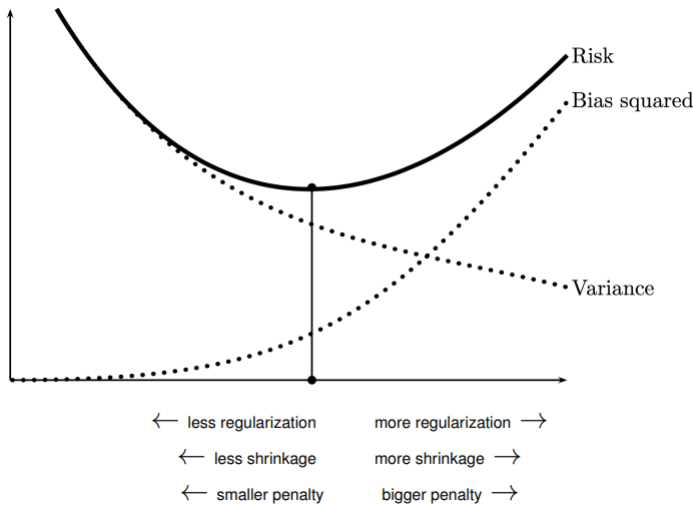


1 BIAS-VARIANCE TRADEOFF

$$\begin{aligned}
 E(\theta - \hat{\theta})^2 &= E(\theta - E\hat{\theta} + E\hat{\theta} - \hat{\theta})^2 \\
 &= E(\theta - E\hat{\theta})^2 - 2E\{(\theta - E\hat{\theta})(\hat{\theta} - E\hat{\theta})\} + E(\hat{\theta} - E\hat{\theta})^2 \\
 &= E(\theta - E\hat{\theta})^2 - 2(\theta - E\hat{\theta})E(\hat{\theta} - E\hat{\theta}) + E(\hat{\theta} - E\hat{\theta})^2 \\
 &= E(\theta - E\hat{\theta})^2 + E(\hat{\theta} - E\hat{\theta})^2 \\
 &= \text{Bias}(\hat{\theta})^2 + \text{Variance}(\hat{\theta})
 \end{aligned}$$



2 CROSS VALIDATION

	Iteration					
Obs	1	2	3	4	...	n
1	valid	train	train	train	...	train
2	train	valid	train	train	...	train
3	train	train	valid	train	...	train
4	train	train	train	valid	...	train
...
n	train	train	valid
MSE	MSE ₁	MSE ₂	MSE ₃	MSE ₄	...	MSE _n

$$\text{LOOCV test error: } CV_{(n)} = \frac{1}{n} \sum_i MSE_i$$

	Iteration					
Obs	1	2	3	4	...	k
1	valid	train	train	train	...	train
2	valid	train	train	train	...	train
3	valid	train	train	train	...	train
4	train	valid	train	train	...	train
...
n-2	train	train	valid
n-1	train	train	valid
n	train	train	valid
MSE	MSE ₁	MSE ₂	MSE ₃	MSE ₄	...	MSE _k

fold 1

fold k

K-Fold: $CV_{(k)} = \sum_b \frac{n_b}{n} MSE_b$ where n_b is the total observations in the b-th fold, and n is the total observations in the entire dataset. Suppose the

fitted values can be written $\hat{Y} = HY$. The leave-one-out-cross-validation error is

$$R_{LOOCV} = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_{(-i)})^2 = \frac{1}{n} \sum_{i=1}^n \left(\frac{Y_i - \hat{Y}_i}{1 - H_{ii}} \right)^2$$

where H_{ii} is the i-th diagonal entry. This is the case for least squares and regularized multiple regression:

$$H = X (X^T X)^{-1} X^T \text{ or } H = X (X^T X + \lambda I)^{-1} X^T$$

3 TREE

Tree Build: (1) Cycle through predictors X_k for $k = 1, \dots, p$. For each X_k :

- (Quantitative X_k) Consider cutpoints s (unique values of X_k) that divide up the region into two parts:

$$R_1(k, s) = \{i \mid X_{ik} < s\} \quad \text{and} \quad R_2(k, s) = \{i \mid X_{ik} \geq s\}$$

- Evaluate (for regression trees):

$$Q_k(s) = \sum_{i \in R_1(k, s)} (y_i - \bar{y}_{R_1})^2 + \sum_{i \in R_2(k, s)} (y_i - \bar{y}_{R_2})^2$$

Find the value of s that minimizes $Q_k(s)$. Call this s_k .

