Supervised Learning II: high-dimensional model selection

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Learning Objectives

- ▶ Model selection, Bias-Variance tradeoff, a Bayesian View
- ▶ How do we handle $p \gg n$ situation in practice?
- Multiple Frequenist & Bayesian approaches

A working example: predicting gene expressions from genetic information

Q. Can we predict gene expressions based on genetic information?

 $\mathsf{DNA} \overset{\mathsf{here?}}{\to} \mathsf{mRNA} \to \mathsf{protein}$

If we could predict gene expression...

$$\mathsf{DNA} \overset{\mathsf{here?}}{\to} \mathsf{mRNA} \to \mathsf{protein}$$

We can guess potential mechanisms of genetic disorders:

$$\mathsf{DNA}\;\mathsf{change} \to \overset{\mathsf{black-box}}{(\cdots)} \to \mathsf{disease}$$

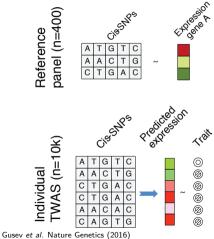
because we can do transcriptome-wide association studies (TWAS):

$$\Delta \mathsf{DNA} \to \mathsf{mRNA}(\Delta \mathsf{DNA}) \overset{\mathsf{test this}}{\to} \mathsf{disease}$$

Gamazon et al. Nature Genetics (2015)

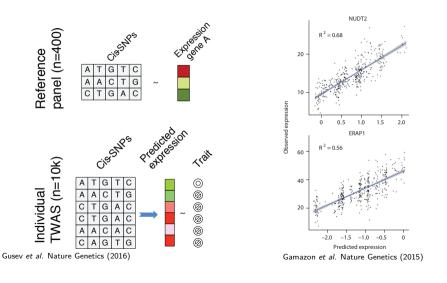
Gusev et al. Nature Genetics (2016)

If we could predict gene expression by genetic information...



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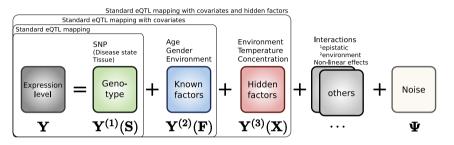
If we could predict gene expression by genetic information...



Today's problem: gene expression prediction

- ▶ We will focus on supervised learning (regression) of gene expression
- ▶ We will revisit the problem to discuss biological aspects in the GWAS lectures

Why regression?



- Handle multiple types of biological and technical factors
- Including all the variables often improve statistical powers
- ▶ What if there are too many variables?

Modeling gene expression as a function of genetic variants

$$\mathbf{y} = \left(\begin{array}{c} y_1 \\ y_2 \\ \vdots \\ y_n \end{array} \right), \quad X = \left(\begin{array}{ccc} X_{11} & \cdots & X_{1p} \\ X_{21} & \cdots & X_{2p} \\ & \cdots & \\ X_{n1} & \cdots & X_{np} \end{array} \right), \quad \theta = \left(\begin{array}{c} \theta_1 \\ \theta_2 \\ \vdots \\ \theta_p \end{array} \right)$$

Multivariate linear regression model:

$$\mathbf{y} = X\theta + \epsilon, \ \epsilon \sim \mathcal{N}(\mathbf{0}, \sigma^2 I)$$
.

Example

- $ightharpoonup \mathbf{y}$: a gene expression measured by RNA-seq / microarray.
- (X_{ij}) : genetic variants at locus j measured on individual i. X can be anything of interest, such as other genes and phenotypes.
- ▶ We can fit the model gene by gene (independence) or all the genes jointly (dependency between genes)

Two major interests in regression analysis

$$\mathbf{y} = \begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix}, \quad X = \begin{pmatrix} X_{11} & \cdots & X_{1p} \\ X_{21} & \cdots & X_{2p} \\ & \cdots & & \\ X_{n1} & \cdots & X_{nn} \end{pmatrix}, \quad \theta = \begin{pmatrix} \theta_1 \\ \theta_2 \\ \vdots \\ \theta_n \end{pmatrix}$$

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Multivariate linear regression model:

$$\mathbf{y} = X \mathbf{\theta} + \epsilon, \, \epsilon \sim \mathcal{N}(\mathbf{0}, \sigma^2 I)$$
 .

1. Estimation of unknown parameters (**posterior probability**):

$$p(\theta|X, \mathbf{y}) \propto p(\mathbf{y}|X, \theta)p(\theta)$$

Two major interests in regression analysis

$$\mathbf{y} = \left(\begin{array}{c} y_1 \\ y_2 \\ \vdots \\ y_n \end{array} \right), \quad X = \left(\begin{array}{ccc} X_{11} & \cdots & X_{1p} \\ X_{21} & \cdots & X_{2p} \\ & \cdots & \\ X_{n1} & \cdots & X_{np} \end{array} \right), \quad \theta = \left(\begin{array}{c} \theta_1 \\ \theta_2 \\ \vdots \\ \theta_p \end{array} \right)$$

Multivariate linear regression model:

$$\mathbf{y} = X\theta + \epsilon, \ \epsilon \sim \mathcal{N}(\mathbf{0}, \sigma^2 I)$$
.

