

# Using Probabilistic Knockoffs of Binary Variables to Control the False Discovery Rate

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July 16, 2015

## 1 Introduction

Variable selection is an essential problem to fitting a regression model. For linear regression, the knockoff filter (Barber and Candès, 2014) offers a method of exact FDR control. However, the method as originally formulated does not extend to other generalized linear models such as logistic regression. This paper offers an extension of this method which will work with binary features in the context of linear regression, but also will extend to other GLMs.

### 1.1 Knockoff Filter

Let us consider the usual setting for linear regression, where  $n$  observations of a variable of interest  $y$  arise from the model

$$\mathbf{y} = X\beta + \mathbf{z}$$

where  $\mathbf{y} \in \mathbb{R}^n$  are the observed values of  $y$ ,  $X \in \mathbb{R}^{n \times p}$  is the matrix of predictor variables,  $\beta \in \mathbb{R}^p$  are the unknown coefficients, and  $\mathbf{z}$  is Gaussian noise. For the purpose of this paper, only the case where  $2p \leq n$  will be considered, though the methods can be extended to  $p \leq n$ . I will refer the  $j$ th column of  $X$  as  $X_j$ , which is  $n$  observations of the random variable  $x_j$ . The random variable  $x_j$  is in turn  $j$ th entry of the random vector valued variable  $\mathbf{x}$ . In the situation where  $\beta$  is sparse and there is reason to expect that  $x_j$  and  $y$  are uncorrelated for many  $j$ , the knockoff filter is a method to select a subset of the  $x_j$  which are likely correlated with  $y$ .

The method specifically seeks to control the false discovery rate (FDR), which is the expected portion of some selection of  $x_j$  which are, in fact, uncorrelated with  $y$ . For a procedure which chooses a subset of variables  $\hat{S} \subseteq \{1, \dots, p\}$ , this is defined as

$$\text{FDR} = \mathbb{E} \left[ \frac{|\{j : \beta_j = 0 \text{ \& } j \in \hat{S}\}|}{\max\{|\hat{S}|, 1\}} \right]$$

FDR is controlled at level  $q$  if FDR is less than  $q$  irrespective of the coefficients  $\beta$ .

The knockoff filter achieves FDR control in several steps, the first of which is creating a set of ‘knockoff’ features  $\tilde{X}_j$  which imitate the original  $X_j$  while being less correlated with  $y$ . In particular, the matrix of knockoffs

$\tilde{X}$  has the same internal correlation structure as  $X$ , the knockoff feature  $\tilde{X}_j$  has the same correlation with other  $X_i$  as  $X_j$  does, but the correlation between  $\tilde{X}_j$  and  $X_j$  is minimized. In other words, where  $\hat{\Sigma} := X^T X$ ,

$$\tilde{X}^T \tilde{X} = \Sigma \text{ and } \tilde{X}^T X = \Sigma - \text{diag}\{\mathbf{s}\}$$

for some vector  $\mathbf{s} \in \mathbb{R}^p$  such that, where  $\text{diag}\{\Sigma\}$  is the vector made from the main diagonal of  $\Sigma$ ,  $\text{diag}\{\Sigma\} - \mathbf{s}$  is small. Since  $\tilde{X}_j$  and  $X_j$  have relatively low correlation, as long as  $X_j$  is created independently of  $\mathbf{y}$ ,  $\tilde{X}_j$  will have lower correlation with  $\mathbf{y}$  than  $X_j$ . In the case where  $X_j$  is uncorrelated with  $\mathbf{y}$ ,  $\tilde{X}_j$  will also be uncorrelated with  $\mathbf{y}$ . How these knockoffs are actually generated will be described shortly.

The second step is to fit a series of Lasso model of  $\mathbf{y}$  on the combined design matrix  $X_L = [X \ \tilde{X}]$  so as to determine the largest value  $\lambda$  at which the coefficient for each  $X_j$  and  $\tilde{X}_j$  is nonzero. The subscript  $L$  refers to the large design matrix with both features and knockoffs.<sup>1</sup> Recall, for a given  $\lambda$ , the estimated coefficient from the Lasso regression will be

$$\beta(\lambda) = \text{argmin}_{\mathbf{b}} \left\{ \frac{1}{2} \|\mathbf{y} - X_L \mathbf{b}\|_2^2 + \lambda \|\mathbf{b}\|_1 \right\}$$

In the general case, the coefficient for one feature in a Lasso regression being first nonzero for a larger value of  $\lambda$  than another feature is an indication that the first feature is a stronger predictor of the outcome than the second. Thus, since, by construction, the knockoff features are weaker predictors than the originals, we would expect the original features to have nonzero coefficients sooner than the knockoff features when the original is a valid predictor. On the other hand, since  $\beta(\lambda)$  only depends on  $X_L$  through the sufficient statistics  $\Sigma_L = X_L^T X_L$  and  $X_L^T \mathbf{y}$ , for null predictors, the coefficients of the original features won't enter any sooner on average than knockoff feature. This can be seen by switching a null  $X_j$  with  $\tilde{X}_j$ ; by construction,  $\Sigma_L$  will be unaltered, while  $E[X_L^T \mathbf{y}]$  will also be unchanged, since  $E[X_j^T \mathbf{y}] = E[\tilde{X}_j^T \mathbf{y}] = 0$ .

