

Ch. 3

Resampling

web.stanford.edu/class/stats202

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- Test/train split
- Cross-validation
- Bootstrap

Not covered: Permutation tests ...

Validation

Thinking about the *true* loss function is important

- Most of the **regression** methods we've studied aim to minimize the RSS, while **classification** methods aim to minimize the 0-1 loss.
- In classification, we often care about certain kinds of error more than others; i.e. the natural loss function is not the 0-1 loss.
- Even if we use a method which minimizes a certain kind of training error, we can *tune* it to optimize our true loss function.
- Example: in the default study we could find the threshold that brings the False negative rate below an acceptable level.

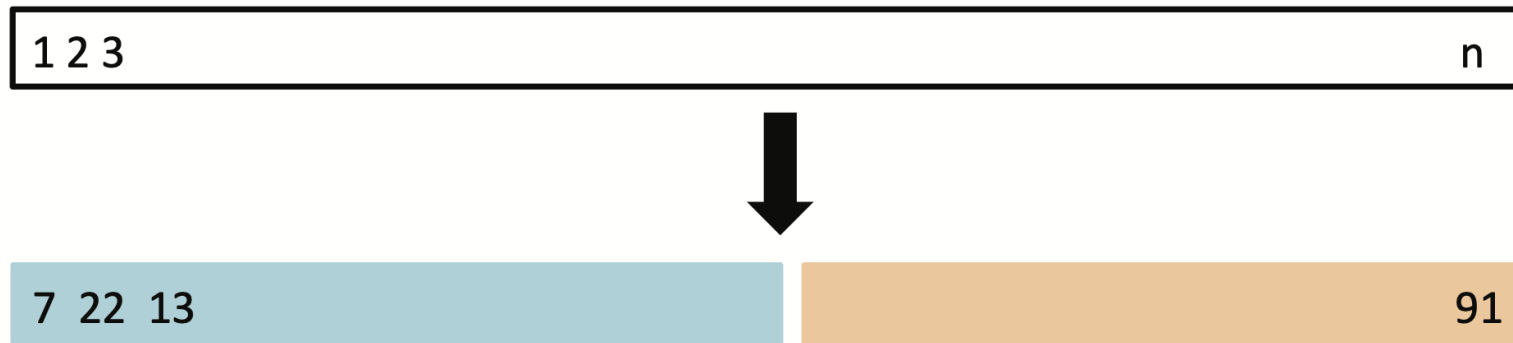
How to choose a supervised method that minimizes the test error

- In addition, *tune* the parameters of each method: maybe
 - *k* in *k*-nearest neighbors.
 - The number of variables to include in forward or backward selection.
 - The order of a polynomial in polynomial regression.

Validation set approach

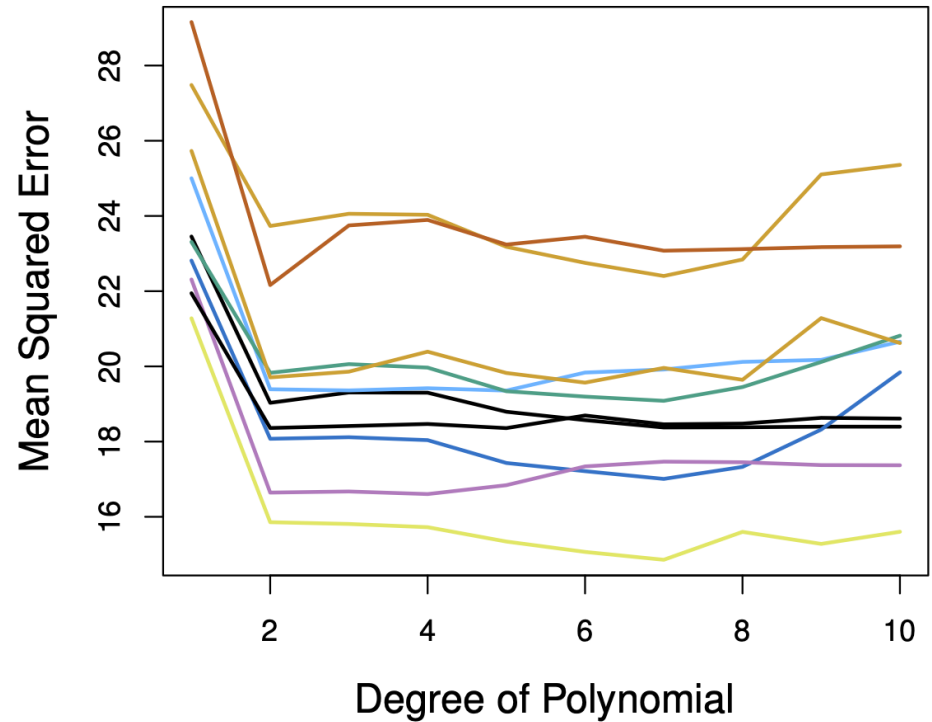
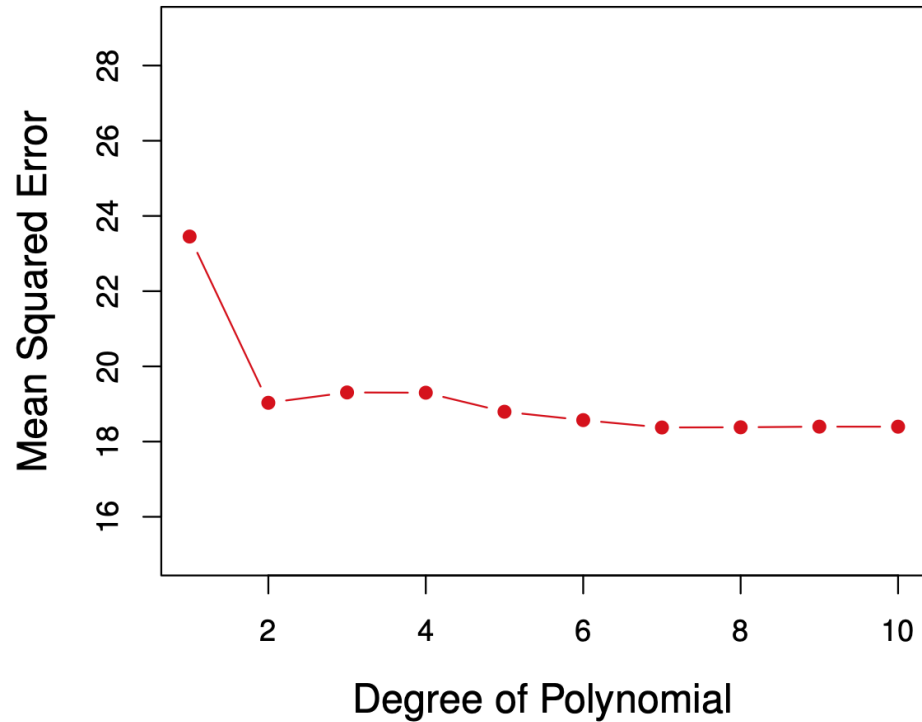
Use of a **validation set** is one way to approximate the test error:

- Divide the data into two parts.
- Train each model with one part.
- Compute the error on the remaining *validation* data.