1. Estimation of unknown parameters (posterior probability):

$$p(\theta|X, \mathbf{y}) \propto p(\mathbf{y}|X, \theta)p(\theta)$$

2. Prediction of future phenotype (posterior prediction):

$$p(\mathbf{y}^{\text{new}}|X^{\text{new}},X,\mathbf{y}) = \int p(\mathbf{y}^{\text{new}}|X^{\text{new}},\theta)p(\mathbf{y}|X,\theta)p(\theta)d\theta$$

Of many important questions, we will try to tackle this one...

$$p \gg n$$

- n: sample size
- p: number of parameters

Today's lecture

Bias-variance tradeoff

High-dimensional multivariate regression

Knock-off filter to control False Discovery Rate

Discussion

A class of models $\hat{f} \in \mathcal{F}$

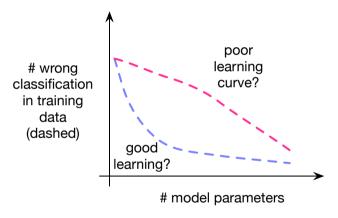
$$\begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix} = \theta_1 \begin{pmatrix} X_{11} \\ X_{21} \\ \vdots \\ X_{n1} \end{pmatrix} + \cdots \theta_p \begin{pmatrix} X_{1p} \\ X_{2p} \\ \vdots \\ X_{np} \end{pmatrix}.$$

- Different number of variables will define a class of potential models
- \blacktriangleright E.g., \mathcal{F}_1 : a class of models with one variable
- $\triangleright \mathcal{F}_2$: a class of models with two variables
- (...)
- $\triangleright \mathcal{F}_q$: a class of models with q variables

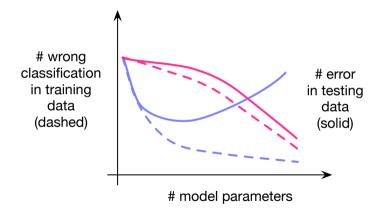
How do we know if one model is better than the other?

- ► Training vs. (unseen) testing data
- ightharpoonup Our hope: training pprox testing

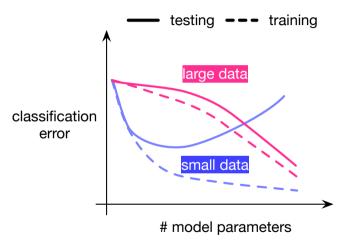
What is a good classifier?



What is a good classifier?



What is a good classifier?



The ultimate goal: generalization error minimization

k-fold CV error \rightarrow leave-one-out CV error \rightarrow generalization error

- No matter what may come, we will still predict as good as this...
- ▶ We will use k-fold cross validation error to estimate generalization error

$$\mathbb{E}\begin{bmatrix} \text{true unknown model} & \text{our attempt} \\ f(X) & -\hat{f}(X) \end{bmatrix}^2 = \mathbb{E}\begin{bmatrix} f(X) & \text{our attempt} \\ -\mathbb{E}[\widehat{f}] + \mathbb{E}[\widehat{f}] & -\hat{f}(X) \end{bmatrix}^2$$

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 (expand the square)
$$= \mathbb{E}\big[(f(X) - \mathbb{E}\big[\hat{f}\big])^2 + (\mathbb{E}\big[\hat{f}\big] - \hat{f}(X))^2 \\ + 2(f(X) - \mathbb{E}\big[\hat{f}\big])(\mathbb{E}\big[\hat{f}\big] - \hat{f}(X)) \end{bmatrix}$$

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$$\mathbb{E}\begin{bmatrix} \text{true unknown model} \\ f(X) & -\hat{f}(X) \end{bmatrix}^2 = \mathbb{E}\begin{bmatrix} f(X) & -\mathbb{E}[\hat{f}] + \mathbb{E}[\hat{f}] & -\hat{f}(X) \end{bmatrix}^2$$

$$(\text{expand the square}) = \mathbb{E}[(f(X) - \mathbb{E}[\hat{f}])^2 + (\mathbb{E}[\hat{f}] - \hat{f}(X))^2 \\ + 2(f(X) - \mathbb{E}[\hat{f}])(\mathbb{E}[\hat{f}] - \hat{f}(X))]$$

$$(\text{rearrange the terms}) = \mathbb{E}[f(X) - \mathbb{E}[\hat{f}]]^2 + \mathbb{E}[\mathbb{E}[\hat{f}] - \hat{f}(X))]^2 \\ + 2\mathbb{E}[f(X) - \mathbb{E}[\hat{f}]]^2 + \mathbb{E}[\mathbb{E}[\hat{f}] - \hat{f}(X)]^2$$

$$= \mathbb{E}[f(X) - \mathbb{E}[\hat{f}]]^2 + \mathbb{E}[\mathbb{E}[\hat{f}] - \hat{f}(X)]^2$$

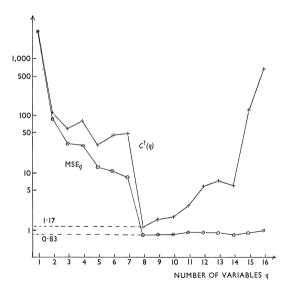
$$= \mathbb{E}[f(X) - \mathbb{E}[\hat{f}]]^2 + \mathbb{E}[\mathbb{E}[\hat{f}] - \hat{f}(X)]^2$$

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Remark: We didn't factor out irreducible errors.

$$\mathbb{E} \begin{bmatrix} \text{true unknown model} & \text{our attempt} \\ f(X) & - & \hat{f}(X) \end{bmatrix}^2 = \underbrace{\mathbb{E} \big[f(X) - \mathbb{E} \big[\hat{f} \big] \big]^2}_{\text{bias}^2} + \underbrace{\mathbb{E} \big[\mathbb{E} \big[\hat{f} \big] - \hat{f}(X) \big] \big]^2}_{\text{variance}}$$

k-fold cross validation in regression modelling (M. Stone 1974)



Today's lecture

Bias-variance tradeof

High-dimensional multivariate regression

Knock-off filter to control False Discovery Rate

Discussion

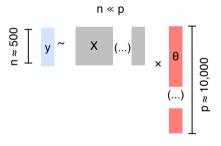
In multivariate regression modelling

Model selection pprox variable selection

Challenges in our $p \gg n$ regression problem

Degeneracy

High degree of freedom, many, many unknown, but very title information



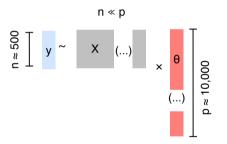
Col-linearity

Variables are somewhat similar to each other

Challenges in our $p \gg n$ regression problem

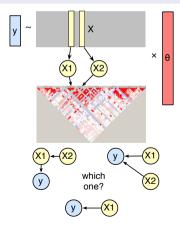
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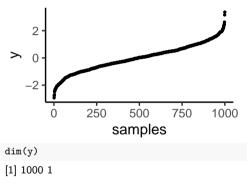


