#### **STAT540**

Lecture 14: Feb 28th 2018

## Supervised learning II

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## Recall: Supervise Learning

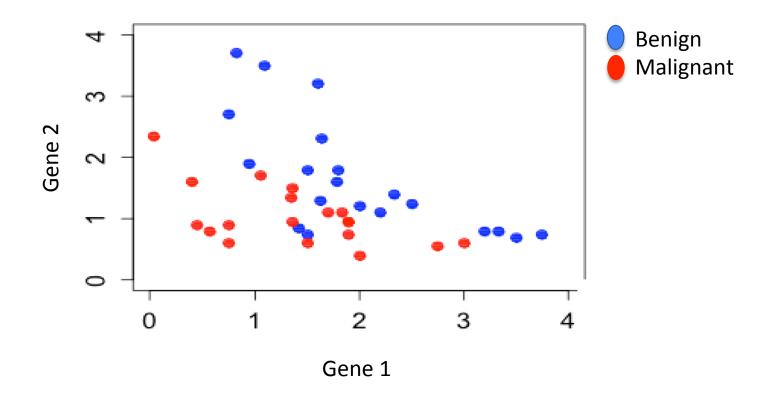
- We have a training data set of n examples in which we know the value of both y and X
- Based on the training data, we will produce a model or a rule to predict y. The model can be parametric or nonparametric.
- We want to predict y on new samples of a "test set" for which we only know X.

How can we find the best-trained model?

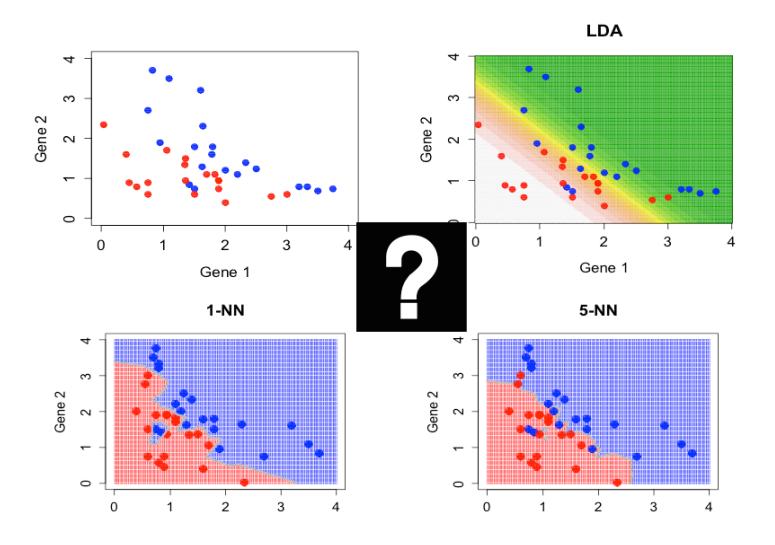
Goal: prediction!

On which samples?
How do we define best?
And based on what information?

Assume we'd like to train a classifier to predict tumor type from gene expression data

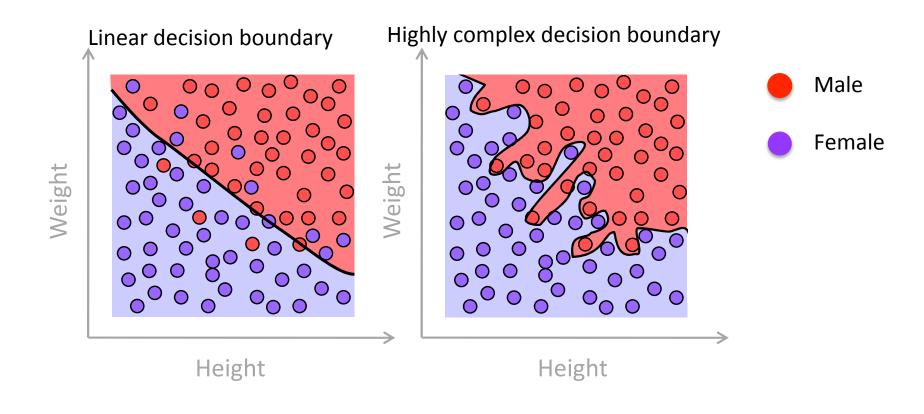


Many methods can be used to build a classifier (ie. define a decision boundary), depending on the exact model and tuning parameters. But which one is better?