This observation leads to the final step. Let  $Z_j$  be the largest  $\lambda$  such that feature  $j$  has a nonzero coefficient and  $\tilde{Z}_j$  the largest  $\lambda$  such that knockoff  $j$  has a nonzero coefficient. Then, define  $W_j$  as

$$W_j = \begin{cases} Z_j & \text{if } Z_j > \tilde{Z}_j \\ -\tilde{Z}_j & \text{if } Z_j < \tilde{Z}_j \\ 0 & \text{if } Z_j = \tilde{Z}_j \end{cases}$$

When  $X_j$  is a null predictor,  $W_j$  will be symmetrically distributed around zero, and when  $X_j$  is true predictor, it will have a distribution skewed positive. Since  $W_j$  with large positive values are more likely to be true predictors, the knockoff filter selects the variables  $\{j : W_j \geq T\}$ , where  $T$  is a threshold defined as

$$T = \min \left\{ t > 0 : \frac{|\{j : W_j \leq -t\}|}{\max\{|\{j : W_j \geq t\}|, 1\}} \leq q \right\}$$

Basic logic of this method is fairly simple. Let  $N_h(t)$  be the random variable for the number of null predictors with  $W_j \leq t$ ,  $N_l(t)$  be the number of null predictors with  $W_j \geq t$ , and  $V_l(t)$  &  $V_h(t)$  be the similar number of true

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<sup>1</sup>Other statistics besides the  $\lambda$ s can also be used in the knockoff method, but are not considered in this paper

predictors. Since the null  $W_j$  are symmetrically distributed around 0,  $E[N_l(t)] = E[N_h(t)]$ . Thus,

$$\begin{aligned}
q &\geq E \left[ \frac{|\{j : W_j \leq -t\}|}{\max\{|\{j : W_j \geq t\}|, 1\}} \right] \\
q &\geq E \left[ \frac{N_l(t) + V_l(t)}{\max\{N_h(t) + V_h(t), 1\}} \right] \\
q &\geq E \left[ \frac{N_l(t)}{\max\{N_h(t) + V_h(t), 1\}} \right] \\
q &\geq E \left[ \frac{N_h(t)}{\max\{N_h(t) + V_h(t), 1\}} \right] \\
q &\geq \text{FDR}
\end{aligned}$$

So FDR is controlled, and since  $V_l(t)$  will tend to be small, it should be controlled fairly tightly.

## 1.2 Original Knockoff Features

The original formulation of the method offers two similar methods of constructing knockoffs. Both of these will, by construction, have exactly the property that

$$\tilde{X}^T \tilde{X} = \Sigma \text{ and } \tilde{X}^T X = \Sigma - \text{diag}\{\mathbf{s}\}.$$

For both methods, the first step is to normalize the matrix  $X$  such that  $X_j^T X_j = 1$  for all  $j$ . Then, let the Gram matrix of  $X_L$  is

$$\Sigma_L = [X \ \tilde{X}]^T [X \ \tilde{X}] = \begin{bmatrix} \Sigma & \Sigma - \text{diag}\{\mathbf{s}\} \\ \Sigma - \text{diag}\{\mathbf{s}\} & \Sigma \end{bmatrix}$$

$A$ , the Schur complement of  $\Sigma$  in  $\Sigma_L$  can be calculated as

$$A = 2 \text{diag}\{\mathbf{s}\} - \text{diag}\{\mathbf{s}\} \Sigma^{-1} \text{diag}\{\mathbf{s}\}$$

For  $\Sigma_L$  to exist,  $\Sigma_L$  must be positive semi-definite, which happens if and only if  $A$  is positive semi-definite, which happens in turn if and only if<sup>2</sup>

$$\text{diag}\{\mathbf{s}\} \succeq 0 \text{ and } 2\Sigma - \text{diag}\{\mathbf{s}\} \succeq 0$$

Given this is true,  $A$  can be factored as  $A = C^T C$ . Combining this with a satisfactory  $\mathbf{s}$  and an orthonormal matrix  $\tilde{U} \in \mathbb{R}^{n \times p}$  such that  $\tilde{U}^T X = 0$ , a  $\tilde{X}$  fulfilling the desired properties can be calculated as

$$\tilde{X} = X(I - \Sigma^{-1} \text{diag}\{\mathbf{s}\}) + \tilde{U}C$$

As mentioned above,  $\mathbf{s}$  should be chosen so as to make  $\text{diag}\{\Sigma\} - \mathbf{s}$  small. Since each  $X_j$  has been normalized, this means that  $\text{diag}\{\Sigma\} = \mathbf{1}$ , so  $\mathbf{1} - \mathbf{s}$  should be minimized in accordance with the restrictions on  $\mathbf{s}$ . The two methods differ in how  $\mathbf{s}$  is chosen:

- *Equi-correlated knockoffs*: Each original features is set to have the same correlation with its knockoff by setting  $\mathbf{s} = 2 \min\{\lambda_{\min}(\Sigma), 1\} \mathbf{1}$ . For all simulations in this paper, this was the method used.

