumption, let us first notice that...
any atom belonging to the safe region $S$ will never satisfy test (8). Hypothesis (16) then simply ensures that

$$S_m \subseteq B(c, 1 - \tau),$$  

(17)

where $S_m$ is the $m$-dimensional unit sphere. In other words, if (16) holds then there exists at least one unit-norm vector not included in the safe sphere $B(c, 1 - \tau)$. This assumption makes sense from a practical point of view since if (17) does not hold, then no atom can be screened anyway.

A consequence of hypotheses (15) and (16) is that we must necessarily have $c \neq 0$. Indeed, if $c = 0$, satisfying (16) requires $\tau > 0$. On the other hand, the first hypothesis (15) combined to $c = 0$ imposes that $\tau \leq 0$ as shown in Lemma 4, Appendix A. Since $\tau > 0$ and $\tau \leq 0$ cannot obviously hold simultaneously, we have that the combination of (15) and (16) discards the case $c = 0$.

III. Joint Screening Tests

In this section, we introduce a new screening procedure having a complexity not depending on the number of atoms in the dictionary (or only in a logarithmic factor for the procedure described in Section III-C). We dub our methodology “joint screening test” because it allows to screen a set of atoms by carrying out one single test. In a first subsection, we derive tests allowing to screen any atom belonging to some specific region $R \subset \mathbb{R}^m$. In a second subsection, we elaborate on the relative effectiveness of the proposed test for different choices of $R$. Finally, in the last two subsections, we discuss the choice of the parameters defining the screening region $R$.

A. Joint screening of a region $R$

Let $A = \{a_i\}_{i=1}^n$ denote the set of atoms of the dictionary and let $S \subset \mathbb{R}^m$ be a safe region (that is $x_\lambda^S(i) = 0 \forall i : a_i \in A \cap R$). The “joint” screening procedure proposed in this paper is a direct consequence of the following observation (which follows directly from (8)):

$$\max_{a \in A} \max_{z \in S} \langle a, z \rangle < 1 \Rightarrow x_\lambda^S(i) = 0 \forall i : a_i \in A \cap R. \quad (18)$$

In order words, if the inequality in the left-hand side of (18) is satisfied, all the atoms $a_i \in A \cap R$ can be safely and jointly screened from problem (1).

In what follows, we will see that the verification of the inequality in the left-hand side of (18) can be done very efficiently for some specific choices of regions $S$ and $R$. First, we will assume that $S$ is a sphere region (9). The joint screening test (18) then takes the simple form:

$$\max_{a \in A} \langle a, c \rangle < \tau \Rightarrow x_\lambda^S(i) = 0 \forall i : a_i \in A \cap R. \quad (19)$$

Moreover, we will consider the two following options for $R$:

$$R = B(t, \epsilon) \triangleq \{a : \|a - t\|_2 \leq \epsilon\}, \quad (20)$$

$$R = D(t, \delta) \triangleq \{a : \langle a, t \rangle \geq \delta, \|a\|_2 \leq 1\}, \quad (21)$$

Algorithm 1 Joint Screening Test

1: **inputs:** $L :$ number of regions, $A :$ set of atoms
2: **procedure** Joint Screening($L, A$)
3: **init:** $A_{\text{scr}} = \emptyset$
4: Select a set of regions $\{R_l\}_{l=1}^L$
5: **for all** $1 \leq l \leq L$ **do**
6: **if** $\max_{a \in R_l} \langle a, c \rangle < \tau$ **then**
7: $A_{\text{scr}} = A_{\text{scr}} \cup (A \cap R_l)$
8: **end if**
9: **end for**
10: **end procedure**
11: **outputs:** $A_{\text{scr}} :$ set of screened atoms

where $t \in \mathbb{R}^m$ and $\epsilon, \delta$ are some parameters. Without loss of generality, we will assume in the rest of the paper that $\|t\|_2 = 1$. The regions $B(t, \epsilon)$ and $D(t, \delta)$ have some easy geometric interpretations: $B(t, \epsilon)$ corresponds to the set of vectors located in a ball of radius $\epsilon$ centered on $t$; $D(t, \delta)$ is a dome including all the vectors of norm smaller than one and having an inner product with $t$ greater than or equal to $\delta$.

For these two choices of regions, the joint screening test defined in (19) admits very simple analytical solutions, as shown by the following result:

**Theorem 1.** \( \max_{a \in B(t, \epsilon)} \langle a, c \rangle < \tau \) if and only if \( \langle t, c \rangle < \tau - \epsilon \|c\|_2 \). \( (22) \) Moreover, \( \max_{a \in D(t, \delta)} \langle a, c \rangle < \tau \) if and only if \( \langle t, c \rangle < \tau \), \( (23) \)

and

$$\delta > \frac{\langle t, c \rangle \tau + \sqrt{\|c\|_2^2 - \langle t, c \rangle^2} \sqrt{\|c\|_2^2 - \tau^2}}{\|c\|_2^2}. \quad (24)$$

A proof of this result can be found in Appendix B. We note from (22)-(24) that the joint screening tests (19) based on a sphere region $B(t, \epsilon)$ or a dome region $D(t, \delta)$ only requires the evaluation of one inner product, namely $\langle t, c \rangle$; nonetheless, if these tests are passed, they allow to screen all the atoms in the regions $B(t, \epsilon)$ and $D(t, \delta)$. In this paper, we will often refer to $t$ as “test vector” since it is the only vector appearing in the joint test associated to region $R$.

Motivated by Theorem 1, we propose the screening procedure described in Algorithm 1. The online complexity of this algorithm is dominated by the operations carried out in steps 4, 6 and 7. If the regions $\{R_l\}_{l=1}^L$ are prespecified once for all in advance, the complexity of this procedure is concentrated in the verification of the tests “$\max_{a \in R_l} \langle a, c \rangle < \tau$”. Now, if one considers sphere or dome regions, we have from Theorem 1 that this operation only requires the evaluation of $L$ inner products. In this case, the overall complexity of the proposed methodology thus scales as $O(Lm)$.

If the choice of the regions $\{R_l\}_{l=1}^L$ is changed “dynamically” (for example, one may want to adapt the choice of

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4This comes straightforwardly from the observation that for any $a_i \in S$, $\max_{a \in S} \langle a, z \rangle \geq \langle a_i, a_i \rangle = 1 \geq \tau$. 

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\{R_i\}_{i=1}^L \text{ to the safe region } S), \text{ the overall complexity of the algorithm must bear additional costs, namely the construction of the region } R_i \text{ and the identification of the set of atoms belonging to it, that is } A \cap R_i. \text{ In Section III-C, we propose a procedure to adapt the size of the regions } \{R_i\}_{i=1}^L \text{ only leading to an increase of the computational cost of the order of } O(L \log_2 n). \text{ In this case, the overall complexity of the proposed procedure thus scales as } O(Ln + L \log_2 n).

These orders of complexity have to be compared to the computational cost of standard screening procedures, that is \(O(mn)\). We thus see that the screening procedure advocated in this section may lead to huge computational savings when the size \(n\) of the dictionary becomes large. However, the price to pay to achieve such a complexity reduction is a decrease of the effectiveness of the screening tests. In particular, as discussed in Section III-B below, the joint screening test for a region \(R\) can only be verified if the standard screening test (8) is passed for all the atoms \(a_i \in A \cap R\). The choice of the regions \(\{R_i\}_{i=1}^L\) will therefore play a major role in the ability of the proposed screening method to identify the zeros of \(x_i^\star\).

We discuss the latter issue in Sections III-C and III-D.