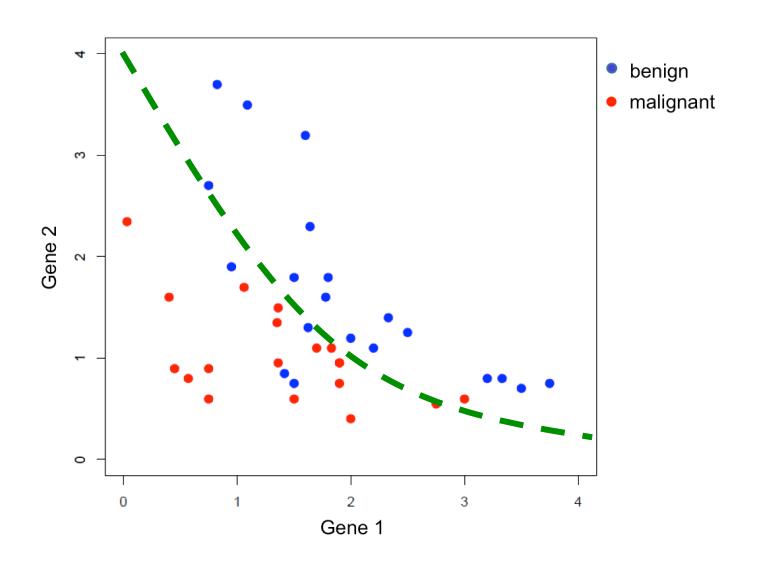
## **Overfitting**

If we allow very complicated predictors, we could overfit the training data:

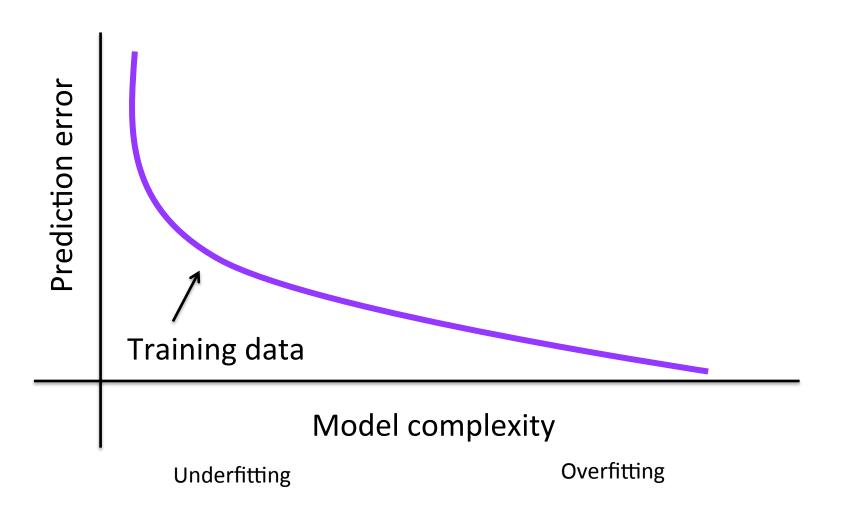


- The best model should predict the class labels of the samples in the *test* set accurately!
- "the model should generalize"

