

Comparing Algorithms for the Sparse Group Lasso

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Abstract

The sparse group lasso is a high-dimensional regression technique that is useful for problems whose covariates have a naturally grouped structure, and where sparsity is encouraged at both the group and individual covariate level. In this paper we discuss two algorithms for this optimization problem, as well as their implementation in Fortran as part of a new R package. This R package is an advance over existing packages, as it is the only one that solves this problem in a sufficiently fast computation time for truly high-dimensional situations.

1 Introduction

The lasso is “a regression analysis method that performs both variable selection and regularization” which uses an l_1 penalty [3] to select a subset of predictors to be nonzero. The minimization problem is of the form

$$\min_{\beta} \frac{1}{2} \|y - X\beta\|_2^2 + \lambda \|\beta\|_1,$$

where X is an n by p data matrix, β is the unknown coefficient vector, and λ is a hyperparameter that enforces the regularization/variable selection. In this problem it is assumed that the response y is linearly related to the predictors (the columns of the data matrix X), with the goal being to estimate the coefficient vector β responsible for this linear relationship. In general it will return a solution with some nonzero entries in the β vector, and the rest zero.

A variant of this, the group lasso [7] is appropriate when there is a natural grouping structure for the coefficients; that is, we assume that the vector of coefficients is partitioned into groups, or subvectors, and, by analogy with regular lasso regression, only a few of the groups are active, i.e., have nonzero coefficients. The group lasso thus performs regularization that has the effect of discarding groups of predictors rather than the predictors themselves; it is of the form

$$\min_{\beta} \frac{1}{2} \left\| y - \sum_{l=1}^m X^{(l)} \beta^{(l)} \right\|_2^2 + \lambda \sum_{l=1}^m \sqrt{p_l} \|\beta^{(l)}\|_2.$$

Note that the grouping structure is explicit in the above equation: the vector of coefficients, β , is thought of as a concatenation of the coefficient subvectors of the various groups $\beta^{(l)}$,

and similarly the data matrix X is the concatenation of submatrices, each submatrix $X^{(l)}$ being composed of the columns that correspond to the particular group. Thus the first part of the equation, $y - \sum_{l=1}^m X^{(l)}\beta^{(l)}$, is identical to the more simply-written equation $y - X\beta$, but is written with this partition in mind.

The second part of the equation, however— $\sum_{l=1}^m \sqrt{p_l} \|\beta^{(l)}\|_2$ —is different than the corresponding part in the original lasso equation. Rather than being an $l1$ norm of the vector β , it is a sum of the (non-squared) $l2$ norms of the coefficient vectors of the various groups. It is interesting to note that it is the non-differentiability of this expression at 0 that accounts for the group-discarding property of the problem, similar to how the $l1$ norm’s non-differentiability at 0 is responsible for the discarding property of coefficients in the original lasso.

As with the original lasso equation, there is only a single tuning parameter λ , whose value determines the strength of regularization. Within the second summation are the relative weights of the groups, p_l , though these are usually determined by the size of the corresponding groups, and so in the rest of this paper this notation is suppressed from the equations.

Finally, in a group-structured problem as above, it may be desirable to enforce sparsity, not only among the groups, but also within the groups. The sparse group lasso [2] does this by solving the following minimization problem

$$\min_{\beta} \frac{1}{2} \left\| y - \sum_{l=1}^m X^{(l)}\beta^{(l)} \right\|_2^2 + (1 - \alpha)\lambda \sum_{l=1}^m \|\beta^{(l)}\|_2 + \alpha\lambda \|\beta\|_1. \quad (1)$$

This equation is very similar to that of the group lasso, and in fact one sees that the only difference is that it adds a second regularization term, the overall $l1$ norm of the full β vector, which we first saw in the original lasso formulation. There is now a second tuning parameter α , which controls the relative emphasis of intra- vs inter- sparsity in the predictors.

The sparse group lasso, like the other two lassos, does not have a closed form solution and thus relies on computational algorithms, which may be very intensive for large datasets and/or many values of λ . The rest of this paper therefore concerns the mitigation of this issue, in particular the following question: if we are solving the sparse group lasso, not for a single value of the tuning parameter λ but a whole parameter space—in this context, a range of values $(\lambda_1, \dots, \lambda_S)$ —then can we shorten the total computational time by making use of the already-computed solution at previous λ ’s in the parameter space to speed up computation at a given λ ?

In this paper we make use of a heuristic called the Strong Rule [4] to help solve this problem, with some success. The strong rule uses the solution at the previous λ_{s-1} to predict which groups will remain inactive upon solution at the current λ_s , and discards those groups before entering into the algorithm. If a significant number of groups are thrown out before entering the algorithm, convergence time can improve significantly.

The R package we have create has two algorithms, both using the strong rule, but in slightly different ways: the **three-step algorithm** and the **four-step algorithm**. Although they perform similarly for the simulated data set used in later sections of this paper, it is suspected that they will each be useful for different scenarios, depending on the size of the data, size of the predictors, and the true underlying group structure. This is explored in the last section before the conclusion.