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<sup>2</sup>A fleshed out version of this argument can be found in the original knockoff paper

- *SDP knockoffs*: The  $\mathbf{s}$  which minimizes the average correlation between knockoff and original features can be found via a semi-definite programming problem:

$$\begin{aligned} & \text{minimize} && \|\mathbf{1} - \mathbf{s}\|_1 \\ & \text{subject to} && \mathbf{0} \preceq \text{diag}\{\mathbf{s}\} \preceq 2\Sigma \end{aligned}$$

This method is significantly more computationally intensive.

### 1.3 Binary Knockoffs

Though the “original” knockoff method, described above, achieves the exact desired knockoff properties, the individual values in the vector  $X_j$  will have little relation to the individual values in  $\tilde{X}_j$ . In particular, these values will often have very different empirical distributions. This effect is particularly noticeable when the random variable  $x_j$  is discrete but  $\tilde{X}_j$  does not even consist of the same set of values. The end result is that for variable selection for other generalized linear models, which do not have the same sufficient statistics as linear regression which knockoffs are designed to hit, the original knockoffs will fail to control FDR.

Thus, this paper offers a new method of generating knockoffs which should offer superior performance with other GLMs. In this new method, the matrix of knockoff features  $\tilde{X}$  will be generated by row from a random vector valued variable  $\tilde{\mathbf{x}}$ , each entry  $\tilde{x}_j$  of which will have the property  $\tilde{x}_j \sim x_j$ . This random variable will also abide by a relaxation of the original knockoff condition:

$$\mathbb{E}[\tilde{\mathbf{x}}^T \tilde{\mathbf{x}}] = \Sigma \quad \text{and} \quad \mathbb{E}[\tilde{\mathbf{x}}^T \mathbf{x} \mid \mathbf{x}] = \Sigma - \text{diag}\{\mathbf{s}\}$$

This will ensure that, at the very least, these knockoffs are a suitable replacement for the original knockoffs for linear regression.

Generating such knockoffs for a completely general case of any  $\mathbf{x}$  is likely infeasible. However, in the specific case where  $\mathbf{x}$  is a random binary vector variable, this paper will demonstrate a method to generate such knockoff variables. Since binary data is extremely common in many areas, this will hopefully serve as a useful tool.

### 1.4 Paper Organization

The rest of this paper will be organized in the following fashion:

- Section 2 will go into more detail about how the original knockoffs breakdown with generalized linear models. In particular, several simulations will demonstrate how they breakdown.
- Section 3 will develop the method and theory for generating binary knockoffs.
- Section 4 will discuss tests of Binary knockoffs in simulation, both in comparison to the original knockoffs with Lasso and for logistic regression by itself.
- Section 5 is the final section, and will contain discussion of the results as well as areas for further work.

## 2 Issues With Deterministic Knockoffs

The knockoff filter and  $W$  statistics have a very natural extension to generalized linear models. Here, where  $l(\beta \mid X, \tilde{X})$  is the log likelihood of coefficients  $\beta$  given the model, the  $L1$  regularized regression model will have estimated coefficient vector

$$\beta(\lambda) = \operatorname{argmin}_{\mathbf{b}} \left\{ l(\beta \mid X, \tilde{X}) + \lambda \|\mathbf{b}\|_1 \right\}$$

The  $Z_j$  and  $\tilde{Z}_j$  are then, once again, the largest  $\lambda$  such that the given original or knockoff feature has a positive coefficient, and then  $W_j$  is constructed exactly as before. The problem with this is that if the given GLM doesn't have the same sufficient statistics as linear regression, there is no theoretical guarantee that the knockoff filter will control FDR. This is since, for null  $X_j$ , there is no theory to guarantee the  $Z_j$  and  $\tilde{Z}_j$  are exchangeable, and thus  $W_j$  is not guaranteed to be symmetrically distributed around 0.