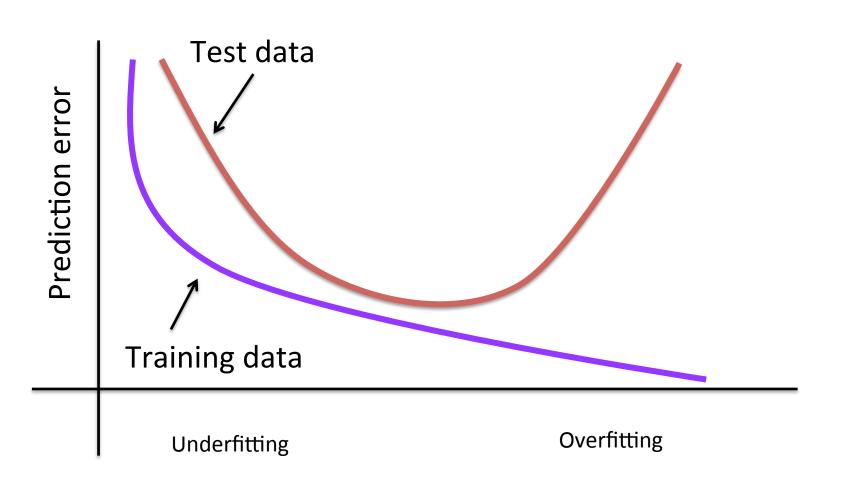
# **Decision boundary**



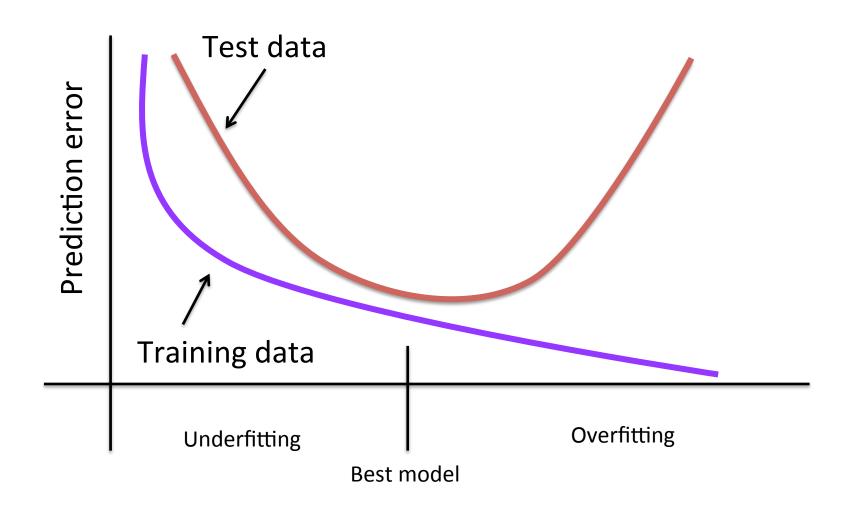
# Error and model complexity



# Error and model complexity



# Error and model complexity



#### **Cross-validation**

- General approach for estimating the error of the model in an "unbiased" way.
- Split the data to many sub-sets, use some to train model and others to test the model's predictions.
  - Training set
  - Validation set
  - Test set

# Cross-validation (CV)

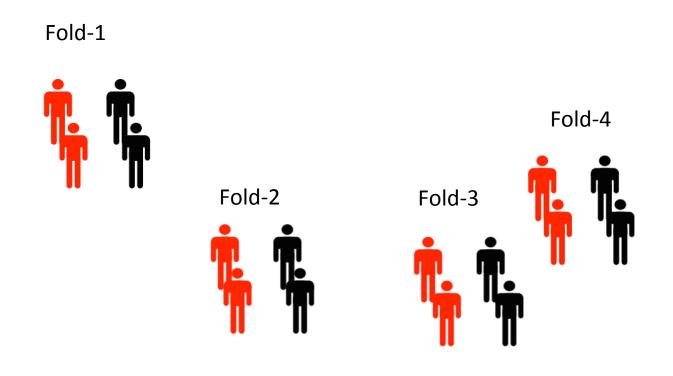
- K-fold cross-validation:
  - 1. Create k partition (folds) of input data
  - 2. Set aside data in one of the partition (fold) for validation
  - 3. Train model on all but the held-out fold
  - 4. Measure cross-validation (CV) error using data from the left-out fold:

$$\mathsf{CV}\;\mathsf{Error}_i = \frac{1}{n_i} \sum_{j \in T_i} L(y_j, \hat{y}_{j(-i)})$$

5. Repeat leaving out for all folds and measure average error

$$\mathsf{CV}\;\mathsf{Error} = \frac{1}{k}\sum_{i=1}^k \mathsf{CV}\;\mathsf{Error}_i$$





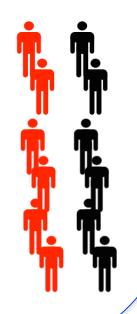
Training data



Validation data







Validation data



Use model to predict class labels for validation fold

Build (train) a model

$$CV\_Error_i = \frac{1}{n_i} \sum_{j \in T_i} L(y_j, \hat{y}_{j(-i)})$$

## K-fold cross-validation

- k can range from 2 to n:
  - Larger k:
    - Variance of true error will be high
    - Computational time will be large
    - + bias of error estimate will be small
  - Smaller k:
    - + reduced computation time
    - + variance of error estimate is small
    - Bias of error estimate is large
- N-fold CV is called "Leave-One-Out" CV
- In practice:
  - Lower k is more reliable, eg., 3-fold CV is standard.

