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# A knockoff filter for high-dimensional selective inference

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## Abstract

This paper develops a framework for testing for associations in a possibly high-dimensional linear model where the number of features/variables may far exceed the number of observational units. In this framework, the observations are split into two groups, where the first group is used to screen for a set of potentially relevant variables, whereas the second is used for inference over this reduced set of variables; we also develop strategies for leveraging information from the first part of the data at the inference step for greater accuracy. In our work, the inferential step is carried out by applying the recently introduced knockoff filter, which creates a knockoff copy—a fake variable serving as a control—for each screened variable. We prove that this procedure controls the *directional* false discovery rate (FDR) in the reduced model controlling for all screened variables; this says that our high-dimensional knockoff procedure ‘discovers’ important variables as well as the directions (signs) of their effects, in such a way that the expected proportion of wrongly chosen signs is below the user-specified level (thereby controlling a notion of Type S error averaged over the selected set). This result is non-asymptotic, and holds for any distribution of the original features and any values of the unknown regression coefficients, so that inference is not calibrated under hypothesized values of the effect sizes. We demonstrate the performance of our general and flexible approach through numerical studies showing more power than existing alternatives. Finally, we apply our method to a genome-wide association study to find locations on the genome that are possibly associated with a continuous phenotype.

**Keywords:** knockoffs, inference in high-dimensional regression models, errors of type S, Lasso, variable selection, (directional) false discovery rate, martingales.

## 1 Introduction

Many modern studies in the sciences take the following form: collect a large amount of data, and then ask which of the potentially many measured variables are possibly associated with a response of interest. A typical example would be a genome-wide association study (GWAS), where one wishes to ‘discover’ which genetic variants are possibly associated with a trait. In such studies, it is common to read genetic variants using single-nucleotide polymorphism (SNP) arrays and then look for associations between the trait and the hundreds of thousands of SNPs. In these types of studies and others, we typically have far many more variables or features (SNPs) than observations (individuals in the study).

Finding statistically significant associations between a response and a large set of potentially explanatory variables requires the specification of a statistical model; in this work, we consider the classical linear regression model, which takes the form

$$Y = \sum_{j=1}^p \beta_j X_j + \epsilon, \quad (1)$$

where  $Y$  is the response variable of interest, the  $X_j$ ’s are the explanatory variables, and  $\epsilon$  is a (stochastic) error term. In the GWAS example,  $Y$  may be the level of HDL cholesterol and  $X_j$  the number of recessive alleles at a given location on the genome. In such applications it is important to keep in mind that the linear relationship (1) is just an approximation of a more complicated and unknown model.

In classical statistics, when we speak of finding associations, we think of testing each of the  $p$  hypotheses  $H_j : \beta_j = 0$ , and one can see that there are a few complications with this viewpoint. The first is that for fixed designs,

the linear model (1) with  $p$  parameters is not identifiable whenever the number  $n$  of samples is smaller than this number  $p$  of features. Formally, testing an unidentifiable model may seem like a problematic proposition. A second complication is that in our GWAS example, it may very well be the case that causal mutations affecting levels of HDL cholesterol, for instance, have not been typed (i.e. the array of SNPs is a subsample of the genome, and does not include the causal mutation). In such studies one is, therefore, led to search for indirect effects. In other words, while the causal factors have not been measured, we nevertheless hope to have measured variables that are sufficiently close or correlated to be picked up by association. In these settings, it is understood that even if there is a true sparse ‘causal’ model, we may end up working with an approximate and non-sparse statistical model of the form (1) in which few, if any, of the features have precisely zero effect (i.e. for most features  $j$ ,  $\beta_j = 0$  is not exactly true); this phenomenon occurs because the causal effects have been folded onto the observed variables. There are two consequences of this: (1) sparsity assumptions, which are traditionally assumed in the literature to relieve ourselves from the identifiability problem, are not applicable<sup>1</sup> and (2) when few or none of the regression coefficients take on the value zero, controlling a classical Type I error typically makes little sense since nearly any selected feature is technically a true positive, and we need a different measure of performance to capture the idea that we would like to correctly identify the meaningful large effects while screening out features with near-zero effects. To summarize our discussion, we have at least two problems:

- Lack of identifiability (at least when  $p > n$ ).
- Possibly correlated features and lack of model sparsity so that few, if any, of the null hypotheses actually hold.

These complications should not occlude the relatively simple goal of a statistical selection procedure, which in the GWAS context can be stated as follows: *understanding that SNPs may be proxies for causal mutations, we would like to find as many proxies or locations on the genome without too many false positives—a false positive being a reported location (SNP) with no causal mutation sitting nearby.* Being guaranteed a sufficiently small fraction of false positives would assure the scientist that most of her discoveries are indeed true and, in some sense, replicable. We are thus interested in reliable methods for finding the large effects, those SNPs with large coefficient magnitudes. This paper develops a framework and methods for getting close to this goal.

## 1.1 Errors of Type S and directional FDR

In a series of papers, Gelman and his collaborators introduce a useful measure they call *error of Type S* (S stands for sign). In their work [9], they argue that “in classical statistics, the significance of comparisons (e. g. ,  $\theta_1 - \theta_2$ ) is calibrated using Type I error rate, relying on the assumption that the true difference is zero, which makes no sense in many applications.” They then propose “a more relevant framework in which a true comparison can be positive or negative, and, based on the data, you can state “ $\theta_1 > \theta_2$  with confidence”, “ $\theta_2 > \theta_1$  with confidence”, or “no claim with confidence”.” In this framework, a Type S error (sometimes called a Type III error in other works) occurs when we claim with confidence that the comparison goes one way when, in fact, it goes the other way.

This point of view is extremely relevant to our (possibly high-dimensional) regression problem and our goal of finding the important effects. When we choose to report a variable, we should be able to state with confidence its direction of effect, i.e. whether  $\beta_j > 0$  or  $\beta_j < 0$ . To press this point, we would surely have little faith in a procedure that would control errors of Type I but would not be able to tell the directions of the effects. Another useful aspect of Type S errors is that small effects  $\beta_j \approx 0$  are generally those for which we cannot have much certainty about their direction, since the size of the effect is comparable to or below the noise level of our estimate. Therefore, if we were concerned by signed errors, we would probably not report these effects as discoveries—arguably a wise thing to do.

To measure our success at selecting only those effects that are large enough to be meaningfully distinguished from noise, we might like to control the mixed directional false discovery rate ( $\text{FDR}_{\text{dir}}$ ) [22, 4] defined as follows: letting  $\hat{S} \subset \{1, \dots, p\}$  be the set of selected features together with estimates  $\widehat{\text{sign}}_j \in \{\pm 1\}$  of the direction of effect,

$$\text{FDR}_{\text{dir}} = \mathbb{E} [\text{FDP}_{\text{dir}}] ,$$

<sup>1</sup>The literature also typically assumes low correlations between variables, which is also not applicable in the GWAS example.

where the mixed directional false discovery proportion ( $\text{FDP}_{\text{dir}}$ ) is given by

$$\text{FDP}_{\text{dir}} = \frac{\left| \left\{ j \in \widehat{S} : \widehat{\text{sign}}_j \neq \text{sign}(\beta_j) \right\} \right|}{|\widehat{S}| \vee 1} \quad (2)$$

with the convention that  $\text{sign}(0) = 0$ . This definition subsumes Type I and Type S errors: a false discovery or error occurs either when a zero effect is selected, or when a nonzero effect is selected but with the incorrect sign. (In the denominator,  $|\widehat{S}| \vee 1$  denotes  $\max\{|\widehat{S}|, 1\}$ ; this maximum is taken so that if we make zero discoveries, then the FDP is calculated as zero.) The term ‘‘mixed’’ comes from this combination of two error types; for our purposes, we consider declaring that  $\beta_j > 0$  to be a sign error whether the truth is that  $\beta_j = 0$  or  $\beta_j < 0$ , and will not distinguish between these two types of errors, and so we will drop the term ‘‘mixed’’ and refer to it simply as the ‘‘directional FDR’’. The directional FDP is then the total number of errors of this (combined) type averaged over the selected set. In regression settings in which many of the  $\beta_j$ ’s are approximately zero but perhaps not exactly zero, controlling the directional FDR may be more appropriate than the ‘‘classical’’ FDR (which counts Type I errors only):

$$\text{FDR} = \mathbb{E}[\text{FDP}], \quad \text{FDP} = \frac{\left| \left\{ j \in \widehat{S} \text{ and } \beta_j = 0 \right\} \right|}{|\widehat{S}| \vee 1},$$

The question now is whether we would know of procedures that can offer such guarantees. Note that controlling the directional FDR has a different flavor than classical FDR, since paraphrasing Gelman et al., the significance is not calibrated using Type I errors which implicitly assumes that some of the  $\beta_j$ ’s are zero. In contrast, we are after a form of inference holding no matter the values of the  $\beta_j$ ’s.

In earlier work [1] we introduced *the knockoff filter*, a new variable selection procedure, which rigorously controls the classical FDR, in the low-dimensional setting where  $p \leq n$ . It should be clear that the equivalent notion (2) associated with Type S errors is in principle more difficult to control since by definition we have

$$\text{FDR}_{\text{dir}} \geq \text{FDR},$$

due to the fact that the classical FDR does not record an error when the  $j$ th feature is correctly included in the model but with the incorrect sign, while the directional FDR does. A first contribution of this paper is to show that the knockoff filter offers more than advertised in our earlier work [1]: indeed, we will find that this filter, with no modifications, actually controls the directional FDR as well as the FDR. In particular, this implies that the knockoff filter is applicable in settings where we do not expect any sparsity but nonetheless wish to test whether our conclusions regarding effect signs are reliable. This addresses one of the complications discussed earlier.

## 1.2 High dimensionality

To address the other complication, namely, the high-dimensionality issue ( $p > n$ ), we propose the following general strategy:

- *Screening step.* In a first step, screen all the features  $\{X_j\}, j = 1, \dots, p$ , as to identify a set  $\widehat{S}_0 \subset \{1, \dots, p\}$  of potentially relevant features with  $|\widehat{S}_0| < n$ . In this paper, we shall regard this step as being quite liberal in the sense that it typically produces a long list, hopefully containing most of the important features (with large effect sizes) but also possibly many features with zero effects  $\beta_j = 0$  or nearly vanishing effects  $\beta_j \approx 0$ .
- *Inference/selection step.* The screening step yields a reduced model

$$Y = \sum_{j \in \widehat{S}_0} \beta_j^{\text{partial}} X_j + \epsilon, \quad (3)$$

where we use the notation  $\beta_j^{\text{partial}}$  to indicate that both the definition and the meaning of the regression coefficients has changed (see below). Then test for associations in this reduced model by controlling the directional FDR.

In our GWAS example, this means that we would first screen for promising SNPs, and then extract from this set a final and smaller list of SNPs we are confident are associated with the phenotype under study (recall that reporting a SNP only means that we are confident a mutation lies nearby). Admittedly, this way of thinking is hardly original, and many researchers have proposed and studied such general strategies; see [29, 27] for a non-exhaustive list of important works among those lines. The originality in our approach lies in (1) the choice of Type S error as the right quantity to control leading to a useful selection strategy, and (2) the design of a statistical procedure achieving exact directional FDR control in the reduced model.

We would like to emphasize the importance of considering the directional FDR rather than the classical (unsigned) FDR. Imagine that our sampled observations  $\mathbf{y} \in \mathbb{R}^n$  have mean  $\mathbf{X}\boldsymbol{\beta}$  and uncorrelated errors. In the reduced model, we wish to provide inference about the *partial regression coefficients*, given by

$$\boldsymbol{\beta}^{\text{partial}} = (\mathbf{X}_{\hat{S}_0}^\top \mathbf{X}_{\hat{S}_0})^{-1} \mathbf{X}_{\hat{S}_0}^\top \mathbf{X} \boldsymbol{\beta}.$$

That is, these are the coefficients if the mean of  $\mathbf{y}$ , i.e.  $\mathbf{X}\boldsymbol{\beta}$ , were regressed onto the features  $\mathbf{X}_{\hat{S}_0}$  only. Even if the original coefficient vector  $\boldsymbol{\beta}$  for the full regression model is exactly sparse with many entries exactly equal to zero, the vector of partial regression coefficients  $\boldsymbol{\beta}^{\text{partial}}$  is nonetheless likely to be dense unless there is special structure within  $\mathbf{X}$ .

Now, consider a feature  $\mathbf{X}_j$  not appearing in the original full model, i.e.  $\beta_j = 0$ . In the partial regression, we may find one of two scenarios:

- The coefficient in the partial regression may be large, that is,  $\beta_j^{\text{partial}} \not\approx 0$ . This typically occurs if  $\mathbf{X}_j$  is highly correlated with some strong signal  $\mathbf{X}_k$  that was missed by the screening step. (For instance, we may have missed a causal SNP but included a close neighbor, instead, in the screened set.) Here, we would generally prefer to include  $\mathbf{X}_j$  in the selected model in any case, since it is a good proxy for the missed relevant feature  $\mathbf{X}_k$ .
- Alternately, the coefficient might remain near zero,  $\beta_j^{\text{partial}} \approx 0$ . This is likely whenever  $\mathbf{X}_j$  is not a proxy for any missed feature. Here, the sign of  $\beta_j^{\text{partial}}$  cannot be estimated with much certainty, and so with directional FDR control, we are likely to exclude  $\mathbf{X}_j$  from our final model.

These considerations hopefully make clear that careful screening followed by directional FDR control might yield a valuable selection procedure, which in our GWAS example would likely be able to report SNPs (locations on the genome) associated with a trait while controlling a very natural notion of false positive rate. On the other hand, a setting where this framework does not apply is that of causal inference, in which one would like to report true causal effects and would prefer not to select variables that, due to correlation, act as proxies to the true causal features.

### 1.3 Comparison with other works

There is of course a vast literature on inference in the regression setting. When  $n > p$ , we have available the sampling distribution of least-squares estimates, which makes the construction of  $p$ -values and confidence intervals possible, although selective inference procedures controlling the FDR and similar criteria are more tricky because of the correlations between such test statistics. For an overview of some of the work when  $n > p$ , we refer the reader to the companion article [1].

There has also been much recent work on the high-dimensional setting  $p > n$ , which is the focus of our work here. One type of approach to high-dimensional inference is to avoid the identifiability problem by making assumptions on the data distribution such as (1) a highly sparse coefficient vector  $\boldsymbol{\beta}$ , and/or (2) a “beta-min” condition which requires nonzero entries of  $\boldsymbol{\beta}$  to not be too close to zero, and/or (3) assumptions on the design matrix such as low-pairwise correlations or placing a random distribution on the features. These types of conditions ensure that, with high probability (asymptotically), a sure screening property will hold: that is, at any place in the method requiring a model selection step, with high probability all the relevant features (i.e. all  $\mathbf{X}_j$  with  $\beta_j \neq 0$ ) will be selected. Under these conditions, it is possible to produce an asymptotically normal estimator for each coefficient  $\beta_j$  which can then yield a  $p$ -value or confidence interval which is asymptotically valid. Methods in this category

include the work of Voorman et al. [26], Belloni et al. [3], and Huang et al. [12]. A different type of result, relying on rapid decay of the error in estimating  $\beta$  in an asymptotic setting instead of requiring a sure screening property, is the debiasing work of Zhang and Zhang [31] and Javanmard and Montanari [16]; see also Voorman et al. [26] for a different but related approach. Lockhart et al. [19] propose a sequential testing procedure, which moves along the Lasso path as variables are added into the model, under the assumption that the signals appear before the false positives along the Lasso path (which holds with high probability asymptotically under similar assumptions, i.e., highly sparse  $\beta$ , the beta-min condition, and a well-behaved design matrix). To contrast these lines of work with our method presented here, our work does not make any assumptions on signal strength or sparsity level or design matrix, and we observe reliable performance in terms of FDR control at even relatively small sample sizes.

In contrast with the asymptotic setting described above, other approaches focus on finite-sample p-values and confidence intervals which do not rely on “high probability” selection events but instead are calculated by conditioning on the screened or selected model. Lee et al. [17] develops exact post-selection inference for the Lasso when applied with a fixed penalty parameter, with methodology that extends to other model selection procedures which can be expressed as linear constraints on  $\mathbf{y}$ . In contrast, Taylor et al. [24] propose methods for sequential selection procedures, such as the path of selected models obtained by tuning the Lasso penalty parameter; in this setting, FDR control can be obtained with sequential hypothesis testing procedures e.g. [11], and the tests can be viewed as asking whether the most recent added feature has a true effect in the partial model fitted so far. Fithian et al. [8] develops general theory for this type of inference after conditioning on (sequential or nonsequential) selection events, termed “data carving”. In earlier work, Leeb and Pötscher [18] studied the impossibility of characterizing the (unconditional) distribution of post-selection estimators, and the PoSI (“post-selection inference”) framework of Berk et al. [5] proposed handling the range of possible selected models by taking a maximum over the set of possibilities. Like this group of methods, our knockoff work also makes no assumptions on the regression design, the value of regression coefficients and asymptotic type events, e.g. that the exact true model would be identified in the model selection step. In practice, the methods in this category may have high power when considering extremely small submodels, but lose power when the selected model being considered grows larger (see Section 5 for numerical illustrations). In contrast our knockoff based method shows good power regardless of the size of the screened model as long as the sample size is not too small in comparison. This may be attributed in part to the fact that our goal is to select a set of features while making sure we do not have too many false positives in this set. This directed goal is quite different from that in this literature and, in particular, we do not aim at performing inference on any single feature. (Once we identify interesting features out of a sea of possibilities, one can always collect additional data to perform inference on a single feature.) This flexibility allows us to choose specially crafted test statistics achieving greater power.