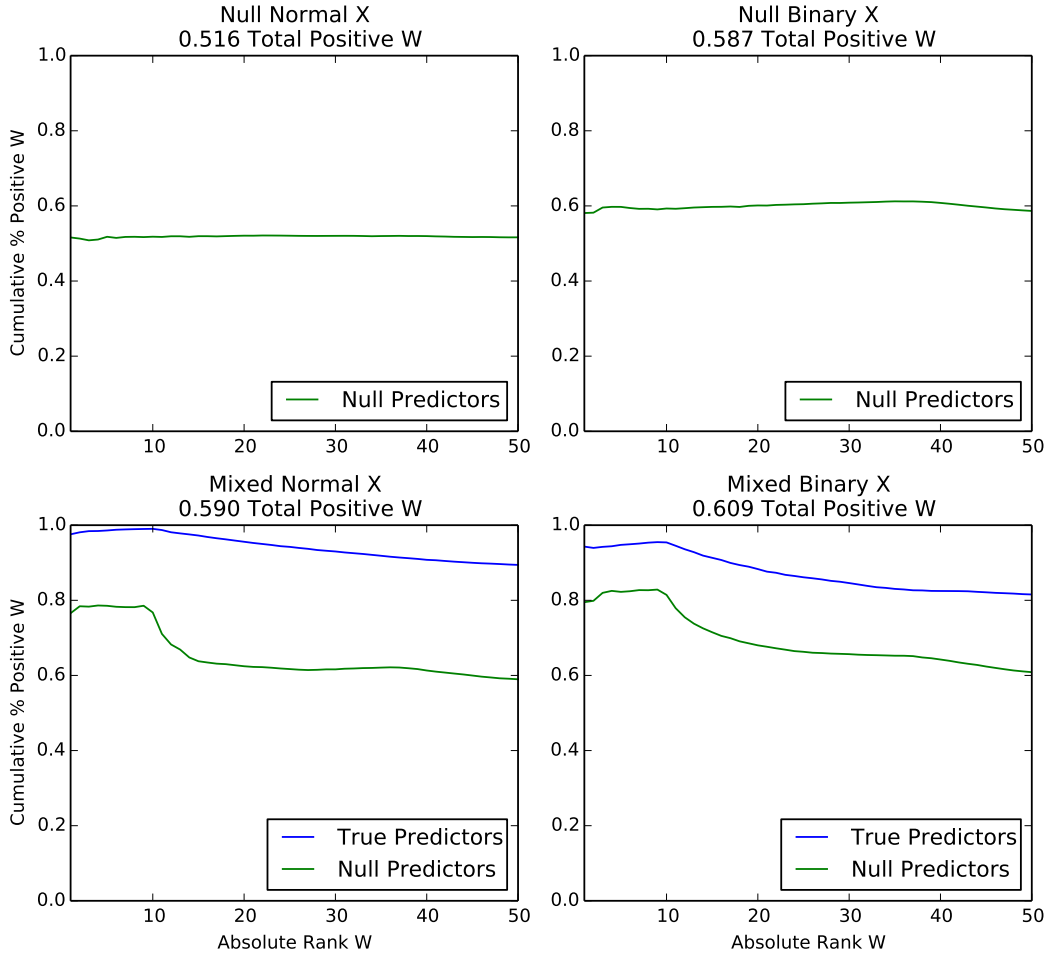


Figure 1: The mean cumulative portion of  $W$  statistic which are positive by absolute rank of the value. The mean is over 1000 simulations. On the left side, the features are drawn from a random standard normal distribution. On the right side, they are drawn as Bernoulli with probability .25 of being 1. The top has 50 features uncorrelated with the outcome, while the bottom has 40 features uncorrelated with the outcome and 10 correlated with it.

To test how bad this problem is, I tested the method using original style knockoffs in logistic regression. The results can be seen in figure 1, which shows cumulatively, starting with the largest absolute value, what portion of the  $W_j$  are positive. For the method to work, for the null predictors, this should be a consistent 50%, indicative of the desired symmetric distribution. This is particularly important for high values, which play the largest roll in selecting a threshold. We see that in the top left corner, when all features are null and normally distributed, that we almost achieve this, with only a small, but consistent, deviation from 50%. However, in the top right, when the predictors are binary, the null originals enter first far more often, which will result in the FDR being too high.

This gets much worse when some true predictors are included, as shown in the bottom row of the figure. For both normal and binary predictors, the originals come in first far more often in the beginning. This will completely ruin FDR control, since the portion of null predictors will be assumed far lower than it actually is. It is worth noting that the particular shape of the curve in the diagram, with the plateau for the null predictors through 10, is partially an artifact of how the totals were tabulated. The mean through the first ten is the mean for null predictors that came in first out of both null and true predictors; since the largest ten  $W_j$  will tend to be true predictors, the average over the null predictors represent the few extreme  $W_j$  which managed to beat out some number of true predictors.

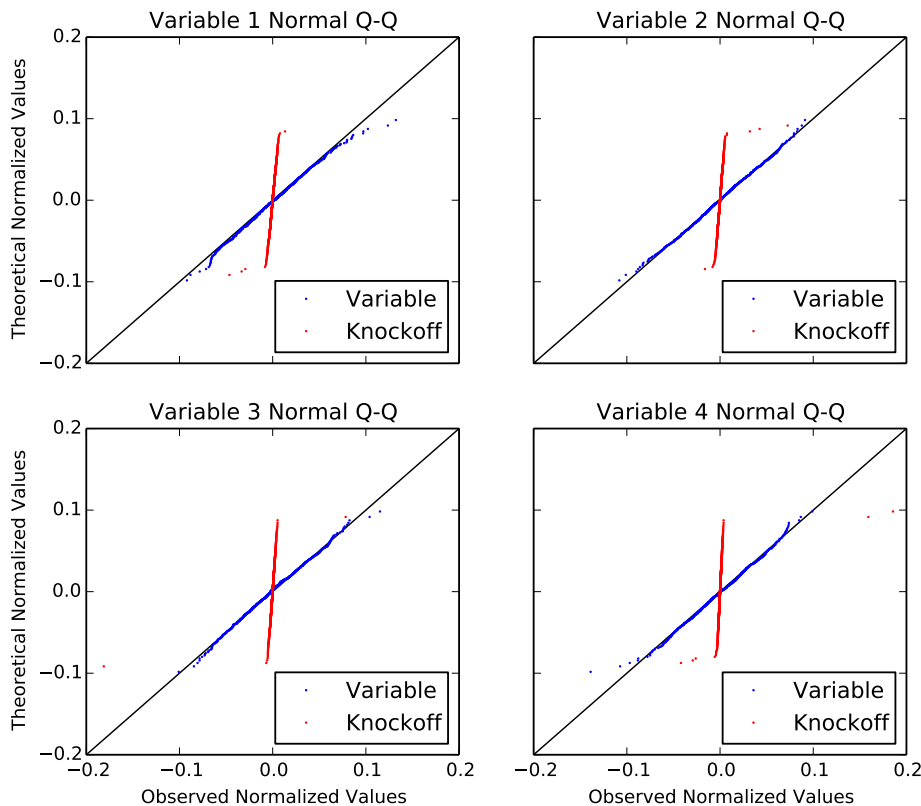


Figure 2: Normal Q-Q of original variables and knockoffs for simulation with 4 variables and 1,000 observations

