Controlled Variable Selection: Knockoff Filters

Yibin Xiong

May 27, 2022

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Controlled Variable Selection Problem

We want to find out which explanatory variables are "truly" associated with the response variable, in the sense of statistical significance.

i.e. $\forall j \text{ test } H_0^{(j)} : Y \perp \!\!\! \perp X_j \mid X_{-j}$. This is to find the *Markov blanket*, which retains information with minimal number of variables.

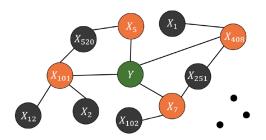


Figure: Markov blanket $\mathcal{S}: Y \perp\!\!\!\perp \{X_j\}_{j \notin \mathcal{S}} \mid \mathcal{S}$

Controlled Variable Selection Problem

Now we have a multiple hypothesis testing problem

> Avoid many false positives: control the false discovery rate (FDR)

Let \hat{S} be the set of covariates we selected and \mathcal{H}_0 be the set of "null" variables, which are defined by the individual null hypotheses.

$$\mathsf{FDR} := \mathbb{E}\left[\mathsf{FDP}
ight] = \mathbb{E}\left[rac{|\hat{S} \cap \mathcal{H}_0|}{\mathsf{max}\{|\hat{S}|,1\}}
ight]$$

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Controlled Variable Selection Problem

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ight]$$

- \circ More liberal than controlling the family-wise error rate $\mathbb{P}\left(|\hat{\mathcal{S}}\cap\mathcal{H}_0|\geq 1\right)$
- Making a false discovery, for example in genome-wide association studies, does not have high real-world costs.

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Idea of Knockoffs

 \triangleright A "copy" of covariate X_j that preserves the correlation structures and serves as a negative control (i.e. no correlation with the response Y)

• "Geometric" assumptions [1]

In matrix form, this is $\tilde{X}^T\tilde{X} = X^TX = \Sigma$, $X^T\tilde{X} = \Sigma - \mathrm{diag}\{s\}$

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Idea of Knockoffs

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• "Geometric" assumptions [1]

$$\begin{split} & \tilde{X}_j^T \tilde{X}_k = X_j^T X_k = 1 \ \ \forall j, k \\ & X_j^T \tilde{X}_k = X_j^T X_k \qquad \ \ \forall j \neq k \\ & X_j^T \tilde{X}_j = 1 - s_j \quad \text{for some } s_j \text{ close to } 1 \end{split}$$

In matrix form, this is $\tilde{X}^T\tilde{X} = X^TX = \Sigma$, $X^T\tilde{X} = \Sigma - \mathrm{diag}\{s\}$

- Compute a statistics that indicates relative importance of the covariate versus its knockoff.
- \triangleright Select variables sequentially until the empirical estimate of FDR hits a threshold.

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Assume $n \ge 2p$ and $y = X\beta + z$, where $z \sim \mathcal{N}(0, \sigma^2 I)$.

Step 1: Construct the knockoffs

We want

$$\begin{bmatrix} X & \tilde{X} \end{bmatrix}^T \begin{bmatrix} X & \tilde{X} \end{bmatrix} = \begin{bmatrix} \Sigma & \Sigma - \mathsf{diag}\{s\} \\ \Sigma - \mathsf{diag}\{s\} & \Sigma \end{bmatrix} \succeq 0$$

By Schur complement calculation, we can construct

$$ilde{X} := X(I - \Sigma^{-1} \mathsf{diag}\{s\}) + ilde{U}C$$

where \tilde{U} orthogonal, $\tilde{U}^TX=0$, and $C^TC=2\mathrm{diag}\{s\}-\mathrm{diag}\{s\}\Sigma^{-1}\mathrm{diag}\{s\}$.

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¹∧ denotes min and ∨ denotes max

Assume $n \ge 2p$ and $y = X\beta + z$, where $z \sim \mathcal{N}(0, \sigma^2 I)$.

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How to choose s?