Additionally, for the non-asymptotic methods summarized here, generally the noise level  $\sigma$  is assumed to be known in order for the computations to be carried out; our method does not require this (except for one of our theoretical results given later). We note that several methods give asymptotic results for estimating  $\sigma$  without prior knowledge, including the square-root Lasso method of Belloni et al. [2], as well as Fan et al. [7]’s procedure for variance estimation after sure screening. However, like the asymptotic literature described above, these procedures rely on strong assumptions such as extreme sparsity in order to enable accurate estimation of  $\sigma$ ; for a procedure not requiring sparsity, see Janson et al. [14].

Finally, we have called attention on Type S errors as a useful error metric for controlled variable selection; this seems to be a new combination, and we believe this is the right framework for this problem in the high-dimensional setting, where strict sparsity assumptions may be violated whenever a reduced model is considered.

## 2 Knockoffs

Since this paper builds upon and extends the knockoff methodology introduced in [1], we first review the essentials of this method. Imagine we have a response  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\beta, \sigma^2\mathbf{I})$  and have reasons to believe that the coefficient vector  $\beta \in \mathbb{R}^p$  is sparse. To find the nonzero coefficients, we may want to fit a Lasso model [25]

$$\min_{\mathbf{b} \in \mathbb{R}^p} \frac{1}{2} \|\mathbf{y} - \mathbf{X}\mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1$$

and let  $\hat{\beta}(\lambda)$  be the solution. A critical question is this: can we estimate the number of false discoveries in the Lasso solution? That is to say, can we guess the number of coordinates with  $\hat{\beta}_j(\lambda) \neq 0$  and  $\beta_j = 0$ ? The knockoff filter provides answers to questions of this kind by constructing a knockoff companion for each variable, which essentially acts as a *control*.

## 2.1 The knockoff idea

For each feature  $\mathbf{X}_j$ , a knockoff copy  $\tilde{\mathbf{X}}_j$  is constructed such that the augmented  $n \times (2p)$  design matrix of features together with knockoffs satisfies

$$[\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}] = \begin{bmatrix} \mathbf{X}^\top \mathbf{X} & \mathbf{X}^\top \tilde{\mathbf{X}} \\ \tilde{\mathbf{X}}^\top \mathbf{X} & \tilde{\mathbf{X}}^\top \tilde{\mathbf{X}} \end{bmatrix} = \begin{bmatrix} \boldsymbol{\Sigma} & \boldsymbol{\Sigma} - \text{diag}\{\mathbf{s}\} \\ \boldsymbol{\Sigma} - \text{diag}\{\mathbf{s}\} & \boldsymbol{\Sigma} \end{bmatrix} \triangleq \mathbf{G}, \quad (4)$$

where the vector  $\mathbf{s} \geq \mathbf{0}$  of course must be small enough that the resulting Gram matrix is positive semidefinite.<sup>2</sup> By definition, we see that the knockoffs exhibit the same correlation structure as the original variables, and that the cross-correlation is also preserved in the sense that for all pairs of distinct variables  $j \neq k$ , we have  $\mathbf{X}_j^\top \mathbf{X}_k = \tilde{\mathbf{X}}_j^\top \mathbf{X}_k$ . The property, which we call *pairwise exchangeability*, has the important consequence that if  $j$  is null, i.e.  $\beta_j = 0$ , then

$$\mathbf{X}_j^\top \mathbf{y} \stackrel{d}{=} \tilde{\mathbf{X}}_j^\top \mathbf{y}, \quad (5)$$

where  $\stackrel{d}{=}$  denotes equality in distribution (to see this, note that both random variables are Gaussian with the same mean and variance). The distributional equality (5) also holds more generally: for any subset  $S$  of nulls (i.e. a set of features  $j$  with  $\beta_j = 0$ ), we have

$$[\mathbf{X} \ \tilde{\mathbf{X}}]_{\text{swap}(S)}^\top \mathbf{y} \stackrel{d}{=} [\mathbf{X} \ \tilde{\mathbf{X}}]^\top \mathbf{y}, \quad (6)$$

where the matrix  $[\mathbf{X} \ \tilde{\mathbf{X}}]_{\text{swap}(S)}$  is obtained from  $[\mathbf{X} \ \tilde{\mathbf{X}}]$  by swapping the columns  $\mathbf{X}_j$  and  $\tilde{\mathbf{X}}_j$  for each  $j \in S$ . In fact, one can say that knockoffs are constructed according to (4) precisely for (6) to hold. To see the value of this last exchangeability property (6), suppose we were using marginal correlations to test for nonzero effects. Since the knockoffs were man-made with a total disregard for the response, they are known to be null and hence we could use them as controls. For instance, to declare that  $\beta_j \neq 0$  with some confidence we would certainly want to see  $|\mathbf{X}_j^\top \mathbf{y}| > |\tilde{\mathbf{X}}_j^\top \mathbf{y}|$ . In other words, the values of  $\tilde{\mathbf{X}}_j^\top \mathbf{y}$  provide meaningful comparisons since they have the same distributions as the corresponding null statistics.

We can now return to our problem of estimating how many of the Lasso discoveries are, in fact, null. To do this, we run the Lasso on the original design augmented with knockoffs,

$$\min_{\mathbf{b} \in \mathbb{R}^{2p}} \frac{1}{2} \|\mathbf{y} - [\mathbf{X} \ \tilde{\mathbf{X}}] \mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1$$

and denote the solution by  $[\hat{\beta}(\lambda) \ \tilde{\beta}(\lambda)]$  (the first  $p$  components are the coefficients of the original variables and the last  $p$  are for the knockoffs). Due to (4) and (6),  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}]$  and  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top \mathbf{y}$  are invariant and distributionally invariant, respectively, to any swap of original null features and knockoffs. As a consequence, for any subset of nulls,

$$[\hat{\beta}(\lambda) \ \tilde{\beta}(\lambda)]_{\text{swap}(S)} \stackrel{d}{=} [\hat{\beta}(\lambda) \ \tilde{\beta}(\lambda)].$$

Hence,  $\hat{\beta}_j(\lambda)$  and  $\tilde{\beta}_j(\lambda)$  have identical distributions whenever  $j$  is null and, in particular,

$$|\{\text{null } j : \hat{\beta}_j(\lambda) \neq 0\}| \stackrel{d}{=} |\{\text{null } j : \tilde{\beta}_j(\lambda) \neq 0\}| \leq |\{j : \tilde{\beta}_j(\lambda) \neq 0\}|.$$

Therefore, *by looking at the number of knockoff variables that are in the Lasso solution, we have an upward biased estimate of the number of Lasso-selected null variables.*

<sup>2</sup>If  $\mathbf{s}$  is chosen so that the Gram matrix is positive semidefinite, then  $\tilde{\mathbf{X}}$  can be constructed to satisfy this matrix equality as long as  $n \geq 2p$ .



## 2.2 Operationalization and FDR control

It is possible to push through the knockoff idea by computing test statistics and a selection rule as to achieve exact FDR control. (One can also control other types of error such as the family-wise error rate (FWER) or the  $k$ -FWER as in [13]). For each variable  $j \in \{1, \dots, p\}$ , we work with a general statistic  $W_j$  obeying a *sufficiency* and an *antisymmetry* property; we will see shortly how this connects to the Lasso regression from above. The sufficiency property says that  $W_j$  depends upon the design matrix  $\mathbf{X}$  only through its covariance, and upon the response  $\mathbf{y}$  through marginal correlations: namely,

$$W_j = w_j([\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}], [\mathbf{X} \ \tilde{\mathbf{X}}]^\top \mathbf{y}) \quad (7)$$

for some function  $w_j$ . The antisymmetry property says swapping  $\mathbf{X}_j$  and  $\tilde{\mathbf{X}}_j$  has the effect of changing the sign of  $W_j$ ,

$$w_j([\mathbf{X} \ \tilde{\mathbf{X}}]_{\text{swap}(S)}, \mathbf{y}) = \begin{cases} w_j([\mathbf{X} \ \tilde{\mathbf{X}}], \mathbf{y}), & j \notin S, \\ -w_j([\mathbf{X} \ \tilde{\mathbf{X}}], \mathbf{y}), & j \in S. \end{cases} \quad (8)$$

In [1], a much discussed example of such a statistic concerns knots at which variables enter the Lasso path: for each feature  $\mathbf{X}_j$  and each knockoff  $\tilde{\mathbf{X}}_j$ , record the first time that this feature or its knockoff enters the Lasso path, i.e. the largest penalty parameter value  $\lambda$  such that  $\hat{\beta}_j \neq 0$  or  $\hat{\tilde{\beta}}_j \neq 0$ ; then set

$$W_j = \left( \text{largest } \lambda \text{ such that } \mathbf{X}_j \text{ or } \tilde{\mathbf{X}}_j \text{ enters Lasso path} \right) \cdot \begin{cases} +1, & \text{if } \mathbf{X}_j \text{ enters before } \tilde{\mathbf{X}}_j, \\ -1, & \text{if } \mathbf{X}_j \text{ enters after } \tilde{\mathbf{X}}_j. \end{cases} \quad (9)$$

Pairwise exchangeability tells us that for a null feature, the original variable is equally likely to enter before or after its knockoff. This says that the sign of a null statistic  $W_j$  is a fair coin flip, and it also holds that the signs of the null  $W_j$ 's are independent of each other as well as of the magnitudes  $|\mathbf{W}|$ .

Now that we have test statistics for each variable, we need a selection rule. Choose a threshold  $T > 0$  by setting<sup>3</sup>

$$T = \min \left\{ t > 0 : \frac{\#\{j : W_j \leq -t\}}{\#\{j : W_j \geq t\}} \leq q \right\}, \quad (10)$$

where  $q$  is the target FDR level. The output of the procedure is the selected model

$$\hat{S} = \{j : W_j \geq T\}.$$

This selection makes sense since the numerator in (10) is an (over)estimate for the number of false discoveries among all reported variables with  $W_j \geq t$ , that is,

$$\#\{j : W_j \leq -t\} \geq \#\{\text{null } j : W_j \leq -t\} \stackrel{d}{=} \#\{\text{null } j : W_j \geq t\}.$$

Hence, the ratio appearing in the right-hand side of (10) is an estimate of the false discovery proportion (FDP) if we were to use the threshold  $t$ . Hence, we can view our selection rule as a step-up rule stopping the first time our estimate falls below our target level. A slightly more conservative procedure, the knockoff+ filter, is given by incrementing the number of negatives by one, replacing the threshold in (10) with the choice

$$T_+ = \min \left\{ t > 0 : \frac{1 + \#\{j : W_j \leq -t\}}{\#\{j : W_j \geq t\}} \leq q \right\}, \quad (11)$$

and setting  $\hat{S} = \{j : W_j \geq T_+\}$ .

The key results in [1] state that knockoff+ controls the FDR, and the knockoff controls a slight modification of the FDR, at the level  $q$ .

These results hold no matter the design or the value of the unknown regression coefficients. Crucially, we emphasize that neither the knockoff procedure nor the FDR controlling property assume any knowledge of the noise level  $\sigma$ .

<sup>3</sup> In practice, we will only choose a value  $t$  from the set of magnitudes of  $\mathbf{W}$ . Abusing notation, we write  $\min\{t > 0 : \dots\}$  to mean  $\min\{t \in \mathcal{W}_+ : \dots\}$ , where  $\mathcal{W}_+ = \{|W_j| : |W_j| > 0, j = 1, \dots, p\}$ .

### 3 Controlling Errors of Type S

Although they are more difficult to control, we have argued that Type S errors are more meaningful for regression problems since we would like to be able to tell the direction of effect with confidence (and not bother reporting those variables for which we cannot reliably tell). Consider the setting of Section 2 where  $n \geq 2p$  and  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\boldsymbol{\beta}, \sigma^2\mathbf{I})$ . Then to estimate the direction of effect—the sign of  $\beta_j$ —note that

$$(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y} \stackrel{\text{ind}}{\sim} \mathcal{N}(s_j \beta_j, 2s_j \sigma^2) \text{ for } j = 1, \dots, p,$$

where  $\mathbf{s} \geq \mathbf{0}$  is from the knockoff construction (4). Hence, a natural estimate for the sign of  $\beta_j$  is

$$\widehat{\text{sign}}_j = \text{sign} \left( (\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y} \right). \quad (12)$$

With this, the knockoff filter with no adjustment whatsoever controls the directional FDR as well as the FDR. To understand intuitively why this error measure, which in principle is harder to control than FDR, is still bounded by the same method, note that for a nonnegative effect ( $\beta_j \geq 0$ ), the probability of choosing a negative sign, i.e.  $\widehat{\text{sign}}_j = -1$ , is in fact highest when  $\beta_j = 0$ ; this error is less likely if  $\beta_j > 0$  since in that case we would have  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}$  be normally distributed with a positive mean.

**Theorem 1.** *Assume  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\boldsymbol{\beta}, \sigma^2\mathbf{I})$  and fix any desired FDR level  $q$ . With the estimated direction effects (12), knockoff+ controls the directional FDR (2); that is,  $\text{FDR}_{\text{dir}} \leq q$ . If we use knockoff instead, then  $\text{mFDR}_{\text{dir}} \leq q$ , where  $\text{mFDR}_{\text{dir}}$  is the slightly modified version defined as*

$$\text{mFDR}_{\text{dir}} = \mathbb{E} \left[ \frac{\left| \left\{ j \in \widehat{S} : \widehat{\text{sign}}_j \neq \text{sign}(\beta_j) \right\} \right|}{|\widehat{S}| + q^{-1}} \right]. \quad (13)$$

This result is more powerful than Theorems 1 and 2 from [1], which established that knockoff+ controls the FDR at level  $q$ , i.e.  $\text{FDR} \leq q$ , and knockoff controls the modified FDR, i.e. the expected ratio between the number of (unsigned) false discoveries  $|\{j \in \widehat{S} \text{ and } \beta_j = 0\}|$  and  $|\widehat{S}| + q^{-1}$  (this denominator is as in (13)).

Our new Theorem 1 is also more delicate to prove. The reason is that when we work with Type I errors as in the original result, the probability of claiming that  $\beta_j \neq 0$  is calculated under the assumption that  $\beta_j = 0$ . When working with Type S errors, however, there is no such calibration since there is no null, and each feature  $\mathbf{X}_j$  might have a nonzero coefficient  $\beta_j$ , although it may close to zero. In that case, the test statistic  $W_j$  will have a different probability of appearing with a positive or negative sign, and we are no longer dealing with i.i.d. and unbiased signs for the null  $W_j$ 's.

Thus in the proof of Theorem 1, we will see that the result is ultimately a consequence of the following martingale inequality regarding a sequence of Bernoulli variables which have varying probabilities of success:

**Lemma 1.** *Suppose that  $B_1, \dots, B_n$  are independent variables, with  $B_i \sim \text{Bernoulli}(\rho_i)$  for each  $i$ , where  $\min_i \rho_i \geq \rho > 0$ . Let  $J$  be a stopping time in reverse time with respect to the filtration  $\{\mathcal{F}_j\}$ , where*

$$\mathcal{F}_j = \{B_1 + \dots + B_j, B_{j+1}, \dots, B_n\}.$$

Then

$$\mathbb{E} \left[ \frac{1 + J}{1 + B_1 + \dots + B_J} \right] \leq \rho^{-1}.$$

In the simpler setting where  $\rho_1 = \dots = \rho_n$ , this result is proved (in a slightly different form) in [1], with the proof relying heavily on the exchangeability of the  $B_j$ 's (when the  $B_j$ 's are determined by the signs of the null  $W_j$ 's, each has distribution  $\text{Bernoulli}(0.5)$ ). The result stated here is more subtle due to the lack of exchangeability.