Upon examination, the issue seems to be that the original style knockoff features have a very different empirical

distribution than the features they are imitating. This is obviously true with the binary features, but even with the normal features, the distributions differ a lot. In figure 2, the distribution of four feature and the original style knockoff are plotted against a normal distribution in Q-Q plots. As you can see, they don't match at all. This is suggestive of a solution; if the knockoff variables match the marginal distribution of the original features better, the result may be more suitable for FDR control in GLMs.

### 3 Random Binary Knockoffs

Random binary knockoffs  $\tilde{\mathbf{x}}$ , which maintain the correlation condition in expectation, fit the bill in this regard. The method to produce them is based heavily on more general methodology to random binary vector variables with internal correlation.

#### 3.1 Random Binary Vector Generation

The full class of random binary vector variables on  $\{0, 1\}^p$  can be specified as multinomial on the  $2^p$  elements of the set. However, in practice, it is generally impractical to specify or estimate all  $2^p$  necessary parameters, so it is useful to, as is desirable for knockoffs, pick a method to match the first two moments. These are the mean vector  $E(\mathbf{x}) = \mathbf{m} \in (0, 1)^p$  and the cross-moment matrix  $E(\mathbf{x}\mathbf{x}^T) = \mathbf{M} \in (0, 1)^{p \times p}$ . Obviously,  $m_i = P(x_i = 1)$ ,  $M_{ij} = P(x_i = x_j = 1)$ , and  $\mathbf{m} = \text{diag}\{\mathbf{M}\}$ . For an arbitrary symmetric  $M$  to be valid cross-moment matrix for some random binary vector variable,  $M - \mathbf{m}\mathbf{m}^T \succeq 0$ , and

$$\max\{0, m_i + m_j - 1\} \leq M_{ij} \leq \min\{m_i, m_j\}$$

for all  $i \neq j$ . Given a qualifying  $M$ , or observed  $X$ , there are then a few methods for generating additional random values.

##### 3.1.1 Gaussian Copula Family

Since multivariate normal distributions are easy to randomly draw from and defined by their first two moments, an obvious choice is to use them to generate random binary vectors. This might be done by finding  $\mu$  and  $\Sigma$  such that for  $\mathbf{z} \sim N_p(\mu, \Sigma)$ ,  $x_i$  can be generated as  $x_i = \text{sign}(z_i)$ , and have the desired first two moments. However, this is only guaranteed to be feasible in the bivariate case. For higher dimensions, this method can generally only provide random binary vectors with approximately the right moments, and the quality of the approximation quickly degenerates as  $p$  increases.

### 3.1.2 $\mu$ -Conditionals family

There exists a more flexible family which will always work for arbitrary  $M$  called  $\mu$ -conditionals. The basic idea is that the  $X$  is generate sequentially as

$$P(x_i = 1 \mid x_1, \dots, x_{i-1}) = \mu \left( a_{ii} + \sum_{k=1}^{i-1} a_{ik} x_k \right)$$

for some monotone function  $\mu : \mathbb{R} \rightarrow (0, 1)$ . This is essentially a binomial family GLM for a link function  $\mu$ . If one takes all of the  $a_{kj}$ , they can form a lower triangular matrix  $A$ , and then the joint density can be expressed as

$$P(\mathbf{x} = \gamma) \propto \mu(\gamma^T A \gamma)$$

If  $\mu$  is chosen such that it is a bijection and differentiable, there is a unique  $A$  such that  $E(\mathbf{x}\mathbf{x}^T) = M$  when generated from this model. The natural choice for  $\mu$  is the logistic link function  $L(x) = \frac{1}{1+e^{-x}}$ , which yields the Ising model, the “binary analogue of the multivariate normal distribution which is the maximum entropy distribution on  $\mathbb{R}^p$  having a given covariance matrix.” Additionally, it has the usual benefit that the coefficients can be viewed as a log odds ratio:

$$a_{ij} = \log \left( \frac{P(x_j = x_k = 1)P(x_j = x_k = 0)}{P(x_j = 0, x_k = 1)P(x_j = 1, x_k = 0)} \right)$$

when  $i \neq j$ . When  $\mathbf{x}$  is generated from this model with  $a_{ij} = 0$ , then  $x_i$  and  $x_j$  are conditionally independent.

There is no closed form to calculate the entries in  $A$  if  $p > 1$ , but they can be derived numerically two ways. The first of these, when one is attempting to replicate the empirical cross-moments from a data matrix  $X$ ,  $a_{1i}$  to  $a_{ii}$  is by fitting successive binomial family GLM regressions. The link function is the given function  $\mu$ , and  $X_i$  is regressed on  $X_1 \dots X_{i-1}$  using maximum likelihood.  $a_{ji}$  for  $i \neq j$  will then be the coefficient on  $X_j$  while  $a_{ii}$  is the intercept of the regression.