- Equi-correlated knockoffs: $\forall j : s_i := 2\lambda_{\min}(\Sigma) \wedge 1^{-1}$
- ullet SDP knockoffs: $\min_{s_j} \sum_j 1 s_j \quad ext{s.t. } 0 \leq s_j \leq 1, \ ext{diag}\{s\} \preceq 2\Sigma$

 1 ∧ denotes min and \vee denotes max 1 denotes min and 2 denotes 2 denotes 3

> Step 2: Compute the statistics for each pair of original and knockoff variables

We consider LASSO coefficients that enable us to screen out the important variables:

$$\hat{\beta}(\lambda) = \arg\min_{b} \frac{1}{2} \|y - \begin{bmatrix} X & \tilde{X} \end{bmatrix} b\|_{2}^{2} + \lambda \|b\|_{1}$$

As λ gets larger, we focus more on the penalization and the solution tends to be more sparse and leaves only the important variables.

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As λ gets larger, we focus more on the penalization and the solution tends to be more sparse and leaves only the important variables.

We define $Z_j := \sup\{\lambda : \hat{\beta}_j(\lambda) \neq 0\}$ as an importance score for each covariate and its knockoff. Then define

$$W_j := Z_j ee ilde{Z_j} \cdot egin{cases} +1, & Z_j > ilde{Z_j} \ -1, & Z_j < ilde{Z_j} \ 0, & Z_j = ilde{Z_j} \end{cases}$$

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 \triangleright Step 3: Define a data-dependent threshold for the statistics We specify a level q for controlling the FDR (e.g. q=0.05).

knockoff:

$$T := \min \left\{ t : \frac{\#\{j : W_j \le -t\}}{\#\{j : W_j \ge t\} \lor 1} \le q \right\}$$

• knockoff+:

$$T := \min \left\{ t : \frac{1 + \#\{j : W_j \le -t\}}{\#\{j : W_j \ge t\} \lor 1} \le q \right\}$$

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knockoff+:

$$T := \min \left\{ t : \frac{1 + \#\{j : W_j \le -t\}}{\#\{j : W_j \ge t\} \lor 1} \le q \right\}$$

Step 4: Sequential selection

Arrange the covariates by descending order of $|W_j|$, and select the covariates that correspond to positive W_j until the quantity exceeds q.

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Theoretical Guarantees: Assumptions

- > What we assumed
 - $n \ge 2p$ (can adapt to $n \ge p$)
 - linear regression model $F_{Y|X} = \mathcal{N}(X\beta, \sigma^2 I)$, used when computing Z_j and showing exchangebility results
 - geometric assumptions
 - sufficiency of the statistics:

W ONLY depends on the Gram matrix and the feature-response inner product

$$W = f(\begin{bmatrix} X & \tilde{X} \end{bmatrix}^T \begin{bmatrix} X & \tilde{X} \end{bmatrix}, \begin{bmatrix} X & \tilde{X} \end{bmatrix}^T y)$$

• antisymmetry of the statistics: $W_j(Z_j, \tilde{Z}_j) = -W_j(\tilde{Z}_j, Z_j)$ swapping X_j and \tilde{X}_j in the augmented design matrix changes the sign of W_j

$$\forall \operatorname{set} S : \forall j \in S : W_j \left(\begin{bmatrix} X & \tilde{X} \end{bmatrix}_{\operatorname{swap}(S)}, y \right) = -W_j \left(\begin{bmatrix} X & \tilde{X} \end{bmatrix}, y \right)$$

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Theoretical Guarantees: Exchangeability

Exchangeability result

For any subset *S* of the *null* variables,

$$\begin{bmatrix} X & \tilde{X} \end{bmatrix}_{\text{swap}(S)}^{T} \begin{bmatrix} X & \tilde{X} \end{bmatrix}_{\text{swap}(S)} = \begin{bmatrix} X & \tilde{X} \end{bmatrix}^{T} \begin{bmatrix} X & \tilde{X} \end{bmatrix}$$
 (1)

$$\begin{bmatrix} X & \tilde{X} \end{bmatrix}_{\text{swap}(S)}^{T} y \stackrel{d}{=} \begin{bmatrix} X & \tilde{X} \end{bmatrix}^{T} y \tag{2}$$

- \circ (1) is a direct consequence of the geometric assumptions, i.e. by our construction.
- Proof of (2) uses the geometric assumption and linear homoskedastic model.
- \circ Exchangeability, combined with antisymmetry of the statistics, is the key for showing i.i.d. signs of null statistics because $M \stackrel{d}{=} M' \Rightarrow f(M) \stackrel{d}{=} f(M')$.

