Rare Feature Selection in High Dimensions

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Abstract

It is common in modern prediction problems for many predictor variables to be counts of rarely occurring events. This leads to design matrices in which many columns are highly sparse. The challenge posed by such “rare features” has received little attention despite its prevalence in diverse areas, ranging from natural language processing (e.g., rare words) to biology (e.g., rare species). We show, both theoretically and empirically, that not explicitly accounting for the rareness of features can greatly reduce the effectiveness of an analysis. We next propose a framework for aggregating rare features into denser features in a flexible manner that creates better predictors of the response. Our strategy leverages side information in the form of a tree that encodes feature similarity.

We apply our method to data from TripAdvisor, in which we predict the numerical rating of a hotel based on the text of the associated review. Our method achieves high accuracy by making effective use of rare words; by contrast, the lasso is unable to identify highly predictive words if they are too rare. A companion R package, called rare, implements our new estimator, using the alternating direction method of multipliers.

1 Introduction

The assumption of parameter sparsity plays an important simplifying role in high-dimensional statistics. However, this paper is focused on sparsity in the data itself, which actually makes estimation more challenging. In many modern prediction problems, the design matrix has many columns that are highly sparse. This arises when the features record the frequency of events (or the number of times certain properties hold). While a small number of these events may be common, there is typically a very large number of rare events, which correspond to features that are zero for nearly all observations. We call these predictors rare features. Rare features are in fact extremely common in many modern data sets. For example, consider the task of predicting user behavior based on past website visits: Only a small number of sites are visited by a lot of the users; all other sites are visited by only a small proportion of users.

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As another example, consider text mining, in which one makes predictions about documents based on the terms used. A typical approach is to create a document-term matrix in which each column encodes a term’s frequency across documents. In such domains, it is often the case that the majority of the terms appear very infrequently across the documents; hence the corresponding columns in the document-term matrix are very sparse (e.g., Forman 2003; Huang 2008; Liu et al. 2010; Wang et al. 2010). In Section 6, we study a text dataset with more than 200 thousand reviews crawled from https://www.tripadvisor.com. Our goal is to use the adjectives in a review to predict a user’s numerical rating of a hotel. As shown in the right panel of Figure 5, the distribution of adjective density, defined as the proportion of documents containing an adjective, is extremely right-skewed, with many adjectives occurring very infrequently in the corpus. In fact, we find that more than 95% of the 7,787 adjectives appear in less than 5% of the reviews. It is common practice to simply discard rare terms which may mean removing most of the terms (e.g., Forman 2003; Huang 2008; Liu et al. 2010; Wang et al. 2010).

Rare features also arise in various scientific fields. For example, microbiome data measure the abundances of a large number of microbial species in a given environment. Researchers use next generation sequencing technologies, clustering these reads into “operational taxonomic units” (OTUs), which are roughly thought of as different species of microbe (e.g., Schloss et al. 2009; Caporaso et al. 2010). In practice, many OTUs are rare, and researchers often aggregate the OTUs to genus or higher levels (e.g., Zhang et al. 2012; Chen et al. 2013; Xia et al. 2013; Lin et al. 2014; Randolph et al. 2015; Shi et al. 2016; Cao et al. 2017) or with unsupervised clustering techniques (e.g., McMurdie and Holmes 2013; Wang and Zhao 2017b) to create denser features. However, even after this step, a large portion of these aggregated OTUs are still found to be too sparse and thus are discarded (e.g., Zhang et al. 2012; Chen et al. 2013; Shi et al. 2016; Wang and Zhao 2017b). The rationale for this elimination of rare OTUs is that there needs to be enough variation among samples for an OTU to be successfully estimated in a statistical model (Ridenhour et al., 2017).

The practice of discarding rare features is wasteful: a rare feature should not be interpreted as an unimportant one since it can be highly predictive of the response. For instance, using the word “ghastly” in a hotel review delivers an obvious negative sentiment, but this adjective appears very infrequently in TripAdvisor reviews. Discarding an informative word like “ghastly” simply because it is rare clearly seems inadvisable. To throw out over half of one’s features is to ignore what may be a huge amount of useful information.

Even if rare features are not explicitly discarded, many existing variable selection methods are unable to select them. The challenge is that with limited examples there is very little information to identify a rare feature as important. Theorem 1 shows that even a single rare feature can render ordinary least squares (OLS) inconsistent in the classical limit of infinite sample size and fixed dimension.

To address the challenge posed by rare features, we propose in this work a method for forming new aggregated features which are less sparse than the original ones and may be more relevant to the prediction task. Consider the following features, which represent the frequency of certain adjectives used in hotel reviews:

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1For example, in the R text mining library tm (Feinerer and Hornik, 2017), removeSparseTerms is a commonly used function for removing any terms with sparsity level above a certain threshold.
While both sets of adjectives express negative sentiments, the first set (which might be summarized as “worry”) seems more mild than the second set (which might be summarized as “horrification”). In predicting the rating of a hotel review, we might find the following two aggregated features more relevant:

\[
\begin{align*}
\widetilde{X}_{\text{worry}} &= X_{\text{worrying}} + X_{\text{depressing}} + \cdots + X_{\text{troubling}} \\
\widetilde{X}_{\text{horrification}} &= X_{\text{horrid}} + X_{\text{hideous}} + \cdots + X_{\text{awful}}.
\end{align*}
\]

The distinction between “horrid” and “hideous” might not matter for predicting the hotel rating, whereas the distinction between a “worry”-related word versus a “horrification”-related word may be quite relevant. Thus, not only are these aggregated features less rare than the original features, but they may also be more relevant to the prediction task. A method that selects the aggregated feature \(\widetilde{X}_{\text{horrification}}\) thereby can incorporate the information conveyed in the use of “hideous” into the prediction task; this same method may be unable to otherwise determine the effect of “hideous” by itself since it is too rare.

Indeed, appropriate aggregation of rare features in certain situations can be key to attaining consistent estimation and support recovery. In Theorem 2, we consider a setting where all features are rare and a natural aggregation rule exists among the features. In that setting, we show that the lasso (Tibshirani, 1996) fails to attain high-probability support recovery (for all values of its tuning parameter), whereas an oracle-aggregator does attain this property. Theorem 2 demonstrates the value of proper aggregation for accurate feature selection when features are rare. This motivates the remainder of the paper, in which we devise a strategy for determining an effective feature aggregation based on data. Our aggregation procedure makes use of side information about the features, which we find is available in many domains. In particular, we assume that a tree is available that represents the closeness of features. For example, Figure 1 shows a tree for the previous word example that is generated via hierarchical clustering over word2vec (Mikolov et al., 2013) embeddings learned from a different data source. The two contours enclose two subtrees resulting from a cut at their joint node. Aggregating the counts in these subtrees leads to the new features \(\widetilde{X}_{\text{worry}}\) and \(\widetilde{X}_{\text{horrification}}\) described above. We give more details of constructing such a tree in Section 3.1.

In Section 2, we motivate our work by providing theoretical results demonstrating the difficulty that OLS and the lasso have with rare features. We further show that correct aggregation of rare features leads to signed support recovery in a setting where the lasso is unable to attain this property. In Section 3, we introduce a tree-based parametrization strategy that translates the feature aggregation problem to a sparse modeling problem. Our main proposal is an estimator formulated as a solution to a convex optimization problem for which we derive an efficient algorithm. In Section 4, we prove a bound on the prediction error for our method. Finally, we demonstrate the empirical merits of the proposed framework through simulation (Section 5) and through the TripAdvisor prediction task (Section 6) described above. In simulation, we examine our method’s robustness to misspecified side information. Quantitative and qualitative comparisons in the TripAdvisor example highlight the advantages of aggregating rare features.
Notation: Given a design matrix $X \in \mathbb{R}^{n \times p}$, let $x_i \in \mathbb{R}^p$ denote the feature vector of observation $i$ and $X_j \in \mathbb{R}^n$ denote the $j$th feature, where $i = 1, \ldots, n$ and $j = 1, \ldots, p$. For a vector $\beta \in \mathbb{R}^p$, let $\text{supp}(\beta) \subseteq \{1, \ldots, p\}$ denote its support (i.e., the set of indices of nonzero elements). Let $S_{\pm}(\beta) := (\text{sign}(\beta_t))_{t=1,\ldots,p}$ encode the signed support of the vector $\beta$. Let $T$ be a $p$-leafed tree with root $r$, set of leaves $\mathcal{L}(T) = \{1, \ldots, p\}$, and set of nodes $\mathcal{V}(T)$ of size $|T|$. Let $T_u$ be the subtree of $T$ rooted by $u$ for $u \in \mathcal{V}(T)$. We follow the commonly-used notions of child, parent, sibling, descendant, and ancestor to describe the relationships between nodes of a tree. For a matrix $A \in \mathbb{R}^{m \times n}$, let $\|A\|_1 = \max_{1 \leq j \leq n} \sum_{i=1}^m |a_{ij}|$ be the matrix-1 norm, $\|A\|_\infty = \|A^T\|_1$ be the matrix-$\infty$ norm, and (for a subset $B$ of $\{1, \ldots, n\}$) $A_B \in \mathbb{R}^{m \times |B|}$ be the submatrix formed by removing the columns of $A$ not in $B$. Let $S_\lambda(\beta_j) = \text{sign}(\beta_j) \cdot \max\{|\beta_j| - \lambda, 0\}$ be the soft-thresholding operator applied to $\beta_j \in \mathbb{R}$. We let $e_j$ denote the vector having a one in the $j$th entry and zero elsewhere.

### 2 Rare Features and the Promise of Aggregation

#### 2.1 The Difficulty Posed by Rare Features

Consider the linear model,

$$y = X\beta^* + \epsilon, \quad \epsilon \sim N(0, \sigma^2 I_n).$$  

where $y = (y_1, \ldots, y_n)^T \in \mathbb{R}^n$ is a response vector, $X \in \mathbb{R}^{n \times p}$ is a design matrix, $\beta^*$ is a $p$-vector of parameters, and $\epsilon \in \mathbb{R}^n$ is a vector of independent Gaussian errors having variance $\sigma^2$. In this paper, we focus on counts data, i.e., $X_{ij}$ records the frequency of an event $j$ in observation $i$. In particular, we will assume throughout that $X$ has non-negative elements.

The lasso (Tibshirani [1996]) is an estimator that performs variable selection, making it well-suited to the $p \gg n$ setting:

$$\hat{\beta}_\lambda^{\text{lasso}} \in \arg\min_{\beta \in \mathbb{R}^p} \frac{1}{2n} \|y - X\beta\|^2_2 + \lambda \|\beta\|_1.$$  

Figure 1: A tree that relates adjectives on its leaves.
When $\lambda = 0$, this coincides with the OLS estimator, which is uniquely defined when $n > p$ and $X$ is full rank:

$$\hat{\beta}_{OLS}(n) = (X^T X)^{-1} X^T y.$$ 

To better understand the challenge posed by rare features, we begin by considering the effect of a single rare feature on OLS in the classical $p$-fixed, $n \to \infty$ regime. We take the $j$th feature to be a binary vector having $k$ nonzeros, where $k$ is a fixed value not depending on $n$. As $n$ increases, the proportion of nonzero elements, $k/n$, goes to 0. We show in Theorem 1 that $\hat{\beta}_{OLS}^j(n)$ does not converge in probability to $\beta^*_j$ with increasing sample size. This establishes that OLS is not a consistent estimator of $\beta^*$ even in a $p$-fixed asymptotic regime.