Otherwise, if one is just working with a desired cross-moment matrix  $M$ , the successive rows of  $A$  can be fit via Newton-Raphson. This is performed successively on each row of  $A$ . If the first  $i - 1$  rows have been fit, then the upper left  $(i - 1) \times (i - 1)$  sub matrix  $A_{-i}$  of  $A$  has already been filled. Next,  $\mathbf{a}_i$ , the first  $i$  entries of the  $i$ th row of  $A$  must be fit, while the rest of the row will be 0. This corresponds to  $\mathbf{m}_i$ , the first  $i$  entries of the  $i$ th row of  $M$ . In other words,  $\mathbf{m}_i = [E(x_i x_j)]_{j=1}^i$ . Finally, let us say that  $\mathbf{x}_{-i}$  is the first  $i - 1$  entries of  $\mathbf{x}$ .  $\mathbf{a}_i$  must satisfy

$$\begin{aligned} \mathbf{m}_i &= E \left( x_i \begin{bmatrix} \mathbf{x}_{-i} \\ x_i \end{bmatrix} \right) \\ \mathbf{m}_i &= E \left( E \left( x_i \begin{bmatrix} \mathbf{x}_{-i} \\ x_i \end{bmatrix} \mid \mathbf{x}_{-i} \right) \right) \\ \mathbf{m}_i &= \sum_{\mathbf{x}_{-i} \in \{0,1\}^{i-1}} P(\mathbf{x}_{-i}) P(x_i = 1 \mid \mathbf{x}_{-i}) \begin{bmatrix} \mathbf{x}_{-i} \\ 1 \end{bmatrix} \end{aligned}$$



When  $\mu$  is the logistic link function  $L$ , this is

$$\mathbf{m}_i = \sum_{\mathbf{x}_{-i} \in \{0,1\}^{i-1}} \frac{1}{c} L(\mathbf{x}_{-i}^T A_{-i} \mathbf{x}_{-i}) L\left(\mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_{-i} \\ 1 \end{bmatrix}\right) \begin{bmatrix} \mathbf{x}_{-i} \\ 1 \end{bmatrix}$$

Where  $c$  is the appropriate normalizing constant. Let us define the quantity on the right in the last line as  $f(\mathbf{a}_i)$ .

This equation  $f(\mathbf{a}_i) = \mathbf{m}_i$  can be solved by successive Newton-Raphson iterations defined by

$$\mathbf{a}_i^{(k+1)} = \left[ Hf(\mathbf{a}_i^{(k)}) \right]^{-1} \left[ f(\mathbf{a}_i^{(k)}) - \mathbf{m}_i \right]$$

To do so, the Hessian matrix is calculated as

$$Hf(\mathbf{a}_i) = \sum_{\mathbf{x}_{-i} \in \{0,1\}^{i-1}} \frac{1}{c} L(\mathbf{x}_{-i}^T A_{-i} \mathbf{x}_{-i}) L' \left( \mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_{-i} \\ 1 \end{bmatrix} \right) \begin{bmatrix} \mathbf{x}_{-i} \\ 1 \end{bmatrix} \begin{bmatrix} \mathbf{x}_{-i}^T & 1 \end{bmatrix}$$

With  $2^{i-1}$  possible values for  $\mathbf{x}_{-i}$ , this can quickly become computationally expensive. Instead, with a series of values  $\mathbf{x}_{-i}^{(k)} \sim \mathbf{x}_{-i}$ , the simulated values

$$f(\mathbf{a}_i) \approx \frac{1}{K} \sum_{k=1}^K L \left( \mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_{-i}^{(k)} \\ 1 \end{bmatrix} \right) \begin{bmatrix} \mathbf{x}_{-i}^{(k)} \\ 1 \end{bmatrix}$$

and

$$Hf(\mathbf{a}_i) \approx \frac{1}{K} \sum_{k=1}^K L' \left( \mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_{-i}^{(k)} \\ 1 \end{bmatrix} \right) \begin{bmatrix} \mathbf{x}_{-i}^{(k)} \\ 1 \end{bmatrix} \begin{bmatrix} [\mathbf{x}_{-i}^{(k)}]^T & 1 \end{bmatrix}$$

can be used.

Though, in theory,  $A$  should always exist, in practice numerical issues may compound to the point that the Newton-Raphson method won't converge. In this case, one can solve instead for  $\mathbf{m}_i^*(\tau)$ , where, for  $\tau \in [0, 1]$

$$\mathbf{m}_i^*(\tau) = (1 - \tau)\mathbf{m}_i + \tau \begin{bmatrix} 0 & \dots & 0 & M_{ii} \end{bmatrix}^T$$

When  $\tau = 0$ , this yields the original problem, while when  $\tau = 1$ , it treats  $x_i$  as independent of  $\mathbf{x}_{-i}$ . The latter will always have the solution

$$\mathbf{a}_i = \begin{bmatrix} 0 & \dots & 0 & \log\left(\frac{M_{ii}}{1-M_{ii}}\right) \end{bmatrix}^T$$

The hope is that for some  $\tau$  close to 0, convergence can be achieved, only causing a slight distortion from the desired cross moments.