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Theoretical Guarantees: A Key Property

i.i.d. signs of null statistics

For any null variable j, conditional on $|W| = (|W_1|, \dots, |W_p|)$,

$$W_j \stackrel{d}{=} -W_j \tag{3}$$

$$\#\{j: \beta_j = 0, W_j \le -t\} \stackrel{d}{=} \#\{j: \beta_j = 0, W_j \ge t\}$$
 (4)

- \circ This makes intuitive sense since we expect W_j to be a large positive value if X_j is a signal and W_j to be close to 0 if X_j is a null variable. For a null X_j , It should be equally very unlikely for W_j to be a positive large number or to be a negative large number.
- This gives us a good proxy for the number of false positives and the empirical FDR

$$\frac{\#\{j:\beta_j=0,W_j\geq t\}}{\#\{j:W_j\geq t\}\vee 1}\approx \frac{\#\{j:\beta_j=0,W_j\leq -t\}}{\#\{j:W_j\geq t\}\vee 1}\leq \frac{\#\{j:W_j\leq -t\}}{\#\{j:W_j\geq t\}\vee 1}$$

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Theoretical Guarantees: FDR Control

For knockoff+, we can guarantee that the FDR is at most q.

 \circ Since T is a stopping time, by optional stopping theorem of supermartingales

$$\mathbb{E}\left[\frac{\#\{j:\beta_j=0,W_j\geq T\}}{1+\#\{j:\beta_j=0,W_j\leq -T\}}\right]\leq \mathbb{E}\left[\frac{\#\{j:\beta_j=0,W_j\geq 0\}}{1+\#\{j:\beta_j=0,W_j\leq 0\}}\right]<1$$

o Main inequalities

$$\begin{split} \mathsf{FDR} &= \mathbb{E}\left[\frac{\#\{j: \beta_j = 0, \, W_j \geq T\}}{\#\{j: \, W_j \geq T\} \vee 1}\right] \\ &= \mathbb{E}\left[\frac{\#\{j: \beta_j = 0, \, W_j \geq T\}}{1 + \#\{j: \beta_j = 0, \, W_j \leq -T\}} \cdot \frac{1 + \#\{j: \beta_j = 0, \, W_j \leq -T\}}{\#\{j: \, W_j \geq T\} \vee 1}\right] \\ &\leq \mathbb{E}\left[\frac{\#\{j: \beta_j = 0, \, W_j \geq T\}}{1 + \#\{j: \beta_j = 0, \, W_j \leq -T\}}\right] \cdot q \\ &\leq q \end{split}$$

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Model-X Knockoffs

- ▷ Assumptions [2]:
 - Exchangeability: $(X, \tilde{X})_{\text{swap}(S)} \stackrel{d}{=} (X, \tilde{X})$
 - Conditional independence: $\tilde{X} \perp \!\!\! \perp Y \mid X$
 - ullet Distribution F_X , used for constructing $ilde{X}$

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Model-X Knockoffs

- ▷ Assumptions [2]:
 - Exchangeability: $(X, \tilde{X})_{\text{swap}(S)} \stackrel{d}{=} (X, \tilde{X})$
 - Conditional independence: $\tilde{X} \perp \!\!\! \perp Y \mid X$
 - ullet Distribution F_X , used for constructing $ilde{X}$
- > Improvements over vanilla knockoffs
 - Doesn't assume $F_{Y|X}$, which we don't exactly know but have to use models to approximate
 - Unsupervised data can be used
 - No geometric assumption, can be applied to high-dimensional settings
 - No sufficiency condition for W_j
 - Not just for homoscedastic linear model, but any regression and classification models



Constructing Knockoffs [2]

ightharpoonup If the components of X are independent, then we can sample \tilde{X} independently from F_X component-wise.

▷ If the components are correlated, use SCIP algorithm:

* SCIP can be take costly runtime in practice as some conditional distribution $\mathcal{L}(X_j \mid X_{-j}, \tilde{X}_{1:j-1})$ can be complicated and we need to compute a conditional distribution in each iteration.