B. Relative effectiveness of the screening tests

It is easy to see from (18) that the choice of region \(R\) is a compromise between the number of atoms that can be jointly screened and the ease of passing the test. Indeed, although large regions allow to screen more atoms, they are also less likely to pass the joint screening test since, for any \(R_1 \subseteq R_2\), we have

\[
\max_{a \in R_1} \max_{z \in S} \langle a, z \rangle \leq \max_{a \in R_2} \max_{z \in S} \langle a, z \rangle.
\]

In particular, letting \(R_1 = \{a_i\}\) and \(R_2 = R\) in the above inequality, we see that passing the joint screening test (18) requires the standard screening test (8) to be verified for any atom \(a_i \in A \cap R\). Hence, quite logically, joint screening test (18) can only lead to inferior screening performance as compared to standard screening test (8).

Another question of interest is the relative effectiveness of the joint sphere and dome tests proposed in (22) and (23)-(24), respectively. The next lemma provides some insights into this question.

**Lemma 1.** The smallest\(^5\) dome containing a set of unit-norm vectors \(U\) is always contained in the smallest sphere containing \(U\).

A proof of this lemma can be found in Appendix C. In view of (25), a direct consequence of Lemma 1 is as follows: if one wishes to jointly screen a set of unit-norm atoms, there always exists a joint dome test leading to screening performance at least as good as the “best” joint sphere test.

C. Choosing the “size” of \(R\)

In this section, we discuss a particular strategy to adapt the size of the regions \(\{R_i\}_{i=1}^L\) in step 4 of Algorithm 1. More specifically, we assume that \(R_i\) corresponds to either a sphere or a dome region and we discuss the choice of the parameters \(\epsilon\) and \(\delta\).

Let us first consider the case when \(R_i\) is a sphere, that is \(R_i = B(t_i, \epsilon_i)\). We assume that the test vector \(t_i\) is given and want to tune the value of \(\epsilon_i\) so that \(R_i\) is the largest sphere passing (if possible) the joint screening test (22). Noticing that the joint sphere test (22) is satisfied as soon as the radius \(\epsilon_i\) verifies

\[
\epsilon_i < \epsilon_{t_i, c} \triangleq \frac{\tau - \langle t_i, c \rangle}{\|c\|_2},
\]

an ideal choice for \(\epsilon_i\) therefore consists in setting the latter as close as possible to \(\epsilon_{t_i, c}\).

We note that computing the value of \(\epsilon_{t_i, c}\) only requires the evaluation of one inner product \(\langle t_i, c \rangle\) and does therefore not imply any computational increase with respect to the case where the regions are predefined once for all (the inner product \(\langle t_i, c \rangle\) has anyway to be computed for the evaluation of the tests (22)-(24)). However, as mentioned previously, another issue arises when varying the size of \(R_i\): the efficient identification of the set of atoms \(A \cap R_i\). We show hereafter that this operation can actually be carried out with a small computational overhead.

Letting the radius \(\epsilon_i\) tend to its largest value \(\epsilon_{t_i, c}\), we have that any atom \(a_i \in A\) having a distance to \(t_i\) strictly smaller than \(\epsilon_{t_i, c}\) will be screened by test (22), that is

\[
\|a_i - t_i\|_2 < \epsilon_{t_i, c} \Rightarrow x_i^\star(i) = 0.
\]

Now, the quantities \(\{\|a_i - t_i\|_2\}_{i=1}^n\) can be precomputed and sorted once for all in advance, so that the identification of the atoms verifying (27) can be done very efficiently (one can for example achieve a complexity scaling as \(O(\log_2 n)\) by using state-of-the-art searching algorithms [26]). As a consequence, the online complexity associated to the implementation of (27) is of the order of \(O(m + \log_2 n)\).\(^6\)

We can apply the same kind of reasoning when \(R_i\) is a dome region, that is \(R_i = D(t_i, \delta_i)\). If \(t_i\) is given, a tight lower bound on the value of \(\delta_i\) verifying the joint dome test is trivially given by the right-hand side of (24), that is

\[
\delta_i > \delta_{t_i, c},
\]

where

\[
\delta_{t_i, c} \triangleq \frac{\langle t_i, c \rangle \tau + \sqrt{\|c\|_2^2 - \langle t_i, c \rangle^2} \sqrt{\|c\|_2^2 - \tau^2}}{\|c\|_2^2}.
\]

Hence, provided that \(\langle t_i, c \rangle < \tau\), letting parameter \(\delta_i\) tend to its smallest value \(\delta_{t_i, c}\) will lead to the screening of any atom \(a_i \in A\) having an inner product with \(t_i\) strictly greater than \(\delta_{t_i, c}\), that is:

\[
\begin{cases}
\langle t_i, c \rangle < \tau \\
\langle t_i, a_i \rangle > \delta_{t_i, c} \Rightarrow x_i^\star(i) = 0.
\end{cases}
\]

\(\hat{O}(m)\) to evaluate the inner product \(\langle t_i, c \rangle\) and \(O(\log_2 n)\) to identify the elements of \(\{\|a_i - t_i\|_2\}_{i=1}^n\) passing the test (27).
Again, the quantities \( \{ (t_l, a_i) \}_{l=1}^n \) can be precomputed and sorted once for all in advance, so that a complexity scaling as \( O(m + \log_2 n) \) can also be achieved here.

Going back to the screening procedure advocated in Algorithm 1, we see that adapting the parameter \( \epsilon_l \) (resp. \( \delta_l \)) for each region \( R_l \) as discussed above is equivalent to applying test (27) (resp. (30)) for each of the \( L \) different test vectors \( t_l \) specifying the regions \( R_l \). The overall complexity of this procedure thus scales as \( O(Lmn + L \log_2 n) \).

We note that tuning the region’s size as described in this section leads to the most effective joint screening test given a set of region centers \( \{ t_l \}_{l=1}^L \) and a safe sphere \( B(c, \tau) \) (that is the test identifying the most zeros of the LASSO solution). This desirable property comes however at the expense of a computational overhead: the online complexity is impacted by an additional logarithmic factor and scales as \( O(Lmn + L \log_2 n) \). This methodology also requires to evaluate the inner products \( \langle t_l, a_i \rangle \) and thus induces an offline complexity of \( O(Lmn) \) which may preclude the use of such strategy for a large number of regions.

D. Choosing the test vectors

In the previous section, we assumed that the test vector \( t_l \) was given and we discussed the (online) tuning of the parameters \( \epsilon_l \) and \( \delta_l \). In this section, we elaborate on the (offline) choice of the test vectors \( \{ t_l \}_{l=1}^L \). The devise of algorithms optimizing the set of test vectors being a broad topic of research, we leave this task for future works. Here, we keep our discussion to a more conceptual level and highlight some guidelines according to which the choice of the test vectors should/could be made.

In our discussion in Section III-B, we emphasized that the joint test of region \( R_l \) in (18) can only be passed if the standard test (8) is successful for any atom \( a_i \in A \cap R_l \). Standard tests thus characterize the best screening performance achievable by the joint procedures advocated in this paper. In what follows, our discussion will be motivated by the latter observation. We introduce the next lemma to support our discussion.

**Lemma 2.** Let \( S = B(c, 1 - \tau) \) be a safe sphere for problem (1)-(2). The standard sphere test (10) based on \( S \) fails for atom \( a_i \in S^m \) if and only if
\[
\| a_i \|_2 < \frac{\tau}{\| c \|_2}.
\]

**Proof:** By definition, the set of unit-norm atoms which do not pass test (10) is given by
\[
\{ a : \langle a, c \rangle \geq \tau, \| a \|_2 = 1 \} = \{ a : \frac{\langle a, c \rangle}{\| c \|_2} \geq \frac{\tau}{\| c \|_2} \} \cap S^m
= D\left( \frac{c}{\| c \|_2}, \frac{\tau}{\| c \|_2} \right) \cap S^m.
\]
Since \( a_i \in S^m \), we obtain the result. Note that we were allowed to divide by \( \| c \|_2 \) in the above expressions because our working hypotheses (see Section II-E) ensure that \( c \neq 0 \).