Schematic of validation set approach.

Example: choosing order of polynomial



Left: validation error as a function of degree. Right: multiple splits into validation and training.

- Polynomial regression to estimate mpg from horsepower in the Auto data.
- **Problem:** Every split yields a different estimate of the error.



Leave one out cross-validation (LOOCV)

- For every $i = 1, \dots, n$:
 - *train the model on every point except i ,*
 - *compute the test error on the held out point.*
- Average the test errors.

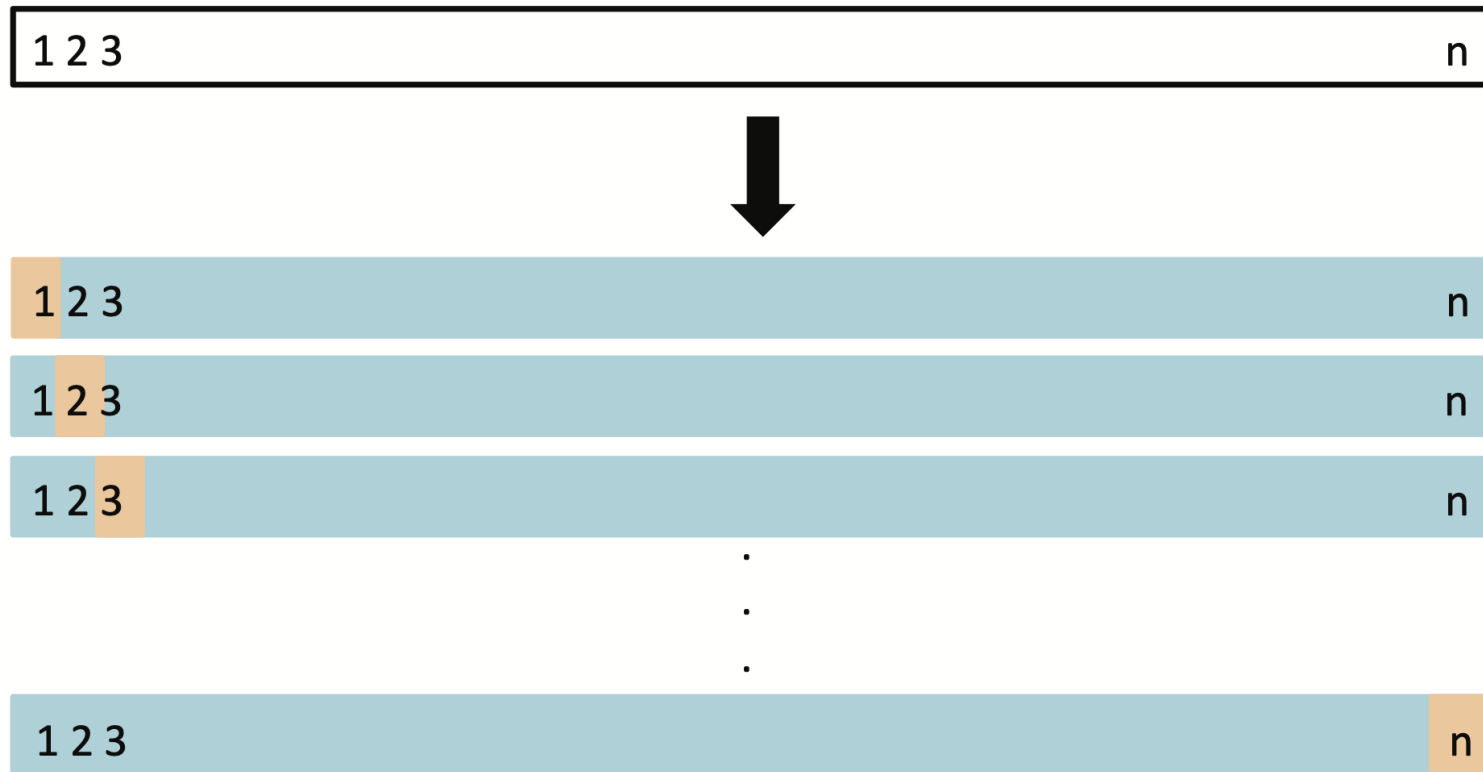
Regression

- Overall error:

$$CV_{(n)} = \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i^{(-i)})^2$$

- Notation $\hat{y}_i^{(-i)}$: prediction for the i sample when learning without using the i th sample.

Schematic for LOOCV



Schematic of leave-one-out cross-validation (LOOCV) set approach.

Requires fitting method n times...

Classification

- Overall error:

$$CV_{(n)} = \frac{1}{n} \sum_{i=1}^n \mathbf{1}(y_i \neq \hat{y}_i^{(-i)})$$

- Here, $\hat{y}_i^{(-i)}$ is predicted label for the i sample when learning without using the i th sample.

Shortcut for linear regression

- Computing $CV_{(n)}$ can be computationally expensive, since it involves fitting the model n times.
- For linear regression, there is a shortcut:

$$CV_{(n)} = \frac{1}{n} \sum_{i=1}^n \left(\frac{y_i - \hat{y}_i}{1 - h_{ii}} \right)^2$$

Handwritten blue annotations: A blue arrow points from the handwritten $y_i - \hat{y}_i$ above the fraction to the numerator of the fraction. Another blue arrow points from the handwritten \hat{y}_i above the fraction to the denominator of the fraction.