# How do we measure error on validation/test set?

#### continuous response

#### Examples:

Squared error loss

$$L(\boldsymbol{y}, \hat{\boldsymbol{y}}) = \|\boldsymbol{y} - \hat{\boldsymbol{y}}\|_{2}^{2} = \sum_{i=1}^{n} (y_{i} - \hat{y}_{i})^{2}$$

Absolute error loss

$$L(y, \hat{y}) = \|y - \hat{y}\|_1 = \sum_{i=1}^{n} |y_i - \hat{y}_i|_1$$

# Binary response/labels

- ► True positive (TP)
- True negative (TN)
- False positive (?Type I error?) (FP)
- False negative (?Type II error?) (FN)
- Accuracy (TP + TN)/N (=1-error rate)
- Sensitivity: TP/(TP+FN) (recall)
- Specificity: TN/(TN + FP)

## Summary of SL and CV so far ...

#### Supervised learning:

- Write down a model → objective function
- Algebraically simplify model/objective as much as possible
- Write down the optimization problem: solve for parameters
   (highly recommend doing the above, and program your own logistic regression function)

#### Overfitting:

- Constantly think about it!
- Overfitting can severely delude you about the accuracy of your model

#### Cross-validation:

- Good fist-pass solution for tuning parameters, finding the "right" model
- Assumption: test and training data are independent (this may not always be the case, especially due to systematic artifacts in genomics)
  - Batch effects result in inflated estimate of accuracy

- In high dimensional biology ("omics studies") we typically have thousands to millions of features/covariates (p>>n problem):
  - Gene expression datasets: >20,000 genes
  - Genotyping datasets: > 1M SNPs
  - DNA Methylation datasets: > 200K methylation sites

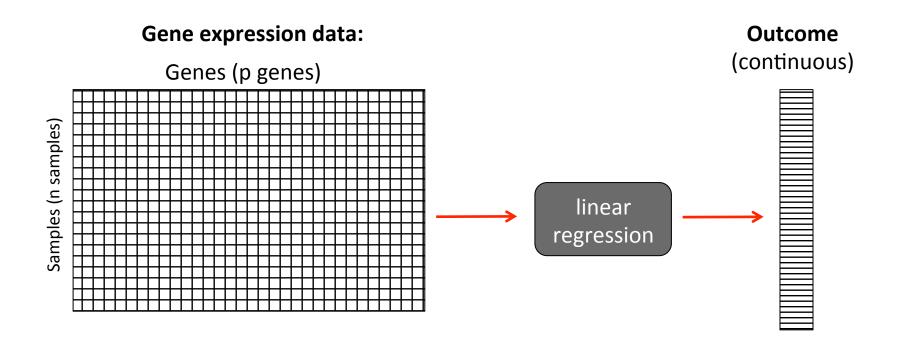
 A main analysis goal is to identify features/covariates that important in predicting a trait/disease/outcome

Complexity regularization through feature selection and penalization

# Case study: why feature selection can help with overfitting

- Problem setup:
  - Gene expression data for n individuals & p genes
  - Response data is continuous
- Goals:
  - Build predictive model for inferring outcome
  - Identify 'important' genes

#### Case study: feature selection can help with overfitting



1. Generate some random data:

X ~ randn(100,1000) : 100 samples and 1000 genes, normally-distributed

Y ~ randn(100,1) : 100 samples, continuous + normally-distributed

#### 2. Predict Y from X using linear regression:

 $\vec{\alpha} = (X^T X)^{-1} X^T \vec{y}$ 

$$\underset{\alpha,b}{\operatorname{argmin}} \sum_{i=1}^{n} (y_i - (b + \alpha^T \vec{x}_i))^2 \quad \text{Scalar notation}$$

$$\underset{\alpha}{\operatorname{argmin}} \quad \|\vec{y} - X\vec{\alpha}\|_2^2$$

$$\underset{\alpha}{\operatorname{argmin}} \quad \|\vec{y} - X\vec{\alpha}\|_2^2$$

$$\underset{\alpha}{\operatorname{matrix notation}}$$

$$= \underset{\alpha}{\operatorname{argmin}} \quad (\vec{y} - X\vec{\alpha})^T (\vec{y} - X\vec{\alpha})$$