To see the connection between Lemma 1 and (directional) FDR control, observe that

$$\begin{aligned} \text{FDP} &= \frac{\#\{j \text{ null} : W_j \geq T_+\}}{1 \vee \#\{j : W_j \geq T_+\}} = \frac{\#\{j \text{ null} : W_j \geq T_+\}}{1 + \#\{j \text{ null} : W_j \leq -T_+\}} \cdot \frac{1 + \#\{j \text{ null} : W_j \leq -T_+\}}{1 \vee \#\{j : W_j \geq T_+\}} \\ &\leq q \cdot \frac{\#\{j \text{ null} : W_j \geq T_+\}}{1 + \#\{j \text{ null} : W_j \leq -T_+\}}, \end{aligned}$$

where the inequality follows from the definition of  $T_+$  (11). Now reorder the indices of the null  $W_j$ 's so that  $|W_{(1)}| \geq |W_{(2)}| \geq \dots$ , where  $|W_{(1)}|$  is the null with the largest magnitude,  $|W_{(2)}|$  the second largest and so on, and let  $B_j = \mathbb{1}_{W_{(j)} < 0}$ . Then we have

$$\frac{\#\{j \text{ null} : W_j \geq T_+\}}{1 + \#\{j \text{ null} : W_j \leq -T_+\}} = \frac{(1 - B_1) + \dots + (1 - B_J)}{1 + B_1 + \dots + B_J} = \frac{1 + J}{1 + B_1 + \dots + B_J} - 1,$$

where  $J$  is the index such that  $|W_{(1)}| \geq \dots \geq |W_{(J)}| \geq T_+ > |W_{(J+1)}| \geq \dots$ ; this last expression is the quantity in Lemma 1. If each  $W_j$ , for a null feature, is equally likely to be positive or negative, then the  $B_j$ 's are i.i.d. Bernoulli(0.5) variables, and we obtain FDR control at level  $q$  by applying Lemma 1 with  $\rho_i = 0.5$ . However, when considering directional FDR control, the  $\beta_j$ 's are not vanishing and the  $W_j$ 's will typically not be symmetric. We refer to Appendix A.2 for details.

## 4 Knockoffs in High Dimensions

In high dimensions, where  $p > n$ , the knockoff construction is no longer possible—in fact, the Gram matrix condition (4) would be possible only if  $\mathbf{s} = \mathbf{0}$ , that is, if  $\tilde{\mathbf{X}}_j = \mathbf{X}_j$  for each feature  $j = 1, \dots, p$ , so that the knockoff procedure would have zero power. In this setting, one straightforward approach would be to use part of the data to reduce the number of features, and a disjoint part of the data to run the knockoff filter. In the next section, we develop this approach, and then find that we can gain substantial power by using a more subtle approach to data splitting.

### 4.1 Feature screening and reusing data

Consider splitting the  $n$  observations into two disjoint groups of size  $n_0$  and  $n_1 = n - n_0$ , used for the purpose of first screening for a smaller set of potentially relevant features, then running a model selection procedure over this reduced list of features, respectively. We denote the two disjoint portions of the data as  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)}) \in \mathbb{R}^{n_0 \times p} \times \mathbb{R}^{n_0}$  and  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)}) \in \mathbb{R}^{n_1 \times p} \times \mathbb{R}^{n_1}$ , and then follow the next two steps:

- **Screening step:** using  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ , we identify a subset  $\hat{S}_0 \subset [p]$  of potentially relevant features, such that  $|\hat{S}_0| < n_1$ .
- **Selection step (splitting):** ignoring any features that were discarded in the screening step, we run the knockoff procedure on the remaining data, that is, on  $(\mathbf{X}_{\hat{S}_0}^{(1)}, \mathbf{y}^{(1)})$ .

This straightforward data splitting approach is a natural extension of the low-dimensional knockoff filter, and it is clear that the approach will control the directional FDR in the final model selection step as long as the screening step correctly captures all the relevant features—those with non-vanishing regression coefficients—a property often referred to as *sure screening* in the literature [6]. (False positives in the screening step, i.e. including too many null features, do not pose a problem).

Of course, there is an inherent loss of power due to the split of the data, since the model selection step uses  $n_1$  rather than  $n$  observations. However, using disjoint data sets for the screening and selection steps is critical, since the distribution of  $\mathbf{y}^{(0)}$  cannot be treated as a Gaussian linear model *after* the screening step has taken place; the screening step is a function of the random variable  $\mathbf{y}^{(0)}$ , and so the following modification of the selection step *would not control the FDR*: ignoring any features that were discarded in the screening step, we run the knockoff procedure on the full data set, i.e. on  $(\mathbf{X}_{\hat{S}_0}, \mathbf{y})$ . The loss of FDR control is not merely theoretical: a null feature  $\mathbf{X}_j$  that is chosen by the screening step is generally more likely to appear as a false positive when running the knockoff filter, leading to a much higher FDR. Surprisingly, though, a simple modification of this procedure is able to retain the FDR control properties of the split-data procedure, while raising power substantially to approach the sensitivity of the full-data procedure:

- **Selection step (with recycling):** we begin by constructing a knockoff matrix on the remaining data  $\tilde{\mathbf{X}}_{\hat{S}_0}^{(1)}$  for  $\mathbf{X}_{\hat{S}_0}^{(1)}$  just as we would in the data splitting version. The difference now is that we concatenate the original design matrix on the first  $n_0$  observations with the knockoff matrix on the next  $n_1$  observations,

$$\tilde{\mathbf{X}}_{\hat{S}_0} = \begin{bmatrix} \mathbf{X}_{\hat{S}_0}^{(0)} \\ \tilde{\mathbf{X}}_{\hat{S}_0}^{(1)} \end{bmatrix}, \quad (14)$$

and run the knockoff filter on the entire data set with  $n$  samples. (Note that on the first split, knockoffs are exact copies.)

The term “recycling” refers to the way that we incorporate the random vector  $\mathbf{y}^{(0)}$ , which was already used in the screening step, for the selection step. After the screening step,  $\mathbf{y}^{(0)}$  has already been observed, and so we need to treat it as a fixed vector (or rather, to condition on its value) in the construction and analysis of the knockoff filter for the selection step.

**Relation to existing work.** We pause here to compare our technique to the data carving methods of Fithian et al. [8]. In that work, as in ours, some part of the data  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  is used to perform an initial screening step, and is then reused for inference along with the remaining data  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$ . However, the mechanism behind reusing the first part of the data is highly different. In Fithian et al. [8]’s work, the first part of the response  $\mathbf{y}^{(0)}$  is reused by leveraging the “remaining randomness” after the screening step:  $\mathbf{y}^{(0)}$  is regarded as a random vector, with distribution given by conditioning on the outcome of the screening step, i.e.  $(\mathbf{y}^{(0)} \mid \hat{S}_0)$ . In contrast, in our “recycling” procedure,  $\mathbf{y}^{(0)}$  can be used in an arbitrary way for the screening step, and so there is no “remaining randomness” in  $\mathbf{y}^{(0)}$ . Instead, we reuse  $\mathbf{y}^{(0)}$  by treating it as a fixed vector;  $\mathbf{y}^{(1)}$  is the only variable treated as random for the purpose of our FDR control results.

More broadly, our method can be considered as similar in flavor to the “screen and clean” methodology of Wasserman and Roeder [27], where an initial screening step (performed via a high-dimensional Lasso), with a tuning parameter chosen by validation, is followed by an inference step on an independent portion of the data, with inference performed via a least-squares regression. This methodology has been applied to genome-wide association studies (GWAS) in [29]. At a high level, our method follows this same overall framework of screening for a low-dimensional submodel, then using new data for low-dimensional inference; however, we will gain power by “recycling” the first part of the data, and more significantly, by using the knockoff filter rather than least-squares for the inference step, which in the low-dimensional setting gives substantial gains in power as it leverages the sparse structure of the true model [1].

## 4.2 Increasing power with signed statistics

Since the knockoff filter with data splitting or with data recycling treats the first portion of the data,  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ , as fixed once the screening step has been performed, we are free to use this data in any way we wish, to try to gather information about the true signals. While the screening step identifies the indices of the variables which are likely to contain signals, we can also use this step to identify probable signs. For example, if the screening step is performed by running the Lasso on  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ , and the  $j$ th feature  $\mathbf{X}_j^{(0)}$  is selected early in this Lasso path, then we can record the sign of the estimated coefficient,  $\text{sign}_j^{(0)}$ ; we can then use this information to look specifically for an effect consistent with this sign in the second phase of our procedure. This will in general increase power, since we are extracting more information from the first part of the data before running the selection procedure on the second part,  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$ .

Without using the sign information, if we were to use the Lasso to produce the statistics  $W_j$  for running the knockoff method, we would begin by computing the Lasso solution  $[\hat{\beta}(\lambda) \tilde{\beta}(\lambda)]$  to either

$$\min_{\mathbf{b} \in \mathbb{R}^{2|\hat{S}_0|}} \frac{1}{2} \|\mathbf{y}^{(1)} - [\mathbf{X}_{\hat{S}_0}^{(1)} \tilde{\mathbf{X}}_{\hat{S}_0}^{(1)}] \mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1$$

for data splitting, or

$$\min_{\mathbf{b} \in \mathbb{R}^{2|\hat{S}_0|}} \frac{1}{2} \|\mathbf{y} - [\mathbf{X}_{\hat{S}_0} \tilde{\mathbf{X}}_{\hat{S}_0}] \mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1$$

for data recycling. Instead, to make use of the sign information gathered at the screening phase, we can consider a sign-restricted Lasso for forming our statistics  $W_j$  for testing each feature  $\mathbf{X}_j$ : in the data splitting version we would be interested in the solution to

$$\begin{aligned} \min_{\mathbf{b} \in \mathbb{R}^{2|\widehat{S}_0|}} \quad & \frac{1}{2} \|\mathbf{y}^{(1)} - [\mathbf{X}_{\widehat{S}_0}^{(1)} \widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}] \mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1 \\ \text{s.t.} \quad & b_j \cdot \text{sign}_j^{(0)} \geq 0 \\ & b_{j+|\widehat{S}_0|} \cdot \text{sign}_j^{(0)} \geq 0 \end{aligned}$$

and similarly for the recycling version. In other words, we are running the same Lasso optimization, but with the added restriction that we will only select the  $j$ th feature or  $j$ th knockoff feature if its estimated effect direction agrees with the sign information gathered at the screening stage.

Why should we expect these signed Lasso statistics to give higher power? Intuitively, we think of the screening step as choosing from  $p$  possible hypotheses—hypothesis  $H_j$  is described by the question, “Does  $\mathbf{X}_j$  appear in the true model?”—to identify those that are most likely to contain a signal. However, we can instead frame this step as considering twice as many hypotheses, the  $2p$  hypotheses corresponding to the signed versions of this question: hypothesis  $H_j^+$  is the question, “Does  $\mathbf{X}_j$  appear in the true model with a positive effect?”, and hypothesis  $H_j^-$  is the question “Does  $\mathbf{X}_j$  appear in the true model with a negative effect?”. With this in mind, if the screening step fits a model to the first part of the data  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ , and this fitted model includes the  $j$ th feature with a positive coefficient, then this indicates that hypothesis  $H_j^+$  is more likely to contain a signal. Therefore, it makes sense that in our selection step we should focus our attention on hypothesis  $H_j^+$ . Of course, it is possible that the true effect is in fact negative, but since this is less likely, we would generally be increasing the noise if we give equal attention to hypotheses  $H_j^+$  and  $H_j^-$ .

### 4.3 Sure screening and directional FDR control

In order to demonstrate the correctness of the selection step with recycling, assume that the screening step is highly likely to find all true signals—that is,  $\widehat{S}_0 \supseteq \text{support}(\boldsymbol{\beta})$  with high probability. Note that we do not assume that the screening step *exactly* selects the true support—while this type of sparsistency result holds for the Lasso in the asymptotic setting (see e.g. [32]), in practice, even with ideal simulated data, it is generally the case that we cannot perfectly separate true signals from false positives using the limited data available, unless the signal is extremely strong and extremely sparse [23]. Instead, this assumption merely requires that there is some sufficiently liberal screening procedure that is likely to capture all the true signals, along with many false positives. In fact, we do not prohibit the possibility that the vast majority of features chosen by the screening step are false positives; we only need to ensure that the number of screened features  $|\widehat{S}_0|$  is small enough that the knockoff filter can then be applied for the selection step.

From a theoretical perspective, we would like to remark that many existing results guarantee that, under some conditions on the design and the strength of the signal, applying the Lasso will nearly always recover a set  $\widehat{S}_0$  that contains the true support without growing too large, see e.g. Zhang and Huang [30, Theorems 1 and 2]. In fact, in extremely high dimensions where screening with the Lasso may not be practical for computational reasons, the Sure Independence Screening result of Fan and Lv [6] guarantees that we can find a sparse superset of  $\text{support}(\boldsymbol{\beta})$  simply by screening for the largest inner products  $\mathbf{X}_j^\top \mathbf{y}$ .

Suppose we fix some chosen method for the screening step, which is constrained only in that it must be a function of the first portion of the data,  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ . Define the sure screening event as

$$\mathcal{E} = \{\widehat{S}_0 \supseteq \text{support}(\boldsymbol{\beta}) \text{ and } |\widehat{S}_0| \leq n_1/2\},$$

and note that  $\mathbb{1}_{\mathcal{E}}$  is a function of  $\mathbf{y}^{(0)}$  when we treat  $\mathbf{X}$  and  $\boldsymbol{\beta}$  as fixed. On this event, directional FDR control of the selection step holds.

**Theorem 2.** *Suppose  $\mathbf{y} \sim \mathcal{N}(\mathbf{X}\boldsymbol{\beta}, \sigma^2\mathbf{I})$ . Then the knockoff-with-data-recycling procedure, with estimated signs  $\widehat{\text{sign}}_j$  as in (12), controls the modified directional FDR at the level*

$$\mathbb{E}[\text{mFDR}_{\text{dir}} \mid \mathcal{E}] \leq q,$$

while if knockoff+ is used in place of the knockoff, then the directional FDR is controlled as

$$\mathbb{E} [\text{FDR}_{\text{dir}} \mid \mathcal{E}] \leq q .$$

In particular, if  $\mathcal{E}$  occurs with probability near 1, then the various forms of the directional FDR are controlled even without conditioning on  $\mathcal{E}$ , by reformulating the results as  $\text{FDR} \leq \text{FDR}_{\text{dir}} \leq q + \mathbb{P}\{\mathcal{E}^c\}$  in the case of knockoff+, and similarly for knockoff.

#### 4.4 Biases

If the screening step misses variables from the model, a bias is introduced which creates a fundamental difficulty. To discuss this, recall that knockoffs are constructed to guarantee the crucial pairwise exchangeability for the nulls (6). Among other things, we have seen that exchangeability has the consequence that null variables are equally likely to be selected by the Lasso as their knockoff companions. When nonzero effects have not been screened, this may no longer be the case. Concretely, imagine that  $\mathbf{X}_k$  has a nonzero effect but was not identified in the screening step. Then since the knockoff construction used only the screened set  $\widehat{S}_0$ , we cannot guarantee that  $\mathbf{X}_j^\top \mathbf{X}_k = \widetilde{\mathbf{X}}_j^\top \mathbf{X}_k$  for  $j \in \widehat{S}_0$ , which in turn may lead to  $\mathbf{X}_j^\top \mathbf{X} \boldsymbol{\beta} \neq \widetilde{\mathbf{X}}_j^\top \mathbf{X} \boldsymbol{\beta}$  and, therefore,

$$\mathbf{X}_j^\top \mathbf{y} \stackrel{d}{\neq} \widetilde{\mathbf{X}}_j^\top \mathbf{y}$$

even when  $j$  is a null feature, i.e.  $\beta_j = 0$ . For example, if  $\mathbf{X}_j$  were strongly correlated with  $\mathbf{X}_k$ , then we could easily imagine that  $\mathbf{X}_j$  would be more likely to enter the Lasso path than its knockoff  $\widetilde{\mathbf{X}}_j$ . In general, and in contrast to the lower dimensional setting, the bias implies that when we trace the Lasso path and count the number of knockoffs that have appeared thus far, we cannot be sure that this number is a good (over)estimate of the number of nulls. As explained before, however, it may be desirable to select  $\mathbf{X}_j$  in this case since it is a proxy for  $\mathbf{X}_k$ . We next reframe this issue in terms of the partial regression coefficients.