Lemma 2 states that the set of unit-norm vectors which cannot be screened by a (standard) sphere test corresponds to a well-defined region, that is \( D\left( \frac{c}{\| c \|_2}, \frac{\tau}{\| c \|_2} \right) \cap S^m \). Now, since the joint test (18) can only be passed if the standard test (8) is verified for all the vectors belonging to \( R_l \), any non-empty intersection between \( R_l \) and \( D\left( \frac{c}{\| c \|_2}, \frac{\tau}{\| c \|_2} \right) \cap S^m \) will lead to a failure of the joint test. We build hereafter on this observation to provide two rules of thumb for the choice of the tests vectors \( \{ t_l \}_{l=1}^L \).

Let us first consider the case where the sizes of the regions \( \{ R_l \}_{l=1}^L \) are chosen once for all in advance. In this context, a first strategy to select the vectors \( \{ t_l \}_{l=1}^L \) (and the size of the regions) could be based on the following (reasonable) requirements: i) each atom \( a_i \in A \) must belong to at least one region \( R_l \); ii) each region must be as small as possible. The first requirement ensures that each atom may potentially be (jointly) screened by some test. The second one intends to “optimize” the probability of passing the joint test, since one may argue that small regions are less likely to have an intersection with the dome \( D\left( \frac{c}{\| c \|_2}, \frac{\tau}{\| c \|_2} \right) \cap S^m \). This suggests the set of test vectors \( \{ t_l \}_{l=1}^L \) should be distributed uniformly in \( A \).

A second option to select the set of test vectors is based on the following connection between the joint screening strategy proposed in (30) and the standard screening procedure (10): considering (30) with \( t_l = -\frac{c}{\| c \|_2} \) is exactly equivalent to applying the standard test (10) on all the atoms of the dictionary \( A \). This can be seen as follows. First, rewriting Lemma 2 in a slightly different way, we have that the set of unit-norm atoms passing test (10) can be written as
\[
\{ a : \langle a, c \rangle < \frac{\tau}{\| c \|_2} \} \cap S^m. \tag{32}
\]
Moreover, particularizing (30) to the specific choice \( t_l = -\frac{c}{\| c \|_2} \), we obtain
\[
\{ a : \langle a, c \rangle < \frac{\tau}{\| c \|_2} \} \cap S^m \Rightarrow x^*_l(i) = 0. \tag{33}
\]
The first inequality in (33) is always satisfied by virtue of our working assumptions (see Section II-E); the second one is equivalent to
\[
a_i \in \{ a : \langle a, c \rangle < \frac{\tau}{\| c \|_2} \} \cap S^m. \tag{34}
\]
Hence, in view of (32), (33) is equivalent to applying the standard test (10) on the atoms of the dictionary \( A \).

This observation leads to our second rule of thumb to select \( \{ t_l \}_{l=1}^L \): when test (30) is considered, the test vectors should be chosen “as close as possible” to \( -\frac{c}{\| c \|_2} \). In particular, as emphasized above, if \( t_l = -\frac{c}{\| c \|_2} \) then one single joint test (30) leads to the screening of all the atoms “screenable” by the standard test (8). Of course, in practice, the actual value of the safe-sphere center \( c \) is not known in advance and depend on many parameters (e.g., the LASSO problem at stake, the method used to construct the safe sphere, etc.).

However, our above observation gives us good clues on how the test vectors should be chosen. When we have at our
disposal a “training set” of sphere center \( \{c\} \), we could for example imagine to “learn” the test vectors from this dataset by imposing that elements of \( \{t^L_i\}_{i=1}^L \) are not “too far” from those in the training set.

IV. FINDING A SAFE REGION

In this section we elaborate on the problem of evaluating efficiently a dual feasible point. As pointed out in Section II-D, the standard “dual scaling” methodology entails an online complexity scaling as \( O(mn) \) in the general case. We propose hereafter two strategies based on “regions” to alleviate this order of complexity. Although presented separately, these two procedures can be combined in practice.

A. Relaxed dual scaling

A first strategy is based on the following observation: the standard dual scaling procedure can be relaxed by noticing that if some \( \beta \in \mathbb{R} \) is such that

\[
\beta \geq \max_{1 \leq i \leq n} \langle a_i, \tilde{z} \rangle, \tag{35}
\]

then the point

\[
z = \beta^{-1} \tilde{z} \tag{36}
\]

is dual feasible.

We propose hereafter a strategy based on the use of regions to compute efficiently such an upper bound \( \beta \). More specifically, let \( \{R_i\}_{i=1}^L \) be a set of (closed) regions of \( \mathbb{R}^m \) such that

\[
A \subseteq \bigcup_{i=1}^L R_i. \tag{37}
\]

Then, obviously, a valid choice for \( \beta \) is as follows:

\[
\beta = \max_{1 \leq i \leq L} \max_{a \in R_i} \langle a, \tilde{z} \rangle. \tag{38}
\]

Now, for the sphere and dome regions specified in (20)-(21), the inner maximum "max\( \max_{n \in R_i} \langle a, \tilde{z} \rangle \)" admits a simple closed-form expression as shown in the following result:

**Theorem 2.** \( \forall \tilde{z} \in \mathbb{R}^m \) we have

\[
\max_{a \in B(t, c)} \langle a, \tilde{z} \rangle = \langle t, \tilde{z} \rangle + c \| \tilde{z} \|_2^2, \tag{39}
\]

\[
\max_{a \in D(t, \delta)} \langle a, \tilde{z} \rangle = \begin{cases} \| \tilde{z} \|_2^2 & \text{if } \delta \leq \frac{\langle t, \tilde{z} \rangle}{\| \tilde{z} \|_2} \\ f(\delta) & \text{otherwise} \end{cases}, \tag{40}
\]

where

\[
f(\delta) \triangleq \delta \langle t, \tilde{z} \rangle + \sqrt{1 - \delta^2 \| \tilde{z} \|_2^2 - \langle t, \tilde{z} \rangle^2}. \tag{41}
\]

We refer the reader to Appendix B for a proof of this result. We see that the expressions (39)-(40) only depend on one inner product, namely \( \langle t, \tilde{z} \rangle \). The identification of a dual feasible point via (36)-(38) can therefore be done through the evaluation of \( L \) inner products. This first strategy to evaluate a dual feasible point has therefore a complexity scaling as \( O(Lm) \) when sphere and dome regions are considered.

The same remark as in Section III applies here: smaller regions usually lead to tightest bounds \( \beta \) but also typically involve larger complexities since more regions may be needed to cover the dictionary \( \mathcal{A} \), see (37). As an extreme example, for the particular choice \( R_i = \{a_l\}, l = 1 \ldots n \), one recovers the standard (brute-force) dual scaling approach.

B. “Dual” screening

Our second strategy is inspired from the joint screening methodologies introduced in Section III. More specifically, our approach can be seen as a “screening method” for dual scaling: for a given \( \tilde{z} \in \mathbb{R}^m \), we propose the use of a joint screening procedure to identify (some of) the atoms \( a_i \in \mathcal{A} \) which do not attain the maximum value of \( \langle a_i, \tilde{z} \rangle \).