**Theorem 1.** Consider the linear model (1) with $X \in \mathbb{R}^{n \times p}$ having full column rank. Further suppose that $X_j$ is a binary vector having (a constant) $k$ nonzeros. It follows that there exists $\eta > 0$ for which

$$\liminf_{n \to \infty} \mathbb{P}\left(\left|\hat{\beta}_{OLS}^j(n) - \beta^*_j\right| > \eta\right) > 0.$$ 

**Proof.** The result follows from taking lim inf$_{n \to \infty}$ of both sides of (7) in Appendix A and observing that $2\Phi\left(-\eta k^{1/2}/\sigma\right)$ does not depend on $n$. \qed

The above result highlights the difficulty of estimating the coefficient of a rare feature. This suggests that even when rare features are not explicitly discarded, variable selection methods may fail to ever select them regardless of their strength of association with the response. Other researchers have also acknowledged the difficulty posed by rare features in different scenarios. For example, in the context of hypothesis testing for high-dimensional sparse binary regression, Mukherjee et al. (2015) shows that when the design matrix is too sparse, any test has no power asymptotically, and signals cannot be detected regardless of their strength. Since the failure is caused by the sparsity of the features, it is therefore natural to ask if “densifying the features” in an appropriate way would fix the problem. As discussed above, aggregating the counts of related events may be a reasonable way to allow a method to make use of the information in rare features.

### 2.2 Aggregating Rare Features Can Help

Given $m$ subsets of $\{1, \ldots, p\}$, we can form $m$ aggregated features by summing within each subset. We can encode these subsets in a binary matrix $A \in \{0, 1\}^{p \times m}$ and form a new design matrix of aggregated features as $\tilde{X} = XA$. The columns of $\tilde{X}$ are also counts, but represent the frequency of $m$ different unions of the $p$ original events. For example, if the first subset is $\{1, 6, 8\}$, the first column of $A$ would be $e_1 + e_6 + e_8$ and the first aggregated feature would be $\tilde{X}_1 = X_1 + X_6 + X_8$, recording the number of times any of the first, sixth, or eighth events occur. A linear model, $\tilde{X}\tilde{\beta}$, based on the aggregated features can be equivalently expressed as a linear model, $X\beta$, in terms of the original features as long as $\beta$ satisfies a set of linear constraints (ensuring that it is in the column space of $A$):

$$\tilde{X}\tilde{\beta} = (XA)\hat{\beta} = X(A\hat{\beta}) = X\beta.$$
The vector $\boldsymbol{\beta}$ lies in the column space of $\mathbf{A}$ precisely when it is constant within each of the $m$ subsets. For example,

$$\text{enforcing } \beta_1 = \beta_6 = \beta_8 \iff \text{aggregating features: } \mathbf{X}_1\beta_1 + \mathbf{X}_6\beta_6 + \mathbf{X}_8\beta_8 = (\mathbf{X}_1 + \mathbf{X}_6 + \mathbf{X}_8)\beta_1 = \tilde{\mathbf{X}}_1\tilde{\beta}_1.$$  (3)

In practice, determining how to aggregate features is a challenging problem, and our proposed strategy in Section 3 will use side information to guide this aggregation.

For now, to understand the potential gains achievable by aggregation, we consider an idealized case in which the correct aggregation of features is given to us by an oracle. In the next theorem, we construct a situation in which (a) the lasso on the original rare features is unable to correctly recover the support of $\beta^*$ for any value of the tuning parameter $\lambda$, and (b) an oracle-aggregation of features makes it possible for the lasso to recover the support of $\beta^*$. For simplicity, we take $\mathbf{X} = \mathbf{I}_n$, which corresponds to the case in which every feature has a single nonzero observation (and $n = p$). We take $\beta^*$ to have $k$ blocks of size $n/k$, with entries that are constant within each block. The last block is all zeros and the minimal nonzero $|\beta_j^*|$, is restricted to lie within a range that expands with $n$ and shrinks with $k$. The oracle approach delivers to the lasso the $k$ aggregated features that match the structure in $\beta^*$. These aggregated features have $n/k$ nonzeros, and thus are not rare features. Having performed the lasso on these aggregated features, we then duplicate the $k$ elements, $n/k$ times per group, to get $\beta^*_{\text{oracle}} \in \mathbb{R}^n$. The lasso with the oracle-aggregator is shown to achieve high-probability signed support recovery whereas the lasso on the original features fails to achieve this property for all values of the tuning parameter $\lambda$.

**Theorem 2.** Consider the linear model $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{e}$ with $\mathbf{X} = \mathbf{I}_n$ and $\beta^* = \tilde{\beta}^* \otimes \mathbf{1}_{n/k}$ for $\tilde{\beta}_i^* = (\tilde{\beta}_1^*, \ldots, \tilde{\beta}_{k-1}^*, 0)$. If $\sigma \sqrt{\frac{4k\log(k^2n)}{n}} < \min_{i=1,\ldots,k-1} |\tilde{\beta}_i^*| \leq \sigma \sqrt{\frac{\log(2(2n/k-1))}{3}}$ where $\tilde{c} = \frac{1}{3}e^{-(\pi/2+2)} - \frac{1}{4} + \frac{1}{\pi}$

(a) The lasso fails to get high-probability signed support recovery:

$$\limsup_{n \to \infty} \sup_{\lambda \geq 0} \mathbb{P} \left( S_{\pm}(\hat{\beta}_{\lambda}^{\text{lasso}}) = S_{\pm}(\beta^*) \right) \leq \frac{1}{e}.$$  

(b) The lasso with an oracle-aggregation of features succeeds in recovering the correct signed support for some $\lambda > 0$:

$$\lim_{n \to \infty} \mathbb{P} \left( S_{\pm}(\hat{\beta}_{\lambda}^{\text{oracle}}) = S_{\pm}(\beta^*) \right) = 1.$$  

**Proof.** These results correspond to Propositions 1 and 2 in Appendix B and are proved there. \qed

### 3 Main Proposal: Tree-Guided Aggregation

In the previous section, we have seen the potential gains achievable through aggregating rare features. In this section, we propose a tree-guided method for aggregating and selecting rare features. We discuss this tree in Section 3.1 introduce a tree-based parametrization strategy in Section 3.2 and propose a new estimator in Section 3.3.
3.1 A Tree to Guide Aggregation

To form aggregated variables, it is infeasible to consider all possible partitions of the features \( \{1, \ldots, p\} \). Rather, we will consider a tree \( T \) with leaves 1, \ldots, \( p \) and restrict ourselves to partitions that can be expressed as a collection of branches of \( T \) (see, e.g., Figure 1). We sum features within a branch to form our new aggregated features.

We would like to aggregate features that are related, and thus we would like to have \( T \) encode feature similarity information. Such information about the features comes from prior knowledge and/or data sources external to the current regression problem (i.e., not from \( y \) and \( X \)). For example, for microbiome data, \( T \) could be the phylogenetic tree encoding evolutionary relationships among the OTUs (e.g., [Matsen et al. 2010] [Tang et al. 2016] [Wang and Zhao 2017a]) or the co-occurrence of OTUs from past data sets. When features correspond to words, closeness in meaning can be used to form \( T \) (e.g., in Section 6, we perform hierarchical clustering on word embeddings that were learned from an enormous corpus).

In (3), we demonstrated how aggregating a set of features is equivalent to setting these features’ coefficients to be equal. To perform tree-guided aggregation, we therefore associate a coefficient \( \beta_j \) with each leaf of \( T \) and “fuse” (i.e., set equal to each other) any coefficients within a branch that we wish to aggregate.

3.2 A Tree-Based Parametrization

In order to fuse \( \beta_u \)’s within a branch, we adopt a tree-based parametrization by assigning a parameter \( \gamma_u \) to each node \( u \) in \( T \) (this includes both leaves and interior nodes). The left panel of Figure 2 gives an example. Let \( \text{ancestor}(j) \cup \{j\} \) be the set of nodes in the path from the root of \( T \) to the \( j \)th feature, which is associated with the \( j \)th leaf. We express \( \beta_j \) as the sum of all the \( \gamma_u \)’s on the path:

\[
\beta_j = \sum_{u \in \text{ancestor}(j) \cup \{j\}} \gamma_u. \quad (4)
\]

This can be written more compactly as \( \beta = A\gamma \), where \( A \in \{0, 1\}^{p \times |T|} \) is a binary matrix with \( A_{jk} := \mathbb{1}_{\{u_k \in \text{ancestor}(j) \cup \{j\}\}} \). The descendants of each node \( u \) define a branch \( T_u \), and zeroing out \( \gamma_v \)’s for all \( v \in \text{descendant}(u) \) fuses the coefficients in this branch, i.e., \( \{\beta_j : j \in L(T_u)\} \). Thus, \( \gamma_{\text{descendant}(u)} = 0 \) is equivalent to aggregating the features \( X_j \) with \( j \in L(T_u) \) (see the right panel of Figure 2).

Another way of viewing this parametrization’s merging of branches is by expressing \( X\beta = XA\gamma \), where \( (XA)_{ik} = \sum_{j=1}^{p} X_{ij}A_{jk} = \sum_{j \in \text{descendant}(u_k) \cup \{u_k\}} X_{ij} \). Aggregates counts over all the descendant features of node \( u_k \). By aggregating nearby features, we allow rare features to borrow strength from their neighbors, allowing us to estimate shared coefficient values that would otherwise be too difficult to estimate. In the next section, we describe an optimization problem that uses the \( \gamma \) parametrization to simultaneously perform feature aggregation and selection.
By zeroing out the $\gamma_i$’s in the gray nodes, we aggregate $\beta$ into two groups indicated by the dashed contours: $\beta_1 = \beta_2 = \beta_3 = \gamma_6 + \gamma_8$ and $\beta_4 = \beta_5 = \gamma_8$. Counts data are aggregated for features sharing the same coefficient: $X\beta = (X_1 + X_2 + X_3)\beta_1 + (X_4 + X_5)\beta_4$.

### 3.3 The Optimization Problem

Our proposed estimator $\hat{\beta}$ is the solution to the following convex optimization problem:

$$
\min_{\beta \in \mathbb{R}^p, \gamma \in \mathbb{R}^{\varepsilon(T)}} \left\{ \frac{1}{2n} \| y - X\beta \|^2_2 + \lambda \left( \alpha \| \gamma - r \|_1 + (1 - \alpha) \| \beta \|_1 \right) \right\} \quad \text{s.t.} \quad \beta = A\gamma.
$$

We apply an $\ell_1$ penalty on non-root $\gamma_u$’s to induce sparsity in $\hat{\gamma}$, which in turn induces fusion of the coefficients in $\hat{\beta}$. In the high-dimensional setting, sparsity in feature coefficients is also desirable. Therefore, we apply an $\ell_1$ penalty on $\beta$ as well. The tuning parameter $\lambda$ controls the overall penalization level while $\alpha$ determines the trade-off between the two types of regularization: fusion and sparsity. In practice, both $\lambda$ and $\alpha$ are determined via cross validation.

When $\alpha = 0$, (5) reduces to a lasso problem in $\beta$; when $\alpha = 1$, (5) reduces to a lasso problem in $\gamma$. Both extreme cases can be efficiently solved with a lasso solver such as glmnet (Friedman et al. 2010). For $\alpha \in (0, 1)$, (5) is a generalized lasso problem (Tibshirani and Taylor, 2011) in $\gamma$, and can be solved in principle using preexisting solvers (e.g., Arnold and Tibshirani 2014). However, better computational performance, in particular in high-dimensional settings, can be attained using an algorithm specially tailored to our problem. We write (5) as a global consensus problem and solve this using alternating direction method of multipliers (ADMM, Boyd et al. 2011). The consensus problem introduces additional copies of $\beta$ and $\gamma$, which decouples the various parts of the problem, leading to efficient ADMM updates:

$$
\min_{\beta^{(1)}, \beta^{(2)}, \beta^{(3)}, \beta \in \mathbb{R}^p, \gamma^{(1)}, \gamma^{(2)}, \gamma \in \mathbb{R}^{\varepsilon(T)}} \left\{ \frac{1}{2n} \| y - X\beta^{(1)} \|^2_2 + \lambda \alpha \| \gamma^{(1)} - r \|_1 + \lambda (1 - \alpha) \| \beta^{(2)} \|_1 \right\}
$$

s.t. $\beta^{(3)} = A\gamma^{(2)}$, $\beta = \beta^{(1)} = \beta^{(2)} = \beta^{(3)}$ and $\gamma = \gamma^{(1)} = \gamma^{(2)}$.