There are already two other existing R packages that perform group lasso, **gglasso** and **sgl**. The advantage of our package over those two are as follows: the **sgl** package has sparsity, but does direct coordinate descent and does not have a heuristic like the strong rule, so it does not take advantage of such a computational speedup. Because of this, **sgl** is too slow to be of use in analyzing the high-dimensional problems that occur commonly, for example in genetic applications.

The **gglasso** package, on the other hand, incorporates such a rule and is computationally fast, but does not incorporate within-group sparsity (i.e., it performs group lasso, not sparse group lasso). When this package is used on a grouped dataset, the solution will have some active groups and some inactive, but within an active group, generally all the coefficients will be nonzero. Our contribution, then, is to provide a package that performs sparse group lasso, and is faster than existing algorithms. The algorithms for this package are written in Fortran, and are based on the algorithm from the **gglasso** package.

In section 2, we describe the algorithm in detail, paying particular attention to the strong rule. In section 3, we show how to use the package, running through an example with simulated data. In section 4, we compare our package to the other existing **sgl** packages, and also compare the two variants of our algorithm with each other.

2 Methodology

2.1 Overview of the algorithm

There is no closed-form solution to the optimization problem in [Equation 1](#) above, so we need a numerical algorithm to find the optimal solution. The problem defined by [Equation 1](#) is convex, since the expression is a sum of convex functions and the feasible set is convex, so there is an optimal solution, and a variety of methods may be used one.

Our package has two different algorithms to accomplish this, which we refer to as the **three-step** and **four-step** algorithms. The general framework for both of our algorithms is based on a block-wise coordinate descent algorithm (see [\[2, 6\]](#)). What this means is that we loop over the groups and, for a given group, update only those variables while holding all other groups constant. In particular, we will use a majorization-minimization coordinate descent scheme; the term 'majorization' comes from the idea that, instead of using the exact equation to determine the step size and direction in every update step, we update according to a simpler expression than [Equation 1](#) that majorizes, or bounds from above, the expression we want to solve for. This is explained in more detail in the following paragraph.

For the rest of this section, we will focus on a particular group k . We hold the coefficients for all other groups fixed, and find an appropriate update step for group k . We note here that, because the loss function in [Equation 1](#) is differentiable and the penalty terms are convex and separable (i.e., they can be decomposed into a sum of functions each only involving a single group), a coordinate descent algorithm is guaranteed to converge to a global optimum [\[5\]](#).

To begin with, we will introduce some notation. Let

$$r_{(-k)} = y - \sum_{l \neq k} X^{(l)} \beta^{(l)}$$

be the partial residual of y , where all the group fits besides that of group k are subtracted from y . Since all groups besides group k are held fixed, we don't need to consider the penalty terms corresponding to those fixed groups. So what we are really interested in minimizing is the following:

$$\frac{1}{2n} \|r_{(-k)} - X^{(k)} \beta^{(k)}\|_2^2 + (1 - \alpha)\lambda \|\beta^{(k)}\|_2 + \alpha\lambda \|\beta^{(k)}\|_1. \quad (2)$$

For ease of notation, we will suppress the superscript (k) from $\beta^{(k)}$, with the understanding that we are really referring to only the k -th group of the coefficient vector. We will also define, using these terms, the unpenalized loss function

$$\ell(r_{(-k)}, \beta) = \frac{1}{2n} \|r_{(-k)} - X^{(k)} \beta\|_2^2,$$

so that our optimization problem for the k -th group becomes $\ell(r_{(-k)}, \beta) + (1 - \alpha)\lambda \|\beta\|_2 + \alpha\lambda \|\beta\|_1$, and we are interested in finding an optimal value, $\hat{\beta}$.

Any global minimum is determined by the subgradient equation, which is similar to a first-derivative test for minima, except the $\|\cdot\|_2$ and $\|\cdot\|_1$ penalty terms are non-differentiable at 0; because of this, the (sub)differential for each coordinate in β (i.e., $\beta^{(k)}$) is not a single value, but a range of possible values. For Equation 2 above, taking the subdifferential and setting equal to zero gives us the following condition that the minimum $\hat{\beta}$ needs to satisfy:

$$\frac{1}{n} X^{(k)T} (r_{(-k)} - X^{(k)} \beta) = (1 - \alpha)\lambda u + \alpha\lambda v, \quad (3)$$

where u is the subgradient of $\|\beta\|_2$ and v is the subgradient of $\|\beta\|_1$. The first is defined to be $\frac{\beta}{\|\beta\|_2}$ if β is a nonzero vector, and is any value in the set $\{u : \|u\|_2 \leq 1\}$ otherwise; the second, v , is defined coordinate-wise as $v_j = \text{sign}(\beta_j)$ if $\beta_j \neq 0$, and is any value $v_j \in \{v_j : |v_j| \leq 1\}$ otherwise.

At this point, it is possible to use Equation 3 to derive an update step and develop a cyclical coordinate-wise algorithm, but it is too computationally expensive, involving repeated large-matrix multiplication ([2]); instead we use the majorization-minimization idea discussed above.