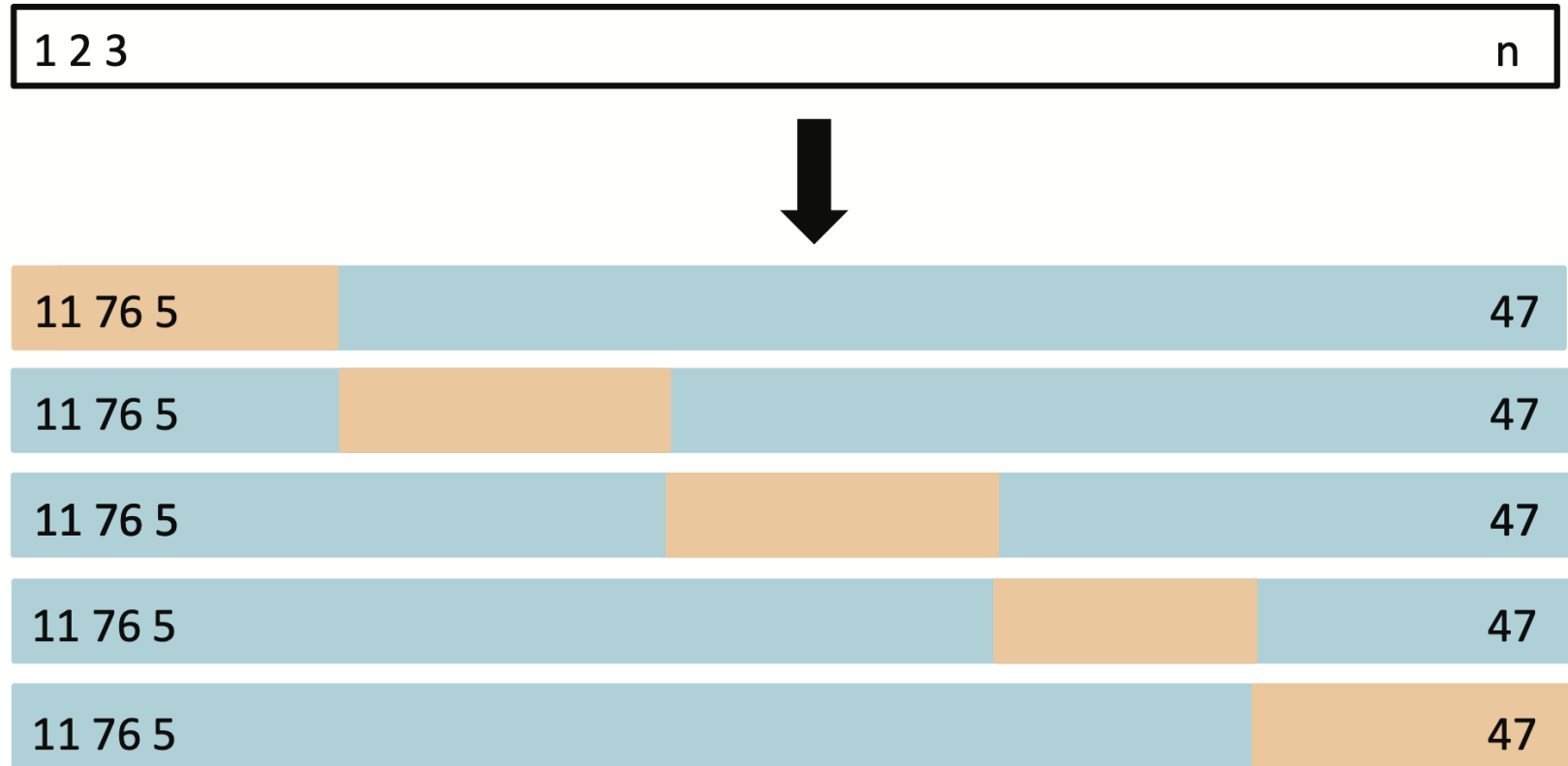
- Above, h_{ii} is the leverage statistic.
- Approximate versions sometimes used for logistic regression...

K -fold cross-validation

Algorithm 5.3? K -fold CV

- Split the data into K subsets or *folds*.
- For every $i = 1, \dots, K$:
 - *train the model on every fold except the i th fold,*
 - *compute the test error on the i th fold.*
- Average the test errors.

Schematic for K -fold CV

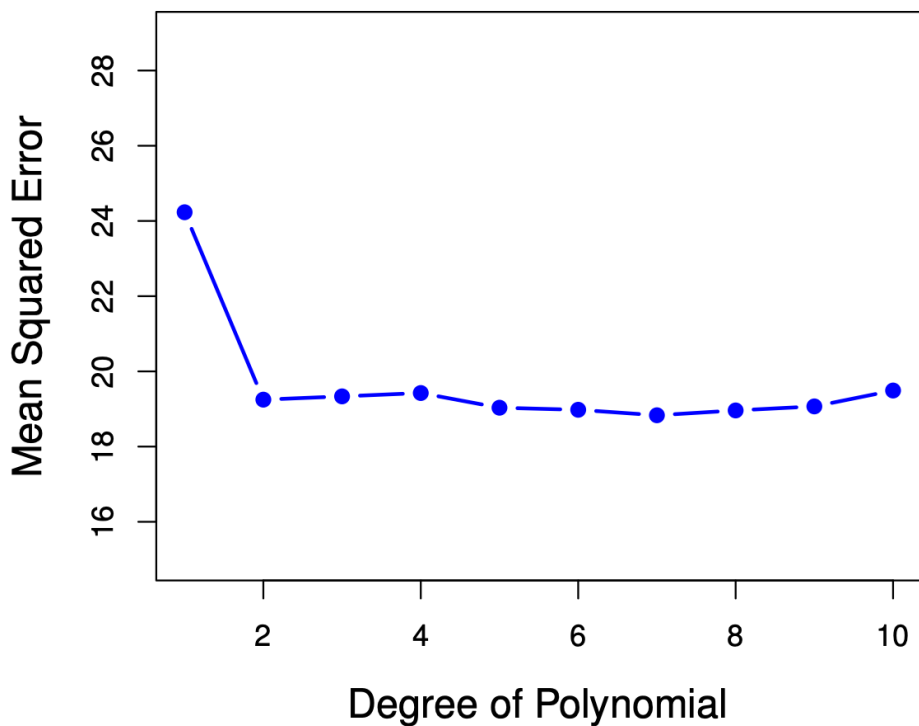


Schematic of K -fold CV fold approach.

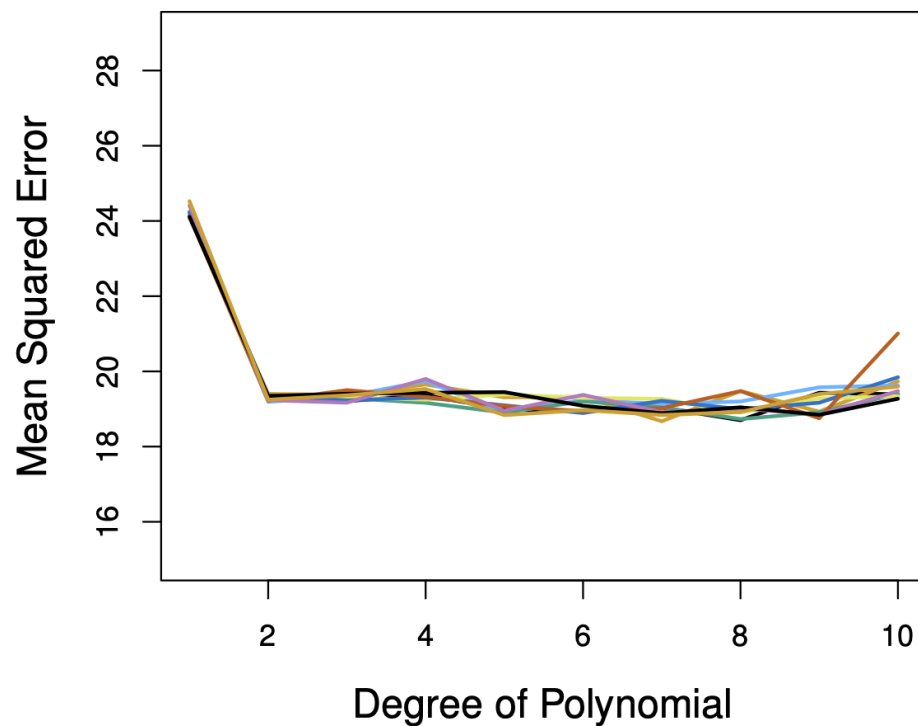
*Unlike LOOCV,
 K -fold has
some randomness*

LOOCV vs. K -fold cross-validation

LOOCV



10-fold CV



Comparison of LOOCV and K -fold CV.