In particular, our ADMM approach requires performing a singular value decomposition (SVD) on $X$, an SVD on $(I_p : -A)$ (these are reused for all $\lambda$ and $\alpha$), and then applying matrix multiplies and soft-thresholdings until convergence. See Algorithm 1 in Appendix C.
Figure 3: In the above tree, $B^* = \{u_1, u_2, u_3, u_4, y_5\}$ has its nodes labeled with black circles.

for details. Appendix [C.1] provides a derivation of Algorithm 1 and Appendix [C.2] discusses a slight modification for including an intercept, which is desirable in practice.

We conclude this section by making connections to some related work. The idea of using a tree as auxiliary information for achieving different tasks appears, for example, in the genomics literature. [Wang and Zhao (2017b)] introduce a penalized regression method with high-dimensional and compositional covariates that uses a phylogenetic tree; however, their goal and use of the tree is fundamentally different from ours. Their tree-based penalty maintains a zero-sum constraint for coefficients in order to perform subcomposition selection rather than feature aggregation. (In fact, in their application to the human gut microbiome study, [Wu et al. 2011] before applying their procedure they begin by manually aggregating 17,000 OTUs to 62 in order to reduce the sparsity of the data.) [Guinot et al. (2017)] considers a similar idea of aggregating genomic features with the help of a hierarchical clustering tree; however, their tree is learned from the design matrix and the prediction task is only used to determine the level of tree cut, whereas our method uses the response to flexibly choose differing aggregation levels across the tree. We consider a strategy similar to theirs, which we call $L1\text{-ag-h}$ in the empirical comparisons. Finally, [Kim et al. 2012] propose a tree-guided group lasso approach in the context of multi-response regression. In their context, the tree relates the different responses and is used to borrow strength across related prediction tasks.

4 Statistical Theory

In this section, we study the prediction consistency of our method. Since $\mathcal{T}$ encodes feature similarity information, throughout the section we require $\mathcal{T}$ to be a “full” tree such that each node is either a leaf or possesses at least two child nodes. We begin with some definitions.

**Definition 1.** We say that $B \subseteq \mathcal{V}(\mathcal{T})$ is an aggregating set with respect to $\mathcal{T}$ if $\{\mathcal{L}(\mathcal{T}_u) : u \in B\}$ forms a partition of $\mathcal{L}(\mathcal{T})$.

The black circles in Figure 3 form an aggregating set since their branches’ leaves are a partition of $\{1, \ldots, 8\}$. We would like to refer to “the true aggregating set $B^*$ with respect to $\mathcal{T}$” and, to do so, we must first establish that there exists a unique coarsest aggregating set corresponding to a vector $\beta^*$. 

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Lemma 1. For any $\beta^* \in \mathbb{R}^p$, there exists a unique coarsest aggregating set $B^* := B(\beta^*, \mathcal{T}) \subseteq \mathcal{V}(\mathcal{T})$ (hereafter “the aggregating set”) with respect to the tree $\mathcal{T}$ such that (a) $\beta^*_j = \beta^*_k$ for $j, k \in \mathcal{L}(\mathcal{T}) \forall u \in B^*$, (b) $|\beta_j^* - \beta_k^*| > 0$ for $j \in \mathcal{L}(\mathcal{T})$ and $k \in \mathcal{L}(\mathcal{T})$ for siblings $u, v \in B^*$.

The lemma (proved in Appendix D) defines $B^*$ as the aggregating set such that further merging of siblings would mean that $\beta^*$ is not constant within each subset of the partition.

Definition 2. Given the triplet $(\mathcal{T}, \beta^*, X)$, we define (a) $\tilde{X} = X A_{B^*} \in \mathbb{R}^{n \times |B^*|}$ to be the design matrix of aggregated features, which uses $B^* = B(\beta^*, \mathcal{T})$ as the aggregating set, and (b) $\bar{\beta}^* \in \mathbb{R}^{|B^*|}$ to be the coefficient vector using these aggregated features: $\bar{\beta}^* = A_{B^*} \beta^*$.

We are now ready to provide a bound on the prediction error of our estimator, which is proved in Appendix D.

Theorem 3 (Prediction Error Bound). Assume $X$ has been scaled so that $\|X_1p\|_2^2 = n$. If we take $\lambda \geq 8\sigma \sqrt{\frac{\log 2p}{n}}$ and $0 \leq \alpha \leq (1 + p^{-1})^{-1}$, then with probability at least $1 - p^{-1}$,

$$\frac{1}{n} \left\| X \bar{\beta} - X \bar{\beta}^* \right\|_2^2 \leq 3\lambda \left( \alpha \left\| \beta^* \right\|_1 + (1 - \alpha) \left\| \beta^* \right\|_1 \right).$$

The above theorem is an example of a slow-rate bound, which is notable for the fact that it places no assumptions on the design matrix $X$ [Dalalyan et al., 2017]. (The condition that $\|X1p\|_2^2 = n$ is easily satisfied by appropriate scaling of $X$). The bound depends on $\|\beta^*\|_1$ and $\|\beta^*\|_1$, which heuristically can be thought of as measuring the number of original and aggregated features that are relevant for making predictions. The following corollary facilitates the interpretation of the prediction bound and demonstrates the effectiveness of our method given a good choice for $\alpha$.

Corollary 1. Assume that $\|\beta^*\|_\infty \leq M$ and $X$ has been scaled so that $\|X1p\|_2^2 = n$. Taking $\lambda = 8\sigma \sqrt{\frac{\log 2p}{n}}$ and $0 \leq \alpha \leq (1 + p^{-1})^{-1}$, we have, with probability at least $1 - p^{-1}$, that

$$\frac{1}{n} \left\| X \bar{\beta} - X \beta^* \right\|_2^2 \leq 24\sigma M \sqrt{\frac{\log 2p}{n}} (\alpha |B^*| + (1 - \alpha)|A^*|),$$

where $A^*$ is the support of $\beta^*$. Furthermore, with $\alpha = \frac{|A^*|}{|A^*| + |B^*|}$, $\frac{1}{n} \left\| X \bar{\beta} - X \beta^* \right\|_2^2 \leq 48\sigma M \sqrt{\frac{\log 2p}{n}} \cdot \min \left(|A^*|, |B^*|\right)$.

Proof. See Appendix F.

The first statement in Corollary 1 establishes that our estimator can make excellent predictions even when $p \gg n$ as long as $(\log p)/n \to 0$ (assuming $|A^*|$ and $|B^*|$ are bounded). The quantity $|A^*|$ is the traditional notion of sparsity appearing throughout the high-dimensional statistics literature. The quantity $|B^*|$ is specific to our framework: it depends both on $\beta^*$ and on the tree $\mathcal{T}$ that guides the aggregation. The second statement in Corollary 1 exhibits the effectiveness of our method. With a properly chosen $\alpha$, we can do well unless both $|A^*|$ and $|B^*|$ are large. This is notable since one can construct extreme examples of $\beta^*$ and $\mathcal{T}$ in which $|A^*| = p$ and $|B^*| = 1$ and in which $|A^*| = 1$ and $|B^*| = p$. That is, our method can do well even when there is no sparsity (as long as there is aggregation) and when there is no aggregation (as long as there is sparsity).
Figure 4: (Left and Middle) two scenarios for varying $k$: $\min_\Lambda \|\hat{\beta}(\Lambda) - \beta^*\|^2_2/p$ versus $k$ for $(n, p, s) = (500, 100, 0)$ and $(n, p, s) = (100, 200, 0.2)$. (Right) degradation of our method with distorted trees: $\min_\Lambda \|X\hat{\beta}(\Lambda) - X\beta^*\|^2_2/n$ versus $\tau$ for $(n, p, s, k) = (100, 200, 0.2, 10)$.

5 Simulation Study

For $k \in \{5, 10, 15, 20, 25, 30\}$, we generate $p$ data points in a $(k-1)$-dimensional latent space, in which $\mu_1, \ldots, \mu_k \in \mathbb{R}^{k-1}$ are taken to be equidistant and as vertices of the unit simplex. We generate $p/k$ latent vectors independently from $N(\mu_i, 0.1^2I_{k-1})$ for $i \in \{1, \ldots, k\}$. We form a tree $T$ by performing hierarchical clustering (using hclust in R Core Team (2016)) on the $p$ vectors, before cutting the tree into $k$ subtrees (the roots of which form $B^*$). We form $A$ corresponding to this tree and generate $\beta^* = A_B^*\beta^*$. The first $k \cdot s$ elements of $\beta^* \in \mathbb{R}^k$ are 0, and the remaining elements are drawn independently from a $N(0, 4)$ distribution. The design matrix $X \in \mathbb{R}^{n \times p}$ is simulated from a Poisson(0.1) distribution. The response $y \in \mathbb{R}^n$ is simulated from $\mathbb{I}$ with $\sigma = \|X\beta^*\|_2/(5n)$. For every method under consideration, we average its performance over 100 repetitions in all the following simulations.

We consider two scenarios, one low-dimensional ($n = 500$, $p = 100$, $s = 0$) and the other high-dimensional ($n = 100$, $p = 200$, $s = 0.2$). We apply our method with the true $T$ and vary the tuning parameters $(\alpha, \lambda)$ along an 8-by-50 grid of values. We compare our method to oracle least squares, in which we perform least squares on $[XA_B^*]_{(k-s+1):k}$, the correctly aggregated features having non-zero $\beta^*$. Oracle least squares represents the best possible performance of any method that attempts to aggregate and select features. In the low-dimensional scenario, we include least squares on the original design matrix $X$, and in the high-dimensional scenario, we include the lasso and ridge regression, which are each computed across a grid of 50 values of the tuning parameter.

To understand the best performance attainable by each method, we measure the best mean-squared estimation error, i.e., $\min_\Lambda \|\hat{\beta}(\Lambda) - \beta^*\|^2_2/p$, where “best” is with respect to each method’s tuning parameter(s) $\Lambda$. The left and the middle panels of Figures 4 shows the performance of the methods in the low-dimensional and high-dimensional scenarios, respectively. Given that our method includes least squares and the lasso as special cases, it is no surprise that our methods have better attainable performance than those methods. These results indicate that our method performs similarly to the oracle when the true number of aggregated features, $k$, is small and degrades as this quantity increases.

Clearly, the performance of our method will depend on the quality of the tree being used. 
In the previous simulations we provided our method with a tree that is perfectly compatible with the true aggregating set. In practice, the tree used may be only an approximate representation of how features should be aggregated. We therefore study the sensitivity of our method to misspecification of the tree. We return to the high-dimensional setting above with $k = 10$, and we generate a sequence of trees that are increasingly distorted representations of how the data should in fact be aggregated.

We begin with a true aggregation of the features into $k$ groups, each of size $p/k$. In each repetition of the simulation, we generate a (random) tree $T$ by performing hierarchical clustering on $p$ random vectors generated similarly as above: for each group $i \in \{1, \ldots, k\}$, we associate a cluster center $\mu_i \in \mathbb{R}^{k-1}$ and generate $p/k$ latent vectors independently from $N(\mu_i, \tau^2 I_{k-1})$. We control the degradation level of the tree by varying the value of $\tau$. When $\tau$ is small, the latent vectors will be well-separated by group so that the tree will have an aggregating set that matches the true aggregation structure (with high probability). As $\tau \in \{0.1, 0.15, 0.2, 0.25, 0.3\}$ increases, the information provided by the tree becomes increasingly weak. The right panel of Figure 4 shows the degradation of our method as $\tau$ increases.