#### 4.5 Main result: directional FDR control in the reduced model

Earlier we argued that we really ought to regard the screened model as an approximate model, and perform inference on the coefficients in this reduced model, a point of view in line with much discussed recent literature [17, 5, 10, 8]. Thus we are interested in the partial regression coefficients

$$\boldsymbol{\beta}^{\text{partial}} = (\mathbf{X}_{\widehat{S}_0}^\top \mathbf{X}_{\widehat{S}_0})^{-1} \mathbf{X}_{\widehat{S}_0}^\top \mathbf{X} \boldsymbol{\beta}$$

that are the coefficients obtained when  $\mathbf{X} \boldsymbol{\beta}$  is regressed onto the screened variables. Since we no longer treat  $\mathbf{y}^{(0)}$  as random after the screening step, we will instead work with the slightly different definition

$$\boldsymbol{\beta}^{\text{partial}} = (\mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{X}_{\widehat{S}_0}^{(1)})^{-1} \mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{X}^{(1)} \boldsymbol{\beta}. \quad (15)$$

In passing, observe that if we have perfect screening, then the coefficients are the same as those in the full model in the sense that  $\beta_j^{\text{partial}} = \beta_j$  for all  $j \in \widehat{S}_0$ , so what we are discussing is essentially an extension of the results from Section 4.3. The main results from this section and this paper assure us that it is possible to adapt the knockoff method to select variables from the screened model and tell their direction of effect with confidence: we give two results, one for arbitrary designs and one for random designs.

Consider first an arbitrary design  $\mathbf{X}$ , an arbitrary coefficient vector  $\boldsymbol{\beta}$ , and an arbitrary screened set  $\widehat{S}_0$ , but assume knowledge of the noise level  $\sigma$  as is common in the literature. To be sure, all the high-dimensional non-asymptotic inference results we know about [17, 5, 19, 11] either require knowledge of  $\sigma$ , or require a setting where the screening step would select a superset of the true model with high probability [7] as in Section 4.3. Likewise, it is absolutely unclear to us how our knockoff filter would proceed without this piece of information. Having said this,  $\sigma$  may be known in many situations where measurement error can be estimated (e.g. a physical measurement).

With  $\sigma$  known, we can essentially map the problem back into another where sure screening occurs. To see why, note that letting  $\mathcal{P}_{\mathbf{X}_{\hat{S}_0}^{(1)}}$  be the orthogonal projection onto the subspace spanned by the screened variables, we have

$$\mathcal{P}_{\mathbf{X}_{\hat{S}_0}^{(1)}}(\mathbf{y}^{(1)}) \sim \mathcal{N}\left(\mathbf{X}_{\hat{S}_0}^{(1)}\boldsymbol{\beta}^{\text{partial}}, \sigma^2\mathcal{P}_{\mathbf{X}_{\hat{S}_0}^{(1)}}\right).$$

Hence, letting  $\mathbf{g} \sim \mathcal{N}(0, \sigma^2\mathbf{I}_{n_1})$  be drawn independently from the data, we have

$$\mathbf{y}_{\#}^{(1)} \triangleq \mathcal{P}_{\mathbf{X}_{\hat{S}_0}^{(1)}}(\mathbf{y}^{(1)}) + \mathcal{P}_{\mathbf{X}_{\hat{S}_0}^{(1)}}^\perp(\mathbf{g}) \sim \mathcal{N}\left(\mathbf{X}_{\hat{S}_0}^{(1)}\boldsymbol{\beta}^{\text{partial}}, \sigma^2\mathbf{I}_{n_1}\right), \quad (16)$$

which is analogous to the setting of Theorem 2, only with  $\boldsymbol{\beta}^{\text{partial}}$  in place of  $\boldsymbol{\beta}$ .

**Theorem 3** (High-dimensional inference with  $\sigma$  known). *After the screening step, replace  $\mathbf{y}^{(1)}$  (the unused part of the response) with the vector  $\mathbf{y}_{\#}^{(1)}$  from (16). Then the knockoff-with-data-recycling procedure controls the modified directional FDR at the level*

$$\text{mFDR}_{\text{dir}} \leq q,$$

while if knockoff+ is used in place of knockoff, then the directional FDR is controlled as

$$\text{FDR}_{\text{dir}} \leq q;$$

here the estimated signs  $\widehat{\text{sign}}_j$  are defined as in (12), and a false discovery is any  $j \in \widehat{S}$  such that  $\widehat{\text{sign}}_j \neq \text{sign}(\beta_j^{\text{partial}})$ .

This result may also be of interest in a low-dimensional setting: when  $n > p$ , we are able to perform the knockoff procedure without a screening step (as in [1]), but may wish to first decrease the number of candidate features with a screening step in order to gain more power by reducing correlations between a feature  $\mathbf{X}_j$  and its knockoff  $\tilde{\mathbf{X}}_j$ . In this type of setting,  $\sigma$  can easily be estimated with high accuracy by calculating the residual sum of squares from the full model.

Our second result takes another perspective on the behavior of the knockoff method after screening, by considering a *random* model for the covariates  $\mathbf{X}$ . If we assume that the features are generated from a Gaussian distribution with arbitrary and unknown correlations, then the theorem below provides directional FDR control without knowing (or estimating)  $\sigma$ . Here, the knockoff procedure works with the true response data  $\mathbf{y}$  rather than the altered vector (16).

**Theorem 4.** *Assume that the rows of  $\mathbf{X}$  are i.i.d. draws from a  $\mathcal{N}(0, \boldsymbol{\Psi})$  distribution, where  $\boldsymbol{\Psi} \in \mathbb{R}^{p \times p}$  is an arbitrary and unknown matrix. Define the expected partial regression coefficients as*

$$\bar{\boldsymbol{\beta}}^{\text{partial}} = \mathbb{E}\left[\boldsymbol{\beta}^{\text{partial}} \mid \mathbf{X}_{\hat{S}_0}^{(1)}, \mathbf{X}^{(0)}, \mathbf{y}^{(0)}\right] = (\mathbf{X}_{\hat{S}_0}^{(1)\top} \mathbf{X}_{\hat{S}_0}^{(1)})^{-1} \mathbf{X}_{\hat{S}_0}^{(1)\top} \mathbb{E}\left[\mathbf{X}^{(1)} \mid \mathbf{X}_{\hat{S}_0}^{(1)}\right] \boldsymbol{\beta},$$

where the expectation is taken by treating the screened features as fixed while the other features are considered random (on the second part of the data set). Then the knockoff-with-recycling procedure controls the modified directional FDR at the level

$$\text{mFDR}_{\text{dir}} \leq q,$$

while if knockoff+ is used, then the directional FDR is controlled as

$$\text{FDR}_{\text{dir}} \leq q;$$

here the estimated signs  $\widehat{\text{sign}}_j$  are defined as in (12), and a false discovery is any  $j \in \widehat{S}$  such that  $\widehat{\text{sign}}_j \neq \text{sign}(\bar{\beta}_j^{\text{partial}})$ .

We emphasize that we do not assume knowledge of the parameters of the Gaussian distribution of  $\mathbf{X}$ , and do not estimate these parameters in the method; in fact the Gaussian assumption is used only to show that we can model the response  $\mathbf{y}$  as

$$\mathbf{y} = \mathbf{X}_{\hat{S}_0} \boldsymbol{\beta}_{\hat{S}_0} + \mathbf{X}_{\hat{S}_0^c} \boldsymbol{\beta}_{\hat{S}_0^c} + \boldsymbol{\epsilon} = \mathbf{X}_{\hat{S}_0} \bar{\boldsymbol{\beta}}_{\hat{S}_0}^{\text{partial}} + \boldsymbol{\epsilon}',$$

where  $\epsilon' = \epsilon + \mathbf{X}_{\widehat{S}_0^c} \boldsymbol{\beta}_{\widehat{S}_0^c} - \mathbb{E} \left[ \mathbf{X}_{\widehat{S}_0^c} \boldsymbol{\beta}_{\widehat{S}_0^c} \mid \mathbf{X}_{\widehat{S}_0} \right]$  is i.i.d. Gaussian noise (with a larger variance than the original noise  $\epsilon$ , due to the noise added from the true signals missed by the screening step). This is where the fact that knockoffs do not need the value of the noise level (in low dimensions) is immensely useful: the knockoff method will provide valid inference no matter the value of the ‘new noise level’.

## 5 Simulations

We now examine the performance of our method on a simulated high-dimensional data set, and compare to several other techniques for inference in low-dimensional and high-dimensional regression.

### 5.1 Data

The size of our simulated data set is given by dimensions  $n = 2000$  and  $p = 2500$ . We generate a true vector of coefficients  $\boldsymbol{\beta} \in \mathbb{R}^p$  by choosing  $k = 30$  locations at random for the true signals, with coefficients  $\beta_j$  chosen randomly from  $\{\pm 4.5\}$ , with the other  $p - k$  entries set to zero. We then generate a design matrix  $\mathbf{X} \in \mathbb{R}^{n \times p}$ , where the rows of  $\mathbf{X}$  are i.i.d. draws from a  $\mathcal{N}(0, \boldsymbol{\Sigma})$  distribution, and the covariance  $\Sigma_{ij} = \rho^{|i-j|}$  has a tapered structure. For each  $\rho \in \{0, 0.25, 0.5, 0.75\}$ , we generate a single matrix  $\mathbf{X}$  and then generate 100 i.i.d. draws of the error  $\epsilon \sim \mathcal{N}(0, \mathbf{I}_n)$ , and set  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \epsilon$ . We use the first  $n_0 = 1000$  observations for the screening step, and the remaining  $n_1 = 1000$  observations for the inference step. The screening step is carried out by running the Lasso, and stopping when  $k_{\max} = 500$  features have entered the Lasso path; these  $k_{\max}$  variables determine the subset  $\widehat{S}_0$  of features for the screening step. All procedures are run with target FDR level  $q = 0.2$ .

### 5.2 Methods

Our simulated experiments compare the following methods:

- Knockoff: with data splitting or data recycling.
- Benjamini-Hochberg (BH) procedure applied to the least-squares regression coefficients after screening.
- Methods based on the exact post-selection inference work of Lee et al. [17]: Truncated-Gaussian method, convolution method, one-step method. The one-step method does not rely on an initial screening step.

For each of these methods, we implement two versions, one which uses information about the estimated signs of the possible nonzero coefficients (the ‘signed’ version), and one which does not. We note that, aside from knockoffs, all other methods require knowledge of the noise level  $\sigma$  in order to run the method. This is discussed more when we present our results.

Details regarding these various methods are given below; we first report our results.

### 5.3 Results

For each correlation setting and for each method tested, we compute the following measures of performance (averaged over 100 iterations):

- False discovery proportion (FDP) relative to the true full model (i.e. the underlying truth is  $\text{support}(\boldsymbol{\beta})$ );
- Directional FDP relative to the true full model (i.e. counting sign errors as well as Type I errors);
- Directional FDP relative to the screened model, that is, the directional FDP for the coefficients in the reduced model,  $\boldsymbol{\beta}^{\text{partial}} = (\mathbf{X}_{\widehat{S}_0}^\top \mathbf{X}_{\widehat{S}_0})^{-1} \mathbf{X}_{\widehat{S}_0}^\top \mathbf{X} \boldsymbol{\beta}$ .



	FDP	dir. FDP	dir. FDP (scr. model)	Power	Power (rel. to screening)
Knockoff (data split)	0.1019	0.1019	0.0375	0.3233	0.3483
Knockoff (data split, signed)	0.0830	0.0830	0.0264	0.3737	0.4032
Knockoff (data recy.)	0.0681	0.0681	0.0261	0.4760	0.5145
Knockoff (data recy., signed)	0.0681	0.0681	0.0261	0.4760	0.5145
Benjamini-Hochberg	0.2219	0.2219	0.0849	0.2623	0.2833
Benjamini-Hochberg (signed)	0.2068	0.2068	0.0895	0.3673	0.3976
Lee et al (Trunc.-Gaus.)	0.0188	0.0188	0.0091	0.0173	0.0186
Lee et al (Trunc.-Gaus., signed)	0.0281	0.0281	0.0129	0.0127	0.0134
Lee et al (convolution)	0.2296	0.2296	0.1264	0.2677	0.2895
Lee et al (convolution, signed)	0.2081	0.2081	0.0880	0.3697	0.3998
Lee et al (one-step)	0.2169	0.2169	—	0.3060	—
Lee et al (one-step, signed)	0.1765	0.1765	—	0.3943	—

**Table 1:** Results from the simulated data experiment with  $\rho = 0$ . (Target FDR level is  $q = 20\%$ .)

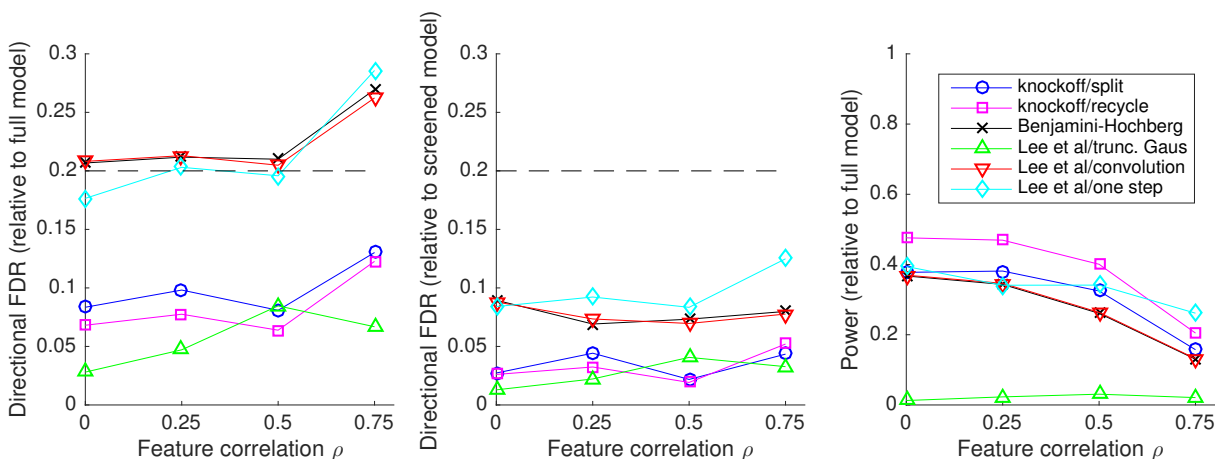
- Power relative to the true full model: the proportion of the true support,  $\text{support}(\beta)$ , which is selected by the method;
- Power relative to the screened set: the proportion of the screened part of the true support, i.e.  $\text{support}(\beta) \cap \widehat{S}_0$ , which is selected by the method.

For the one-step version of [17]’s method, since there is no separate screening step, we omit the directional FDP and power relative to the screened model.

Results for all methods, under the setting  $\rho = 0$  (i.e. the features are drawn independently), are given in Table 1. We see that the knockoff with recycling methods are the most powerful among all methods considered. All methods are successful at controlling the FDR near or below the target level of 20% (with a few methods slightly above; we comment more on this below). Among all methods, knockoff with recycling shows the highest power by a substantial margin, and at the same time has lower FDR than all the other methods with the exception of the truncated-Gaussian version of Lee et al. [17]’s method which has extremely low power; we explain the reason for this later when details for implementing the method are given.

Next, to see the effect of correlation, we plot performance against  $\rho$ . To reduce clutter in the plots we include only the signed versions of each method, as we know the unsigned versions to be less powerful. We display the directional FDP for the full model and the screened models, and the power relative to the full model (note that the one-step version of Lee et al. [17]’s method does not begin with a screening step, and so this method is omitted from the screened FDR plot).

The knockoff with recycling method has superior power across all values of  $\rho$ , followed by the knockoff with data splitting method, except at  $\rho = 0.75$  where the one-step [17] method has slightly higher power (but loses FDR control). All methods are able to (approximately) control the various measures of FDR at the target level  $q = 20\%$  for  $\rho = 0, 0.25, 0.5$ , but the non-knockoff methods lose FDR control at  $\rho = 0.75$ . The directional FDP within the reduced (screened) model is in fact quite low for all methods; this is to be expected, since a sign error is easiest to make for a coefficient whose true value is zero; because partial model coefficients  $\beta_j^{\text{partial}}$  are nonzero in general, sign errors become more unlikely and all procedures are conservative. As before, the knockoff methods simultaneously show higher power and lower FDR than competing methods. Note that for large correlation ( $\rho = 0.75$ ) we observe fairly low power for all methods; in part, this may be due to selecting features  $\mathbf{X}_j$  which are highly correlated to one of the true effects, rather than the effect itself, but mainly it arises from the difficulty of distinguishing between similar features which leads to a low number of selections.



**Figure 1:** Results from the simulated data experiment, plotted against feature correlation  $\rho$ .

**The noise level  $\sigma$**  In practice,  $\sigma$  might be estimated by using the set of features  $\widehat{S}_0$  selected in the screening step, and then projecting the independent second part of the response  $\mathbf{y}^{(1)}$  off of the corresponding subspace:

$$\sigma^2 \approx \widehat{\sigma}^2 = \frac{\|\mathcal{P}_{\mathbf{X}_{\widehat{S}_0}^{(1)}}^\perp(\mathbf{y}^{(1)})\|_2^2}{n_1 - \text{rank}(\mathbf{X}_{\widehat{S}_0}^{(1)})}.$$

This estimate will be highly accurate in scenarios where the set  $\widehat{S}_0$  contains (nearly) all of the true signals and  $n_1$  is substantially larger than  $|\widehat{S}_0|$ . The simulation settings chosen here result in high power<sup>4</sup> (typically  $> 90\%$ ) in this screening step, so that estimating  $\sigma$  would typically be accurate in this regime; in a more low-power setting, estimating  $\sigma$  could be problematic.