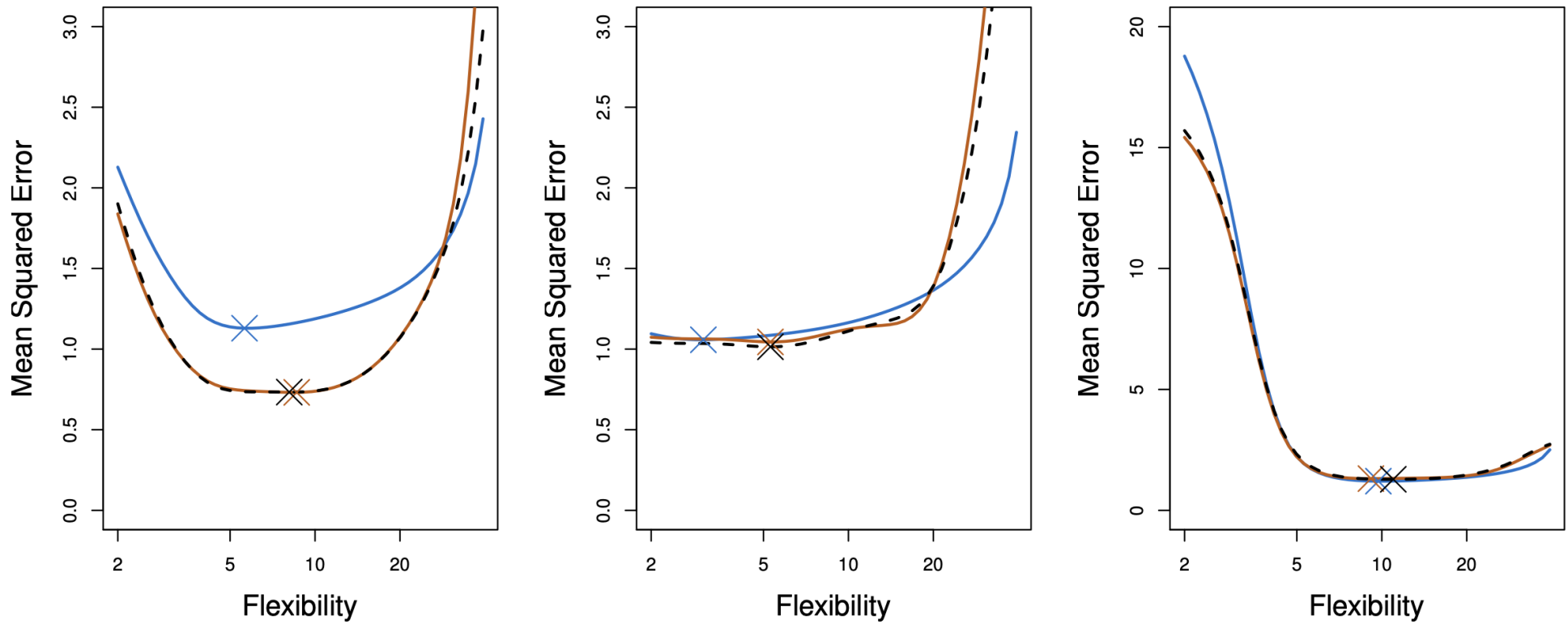
Much less randomness than single test/train split...

Common choice for k :
5, 10, n \rightarrow LOOCV

Comments

- K -fold CV depends on the chosen split (somewhat).
- In K -fold CV, we train the model on less data than what is available to LOOCV. This introduces *some* bias into the estimates of test error.
- In LOOCV, the training samples highly resemble each other. This increases the *some* variance of the test error estimate.
- n -fold CV is equivalent LOOCV.

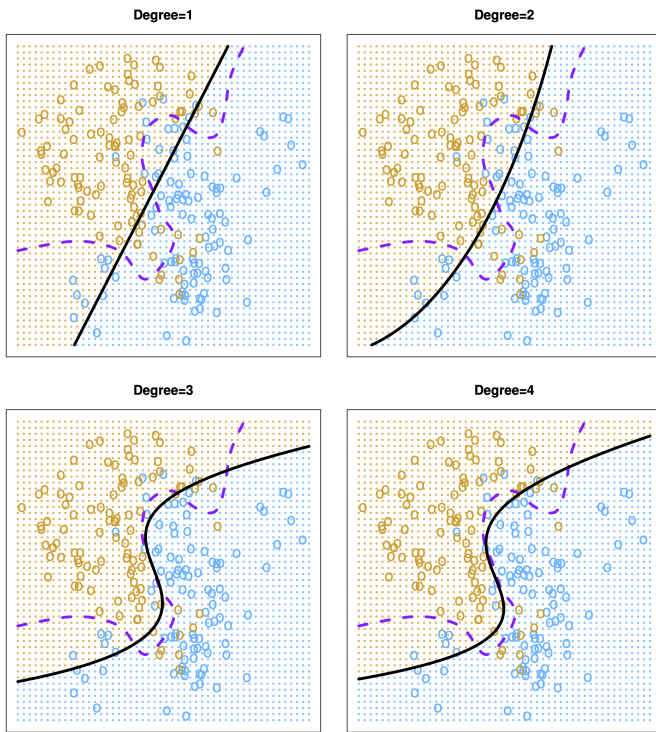
Choosing an optimal model



Comparison of LOOCV and K -fold CV to test MSE.

Even if the error estimates are off, choosing the model with the minimum cross validation error (10 fold in orange) often leads to a method with near minimum ~~test~~ error.