6 Application to Hotel Reviews

Wang et al. (2010) crawled TripAdvisor.com to form a dataset of 235,793 reviews and ratings of 1,850 hotels by users between February 14, 2009 and March 15, 2009. While there are several kinds of ratings, we focus on a user’s overall rating of the hotel (on a 1 to 5 scale), which we take as our response. We form a document-term matrix $X$ in which $X_{ij}$ is the number of times the $i$th review uses the $j$th adjective. We begin by converting words to lower case and keeping only adjectives (as determined by WordNet Fellbaum 1998; Wallace 2007; Feinerer and Hornik 2016). After removing reviews with missing ratings, we are left with 209,987 reviews and 7,787 distinct adjectives. The left panel of Figure 5 shows the distribution of ratings in the data: nearly three quarters of all ratings are above 3 stars. The extremely right-skewed distribution in the right panel of Figure 5 shows that all but a small number of adjectives are highly rare (e.g., over 90% of adjectives are used in fewer than 0.5% of reviews).

Rather than discard this large number of rare adjectives, our method aims to make productive use of these by leveraging side information about the relationship between adjectives. We construct a tree capturing adjective similarity as follows. We start with word embeddings in a 100-dimensional space that were pre-trained by GloVe (Pennington et al., 2014) on the Gigaword5 and Wikipedia2014 corpora. We also obtain a list of adjectives, which the NRC Emotion Lexicon labels as having either positive or negative sentiments (Mohammad and Turney, 2013). We use five nearest neighbors classification within the 100-dimensional space of word embeddings to assign labels to the 5,795 adjectives that have not been labeled in the NRC Emotion Lexicon. This sentiment separation determines the two main branches of the tree $T$. Within each branch, we perform hierarchical clustering of the word embedding vectors. Figure 6 depicts such a tree with 2,397 adjectives (as leaves).

\footnote{Data source: http://times.cs.uiuc.edu/~wang296/Data/}

\footnote{Data source: http://nlp.stanford.edu/data/glove.6B.zip}
| Rating | Proportion |
|--------|------------|
| 1      | 0.066      |
| 2      | 0.085      |
| 3      | 0.105      |
| 4      | 0.308      |
| 5      | 0.436      |

Figure 5: (Left) distribution of TripAdvisor ratings. (Right) only 414 adjectives appear in more than 1% of reviews; the histogram gives the distribution of usage-percentages for those adjectives appearing in fewer than 1% of reviews.

Figure 6: Tree $\mathcal{T}$ over 2,397 adjectives: the left subtree is for adjectives with negative sentiment and the right subtree is for adjectives with positive sentiment.
We compare our method to four other approaches, meant to represent variations of how the lasso is typically applied when rare features are present (see Figure 7 for a schematic). The most common and straightforward approach, which we refer to as \( L1 \), is to simply apply the lasso on the features without making any adjustment for rare features. A second approach, which we refer to as \( L1\text{-dense} \), applies the lasso after first discarding any adjectives that are in fewer than 0.5% of reviews. The third and fourth approaches apply the lasso with features aggregated according to the tree in an unsupervised manner. The third approach, \( L1\text{-ag-h} \), aggregates features that are in the same cluster after cutting the dendrogram at a certain height. In addition to the lasso tuning parameter, the height at which we cut the tree is a second tuning parameter (chosen along an equally-spaced grid of ten values). The fourth approach, \( L1\text{-ag-d} \), performs merges in a bottom-up fashion along the tree until all aggregated features have density above some threshold. This threshold is an additional tuning parameter (chosen along an equally spaced grid of ten values between 0.001 and 0.1).

We hold out 40,000 ratings and reviews as a test set. To observe the performance of these methods over a range of training set sizes, we consider a nested sequence of training sets, ranging from 1% to 100% of the reviews not included in the test set. For all methods, we use five-fold cross validation to select tuning parameters and threshold all predicted ratings to be within the interval \([1, 5]\). Table 1 displays the mean squared prediction error (MSPE) on the test set for each method and training set size.

As the size of the training set increases, all methods except for the lasso with aggregation based on density (\( L1\text{-ag-d} \)) achieve lower MSPE. Among the four lasso-related methods, \( L1 \)
Figure 8: Trees for 2,397 adjectives on the leaves with branches colored based on $\hat{\beta}$ estimated with the lasso (Top) and our method (Bottom), respectively. Red branch, blue branch and gray branch correspond to negative, positive and zero $\hat{\beta}_j$, respectively. Darker color indicates larger magnitude of $\hat{\beta}_j$ and lighter color indicates smaller magnitude of $\hat{\beta}_j$.

and L1-ag-h outperform the other two. As the training set size $n$ increases, the number of features $p$ also increase but at a relatively slower rate. We notice that when $n/p$ is less than 10.51, our method outperforms the other four lasso-related methods. As $n/p$ increases beyond 10.51, i.e., in the statistically easier regimes, L1 and L1-ag-h attain performance comparable to our method.

To better understand the difference between our method and the lasso, we color the branches of the tree generated in the $n = 1,700$ and $p = 2,397$ case (i.e., proportion is 1%) according to the sign and magnitude of $\hat{\beta}$ for the two methods. The lower tree in Figure 8 corresponds to our method and has many nearby branches sharing the same color in (red or blue), indicating that the corresponding adjective counts have been merged. By contrast, the upper tree in Figure 8 which corresponds to the lasso, shows that the solution is sparser and does not have branches of similar color. Inspection of the merged branches from our method reveals words of similar meaning and sentiment being aggregated. To demonstrate that our method selects rare words whereas the lasso does not, we plot $\{|\hat{\beta}_j|\}$ against the percentage of reviews containing an adjective in Figure 9. The rarest word selected by the lasso is “filthy”, which appears in 0.47% of reviews. By contrast, our method selects many words that are far more rare: at the extreme of rarest words, our method selects 797 words that appear in only 0.059% of reviews. Our method is able to select rare words through aggregation. It aggregates 2,244 words into 224 clusters, leaving the remaining 153 words as singletons. Over 70% of these singletons are dense words (where, for this discussion, we call a word “dense” if it appears in at least 1% of reviews and “rare” otherwise). This is four times higher than the percentage of dense words in the original training data. Of the 224 aggregated clusters, 42% are made up entirely of rare words. After aggregation, over half of the clusters become dense features.

Table 2 shows the density and estimated coefficient values for eight words falling in a particular subtree of $T$. The words “heard” and “loud” occur far more commonly than the other six words. We see that the lasso only selects these two words whereas selects all eight words (assigning them negative coefficient values). Our experience with staying at hotels
In this paper, we focus on the challenge posed by highly sparse data matrices, which have become increasingly common in many areas, including biology and text mining. While much work has focused on addressing the challenges of high dimensional data, relatively little attention has been given to the challenges of sparsity in the data. We show, both theoretically and empirically, that not explicitly accounting for the sparsity in the data hurts one’s prediction errors and one’s ability to perform feature selection. Our proposed method is able to make productive use of highly sparse features by creating new aggregated features based on side information about the original features. In contrast to simpler tree-based aggregation strategies that are occasionally used as a pre-processing step in biological applications, our

\[ \beta_X^{\text{lasso}} = \begin{bmatrix} -0.057 \\ -0.147 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \beta_X^{\text{ours}} = \begin{bmatrix} -0.128 \\ -0.128 \\ -0.039 \\ -0.039 \\ -0.039 \\ -0.039 \\ -0.039 \\ -0.039 \end{bmatrix} \]

Table 2: Term density and estimated coefficient for adjectives in the selected group

7 Conclusion

In this paper, we focus on the challenge posed by highly sparse data matrices, which have become increasingly common in many areas, including biology and text mining. While much work has focused on addressing the challenges of high dimensional data, relatively little attention has been given to the challenges of sparsity in the data. We show, both theoretically and empirically, that not explicitly accounting for the sparsity in the data hurts one’s prediction errors and one’s ability to perform feature selection. Our proposed method is able to make productive use of highly sparse features by creating new aggregated features based on side information about the original features. In contrast to simpler tree-based aggregation strategies that are occasionally used as a pre-processing step in biological applications, our

\[ \text{The term density is computed over train set.} \]
method adaptively learns the feature aggregation in a supervised manner. In doing so, our methodology not only overcomes the challenges of data sparsity but also produces features that may be of greater relevance to the particular prediction task of interest.

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Appendices

A Failure of OLS in the Presence of A Rare Feature

**Theorem 4.** Consider the linear model (1) with $X \in \mathbb{R}^{n \times p}$ having full column rank. Further suppose that $X_j$ is a binary vector having $k$ nonzeros. It follows that

$$
\mathbb{P} \left( |\hat{\beta}_{\text{OLS}}^j(n) - \beta_j^*| > \eta \right) \geq 2 \Phi \left( -\eta k^{1/2}/\sigma \right) \quad \text{for any } \eta > 0,
$$

where $\Phi(\cdot)$ is the cumulative distribution function of a standard normal variable.

**Proof.** The distribution of the OLS estimator is $\hat{\beta}_{\text{OLS}}(n) \sim N(\beta^*_j, \sigma^2[(X^T X)^{-1}]_{jj})$. By applying blockwise inversion (see, e.g., Bernstein [2009]), with the $j$th row/column of $X^T X$ in its own “block”, we get

$$
[(X^T X)^{-1}]_{jj} = [X_j^T X_j - X_j^T X_{-j} (X_{-j}^T X_{-j})^{-1} X_{-j}^T X_j]^{-1}
= [\|X_j\|^2 - \|X_{-j}^T X_{-j}\|^{-1/2} X_{-j}^T X_j \|X_j\|^2]^{-1}
\geq \|X_j\|^{-2} = k^{-1}.
$$

Thus,

$$
\mathbb{P} \left( |\hat{\beta}_{\text{OLS}}(n) - \beta_j^*| > \eta \right) = 2 \Phi \left( -\frac{\eta}{\sigma \sqrt{[(X^T X)^{-1}]_{jj}}} \right) \geq 2 \Phi \left( -\eta k^{1/2}/\sigma \right)
$$

where $\Phi(\cdot)$ is the distribution function of a standard normal variable. □

B Proof of Theorem 2

In the setting of Theorem 2, we have $X = I_n \in \mathbb{R}^{n \times n}$ for $\beta^*$ and $\tilde{X} = I_k \otimes 1_{n/k} \in \mathbb{R}^{n \times k}$ for $\tilde{\beta}^*$. Clearly $X \beta^* = \tilde{X} \tilde{\beta}^*$. The two estimators, oracle lasso on the aggregated data ($\tilde{X}$) and lasso on the original data ($X$), are defined below.

- Oracle lasso estimator $\hat{\beta}_\lambda^{\text{oracle}} = \tilde{\beta}_\lambda^{\text{oracle}} \otimes 1_{n/k}$ where $\tilde{\beta}_\lambda^{\text{oracle}}$ is the unique solution to

$$
\min_{\tilde{\beta} \in \mathbb{R}^k} \frac{1}{2n} \|y - \tilde{X} \tilde{\beta}\|_2^2 + \lambda \|\tilde{\beta}\|_1.
$$
• Lasso estimator $\hat{\beta}_\lambda^{\text{lasso}}$ is defined in (2).