Solution for a

### Toy example: how well can we predict y from X?

Generate some random data:

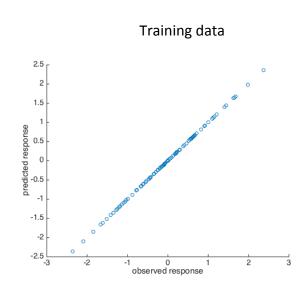
X ~ randn(100,1000) : 100 samples and 1000 genes, normally-distributed

Y ~ randn(100,1)
 : 100 samples, continuous + normally-distributed

#### "Pseudo-code"

```
X = randn(100,1000);
y = randn(100,1);
[a,b] = corr(X,y);
figure,hist(b)
sum(b<.05)

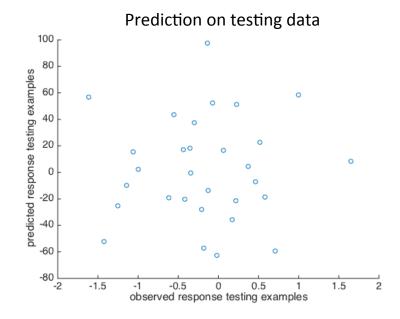
Xo = [ones(100,1) X];
c = (Xo'*Xo)\(Xo'*y);
pr = Xo*c;
figure,plot(y,pr,'o');</pre>
```



NOTE: matrix inversion not stable/reliable when p>n

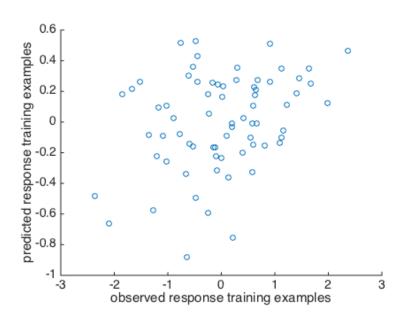
#### Demo: how well can we predict y from X?

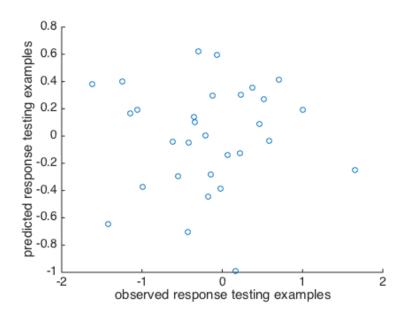




What's the main cause of this severe overfitting? Linear model should be simple enough ??

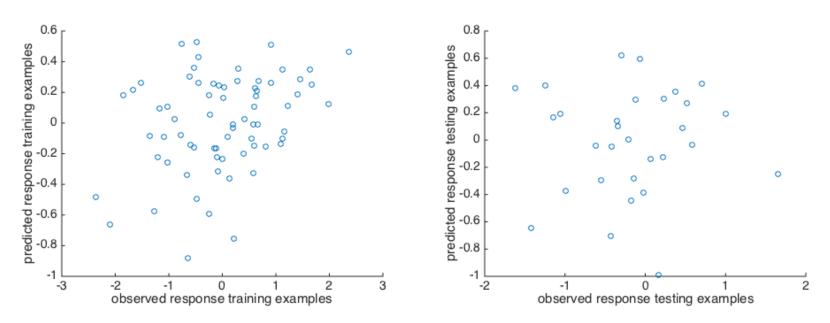
 Reduce the number of features: randomly choose 10 of the 1000 features





What's the main cause of this severe overfitting? Linear model should be simple enough ??