Our procedure is based on the following simple observations. First, for any subset \( \mathcal{A} \subseteq \mathbb{R} \) we obviously have

\[
\max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \leq \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle. \tag{42}
\]

Moreover, any region \( R \subset \mathbb{R}^m \) such that \( \mathcal{R} \cap \mathcal{A} \neq \emptyset \) leads to

\[
\max_{a \in R \cap \mathcal{A}} \langle a, \tilde{z} \rangle \leq \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle. \tag{43}
\]

Therefore, combining (42) and (43), we have

\[
\max_{a \in R} \langle a, \tilde{z} \rangle < \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \Rightarrow \arg \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \notin R \cap \mathcal{A}. \tag{44}
\]

Interestingly, we note that the inequality in the left-hand side of (44) is equivalent to the joint screening test (19) introduced in Section III by making the following substitutions:

\[
c \leftrightarrow \tilde{z} \tag{45}
\]

\[
t \leftrightarrow \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle.
\]

Nevertheless, passing test (44) allows us to draw a quite different conclusion from that obtained for conventional “safe” screening: if the test is verified, one is ensured that \( \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \) is not attained in \( \mathcal{R} \cap \mathcal{A} \). We will therefore refer to the methodologies based on (44) as “dual screening” since, similarly to safe screening, it allows for a reduction of the dimensionality of the dictionary but with “dual scaling” as a target objective (or more specifically, the evaluation of \( \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \)).

Because of the similarity between (19) and (44), all the results presented in Section III may be reused to implement efficiently dual screening with the substitutions (45). In particular, if one chooses \( \mathcal{R} \) to be a sphere or a dome, one may exploit the expressions stated in Theorem 1 to evaluate \( \max_{a \in \mathcal{R}} \langle a, \tilde{z} \rangle \) by computing one single inner product. Evaluating \( \max_{a \in \mathcal{R}} \langle a, \tilde{z} \rangle \) for \( L \) different (sphere or dome) regions thus leads to a complexity scaling as \( O(Lm) \). On the other hand, computing the other side of the inequality in (44), that is \( \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle \), requires the evaluation of \( \text{card}(\mathcal{A}) \) inner products, resulting in a complexity scaling as \( O(\text{card}(\mathcal{A})m) \). Moreover, if the size of the regions are dynamically adapted as suggested in Section III-C, an additional cost of \( O(L \log_2 n) \) has to be added to the overall complexity.

“Dual screening” can thus be implemented with a complexity scaling at most as \( O(Lm + \text{card}(\mathcal{A})m + L \log_2 n) \). If the test vectors \( \{t_i\}_{i=1}^L \) defining the \( L \) regions are included in \( \mathcal{A} \), the
complexity can even be reduced to $O(\text{card}(\mathcal{A})m + L \log_2 n)$ since the same inner products do not have to be evaluated twice. A summary of the operations performed by dual screening is provided in Algorithm 2.

As a final remark, let us notice that the same discussion as in Section III-D applies here for the choice of the test vectors $\{c_l\}_{l=1}^L$. As for $\mathcal{A}$, we have that any $\mathcal{A} \subseteq \mathcal{A}$ leads to a valid lower bound on $\max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle$. In practice, since the maximum can in principle be reached at any point of the dictionary, choosing $\mathcal{A}$ as a regular subsampling of $\mathcal{A}$ seems nevertheless to be a good rule of thumb.

V. NUMERICAL EXPERIMENTS

In this section we evaluate the effectiveness of the proposed methodologies via numerical simulations. As the procedures introduced in this paper aim at screening groups of “similar” atoms, one may expect them to provide significant gains for dictionaries whose atoms are somehow “clustered” on the unit sphere. Hereafter, we focus on two sparse-representation problems dealing with this type of dictionaries.

A first problem is the deconvolution of a mixture of Gaussian functions, where the atoms of the dictionaries take the form:

$$a_i(j) \propto \exp \left( -\frac{1}{2\sigma^2} \left( \frac{j-1}{m-1} - \frac{i-1}{n-1} \right)^2 \right),$$  \hspace{1cm} (46)

for $i = 1 \ldots n$ and $j = 1 \ldots m$. The dictionary thus contains a set of Gaussians with means uniformly sampled in $[0, 1]$. In our simulations, we set $\sigma = 5 \times 10^{-2}$, $m = 50$ and $n = 1024$.

A second problem focuses on sparse decompositions on the well-known MNIST database [27]. We consider a simulation setup similar to the one used in [13]. In that configuration, the atoms of the dictionary are patches of $28 \times 28$ pixels representing handwritten digits. The dictionary considered in our simulations is made up of 1000 patches (100 for each digit) taken from the MNIST training database.

The evaluation of the proposed procedures is organized as follows. In Section V-A, we study the tightness of the upper bounds proposed in Section IV-A for relaxed dual scaling, and illustrate its impact on the radius of the GAP safe sphere. In Section V-B, we assess the performance of the dual screening methodology advocated in Section IV-B. In the next subsection, we illustrate the tradeoff between complexity and screening performance achievable by the joint procedures described in Section III. In Section V-D, we study the behavior of joint screening when the number of atoms tends to infinity in the Gaussian deconvolution problem. Finally, in Section V-E, we study the computational savings which can be obtained in the LASSO implementation by combining the different methodologies proposed in this paper.

Most of our simulation results pertain to the Gaussian deconvolution problem since its dictionary has a desirable behavior of joint screening when the number of atoms tends to infinity in the Gaussian deconvolution problem. Finally, in Section V-D, we study the computational savings which can be obtained in the LASSO implementation by combining the different methodologies proposed in this paper.

A. Relaxed dual scaling

We first discuss the effectiveness of the relaxed dual scaling presented in Section IV-A. We remind the reader that “relaxed dual scaling” is based on the evaluation of an upper bound $\beta$ verifying (35); this upper bound is then used to find a dual feasible point as in (36) which, in turn, may serve in the construction of a safe region (see for example (11) and (12) in Section II-C).

In Fig. 1a, we illustrate the tightness of the upper bound presented in Theorem 2. We consider the following metric:

$$\Delta = \beta - \max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle,$$  \hspace{1cm} (47)

where $\beta$ is defined in (38). We generate $\tilde{z}$ as the Gaussian random linear combination of $5$ atoms of $\mathcal{A}$. The results are averaged over 200 realizations. The plain curves correspond to the averaged value of $\Delta$ for sphere (blue) and dome (red) regions; the shaded areas represent the set of realizations of $\Delta$. The horizontal axis corresponds to the number of regions $L$ considered in the evaluation of $\beta$. The centers of the regions $\{R_l\}_{l=1}^L$ are chosen according to a uniform subsampling of the atoms (46), that is:

$$c_l = a_l/\tilde{z} \text{ for } l = 1 \ldots L.$$  \hspace{1cm} (48)

The size of the regions are set so that $\mathcal{A} \subseteq \cup_{l=1}^L R_l$. We see in Fig. 1a that the precision of the upper bound improves as the number of regions increase. We also note that the dome region leads to more accurate results than spherical regions.

In Fig. 1b, we illustrate the impact of the proposed relaxation on the radius of the GAP sphere (12). We generated the results as follows. We build vectors $y$ as Gaussian random combinations of $10$ atoms of $\mathcal{A}$. We run a FISTA algorithm [3] to solve the LASSO problem (1) with $y$ as input and $\lambda = 0.1 \lambda_{\text{max}}$. We finally construct a GAP safe sphere at each iteration of FISTA as follows: \(i\) we set $\tilde{x} = \lambda^{-1} (y - \lambda \tilde{x})$; \(ii\) we identify a dual feasible point via (36) and use (12) to compute the radius of the GAP sphere. Fig. 1b displays the radius obtained as a function of the number of regions used in the computation of the upper bound $\beta$. The results are averaged over 200 realizations of $y$. We see that, at a given iteration of FISTA, the radius of the sphere quite logically decreases with the number of regions used in the computation of $\beta$. 