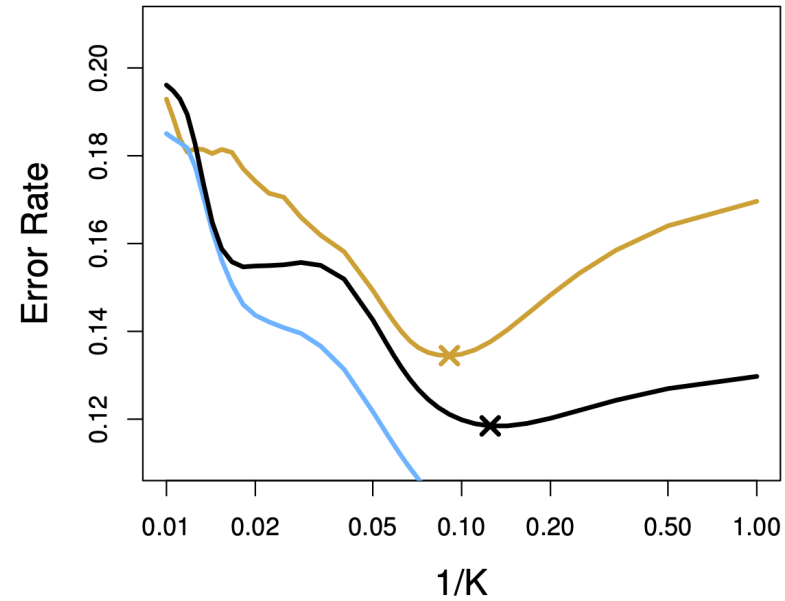
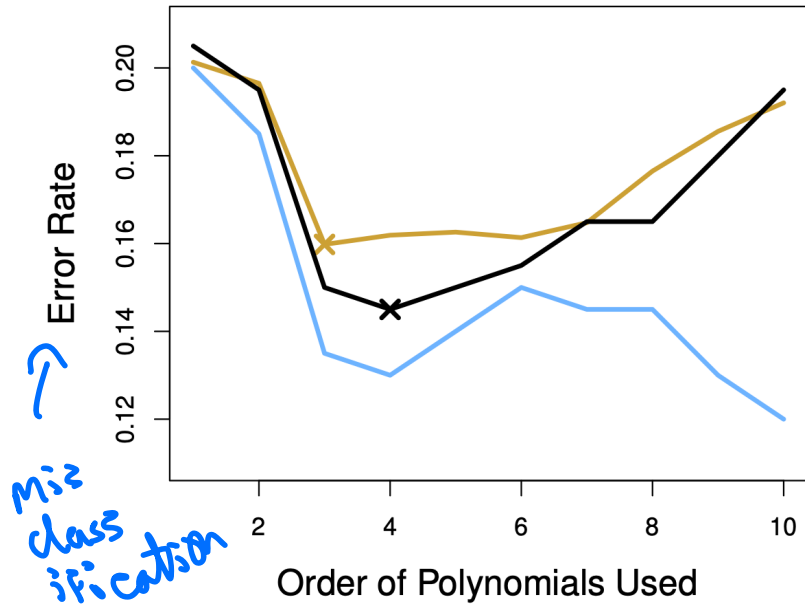
population



In a classification problem, things look similar.

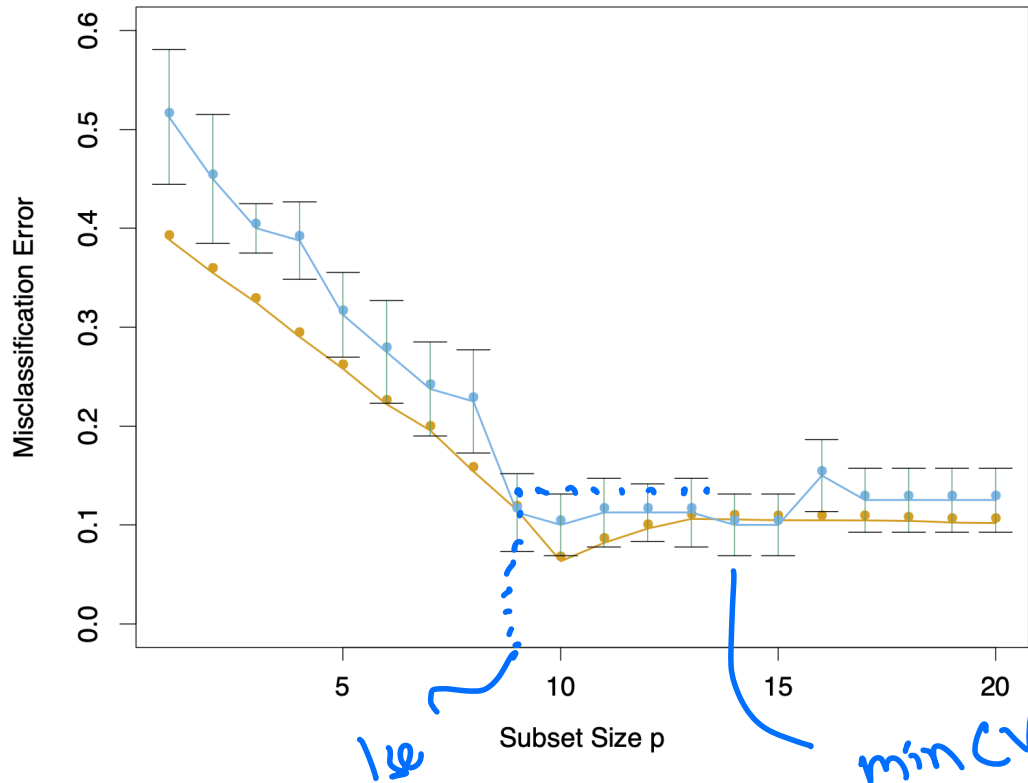
- Logistic regression with polynomial predictors of increasing degree. (— — — — —)
- — — — — — Bayes boundary

Choosing an optimal model



- Cubic model has best test error.
- Quartic has best CV.
- Curves look similar.
- Q: Why doesn't *training error* keep decreasing?

The one standard error (ISE) rule of thumb



Goal's
"simpler" model
w/ similar
CV to min. CV...

- Forward stepwise selection (we'll see in more detail shortly)
- 10-fold cross validation, True test error
- **I-SE rule of thumb:**
 - A number of models with $10 \leq p \leq 15$ have almost the same CV error.
 - The vertical bars represent 1 standard error in the test error from the 10 folds.
 - Choose the simplest model whose CV error is no more than one standard error above the model with the lowest CV error.