In our experiments, we observe that some of these methods, which use the true value of  $\sigma$ , actually result in an FDR level that is slightly higher than the target level  $q = 20\%$ , even at  $\rho = 0$ . The reason is that in the reduced model, there is a source of extra variation caused by the missed variables so that the real noise level is, in fact, higher than that in the full model. If we were to repeat this experiment with lower signal strength (not shown here), so that the accuracy of the screening step is reduced, this problem becomes more noticeable with more inflation of the FDR; note that the knockoff methods are not sensitive to this issue as there is no need to estimate  $\sigma$ .

## 5.4 Implementation

We now describe the details for implementing all of the methods described above.

### 5.4.1 Knockoff variants

We test several variants of the knockoff filter and for each, we split the data, using  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  for the screening step and  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$  for inference, with  $n_0 = 1000$  observations used for screening and  $n_1 = n - n_0 = 1000$  used for inference. We compare the performance of data splitting versus data recycling, as described in Section 4.1.<sup>5</sup> Furthermore we compare two different constructions for the statistics  $W_j$ , the Lasso and the sign-constrained Lasso as in Section 4.2. This leads to a total of four versions of the knockoff procedure. In practice, we observed that the knockoff with data recycling actually gave identical performance with both the unsigned or signed version; this is probably because recycling the data  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  from the screening step preserves the sign information,  $\text{sign}_j^{(0)}$ , implicitly. For each version, the knockoff matrix is calculated using the equivariant construction from [1].

<sup>4</sup>Here, high power means a high percentage of true signals picked up in the screened set.

<sup>5</sup>Note that we do not assume that  $\sigma^2$  is known, and do not use the  $\mathbf{y}_\#^{(1)}$  construction of Theorem 3.

### 5.4.2 Methods based on the Benjamini-Hochberg procedure

We next consider using the Benjamini-Hochberg procedure to correct for multiple comparisons on a low-dimensional multiple linear regression. After performing the screening step, we use the second part of the data  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$  to run a least squares regression,

$$\widehat{\boldsymbol{\beta}}_{\widehat{S}_0} = (\mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{X}_{\widehat{S}_0}^{(1)})^{-1} \mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{y}^{(1)},$$

and compute (dependent) p-values for each feature. If we assume that the screening step captures all true signals, then it would be the case that

$$\mathbf{y}^{(1)} \sim \mathcal{N}(\mathbf{X}_{\widehat{S}_0}^{(1)} \boldsymbol{\beta}_{\widehat{S}_0}, \sigma^2 \mathbf{I}_{n_1}) \quad \Rightarrow \quad \widehat{\boldsymbol{\beta}}_{\widehat{S}_0} \sim \mathcal{N}(\boldsymbol{\beta}_{\widehat{S}_0}, \sigma^2 (\mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{X}_{\widehat{S}_0}^{(1)})^{-1}),$$

and we can therefore compute p-values for the  $\beta_j$ 's via the standardized z-scores

$$\frac{\widehat{\beta}_j}{\sigma \sqrt{((\mathbf{X}_{\widehat{S}_0}^{(1)\top} \mathbf{X}_{\widehat{S}_0}^{(1)})^{-1})_{jj}}}.$$

If the screening step misses some true signals (as is generally the case), we nonetheless hope that the resulting p-values are approximately valid since only a small amount of signal would typically be missed. Note that this procedure uses the known value of  $\sigma$ .

We consider two versions of this method: an “unsigned” version, where these z-scores are converted into two-sided p-values to test whether  $\beta_j = 0$ ; and, a “signed” version with a one-sided p-value, where the signs from the screening step,  $\text{sign}_j^{(0)}$  for  $j \in \widehat{S}_0$ , are used to determine which direction to test. As for the knockoff, we expect the signed version to give greater power; in this case, by moving from two-sided to one-sided p-values, true effects will typically have their p-values reduced by a factor of two, allowing for more discoveries by the BH procedure.

### 5.4.3 Methods based on techniques of Lee et al. [17]

Next, we examine the post-selection inference techniques of [17] for the inference step. We begin as before, using the first part of the data  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  to screen for a set of candidate features  $\widehat{S}_0$ , with estimated effect signs  $\text{sign}_j^{(0)}$  for  $j \in \widehat{S}_0$ . The screening step is carried out with the Lasso, with some tuning parameter  $\lambda$ . Although  $\lambda$  is in fact data-dependent (it is chosen as the point along the Lasso path that produces the desired number of selected features), we proceed as though it was chosen independently of the data. As in the work of [17], the event that the screened set and signs are given by  $\widehat{S}_0$  and  $\text{sign}^{(0)}$  can be represented as a set of affine constraints,

$$\mathbf{A} \mathbf{y}^{(0)} \geq \mathbf{b},$$

where the inequality holds elementwise, and the matrix  $\mathbf{A}$  and the vector  $\mathbf{b}$  depend implicitly on  $\mathbf{X}^{(0)}$ , on  $\widehat{S}_0$ , and on  $\text{sign}^{(0)}$ .

**Truncated-Gaussian method** Our first approach is to use the methods of [17] directly. Fixing a single  $j \in \widehat{S}_0$  and defining

$$\boldsymbol{\eta} = \mathcal{P}_{\mathbf{X}_{\widehat{S}_0 \setminus j}}^{\perp}(\mathbf{X}_j),$$

their work shows that  $\boldsymbol{\eta}^{\top} \mathbf{y}$  is distributed as a truncated Gaussian, with (pre-truncation) mean  $\boldsymbol{\eta}^{\top} \mathbf{X} \boldsymbol{\beta}$  and variance  $\sigma^2 \|\boldsymbol{\eta}\|_2^2$ , truncated to an interval  $[c, d]$  whose endpoints are determined by the affine constraints  $\mathbf{A} \cdot \mathbf{y}^{(0)} \geq \mathbf{b}$  and by conditioning on  $\mathcal{P}_{\boldsymbol{\eta}}^{\perp}(\mathbf{y})$ . We can write this as

$$\boldsymbol{\eta}^{\top} \mathbf{y} \sim \mathcal{TN}(\boldsymbol{\eta}^{\top} \mathbf{X} \boldsymbol{\beta}, \sigma^2 \|\boldsymbol{\eta}\|_2^2; c, d).$$

Then, noting that  $\boldsymbol{\eta}^{\top} \mathbf{X} \boldsymbol{\beta}$  is nonzero if and only if  $\mathbf{X}_j$  has a nonzero coefficient in the reduced model (i.e. regression onto  $\mathbf{X}_{\widehat{S}_0}$ ), we compute a p-value, using either a two-sided test, or a one-sided test whose direction is determined by the estimated sign,  $\text{sign}_j^{(0)}$ . This is repeated for each  $j \in \widehat{S}_0$ . Then the BH procedure is run on the resulting p-values.

**Convolution method** The truncated-Gaussian method described above gives valid post-selection p-values, but empirically can have quite low power, as was shown in our results above. The reason is that by conditioning on  $\mathcal{P}_{\boldsymbol{\eta}}^{\perp}(\mathbf{y})$ , much of the randomness in  $\mathbf{y}$  is lost—in particular, even though  $\mathbf{y}^{(1)}$  has not been used at all in the selection step, we have conditioned on much of the information in  $\mathbf{y}^{(1)}$ . As an alternative, we can consider separating the roles of  $\mathbf{y}^{(0)}$  and  $\mathbf{y}^{(1)}$  in the following way. First, define

$$\boldsymbol{\eta}^{(0)} = \mathcal{P}_{\mathbf{X}_{\mathcal{S}_0 \setminus j}^{(0)}}^{\perp} \left( \mathbf{X}_j^{(0)} \right) \text{ and } \boldsymbol{\eta}^{(1)} = \mathcal{P}_{\mathbf{X}_{\mathcal{S}_0 \setminus j}^{(1)}}^{\perp} \left( \mathbf{X}_j^{(1)} \right).$$

We will condition on the event  $\mathbf{A} \cdot \mathbf{y}^{(0)} \geq \mathbf{b}$ , and on the value of  $\mathcal{P}_{\boldsymbol{\eta}^{(0)}}^{\perp}(\mathbf{y}^{(0)})$ . Then, following the work of [17], after conditioning,

$$\boldsymbol{\eta}^{(0)\top} \mathbf{y}^{(0)} \sim \mathcal{TN}(\boldsymbol{\eta}^{(0)\top} \mathbf{X}^{(0)} \boldsymbol{\beta}, \sigma^2 \|\boldsymbol{\eta}^{(0)}\|_2^2; c, d),$$

where  $[c, d]$  is the truncation interval calculated from the conditioning step. Furthermore,

$$\boldsymbol{\eta}^{(1)\top} \mathbf{y}^{(1)} \sim \mathcal{N}(\boldsymbol{\eta}^{(1)\top} \mathbf{X}^{(1)} \boldsymbol{\beta}, \sigma^2 \|\boldsymbol{\eta}^{(1)}\|_2^2),$$

with no truncation since no information about  $\mathbf{y}^{(1)}$  has been observed so far. Finally,  $\boldsymbol{\eta}^{(0)\top} \mathbf{y}^{(0)}$  and  $\boldsymbol{\eta}^{(1)\top} \mathbf{y}^{(1)}$  are independent. Therefore,

$$\boldsymbol{\eta}^{(0)\top} \mathbf{y}^{(0)} + \boldsymbol{\eta}^{(1)\top} \mathbf{y}^{(1)} \sim \mathcal{TN}(\boldsymbol{\eta}^{(0)\top} \mathbf{X}^{(0)} \boldsymbol{\beta}, \sigma^2 \|\boldsymbol{\eta}^{(0)}\|_2^2; c, d) * \mathcal{N}(\boldsymbol{\eta}^{(1)\top} \mathbf{X}^{(1)} \boldsymbol{\beta}, \sigma^2 \|\boldsymbol{\eta}^{(1)}\|_2^2),$$

where the “\*” denotes a convolution. Now, if the coefficient on feature  $j$  (in the reduced model) is zero, then we would expect that  $\boldsymbol{\eta}^{(0)\top} \mathbf{X}^{(0)} \boldsymbol{\beta}$  and  $\boldsymbol{\eta}^{(1)\top} \mathbf{X}^{(1)} \boldsymbol{\beta}$  are both approximately zero, at least in the setting where the  $n$  data points (both the  $\mathbf{X}$  and  $\mathbf{y}$  values) are i.i.d. draws from some population. So to test this hypothesis, we can produce an approximately valid p-value by testing whether  $\boldsymbol{\eta}^{(0)\top} \mathbf{X}^{(0)} \boldsymbol{\beta} = \boldsymbol{\eta}^{(1)\top} \mathbf{X}^{(1)} \boldsymbol{\beta} = 0$ , with either a two-sided test, or a one-sided test using the value of  $\text{sign}_j^{(0)}$  produced by the screening step. In order to generate this p-value, we can analytically compute the cumulative distribution function of this convolution, which is not too difficult since we are in a univariate setting for each  $j$ . Then the BH procedure is run on the resulting p-values.

We remark that the empirical FDR and power of this convolution method are very similar to those obtained by using the BH procedure on the least-squares regression coefficients obtained only from the second part of the data,  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$ . This is for a similar reason as the low power of the truncated-Gaussian version of this method: the screening step involves a high number of variables entering the Lasso path, which leads to a high number of affine constraints on  $\mathbf{y}^{(0)}$  (or, in the truncated-Gaussian version, on  $\mathbf{y}$ ). Therefore, there is very little information in the remaining randomness of  $\mathbf{y}^{(0)}$ ; most of the information used for constructing the convolution p-values comes from the randomness of the untouched portion of the response,  $\mathbf{y}^{(1)}$ . In practice, then, the resulting p-values are not substantially different from those obtained by simply taking a least-squares model for  $\mathbf{y}^{(1)}$  on its own without incorporating  $\mathbf{y}^{(0)}$ , as is done by the BH procedure.

**One-step method** Finally, we consider applying the results of [17] as originally proposed, i.e. without splitting into a screening step and an inference step. For any fixed  $\lambda$ , we can run the Lasso on  $(\mathbf{X}, \mathbf{y})$  with that value of  $\lambda$  which selects a set of features  $\hat{\mathcal{S}}_{\text{Lasso}}$ , and then use [17]’s polytope method for producing a (two-sided or one-sided) p-value for each  $j \in \hat{\mathcal{S}}_{\text{Lasso}}$ . Then as the final step, we run the BH procedure on these p-values. However, one difficulty here is that we do not know ahead of time a good value of  $\lambda$  to use. To ensure a fair comparison with this method, note that we cannot assume prior knowledge of the true sparsity level; given the dimensions of the problem we assume that a sparsity bound of 100 is reasonable, and will run the Lasso until 100 features are selected. We then proceed as though the value of  $\lambda$  were chosen independently of the data. We compute a two-sided (unsigned) or one-sided (signed) p-value, and run the BH procedure on the resulting p-values.

## 6 Real Data Experiments

We next implement our high-dimensional knockoff method on a genome wide association study (GWAS) data set. The data comes from the Northern Finland Birth Cohort 1966 (NFBC1966) [21, 15], made available through the

dbGaP database (accession number phs000276.v2.p1). Here, 5402 SNP arrays from subjects born in Northern Finland in 1966 are recorded, as well as a number of phenotype variables measured when the subjects were 31 years old.

## 6.1 Methods

**Data pre-processing.** Before applying knockoffs, the data needs to be prepared and our early pre-processing follows Sabatti et al. [21] and Janson et al. [14]. Genotype features from the original data set were removed if they met any of the following conditions:

- Not a SNP (some were, e.g., copy number variations)
- Greater than 5% of values were missing
- All nonmissing values belonged to the same nucleotide
- SNP location could not be aligned to the genome
- A  $\chi^2$  test rejected Hardy-Weinberg equilibrium at the 0.01% level
- On chromosome 23 (sex chromosome)

The remaining missing values were assumed to take the population frequency of the major allele. In the end, we have a total of  $p = 328,934$  SNP features.

For each phenotype, we performed further processing on the response variables. Triglycerides were log-transformed. C-reactive protein (CRP) was also log-transformed after adding 0.002 mg/l (half the detection limit) to any values that were recorded as zero. Subjects were excluded from the triglycerides, HDL cholesterol, and LDL cholesterol if they were on diabetic medication or had not fasted before blood collection (or if either value was missing), or if they were pregnant, or if their respective phenotype measurement was more than three standard deviations from the mean, after correcting for sex, oral contraceptive use, and pregnancy. For the four phenotypes of interest to us, namely, CRP, HDL, LDL and triglycerides, the sample sizes are respectively 5290, 4700, 4682 and 4644. Due to space limitation, we report our findings on HDL and LDL only.

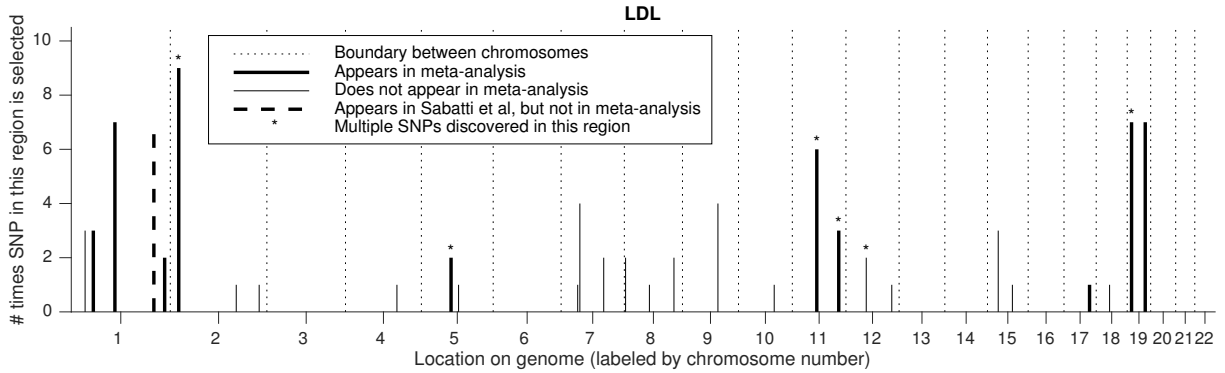
Finally, in order to correct for population stratification, we regressed the response and the features (SNPs) on the top five principal components of the design matrix in exactly the same fashion as suggested in Price et al. [20].

**Data processing with knockoffs.** Now that we have a response/design pair  $(\mathbf{y}, \mathbf{X})$ , we discuss the implementation of our full GWAS processing pipeline.