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Exchangeability Results

Exchangeability of $Y \mid (X, \tilde{X})$

For any subset S of the *null* variables,

$$Y \mid (X, \tilde{X})_{\mathsf{swap}(S)} \stackrel{d}{=} Y \mid (X, \tilde{X})$$
 (5)

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Exchangeability Results

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For any subset S of the *null* variables,

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 (5)

- $p_{Y|(X,\tilde{X})_{\text{swap}(S)}}(y|(x,\tilde{x})) = p_{Y|(X,\tilde{X})}(y|(x,\tilde{x})_{\text{swap}(S)}) = p_{Y|X}(y|x'),$ where $x_i' = \tilde{x}_i$ if $i \in S$ and $x_i' = x_i$ otherwise. (by conditional indep.)
- $\forall j \in S$, since $Y \perp \!\!\! \perp X_j \mid X_{-j}$,

$$p_{Y|X}(y|x'_{j}, x'_{-j}) = p_{Y|X}(y|\tilde{x}_{j}, x'_{-j}) = p_{Y|X}(y|x_{j}, x'_{-j})$$

This shows that $Y \mid (X, \tilde{X})_{\text{swap}(S)} \stackrel{d}{=} Y \mid (X, \tilde{X})_{\text{swap}(S \setminus \{j\})}$. Repeat this process for all j gives us the result.

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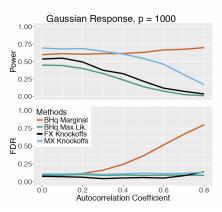
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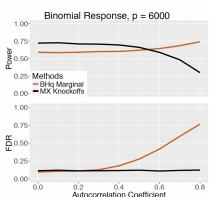
Theoretical Guarantees

- ightharpoonup This and exchangeability of (X, \tilde{X}) implies the exchangeability of the *joint* distribution.
- \triangleright Then any antisymmetric statistics in the form $W_j = w_j(\begin{bmatrix} X & \tilde{X} \end{bmatrix}, y)$ will have i.i.d. signs for the nulls. FDR control follows from this property.
- \triangleright No sufficiency assumption! The choice of Z_j can be more flexible and even produced by ML models.
 - LASSO coefficient difference: $Z_j = |\hat{\beta}_j|$, $W_j = |\hat{\beta}_j| |\hat{\beta}_{j+p}|$
 - * Can use cross-validation to choose regularization parameter λ
 - * Can apply to GLMs
 - Z_j = feature importance score in random forests
 - Data adaptive: apply random forests and LASSO, choose Z_j to be the feature importance measure corresponding to the model with smaller cross-validation error

Comparison with Other FDR Control Methods

▷ Canonical: produce p-values + Benjamini Hochberg (BHq) method





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Motivations

- Variable selection problem: Identify which SNPs, out of millions of candidates, influence the risk of a particular disease or a trait
- Genome data particularly fit the assumptions of Model-X knockoff (know F_X and a lot of unsupervised data)
- Apply hidden Markov model (HMM) to deal with linkage disequilibrium, i.e. dependence between nearby alleles on a genome.
- HMM has relatively simple close-forms for SCIP algorithm
- ullet Computationally efficient algorithm for constructing knockoffs, $\mathcal{O}(np)$

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SCIP for Markov Chains [4]

chain generates the jth knockoff variable \tilde{X}_j by sampling from

$$\mathbb{P}\left[\tilde{X}_{j} = \tilde{x}_{j} \middle| X_{-j} = x_{-j}, \tilde{X}_{1:(j-1)} = \tilde{x}_{1:(j-1)}\right] = \begin{cases}
\frac{q_{1}(\tilde{x}_{1}) Q_{2}(x_{2} | \tilde{x}_{1})}{\mathcal{N}_{1}(x_{2})}, & j = 1, \\
\frac{Q_{j}(\tilde{x}_{j} | x_{j-1}) Q_{j}(\tilde{x}_{j} | \tilde{x}_{j-1}) Q_{j+1}(x_{j+1} | \tilde{x}_{j})}{\mathcal{N}_{j-1}(\tilde{x}_{j}) \mathcal{N}_{j}(x_{j+1})}, & 1 < j < p, \\
\frac{Q_{p}(\tilde{x}_{p} | x_{p-1}) Q_{p}(\tilde{x}_{p} | \tilde{x}_{p-1})}{\mathcal{N}_{p-1}(\tilde{x}_{p}) \mathcal{N}_{p}(1)}, & j = p,
\end{cases}$$
(4)