The wrong way to do cross validation

- *Reading:* Section 7.10.2 of The Elements of Statistical Learning.
- We want to classify 200 individuals according to whether they have cancer or not.
- We use logistic regression onto 1000 measurements of gene expression.
- **Proposed strategy:**
 1. *Using all the data, select the 20 most significant genes using z -tests.*
 2. *Estimate the test error of logistic regression with these 20 predictors via 10-fold cross validation.*

- To see how that works, let's use the following simulated data:
 1. *Each gene expression is standard normal and independent of all others.*
 2. *The response (cancer or not) is sampled from a coin flip — no correlation to any of the “genes”.*
- **Q: What should the misclassification rate be for any classification method using these predictors?**
- **A: Roughly 50%.**

- We run this simulation, and obtain a CV error rate of 3%!
- Why?
 - *Since we only have 200 individuals in total, among 1000 variables, at least some will appear correlated with the response.*
 - *We had run variable selection using all the data, so the variables we select have some correlation with the response in every subset or fold in the cross validation.*

The right way to do cross validation

1. Divide the data into 10 folds.
 2. For $i = 1, \dots, 10$:
 1. *Using every fold except i , perform the variable selection and fit the model with the selected variables.*
 2. *Compute the error on fold i .*
 3. *Average the 10 test errors obtained.*
- In our simulation, this produces an error estimate of close to 50%.
 - **Moral of the story:** Every aspect of the learning method that involves using the data — variable selection, for example — must be cross-validated.

Bootstrap

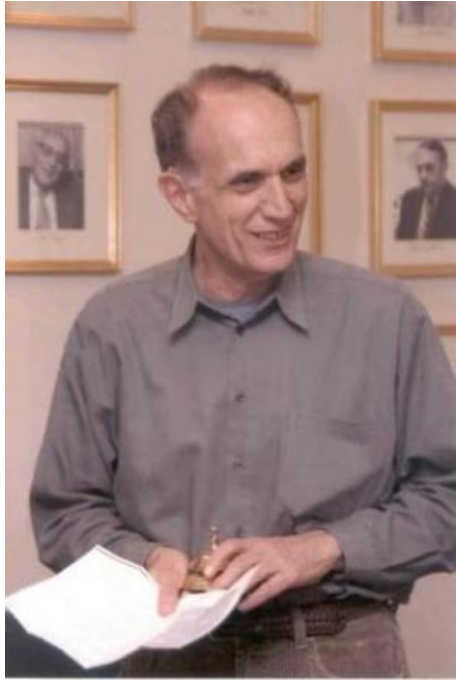
- Another resampling technique often seen in practice.

Cross-validation vs. the Bootstrap

- **Cross-validation:** provides **estimates** of the (test) **error**
- **The Bootstrap:** provides the (standard) **error** of **estimates**



Bootstrap



Brad Efron

- One of the most important techniques in all of Statistics.
- Computer intensive method.
- Popularized by Brad Efron ← Stanford pride!

Standard errors in linear regression from a sample of size n

```
Advertising = read.csv('https://www.statlearning.com/s/Advertising.csv')
M.sales = lm(sales ~ TV, data=Advertising)
summary(M.sales)
```

```
##
## Call:
## lm(formula = sales ~ TV, data = Advertising)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.3860 -1.9545 -0.1913  2.0671  7.2124
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.032594   0.457843   15.36  <2e-16 ***
## TV           0.047537   0.002691   17.67  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.259 on 198 degrees of freedom
## Multiple R-squared:  0.6119, Adjusted R-squared:  0.6099
## F-statistic: 312.1 on 1 and 198 DF, p-value: < 2.2e-16
```

uses the model:

$$Y_i = \beta_0 + \beta_1 X_i + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma^2)$$

Classical way to compute Standard Errors

- **Example:** Estimate the variance of a sample x_1, x_2, \dots, x_n :
- Unbiased estimate of σ^2 :

$$\hat{\sigma}^2 = \frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2.$$

- What is the Standard Error of $\hat{\sigma}^2$?

- Assume that x_1, \dots, x_n are normally distributed with common mean μ and variance σ^2 .
- Then $\hat{\sigma}^2(n-1)$ has a χ -squared distribution with $n-1$ degrees of freedom.
- For large n , $\hat{\sigma}^2$ is normally distributed around σ^2 .
- The SD of this sampling distribution is the Standard Error.

CI: $\hat{\sigma}^2 \pm 2 \cdot SE(\hat{\sigma}^2)$

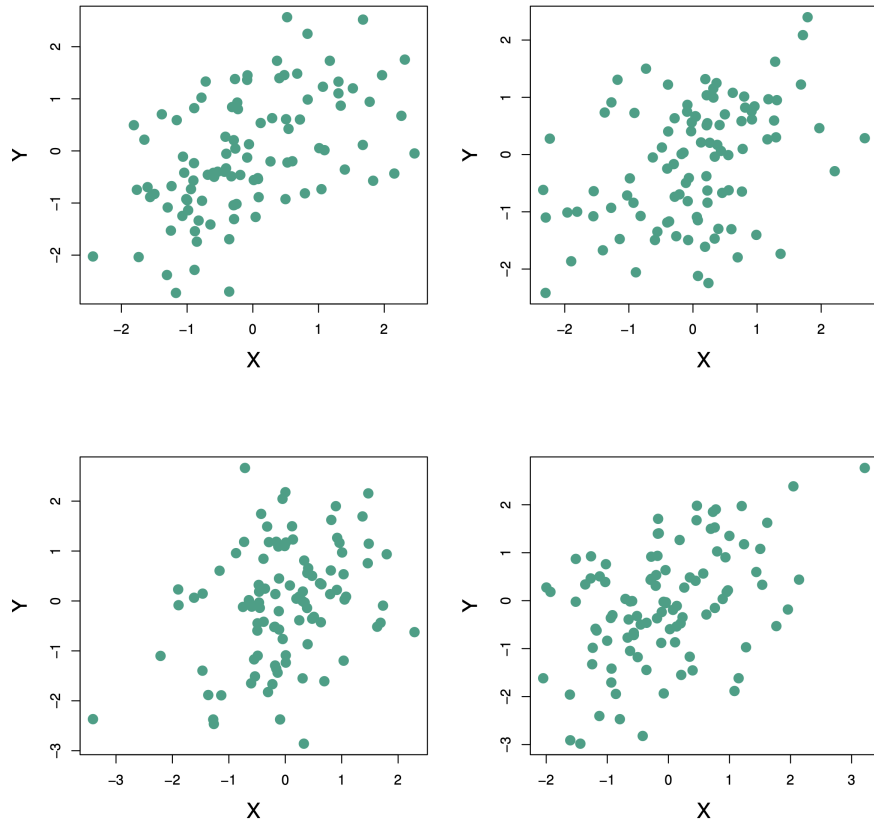
Assumptions

can compute $SE(\hat{\sigma}^2)$

Limitations of the classical approach

- This approach has served statisticians well for many years; however, what happens if:
 - *The distributional assumption — for example, x_1, \dots, x_n being normal — breaks down?*
 - *The estimator does not have a simple form and its sampling distribution cannot be derived analytically?*
- Bootstrap can handle (at least some of) these departures from the usual assumptions!

Example: Investing in two assets



- Suppose that X and Y are the returns of two assets.
- These returns are observed every day: $(x_1, y_1), \dots, (x_n, y_n)$.