### 3.2 Generating Binary Knockoffs

This theory provides the tools to generate random binary knockoffs. This is done sequentially as two steps, the first of which is to come up with the target covariance matrix for  $\mathbf{x}_L = [\mathbf{x} \ \tilde{\mathbf{x}}]$ . Much as before with the original knockoffs, both the equi-correlated and SDP method can be used to select  $\mathbf{s}$  such that  $\text{diag}\{\Sigma\} - \mathbf{s}$  is small and

$$\Sigma_L = \begin{bmatrix} \Sigma & \Sigma - \text{diag}\{\mathbf{s}\} \\ \Sigma - \text{diag}\{\mathbf{s}\} & \Sigma \end{bmatrix} \succeq 0$$

Additionally though, the moment condition must hold for this to correspond to a proper random binary vector. If  $\mathbf{m}_L = E(\mathbf{x}_L) = [\mathbf{m} \ \mathbf{m}]$ , then the desired cross moment matrix of the joint distribution is

$$M_L = \Sigma_L + \mathbf{m}_L \mathbf{m}_L^T$$

So it must be the case that

$$\max\{0, \mathbf{m}_{L,i} + \mathbf{m}_{L,j} - 1\} \leq \Sigma_{L,ij} + \mathbf{m}_i \mathbf{m}_j \leq \min\{\mathbf{m}_{L,i}, \mathbf{m}_{L,j}\}$$

However, since  $\Sigma$  and  $\mathbf{m}$  are from an actual random binary vector, the entries of  $\Sigma$  satisfy this property by default. Only off diagonal entries which have had  $\mathbf{s}$  subtracted from them could possibly violate this condition. Furthermore, for these entries, the goal is to make  $\Sigma_{L,ij}$  as close to 0 as possible. Since the condition is always satisfied in a neighborhood of  $M_{L,ij} = \mathbf{m}_{L,j} \mathbf{m}_{L,i}$ , this implies that this method should normally be satisfied. For the SDP method though, the restriction can be built directly into the optimization problem, yielding the updated problem

$$\begin{aligned} & \text{minimize} \quad \|\mathbf{1} - \text{diag}\{\Sigma\}^{-1} \mathbf{s}\|_1 \\ & \text{subject to} \quad 0 \preceq \text{diag}\{\mathbf{s}\} \preceq 2\Sigma \\ & \quad \quad \quad 2\mathbf{m}_i - 1 \leq \Sigma_{ii} - \mathbf{s}_i + \mathbf{m}_i^2 \leq \mathbf{m}_i \quad \forall i \end{aligned}$$

replacing  $\mathbf{s}$  with  $\text{diag}\{\Sigma\}^{-1} \mathbf{s}$  in the objective is to account for not normalizing  $X$ , as is usually done with the original knockoffs.

Once a proper cross moment matrix  $M_L$  has been selected, one could simply apply the Newton-Raphson method to fit a corresponding  $A$  matrix, and then generate  $\tilde{\mathbf{x}}$  sequentially conditioned on  $x$ , as  $\tilde{x}_i \mid \mathbf{x}, \tilde{x}_1, \dots, \tilde{x}_{i-1}$ . However, there are a few computational wrinkles which can be chosen to speed up the process:

1. If the whole  $A$  matrix is being fit, then the upper half of the matrix, corresponding to  $\mathbf{x}$ , can be fit via the regression method, since they arise from real data  $X$ . This will tend to be quicker, since the calculation lends itself to parallel computing, and the data set will often be smaller than the space of all binary vectors or a simulation of that space. The second half of the matrix still must be fit via Newton-Raphson.
2. One can avoid fitting the first half of the  $A$  matrix entirely though if performing Newton-Raphson with by using the actual observed values in  $X$  to simulate  $\mathbf{x}$ . This can be done by either bootstrapping rows from  $X$  or using some number of copies of  $X$  exactly. The advantage of this is the saved computation and that  $\tilde{x}$  should be built to match the correlation condition more exactly. The downside is that, since these values won't be from the Ising model, the theoretical guarantee of a suitable  $A$  may no longer hold.
3. As  $A$  is being fit, even the parts of  $\mathbf{x}_{-i}$  corresponding to knockoffs need not be redrawn for each Newton-Raphson iteration or each successive  $i$ . This saves computation, and the multiplication

$$\begin{bmatrix} \mathbf{x}_{-i}^{(k)} \\ 1 \end{bmatrix} \begin{bmatrix} [\mathbf{x}_{-i}^{(k)}]^T & 1 \end{bmatrix}$$

doesn't need to be recomputed for each Newton-Raphson iteration, and the upper left portion,  $\mathbf{x}_{-i}^{(k)}[\mathbf{x}_{-i}^{(k)}]^T$  doesn't have to be recomputed for successive  $i$ . This may result in slight deviations in any particular draw compounding into a more severe error over time.