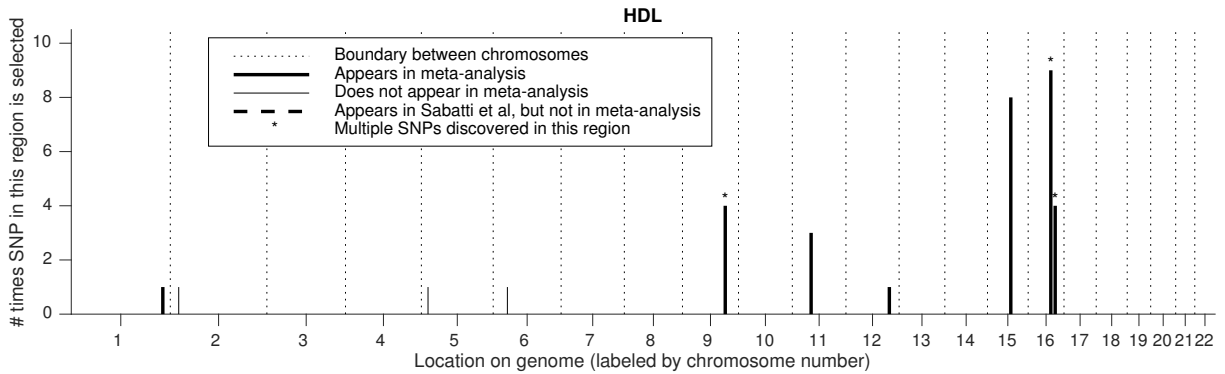
1. **Data splitting with random rotations.** In Section 4.1, we discuss splitting the data  $(\mathbf{X}, \mathbf{y})$  into two parts,  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  and  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$ , with the first part used for screening and the second for inference; in that section, our discussion centers on splitting by partitioning the  $n$  observations into two groups. In practice, for settings such as GWAS where the design matrix  $\mathbf{X}$  is naturally somewhat sparse, this may be problematic as splitting the set of observations can dramatically increase conditioning problems caused by sparsity. Here we take a different approach to splitting. Under the Gaussian linear model, since the i.i.d. Gaussian noise term  $\epsilon \in \mathbb{R}^n$  has a distribution that is unchanged by rotation, we can rotate the data with a randomly chosen orthonormal matrix  $\mathbf{U} \in \mathbb{R}^{n \times n}$ , to obtain  $(\mathbf{X}', \mathbf{y}') = (\mathbf{U} \mathbf{X}, \mathbf{U} \mathbf{y})$ . The original linear model is preserved; as long as the rotation was chosen independently of the data, our model is now

$$\mathbf{y}' = \mathbf{X}' \boldsymbol{\beta} + \boldsymbol{\epsilon}',$$

where  $\boldsymbol{\epsilon}' = \mathbf{U} \boldsymbol{\epsilon} \sim \mathcal{N}(0, \sigma^2 \mathbf{I}_n)$ . (Note that  $\boldsymbol{\beta}$  is unchanged from the original model.) After rotation, the new design matrix  $\mathbf{X}'$  is now dense, and we are able to split the rotated data into a set of  $n_0$  data points (for screening) and  $n_1 = n - n_0$  data points (for inference) without matrix conditioning issues. From this point on, the partitioned data sets  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  and  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$  are assumed to be taken from the rotated data, without further mention. We take  $n_0 = 1900$ .



**Figure 2:** Results of GWAS experiment for the LDL phenotype. The heights of the lines show the number of trials (out of 10 trials) for which at least one SNP in this region was selected; the line type shows whether this same region was identified in [28] and/or [21]. Regions where more than one SNP was selected (across the 10 trials) are marked with a ‘\*’. (See Section 6.2 for details.)



**Figure 3:** Results of GWAS experiment for the HDL phenotype (same interpretation as in Figure 2).

2. **Feature pre-screening with correlations.** The original number of features (SNPs) is 328,934, which is a bit large to easily run the Lasso for feature screening. As suggested in [29] (where the screen-and-clean methodology is applied to GWAS), we begin with a pre-screening step that looks only at marginal correlations: using the first part of the data  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$ , we select the set  $\hat{S}_{\text{pre}} \subset [p]$  of 26,300 features with the largest magnitude correlations  $|\mathbf{X}_j^{(0)\top} \mathbf{y}^{(0)}|$ .
3. **Feature screening with Lasso.** We then run the Lasso on  $(\mathbf{X}_{\hat{S}_{\text{pre}}}^{(0)}, \mathbf{y}^{(0)})$  using the 26,300 pre-screened features as covariates, and define the screened set of features  $\hat{S}_0$  to be the first  $n_1/4$  features, which enter the Lasso path on this reduced data set.
4. **Knockoff filter.** Next we bring back the held out part of the data,  $(\mathbf{X}^{(1)}, \mathbf{y}^{(1)})$ . We apply the knockoff filter with recycling as defined in Section 4.1, with statistics determined by the sign-restricted Lasso introduced in Section 4.2. Throughout, we use target FDR level  $q = 0.2$ .
5. **Repeat.** We then repeat all these steps, with a new random rotation matrix  $\mathbf{U} \in \mathbb{R}^{n \times n}$ , for a total of 10 repetitions. In particular, we are interested in examining whether any selected SNPs appear consistently across these 10 repetitions of our method.

Selection frequency (by region)	Selection frequency (by SNP)	SNP name	Chromosome	Base pair position	Nearby SNPs found in Willer et al. [28]	Nearby SNPs found in Sabatti et al. [21]
9	7	rs693	2	21232195	rs1367117	rs693
	4	rs3923037		21148274		
	4	rs754524		21311541		
	2	rs6754295		21206183		
	1	rs1429974		21300770		
7	7	rs646776	1	109818530	rs629301	rs646776
7	7	rs4844614	1	207875175		rs4844614
7	7	rs157580	19	45395266	rs4420638	rs157580
7	5	rs11668477	19	11195030	rs6511720	rs11668477
	2	rs11878377		10965270		
	2	rs1541596		10987013		
	1	rs10409243		10332988		
6	1	rs688		11227602		
	2	rs174556	11	61580635	rs174546	rs174537
	2	rs174450		61641542		
	1	rs579383		61536583		
1	rs1535	61597972		rs174546		
						rs174556
						rs1535
4	4	rs2728487	7	47209007		
4	4	rs9696070	9	89230779		
3	3	rs1342165	1	34800325		
3	3	rs557435	1	55520864	rs2479409	
3	3	rs4906908	15	27040082		
3	2	rs579163	11	116713630	rs964184	
	1	rs518181		116772787		
	1	rs11216267		116952392		
2	2	rs2802955	1	235015199	rs514230	
2	2	rs10953541	7	107244545		
2	2	rs905502	8	3134810		
2	2	rs1897318	8	124864404		
2	1	rs10062361	5	74565153	rs12916	
	1	rs6896136		74787310		
2	1	rs12427378	12	51074199		
	1	rs2139930		51089287		
1	1	rs7574918	2	165939179		
1	1	rs6749903	2	223653986		
1	1	rs3733262	4	129439663		
1	1	rs981862	5	93615466		
1	1	rs995124	7	41764992		
1	1	rs2351643	8	63076996		
1	1	rs945559	10	89823147		
1	1	rs1955105	12	115344782		
1	1	rs2456930	15	62687339		
1	1	rs4433842	17	64322683	rs1801689	
1	1	rs4799847	18	33686203		

**Table 2:** Results of GWAS experiment for the LDL phenotype (see Section 6.2 for details and interpretation of the results). Physical reference positions for SNPs were drawn from Human Genome Build 37/HG19.

Selection frequency (by region)	Selection frequency (by SNP)	SNP name	Chromosome	Base pair position	Nearby SNPs found in Willer et al. [28]	Nearby SNPs found in Sabatti et al. [21]
9	9	rs3764261	16	56993324	rs3764261	rs3764261
	9	rs7499892		57006590		
8	8	rs1532085	15	58683366	rs1532085	rs1532085
4	2	rs2575875	9	107662494	rs1883025	
	2	rs2740486		107666513		
4	2	rs255049	16	68013471	rs16942887	rs255049
	2	rs255052		68024995		
3	3	rs7120118	11	47286290	rs3136441	rs2167079 rs7120118
1	1	rs12139970	1	230406460	rs4846914	
1	1	rs6728178	2	21193946		
1	1	rs173738	5	16725880		
1	1	rs2817056	6	35734051		
1	1	rs2375016	12	109227914	rs7134594	

**Table 3:** Results of GWAS experiment for the HDL phenotype (see Section 6.2 for details and interpretation of the results). Physical reference positions for SNPs were drawn from Human Genome Build 37/HG19.

## 6.2 Results

Our results for the LDL phenotype are reported in Table 2 and displayed in Figure 2. In total, over the 10 trials (the random splits of the data), 44 different SNPs are selected. However, as nearby SNPs are extremely correlated, we consider SNPs whose positions are within  $10^6$  base pairs of each other, to be in the same “region”; at this level, in total over the 10 trials, there are 29 distinct regions discovered. In Table 2 we show, for each region, the selection frequency of any SNP in that region, i.e. the number of trials out of 10 for which at least one SNP in this region was selected (we also display the selection frequency for the individual SNPs). We also show any SNPs in the same region (defined again as a distance of  $\leq 10^6$  base pairs) which were identified as associated with LDL in the meta-analysis of Willer et al. [28]; this meta-analysis works with an extremely large sample size, and therefore can be viewed as providing a form of “ground truth”. Comparing against the findings of this meta-analysis, we can try to estimate the FDR of our method as follows: for each trial, we count each selected SNP as a discovery, and label it as a false discovery if there is no SNP in the meta-analysis from the same region. We then average this false discovery proportion over the 10 trials, and find an estimated FDR of 32.61%. We also compare against the findings of Sabatti et al. [21], which analyzes the same data set that we use; this comparison therefore should not be viewed as independent validation, but rather as checking that our analysis agrees with existing work on the same data set. In Figure 2, we display these findings visually.

For the HDL phenotype, our results are shown in Table 3 and in Figure 3. There are 13 SNPs discovered at least once in the 10 trials; once grouped into regions, there are 10 distinct regions. Again estimating the FDR by comparing against Willer et al. [28]’s meta-analysis, we estimate an FDR of 4.29%. This low number of discoveries, and perhaps conservative FDR, can probably be attributed to fact that this data set has a relatively small sample size, and fairly weak signal; we would not expect a large number of discoveries in this setting.

## 6.3 Additional simulations

We conclude this section with a short simulation study assessing directional FDR control and power in a setting which employs a real genotype matrix as a design but a computer generated response.

- We extract a subset of SNPs with fairly low correlations from the data set processed after performing the five tasks described at the top of Section 6.1. This is done by applying the PLINK `clump`<sup>6</sup> command using

<sup>6</sup>For details about this procedure, see <http://pngu.mgh.harvard.edu/~purcell/plink/clump.shtml>.



	Target $q$	FDR	dir. FDR	Power	Power (rel. to screening)
Knockoff (data split)	0.1	0.094	0.080	0.339	0.534
Knockoff (data split, signed)	0.1	0.090	0.090	0.403	0.632
Knockoff (data recy.)	0.1	0.085	0.078	0.470	0.737
Knockoff (data split)	0.2	0.190	0.182	0.452	0.709
Knockoff (data split, signed)	0.2	0.180	0.189	0.502	0.785
Knockoff (data recy.)	0.2	0.175	0.154	0.532	0.833

**Table 4:** Performance of the knockoff filter averaged over 50 trials. We do not report the values for knockoff (data recy., signed) since the results are identical to those of the recycling version. The power is the fraction of true variables selected among all true positives while the power (rel. to screening) is the fraction of true variables selected among all true positives that have been screened in.

a significance threshold for index SNPs of 0.2, a physical distance window of 1 kb, a linkage disequilibrium threshold for clumping of  $r^2 = 0.1$ , and HDL as a response. This yields a matrix with 26,315 SNPs with a maximum pairwise correlation equal to 0.316. We proceed by regressing out the top five principal components of each SNP feature as in Section 6.1, and then normalize the columns. The resulting  $4907 \times 26315$  design  $\mathbf{X}$  is fixed throughout the rest of the study.

- For each run, we generate a response  $\mathbf{y}$  from the model  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$ , where  $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0}, \mathbf{I}_n)$  and  $\boldsymbol{\beta}$  has  $k = 40$  nonzero amplitudes equal to  $\pm 4.48$ , each with equal probability, at locations selected uniformly at random.
- We then apply the knockoff procedure applying data splitting with random rotations as earlier. Throughout, we work with  $n_1 = 3000$  samples for the inference step,  $n_0 = 1907$  samples for screening step, and a target size for the screened set equal to  $n_1/4 = 750$  SNPs.

The results, averaged over 50 trials, are reported in Table 4. These results confirm our earlier findings: all knockoff methods control the FDR and the directional FDR. In addition, we see a gain in power as we move from data splitting to data splitting + sign consistency, to data recycling with or without sign consistency (since these two options give identical selections in these experiments, as was the case in our earlier simulations).

## 7 Summary

We have discussed a ‘screen + knockoff’ approach to controlled variable selection, which should appear very natural to practitioners; in addition, we develop the ‘recycling’ technique to reuse data rather than discarding the data used for the screening step, thus improving power. A natural question is thus what sort of inference properties would such a procedure offer? By focusing on Type I + Type S errors, we have shown that screen + knockoff is guaranteed to have a form of reproducibility in that the directional FDR is rigorously under control. This result makes no assumption on the design matrix nor on the values of the regression coefficients, and holds in finite samples; our contribution is, therefore, very different in spirit from most of the results published in the literature on high-dimensional inference, and employs mathematical arguments centered in martingale theory which are naturally also very different from the techniques used in the related literature.

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## A Proofs

### A.1 A general form of directional FDR control

Our results, namely, Theorems 1–4, are all special cases of the general statement below. Throughout,  $\widehat{\text{sign}}_j$  is defined as in (12), i.e.  $\widehat{\text{sign}}_j = \text{sign} \left( (\mathbf{X}_j - \widetilde{\mathbf{X}}_j)^\top \mathbf{y} \right)$ . Also, we shall say that a positive semidefinite matrix  $\mathbf{M} \in \mathbb{R}^{2p \times 2p}$  satisfies the *pairwise exchangeability condition* if  $M_{j,k} = M_{j,k+p} = M_{j+p,k} = M_{j+p,k+p}$  for all  $j \neq k \in \{1, \dots, p\}$  and  $M_{j,j} = M_{j+p,j+p}$  for all  $j \in \{1, \dots, p\}$ .

**Theorem 5.** Suppose  $\mathbf{y} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Theta})$  for some mean vector  $\boldsymbol{\mu} \in \mathbb{R}^n$  and some covariance  $\boldsymbol{\Theta} \in \mathbb{R}^{n \times n}$ . Let  $\mathbf{X}, \tilde{\mathbf{X}} \in \mathbb{R}^{n \times p}$  be any fixed matrices such that  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top \cdot \boldsymbol{\Theta} \cdot [\mathbf{X} \ \tilde{\mathbf{X}}]$  obeys the pairwise exchangeability condition. Let  $\mathbf{W} = (W_1, \dots, W_p)$  be any statistic satisfying the sufficiency and antisymmetry properties (7) and (8). Finally, let  $V_j = \mathbb{1} \left\{ \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\}$  be the indicator of a sign error on feature  $j$ . Then the knockoff+ method controls a directional FDR defined as

$$\text{FDR}_{\text{dir}} = \mathbb{E} \left[ \frac{\left| \left\{ j \in \hat{S} \text{ and } V_j = 1 \right\} \right|}{1 \vee |\hat{S}|} \right] \leq q.$$

If the knockoff method is used instead, then a modified directional FDR is controlled:

$$\text{mFDR}_{\text{dir}} = \mathbb{E} \left[ \frac{\left| \left\{ j \in \hat{S} \text{ and } V_j = 1 \right\} \right|}{|\hat{S}| + q^{-1}} \right] \leq q.$$

The rest of this section shows how all of our results follow as special cases.

**Proof of Theorem 1** This is straightforward since the result is obtained by taking  $\boldsymbol{\mu} = \mathbf{X}\boldsymbol{\beta}$  and  $\boldsymbol{\Theta} = \sigma^2 \mathbf{I}_n$  in the distribution of  $\mathbf{y}$ , and noting that  $\text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) = \text{sign}(\beta_j)$  for all  $j$  such that  $\mathbf{X}_j \neq \tilde{\mathbf{X}}_j$ . (We ignore the trivial case where  $s_j = 0$  implying  $\mathbf{X}_j = \tilde{\mathbf{X}}_j$ , for in this case we would get  $W_j = 0$  and thus feature  $j$  could never be selected.)