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**Algorithm 2 Dual Screening Test**

1: inputs: $L$: number of regions, $\mathcal{A}$: set of atoms, $\tilde{A}$: subset of atoms, $\tilde{z}$: dual variable
2: procedure DUAL SCREENING($L, \mathcal{A}, \tilde{A}$)
3: \hspace{1cm} init: $\mathcal{A}_{\text{scr}} = \emptyset$
4: \hspace{1cm} Evaluate $\max_{a \in \mathcal{A}} \langle a, \tilde{z} \rangle$
5: \hspace{1cm} Select a set of regions $\{R_l\}_{l=1}^L$
6: \hspace{1cm} for all $1 \leq l \leq L$ do
7: \hspace{1.5cm} if $\max_{a \in R_l} \langle a, \tilde{z} \rangle < \max_{a \in \tilde{A}} \langle a, \tilde{z} \rangle$ then
8: \hspace{2cm} $\mathcal{A}_{\text{scr}} = \mathcal{A}_{\text{scr}} \cup (\mathcal{A} \cap R_l)$
9: \hspace{1cm} end if
10: \hspace{1cm} end for
11: end procedure
12: outputs: $\mathcal{A}_{\text{scr}}$: set of screened atoms
B. Dual screening

We now illustrate the performance of the dual screening methodology presented in Section IV-B. We apply Algorithm 2 to random realizations of the dual variable: $\tilde{z}$ is generated as a Gaussian random linear combination of 5 atoms of $A$. Both the elements of $\tilde{A}$ and the test vectors $\{\mathbf{t}_l\}_{l=1}^{L}$ defining the regions used in Algorithm 2 are chosen as a regular subsampling of $L$ atoms of $A$, i.e.,

$$\tilde{A} = \{\mathbf{t}_l\}_{l=1}^{L} = \{\mathbf{a}_l \tilde{z} : l = 1 \ldots L\}. \quad (49)$$

The following figures of merit are represented in Fig. 2: (a) the percentage of atoms identified by dual screening; (b) the computational gain induced by dual screening. The results are averaged over 50 realizations of $\tilde{z}$. The performance of dual screening is shown for both dome and sphere regions.

Regarding Fig. 2b, we consider the following procedure to generate the figure of merit: i) we apply Algorithm 2 to identify a set of atoms, say $A_{scr}$, which do not attain the maximum value of $\langle a, \tilde{z} \rangle$; ii) we evaluate $\max_{a \in A} \langle a, \tilde{z} \rangle$ as

$$\max_{a \in A} \langle a, \tilde{z} \rangle = \max_{a \in A} \max_{\tilde{z}} \langle a, \tilde{z} \rangle. \quad (50)$$

We note that the right-hand side of (50) only requires the evaluation of $\max_{a \in A} \langle a, \tilde{z} \rangle$. If $L$ regions are considered in Algorithm 2, the above procedure then only requires the computation of $L + \card(A \setminus A_{scr})$ inner products to evaluate $\max_{a \in A} \langle a, \tilde{z} \rangle$. This complexity has to be compared to the $n$ inner products needed for a brute-force evaluation of $\max_{a \in A} \langle a, \tilde{z} \rangle$. The figure of merit represented in Fig. 2b illustrates this ratio and is defined as

$$\text{computational gain} = \frac{L + \card(A \setminus A_{scr})}{n}. \quad (51)$$

In Fig. 2a, we see that the percentage of atoms identified by dual screening logically increases as the number of regions increases. More than 90% of the atoms not attaining the maximum value of $\langle a, \tilde{z} \rangle$ can be identified as soon as $\log_2(L) \geq 4$. We also notice that the dome regions lead to slightly better results than the sphere regions.

In Fig. 2b, we note that the ability of dual screening to reduce the number of atoms allows for important savings in terms of computational complexity. In particular, considering the case where $\log_2(L) \geq 4$, we see that the two-step procedure discussed above is able to evaluate $\max_{a \in A} \langle a, \tilde{z} \rangle$ with a complexity roughly ten times smaller than the one required by a brute-force approach.
C. Complexity/performance tradeoff of joint screening

As mentioned in Section III, the complexity of joint screening evolves linearly with the number \( L \) of regions. Hence, using a few regions leads to screening procedures with low computational cost. On the other hand, the use of a small number of regions may degrade performance since they can only partially or roughly cover the dictionary. Hereafter, we thus provide numerical simulations illustrating the tradeoff between complexity and screening performance achievable by joint screening.

More specifically, we emphasize how: \( i) \) the quality of the safe sphere \( B(\mathbf{c}, 1 - \tau) \) and the number \( L \) of regions may impact the screening performance (Fig. 3a and 3b); \( ii) \) the use of the proposed joint screening procedure can reduce the computational cost needed to attain some given screening performance (Fig. 3c). In the next section, joint screening is combined with optimization algorithms addressing the LASSO problem and the overall computational gain induced by the proposed method is demonstrated.

Our simulation setup is as follows. We consider the Gaussian deconvolution problem with dictionary (46). The observation vectors used as inputs of the LASSO problem are generated as Gaussian random linear combinations of 5 atoms of the dictionary. For each instance of the LASSO problem, the penalization parameter \( \lambda \) is chosen so that \( \lambda / \lambda_{\text{max}} = 0.3 \). A “high-accuracy” primal solution, say \( \mathbf{x}_{\text{cvx}} \), is computed with a CVX solver [28] and a dual feasible point, say \( \mathbf{z}_{\text{cvx}} \), is then built by dual scaling of \( \mathbf{y} - \mathbf{A} \mathbf{x}_{\text{cvx}} \). The safe sphere \( B(\mathbf{c}, 1 - \tau) \) used in our simulations obeys

\[
\mathbf{c} = \mathbf{z}_{\text{cvx}}, \\
1 - \tau = r_0 + r_{\text{gap}}
\]

(52)

where \( r_0 \in [10^{-4}, 1] \) is a simulation parameter and

\[
r_{\text{gap}} = \sqrt{2 \over \lambda^2} P_{\lambda}(\mathbf{y}, \mathbf{x}_{\text{cvx}}) - D_{\lambda}(\mathbf{y}, \mathbf{z}_{\text{cvx}}).
\]

In our joint screening procedure, the centers of the regions \( \{ R_l \}_{\ell=1}^L \) are chosen according to a uniform subsampling of the dictionary (46), i.e.,

\[
t_l = a_l \mathbf{z}_{\text{cvx}} \quad \text{for } l = 1 \ldots L.
\]

(53)

We consider regions with “dome” geometry although sphere regions lead sensibly to the same type of results. The size of the regions is optimized via the procedure described in Section III-C.

Fig. 3 represents different figures of merit illustrating the complexity/performance tradeoff achievable by joint screening. All the results are averaged over 50 simulation trials. They are plotted as a function of the (logarithm of the) radius of the safe sphere (\( x \) axis) and the number of regions used in joint screening (\( y \) axis).

Fig. 3a illustrates the percentage of zeros of \( \mathbf{x}_{\lambda}^* \) identified by joint screening. The last row of this figure (i.e., \( \log_2(L) = 10 \)) represents the performance attained by standard screening (10). For a given radius \( 1 - \tau \) (i.e., a vertical line in Fig. 3a), this figure thus shows how screening performance degrades when the number of regions used in joint screening (and therefore the computational complexity of the screening test) decreases. Hence, as far as the safe spheres of the form (52) are concerned, Fig. 3a provides a full picture of the complexity/performance tradeoff achievable by joint screening. Fig. 3b gives a different perspective on the same characterization: it represents the ratio between the number of zeros identified by joint and standard screening procedures. We see that, over a wide range of radii \( 1 - \tau \), the number of zeros identified by joint screening only slightly degrades with respect to standard screening as long as the number of regions \( L \) is sufficiently large (\( \log_2(L) \geq 5 \)).