**Proposition 1** (Support recovery of oracle lasso). Suppose $\min_{i=1,\ldots,k-1} |\tilde{\beta}_i^*| > \sigma \sqrt{4k \log(k^2n)/n}$. With $\lambda = \sigma \sqrt{\log(k^2n)/kn}$, the oracle lasso recovers the correct signed support successfully:

$$
\lim_{n \to \infty} \mathbb{P} \left( S_\pm(\beta^{\text{oracle}}_\lambda) = S_\pm(\beta^*) \right) = 1.
$$

**Proof.** Since $\tilde{X}^T \tilde{X} = \frac{n}{k} I_k$, the scaled matrix $\sqrt{\frac{2}{n}} \tilde{X}$ is orthogonal. Orthogonality implies that

$$
\hat{\beta}_\lambda^{\text{oracle}} = S \left( \left( \sqrt{\frac{k}{n}} \tilde{X}^T \right) \left( \sqrt{\frac{k}{n}} y \right), \lambda k \right) = S \left( \frac{k}{n} \tilde{X}^T y, \lambda k \right)
$$

where $\frac{k}{n} \tilde{X}^T y = \frac{k}{n} \tilde{X}^T \tilde{X} \beta^* + \frac{k}{n} \tilde{X}^T \epsilon = \beta^* + \frac{k}{n} \tilde{X}^T \epsilon \sim N_k(\beta^*, \frac{k^2}{n} I_k)$. By the Chernoff bound for normal variables, for any $t > 0$,

$$
\mathbb{P} \left( \left| \frac{k}{n} (\tilde{X}_j^T y - \tilde{\beta}_j^*) \right| > t \right) \leq 2 \exp \left( -\frac{t^2}{2k \sigma^2 / n} \right) \quad \text{for } j = 1, \ldots, k.
$$

Choosing $t = \sigma \sqrt{\frac{k \log(k^2n)}{n}}$ and applying a union bound yields

$$
\mathbb{P} \left( \left\| \frac{k}{n} \tilde{X}^T y - \tilde{\beta}^* \right\|_\infty > \sigma \sqrt{\frac{k \log(k^2n)}{n}} \right) \leq 2k \exp \left( -\frac{\sigma^2 k \log(k^2n)/n}{2k \sigma^2 / n} \right) = 2/k^{n/2}.
$$

Hence, with probability at least $1 - \frac{2}{\sqrt{n}}$, we have $\left\| \frac{k}{n} \tilde{X}^T y - \tilde{\beta}^* \right\|_\infty \leq \sigma \sqrt{\frac{k \log(k^2n)}{n}} = \lambda k$, due to our choice of $\lambda = \sigma \sqrt{\log(k^2n)/kn}$. Under $\left\| \frac{k}{n} \tilde{X}^T y - \tilde{\beta}^* \right\|_\infty \leq \lambda k$, the following results hold.

• By $\tilde{\beta}_k^*$ is 0 and

$$
\left| \frac{k}{n} (\tilde{X}_k^T y) \right| = \left| \frac{k}{n} (\tilde{X}_k^T y - \tilde{\beta}_k^*) \right| \leq \left| \frac{k}{n} \tilde{X}^T y - \tilde{\beta}^* \right|_\infty \leq \lambda k,
$$

we have $\hat{\beta}_\lambda^{\text{oracle}} = S \left( \frac{k}{n} (\tilde{X}_k^T y), \lambda k \right) = 0$ and $\hat{\beta}^{\text{oracle}} - \beta^{\text{oracle}} = \hat{\beta}_\lambda^{\text{oracle}} = \tilde{\beta}_k = \beta_k^*$ for all $\ell > \frac{k-1}{k} n$.

• For $j = 1, \ldots, k - 1$, since $\left| \frac{k}{n} (\tilde{X}_j^T y - \tilde{\beta}_j^*) \right| \leq \lambda k$ and $\left| \tilde{\beta}_j^* \right| \geq \min_{i=1,\ldots,k-1} \left| \beta_i^* \right| > 2\lambda k$, we must have $\frac{k}{n} (\tilde{X}_j^T y)$ and $\tilde{\beta}_j^*$ share the same sign. Moreover, we either have

$$
\left| \frac{k}{n} (\tilde{X}_j^T y) \right| = \left| \tilde{\beta}_j^* \right| > \lambda k
$$
or \( \left| \frac{k}{n} (\widetilde{X}_j)^T y \right| < \hat{\beta}_j^* \) in which case \( \left| \frac{k}{n} (\widetilde{X}_j)^T y - \hat{\beta}_j^* \right| = \left| \frac{k}{n} (\widetilde{X}_j)^T y \right| - \left| \hat{\beta}_j^* \right| = \left| \hat{\beta}_j^* \right| - \left| \frac{k}{n} (\widetilde{X}_j)^T y \right| \leq \lambda k \) and therefore

\[
\left| \frac{k}{n} \left( \frac{1}{n} X_j^T y \right) \right| \geq \left| \hat{\beta}_j^* \right| - \lambda k \geq 2\lambda k - \lambda k = \lambda k.
\]

Thus, \( \left| \frac{k}{n} (\widetilde{X}_j)^T y \right| > \lambda k \) for \( j = 1, \ldots, k - 1 \). By definition of \( \hat{\beta}_\lambda^{\text{oracle}} \) and (8), for \( \frac{k-1}{k} n < \ell \leq \frac{k}{k} n \),

\[
\hat{\beta}_\lambda^{\text{oracle}} = \hat{\beta}_\lambda^{\text{oracle}} = S \left( \frac{k}{n} (\widetilde{X}_j)^T y, \lambda k \right) = \frac{k}{n} (\widetilde{X}_j)^T y \left( 1 - \frac{\lambda k}{\left| \frac{k}{n} (\widetilde{X}_j)^T y \right|} \right)
\]

which is of the same sign as \( \hat{\beta}_j^* \) (and the same sign as \( \beta_j^* \)).

In the above two bullet points, we have shown \( S_{\pm}(\hat{\beta}_\lambda^{\text{oracle}}) = S_{\pm}(\beta^*) \) holds with probability at least \( 1 - \frac{2}{\sqrt{n}} \). Hence,

\[
\lim_{n \to \infty} \mathbb{P} \left( S_{\pm}(\hat{\beta}_\lambda^{\text{oracle}}) = S_{\pm}(\beta^*) \right) \geq \lim_{n \to \infty} \left( 1 - \frac{2}{\sqrt{n}} \right) = 1.
\]

Since \( \limsup_{n \to \infty} \mathbb{P} \left( S_{\pm}(\hat{\beta}_\lambda^{\text{oracle}}) = S_{\pm}(\beta^*) \right) = 1 \), the limit for \( \mathbb{P} \left( S_{\pm}(\hat{\beta}_\lambda^{\text{oracle}}) = S_{\pm}(\beta^*) \right) \) is 1.

**Lemma 2.** Suppose \( \varepsilon \sim N_n(0, \sigma^2 I_n) \) and \( \tilde{c} = \frac{1}{3} e^{(\pi/2)^{-1}} \sqrt{\frac{1}{4} + \frac{1}{\pi}} \). Then

\[
\mathbb{P} \left( \max_{j=1,\ldots,n} |\varepsilon_j| \leq \frac{2\sigma}{\sqrt{3}} \sqrt{\log(2\tilde{c}n)} \right) \leq \left( 1 - \frac{1}{n} \right)^n.
\]

**Proof.** Let \( Z \) be a standard Gaussian variable. Theorem 2.1 of [Côté et al. (2012)](http://example.com) provides a lower bound for the Gaussian Q function (i.e., \( \mathbb{P}(Z > z) \)). Choosing \( \kappa = \frac{3}{2} \) in their Theorem 2.1 yields

\[
\mathbb{P}(Z > z) \geq \left( \frac{1}{3} e^{(\pi/2)^{-1}} \sqrt{\frac{1}{4} + \frac{1}{\pi}} \right) \frac{e^{-\frac{3\varepsilon^2}{4}}}{\tilde{c}}
\]

where \( \tilde{c} = \frac{1}{3} e^{(\pi/2)^{-1}} \sqrt{\frac{1}{4} + \frac{1}{\pi}} \) is independent of \( z \). Since \( \varepsilon_1 = \sigma Z \), we have for any \( \eta > 0 \)

\[
\mathbb{P}(\varepsilon_1 > \eta) \geq \tilde{c} e^{-\frac{3\eta^2}{4\sigma^2}} \quad \Rightarrow \quad \mathbb{P}(|\varepsilon_1| > \eta) \geq 2\tilde{c} e^{-\frac{3\eta^2}{4\sigma^2}}.
\]

Moreover,

\[
\mathbb{P} \left( \max_{j=1,\ldots,n} |\varepsilon_j| \leq \eta \right) = \mathbb{P}(|\varepsilon_1| \leq \eta)^n = (1 - \mathbb{P}(|\varepsilon_1| > \eta))^n \leq \left( 1 - 2\tilde{c} e^{-\frac{3\eta^2}{4\sigma^2}} \right)^n.
\]
Plugging in $\eta = \frac{2\sigma}{\sqrt{3}} \sqrt{\log (2\tilde{c}n)}$ in the above inequality yields
\[
\mathbb{P} \left( \max_{j=1,\ldots,n} |\epsilon_j| \leq \frac{2\sigma}{\sqrt{3}} \sqrt{\log (2\tilde{c}n)} \right) \leq \left( 1 - \frac{1}{n} \right)^n.
\]

\[\square\]

**Proposition 2** (Failure of support recovery of lasso). Suppose \( \min_{i=1,\ldots,k-1} |\beta_i^*| \leq \sigma \sqrt{\frac{\log(2\tilde{c}(k-1)n/k)}{3}} \) where $\tilde{c} = \frac{1}{3}e^{(\pi/2+2)^{-1}} \sqrt{\frac{1}{4} + \frac{1}{\pi}}$. The lasso fails to get high-probability signed support recovery:
\[
\limsup_{n \to \infty} \sup_{\lambda \geq 0} \mathbb{P} \left( S_\pm(\beta_\lambda^{\text{lasso}}) = S_\pm(\beta^*) \right) \leq \frac{1}{e}.
\]

**Proof.** The lasso solution can be simplified to $\hat{\beta}_\lambda^{\text{lasso}} = S(y, \lambda)$. Since $\beta_i^* \neq 0$ for $\ell \leq k-1$, and $\beta_i^* = 0$ for $\ell > k-1$, the following is a necessary condition for $\hat{\beta}_\lambda^{\text{lasso}}$ to recover the correct signed support:
\[
\exists \lambda \text{ s.t. } |y_\ell| > \lambda \text{ for } \ell \leq \frac{k-1}{k} n \text{ and } |y_\ell| \leq \lambda \text{ for } \ell > \frac{k-1}{k} n \iff \min_{\ell \leq \frac{k-1}{k} n} |y_\ell| > \max_{\ell > \frac{k-1}{k} n} |y_\ell|.
\]

Define $\hat{i} := \arg\min_{i=1,\ldots,k-1} |\beta_i^*|$ and $\mathcal{A} := \left\{ \max_{\ell > \frac{k-1}{k} n} |\epsilon_\ell| \leq \frac{2\sigma}{\sqrt{3}} \sqrt{\log \left( \frac{2\tilde{c}(k-1)n}{k} \right)} \right\}$. Then
\[
\mathbb{P} \left( S_\pm(\beta_\lambda^{\text{lasso}}) = S_\pm(\beta^*) \right)
\leq \mathbb{P} \left( \min_{\ell \leq \frac{k-1}{k} n} |y_\ell| > \max_{\ell > \frac{k-1}{k} n} |y_\ell| \right)
\leq \mathbb{P} \left( \min_{\ell > \frac{k-1}{k} n} |y_\ell| > \max_{\ell > \frac{k-1}{k} n} |y_\ell| \right)
\leq \mathbb{P} \left( \hat{\beta}_{\hat{i}}^* + \min_{\frac{k-1}{k} n < \ell \leq \frac{1}{k} n} |\epsilon_\ell| > \max_{\ell > \frac{1}{k} n} |\epsilon_\ell| \right)
\leq \mathbb{P} \left( \hat{\beta}_{\hat{i}}^* + \min_{\frac{k-1}{k} n < \ell \leq \frac{1}{k} n} |\epsilon_\ell| > \frac{2\sigma}{\sqrt{3}} \sqrt{\log \left( \frac{2\tilde{c}(k-1)n}{k} \right)} \right) + \mathbb{P}(\mathcal{A})
\leq \mathbb{P} \left( \left| \epsilon_{\hat{i}} \right| > \frac{2\sigma}{\sqrt{3}} \sqrt{\log \left( \frac{2\tilde{c}(k-1)n}{k} \right)} - |\hat{\beta}_{\hat{i}}^*| \right)^{\frac{\hat{\mathbb{c}}}{p}} + \mathbb{P}(\mathcal{A}) \quad \text{(by } \epsilon_i \text{ being i.i.d.)}
\leq \mathbb{P} \left( \left| \epsilon_{\hat{i}} \right| > \frac{\sigma}{\sqrt{3}} \sqrt{\log \left( \frac{2\tilde{c}(k-1)n}{k} \right)} \right)^{\frac{\hat{\mathbb{c}}}{p}} + \mathbb{P}(\mathcal{A}) \quad \text{(by } |\hat{\beta}_{\hat{i}}^*| \leq \sigma \sqrt{\frac{\log(2\tilde{c}(k-1)n/k)}{3}} \)
\[ \leq \left[ 2 \exp \left( -\frac{1}{2\sigma^2} \cdot \frac{\sigma^2}{3} \log \left( \frac{2\sigma(k-1)}{k} n \right) \right) \right]^{\frac{n}{k}} + \left( 1 - \frac{k}{n} \right)^{\frac{n}{k}} \] (by Chernoff ineq and Lemma 2)

\[ \leq 2^{n/k} \exp \left( -\frac{n}{6k} \log \left( \frac{2\sigma(k-1)}{k} n \right) \right) + \left( 1 - \frac{k}{n} \right)^{\frac{n}{k}} \]

\[ = 2^{n/k} \left( \frac{2\sigma(k-1)}{k} n \right)^{-n/(6k)} + \left( 1 - \frac{k}{n} \right)^{\frac{n}{k}} \]

which holds for all \( \lambda \geq 0 \). In particular,

\[ \sup_{\lambda \geq 0} \mathbb{P} \left( S_{\pm} (\hat{\beta}_\lambda) = S_{\pm} (\beta^*) \right) \leq \left( \frac{\sigma(k-1)}{32k} n \right)^{-n/(6k)} + \left( 1 - \frac{k}{n} \right)^{\frac{n}{k}}. \]