The more general form of Theorem 5 also allows us to consider other settings, such as those involving variable screening in high dimensions. For instance, our next proof concerns the testing of regression coefficients in the full model under the sure screening property.

**Proof of Theorem 2** We prove directional FDR control by conditioning on  $\mathbf{y}^{(0)}$ . For any  $\mathbf{y}^{(0)}$  such that the event  $\mathcal{E}$  holds, we will show that for the knockoff procedure,

$$\mathbb{E} \left[ \text{mFDR}_{\text{dir}} \mid \mathbf{y}^{(0)} \right] \cdot \mathbb{1}_{\mathcal{E}} \leq q, \quad (17)$$

and for the knockoff+,

$$\mathbb{E} \left[ \text{FDR}_{\text{dir}} \mid \mathbf{y}^{(0)} \right] \cdot \mathbb{1}_{\mathcal{E}} \leq q. \quad (18)$$

From this point on we treat  $\mathbf{y}^{(0)}$  as fixed. The conditional distribution of the response  $\mathbf{y}$  is given by

$$(\mathbf{y} \mid \mathbf{y}^{(0)}) \sim \mathcal{N} \left( \begin{bmatrix} \mathbf{y}^{(0)} \\ \mathbf{X}^{(1)} \boldsymbol{\beta} \end{bmatrix}, \begin{bmatrix} 0 & 0 \\ 0 & \sigma^2 \mathbf{I}_{n_1} \end{bmatrix} \right). \quad (19)$$

If  $\mathbf{y}^{(0)}$  is such that the event  $\mathcal{E}$  occurs, then we can simplify this to

$$(\mathbf{y} \mid \mathbf{y}^{(0)}) \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Theta}), \text{ where } \boldsymbol{\mu} = \begin{bmatrix} \mathbf{y}^{(0)} \\ \mathbf{X}_{\hat{S}_0}^{(1)} \boldsymbol{\beta}_{\hat{S}_0} \end{bmatrix} \text{ and } \boldsymbol{\Theta} = \begin{bmatrix} 0 & 0 \\ 0 & \sigma^2 \mathbf{I}_{n_1} \end{bmatrix}, \quad (20)$$

since  $\beta_j = 0$  for all  $j \notin \hat{S}_0$  when  $\mathcal{E}$  occurs. Define  $\boldsymbol{\Sigma}_{\hat{S}_0}^{(1)} = \mathbf{X}_{\hat{S}_0}^{(1)\top} \mathbf{X}_{\hat{S}_0}^{(1)}$ . Recall that  $\tilde{\mathbf{X}}_{\hat{S}_0}^{(0)} = \mathbf{X}_{\hat{S}_0}^{(0)}$  by (14), and that  $\tilde{\mathbf{X}}_{\hat{S}_0}^{(1)}$  satisfies

$$\begin{bmatrix} \mathbf{X}_{\hat{S}_0}^{(1)} & \tilde{\mathbf{X}}_{\hat{S}_0}^{(1)} \end{bmatrix}^\top \begin{bmatrix} \mathbf{X}_{\hat{S}_0}^{(1)} & \tilde{\mathbf{X}}_{\hat{S}_0}^{(1)} \end{bmatrix} = \begin{bmatrix} \boldsymbol{\Sigma}_{\hat{S}_0}^{(1)} & \boldsymbol{\Sigma}_{\hat{S}_0}^{(1)} - \text{diag}\{\mathbf{s}\} \\ \boldsymbol{\Sigma}_{\hat{S}_0}^{(1)} - \text{diag}\{\mathbf{s}\} & \boldsymbol{\Sigma}_{\hat{S}_0}^{(1)} \end{bmatrix} \quad (21)$$

for some vector  $\mathbf{s} \geq 0$ , by the knockoff construction. We then see that

$$[\mathbf{X}_{\widehat{S}_0} \quad \widetilde{\mathbf{X}}_{\widehat{S}_0}]^\top \Theta [\mathbf{X}_{\widehat{S}_0} \quad \widetilde{\mathbf{X}}_{\widehat{S}_0}] = \sigma^2 [\mathbf{X}_{\widehat{S}_0}^{(1)} \quad \widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}]^\top [\mathbf{X}_{\widehat{S}_0}^{(1)} \quad \widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}],$$

is a pairwise exchangeable matrix. At this point, we have satisfied the conditions of Theorem 5. Now what is a sign error in Theorem 5? We calculate that for any  $j \in \widehat{S}_0$ ,

$$(\mathbf{X}_j - \widetilde{\mathbf{X}}_j)^\top \boldsymbol{\mu} = (\mathbf{X}_j^{(1)} - \widetilde{\mathbf{X}}_j^{(1)})^\top \mathbf{X}_{\widehat{S}_0}^{(1)} \boldsymbol{\beta}_{\widehat{S}_0} = \sum_{k \in \widehat{S}_0} (\mathbf{X}_j^{(1)} - \widetilde{\mathbf{X}}_j^{(1)})^\top \mathbf{X}_k^{(1)} \cdot \beta_k = s_j \cdot \beta_j,$$

where the first equality holds on the event  $\mathcal{E}$  (i.e.  $\beta_k = 0$  for  $k \notin \widehat{S}_0$ ), and the third equality uses the Gram matrix condition (21). Hence, since  $s_j > 0$  whenever  $\mathbf{X}_j \neq \widetilde{\mathbf{X}}_j$ , an error  $\widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \widetilde{\mathbf{X}}_j)^\top \boldsymbol{\mu})$  is the same as  $\widehat{\text{sign}}_j \neq \text{sign}(\beta_j)$ , which completes the proof.

We now move on to our results concerning regression coefficients from the reduced model.

**Proof of Theorem 3** Recall that  $\mathbf{y}_\#^{(1)} \mid \mathbf{y}^{(0)} \sim \mathcal{N}(\mathbf{X}_{\widehat{S}_0}^{(1)} \boldsymbol{\beta}^{\text{partial}}, \sigma^2 \mathbf{I}_{n_1})$  so we can write

$$\left( \begin{bmatrix} \mathbf{y}^{(0)} \\ \mathbf{y}_\#^{(1)} \end{bmatrix} \mid \mathbf{y}^{(0)} \right) \sim \mathcal{N} \left( \begin{bmatrix} \mathbf{y}^{(0)} \\ \mathbf{X}_{\widehat{S}_0}^{(1)} \boldsymbol{\beta}^{\text{partial}} \end{bmatrix}, \begin{bmatrix} 0 & 0 \\ 0 & \sigma^2 \mathbf{I}_{n_1} \end{bmatrix} \right).$$

This is now the exact setting as in the proof of Theorem 2 (see (19)), except with  $\boldsymbol{\beta}^{\text{partial}}$  in place of  $\boldsymbol{\beta}$ , and so the remainder of the proof proceeds identically.

**Proof of Theorem 4** This last proof is more subtle and for this, we treat  $\mathbf{X}$  as random in addition to  $\mathbf{y}$ , but will condition on  $\mathbf{X}^{(0)}$  and on the screened features  $\mathbf{X}_{\widehat{S}_0}^{(1)}$  and knockoffs  $\widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}$  as well as on  $\mathbf{y}^{(0)}$ . By the assumption that the rows of  $\mathbf{X}$  are i.i.d. draws from  $\mathcal{N}(0, \boldsymbol{\Psi})$ , we can write

$$\mathbf{X}_{\widehat{S}_0}^{(1)} = \mathbf{X}_{\widehat{S}_0}^{(1)} \cdot \boldsymbol{\Gamma} + \mathbf{G} \cdot \boldsymbol{\Lambda}^{1/2},$$

where  $\boldsymbol{\Gamma}$  and  $\boldsymbol{\Lambda}$  are the fixed unknown matrices given by

$$\boldsymbol{\Gamma} = (\boldsymbol{\Psi}_{\widehat{S}_0, \widehat{S}_0})^{-1} \cdot \boldsymbol{\Psi}_{\widehat{S}_0, \widehat{S}_0^c}$$

and the Schur complement

$$\boldsymbol{\Lambda} = \boldsymbol{\Psi}_{\widehat{S}_0^c, \widehat{S}_0^c} - \boldsymbol{\Psi}_{\widehat{S}_0^c, \widehat{S}_0} \cdot (\boldsymbol{\Psi}_{\widehat{S}_0, \widehat{S}_0})^{-1} \cdot \boldsymbol{\Psi}_{\widehat{S}_0, \widehat{S}_0^c},$$

and where  $\mathbf{G} \in \mathbb{R}^{n_1 \times (p - |\widehat{S}_0|)}$  has i.i.d. standard normal entries drawn independently from  $(\mathbf{X}^{(0)}, \mathbf{y}^{(0)})$  and from  $(\mathbf{X}_{\widehat{S}_0}^{(1)}, \widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}, \boldsymbol{\epsilon}^{(1)})$ . Then

$$\mathbf{y}^{(1)} = \mathbf{X}^{(1)} \boldsymbol{\beta} + \boldsymbol{\epsilon}^{(1)} = \mathbf{X}_{\widehat{S}_0}^{(1)} \cdot (\boldsymbol{\beta}_{\widehat{S}_0} + \boldsymbol{\Gamma} \boldsymbol{\beta}_{\widehat{S}_0^c}) + \mathbf{G} \cdot \boldsymbol{\Lambda}^{1/2} \boldsymbol{\beta}_{\widehat{S}_0^c} + \boldsymbol{\epsilon}^{(1)},$$

and note that

$$\boldsymbol{\beta}_{\widehat{S}_0} + \boldsymbol{\Gamma} \boldsymbol{\beta}_{\widehat{S}_0^c} = \overline{\boldsymbol{\beta}}^{\text{partial}}$$

by definition of the expected partial regression coefficients. Therefore,

$$(\mathbf{y} \mid \mathbf{X}^{(0)}, \mathbf{y}^{(0)}, \mathbf{X}_{\widehat{S}_0}^{(1)}, \widetilde{\mathbf{X}}_{\widehat{S}_0}^{(1)}) \sim \mathcal{N} \left( \begin{bmatrix} \mathbf{y}^{(0)} \\ \mathbf{X}_{\widehat{S}_0}^{(1)} \overline{\boldsymbol{\beta}}^{\text{partial}} \end{bmatrix}, \begin{bmatrix} 0 & 0 \\ 0 & (\boldsymbol{\beta}_{\widehat{S}_0^c}^\top \boldsymbol{\Lambda} \boldsymbol{\beta}_{\widehat{S}_0^c} + \sigma^2) \mathbf{I}_{n_1} \end{bmatrix} \right).$$

We are now in the same setting as in the proof of Theorem 2 (see (19)), except with  $\overline{\boldsymbol{\beta}}^{\text{partial}}$  in place of  $\boldsymbol{\beta}$  and with a new variance level that has increased due to the randomness in the missed signals. The remainder of the proof thus proceeds identically.

## A.2 Key lemmas

The proof of Theorem 5 relies on two key lemmas: Lemma 1 earlier which treats non-i.i.d. Bernoulli sequences, and the following result regarding the statistics  $\mathbf{W}$  arising in the knockoff procedure.

**Lemma 2.** *With the assumptions from Theorem 5, let  $\mathcal{V}$  be the  $\sigma$ -algebra generated by the random variables  $\{(\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y}, |(\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y}|\}$ , and define the vector  $\mathbf{S} = (S_1, \dots, S_p)$  of signs as*

$$S_j = \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}) \cdot \text{sign}(W_j).$$

Then the following holds:

- $|\mathbf{W}|$  and  $\mathbf{S}$  belong to  $\mathcal{V}$ .
- The signs of  $W_j$  are mutually independent after conditioning on  $\mathcal{V}$ .
- For each  $j = 1, \dots, p$ , if  $S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu})$ , then

$$\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\} \geq 1/2.$$

Before presenting the formal proof, we give an intuitive explanation for why the probabilities for  $\text{sign}(W_j)$  work in our favor; that is, why we are able to obtain  $\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\} \geq 1/2$ , which ensures that we are more likely to over- rather than under-estimate the number of false positives. This is similar to the discussion for the low-dimensional setting as in (12). In this case, for the high-dimensional setting, we see that if  $S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu})$ , then:

- If  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu} \geq 0$ , then  $\text{sign}(W_j) = -1$  whenever  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y} > 0$ ;
- If  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu} \leq 0$ , then  $\text{sign}(W_j) = -1$  whenever  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y} < 0$ .

Of course,  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}$  is a normal random variable whose mean is given by  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}$ . If this mean is nonnegative, then the random variable  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}$  is more likely to be positive than negative; if this mean is nonpositive, then the opposite is true. Either way, we see that  $\text{sign}(W_j) = -1$  has probability at least  $1/2$ .

*Proof.* First, by the sufficiency property,  $\mathbf{W}$  is a function of  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}]$  and  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top \mathbf{y}$  or, equivalently, is of the form

$$\mathbf{W} = \mathbf{w}\left([\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}], (\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y}, |(\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y}|, \text{sign}((\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y})\right)$$

for some function  $\mathbf{w}$ . Second, the antisymmetry property implies that flipping the signs of any subset of the last argument of the function  $\mathbf{w}$  flips the signs of the corresponding outputs. (Of course, for any  $j$  such that  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y} = 0$ , the antisymmetry property implies that  $W_j = 0$ ; we ignore these features in our proof from this point on as they can never be selected by our method.) This property makes clear that  $\mathcal{V}$  determines  $\mathbf{W}$  up to a sign change, so that  $|\mathbf{W}| \in \mathcal{V}$ . Furthermore, define a vector of signs  $\mathbf{S}$  such that

$$|\mathbf{W}| = \mathbf{w}\left([\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}], (\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y}, |(\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y}|, \mathbf{S}\right).$$

Clearly,  $\mathbf{S} \in \mathcal{V}$  and, by the antisymmetry property, we also see that

$$\mathbf{w}\left([\mathbf{X} \ \tilde{\mathbf{X}}]^\top [\mathbf{X} \ \tilde{\mathbf{X}}], (\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y}, |(\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y}|, \mathbf{S} \cdot \text{sign}(\mathbf{W})\right) = \mathbf{W}.$$

This equality means that  $\mathbf{S} \cdot \text{sign}(\mathbf{W})$  must be equal to  $\text{sign}((\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y})$  or, expressed differently,  $\mathbf{S} = \text{sign}(\mathbf{W}) \cdot \text{sign}((\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y})$  thereby coinciding with the definition given in the statement of the lemma. This establishes the first claim.

Next, an elementary calculation shows that

$$\begin{bmatrix} (\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y} \\ (\mathbf{X} - \tilde{\mathbf{X}})^\top \mathbf{y} \end{bmatrix} \sim \mathcal{N} \left( \begin{bmatrix} (\mathbf{X} + \tilde{\mathbf{X}})^\top \boldsymbol{\mu} \\ (\mathbf{X} - \tilde{\mathbf{X}})^\top \boldsymbol{\mu} \end{bmatrix}, \begin{bmatrix} (\mathbf{X} + \tilde{\mathbf{X}})^\top \boldsymbol{\Theta} (\mathbf{X} + \tilde{\mathbf{X}}) & 0 \\ 0 & \text{diag}\{\mathbf{d}\} \end{bmatrix} \right), \quad (22)$$

where  $\mathbf{d} = (d_1, \dots, d_p) \in \mathbb{R}^p$  is some nonnegative vector. The form of the covariance term arises from the fact that  $(\mathbf{X} - \tilde{\mathbf{X}})^\top \boldsymbol{\Theta} (\mathbf{X} + \tilde{\mathbf{X}}) = 0$  and  $(\mathbf{X} - \tilde{\mathbf{X}})^\top \boldsymbol{\Theta} (\mathbf{X} - \tilde{\mathbf{X}})$  is diagonal, according to the pairwise exchangeability assumption on  $[\mathbf{X} \ \tilde{\mathbf{X}}]^\top \boldsymbol{\Theta} [\mathbf{X} \ \tilde{\mathbf{X}}]$ . Therefore, the terms  $(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}$  are mutually independent, and are independent from  $(\mathbf{X} + \tilde{\mathbf{X}})^\top \mathbf{y}$ . Also, since  $\mathbf{S} \in \mathcal{V}$  the terms  $\text{sign}(W_j) = S_j \cdot \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y})$  are mutually independent after conditioning on  $\mathcal{V}$ , proving our second claim.