- We have a fixed amount of money to invest and we will invest a fraction α on X and a fraction $(1 - \alpha)$ on Y .
- Therefore, our return will be

$$\alpha X + (1 - \alpha)Y.$$

- Our goal will be to minimize the variance of our return as a function of α .
- One can show that the optimal α is:

Truth



$$\alpha = \frac{\sigma_Y^2 - \text{Cov}(X, Y)}{\sigma_X^2 + \sigma_Y^2 - 2\text{Cov}(X, Y)}.$$

- **Proposal:** Use an estimate:

$$\hat{\alpha} = \frac{\hat{\sigma}_Y^2 - \widehat{\text{Cov}}(X, Y)}{\hat{\sigma}_X^2 + \hat{\sigma}_Y^2 - 2\widehat{\text{Cov}}(X, Y)}.$$

Estimate



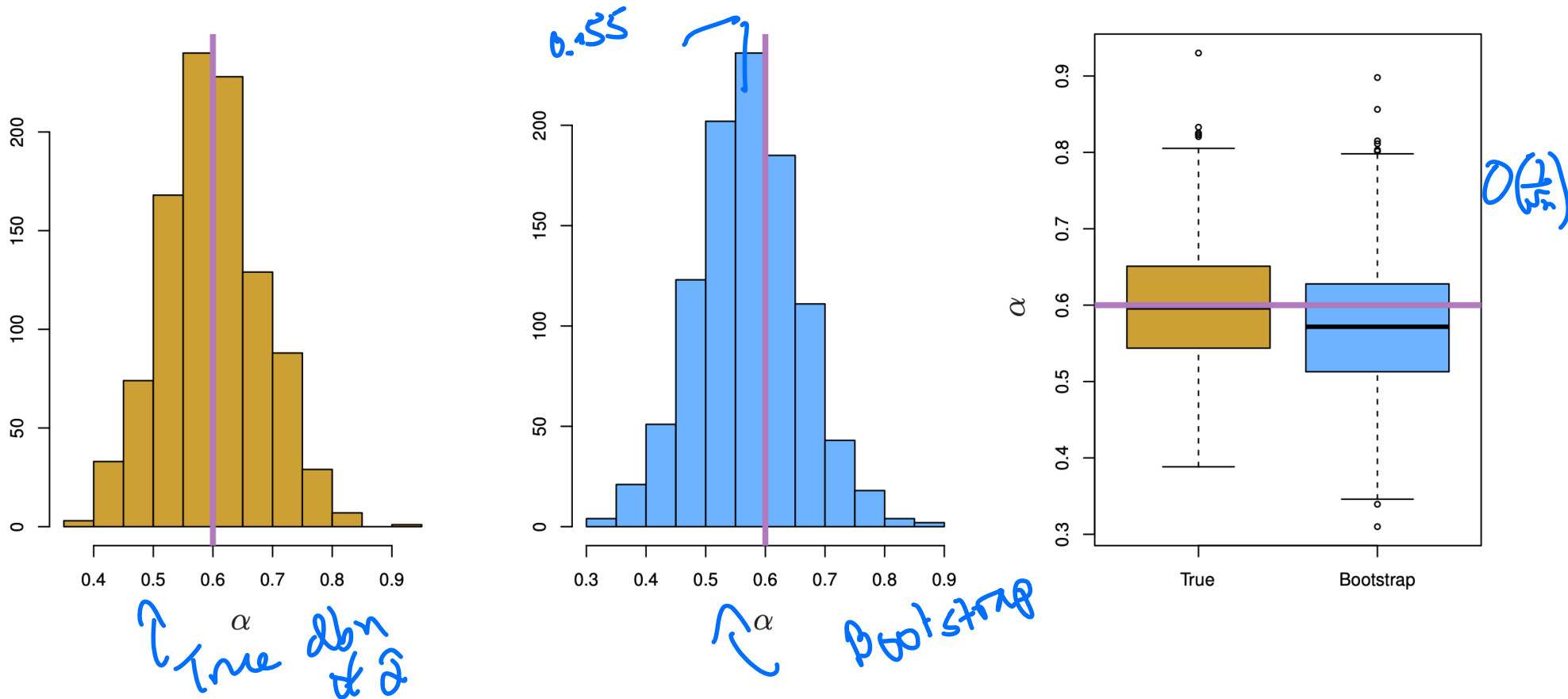
CI =

$$\hat{\alpha} \pm 2 \cdot \text{SE}(\hat{\alpha})$$

How do we get this?

- Suppose we compute the estimate $\hat{\alpha} = 0.55$ using the samples $(x_1, y_1), \dots, (x_n, y_n)$.
- How sure can we be of this value? (*A little vague of a question.*)
- If we had sampled the observations in a different 100 days, would we get a wildly different $\hat{\alpha}$? (*A more precise question.*)

Resampling the data from the true distribution



- In this thought experiment, we know the actual joint distribution $P(X, Y)$, so we can resample the n observations to our hearts' content.

- True distribution of $\hat{\alpha}$

$$SE(\text{Bootstrap}) \approx SE(\text{Truth})$$

Computing the standard error of $\hat{\alpha}$

- We will use S samples to estimate the standard error of $\hat{\alpha}$.

- For each sampling of the data, for $1 \leq s \leq S$

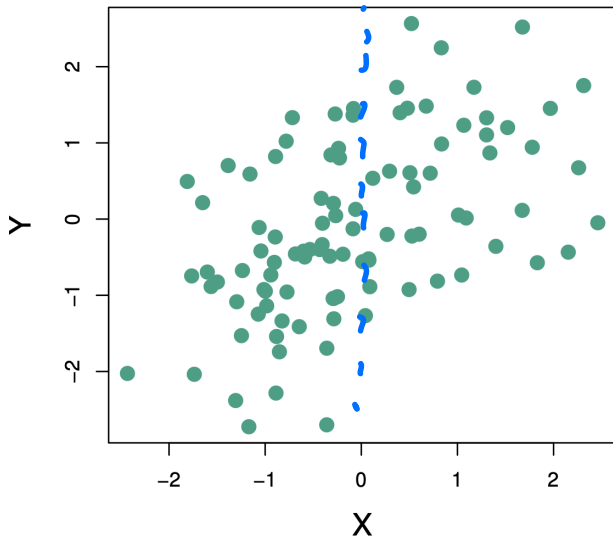


$$(x_1^{(s)}, \dots, x_n^{(s)})$$

we can compute a value of the estimate $\hat{\alpha}^{(1)}, \hat{\alpha}^{(2)}, \dots$

- The Standard Error of $\hat{\alpha}$ is approximated by the standard deviation of these values.