Taking \( \lim \sup \) on both side yields

\[ \lim_{n \to \infty} \sup_{\lambda \geq 0} \mathbb{P} \left( S_{\pm} (\hat{\beta}_\lambda) = S_{\pm} (\beta^*) \right) \leq \lim_{n \to \infty} \left( \frac{\sigma(k-1)}{32k} n \right)^{-n/(6k)} + \lim_{n \to \infty} \left( 1 - \frac{k}{n} \right)^{\frac{n}{k}} = 0 + \frac{1}{e} = \frac{1}{e}. \]

\[
\text{C Consensus ADMM for Solving Problem } \tag{5}
\]

The ADMM algorithm is given in Algorithm 1. Let \( X = \text{SVD}_{\text{compact}}(\tilde{U}, \tilde{D}, \tilde{V}) \) be the compact singular value decomposition of \( X \), where \( \tilde{D} \in \mathbb{R}^{\min(n,p) \times \min(n,p)} \) is a diagonal matrix with non-zero singular values on the diagonal, and \( \tilde{U} \in \mathbb{R}^{n \times \min(n,p)} \) and \( \tilde{V} \in \mathbb{R}^{p \times \min(n,p)} \) contain the left and right singular vectors in columns corresponding to non-zero singular values, respectively. Similarly, we have \( (I_p \cdot -A) = \text{SVD}_{\text{compact}}(\cdot, \cdot, \tilde{Q}) \) where \( \tilde{Q} \in \mathbb{R}^{(p+|T|) \times p} \) contains \( p \) right singular vectors corresponding to non-zero singular values.

\[
\text{C.1 Derivation of Algorithm } \tag{6}
\]

The ADMM updates involve minimizing the augmented Lagrangian of the global consensus problem (6),

\[ L_\rho(\beta^{(1)}, \beta^{(2)}, \beta^{(3)}, \gamma^{(1)}, \gamma^{(2)}, \beta, \gamma; \nu^{(1)}, \nu^{(2)}, \nu^{(3)}, u^{(1)}, u^{(2)}) \]

\[ = \frac{1}{2n} \| y - X\beta^{(1)} \|_2^2 + \lambda \alpha \| \gamma^{(1)}_r \|_1 + \lambda(1 - \alpha) \| \beta^{(2)} \|_1 + 1_{\infty} \{ \beta^{(3)} = A\gamma^{(2)} \} \]

\[ + \sum_{i=1}^3 \left( \nu^{(i)T} (\beta^{(i)} - \beta) + \frac{\rho}{2} \| \beta^{(i)} - \beta \|_2^2 \right) + \sum_{j=1}^2 \left( u^{(j)T} (\gamma^{(j)} - \gamma) + \frac{\rho}{2} \| \gamma^{(j)} - \gamma \|_2^2 \right). \]
Algorithm 1 Consensus ADMM for Solving Problem

Input: $y, X, A, n, p, |T|, \lambda, \alpha, \rho, \epsilon_{abs}, \epsilon_{rel}, \text{maxite}.$

1. $X = \text{SVD}_{\text{compact}}(\cdot, \tilde{D}, \tilde{V})$
2. $(I_p : -A) = \text{SVD}_{\text{compact}}(\cdot, \cdot, \tilde{Q})$
3. $\beta^0 \leftarrow \beta^{(i)0} \leftarrow v^{(i)0} \leftarrow 0 \in \mathbb{R}^p \ \forall i = 1, 2, 3$
4. $\gamma^0 \leftarrow \gamma^{(j)0} \leftarrow u^{(j)0} \leftarrow 0 \in \mathbb{R}^{|T|} \ \forall j = 1, 2$
5. continue $\leftarrow \text{true}$
6. $k \leftarrow 0$
7. while $k < \text{maxite}$ and continue do
8. $k \leftarrow k + 1$
9. $\beta^{(1)k} \leftarrow \left[\tilde{V} \text{diag}\left(\frac{1}{D^T D_{ii} + n \rho}\right)\tilde{V}^T + \frac{1}{n \rho} (I_p - \tilde{V} \tilde{V}^T)\right] (X^T y + n \rho \beta^{k-1} - n v^{(1)k-1})$
10. $\beta^{(2)k} \leftarrow S\left(\beta^{k-1} - \frac{1}{\rho} u^{(2)k-1}, \frac{\lambda(1-\alpha)}{\rho}\right) \ \forall \ell = 1, \ldots, p$
11. $\gamma^{(1)k} \leftarrow \left\{S\left(\gamma^{k-1} - \frac{1}{\rho} u^{(1)k-1}, \frac{\lambda \alpha}{\rho}\right) \text{ if } \ell \in \{1, \ldots, |T|\} \setminus \{r\}
12. \gamma^{(2)k} \leftarrow \left(\frac{\beta^{(3)k}}{\gamma^{(3)k}}\right) \left(\beta^{(1)k} + \beta^{(2)k} + \beta^{(3)k}\right) / 3$
13. $\beta^k \leftarrow (\beta^{(1)k} + \beta^{(2)k} + \beta^{(3)k}) / 3$
14. $\gamma^k \leftarrow (\gamma^{(1)k} + \gamma^{(2)k}) / 2$
15. $v^{(i)k} \leftarrow v^{(i)k-1} + \rho (\beta^{(i)k} - \beta^k) \ \forall i = 1, 2, 3$
16. $u^{(j)k} \leftarrow u^{(j)k-1} + \rho (\gamma^{(j)k} - \gamma^k) \ \forall j = 1, 2.$
17. if $\sqrt{\sum_{i=1}^{3} \|\beta^{(i)k} - \beta^k\|^2} + 2 \|\gamma^k - \gamma^{k-1}\|^2 \leq \epsilon_{abs} \sqrt{3p + 2|T|} + \epsilon_{rel} \sqrt{\sum_{i=1}^{3} \|\gamma^{(i)k}\|^2_2} \max \left\{\sqrt{\sum_{i=1}^{3} \|\beta^{(i)k}\|^2_2} + \sum_{j=1}^{3} \|\gamma^{(j)k}\|^2_2, \sqrt{\sum_{i=1}^{3} \|v^{(i)k}\|^2_2} + \sum_{j=1}^{3} \|u^{(j)k}\|^2_2\right\}$
18. continue $\leftarrow \text{false}$
19. end if
20. end while
Output: $\beta^k, \gamma^k$
1. Update $\beta^{(1)}$.

$$
\beta^{(1)k+1} := \arg \min_{\beta^{(1)} \in \mathbb{R}^p} \left\{ \frac{1}{2n} \left\| y - X \beta^{(1)} \right\|_2^2 + \langle v^{(1)k}, (\beta^{(1)} - \beta^k) \rangle + \frac{\rho}{2} \left\| \beta^{(1)} - \beta^k \right\|_2^2 \right\}.
$$

Let $X = \text{SVD}(U, D, V)$ be the singular value decomposition of $X$, where $U \in \mathbb{R}^{n \times n}$ contains left singular vectors in columns, $V \in \mathbb{R}^{p \times p}$ contains right singular vectors in columns, and $D \in \mathbb{R}^{n \times p}$ is a rectangular diagonal matrix with decreasing singular values on the diagonal. First order condition to the above problem gives us:

$$
(X^T X + n \rho I_p)\beta^{(1)k+1} = X^T y + n \rho \beta^k - n v^{(1)k}
$$

$$
\Rightarrow V(D^T D + n \rho I_p) V^T \beta^{(1)k+1} = X^T y + n \rho \beta^k - n v^{(1)k}
$$

$$
\Rightarrow \beta^{(1)k+1} = V \text{diag} \left( ([D^T D]_{ii} + n \rho)^{-1} \right) V^T \left( X^T y + n \rho \beta^k - n v^{(1)k} \right).
$$

When $n \geq p$, we have

$$
\beta^{(1)k+1} = \widetilde{V} \text{diag} \left( ([\widetilde{D}^T \widetilde{D}]_{ii} + n \rho)^{-1} \right) \widetilde{V}^T \left( X^T y + n \rho \beta^k - n v^{(1)k} \right). \quad (9)
$$

When $n < p$, the SVD can be expressed in a compact form: $D = (\widetilde{D} : 0)$ and $V = (\widetilde{V} : \widetilde{V}_\perp)$ where $\widetilde{D} \in \mathbb{R}^{n \times n}$ and $\widetilde{V} \in \mathbb{R}^{p \times n}$ are from the compact SVD of $X$, and $\widetilde{V}_\perp \in \mathbb{R}^{p \times (p-n)}$. Thus,

$$
V \text{diag} \left( ([D^T D]_{ii} + n \rho)^{-1} \right) V^T = \left( \widetilde{V} : \widetilde{V}_\perp \right) \text{diag} \left( ([D^T D]_{ii} + n \rho)^{-1} \right) \left( \widetilde{V}^T \widetilde{V}_\perp \right)
$$

$$
= \widetilde{V} \text{diag} \left( ([\widetilde{D}^T \widetilde{D}]_{ii} + n \rho)^{-1} \right) \widetilde{V}^T + \widetilde{V}_\perp \widetilde{V}_\perp^T / (n \rho)
$$

$$
= \widetilde{V} \text{diag} \left( ([\widetilde{D}^T \widetilde{D}]_{ii} + n \rho)^{-1} \right) \widetilde{V}^T + (I_p - \widetilde{V} \widetilde{V}^T) / (n \rho).
$$

So when $n < p$,

$$
\beta^{(1)k+1} = \left[ \widetilde{V} \text{diag} \left( ([\widetilde{D}^T \widetilde{D}]_{ii} + n \rho)^{-1} \right) \widetilde{V}^T + (I_p - \widetilde{V} \widetilde{V}^T) / (n \rho) \right] \left( X^T y + n \rho \beta^k - n v^{(1)k} \right). \quad (10)
$$

Since $\widetilde{V} = V$ when $n \geq p$ and $VV^T = I_p$, we have (10) boil to (9) in that case.