Since the unpenalized loss $\ell(r_{(-k)}, \beta)$ is a quadratic function in β , it is equal to its second order Taylor expansion about any point β_0 in the parameter space—indeed, this is the definition of a function being quadratic. We thus start with the following equality for any given β_0 (recall that $\beta_0 = \beta_0^{(k)}$):

$$\forall \beta, \ell(\beta) = \ell(\beta_0) + (\beta - \beta_0)^T \nabla \ell(\beta_0) + \frac{1}{2} (\beta - \beta_0)^T H (\beta - \beta_0), \quad (4)$$

where the gradient $\nabla \ell$ is the first total derivative of ℓ (evaluated at β_0) and H , the Hessian, is the second total derivative. Note that we have again suppressed notation, $\ell(\beta) = \ell(r_{(-k)}, \beta)$, since $\beta = \beta^{(k)}$ is the only variable. Recall that ∇ is the vector of first partial derivatives of ℓ with respect to each coordinate of β , evaluated at β_0 , and H is a $p \times p$ matrix

of mixed partial derivatives of ℓ . In this particular case, a short computation shows that the Hessian is simply written in terms of X : $H = X^T X$.

The matrix X is, for the problems we are interested in solving, very large, and so computing $X^T X$, storing it in memory, and inverting, is going to be an issue, especially since we will be doing update steps many times. What we can do, and will do, is replace this matrix with a much simpler one, tI , a diagonal matrix with the value of t selected to be such that this dominates the Hessian (in the sense that $tI - H$ is positive definite). For our algorithm we choose the largest eigenvalue of the Hessian and use that for t . We get the following inequality:

$$\forall \beta, \beta_0, \ell(\beta) \leq \ell(\beta_0) + (\beta - \beta_0)^T \nabla \ell(\beta_0) + \frac{1}{2t} (\beta - \beta_0)^T (\beta - \beta_0). \quad (5)$$

We take the original minimization problem (Equation 2) and replace the loss ℓ with the right-hand side of Equation 5. Thus Equation 2 is now dominated (majorized) by the following expression

$$M(\beta) = \ell(\beta_0) + (\beta - \beta_0)^T \nabla \ell(\beta_0) + \frac{1}{2t} \|\beta_0 - \beta\|_2^2 + (1 - \alpha)\lambda \|\beta\|_2 + \alpha\lambda \|\beta\|_1, \quad (6)$$

which no longer involves the large matrix multiplication that using the original loss function would have confronted us with.

The optimal value $\hat{\beta}$ for $M(\beta)$ is determined by its subgradient equation, which is similar to that of Equation 3:

$$\frac{1}{t}(\beta - (\beta_0 - t\nabla \ell)) + (1 - \alpha)\lambda u + \alpha\lambda v = 0, \quad (7)$$

with u and v as before. If we solve this for β in terms of β_0 , paying close attention to the conditions for the subdifferentials when β is and isn't 0, we get the following equation:

$$\hat{\beta} = U(\beta_0) = \left(1 - \frac{t(1 - \alpha)\lambda}{\|S(\beta_0 - t\nabla \ell(\beta_0), t\alpha\lambda)\|_2}\right)_+ S(\beta_0 - t\nabla \ell(\beta_0), t\alpha\lambda), \quad (8)$$

where S is the coordinate-wise soft threshold operator, defined by a vector γ and scalar b according to

$$(S(\gamma, b))_j = \text{sign}(\gamma_j)(|\gamma_j| - b)_+, \quad (9)$$

i.e., for each coordinate in the vector, it shrinks that coordinate in magnitude by the amount b , and sets it to zero if the magnitude of that coordinate was smaller than b to begin with.

Equation 8 defines the update step for any given group k , via $\beta \leftarrow U(\beta)$. At a point β_{old} , find the majorizing convex function M that dominates the objective function—centered at that β_{old} —and choose the new value of beta to be the minimizer of majorized function, $\beta_{new} = U(\beta_{old})$. This update step has the advantage that it is easy to compute, and is guaranteed to converge to the optimum $\beta = \beta^{(k)}$ for that given group.

By examining the update step we see that it is possible for the whole group to be set to zero (made inactive) because of the threshold operator $()_+$ in the first part of the expression, and it is possible also for individual components of $\beta^{(k)}$ to be zeroed out from the coordinate-wise threshold $S()$. So this algorithm setup enforces at both the group and individual level.

Because the optimization problem is convex, it can be shown that this type of descent algorithm is guaranteed to converge to the optimal solution. That is, it does not get ‘stuck’ at any inflection points or local minima. Therefore, if that was all the algorithm did, there would be no need to check the KKT conditions for optimality.

However, our algorithms both make use of the sequential strong rule, a heuristic that predicts, before computation, which groups will remain inactive, and discards them; this results in significant computational savings, but because this pre-processing prediction is not always correct, we will need to do a KKT check [1] after convergence to make sure the initial prediction was accurate. This is described in the next section.

2.2 Strong Rule and KKT Check

As mentioned above, the strong rule [4] is easy and fast to perform, discarding large numbers of predictors before computation, but it is not guaranteed to be correct, so it becomes necessary to double-check the solution after convergence, to make sure active groups were not accidentally discarded.

The version of the strong rule used here is called the **sequential strong rule**; it makes use of the fact that we are solving for a sequence $\{\lambda_1 \geq \lambda_2 \geq \dots, \lambda_S\}$ of lambda parameters, rather than a single value. At each λ_s , we rely on the fact that we have solved the problem for the previous λ_{s-1} , and use this information to quickly discard many predictors. Without loss of generality, for the rest of this section assume that the problem has already been solved for λ_{s-1} .