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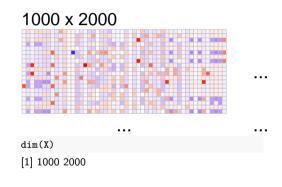
Variables are somewhat similar to each other



A working example - data

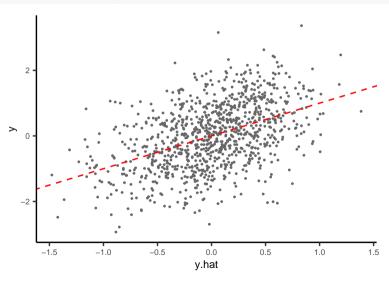


There are 20 true non-zero variables.

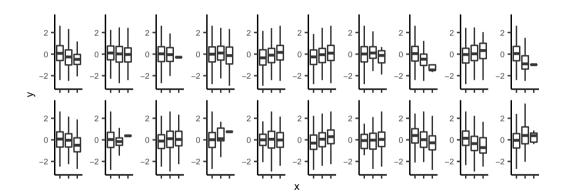


True causal variables explain a large fraction of variation

```
.lm <- lm(y ~ X[, sim$causal, drop = FALSE] - 1)
```



Variant-by-variant correlations



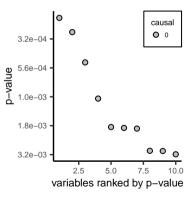
How do we know "causal" variables from 2,000 variables?

Let's try out one by one and rank them by univariate cor.test(x,y)

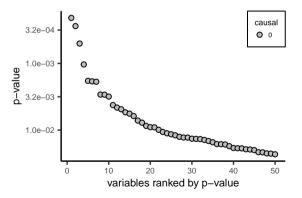
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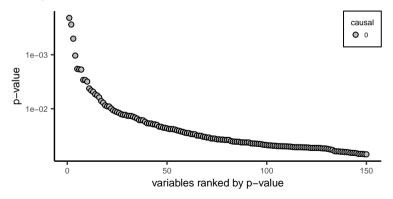
cor.test(x,y)



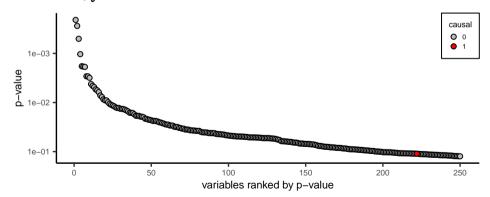
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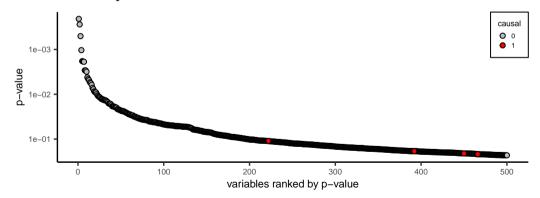
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Let's try out one by one and rank them by univariate



- Classical variable selection by univariate (one-by-one) tests will not work for a $p\gg n$ regression problem
- Especially if we have col-linearity in the design matrix X

Can we get helped by multivariate regression?

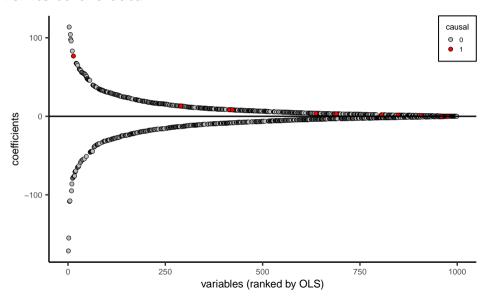
$$lm.out \leftarrow lm(y \sim X - 1)$$

If you look at the coefficients:

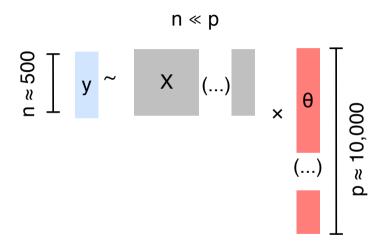
	Estimate	Std. Error	t value	Pr(> t)
X1	1.582654	0	117826708638	0
X2	-15.949781	0	-134571520044	0
X3	1.401209	0	117831497502	0
X4	-5.515155	0	-61749749454	0
X5	6.827798	0	66652250040	0
X6	-15.180671	0	-107848045369	0

Anything strange? Hint: $\hat{\theta} = (X^{\top}X)^{-1}X^{\top}y$.

OLS overfits to the data



Can we get helped by multivariate regression?



OLS (a.k.a. MLE/MSE) is degenerate if $p \gg n$

Variable selection in high-dimensional genotype matrix $(n \ll p)$

Regression analysis = projecting the observed y vector on to column space of $\{x_j: j \in [p]\}$,

$$\begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix} = \theta_1 \begin{pmatrix} X_{11} \\ X_{21} \\ \vdots \\ X_{n1} \end{pmatrix} + \cdots \theta_p \begin{pmatrix} X_{1p} \\ X_{2p} \\ \vdots \\ X_{np} \end{pmatrix}.$$

Variable selection = column selection.

Intuitive idea : choose the best combination of variables. $\rightarrow 2^p$ choices (even harder).

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Variable selection = column selection.

- Intuitive idea : choose the best combination of variables. $\rightarrow 2^p$ choices (even harder).
- lacktriangle Alternative idea : make as many $heta_i$'s nearly zero values.
- What prior does: penalize $|\theta_j|>0$ so that only the strong enough variables take non-zero values.