with the normalization functions $\mathcal{N}_j: \mathcal{X} \mapsto \mathbb{R}_+$ defined recursively as

$$\mathcal{N}_{j}(k) = \begin{cases}
\sum_{l \in \mathcal{X}} q_{1}(l) Q_{2}(k|l), & j = 1, \\
\sum_{l \in \mathcal{X}} Q_{j}(l|x_{j-1}) Q_{j}(l|\tilde{x}_{j-1}) Q_{j+1}(k|l), & 1 < j < p, \\
\mathcal{N}_{j-1}(l), & 1 < j < p,
\end{cases}$$

$$\sum_{l \in \mathcal{X}} \frac{Q_{p}(l|x_{p-1}) Q_{p}(l|\tilde{x}_{p-1})}{\mathcal{N}_{p-1}(l)}, & j = p.$$
(5)

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SCIP for HMM [4]

 \triangleright General structure (with param. (π, A, B) specified for genetics context)

Algorithm 3 Knockoff copies of a hidden Markov model

- 1: sample $z=(z_1,\ldots,z_p)$ from $\mathbb{P}[Z|X=x]$, using a forward-backward procedure
- 2: sample a knockoff copy $\tilde{z}=(\tilde{z}_1,\ldots,\tilde{z}_p)$ of $z=(z_1,\ldots,z_p),$ using Algorithm 2
- 3: sample \tilde{x} from the conditional distribution of X given $\tilde{Z} = \tilde{z}$.

Sample a path of hidden states: "soft" version of Viterbi algorithm Instead of taking the arg max for backward pass in Viterbi algorithm, we sample from a probability distribution to get the previous state.

Algorithm 4 Forward-backward sampling (forward pass)

- 1: **initialize** t = 1, $\alpha_0 = 1$, $Q_1(k|l) = q_1(k)$ for all k, l, $\beta_j(k) = f_j(x_j|k)$
- 2: **for** j = 1 **to** p 1 **do**
- 3: **compute** the forward probabilities $\alpha_j = (Q_j \alpha_{j-1}) \odot \beta_j$
- 4: end for.

${\bf Algorithm~5~Forward\hbox{-}backward~sampling~(backward~pass)}$

- 1: **initialize** j = p, $Q_{p+1}(k|l) = 1$ for all k, l
- 2: for j = p to 1 (backward) do
- 3: sample z_j according to $\pi_j(z_j) = \frac{Q_{j+1}(z_{j+1}|z_j)\alpha_j(z_j)}{\sum_i Q_{j+1}(z_{j+1}|k)\alpha_j(k)}$
 - 4: end for.

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Approximate Knockoff Constructions

ightharpoonup We want (X, \tilde{X}) and $(X, \tilde{X})_{\mathsf{swap}(S)}$ to have the same *first two moments*.

This is equivalent to

$$\mathbb{E}\left[X\right] = \mathbb{E}\left[\tilde{X}\right], \ \mathsf{Cov}(X, \tilde{X}) = \begin{bmatrix} \Sigma & \Sigma - \mathsf{diag}\{s\} \\ \Sigma - \mathsf{diag}\{s\} & \Sigma \end{bmatrix}$$

* If $X \sim \mathcal{N}(0, \Sigma)$, then matching the first two moments is equivalent to matching the distributions.

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* If $X \sim \mathcal{N}(0, \Sigma)$, then matching the first two moments is equivalent to matching the distributions.

 \triangleright Moment matching \Rightarrow "worst" function matching

Define the **maximum mean discrepancy** (MMD) between two distributions as

$$\mathcal{D}_{\mathsf{MMD}}(P_X, P_Z) := \sup_{\|f\|_{\mathcal{H}_K} = 1} \left| \mathbb{E}_{X \sim P_X}[f(X)] - \mathbb{E}_{Z \sim P_Z}[f(Z)] \right|$$

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MMD Estimation (General)

By Cauchy-Schwarz and reproducing property of kernel,

$$\mathcal{D}_{\mathsf{MMD}}(P_X, P_Z)^2 = \mathbb{E}_{X, X'} [k(X, X')] - 2\mathbb{E}_{X \sim P_X, Z \sim P_Z} [k(X, Z)] + \mathbb{E}_{Z, Z'} [k(Z, Z')]$$