The motivation for the strong rule comes from the KKT stationarity condition, which is similar to the first derivative test for minima [1]. Explicitly, this is the condition that the subdifferential equations (see Equation 3) are satisfied at the proposed minimum $\hat{\beta}^{(k)}(\lambda_s)$. Note that we are still focusing on a given group k , but we are emphasizing the dependence on λ now.

From Equation 3 we derive the condition used in the algorithm to check the KKT stationarity condition. Because the algorithm is guaranteed to converge to the optimum for all active groups, we only need to check the condition required for $\hat{\beta}^{(k)} = 0$ to be the solution (at a given λ). First, the subgradient equations reduce to the following:

$$X^{(k)T} r_{(-k)}/n - \alpha \lambda v = (1 - \alpha) \lambda u,$$

where u and v are the subdifferentials of the $l - 2$ and $l - 1$ norms, as in section 2.1. We claim that if the following inequality

$$\|S(X^{(k)T} r_{(-k)}/n, \alpha \lambda)\|_2 \leq (1 - \alpha) \lambda.$$

is satisfied (where S is the soft-threshold operator), then $\hat{\beta}^{(k)} = 0$ is the minimum for that group at that particular lambda. The reason for this is that we can find a subgradient v such that $X^{(k)T} r_{(-k)}/n - \alpha \lambda v = S(X^{(k)T} r_{(-k)}/n, \alpha \lambda)$, and if the above inequality is satisfied, we can also find a subgradient u such that the subgradient equations are satisfied.

So we now have that the KKT stationarity condition is precisely the inequality above for inactive groups, and this is what is checked after convergence in our algorithm, for all

the groups that were either discarded or otherwise remained inactive. For the rest of this section, we will denote the left-hand side of the inequality by

$$c_k := c_k(\lambda) = S(X^{(k)T} r_{(-k)} / n, \alpha \lambda),$$

The sequential strong rule checks if the following inequality holds, and discards the j -th group if so:

$$|c_j(\lambda_{s-1})| < (1 - \alpha)(2\lambda_s - \lambda_{s-1}) \quad (10)$$

The reasoning is as follows: consider $c_j(\lambda)$ as a function of λ . The key point is that, if this function c_j were $(1 - \alpha)$ -Lipschitz, by definition it would satisfy

$$|c_j(\lambda) - c_j(\tilde{\lambda})| \leq (1 - \alpha)|\lambda - \tilde{\lambda}|$$

Now suppose it were Lipschitz and also that $c_j(\lambda_{s-1})$ were known, i.e. we have solved the problem for λ_{s-1} . Then, when the strong rule is satisfied, we combine the two previous inequalities to get

$$|c_j(\lambda_s)| \leq (1 - \alpha)(|c_j(\lambda_s) - c_j(\lambda_{s-1})| + |c_j(\lambda_{s-1})|) < (1 - \alpha)(\lambda_{s-1} - \lambda_s + 2\lambda_s - \lambda_{s-1})$$

which is precisely the KKT stationarity condition at λ_s . Thus, if the strong rule condition were satisfied at this group (and assuming the Lipschitz condition, which is not always true), it follows that β_j is inactive for the current value λ_s . Since we made the Lipschitz assumption, which essentially says that c_j does not change "too fast" as a function of λ , we need to check after performing the algorithm on the other groups that this group is indeed inactive. In fact, as shown in the strong rules paper (), it is very often the case that the c_j 's are $(1 - \alpha)$ -Lipschitz.

2.3 The three-step and four-step algorithms

There are two algorithms in our package that perform sparse group lasso: the three-step algorithm and the four-step algorithm. Both algorithms use the majorized coordinate-descent update step, and mainly differ in how they use the strong rule and how they store the active and potentially active groups. Before discussing these in detail, we need some notation.

First, let $\mathcal{S}_\lambda(A)$ be a function which performs the strong rule check on a set of groups A at λ , and returns the set A' of groups in A that pass the strong rule check. For each individual group in the set A , it checks the inequality in [Equation 10](#) (the sequential strong rule). Recall that the strong rule check at a given λ_k actually involves both λ_k and λ_{k-1} ; this is suppressed in this notation, with this understanding.

Similarly, the function $\text{KKT}_\lambda(A)$ performs the KKT check described in the previous section, and returns the subset A' of groups that fail the KKT check. The idea for both of these functions is to keep track of which groups are potentially active (nonzero) for the given λ .