Reconciling two related concepts – MLE and MSE

Equivalence of maximum-likelihood estimation and mean square error minimization (isotropic Gaussian error distribution).

[MLE] Find θ maximizing

$$\ln p(\mathbf{y}|X,\theta) = -\frac{1}{2\sigma^2} \sum_{i=1}^{n} (y_i - \mathbf{x}_i \theta)^2 + \text{const.}$$

without prior contribution of parameter, and σ is known.

[MSE] Find θ minimizing

$$\sum_{i=1}^{n} (y_i - \mathbf{x}_i \theta)^2.$$

Minimization of the convex loss function:

$$L(\theta) = (\mathbf{y} - X\theta)^{\top} (\mathbf{y} - X\theta)$$

Minimization of the convex loss function:

$$L(\theta) = (\mathbf{v} - X\theta)^{\top} (\mathbf{v} - X\theta)$$

We can optimize setting the derivative with respect to θ to zero:

$$\nabla_{\theta} L = X^{\top} (\mathbf{y} - X\theta) = 0$$

$$\mathbf{y}^{\top}X = X^{\top}X\theta \implies \hat{\theta}_{MLE} = (X^{\top}X)^{-1}X^{\top}y.$$

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- $\blacktriangleright \text{ Approximately, } p(\theta|\mathbf{y},X) \approx \mathcal{N}\Big(\theta\Big|\hat{\theta}_{MLE},\sigma^2(X^\top X)^{-1}\Big).$
- ▶ How hard is $(X^TX)^{-1}$ (i.e., inverse of $p \times p$ matrix)?

Minimization of the convex loss function:

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- $\blacktriangleright \text{ Approximately, } p(\theta|\mathbf{y},X) \approx \mathcal{N} \Big(\theta \Big| \hat{\theta}_{MLE}, \sigma^2(X^\top X)^{-1} \Big).$
- ▶ How hard is $(X^TX)^{-1}$ (i.e., inverse of $p \times p$ matrix)?
 - ▶ What if $n \ll p$? What if we want to include $p(\theta)$?

Bayesian/regularization idea to add the missing probability component

We've been discussing the conditional likelihood

$$p(\mathbf{y}|X,\theta)$$

without a prior probability of regression coefficients,

$$p(\theta)$$

What will be a suitable prior distribution of θ ?

Recall: Reconciling two related concepts - MLE and MSE

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without prior contribution of parameter, and σ is known.

[MSE] Find θ minimizing

$$\sum_{i=1}^{n} (y_i - \mathbf{x}_i \theta)^2.$$

Ridge regression, a linear regression with Gaussian prior (L2)

Prior distribution

$$p(\theta) = \mathcal{N}(\theta|\mathbf{0}, \lambda^{-1}I) \propto \exp\left(-\frac{\lambda}{2}\|\theta\|^2\right)$$

where

$$\| heta\|^2 = \sum_{j=1}^p heta_j^2,$$
 L2-norm.

Maximize

$$\ln p(\mathbf{y}|X,\theta) + \ln p(\theta|\lambda) = -\frac{1}{2\sigma^2} \sum_{i=1}^n (y_i - \mathbf{x}_i \theta)^2 - \frac{\lambda}{2} \|\theta\|^2$$

Minimize L_2 -regularized error

$$\sum_{i=1}^n (y_i - \mathbf{x}_i \theta)^2 + \frac{\lambda}{2} \|\theta\|^2$$

Lasso regression, a linear regression with Laplace prior (L1)

Prior distribution

$$p(\theta) = \mathsf{Laplace}(\theta|\lambda) \propto \exp{(-\lambda\|\theta\|_1)}$$

where

$$\| heta\|_1 = \sum_{j=1}^p | heta_j|, \ \mathsf{L1} ext{-norm}.$$

Maximize

$$\ln p(\mathbf{y}|X,\theta) + \ln p(\theta|\lambda) = -\frac{1}{2\sigma^2} \sum_{i=1}^{n} (y_i - \mathbf{x}_i \theta)^2 - \lambda \|\theta\|_1$$

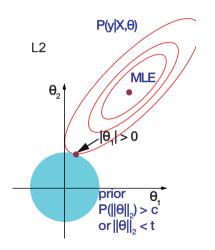
Minimize L_1 -regularized error

$$\sum_{i=1}^n (y_i - \mathbf{x}_i \theta)^2 + \lambda \|\theta\|_1$$

(Tibshirani, 1996)

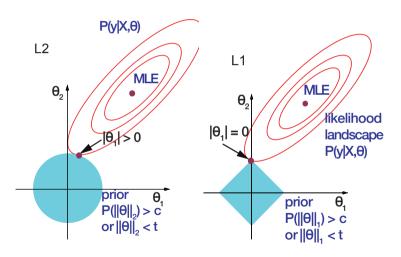
Geometric intuition of regularization.

Consider a simple regression model: $y_i = \theta_1 X_{i1} + \theta_2 X_{i2}.$



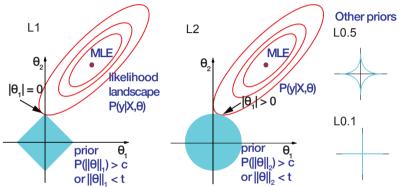
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Geometric intuition of regularization.

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- Both regularization priors shrink the coefficients toward zero.
- \blacktriangleright But only L1 can effectively "select" variables; although we want L_0 .

Hastie, Tibshirani, Friedman, The Elements of Statistical Learning.

Posterior inference of the regularized regression models

Our goal is to estimate (1) posterior distribution

$$p(\theta|\mathbf{y}, X) = \frac{p(\mathbf{y}|X, \theta)p(\theta)}{p(y|X)}.$$

Then (2) using $p(\theta|\mathbf{y},X)$, predict $p(\mathbf{y}^{\star}|\mathbf{y},X)$ by averaging over all possible θ sampled from the estimated posterior distribution.