 Reduce the number of features: randomly choose 10 of the 1000 features



#### Aren't there better ways of filtering the genes?

- Correlation between expression of gene and outcome
   Common mistake don't look at test data when filtering
- Filter genes based on mean/std/prior knowledge

#### Feature selection

- The "filter" approach:
  - Don't look at the labels/response: e.g., only keep genes with STD/mean > threshold
  - Consider the labels/response: e.g., only keep genes significantly correlated with response (note: must be careful to do this in a proper, nested, CV framework)
- The "wrapper" approach:
  - Identifying features that lead to good performance by the specific classifier
    - Cross-validation
- The "embedded" approach:
  - Modify the objective function to identify a reduced feature set intrinsically
    - Regularization/penalization

### Feature selection in linear regression

#### Best subset regression:

- Finds subset of size k with smallest error (e.g., mean squared error).
- Unfeasible for omics studies, because p-choose-k is huge!! (e.g., >10^10)

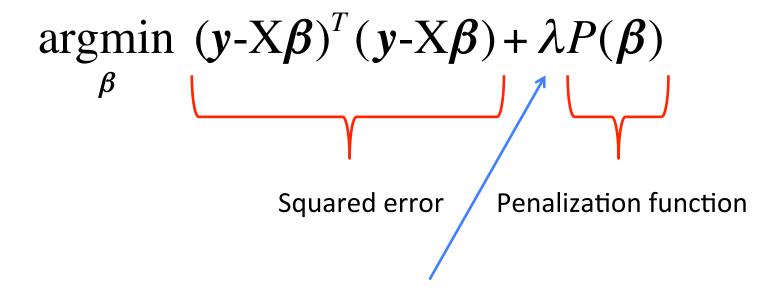
#### Forward/backward stepwise regression

 Sequentially add the best covariate that most improves the fit (e.g., minimizes prediction error)

#### Regularization methods (shrinkage/penalization)

 Modify the objective function, to explicitly penalize "magnitude" of coefficients

## Regularized regression



Penalization (tuning) parameter

<sup>\*\*</sup> Note change in notation: use bold lower case letters for vectors, upper case letters for matrices, lower case letters for scalars \*\*

argmin 
$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda P(\boldsymbol{\beta})$$

Squared error Penalization function

$$P(\boldsymbol{\beta}) = \|\boldsymbol{\beta}\|_2^2 = \sum_{i=1}^p \beta_i^2$$
Ridge regression: L2 norm ("squared") penalty function

(Hoerl and Kennard, Technometrics, 1970)

argmin 
$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda P(\boldsymbol{\beta})$$

Squared error Penalization function

$$P(\boldsymbol{\beta}) = \|\boldsymbol{\beta}\|_2^2 = \sum_{i=1}^p \beta_i^2$$
Ridge regression: L2 norm ("squared") penalty function

 $\lambda \ge 0$  is the penalization parameter that we can "tune"

- When  $\lambda = 0$  we get the linear regression estimate
- When  $\lambda = \infty$  what happens?
- For  $\lambda$  in between 0 and infinity we are balancing error term vs penalty

$$\hat{\boldsymbol{\beta}} = \underset{\boldsymbol{\beta}}{\operatorname{argmin}} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^{T} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \|\boldsymbol{\beta}\|_{2}^{2}$$
Squared error Penalization function

$$\boldsymbol{\beta}^{ridge} = (X^T X + \lambda I)^{-1} X^T \mathbf{y}$$

$$\underset{\beta}{\operatorname{argmin}} \ (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda P(\boldsymbol{\beta})$$

$$\operatorname{Squared error} \quad \operatorname{Penalization function}$$

$$P(\boldsymbol{\beta}) = \|\boldsymbol{\beta}\|_2^2 = \sum_{i=1}^p \beta_i^2$$
 Ridge regression: L2 norm ("squared") penalty function

#### **Important details**:

- How do you choose  $\lambda$ ? Need nested CV to tune parameter and estimate test error.
- Requires standardization of the covariates (columns of X) :
  - the covariates need to be on the same "scale"
- Since columns standardized no intercept required

argmin 
$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda P(\boldsymbol{\beta})$$