Both of these functions take in only a subset of the groups of coefficients, rather than being run on the whole set each time; this is to save time and reduce redundancy. It would not make sense to run a KKT check on those groups that are already known to be active (for the given λ), because the whole point is to figure out which groups are mistakenly put down

Algorithm 1 Three-step Algorithm

Input: $\Lambda = \{\lambda_0 > \lambda_1 > \dots > \lambda_K\}$, \mathcal{E} , \mathcal{A}
Set $\mathcal{E} = \mathcal{A} = \emptyset$; set $d = \epsilon + 1$
Step 1: $\mathcal{E} \leftarrow \mathcal{E} \cup \mathcal{S}(\lambda_{k-1}, \mathcal{E}^c)$
Step 2:
 while $d > \epsilon$ **do**
 for $l = 1$ to m **do**
 $\beta^{(l)} \leftarrow \Gamma(\beta^{(l)})$
 If $\beta^{(l)} \neq 0$ put $\beta^{(l)} \in \mathcal{A}$
 end for
 $d \leftarrow \max_l \|\beta_{k-1}^{(l)} - \beta_k^{(l)}\|$
 end while
Step 3: $\mathcal{E} \leftarrow \mathcal{E} \cup KKT(\mathcal{E}^c)$; if $KKT(\mathcal{E}^c) \neq \emptyset$, go back to step 2.
return β vector for λ_k
 $\lambda_k \leftarrow \lambda_{k+1}$
Return to step 1

as 'inactive'. Similarly for the strong rule check, it would be a waste of time to run that inequality on groups that are already known or suspected of being active, since the point of the strong rule check is to separate those suspected of being active from those that are not, and only updating the coefficient estimates for the suspected active groups.

Thus we need to keep track of the active and suspected active groups. First, let \mathcal{E} be the set of groups that are suspected of being active at a given λ ; this is the subset of groups that we will perform the update step on, repeatedly until convergence. It is important to note that there is no mention of λ for this set—this set is only increasing in membership, and gets passed on from one λ to the next. In other words, once a group is suspected of being active and gets put in \mathcal{E} , it never leaves this set, and if group l is put in \mathcal{E} for λ_{k-1} , it is automatically included in this set when we start the algorithm for the next value, λ_k .

The set \mathcal{A} is the set of groups that are actually active, i.e. nonzero, for a given λ . This set is also never-decreasing, so if a group becomes active for λ_k , it stays in that set for every subsequent lambda. This set is used in addition to \mathcal{E} in the three-step algorithm, because we use a warm-start for β^* every time we progress to the next λ , and we only want to keep track of the small set of nonzero coefficients for the warm start. This set is not used in the four-step algorithm.

Next, let \mathcal{E} be the set of indices for the groups that are potentially active (nonzero) at λ_k . There are two ways in which groups get added to \mathcal{E} : if a group passes the strong rule check at any point it gets added, and if a group fails the KKT check at the end of convergence, it gets added. \mathcal{E} is the main set that we keep track of, and is used in both algorithms; this is the set of groups that we actually perform the update step on. Similarly to \mathcal{A} , this set is ever-increasing—once a group gets added to \mathcal{E} , it remains there from then on, for all subsequent λ . For both \mathcal{E} and \mathcal{A} , it is possible that a group is active for λ_k but is inactive for a subsequent λ , but this is rare, and since the set of active groups is usually very small (for any λ), it does not pose a problem to pass the sets over from λ_{k-1} to λ_k .

First we discuss the three-step algorithm, [Algorithm 1](#). In the initialization (step 0) of the algorithm, we set the lambda path (the decreasing set of λ 's which comprise the parameter space), and start keeping track of two sets, $\mathcal{E} = \emptyset = \mathcal{A}$, which are initially empty. Both of these sets grow as the algorithm is run; predictors get put into these groups if they pass certain checks, but never leave once they are put in.

Without loss of generality assume that we have run the algorithm for a few lambdas, and are at $\lambda = \lambda_k$. The first step (step 1) of the algorithm is to run the strong rule check on all predictor groups in \mathcal{E}^c , and every group that passes the strong rule (which is computed using the gradient at the previous lambda) gets put in the set \mathcal{E} . So, as discussed above, \mathcal{E} is essentially keeping track of every predictor that has ever passed the strong rule check—these are candidates for active groups.

In the second step (step 2), we loop over \mathcal{E} , performing the update step until convergence. Again, this is a type of coordinate descent, but we are saving a lot of time by keeping all groups in \mathcal{E}^c zero and only updating on those suspected of being active. Now, although \mathcal{E} is keeping track of the 'strong set', any time a group actually becomes active (i.e. is updated to be nonzero), it gets put in \mathcal{A} , the 'active' set. This is because while we save the indices of the potentially-active groups, we only save the values of the actually active groups, to use as a warm start when moving from λ_{k-1} to λ_k .

Finally, after we have converged (the update step for all groups is changing values by less than a small, pre-determined ϵ), we need to perform the KKT check to make sure that we didn't accidentally leave some active groups at 0. Again, if we were not using the strong rule check, this would be unnecessary. The only potential violators are in the complement of \mathcal{E} , so: run the KKT check on \mathcal{E}^c , throw any violators into \mathcal{E} and go back to step 2. If there are no violators, we have found the solution at the given λ_k , so we save the values in \mathcal{A} , as well as the gradients, and move on to λ_{k+1} .

The four-step algorithm, [Algorithm 2](#), has a slight refinement over the three-step. It is as follows. First note that there is only one set to keep track of, the set \mathcal{E} . The setup is the same.

Assume we have solved the problem for λ_{k-1} . We loop over \mathcal{E} , which was passed over from λ_{k-1} , and update until convergence. The difference here is that we do not perform the strong check first. After we have run the update loop until convergence on our set, we then perform the strong rule on the complement, \mathcal{E}^c . For any groups that pass the strong rule, we run the kkt check; if there are any violators, put them in \mathcal{E} and go back to step 1.