In reality, we only have n samples



$$\hat{P}(X > 0) \approx 40\%$$

an estimate of $P(X > 0)$

$$\hat{E}[\beta(X, Y)]$$

A single panel of Fig 5.9

- However, these samples can be used to approximate the joint distribution of X and Y .

$\text{Var}(\hat{\alpha}) \approx$ function of Joint Obs of X & Y .

- **The Bootstrap:** Sample from the *empirical distribution*:

$$\widehat{P}(X, Y) = \frac{1}{n} \sum_{i=1}^n \delta_{(x_i, y_i)}.$$

- Equivalently, resample the data by drawing n samples *with replacement* from the actual observations.
- *Why it works:* variances computed under the empirical distribution are good approximations of variances computed under the true distribution (in many cases).

$$\text{Var}_P(g) \approx \text{Var}_{\widehat{P}_B}(g)$$

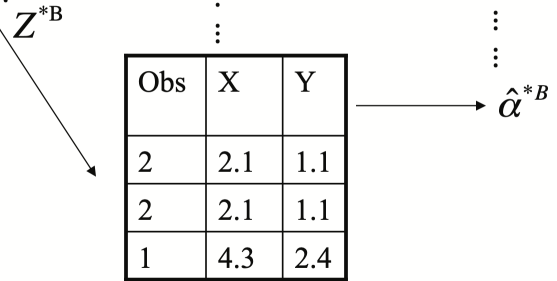
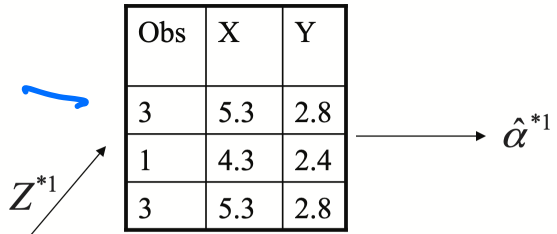
A schematic of the Bootstrap

$n=100$

Obs	X	Y
1	4.3	2.4
2	2.1	1.1
3	5.3	2.8

Original Data (Z)

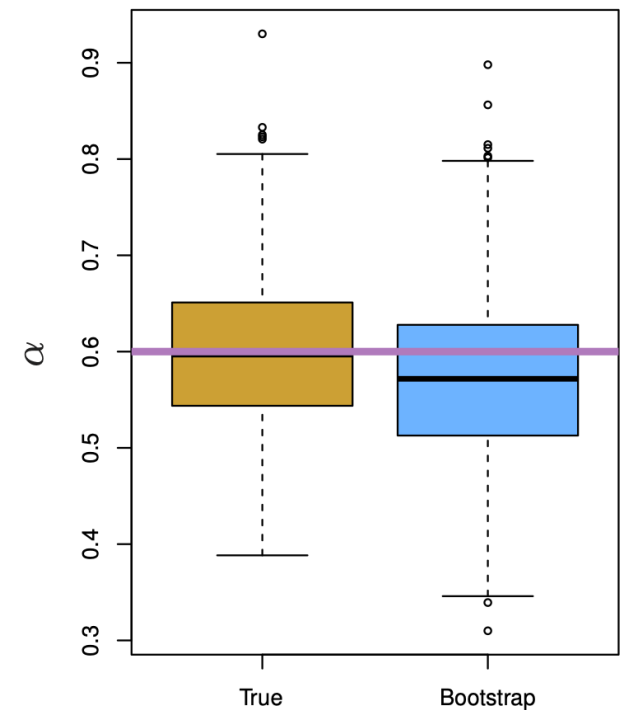
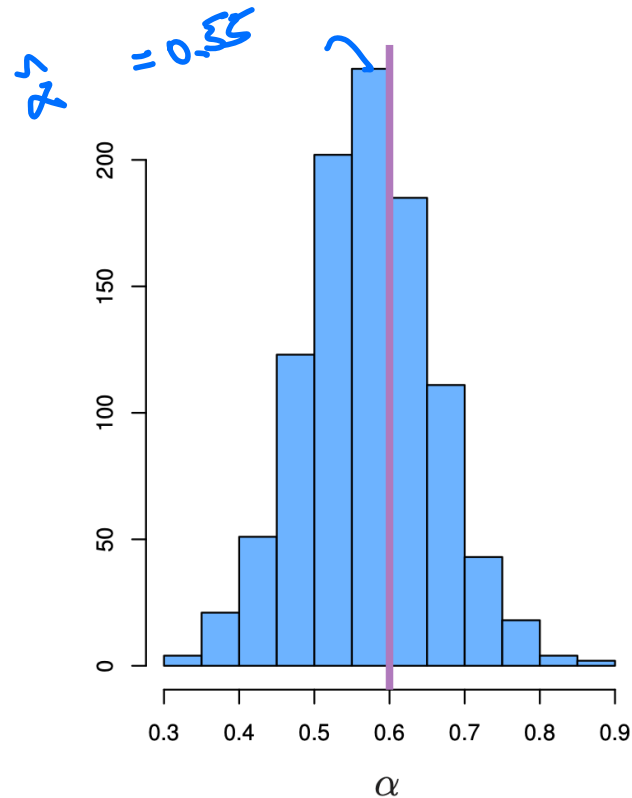
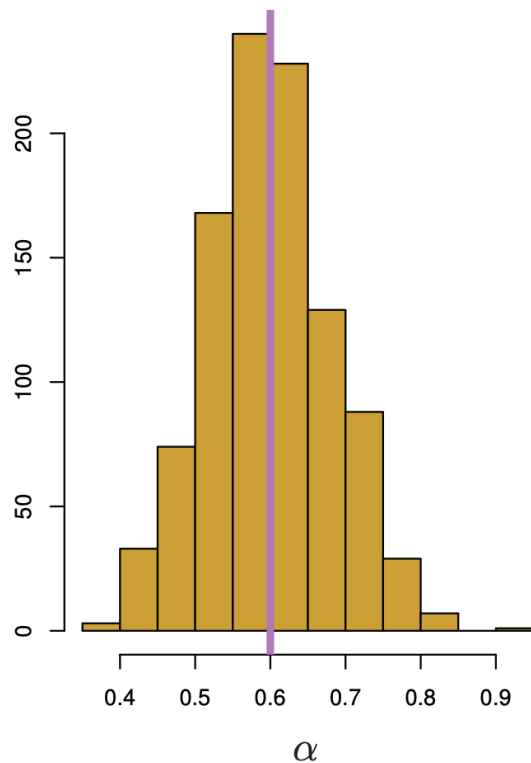
$n=100$



A single dataset

$B \approx 1000$

Comparing Bootstrap sampling to sampling from the true distribution



- Left panel is population distribution of $\hat{\alpha}$ – centered (approximately) around the true α .
- Middle panel is bootstrap distribution of $\hat{\alpha}$ – centered (approximately) around observed $\hat{\alpha}$.