- ▶ Usually posterior prediction (2) is can be easily simulated with accurate estimation of posterior distribution (1).
- Posterior inference can be done analytically or not, depending on the choice of $p(\theta)^1$.

 $^{^1}$ We term prior $p(\theta)$ a conjugate prior if its posterior $p(\theta|\mathbf{y},X)$ is of the same type of distribution.

$$\ln p(\boldsymbol{\theta}|\mathbf{y}, X) = -\frac{1}{2\sigma^2}(\mathbf{y} - X\boldsymbol{\theta})^\top (\mathbf{y} - X\boldsymbol{\theta}) - \frac{\lambda}{2}\boldsymbol{\theta}^\top \boldsymbol{\theta} + \text{const.}$$

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By taking derivative with respect to θ and setting it the zero vector:

$$\nabla_{\theta} = -\frac{1}{2} X^{\top} (\mathbf{y} - X\theta) - \lambda \theta = 0$$

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$$X^{\mathsf{T}}\mathbf{y} = (X^{\mathsf{T}}X + \lambda\sigma^2 I)\theta \implies \hat{\theta} = (X^{\mathsf{T}}X + \lambda\sigma^2 I)^{-1}X^{\mathsf{T}}\mathbf{y}$$

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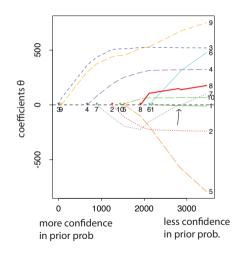
$$\nabla_{\theta} = -\frac{1}{\sigma^2} X^{\top} (\mathbf{y} - X\theta) - \lambda \theta = 0$$

Rearranging the equation:

$$X^{\top}\mathbf{v} = (X^{\top}X + \lambda\sigma^2I)\theta \implies \hat{\theta} = (X^{\top}X + \lambda\sigma^2I)^{-1}X^{\top}\mathbf{v}$$

Remark: For $n \ll p$, the inverse $(X^\top X)^{-1}$ may not exists, but $(X^\top X + \lambda \sigma^2 I)^{-1}$ can exist with a proper λ .

We can solve L1-regularized regression numerically



Algorithms from statistics:

- Figure 1. Efron et al. Least Angle Regression (2002)
- Hans *et al.*, Shotgun search (2007)
- Friedman et al., glmnet (2010)
 - Figueiredo et al. PAMI (2003)
 - Seeger et al. JMLR (2008)

In practice, the greedy algorithm of glmnet works so well

Goal:

$$\min_{\boldsymbol{\theta}} \quad \overbrace{(\mathbf{y} - X\boldsymbol{\theta})^{\top}(\mathbf{y} - X\boldsymbol{\theta})}^{\text{RSS}} + \underbrace{\lambda \alpha \|\boldsymbol{\theta}\|_{1}}_{\text{variable selection}} + \underbrace{\lambda (1 - \alpha) \|\boldsymbol{\theta}\|_{2}}_{\text{shrinkage}}$$

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The variable-by-variable update equation makes sense:

For each θ_i ,

$$\hat{\theta}_{j}^{\mathrm{glmnet}} \leftarrow \frac{S\left(\sum_{i=1}^{n} X_{ij}(y_{i} - \hat{y}_{i}^{(-j)}), \lambda\alpha\right)}{\sum_{i=1}^{n} X_{ij}^{2} + \lambda(1-\alpha)} \quad \text{vs.} \quad \theta_{j}^{\mathrm{MLE}} \leftarrow \frac{\sum_{i=1}^{n} X_{ij}\left(y_{i} - \sum_{k \neq j} X_{ik}\hat{\theta}_{k}\right)}{\sum_{i=1}^{n} X_{ij}^{2}}$$

Friedman et al., Regularization Paths for Generalized Linear Models via Coordinate Descent (2010)

In practice, the greedy algorithm of glmnet works so well Goal:

$$\min_{\boldsymbol{\theta}} \quad \overbrace{(\mathbf{y} - X\boldsymbol{\theta})^{\top}(\mathbf{y} - X\boldsymbol{\theta})}^{\text{RSS}} + \underbrace{\lambda \alpha \|\boldsymbol{\theta}\|_{1}}_{\text{variable selection}} + \underbrace{\lambda (1 - \alpha) \|\boldsymbol{\theta}\|_{2}}_{\text{shrinkage}}$$

The variable-by-variable update equation makes sense:

For each θ_i ,

$$\hat{\theta}_{j} \leftarrow \frac{\sum_{i=1}^{n} X_{ij} \quad \overbrace{(y_{i} - y_{i}^{(-j)})}^{\text{residual w/o the variable } \theta_{j}}, \lambda \alpha}{\sum_{i=1}^{n} X_{ij}^{2} + \underbrace{\lambda(1 - \alpha)}_{\text{shrinkage}}}$$

where $S(z,\tau)$ will set it to zero if $|z|<\tau$.

Cross-validation: How do we tune hyper-parameters (e.g., λ)?

- 1. Divide the total training data $\mathcal{D}^{\text{train}} = \{(X, y)\}$ into two parts:
 - (1) cross-validation training $\{(X,y)\}$ and
 - (2) CV testing data $\{(X^{\star}, y^{\star})\}$
- 2. For each different (λ, α) combination,
 - $\blacktriangleright \ \, \text{Train coefficients} \,\, \theta \,\, \text{using CV training} \,\, \{(X,y)\} \subset \mathcal{D}^{\text{train}}$
 - ► Test how well $\sum_{j} X_{ij}^{\star} \hat{\theta}_{j}$ predicts y^{\star} ?
- 3. Choose the optimal $(\lambda^\star, \alpha^\star)$

How do we tune hyper-parameters (e.g., λ)?

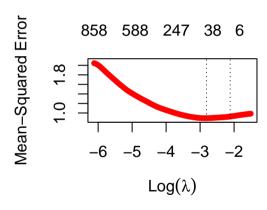
Well, in R, we simply run

How do we tune hyper-parameters (e.g., λ)?