Otherwise, we run the KKT check on the full complement \mathcal{E}^c . Again, if there are any violators, we put them in \mathcal{E} and go back to step 1. If there are no violators, we are done, and we move on to the next λ in the sequence.

3 Example

In this section we provide a worked-through example of how the package is used.

First, we generate some random data. There will be $n = 100$ observations and $p = 200$ predictors. The predictors will be partitioned into groups of 5, so e.g. the first five predictors form the first group, and so on. Some of the groups will be inactive (0), and within a given

Algorithm 2 Four-step Algorithm

Input: $\Lambda = \{\lambda_0 > \lambda_1 > \dots > \lambda_K\}$, \mathcal{E}

Set $\mathcal{E} = \emptyset$; set $d = \epsilon + 1$

Step 1:

while $d > \epsilon$ **do**

for $l = 1$ to m **do**

$\beta^{(l)} \leftarrow \Gamma(\beta^{(l)})$

 If $\beta^{(l)} \neq 0$ put $\beta^{(l)} \in \mathcal{A}$

end for

$d \leftarrow \max_l \|\beta_{k-1}^{(l)} - \beta_k^{(l)}\|$

end while

Step 2: Compute $S = \mathcal{S}(\lambda_{k-1}, \mathcal{E}^c)$

Step 3: $\mathcal{E} \leftarrow \mathcal{E} \cup KKT(S)$; if $KKT(S) \neq \emptyset$, go back to step 1.

Step 4: $\mathcal{E} \leftarrow \mathcal{E} \cup KKT(\mathcal{E}^c)$; if $KKT(\mathcal{E}^c) \neq \emptyset$, go back to step 1.

return β vector for λ_k

$\lambda_k \leftarrow \lambda_{k+1}$

Return to step 1

active group, some of the variables will be 0. The goal is to learn exactly this information.

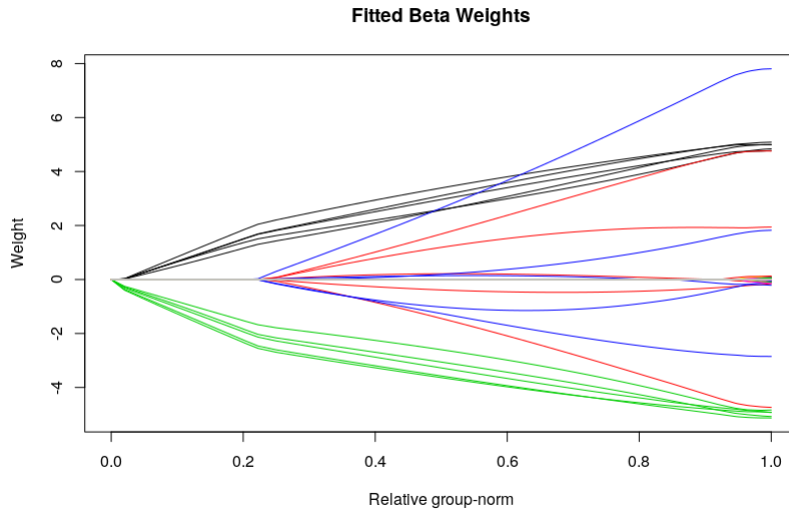
Once we make a random design matrix X and the true β vector (which has the group structure mentioned above), we form the response vector y according to $y = X\beta + \epsilon$. The following code generates the data for this example.

```
set.seed(1010)
n <- 100
p <- 200
X <- matrix(data = rnorm(n*p, mean=0, sd=1), nrow = n, ncol = p)
eps <- rnorm(n, mean = 0, sd=1)
beta_star <- c(rep(5,5), c(5,-5,2,0,0), rep(-5,5), c(2,-3,8,0,0), rep(0,(p-20)))
y <- X%*%beta_star + eps
groups <- rep(1:(p/5), each=5)
```

Since we generated the data according to the above equation, we know the true value of β , in particular which groups are active and which predictors within active groups are nonzero. We want to use the `sparsegl` package to backsolve: given X , y and the group partition information (how the predictors are divided up into groups, but not the values), how can we best estimate the predictors β ?

To reiterate, we need to know beforehand how the predictors are divided up into groups; the algorithm takes that in, and does not learn it. Also note that the groups in β are contiguous. The data needs to be grouped in such a way before we can apply our package.

This package will estimate β for a whole path of λ weights. For each λ , it will find the optimal solution for that weight, according to equation [jblankj](#). The lambda path can be explicitly specified as an input, but otherwise it creates its own set of λ , first finding the smallest value of λ that forces all predictors to be zero, and decrementing logarithmically 100 times, to get a set of 100 decreasing λ 's. For this particular dataset, the lambdas range from 0.636 to 0.00636, with log-constant decremental step-size.



of predictor weights, colored by group, against the relative group norm. This shows how the groups and predictors enter and exit the model as a function of the λ parameter.