Combining the second and third trick leads to the final formulation. Rather than  $K$  simulations of  $\mathbf{x}$ , the simulation is started with the matrix  $X_F$ , which is  $X$  stacked up  $m$  times to get  $n \times m = K' \geq K$  rows. The following process is then repeated for  $p < i \leq 2p$ :

- Where  $\mathbf{x}_F^{(k)}$  is the  $k$ th row of  $X_F$ , the row  $\mathbf{a}_i$  is fit by Newton-Raphson iterations with

$$f(\mathbf{a}_i) \approx \frac{1}{K'} \sum_{k=1}^{K'} \mu \left( \mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_F^{(k)} \\ 1 \end{bmatrix} \right) \begin{bmatrix} \mathbf{x}_F^{(k)} \\ 1 \end{bmatrix}$$

and

$$Hf(\mathbf{a}_i) \approx \frac{1}{K'} \sum_{k=1}^{K'} \mu' \left( \mathbf{a}_i^T \begin{bmatrix} \mathbf{x}_F^{(k)} \\ 1 \end{bmatrix} \right) \begin{bmatrix} \mathbf{x}_F^{(k)} \\ 1 \end{bmatrix} \begin{bmatrix} [\mathbf{x}_F^{(k)}]^T & 1 \end{bmatrix}$$

- If the iterations won't converge, the relaxed equation  $f(\mathbf{a}_i) = m_i^*(\tau)$  is attempted instead for increasing values of  $\tau$  until it converges.
- After  $\mathbf{a}_i$  is fit, a new column  $X_i$  is drawn as independent Bernoulli with probability vector  $\mu(X_F \mathbf{a}_i)$ .
- $X_F$  is updated to

$$X_F = [X_F \ X_i]$$

At the end, the any  $n$  rows of  $X_F$  corresponding to the rows of  $X$  can be taken as  $X_L$ . Any such set should have the desired distribution for  $\tilde{X}$ .

## 4 Bernoulli Knockoff Performance

For each of thses, exaimine these situations:

- $X$  arises out of the assumed Isling model, with no high order interactions.
- $X$  does not arise out of this model, and does have higher order interactions. Could possibly model this by drawing the vector  $\mathbf{x}$  or subsets of it as multinomial with probabilities from a Dirichlet distribution.
- $X$  is from a real world data set, likely something in genetics.
- $y$  is normally distributed around  $X\beta$ .
- $y$  is drawn from some other distribution, possibly skewed, heavy tailed, or light tailed.
- $y$  is from a real world data set.

## 4.1 Gram Matrix Comparison

## 4.2 Binary vs. Determinist Knockoffs in LASSO

## 4.3 Binary Knockoffs in other Regularized GLMS

# 5 Discussion

## 5.1 Areas for Further Work

# 6 Further Work and Simulations

As I see it, further simulation work for my paper breaks down into three logical groups: comparison of random Bernoulli knockoffs to the original Knockoffs in LASSO, evaluation of Bernoulli knockoffs in other L1 regularized GLMs, and expanding random knockoffs to more general sorts of variables.

## 6.1 Comparison to Original Knockoffs in LASSO

The basic idea is to compare how the two sorts of knockoffs compare when  $X$  is binary and we are fitting a LASSO regression. Do they select the same variables? Do the binary knockoffs control FDR more or less conservatively? Situations to test:

- $X$  arises out of the assumed Ising model, with no high order interactions.
- $X$  does not arise out of this model, and does have higher order interactions. Could possibly model this by drawing the vector  $\mathbf{x}$  or subsets of it as multinomial with probabilities from a Dirichlet distribution.
- $X$  is from a real world data set, likely something in genetics.
- $y$  is normally distributed around  $X\beta$ .
- $y$  is drawn from some other distribution, possibly skewed, heavy tailed, or light tailed.
- $y$  is from a real world data set.

## 6.2 Evaluation of Binary Knockoffs in other GLMS

The one of the most interest would be logits. It would be good to see how successful the binary knockoffs are in controlling FDR without the theoretical guarantees that LASSO provides.

- $X$  arises out of the Ising model, in which case it seems like the knockoffs should control FDR.
- $X$  has higher order interactions, which might make the knockoffs perform poorly.
- $X$  is from a real world data set, likely something in genetics.

- $y$  is simulated based on the assumptions of the regression model.
- $y$  is simulated to violate assumptions of the regression model.
- $y$  is from a real world data set.

### 6.3 Generalizations/Harebrained Ideas

I have two seeds of ideas for extensions if I have enough time.

1. Still with binary data, one might be able to simulate binary variables with higher order interactions in the generation of  $X$  by including higher order interactions in the regression of  $X_i$  on  $X_{-i}$ . This would lead to  $A$  being a matrix of higher dimension. Even if this worked, extending the method to knockoffs may not be obvious.
2. In the general case where  $X$  is not binary, I can almost imagine a method set up along similar lines to the binary case.
  - The desired covariance matrix could be chosen as in the original knockoff paper.
  - Each  $x_i$ 's marginal distribution would be approximated by a kernel density estimate on  $X_i$ .
  - A  $x_i \mid x_1, \dots, x_{i-1}$  would be drawn from some reweighing of this marginal to achieve the proper covariance. For instance, if  $F_i^{-1}$  is the inverse CDF of the marginal kernel density for  $x_i$  and  $u_i \mid x_1, \dots, x_{i-1}$  is a RV on  $(0, 1)$ , then  $x_i = F_i^{-1}(u_i)$ .
  - Maybe fit generalized additive model for each successive  $x_i$  with kernel regression for  $x_1, \dots, x_{i-1}$  to predict mean. Then, skew marginal of  $x_i$  until it has that mean.