Fig. 3c yet provides another insight on the complexity/performance tradeoff achieved by joint screening. Here, the screening performance is fixed and one evaluates the reduction of computational cost allowed by joint screening. To this end, we consider the following “two-step” screening procedure: \( i) \) we first apply joint screening on \( L \) regions and discard all the atoms, say \( \mathcal{A}_{\text{sc}} \), belonging to the screened regions; \( ii) \) we then apply standard screening tests on the remaining atoms \( \mathcal{A} \setminus \mathcal{A}_{\text{sc}} \).

The screening performance of this two-step procedure is by
tends to a constant ratio when the size of the dictionary becomes large. This asymptotic behavior attests to the ability of the approach to successfully manage high-dimensional (or even continuous) problems.

### E. Complexity savings

As a final assessment of the performance of joint screening, we evaluate the overall computational gain induced by the proposed method in the resolution of LASSO problems. More specifically, the computational complexity of different optimization procedures (with and without joint screening) are compared in terms of total number of operations needed to compute a (set of) target solution(s) $\mathbf{x}^*_\lambda$. Depending on the type of implementation (sequential or parallel), the results obtained in this section can thus be interpreted as either computational or energy savings.

We focus on the two experimental setups described at the beginning of this section, namely the Gaussian deconvolution and the “MNIST” sparse representation problems. In the former, the observation vector $\mathbf{y}$ is built as the Gaussian random linear combination of 5 atoms. In the latter, $\mathbf{y}$ is randomly chosen in a subset of the MNIST testing database.

The computational gain induced by joint screening is evaluated on two different optimization procedures. The first one is the well-known FISTA procedure, an accelerated proximal gradient algorithm introduced in [3]. The second corresponds to a Frank-Wolfe (FW) algorithm [8] applied to an epigraph formulation of the LASSO problem, as described in [29, Lemma 12]. We consider a “continuation method” to compute $\mathbf{x}^*_\lambda$ for some $\lambda = \lambda_{\text{target}}$: the LASSO problem is solved for a decreasing sequence of $\lambda$ (down to $\lambda = \lambda_{\text{target}}$) and initialized with a “warm start” for each new value of $\lambda$. We stop the iterations of the algorithm when a dual gap of $5.10^{-3}$ is attained.

The standard implementations of FISTA and FW are compared with two “screening-based” alternatives. In one implementation, the iterations of the optimization algorithm are intertwined with standard GAP sphere screening tests. In the other, joint screening (in combination with dual screening for the computation of the GAP sphere) is applied at each iteration of the optimization procedures. The center $\mathbf{c}$ of the GAP sphere is constructed by dual scaling of $\mathbf{y} - \mathbf{A}\hat{x}$, where $\hat{x}$ denotes the estimate of the optimization algorithm at a given iteration.

The following setup is considered for the parameters of the joint (and dual) screening. In the Gaussian deconvolution problem, the region centers $\{t_l\}_{l=1}^L$ are chosen as a regular subsampling of the dictionary, see (53). For MNIST, the $L$ centers are computed by applying the well-known “K-means” algorithm [30] on the atoms of the dictionary $\mathcal{A}$. Both the “sphere” and “dome” geometries are considered. The radii of the regions are optimized by using the methodology described in Section III-C. As far as FISTA is concerned, joint screening is used to implement the “two-step” procedure described in Section V-C (the same screening performance as standard screening is therefore achieved but at potentially lower computational cost).
Fig. 5 provides different figures of merit illustrating the reduction of complexity induced by joint screening. The first two rows represent the performance obtained in the Gaussian deconvolution problem, for FISTA and FW respectively. The last two rows deal with the MNIST problem for FISTA and FW, respectively. All the results are averaged over 50 trials.

The results in the first column characterize the average number of operations carried out by each procedure to solve the LASSO problem for \( \lambda/\lambda_{\text{max}} = 0.6 \). The results in the second column correspond to the average computational gain induced by joint screening over standard screening for \( \lambda/\lambda_{\text{max}} = 0.6 \). For one given instance of LASSO, the “computational gain” is defined as

\[
\text{computational gain} = 1 - \frac{N_{\text{joint}}}{N_{\text{std}}}, \tag{54}
\]

where \( N_{\text{std}} \) (resp. \( N_{\text{joint}} \)) is the total number of operations carried out by the optimization procedure with standard (resp. joint) screening. The third column illustrates the average computational gain as a function of \( \lambda/\lambda_{\text{max}} \) for some particular values of \( L \) (\( L = 2^7 \) for the first two rows and \( L = 100 \) for the last two).

In the counting of the operations, we restricted our attention to multiplications since they entail a much higher computational burden than additions in floating-point arithmetic. The number of operations is evaluated “smartly”, that is each computation which can be reused latter on by the procedure is not counted twice. For example, one iteration of FISTA/FW with or without standard screening roughly requires the same computational burden since all the inner products needed to implement standard screening are already computed within the main recursion of FISTA/FW.

In a nutshell, one iteration of FISTA with standard screening requires \( O(mn) \) operations (we remind the reader that, when dynamic screening is applied, \( n \) represents the number of atoms in the dictionary at one given iteration, see Section II-D). On the other hand, joint screening (cf. Algorithm 1) entails a complexity scaling as \( O(L \log_2 n + m) \). Letting \( n_{\text{js}} \) be the number of atoms in the dictionary after joint screening, applying a FISTA update and standard screening then requires \( O(n_{\text{js}} m) \) operations. Hence, if \( m(L + n_{\text{js}}) + L \log_2 n \leq mn \), the “two-step” screening procedure considered here leads to some computational savings. This happens for example when many atoms can be screened from a few joint tests (i.e., \( L \) and \( n_{\text{js}} \) are small compared to \( n \)).

Results in Fig. 5 (rows 1 and 3) show that this situation occurs in our numerical experiments: procedures with joint screening achieve convergence with fewer operations than those with standard (or no) screening. For example, for \( \lambda/\lambda_{\text{max}} = 0.6 \), the results in the second column emphasize that an average gain of roughly 50% to 60% may be attained for proper choices of \( L \). We also note that dome regions usually lead to slightly better performance than sphere regions. In the last column of Fig. 5, we notice that a gain can be obtained in wide range of \( \lambda \)'s although to a lesser extent when \(- \log_{10}(\lambda/\lambda_{\text{max}}) \) increases. This is in good accordance with typical results of safe screening where the performance degrades for lower values of the penalization parameter.

The same conclusions carry over for the simulations involving the FW procedure (Fig. 5, rows 2 and 4). We note that the complexity of one FW iteration is dominated by the so-called “atom selection” step:

\[
\text{Find } a_{\max} \in \arg \max_{a \in A}(a, r), \tag{55}
\]

where \( r = y - A \hat{x} \) and \( \hat{x} \) is the current FW iterate. The (brute-force) implementation of (55) results in a complexity of \( O(mn) \) per iteration. Similarly to FISTA, adding standard screening into FW recursions only induces a marginal cost since all the inner products needed to implement (10) are already computed in the (brute-force) evaluation of (55).

The joint methodologies introduced in this paper can help to reduce this order of complexity as follows. We first note that (55) can be solved efficiently by using the dual screening technique presented in Section V-B, see Algorithm 2. This requires \( O(m(L + n_{\text{ds}}) + L \log_2 n) \) operations where \( n_{\text{ds}} \) is the number of atoms not solution of (55), which were not identified by dual screening. Applying joint screening then only requires \( O(L \log_2 n) \) additional operations, since the inner products \( \{t_{ij}, c\}_{j=1}^{m} \) have already been computed (up to some constant) in the dual-screening step. The overall complexity of one FW iteration with dual/joint screening thus scales as \( O(m(L + n_{\text{ds}}) + 2L \log_2 n) \). If \( L \) and \( n_{\text{ds}} \) are much smaller than \( n \), this order of complexity may become more favorable than \( O(mn) \).