2. Update $\beta^{(2)}$.

$$
\beta^{(2)k+1} := \arg \min_{\beta^{(2)} \in \mathbb{R}^p} \left\{ \frac{1}{2} \left\| \beta^{(2)} - \left( \beta^k - \frac{1}{\rho} v^{(2)k} \right) \right\|_2^2 + \lambda(1 - \alpha) \| \beta^{(2)} \|_1 \right\}.
$$

The solution is simply elementwise soft-thresholding:

$$
\beta^{(2)k+1}_\ell = S \left( \frac{\beta^k_\ell - \frac{1}{\rho} v^{(2)k}_\ell}{\rho}, \frac{\lambda(1 - \alpha)}{\rho} \right) \quad \forall \ell = 1, \ldots, p.
$$
3. Update $\gamma^{(1)}$.

$$
\gamma^{(1)k+1} := \arg \min_{\gamma^{(1)} \in \mathbb{R}^{(|T|)}} \left\{ \frac{\rho}{2} \left\| \gamma^{(1)} - \left( \gamma^k - \frac{1}{\rho} u^{(1)k} \right) \right\|_2^2 + \lambda \alpha \| \gamma^{(1)}_r \|_1 \right\}.
$$

Since root $\gamma^{(1)}_r$ is not penalized, the solution is the following:

$$
\gamma^{(1)k+1}_\ell = \begin{cases} 
S \left( \gamma^{(1)k}_\ell - \frac{1}{\rho} u^{(1)k}_\ell, \frac{\lambda_\alpha}{\rho} \right) & \text{if } \ell \in \{1, \ldots, |T|\} \setminus \{r\} \\
\gamma^{(1)k}_\ell - \frac{1}{\rho} u^{(1)k}_\ell & \text{if } \ell = r.
\end{cases}
$$

4. Joint update of $\beta^{(3)}$ and $\gamma^{(2)}$.

$$
\left( \begin{array}{c} \beta^{(3)k+1} \\ \gamma^{(2)k+1} \end{array} \right) := \arg \min_{\beta^{(3)} \in \mathbb{R}^p, \gamma^{(2)} \in \mathbb{R}^{|T|}} \left\{ \left\| \beta^{(3)} - \left( \beta^k - \frac{1}{\rho} v^{(3)k} \right) \right\|_2^2 + \left\| \gamma^{(2)} - \left( \gamma^k - \frac{1}{\rho} u^{(2)k} \right) \right\|_2^2 \right\}
$$

\[ \text{s.t. } (I_p : -A) \left( \begin{array}{c} \beta^{(3)} \\ \gamma^{(2)} \end{array} \right) = 0.\]

The solution is the projection of $\left( \begin{array}{c} \beta^k \\ \gamma^k \end{array} \right) - \frac{1}{\rho} \left( v^{(3)k} \\ u^{(2)k} \right)$ onto the null space of $(I_p : -A)$. Let $(I_p : -A) = \text{SVD}(\cdot, Q)$ where $Q = (\tilde{Q} : \tilde{Q}_\perp) \in \mathbb{R}^{(p+|T|):(p+|T|)}$ contains all the right singular vectors in columns. So $I_{p+|T|} = QQ^T = \tilde{Q} \tilde{Q}^T + \tilde{Q}_\perp \tilde{Q}_\perp^T$. Since $\tilde{Q}$ corresponds to non-zero singular values of $(I_p : -A)$ by construction, we have $\tilde{Q}_\perp$ corresponds to the zero singular values, making itself an orthonormal basis for the null space of $(I_p : -A)$. Thus,

$$
\left( \begin{array}{c} \beta^{(3)k+1} \\ \gamma^{(2)k+1} \end{array} \right) = \tilde{Q}_\perp (\tilde{Q}_\perp \tilde{Q}_\perp)^{-1} \tilde{Q}_\perp^T \left[ \left( \begin{array}{c} \beta^k \\ \gamma^k \end{array} \right) - \frac{1}{\rho} \left( v^{(3)k} \\ u^{(2)k} \right) \right]
$$

5. Update global variables $\beta$ and $\gamma$.

$$
\beta^{k+1} := \arg \min_{\beta \in \mathbb{R}^p} \sum_{i=1}^3 \left\| \beta - \left( \beta^{(i)k+1} + \frac{1}{\rho} v^{(i)k} \right) \right\|_2^2 = \bar{\beta}^{k+1} + \bar{v}^k \quad (11)
$$

$$
\gamma^{k+1} := \arg \min_{\gamma \in \mathbb{R}^{|T|}} \sum_{j=1}^2 \left\| \gamma - \left( \gamma^{(j)k+1} + \frac{1}{\rho} u^{(j)k} \right) \right\|_2^2 = \bar{\gamma}^{k+1} + \bar{u}^k \quad (12)
$$

where $\bar{\beta}^k := \frac{\beta^{(1)k+1} + \beta^{(2)k+1} + \beta^{(3)k}}{3}$, $\bar{v}^k := \frac{v^{(1)k} + v^{(2)k} + v^{(3)k}}{3}$, $\bar{\gamma}^k := \frac{\gamma^{(1)k+1} + \gamma^{(2)k}}{2}$ and $\bar{u}^k := \frac{u^{(1)k} + u^{(2)k}}{2}$.
6. Update dual variables.

\[ \mathbf{v}^{(1)k+1} := \mathbf{v}^{(i)k} + \rho(\mathbf{\beta}^{(i)k+1} - \mathbf{\beta}^{k+1}) \quad \text{for} \quad i = 1, 2, 3, \]
\[ \mathbf{u}^{(1)k+1} := \mathbf{u}^{(j)k} + \rho(\mathbf{\gamma}^{(j)k+1} - \mathbf{\gamma}^{k+1}) \quad \text{for} \quad j = 1, 2. \]

Similarly, averaging the updates for \( u \) and the updates for \( v \) gives

\[ \mathbf{\hat{v}}^{k+1} = \mathbf{\hat{v}}^k + \rho(\mathbf{\bar{\beta}}^{k+1} - \mathbf{\beta}^{k+1}) \quad \text{(13)} \]
\[ \mathbf{\hat{u}}^{k+1} = \mathbf{\hat{u}}^k + \rho(\mathbf{\bar{\gamma}}^{k+1} - \mathbf{\gamma}^{k+1}) \quad \text{(14)} \]

Substituting (11) and (12) into (13) and (14) yields that \( \mathbf{\hat{v}}^{k+1} = \mathbf{\hat{u}}^{k+1} = 0 \) after the first iteration.

Using \( \mathbf{\beta}^k = \mathbf{\bar{\beta}}^k \) and \( \mathbf{\gamma}^k = \mathbf{\bar{\gamma}}^k \) in the above updates, the updates become Lines 9-16 of Algorithm 1. Next, we follow Section 3.3.1 in Boyd et al. (2011) to determine the termination criteria. We first write Problem (6) in the same form as Problem (3.1) in Boyd et al. (2011) which is presented below in typewriter font:

\[ \min_{x,z} \{ f(x) + g(z) \text{ s.t. } Ax + Bz = c \} \]

where

\[
A = I_{3p+2|\mathcal{T}|}, B = - \begin{pmatrix} I_p & 0 \\ I_p & 0 \\ 0 & I_{|\mathcal{T}|} \\ 0 & I_{|\mathcal{T}|} \end{pmatrix}, \quad c = 0, \quad x = \begin{pmatrix} \mathbf{\beta}^{(1)} \\ \mathbf{\beta}^{(2)} \\ \mathbf{\beta}^{(3)} \\ \mathbf{\gamma}^{(1)} \\ \mathbf{\gamma}^{(2)} \end{pmatrix} \quad \text{and} \quad z = \begin{pmatrix} \mathbf{\beta} \\ \mathbf{\gamma} \end{pmatrix}.
\]

The primal and dual residuals are

\[
\mathbf{r}^{k+1} = Ax^{k+1} + Bz^{k+1} - c = \begin{pmatrix} \beta^{(1)k+1} - \beta^{k+1} \\ \beta^{(2)k+1} - \beta^{k+1} \\ \beta^{(3)k+1} - \beta^{k+1} \\ \gamma^{(1)k+1} - \gamma^{k+1} \\ \gamma^{(2)k+1} - \gamma^{k+1} \end{pmatrix} \quad \text{and} \quad \mathbf{s}^{k+1} = \rho A^T B(z^{k+1} - z^k) = \rho \begin{pmatrix} \beta^{k+1} - \beta^k \\ \beta^{k+1} - \beta^k \\ \beta^{k+1} - \beta^k \\ \gamma^{k+1} - \gamma^k \\ \gamma^{k+1} - \gamma^k \end{pmatrix}.
\]

By Condition (3.12) in Boyd et al. (2011), the ADMM algorithm stops when both residuals are small. In our case, the termination criteria are the following.

1. The primal residual is small:

\[
\sqrt{\sum_{i=1}^{3} \| \mathbf{\beta}^{(i)k} - \mathbf{\beta}^k \|^2_2 + \sum_{j=1}^{2} \| \mathbf{\gamma}^{(j)k} - \mathbf{\gamma}^k \|^2_2} \leq \sqrt{3p + 2|\mathcal{T}|} \cdot \epsilon^{abs} + \epsilon^{rel} \cdot \max \left\{ \sqrt{\sum_{i=1}^{3} \| \mathbf{\beta}^{(i)k} \|^2_2 + \sum_{j=1}^{2} \| \mathbf{\gamma}^{(j)k} \|^2_2}, \sqrt{3 \| \mathbf{\beta}^k \|^2_2 + 2 \| \mathbf{\gamma}^k \|^2_2} \right\}.
\]

2. The dual residual is small:

\[
\rho \sqrt{3 \| \mathbf{\beta}^k - \mathbf{\beta}^{k-1} \|^2_2 + 2 \| \mathbf{\gamma}^k - \mathbf{\gamma}^{k-1} \|^2_2} \leq \sqrt{3p + 2|\mathcal{T}|} \cdot \epsilon^{abs} + \epsilon^{rel} \cdot \sqrt{\sum_{i=1}^{3} \| \mathbf{\beta}^{(i)k} \|^2_2 + \sum_{j=1}^{2} \| \mathbf{\gamma}^{(j)k} \|^2_2}.
\]
C.2 Treatment of Intercept in Problem (5)

When an intercept \( \beta_0 \) is included in the least squares, Problem (5) becomes:

\[
\min_{\beta_0 \in \mathbb{R}, \beta \in \mathbb{R}^p, \gamma \in \mathbb{R}^{|T|}} \left\{ \frac{1}{2n} \| y - X\beta - \beta_0 \|^2 + \lambda (\alpha \|\gamma\|_1 + (1 - \alpha) \|\beta\|_1) \right\}.
\]  

(15)

First-order condition of the solution \((\hat{\beta}_0, \hat{\beta})\) yields that

\[
\frac{\partial}{\partial \beta_0} \frac{1}{2n} \| y - X\beta - \beta_0 \|^2 \bigg|_{(\beta_0, \beta) = (\hat{\beta}_0, \hat{\beta})} = \frac{1}{n} \left[ 1 - 1^T_n (1_n \hat{\beta}_0 - (y - X\hat{\beta})) \right] = \frac{1}{n} (n \hat{\beta}_0 - 1^T_n (y - X\hat{\beta})) = 0.
\]

So \( \hat{\beta}_0 = \frac{1}{n} 1^T_n (y - X\hat{\beta}) \) where \( 1_n \in \mathbb{R}^n \) is a column vector. Plugging \( \hat{\beta}_0 \) in Problem (15) yields

\[
\min_{\beta \in \mathbb{R}^p, \gamma \in \mathbb{R}^{|T|}} \left\{ \frac{1}{2n} \| (I_n - \frac{1}{n} 1^T_n 1^T_n) y - (I_n - \frac{1}{n} 1^T_n 1^T_n) X\beta \|^2 + \lambda (\alpha \|\gamma\|_1 + (1 - \alpha) \|\beta\|_1) \right\}
\]

which can now be solved using our consensus ADMM algorithm.

D Proof of Lemma 1

We first show existence of such \( B^* \) by providing a feasible procedure to find \( B^* \). Suppose \( \beta^* \) has at least two distinct values (otherwise \( B^* = \{r\} \) trivially). Start with \( B = \mathcal{L}(T) \) so that the first constraint is satisfied. If for siblings \( u, v \) in \( B \) such that the second constraint is violated, by construction \( \beta_j^* = \beta_k^* \) for \( j \in \mathcal{L}(T_u) \) and \( k \in \mathcal{L}(T_v) \). So we replace \( u, v \) in \( B \) with their parent node. We repeat the above steps until the second constraint is satisfied, while holding the first constraint. Thus, \( B \) satisfies the two requirements for \( B^* \).