In addition to lambda we also need to set α , which controls the relative emphasis on inter- vs intra- group sparsity. The default is $\alpha = 0.05$. Here is the code that runs the algorithm and stores the results in an object called `myparse1`.

```

myparse1 <- sparsegl(x = X, y = y, group = groups,
                    pen = "sparsegl", algorithm = "threestep")

```

With the above line of code, we have run the algorithm that solves the problem for the default lambda space, and created a `sparsegl` object. The main data in that object is the B matrix, which gives the estimated beta vector for each value of λ . Note that, when calling this function, we must give it the group structure, and also specify the threestep vs the fourstep algorithm. Finally, the 'pen' flag specifies that we want to perform sparse group lasso; there is also the option to just perform group lasso.

If we look now at the B matrix, we see that, for a particular range of lambdas, the algorithm was able to deduce correctly the active groups, the active predictors within those groups, and accurately estimate their weights.

;;see beta matrix;;

It is illustrative to look at a graph of the predictors against lambda, to see when the various predictors become active. For visualization reasons, we instead plot on the x-axis, not lambda but an equivalent measure, the relative group norm. This is equivalent to graphing against lambda, since as lambda decreases, the group-norm (which is the sum of L_2 norms of all the groups in beta) of the fitted beta increases. This type of graph is produced by a built-in function of the `sparsegl` package. All predictors are plotted, and each are colored by group membership, which is supplied as input. See the figure below.

We can see that there are four active groups (all other groups remain 0 for all values on the x-axis): black, green, red and blue. By comparing this graph with the true beta in the code above, we can get a measure of how the algorithm is performing across the various lambda values.

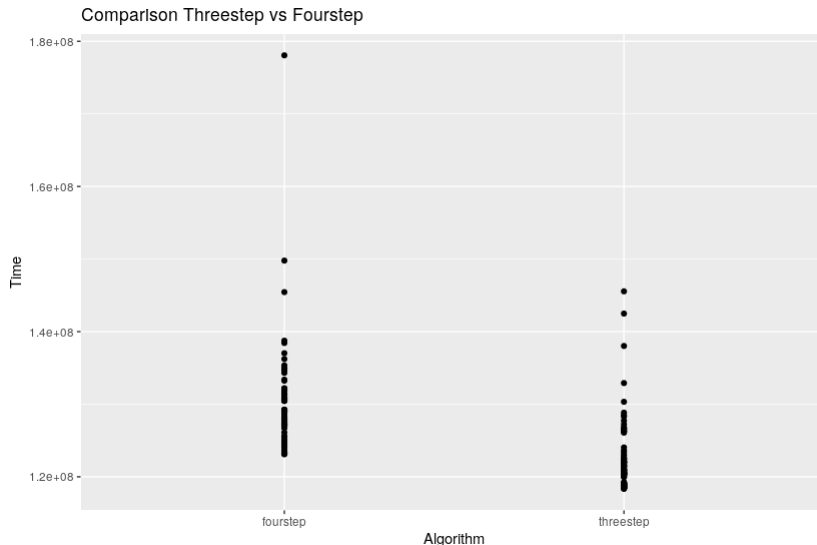


Figure 1: A graph comparing the run-times of the threestep and fourstep algorithms. The fourstep algorithm is slightly faster on average.

The black group (which we see has 5 members) quickly becomes active as λ is decreased, and eventually all values settle at a value of 5. This is evidently the first group, which was set to five 5's. Similarly, the green group becomes active and converges to five -5 's; this is third group. The other two groups are active but have predictors that are 0—we can see that the red group, for instance, has a 5, a 2, and a -5 , and must be the second group.

From comparing this output graph with the true β , with which the data was generated, one might ask what the optimal λ , is, which recovers the true structure. In this case, it appears the small end of the λ path results in the most accurate estimates.

4 Comparison

First we will compare the two algorithms within the `sparsegl` function, `threestep` and `fourstep`, for both accuracy and speed. Then, we compare our package with two other competing packages, the `SGL` package (which performs sparse group lasso, without predictor-discarding rules) and the `gglasso` package (which only performs group lasso, but uses predictor-discarding rules). Since the main contribution of this package is a fast algorithm for sparse group lasso, we pay particular attention to the speed difference between our algorithms and `SGL`.

For all comparisons, we use the R package `microbenchmark`, which compares two or more operations by performing them repeatedly (100 for our analysis) and collecting the times to perform each operation.

We can see that there is not a big difference in the time it takes to perform the `threestep` algorithm vs the `fourstep` algorithm. This is possibly a result of the simulated data used, and we believe that for some large datasets, the `fourstep` algorithm will outperform the `threestep`.

Next, we compare our package with the `gglasso` package, which performs regular group