We illustrate this trend in rows 2 and 4 of Fig. 5. Similarly to FISTA, we see that joint screening may lead to significant gains in the implementation of FW: for proper choices of \( L \), average computational gains larger than 60% may be obtained. For the MNIST simulation (row 4, column 3), we see that the average computational gain is less dependent on \( \lambda \). As far as this simulation setup is concerned, we noted that this is due to the fact that dual screening always allows for important gains in the implementation of (55). Hence, even when safe screening becomes more difficult (i.e., \( \lambda \) decreases), complexity reduction is still possible via dual screening.

VI. CONCLUSIONS

In this paper, we proposed several methodologies to improve the tradeoff “complexity/effectiveness” of safe screening tests for LASSO. Our procedures are based on the following general philosophy: we gather subsets of atoms in some regions with “desirable” geometries (e.g., spheres or domes) and exploit the latter to deduce closed-form expressions of the optimization problems encountered in the construction of the safe screening test. A first procedure relying on this principle is the so-called “joint screening test” (Section III) which enables the rejection of all the atoms belonging to some region by performing one single test. Other procedures grounded on this philosophy are the “relaxed dual scaling” and “dual screening” procedures proposed in Section IV, which offer some low-complexity alternatives to compute a dual feasible point of the LASSO problem. We showed through numerical simulations that the proposed methodologies lead to significant computational gain in the implementation of safe screening tests and standard optimization procedures.
Figure 5. First column: overall number of operations required to achieve convergence; second and third columns: average computational gain induced by joint screening over standard screening. First and third rows: FISTA; second and fourth rows: FW. The first two rows deal with the Gaussian deconvolution setup; the last two with the MNIST sparse-representation problem.
APPENDIX A
MISCELLANEOUS TECHNICAL LEMMAS

In this appendix we prove two technical lemmas which will be useful in the derivation of our main results. The first lemma (Lemma 3) characterizes the properties of some functions appearing in the dome joint screening procedure. The second lemma (Lemma 4) establishes a relationship between the (norm of the) center c and the radius $\tau$ of any safe sphere.

Lemma 3. Let

$$f(\xi) = A\xi + \sqrt{1 - A^2}\sqrt{1 - \xi^2}. \quad (56)$$

The following assertions hold:

(a) If $A \in [-1, 1]$, $f$ is concave over $[-1, 1]$
(b) If $A \in (-1, 1)$, $f$ is strictly concave over $[-1, 1]$
(c) If $A \in [-1, 1]$, the function $g(\xi) = \max_{\xi \leq \xi' \leq 1} f(\xi')$ can be written as

$$g(\xi) = \begin{cases} f(A) & \text{if } \xi < A \\ f(\xi) & \text{otherwise} \end{cases} \quad (57)$$

in the interval $\xi \in [-1, 1]$.

(d) If $A \in [-1, 1]$, $g$ is concave and non-increasing over the interval $[-1, 1]$
(e) If $A \in (-1, 1)$, $g$ is strictly concave and strictly decreasing over the interval $[A, 1]$.

Proof: ((a) and (b)) If $A = \pm 1$, $f$ is linear and therefore concave. If $A \in (-1, 1)$, $f$ is the sum of two terms. The first one is linear and therefore concave. The second corresponds to the equation of a “half-circle” and is thus strictly concave. Hence, $f$ is strictly concave for $A \in (-1, 1)$.

(c) If $|A| < 1$, we note that the maximum value of $f(\xi')$ over $[-1, 1]$ is unique and obtained for $\xi' = A$, by virtue of the strict concavity of $f$. Then, for $|A| < 1$ and $\xi \leq A$,

$$\max_{\xi \leq \xi' \leq 1} f(\xi') = f(A) = 1,$$

since $A \in [\xi, 1]$, and for $\xi > A$,

$$\max_{\xi \leq \xi' \leq 1} f(\xi') = f(\xi),$$

due to the strictly decreasing behavior of $f$ over $[\xi, 1]$.

The case $|A| = 1$ leads to trivial solutions. If $A = 1$, we have

$$\max_{\xi \leq \xi' \leq 1} f(\xi') = \max_{\xi \leq \xi' \leq 1} \xi' = 1 = f(A) \quad \forall \xi \in [-1, 1].$$

If $A = -1$, we have

$$\max_{\xi \leq \xi' \leq 1} f(\xi') = \max_{\xi \leq \xi' \leq 1} -\xi' = -\xi = f(\xi) \quad \forall \xi \in [-1, 1].$$

Eq. (57) merges all the different cases in a synthetic way.

(d) and (e) The concavity and the non-increasing (resp. the strict concavity and the strictly decreasing) nature of $g$ over $[-1, 1]$ (resp. $[A, 1]$) for $A \in [-1, 1]$ (resp. $A \in (-1, 1)$) follows from the definition of $g$ and the concavity (resp. strict concavity) of $f$.

The next lemma relates the center and the radius of any safe sphere test. It is used in the proof of Theorem 1 in Appendix B.

Lemma 4. Let $S = B(c, 1 - \tau)$ be a safe sphere for problem (1)-(2) with penalization parameter $\lambda < \lambda_{\text{max}}$ (that is $z^*_\lambda \in S$). Then, we have

$$\tau \leq ||c||_2. \quad (58)$$

Proof: If $S = \{z : ||z - c||_2 \leq 1 - \tau\}$ is a safe region, then

$$||z^*_\lambda - c||_2 \leq 1 - \tau, \quad (59)$$

which leads, by using a triangle inequality, to

$$||z^*_\lambda||_2 - 1 + \tau \leq ||c||_2. \quad (60)$$

Now, if $\lambda < \lambda_{\text{max}}$, we have

$$||z^*_\lambda||_2 \geq 1. \quad (61)$$

The latter claim follows from the following arguments. If $\lambda < \lambda_{\text{max}}$, we necessarily have $x^*_\lambda(i) > 0$ for some $i \in [1, \ldots, n]$. From the optimality condition (7), we have for such $i$: $(a_i, z^*_\lambda) = 1$. Hence, we obtain (61) by using the Cauchy-Schwarz inequality:

$$||z^*_\lambda||_2 \geq (a_i, z^*_\lambda) = 1.$$

Finally, we obtain the main result (58) by combining (60) and (61).

APPENDIX B
PROOFS OF THEOREMS 1 AND 2

In this appendix we provide a proof to the results stated in Theorems 1 and 2. The proof is divided in two parts: in Appendix B-A we address the case of a spherical region whereas in Appendix B-B we focus on a dome region.

A. Sphere region

Let us first notice that the sphere region $B(t, \epsilon)$ can be written as

$$B(t, \epsilon) = \{a = t + z : ||z||_2 \leq \epsilon\}. \quad (64)$$

Therefore, $\forall \tilde{z} \in \mathbb{R}^m$ we have

$$\max_{a \in B(t, \epsilon)} \langle a, \tilde{z} \rangle = \langle t, \tilde{z} \rangle + \max_{||z||_2 \leq \epsilon} \langle z, \tilde{z} \rangle = \langle t, \tilde{z} \rangle + \epsilon ||\tilde{z}||_2, \quad (65)$$

where the last equality is a consequence of the tightness of the Cauchy-Schwarz inequality. The result stated in Theorem 2 for the sphere region $B(t, \epsilon)$ corresponds to (65). Theorem 1 easily follows from (65) by choosing $\tilde{z} = c$.

8This statement can be proved as follows. If $x^*_\lambda = 0$, then we have $z^*_\lambda = y/\lambda$ from (7). Now, we must have, by dual feasibility:

$$\max_i (a_i, z^*_\lambda) \leq 1. \quad (62)$$

Plugging $z^*_\lambda = y/\lambda$ into this inequality, we obtain

$$\lambda_{\text{max}} \equiv \max_i (a_i, y) \leq \lambda. \quad (63)$$

Therefore, by contraposition, if $\lambda < \lambda_{\text{max}}$ then $x^*_\lambda \neq 0$. 