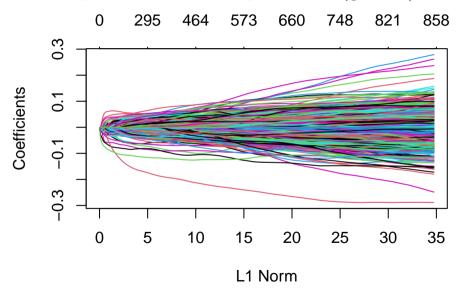
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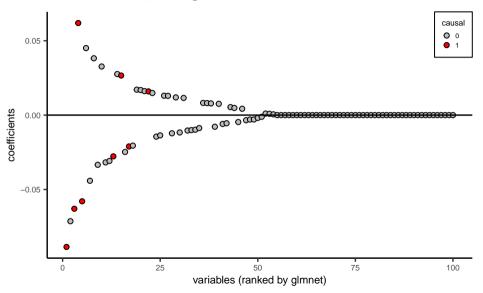
Well, in R, we simply run



Revisit our working example with L1-regularization (glmnet)



At the optimal λ found by cv.glmnet

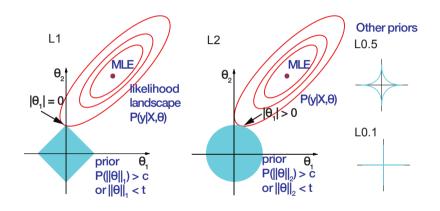


Bias-variance tradeoff explains why a regularized regression works in practice

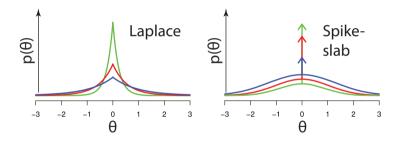
$$\min_{\boldsymbol{\theta}} \quad \overbrace{(\mathbf{y} - X\boldsymbol{\theta})^{\top}(\mathbf{y} - X\boldsymbol{\theta})}^{\approx \text{bias}} + \underbrace{\lambda \alpha \|\boldsymbol{\theta}\|_1}_{\text{variable selection}} + \underbrace{\lambda (1 - \alpha) \|\boldsymbol{\theta}\|_2}_{\text{shrinkage}}$$

▶ The second and the third terms control the model variance

Can we try out different prior (regularization)?



Bayesian spike-and-slab prior to achieve L0 norm



Hern'andez-Lobato {et al.} (2015)

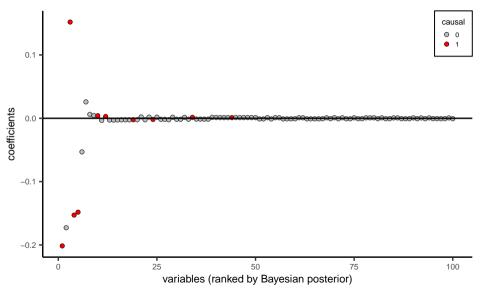
Bayesian spike-and-slab prior to select variables (literally)

With **indicator** variables, $z_1, \dots, z_p \in \{0, 1\}$,

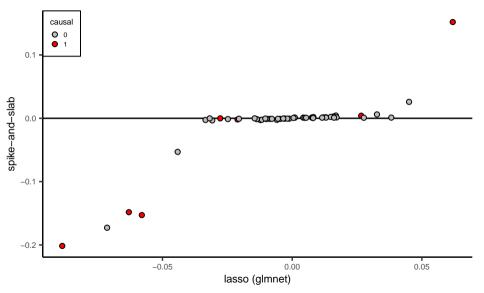
$$\left(\begin{array}{c} y_1 \\ y_2 \\ \vdots \\ y_n \end{array} \right) = z_1 \beta_1 \left(\begin{array}{c} X_{11} \\ X_{21} \\ \vdots \\ X_{n1} \end{array} \right) + \cdots z_1 \beta_p \left(\begin{array}{c} X_{1p} \\ X_{2p} \\ \vdots \\ X_{np} \end{array} \right),$$

$$\mathbf{y} = X\theta + \epsilon, \quad \theta_j | z_j = 1 \sim \mathcal{N}(\beta_j, \sigma_j^2), \ \forall j.$$

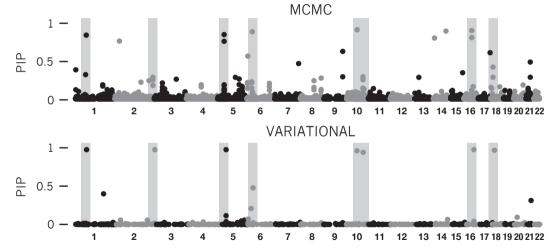
Bayesian inference with sparse Bayesian prior



Bayesian inference with sparse Bayesian prior



A Bayesian approach successfully handles high-dimensional regression problems



Today's lecture

Bias-variance tradeoff

High-dimensional multivariate regression

Knock-off filter to control False Discovery Rate

Discussion

multiple hypothesis testing!

Many variables to test for their non-zero-ness \rightarrow

False discovery rate in high-dimensional variable selection

$$FDR(\tau) = \frac{\sum_{j=1}^{p} I\{|\hat{\theta}_{j}| > \tau \wedge \theta_{j} = 0\}}{\max\{1, \sum_{j=1}^{p} I\{|\hat{\theta}_{j}| > \tau\}\}}$$

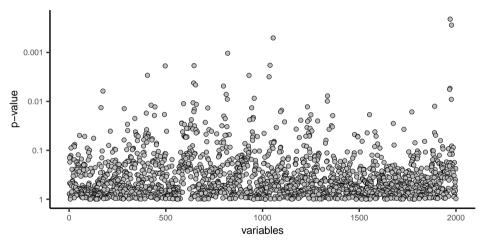
where

- $ightharpoonup \hat{\theta}_j$: estimation using data
- $\triangleright \theta_j$: true random variable

Can we simply attempt to control FDR as in DEG analysis?