Squared error Penalization function

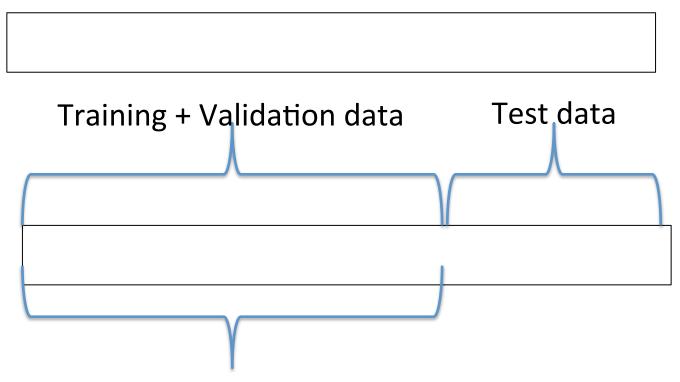
$$P(\boldsymbol{\beta}) = \|\boldsymbol{\beta}\|_2^2 = \sum_{i=1}^p \beta_i^2$$
Ridge regression: L2 norm ("squared") penalty function

#### Choosing the penalization parameter:

To choose the parameter and assess testing error we need to do nested cross-validation. Why?

#### **Nested cross-validation**





Do k-fold CV here to find tuning parameter, report results on test data

$$\hat{\boldsymbol{\beta}} = \underset{\boldsymbol{\beta}}{\operatorname{argmin}} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^{T} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \|\boldsymbol{\beta}\|_{2}^{2}$$
Squared error Penalization function

#### Probabilistic interpretation:

$$L(\theta \mid Data) = L(\theta \mid X, y)$$

$$= p(y \mid X, \theta)p(\theta) = N(y \mid X\beta, \sigma)N(\beta \mid 0, v)$$
Likelihood Prior

# Regularized regression: lasso

$$\hat{\boldsymbol{\beta}} = \underset{\boldsymbol{\beta}}{\operatorname{argmin}} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^{T} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \|\boldsymbol{\beta}\|_{1}$$

$$\|\boldsymbol{\beta}\|_1 = \sum_{i=1}^p |\beta_i|$$
 L1 norm penalty

- Proposed by Tibshirani (1996)
- Lasso is an acronym: Least Absolute Selection and Shrinkage Operator
- The only difference between ridge and lasso regularization is that ridge uses L2 norm vs lasso uses L1 norm. But turns out that the solutions to lasso and ridge behaves very differently.

$$\hat{\boldsymbol{\beta}}_{lasso} = \underset{\boldsymbol{\beta}}{\operatorname{argmin}} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^{T} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \|\boldsymbol{\beta}\|_{1}$$

#### As before:

• The tuning parameter  $\lambda \ge 0$  controls the strength of the penalty. What happens at the 0 and infinity?

#### But now:

- For  $\lambda \ge 0$  between the two extreme setting, we are balancing two ideas: minimizing the squared error, and penalizing the magnitude of the coefficient. But the L1 penalty causes some coefficients to bet set to **zero exactly**.
- Because some coefficients are set to zero exactly, lasso performs variable selection.
- No closed form solution: requires numerical optimization.
  - LARS algorithm
  - ADMM algorithm \*\*

### Comparing lasso and ridge

- Predictive performance: lasso and ridge are typically comparable
- Interpretation: lasso has a big advantage because it leads to variable selection

#### Some limitations and considerations

 If p>>n, the lasso can select at most n features (rest of the coefficients will be set to 0).

 If there is a group of highly correlated features, the lasso will choose only one among them (arbitrarily).

Sensitivity to the choice of penalization parameter.

## The elastic net: combined L2 and L1 penalty

$$\hat{\boldsymbol{\beta}} = \underset{\boldsymbol{\beta}}{\operatorname{argmin}} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^{T} (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda ((1 - \alpha) \|\boldsymbol{\beta}\|_{1} + \alpha \|\boldsymbol{\beta}\|_{2}^{2})$$

- Convex combination of the L1 and L2 penalty
- Addresses the shortcoming of the lasso in the presence of correlated features.
- But now we have to set 2 parameters.

#### Discussion

- Regularization methods can be extended to other models beyond linear regression (e.g., logistic regression)
- Designing variable penalization functions is an active area of research (e.g., fused lasso, group lasso, etc)
- How do we choose the regularization/penalty parameter?
  - Cross-validation

# Two common mistakes when applying supervised learning

 Do "feature" selection on entire data, and then build classifier

#### Do NOT do nested CV

 If you are learning parameters and reporting error, you should have training, validation, and test data splits.