(2) Find the predictor X_k with the minimum $Q_1(s_1), Q_2(s_2), \dots, Q_p(s_p)$.

Make the first binary partition along predictor X_k at cut point s_k .

Cost-complexity pruning:

$$C(T) = \sum_{m=1}^{|T|} \sum_{i \in R_m} (y_i - \hat{y}_{R_m})^2 + \alpha |T|$$

$\alpha = 0$ implies the full tree, Larger α implies higher penalty for complexity of model. With increasing α :

(1) Grow a big tree on a training set. (2) Obtain a nested set of subtrees $T_L \subset \dots \subset T_2 \subset T_1 \subset T$ corresponding to a sequence of α values. (3) Use K-fold cross-validation to identify the subtree that does best.

Classification Tree Impurity measures: Define node proportion of class

$$k: \hat{p}_{mk} = \frac{1}{N_m} \sum_{x_i \in R_m} I(y_i = k) \text{ and } k(m) = \arg \max_k \hat{p}_{mk}$$

- Misclassification error: $1 - \hat{p}_{mk(m)}$

- Gini index: $\sum_{k=1}^K \hat{p}_{mk} (1 - \hat{p}_{mk})$

- Entropy: $-\sum_{k=1}^K \hat{p}_{mk} \log \hat{p}_{mk}$

Bagging

Regression trees: Create B bootstrap samples, grow tree (without pruning) using each $\hat{f}^{*1}, \hat{f}^{*2}, \dots, \hat{f}^{*B}$. For prediction at x , we take an average:

$$\hat{f}_{bag}(x) = \frac{1}{B} \sum_{b=1}^B \hat{f}^{*b}(x)$$

Classification trees: $\hat{f}_{bag}(x)$ is decided by majority vote.

OOB Estimation: For each bagged tree, we can make predictions for the OOB observations. At the end, we can aggregate over all predictions for the i-th observation to arrive at a OOB prediction \hat{y}_i . We can compute prediction error based on these OOB predictions $\hat{y}_1, \dots, \hat{y}_n$.

Random Forests:

(1) For $b=1$ to B:

(a) Draw a bootstrap sample Z^* of size n from the training data

(b) Grow a random-forest tree T_b to the bootstrapped data, recursively repeating following steps, until minimum node size reached: i. Select m variables at random from the p variables ii. Pick the best variable/split-point among the m iii. Split the node into two children nodes

(2) Output the ensemble of trees $\{T_b\}_{b=1}^B$. To make a prediction at a new point x :

Regression: Average $\hat{f}_{rf}^B(x) = \frac{1}{B} \sum_{b=1}^B T_b(x)$

Classification: Majority vote of the individual trees

4 PCA

Algorithm (1) Center the data: $x_i \mapsto x_i - \frac{1}{n} \sum_{j=1}^n x_j = x_i - \bar{x}$ (2) Compute

the $d \times d$ sample covariance $S = \frac{1}{n} \sum_{i=1}^n x_i x_i^T$. Note that $\frac{1}{n} \sum_i (x_{ij} - \bar{x})^2$

is the sample variance of j th coordinate of data. (3) Find the first k eigenvectors of S , $\phi_1, \dots, \phi_k \in \mathbb{R}^d$, $S\phi_j = \lambda_j \phi_j$ (4) Project the data onto those k vectors: $x_i \mapsto \bar{x} + \left(\phi_1^T x_i\right) \phi_1 + \dots + \left(\phi_k^T x_i\right) \phi_k$

PCA is an unsupervised method

- Finds directions of greatest variation in the data
- The directions are called the principal vectors; the weightings on the vectors are called the principal components
- The first few vectors may be interpretable
- Orthogonality makes interpretation difficult for the higher components
- Can be used for visualization or dimensionality reduction