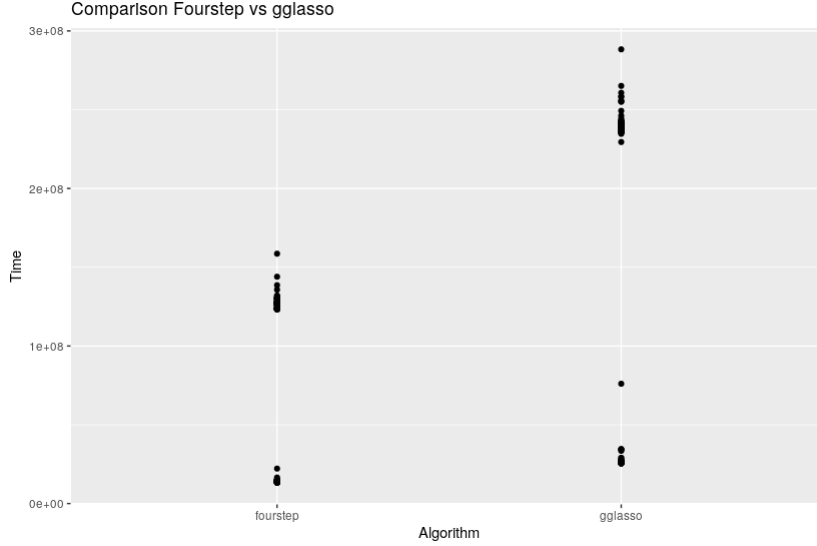


Figure 2: A graph comparing the run-times of the fourstep algorithm with the gglasso package. The fourstep algorithm is slightly faster.

lasso. For this comparison we set α to be zero in our algorithm, so that it also performs regular group lasso.

We see that our package actually outperforms gglasso, even though the gglasso incorporates a similar strong rule, and is overall very close to our threestep algorithm. This gives evidence that the fourstep algorithm can outperform the threestep in at least some circumstances. So even without considering the added functionality of sparsegl to incorporate sparseness, our sparsegl algorithm seems to be an improvement on the gglasso package for performing group lasso.

Finally, we look at the only other existing package that performs sparse group lasso, the SGL package.

Here we see that our fourstep algorithm is substantially faster than SGL in performing sparse group lasso. In fact, we needed to decrease the number of times that microbenchmark ran the two algorithms, since the default of 100 tests was too much for this computer, it did not finish the job in an hour.

Recall the dataset we used for these comparisons, with $n = 100$ and $p = 200$. It is clear that SGL cannot be used for very large datasets, and thus the sparsegl package represents real progress.

We also compare the actual output, in particular the beta matrix, to confirm that they are arriving at the same answers. For this comparison, the lambda path is about the same, but for the other packages (gglasso, SGL), the lambda path will in general be different, so some care must be taken in comparing the beta matrices.

5 Conclusion

Putting this here in case I screw up [4]

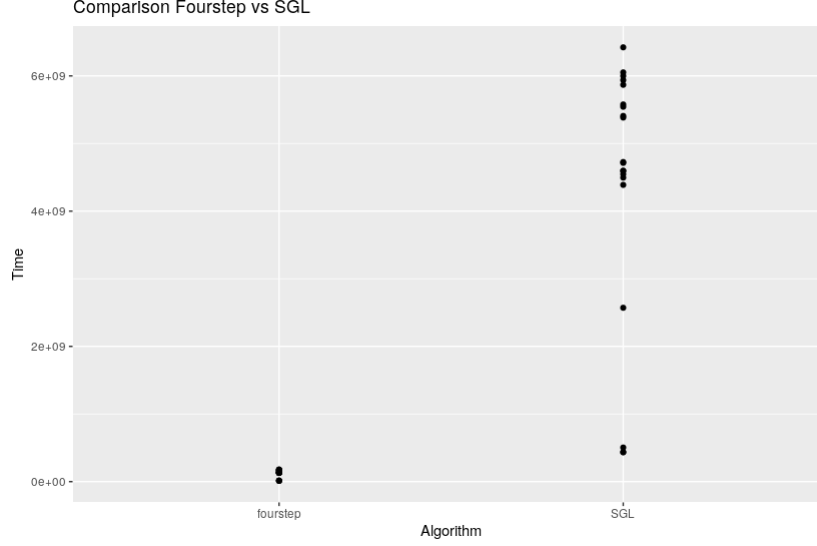


Figure 3: A graph comparing the run-times of the fourstep algorithm with the SGL package. The fourstep algorithm is substantially faster than SGL in performing sparse group lasso.

Then I want to put this [6] here.
And finally I recall the work of [2] for the people.

Algorithm 3 Three-step Algorithm

Input: $\lambda_0, \lambda_1, \dots, \mathcal{E}, \mathcal{A}$

Set \mathcal{E} and \mathcal{A} to \emptyset

▷ Step 0

for $i = 1$ to n **do**

$x_i \leftarrow d + Tx_{i-1|i-1}, P_i \leftarrow Q + TP_{i-1|i-1}T^\top$

▷ Predict current state

$\tilde{y}_i \leftarrow c + Zx_i, F_i \leftarrow G + ZP_iZ^\top$

▷ Predict current observation

$v_i \leftarrow y_i - \tilde{y}_i, K_i \leftarrow P_iZ^\top F_i^{-1}$

▷ Forecast error and Kalman gain

$x_{i|i} \leftarrow x_i + K_iv_i, P_{i|i} \leftarrow P_i - P_iZ^\top K_i$

▷ Update

$\ell(\theta) = \ell(\theta) - v_i^\top F_i^{-1}v_i - \log(|F_i|)$

end for

return $\tilde{Y} = \{\tilde{y}_i\}_{i=1}^n, x = \{x_i\}_{i=1}^n, \tilde{X} = \{x_{i|i}\}_{i=1}^n, P = \{P_i\}_{i=1}^n, \tilde{P} = \{P_{i|i}\}_{i=1}^n, \ell(\theta)$

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