B. Dome region

We assume \( \|t\|_2 = 1 \). We first note that the dome region \( D(t, \delta) \) can be written as

\[
D(t, \delta) = \{ a = at + z : z \in Z, \delta \leq a \leq 1 \},
\]

where

\[
Z = \{ z : z \in (\text{span}[t])^\perp, \|z\|_2 \leq \sqrt{1 - \alpha^2} \}.
\]

Therefore, \( \forall z \in \mathbb{R}^m \) we have

\[
\max_{a \in D(t, \delta)} \langle a, z \rangle = \max_{\alpha \leq \alpha \leq 1} \left( \alpha \langle t, z \rangle + \max_{z \in Z} (\langle z, z \rangle) \right)
\]

\[
= \max_{\delta \leq \alpha \leq 1} \left( \alpha \langle t, z \rangle + \max_{z \in Z} (\langle z, P^+_t(\delta) \rangle) \right)
\]

\[
= \max_{\delta \leq \alpha \leq 1} \left( \alpha \langle t, z \rangle + \sqrt{1 - \alpha^2} \|P^+_t(\delta)\|_2 \right).
\]

where \( P^+_t(\delta) = z - \langle t, z \rangle t \) denotes the orthogonal projector onto \( (\text{span}[t])^\perp \). The last equality is a consequence of the tightness of the Cauchy-Schwarz inequality.

Using Lemma 3(c) in Appendix A with \( A = (\frac{t}{\|t\|_2}) \), we obtain that

\[
g(\delta) = \left\{ \begin{array}{ll}
\|z\|_2 & \text{if } \delta < \langle \frac{t}{\|t\|_2}, z \rangle \\
\delta(t, z) + \sqrt{1 - \delta^2} \|P^+_t(z)\|_2 & \text{otherwise} \end{array} \right.
\]

(68)

This corresponds to the result stated in Theorem 2.

Setting \( z = c \) in the definition of \( g(\delta) \), the joint dome test “\( \max_{a \in D(t, \delta)} \langle a, c \rangle < \tau \)” can thus be simply rewritten as

\[
\tau > g(\delta).
\]

(69)

The expressions (23)-(24) stated in Theorem 1 can then be obtained as follows. First, satisfying (69) necessarily requires that

\[
\tau > \min_{\delta \in [-1, 1]} g(\delta) = g(1) = \langle t, c \rangle,
\]

(70)

where the first equality follows from the non-increasing nature of \( g \) (Lemma 3(d)) and the second from its definition (68). Inequality (70) corresponds to the condition enforced by (23).

Moreover, we have from Lemma 4 in Appendix A that\(^9\)

\[
\tau \leq \|c\|_2
\]

(71)

provided that \( \tau \) is associated to the radius of a safe sphere. Therefore, if (23) holds, owing to the continuity of \( g \) and the fact that it is strictly decreasing over \( \left[ \frac{\|t\|_2}{\|c\|_2}, 1 \right] \) (see Lemma 3(e)), there exists \( \delta_{t,c} \in \left[ \frac{\|t\|_2}{\|c\|_2}, 1 \right] \) such that \( g(\delta_{t,c}) = \tau \). Using the expression of \( g \) over \( \left[ \frac{\|t\|_2}{\|c\|_2}, 1 \right] \) in (68), we find

\[
\delta_{t,c} = \frac{\langle t, c \rangle \tau + \sqrt{\|c\|_2^2 - \langle t, c \rangle^2} \sqrt{\|c\|_2^2 - \tau^2}}{\|c\|_2^2}.
\]

(72)

\(^9\)Note that the assumption “\( \lambda < \lambda_{\max} \)” in Lemma 4 is satisfied by virtue of our working hypotheses (see Section II-E).

\(^{10}\)Note that \( c \neq 0 \) because of working hypotheses in Section II-E.

Invoking again the strict decrease of \( g \) over \( \left[ \frac{\|t\|_2}{\|c\|_2}, 1 \right] \) (see Lemma 3(e)), we have that \( \tau = g(\delta_{t,c}) > g(\delta) \) if and only if \( \delta > \delta_{t,c} \).

Combining this condition with the expression of \( \delta_{t,c} \) in (72), we obtain (24).

APPENDIX C

PROOF OF LEMA 1

First note that the volume of a dome \( D(t, \delta) \) is a decreasing function of \( \delta \), irrespective of the test vector \( t \). Hence, the smallest dome including all the elements of \( U \) is given by \( D(t^*, \delta^*) \) with (without loss of generality, we assume that the vector \( t \) defining the dome has a unit norm):\(^{10}\)

\[
t^* = \arg \max_{t : \|t\|_2 = 1} \inf \{ a : \|a - t\|_2 \}
\]

(73)

\[
\delta^* = \min_{a \in U} \|a - t^*\|_2.
\]

(74)

On the other hand, the minimum-volume sphere covering all the elements of \( U \) is given by \( B(t^*, \epsilon^*) \) with

\[
t^* = \arg \min_{t : \|t\|_2 = 1} \inf \{ a : \|a - t\|_2 \},
\]

(75)

\[
\epsilon^* = \max_{a \in U} \|a - t^*\|_2.
\]

(76)

We first show that the optimal parameters \( (t^*, \delta^*) \) and \( (\tilde{t}^*, \epsilon^*) \) are related as follows

\[
\tilde{t}^* = \tilde{\delta} t^*,
\]

(77)

\[
\epsilon^* = \sqrt{1 - \tilde{\delta}^2},
\]

(78)

where

\[
\tilde{\delta} = \max(0, \delta^*).
\]

(79)

Indeed, setting \( \tilde{t} = \beta a \) with \( \beta \geq 0 \) and \( \|a\|_2 = 1 \), (75) can also be rewritten as

\[
(\beta^*, \epsilon^*) = \arg \min_{\beta \geq 0, \|u\|_2 = 1} \inf \{ a : \|a - \beta u\|_2 \}
\]

\[
= \arg \min_{\beta \geq 0, \|u\|_2 = 1} \left( \beta^2 - 2 \beta \inf_{a \in U} \langle u, a \rangle \right).
\]

(80)

From (80), we clearly have that \( u^* = \arg \max_{\|u\|_2 = 1} \inf_{a \in U} \langle u, a \rangle \). In view of (73), we thus have \( u = \tilde{t}^* \). Taking this fact into account, we deduce

\[
\beta^* = \arg \min_{\beta \geq 0} \left( \beta^2 - 2 \beta \epsilon^* \right) = \tilde{\delta},
\]

where \( \tilde{\delta} \) is defined in (79), and thus \( \tilde{t}^* = \delta t^* \). Plugging \( \tilde{t}^* = \delta t^* \) in (76) and using the definition of \( \delta^* \) in (74), we find

\[
\epsilon^* = \sqrt{1 - \tilde{\delta}^2}.
\]

(81)

This shows (77)-(78).

We now prove the result of the lemma, that is

\[
D(t^*, \delta^*) \subseteq B(\tilde{t}^*, \epsilon^*).
\]

This statement can be equivalently rewritten as

\[
\forall a \in D(t^*, \delta^*) : \|a - \tilde{t}^*\|_2 \leq 1 - \tilde{\delta}^2.
\]
If $\delta = 0$, the inequality is satisfied since $\|a\|_2 \leq 1 \forall a \in D(t^*, \delta^*)$. If $\delta = \delta^*$, the inequality is also verified because

$$\|a - \delta^* t^*\|_2^2 = 1 + (\delta^*)^2 - 2\delta^* \langle t^*, a \rangle \leq 1 - (\delta^*)^2,$$

where the last inequality follows from the fact that

$$\forall a \in D(t^*, \delta^*): \langle t^*, a \rangle \geq \delta^*.$$

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