Suppose \( B^* \) and \( \bar{B}^* \) are different aggregating sets for \( \beta^* \). Without loss of generality, suppose there exists \( u \in \bar{B}^* \) but \( u \notin B^* \). Then \( u \) is a descendant or an ancestor of some nodes in \( B^* \); for either case the second constraint will be violated. Thus, such \( u \) does not exist and \( \bar{B}^* = B^* \).

The existence and uniqueness of \( A^* \) follow from the definition of support of \( \beta^* \).

E Proof of Theorem 3

We follow the proof strategy used in Theorem 1 of [Lou et al. (2016)] to prove this theorem. If \((\beta, \gamma)\) is a solution to Problem (5), then we have

\[
\frac{1}{2n} \| y - X\beta \|^2 + \lambda \Omega(\hat{\beta}, \hat{\gamma}) \leq \frac{1}{2n} \| y - X\beta \|^2 + \lambda \Omega(\beta, \gamma)
\]

for any \((\beta, \gamma)\) such that \( \beta = A\gamma \), where \( \Omega(\beta, \gamma) = \alpha \|\gamma\|_1 + (1 - \alpha) \|\beta\|_1 \). Let \((\beta^*, \gamma^*)\) be such that

\[
\beta^* = A_{B^*}\hat{\beta}^* \quad \text{and} \quad \gamma^*_\ell = \begin{cases} \hat{\beta}^*_\ell & \text{if } \ell \in B^* \\ 0 & \text{otherwise} \end{cases}
\]

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Plugging in $y = X\beta^* + \varepsilon$ and $(\beta, \gamma) = (\beta^*, \gamma^*)$, with some algebra we have

$$\frac{1}{2n} \left\| X\hat{\beta} - X\beta^* \right\|^2_2 + \lambda\Omega(\hat{\beta}, \hat{\gamma}) \leq \lambda\Omega(\beta^*, \gamma^*) + \frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)}$$

(16)

where $\hat{\Delta}^{(\beta^*)} = \hat{\beta} - \beta^*$. By $\hat{\beta} = A\hat{\gamma}$ and $\beta^* = A\gamma^*$ (and writing $\hat{\Delta}^{(\gamma^*)} = \hat{\gamma} - \gamma^*$),

$$\frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} = \frac{1}{n} \varepsilon^T XA\hat{\Delta}^{(\gamma^*)}.$$  

Define $V_j := \frac{1}{\sqrt{n}} X_j^T \varepsilon$ for $j = 1, \ldots, p$ and $U_\ell := \frac{1}{\sqrt{n}} A_\ell^T X^T \varepsilon$ for $\ell = 1, \ldots, |T|$. Then

$$\frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} = \frac{1}{\sqrt{n}} \sum_{j=1}^p V_j \hat{\Delta}_j^{(\beta^*)}$$

and

$$\frac{1}{n} \varepsilon^T XA\hat{\Delta}^{(\gamma^*)} = \frac{1}{\sqrt{n}} \sum_{\ell=1}^{|T|} U_\ell \hat{\Delta}_\ell^{(\gamma^*)}.$$  

Moreover, for any $j = 1, \ldots, p$, there is a leaf $u_\ell \in T$ such that $X_j = XA_\ell$. Writing $V = (V_1, \ldots, V_p)$ and $U = (U_1, \ldots, U_{|T|})$, we have $\|V\|_\infty \leq \|U\|_\infty$ hold with probability one.

We next bound $\frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} = (1 - \alpha) \frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} + \alpha \frac{1}{n} \varepsilon^T XA\hat{\Delta}^{(\gamma^*)}$ in absolute value, where $0 \leq \alpha \leq (1 + p^{-1})^{-1}$.

$$\left| \frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} \right| \leq (1 - \alpha) \left| \frac{1}{\sqrt{n}} \sum_{j=1}^p V_j \hat{\Delta}_j^{(\beta^*)} \right| + \alpha \left| \frac{1}{\sqrt{n}} \sum_{\ell=1}^{|T|} U_\ell \hat{\Delta}_\ell^{(\gamma^*)} \right|$$

$$\leq (1 - \alpha) \frac{1}{\sqrt{n}} \sum_{j=1}^p |V_j| \cdot |\hat{\Delta}_j^{(\beta^*)}| + \alpha \frac{1}{\sqrt{n}} \sum_{\ell=1}^{|T|} |U_\ell| \cdot |\hat{\Delta}_\ell^{(\gamma^*)}|$$

$$\leq (1 - \alpha) \frac{1}{\sqrt{n}} \|V\|_\infty \|\hat{\Delta}^{(\beta^*)}\|_1 + \alpha \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\gamma^*)}\|_1$$

$$\leq (1 - \alpha) \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\beta^*)}\|_1 + \alpha \frac{1}{\sqrt{n}} \|U\|_\infty \left( \|\hat{\Delta}^{(\gamma^*)}\|_1 + \|\hat{\Delta}^{(\gamma^*)}\|_1 \right)$$

$$\leq (1 - \alpha + p^{-1} \alpha) \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\beta^*)}\|_1 + 2\alpha \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\gamma^*)}\|_1$$

(17)

where the last inequality follows from observing that $\hat{\Delta}^{(\beta^*)} = A_{\beta^r} \hat{\Delta}^{(\gamma^*)}_r + 1_p \hat{\Delta}^{(\gamma^*)}$ and

$$p|\hat{\Delta}^{(\gamma^*)}_r| = \|1_p \hat{\Delta}^{(\gamma^*)}_r\|_1 \leq \|\hat{\Delta}^{(\beta^*)}\|_1 + \|A_{\beta^r} \hat{\Delta}^{(\gamma^*)}_r\|_1 \leq \|\hat{\Delta}^{(\beta^*)}\|_1 + \|A_{\beta^r}\|_1 \|\hat{\Delta}^{(\gamma^*)}_r\|_1 \leq \|\hat{\Delta}^{(\beta^*)}\|_1 + p \|\hat{\Delta}^{(\gamma^*)}_r\|_1.$$  

When $\alpha \leq (1 + p^{-1})^{-1}$, we have $(1 - \alpha) \geq p^{-1} \alpha$ and then $(1 - \alpha + p^{-1} \alpha) \leq 2(1 - \alpha)$. Thus, (17) becomes

$$\left| \frac{1}{n} \varepsilon^T X\hat{\Delta}^{(\beta^*)} \right| \leq 2(1 - \alpha) \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\beta^*)}\|_1 + 2\alpha \frac{1}{\sqrt{n}} \|U\|_\infty \|\hat{\Delta}^{(\gamma^*)}\|_1$$

(18)
Since \( \varepsilon \sim N_n(0, \sigma^2 I_n) \), \( U_\ell \sim N \left( 0, \frac{\| X A_\ell \|_2^2 \sigma^2}{n} \right) \) for \( \ell = 1, \ldots, |T| \). By Lemma 6.2 of Bühlmann and van de Geer (2011), we have for \( x > 0 \)

\[
P \left( \frac{\| U \|_\infty}{2\sqrt{n}} > \frac{\| X A \|_2 \sigma}{\sqrt{2n}} \sqrt{x + \log |T|} \right) \leq 2e^{-x}. 
\]

By the construction of \( T \), each internal node has at least 2 child nodes. To go up to the next level from the leaf nodes, only one node “survives” among its siblings. For \( T \) with \( p \) leaf nodes, there must be at most \( p - 1 \) internal nodes where the maximum number is achieved when \( T \) is a full binary tree. Thus, \( |T| \leq 2p \). Moreover, \( \max_{\ell=1, \ldots, |T|} \| X A_\ell \|_2 \leq \| X 1_p \|_2 = \sqrt{n} \) since \( X \) has non-negative elements. We therefore have

\[
P \left( \frac{\| U \|_\infty}{2\sqrt{n}} > \nu \right) \leq 2e^{-x} \quad \text{for } \nu = \frac{\sigma}{\sqrt{2n}} \sqrt{x + \log 2p}. 
\]

Choosing \( x = \log 2p \), we have \( \nu = \frac{\sigma}{\sqrt{2n}} \sqrt{\log 2p} \) and \( \| U \|_\infty / \sqrt{n} \leq 2\nu \) hold with probability at least \( 1 - p^{-1} \). Thus, we have the following inequality holding with high probability:

\[
\left| \frac{1}{n} \varepsilon^T X \hat{\Delta}^{(\beta^*)} \right| \leq 4(1 - \alpha)\nu  \| \hat{\Delta}^{(\beta^*)} \|_1 + 4\alpha\nu  \| \hat{\Delta}^{(\gamma^*)} \|_1. 
\] (19)

Let \( \lambda \geq 8\nu \) and \( 0 \leq \alpha \leq (1 + p^{-1})^{-1} \). By (16) and (19), the following holds with probability at least \( 1 - p^{-1} \):

\[
\frac{1}{2n} \left\| X \hat{\beta} - X \beta^* \right\|_2^2 \leq \frac{1}{2} \lambda \Omega(\hat{\Delta}^{(\beta^*)}, \hat{\Delta}^{(\gamma^*)}) - \lambda \Omega(\hat{\beta}, \hat{\gamma}) + \lambda \Omega(\beta^*, \gamma^*) 
\]

\[
\leq \frac{1}{2} \left( \lambda \Omega(\beta^*), \gamma^* \right) - \lambda \Omega(\beta, \gamma) + \lambda \Omega(\beta^*, \gamma^*) \quad \text{(by triangle inequality)}
\]

\[
\leq \frac{3}{2} \lambda \Omega(\beta^*, \gamma^*) = \frac{3}{2} \lambda \left( \alpha \left\| \beta^* \right\|_1 + (1 - \alpha) \left\| \beta^* \right\|_1 \right). 
\]

F \quad \textbf{Proof of Corollary 1}

The first statement follows immediately from observing that \( \| \hat{\beta}^* \|_1 \leq M|B^*| \) and \( \| \beta^* \|_1 \leq M|A^*| \).

To show the second statement, we start by showing that \( \alpha = \frac{|A^*|}{|A^*| + |B^*|} \leq (1 + p^{-1})^{-1} \) for all \( p \). Since \( |B^*| \geq 1 \) and \( |A^*| \leq p \), the following holds for all \( p \):

\[
|A^*| \leq p \cdot |B^*| \quad \Leftrightarrow \quad |A^*| + p^{-1}|A^*| \leq |A^*| + |B^*| \quad \Leftrightarrow \quad \frac{|A^*|}{|A^*| + |B^*|} \leq (1 + p^{-1})^{-1}. 
\]

From Theorem 8 we have

\[
\frac{1}{n} \left\| X \hat{\beta} - X \beta^* \right\|_2^2 \leq 3\lambda M (\alpha |B^*| + (1 - \alpha)|A^*|) 
\]

\[
= 24\sigma M \sqrt{\frac{\log 2p}{2n}} \cdot (\alpha |B^*| + (1 - \alpha)|A^*|) \quad \text{(by plugging in } \lambda \text{)}
\]

\[28\]
\[ 48 \sigma M \sqrt{\frac{\log 2}{n}} \left( \frac{1}{|A^*|} + \frac{1}{|B^*|} \right)^{-1} \text{ (by plugging in } \alpha) \]
\[ \leq 48 \sigma M \sqrt{\frac{\log 2}{n}} \cdot \min \left( |A^*|, |B^*| \right). \]

This final inequality follows since, for any \( a, b > 0 \), \( (1/a + 1/b)^{-1} \leq (1/a + 0)^{-1} = a \), which establishes by symmetry in \( a \) and \( b \) that \( (1/a + 1/b)^{-1} \leq \min\{a, b\} \).

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