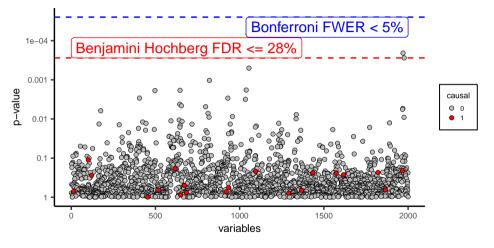
- 1. Perform variable-by-variable association tests
- 2. Combine p-values
- 3. Run multiple hypothesis correction (e.g., Bonferroni, Benjamini-Hochberg)

Can we simply attempt to control FDR as in DEG analysis?



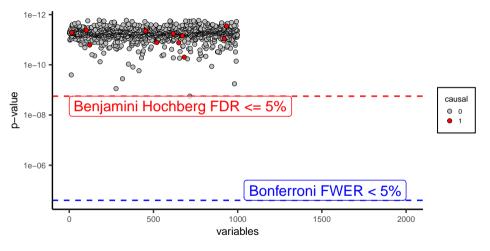
Variant-by-variant tests fail to control false discovery rate. Why?

Can we simply attempt to control FDR as in DEG analysis?



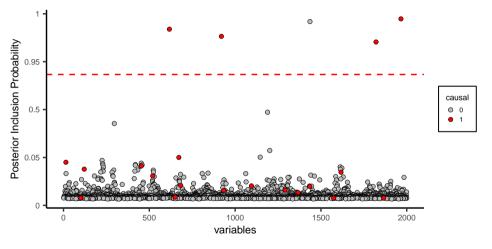
Variant-by-variant tests fail to control false discovery rate. Why?

How about using multivariate OLS results?



What happened to the other 1000 variables?

Bayesian posterior inclusion probability can help



lacktriangle Okay, but what is FDR? Can we consider (1— PIP) as FDR?

How we estimate the False Discovery Rate for non-zero regression coefficient?

- What should be the null distribution of regression coefficient?
- ▶ Is it t-distributed (the default option of lm)?

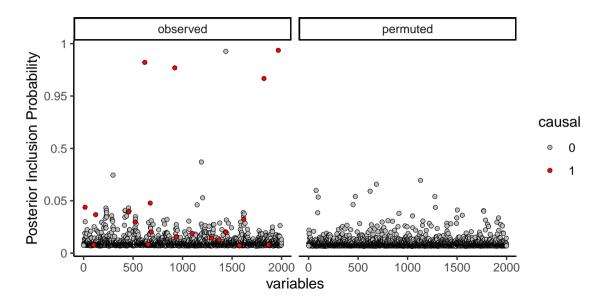
First attempt: Construct "null" regression data by sample permutation?

```
set.seed(17)
X.perm <- apply(X, 2, sample)</pre>
```

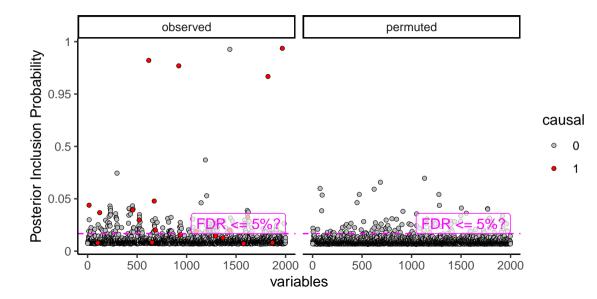
- ▶ What are we missing?
- lt is not clear whether we can control Type-I error.

$$\mathbf{y} \sim [X, \quad \tilde{X}]$$

Can we learn FDR cutoff from the permuted coefficients?



Can we learn FDR cutoff from the permuted coefficients?



Can we calibrate FDR using the permuted data?

Not really...

- Let ρ_i be estimated posterior probability $p(\theta_i \neq 0|\text{data})$
- empirical False Discovery Rate =

$$\frac{\sum_{j} I\{\rho_{j} > \tau \wedge \theta_{j} = 0\}}{\sum_{j} I\{\rho_{j} > \tau\}}$$

In this example, we have 93 %

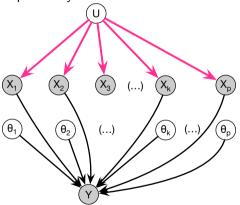
▶ What have we missed?

What went wrong?

- 1. We need to apply different threshold levels for different varaibles
- 2. We didn't consider correlation (col-linearity) structures between variables
- 3. Naive permutation steps break the covariance structure in X

KO Idea 1: Preserve dependency structure between variables

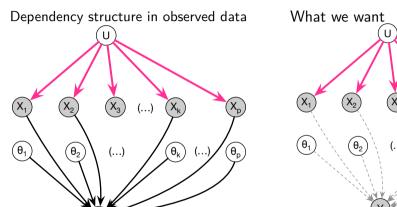
Dependency structure in observed data

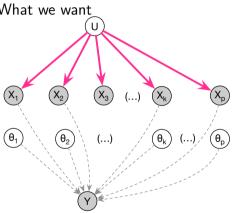


KO Idea 1: Preserve dependency structure between variables

Dependency structure in observed data What permutation did... θ_1 θ_2 (...)