An unbiased estimate of this quantity is

$$\hat{\mathcal{D}}_{MMD}(\mathbf{X}, \mathbf{Z})^{2} = \frac{1}{n(n-1)} \sum_{i=1}^{n} \sum_{j \neq i} \left[k(X^{i}, X^{j}) + k(Z^{i}, Z^{j}) \right]$$
$$-\frac{2}{n^{2}} \sum_{i=1}^{n} \sum_{j=1}^{n} k(X^{i}, Z^{j})$$

where $\mathbf{X}, \mathbf{Z} \in \mathbb{R}^{n \times p}$ are design matrices.

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Deep Knockoff Machine [3]

ightarrow Generate $ilde{X}$ using deep neural networks with X and random noise V

$$\tilde{X}:=f_{\theta}(X,V)$$

ightarrow Ensure $\hat{\mathcal{D}}_{\mathrm{MMD}}((X, \tilde{X}), (X, \tilde{X})_{\mathrm{swap}(j)})^2$ for every j is small

We randomly partition X into $X', X'' \in \mathbb{R}^{\frac{n}{2} \times p}$ to obtain *unbiased* estimate. Define the loss function as

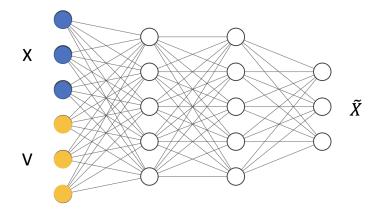
$$J_{\mathsf{MMD}}(X,\tilde{X}) = \hat{\mathcal{D}}_{\mathsf{MMD}}((X',\tilde{X}'),(\tilde{X}'',X''))^2 + \hat{\mathcal{D}}_{\mathsf{MMD}}((X',\tilde{X}'),(X'',\tilde{X}'')_{\mathsf{swap}(S)})^2$$

where S is a uniformly random subset of [p] where each index have 1/2 probability of being in S.

- → Minimize this loss function using stochastic gradient descent

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Deep Knockoff Machine: NN Architecture



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Deep Knockoff Machine: Algorithm [3]

Algorithm 1: Training a deep knockoff machine

Input: $X \in \mathbb{R}^{n \times p}$ – Training data.

 γ – Higher-order penalty hyperparameter.

 λ – Second-order penalty hyperparameter.

 δ – Decorrelation penalty hyperparameter.

 θ_1 – Initialization values for the weights and biases of the network.

 μ – Learning rate.

T – Number of iterations.

Output: f_{θ_T} – A knockoff machine.

Procedure:

for t = 1 : T do

Sample the noise realizations: $V^i \sim \mathcal{N}(0, I)$, for all $1 \leq i \leq n$;

Randomly divide X into two disjoint mini-batches X', X'';

Pick a subset of swapping indices $S \subset \{1, \dots, p\}$ uniformly at random;

Generate the knockoffs as a deterministic function of θ :

$$\tilde{X}^i = f_{\theta_t}(X^i, V^i)$$
, for all $1 \le i \le n$;

Evaluate the objective function, using the batches and swapping indices fixed above:

$$J_{\theta_{\star}}(\mathbf{X}, \tilde{\mathbf{X}}) = \gamma J_{\text{MMD}}(\mathbf{X}, \tilde{\mathbf{X}}) + \lambda J_{\text{second-order}}(\mathbf{X}, \tilde{\mathbf{X}}) + \delta J_{\text{decorrelation}}(\mathbf{X}, \tilde{\mathbf{X}});$$

Compute the gradient of $J_{\theta_t}(\mathbf{X}, \tilde{\mathbf{X}})$, which is now a deterministic function of θ ;

Update the parameters: $\theta_{t+1} = \theta_t - \mu \nabla_{\theta_t} J_{\theta_t}(\mathbf{X}, \tilde{\mathbf{X}});$

end



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References

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- [4] Matteo Sesia, Chiara Sabatti, and Emmanuel J Candès. "Gene hunting with hidden Markov model knockoffs". In: *Biometrika* 106.1 (2019), pp. 1–18.

Recommended resources: Prof. Sesia's website, Prof. Janson's talk, Prof. Candès' talk, Philp Anderson's video on FDR introduction

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