Finally, observe that if  $Z \sim \mathcal{N}(\theta, \sigma^2)$ , then it follows from a simple calculation that

$$\frac{\mathbb{P}\{\text{sign}(Z) = -1 \mid |Z|\}}{\mathbb{P}\{\text{sign}(Z) = +1 \mid |Z|\}} = \exp\left(-\frac{2\theta|z|}{\sigma^2}\right).$$

Now since  $\mathbb{P}\{\text{sign}(W_j) = \pm 1 \mid \mathcal{V}\} = \mathbb{P}\left\{S_j \cdot \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}) = \pm 1 \mid \mathcal{V}\right\}$ , applying the above formula gives

$$\frac{\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\}}{\mathbb{P}\{\text{sign}(W_j) = +1 \mid \mathcal{V}\}} = \exp\left(-\frac{2S_j \cdot (\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu} \cdot |(\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}|}{d_j}\right).$$

Clearly, if  $S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu})$ , then the argument in the exponential in the right-hand side of this last inequality is positive and thus,  $\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\} \geq 1/2$ .  $\square$

The original knockoff paper [1] worked in the simpler setting where the signs of  $W_j$  for the nulls are i.i.d. unbiased. If  $\mathcal{H}_0$  is the set of nulls and  $T > 0$  the adaptive threshold of the knockoff filter, [1] established that the i.i.d. property for the signs gives

$$\mathbb{E} \left[ \mathbb{E} \left[ \frac{|\{j \in \mathcal{H}_0 : W_j \geq T\}|}{1 + |\{j \in \mathcal{H}_0 : W_j \leq -T\}|} \mid |\mathbf{W}| \right] \right] \leq 1.$$

Here, we use Lemma 1 to develop a similar bound when the signs are no longer i.i.d. unbiased but are, instead, independent with at most a 50% chance of being positive conditionally on  $\mathcal{V}$ .

**Corollary 1.** *Suppose  $\mathcal{M} \subset \{1, \dots, p\}$  is a random set belonging to  $\mathcal{V}$  and chosen such that for each  $j \in \mathcal{M}$ ,  $|W_j| > 0$  and  $\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\} \geq \rho$ . Letting  $T > 0$  be the adaptive threshold of either the knockoff or knockoff+ filter, then*

$$\mathbb{E} \left[ \frac{|\{j \in \mathcal{M} : W_j \geq T\}|}{1 + |\{j \in \mathcal{M} : W_j \leq -T\}|} \mid \mathcal{V} \right] \leq \rho^{-1} - 1. \quad (23)$$

*Proof.* The proof is straightforward and only consists in rewriting the left-hand side of (23) in such a way that we recognize the formulation from Lemma 1. To begin with, we can treat the ordering of  $|\mathbf{W}|$  as fixed since Lemma 2 gives  $|\mathbf{W}| \in \mathcal{V}$ . Now assume without loss of generality that  $\mathcal{M} = \{1, \dots, m\}$  and reorder the indices of the  $W_j$ 's in  $\mathcal{M}$  so that  $|W_{(1)}| \geq |W_{(2)}| \geq \dots \geq |W_{(m)}|$ . Set  $B_j = \mathbb{1}_{W_{(j)} < 0}$ . Next we will condition also on  $\text{sign}(W_j)$  for all  $j \notin \mathcal{M}$ . Let  $\tilde{\mathcal{V}}$  be the larger  $\sigma$ -algebra generated by  $\mathcal{V}$  and  $\{\text{sign}(W_j) : j \notin \mathcal{M}\}$ . By definition of  $\mathcal{M}$ , when we condition on  $\mathcal{V}$ , we have  $B_j \stackrel{\perp}{\sim} \text{Bernoulli}(\rho_j)$  with  $\rho_j \geq \rho$  for all  $j \in \mathcal{M}$ . By Lemma 2, the same is still true even after conditioning on  $\{\text{sign}(W_j) : j \notin \mathcal{M}\}$  also, since the signs of  $\mathbf{W}$  are mutually independent conditional on  $\mathcal{V}$ . To summarize, we have

$$(B_j)_{j \in \mathcal{M}} \mid \tilde{\mathcal{V}} \stackrel{\perp}{\sim} \text{Bernoulli}(\rho_j),$$

with  $\rho_j \geq \rho$  for all  $j \in \mathcal{M}$ .

Next, we can write

$$\frac{\#\{j \in \mathcal{M} : W_j \geq T\}}{1 + \#\{j \in \mathcal{M} : W_j \leq -T\}} = \frac{(1 - B_1) + \dots + (1 - B_J)}{1 + B_1 + \dots + B_J} = \frac{1 + J}{1 + B_1 + \dots + B_J} - 1,$$

where  $J$  is the index such that  $|W_{(1)}| \geq \dots \geq |W_{(J)}| \geq T > |W_{(J+1)}| \geq \dots \geq |W_{(m)}|$ . After conditioning on  $\tilde{\mathcal{V}}$ , so that we can treat  $|\mathbf{W}|$  and  $\{\text{sign}(W_j) : j \notin \mathcal{M}\}$  as fixed, we observe that the index  $J$  can be expressed as a stopping time, in reverse time, with respect to the filtration  $\{\mathcal{F}_j\}$  given by

$$\mathcal{F}_j = \{B_1 + \dots + B_j, B_{j+1}, \dots, B_m\}.$$

The conclusion now follows from Lemma 1.  $\square$

### A.3 Proof of Theorem 5

First, consider control of  $\text{mFDR}_{\text{dir}}$  under the knockoff. Since  $j \in \hat{S}$  if and only if  $W_j \geq T$  where  $T$  is our adaptive threshold, the modified directional FDR is given by

$$\begin{aligned} \text{mFDR}_{\text{dir}} &= \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{|\{j : W_j \geq T\}| + q^{-1}} \right] \\ &= \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{1 + |\{j : W_j \leq -T\}|} \cdot \frac{1 + |\{j : W_j \leq -T\}|}{|\{j : W_j \geq T\}| + q^{-1}} \right] \\ &\leq q \cdot \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{1 + |\{j : W_j \leq -T\}|} \right] \end{aligned}$$

since  $|\{j : W_j \leq -T\}| \leq q \cdot |\{j : W_j \geq T\}|$  by definition of  $T$ . Now rewrite the set of sign errors as

$$\begin{aligned} \left\{ j : W_j \geq T, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} &= \left\{ j : W_j \geq T, \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}) \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \\ &= \left\{ j : W_j \geq T, S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\}, \end{aligned}$$

where the first equality follows from the definition of  $\widehat{\text{sign}}_j$  in (12), and the second from the definition  $S_j = \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \mathbf{y}) \cdot \text{sign}(W_j)$  as in Lemma 2 (since  $\text{sign}(W_j) = +1$  for all  $j$  in this set). Define  $\widehat{\mathcal{H}}_0 = \{j : S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu})\}$  and let  $\mathcal{V}$  be as in Lemma 2. By the tower law we obtain

$$\begin{aligned} \text{mFDR}_{\text{dir}} &\leq q \cdot \mathbb{E} \left[ \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T, S_j \neq \text{sign}((\mathbf{X}_j - \tilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{1 + |\{j : W_j \leq -T\}|} \middle| \mathcal{V} \right] \right] \\ &= q \cdot \mathbb{E} \left[ \mathbb{E} \left[ \frac{\left| \left\{ j \in \widehat{\mathcal{H}}_0 : W_j \geq T \right\} \right|}{1 + |\{j : W_j \leq -T\}|} \middle| \mathcal{V} \right] \right] \\ &\leq q \cdot \mathbb{E} \left[ \mathbb{E} \left[ \frac{\left| \left\{ j \in \widehat{\mathcal{H}}_0 : W_j \geq T \right\} \right|}{1 + \left| \left\{ j \in \widehat{\mathcal{H}}_0 : W_j \leq -T \right\} \right|} \middle| \mathcal{V} \right] \right]. \end{aligned}$$

Next, note that  $\widehat{\mathcal{H}}_0 \in \mathcal{V}$  since  $\mathbf{S} \in \mathcal{V}$  by Lemma 2, and so inside of the conditional expectation, we can treat the set  $\widehat{\mathcal{H}}_0$  as fixed. Lemma 1 proves that conditional on  $\mathcal{V}$ , the signs of  $\mathbf{W}$  are independent, with  $\mathbb{P}\{\text{sign}(W_j) = -1 \mid \mathcal{V}\} \geq 1/2$  for all  $j \in \widehat{\mathcal{H}}_0$ . Therefore, applying Corollary 1 with  $\rho = 1/2$  gives

$$\mathbb{E} \left[ \frac{\left| \left\{ j \in \widehat{\mathcal{H}}_0 : W_j \geq T \right\} \right|}{1 + \left| \left\{ j \in \widehat{\mathcal{H}}_0 : W_j \leq -T \right\} \right|} \middle| \mathcal{V} \right] \leq 1,$$



which concludes the argument.

The proof for  $\text{FDR}_{\text{dir}}$ , when using knockoff+ instead of knockoff, follows similarly: we have

$$\begin{aligned} \text{FDR}_{\text{dir}} &= \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T_+, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \widetilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{1 + |\{j : W_j \leq -T_+\}|} \cdot \frac{1 + |\{j : W_j \leq -T_+\}|}{1 \vee |\{j : W_j \geq T_+\}|} \right] \\ &\leq q \cdot \mathbb{E} \left[ \frac{\left| \left\{ j : W_j \geq T_+, \widehat{\text{sign}}_j \neq \text{sign}((\mathbf{X}_j - \widetilde{\mathbf{X}}_j)^\top \boldsymbol{\mu}) \right\} \right|}{1 + |\{j : W_j \leq -T_+\}|} \right], \end{aligned}$$

where the last step uses the (slightly more conservative) definition of the threshold  $T_+$  for the knockoff+ procedure. From then on, the argument is the same as before.

#### A.4 Proof of Lemma 1

We first give a slight generalization of Lemma 4 in [1]:

**Lemma 3.** *Suppose that  $B_1, \dots, B_n \stackrel{\text{iid}}{\sim} \text{Bernoulli}(\rho)$ . Let  $J$  be a stopping time in reverse time with respect to the filtration  $\{\mathcal{F}_j\}$ , where  $\mathcal{F}_j \ni B_1 + \dots + B_j, B_{j+1}, \dots, B_n$ , and where the variables  $B_1, \dots, B_j$  are exchangeable with respect to  $\mathcal{F}_j$ . Then*

$$\mathbb{E} \left[ \frac{1 + J}{1 + B_1 + \dots + B_J} \right] \leq \rho^{-1}.$$

*Proof of Lemma 3.* Define the sum

$$S_j = B_1 + \dots + B_j \in \mathcal{F}_j,$$

and define the process

$$M_j = \frac{1 + j}{1 + B_1 + \dots + B_j} = \frac{1 + j}{1 + S_j} \in \mathcal{F}_j.$$

In [1] it is shown that  $\mathbb{E}[M_n] \leq \rho^{-1}$ , therefore, by the optional stopping time theorem it suffices to show that  $\{M_j\}$  is a supermartingale with respect to  $\{\mathcal{F}_j\}$ . First, since  $\{B_1, \dots, B_{j+1}\}$  are exchangeable with respect to  $\mathcal{F}_{j+1}$ , we have

$$\mathbb{P}\{B_{j+1} = 1 \mid \mathcal{F}_{j+1}\} = \frac{S_{j+1}}{1 + j}.$$

Therefore, if  $S_{j+1} > 0$ ,

$$\begin{aligned} \mathbb{E}[M_j \mid \mathcal{F}_{j+1}] &= \frac{1 + j}{1 + S_{j+1}} \cdot \mathbb{P}\{B_{j+1} = 0 \mid \mathcal{F}_{j+1}, S_{j+1}\} + \frac{1 + j}{1 + S_{j+1} - 1} \cdot \mathbb{P}\{B_{j+1} = 1 \mid \mathcal{F}_{j+1}, S_{j+1}\} \\ &= \frac{1 + j}{1 + S_{j+1}} \cdot \frac{1 + j - S_{j+1}}{1 + j} + \frac{1 + j}{1 + S_{j+1} - 1} \cdot \frac{S_{j+1}}{1 + j} \\ &= \frac{1 + j - S_{j+1}}{1 + S_{j+1}} + 1 = \frac{1 + (j + 1)}{1 + S_{j+1}} = M_{j+1}. \end{aligned}$$

If instead  $S_{j+1} = 0$ , then trivially  $S_j = 0$  also, and so  $M_j = 1 + j < 2 + j = M_{j+1}$ . This proves that  $\{M_j\}$  is a supermartingale with respect to  $\{\mathcal{F}_j\}$ , as desired.  $\square$

**Corollary 2.** *Suppose that  $\mathcal{A} \subseteq [n]$  is fixed, while  $B_1, \dots, B_n \stackrel{\text{iid}}{\sim} \text{Bernoulli}(\rho)$ . Let  $J$  be a stopping time in reverse time with respect to the filtration  $\{\mathcal{F}_j\}$ , where  $\mathcal{F}_j \ni \sum_{i \leq j, i \in \mathcal{A}} B_i$ , and the variables  $\{B_i : i \leq j, i \in \mathcal{A}\}$  are exchangeable with respect to  $\mathcal{F}_j$ . Then*

$$\mathbb{E} \left[ \frac{1 + |\{i \leq J : i \in \mathcal{A}\}|}{1 + \sum_{i \leq J, i \in \mathcal{A}} B_i} \right] \leq \rho^{-1}.$$

*Proof of Corollary 2.* Let  $\mathcal{A} = \{i_1, \dots, i_m\}$  where  $1 \leq i_1 < \dots < i_m \leq n$ . Then by considering the i.i.d. sequence

$$B_{i_1}, \dots, B_{i_m}$$

in place of  $B_1, \dots, B_n$ , we see that this result is equivalent to Lemma 3.  $\square$

*Proof of Lemma 1.* We may assume  $\rho < 1$  to avoid the trivial case. We now create a different construction for the  $B_i$ 's. First, generate a random set  $\mathcal{A} \subseteq [n]$  where for each  $i$ , independently,

$$\mathbb{P}\{i \in \mathcal{A}\} = \frac{1 - \rho_i}{1 - \rho}.$$

Next, define variables

$$Q_1, \dots, Q_n \stackrel{\text{iid}}{\sim} \text{Bernoulli}(\rho),$$

which are generated independently of the random set  $\mathcal{A}$ . Finally, define

$$B_i = Q_i \cdot \mathbb{1}_{i \in \mathcal{A}} + \mathbb{1}_{i \notin \mathcal{A}}. \quad (24)$$

Then, clearly, the  $B_i$ 's are mutually independent with  $\mathbb{P}\{B_i = 1\} = \rho_i$ , as required by the lemma. Next, since  $B_i = Q_i \cdot \mathbb{1}_{i \in \mathcal{A}} + \mathbb{1}_{i \notin \mathcal{A}}$  for all  $i$ , we have

$$\frac{1 + J}{1 + B_1 + \dots + B_J} = \frac{1 + |\{i \leq J : i \in \mathcal{A}\}| + |\{i \leq J : i \notin \mathcal{A}\}|}{1 + \sum_{i \leq J, i \in \mathcal{A}} Q_i + |\{i \leq J : i \notin \mathcal{A}\}|} \leq \frac{1 + |\{i \leq J : i \in \mathcal{A}\}|}{1 + \sum_{i \leq J, i \in \mathcal{A}} Q_i},$$

where the last step uses the identity  $\frac{a+c}{b+c} \leq \frac{a}{b}$  whenever  $0 < b \leq a$  and  $c \geq 0$ . Therefore, it will be sufficient to bound the right-hand side. We will use Corollary 2 to prove that

$$\mathbb{E} \left[ \frac{1 + |\{i \leq J : i \in \mathcal{A}\}|}{1 + \sum_{i \leq J, i \in \mathcal{A}} Q_i} \middle| \mathcal{A} \right] \leq \rho^{-1}, \quad (25)$$

which will be sufficient to prove the lemma by applying the tower law of expectations.

To prove (25), first let  $\tilde{Q}_i = Q_i \cdot \mathbb{1}_{i \in \mathcal{A}}$ , and define a filtration  $\{\mathcal{F}'_j\}$  where  $\mathcal{F}'_j$  is the  $\sigma$ -algebra generated as

$$\mathcal{F}'_j = \sigma \left( \left\{ \tilde{Q}_1 + \dots + \tilde{Q}_j, \tilde{Q}_{j+1}, \dots, \tilde{Q}_n, \mathcal{A} \right\} \right).$$

Next, for any  $j$ , by (24) we see that

$$B_1 + \dots + B_j, B_{j+1}, \dots, B_n \in \mathcal{F}'_j \quad \Rightarrow \quad \mathcal{F}'_j \supseteq \mathcal{F}_j,$$

and so  $T$  is a stopping time (in reverse time) with respect to  $\{\mathcal{F}'_j\}$  also. We also see that trivially, the variables  $\{Q_i : i \leq j, i \in \mathcal{A}\}$  are exchangeable with respect to  $\mathcal{F}'_j$  (since the  $Q_i$ 's are i.i.d. and are independent from  $\mathcal{A}$ ). Finally, since the  $Q_i$ 's are independent from  $\mathcal{A}$ , the desired bound (25) follows directly from Corollary 2 after conditioning on  $\mathcal{A}$ .  $\square$