KO Idea 1: Preserve dependency structure between variables





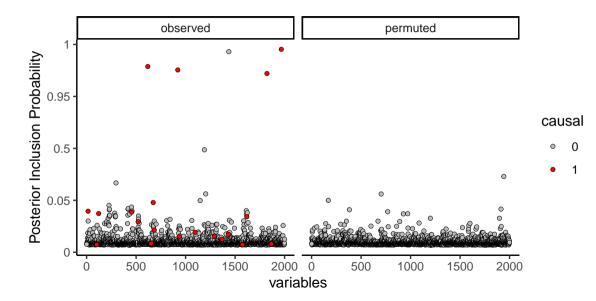
Second attempt: Construct "null" regression data by permutation preserving inter-variable dependency

```
set.seed(17)
X.perm <- X[sample(nrow(X)), ]</pre>
```

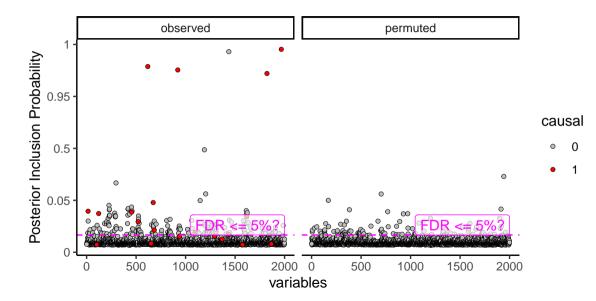
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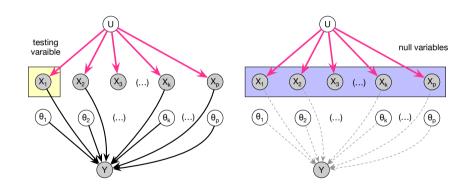
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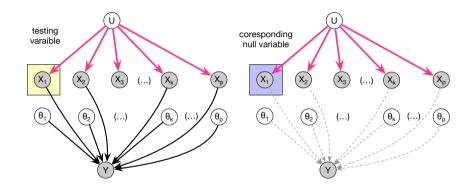
In this example, we have 93 %

What are we still missing?

Is our comparison scheme fair? We comparing one variable against all the null variables



KO Idea 2: Matched comparison: X_j vs. \tilde{X}_j



Construct a knockoff matrix preserving both correlation structures

Knock-off filter

Given $X=(X_1,\dots,X_p)$, a new family of random variables, $\tilde X=(\tilde X_1,\dots,\tilde X_p)$ are considered a valid "knockoff" filter if

- 1. \tilde{X} is independent of Y given X
- 2. distribution of (X,\tilde{X}) remain invariant to any swapping between the original and knockoff variables.

E.g.,

Construct a knockoff matrix preserving both correlation structures

Knock-off filter

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E.g.,

$$(X_1, \textcolor{red}{X_2}, X_3, \tilde{X}_1, \textcolor{red}{\tilde{X}_2}, \tilde{X}_3) \stackrel{d}{=} (X_1, \textcolor{red}{\tilde{X}_2}, X_3, \tilde{X}_1, \textcolor{red}{X_2}, \tilde{X}_3)$$

Construct a knockoff matrix preserving both correlation structures

Knock-off filter

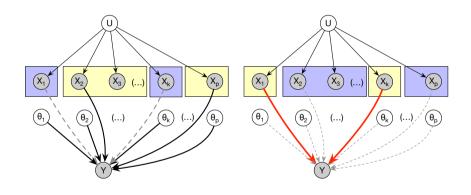
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E.g.,

$$\begin{split} (X_1, & X_2, X_3, \tilde{X}_1, \tilde{X}_2, \tilde{X}_3) \stackrel{d}{=} (X_1, \tilde{X}_2, X_3, \tilde{X}_1, X_2, \tilde{X}_3) \\ (X_1, & X_2, X_3, \tilde{X}_1, \tilde{X}_2, \tilde{X}_3) \stackrel{d}{=} (\tilde{X}_1, \tilde{X}_2, X_3, X_1, X_2, \tilde{X}_3) \\ (\ldots) \end{split}$$

Knockoff filter (null design matrix) preserves swap exchangeability



What would happen if we replace some variable X_k with its

remain unchanged?

knock-off copy $ilde{X}_k$ whilst dependence with all the other variables

1. Fit $X \sim WZ$ matrix factorization

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- 2. Predict $\hat{X} \leftarrow \hat{U}\hat{Z}$

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- 2. Predict $\hat{X} \leftarrow \hat{U}\hat{Z}$
- 3. Take residuals $\epsilon = X \hat{X}$
- 4. Add permuted residuals $\tilde{\epsilon},$ i.e., $\tilde{X}=\hat{X}+\tilde{\epsilon}$

Zhu et al. DeepLINK: Deep learning inference using knockoffs with applications to genomics (2021)

Knockoff statistics

$$\mathbf{y} \sim [X, \tilde{X}_{\text{knockoff}}]$$

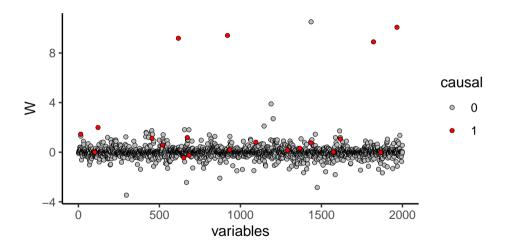
For each variable j (Lasso):

$$W_j = |\hat{\theta}_j| - |\tilde{\theta}_j|$$

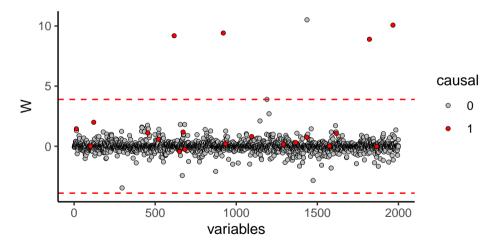
For each variable j (Bayesian PIP):

$$W_j = \hat{\rho}_j - \tilde{\rho}_j$$

Knockoff statistics: What is FDR here?



Knockoff statistics: What is FDR here?



Today's lecture

Bias-variance tradeof

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Discussion

Other methods that we haven't had a chance to discuss

- ► Ensemble learning
 - ▶ Boosting, Model-averaging
- Bayesian non-parametric models
 - We select models by *not* selecting a model
 - Gaussian process
- Deep neural network model