Model Assessment and Selection

Model selection:

- Estimate performance of models to choose best one.

Model assessment:

- Given the final chosen model, estimate prediction error on new data.

Best approach in data rich environment:
randomly split data three ways.

Less data: approx. validation step by analytic formula (e.g. AIC) or re-use sample (cross-validation and bootstrap).

Model Assessment and Selection

Readings:

- An Introduction to Statistical Learning *(Ch. 2 and 5).*
- In The Elements of Statistical Learning *(Ch 7.)*

The regression function $f(x)$

- Is also defined for vector X; e.g. $f(x) = f(x_1, x_2, x_3) = E(Y|X_1 = x_1, X_2 = x_2, X_3 = x_3)$
- Is the *ideal* or *optimal* predictor of Y with regard to mean-squared prediction error: $f(x) = E(Y|X = x)$ is the function that minimizes $E[(Y - g(X))^2|X = x]$ over all functions g at all points $X = x$.
- $\epsilon = Y - f(x)$ is the *irreducible* error — i.e. even if we knew $f(x)$, we would still make errors in prediction, since at each $X = x$ there is typically a distribution of possible Y values.
- For any estimate $\hat{f}(x)$ of $f(x)$, we have

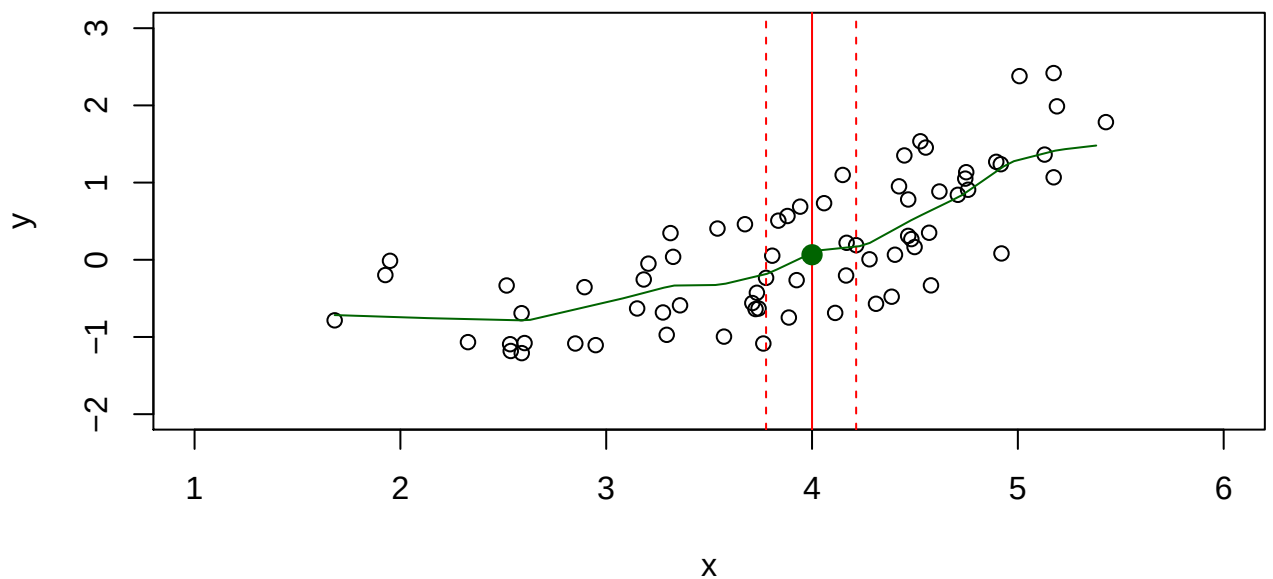
$$E[(Y - \hat{f}(X))^2|X = x] = \underbrace{[f(x) - \hat{f}(x)]^2}_{\textit{Reducible}} + \underbrace{\text{Var}(\epsilon)}_{\textit{Irreducible}}$$

How to estimate f

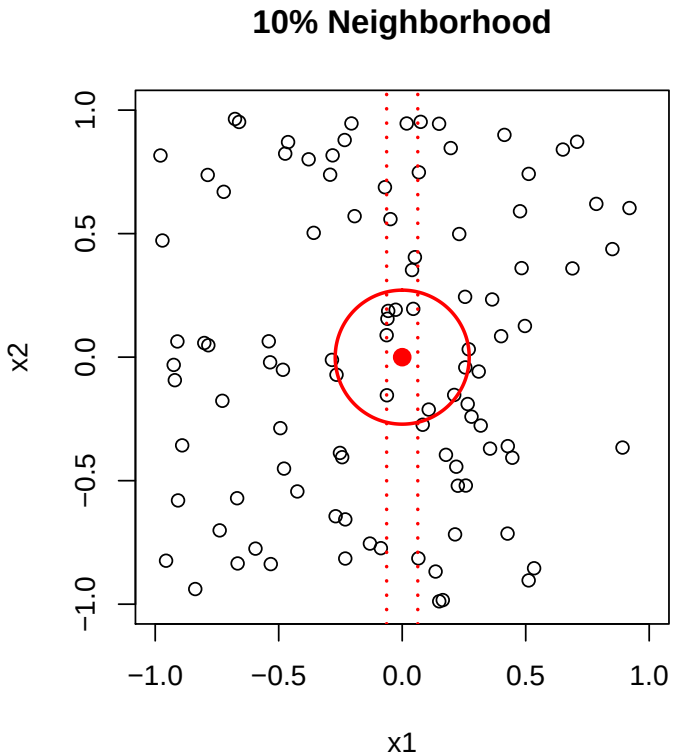
- Typically we have few if any data points with $X = 4$ exactly.
- So we cannot compute $E(Y|X = x)$!
- Relax the definition and let

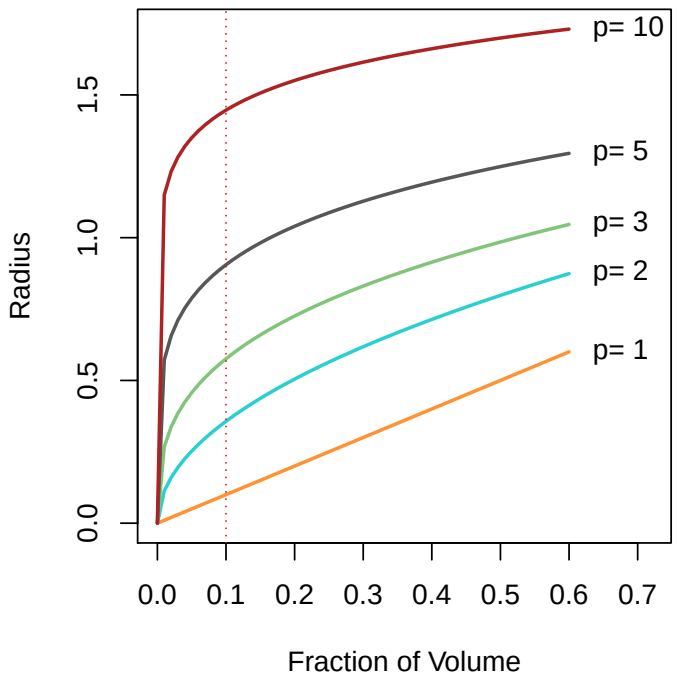
$$\hat{f}(x) = \text{Ave}(Y|X \in \mathcal{N}(x))$$

where $\mathcal{N}(x)$ is some *neighborhood* of x.



The curse of dimensionality





Parametric and structured models

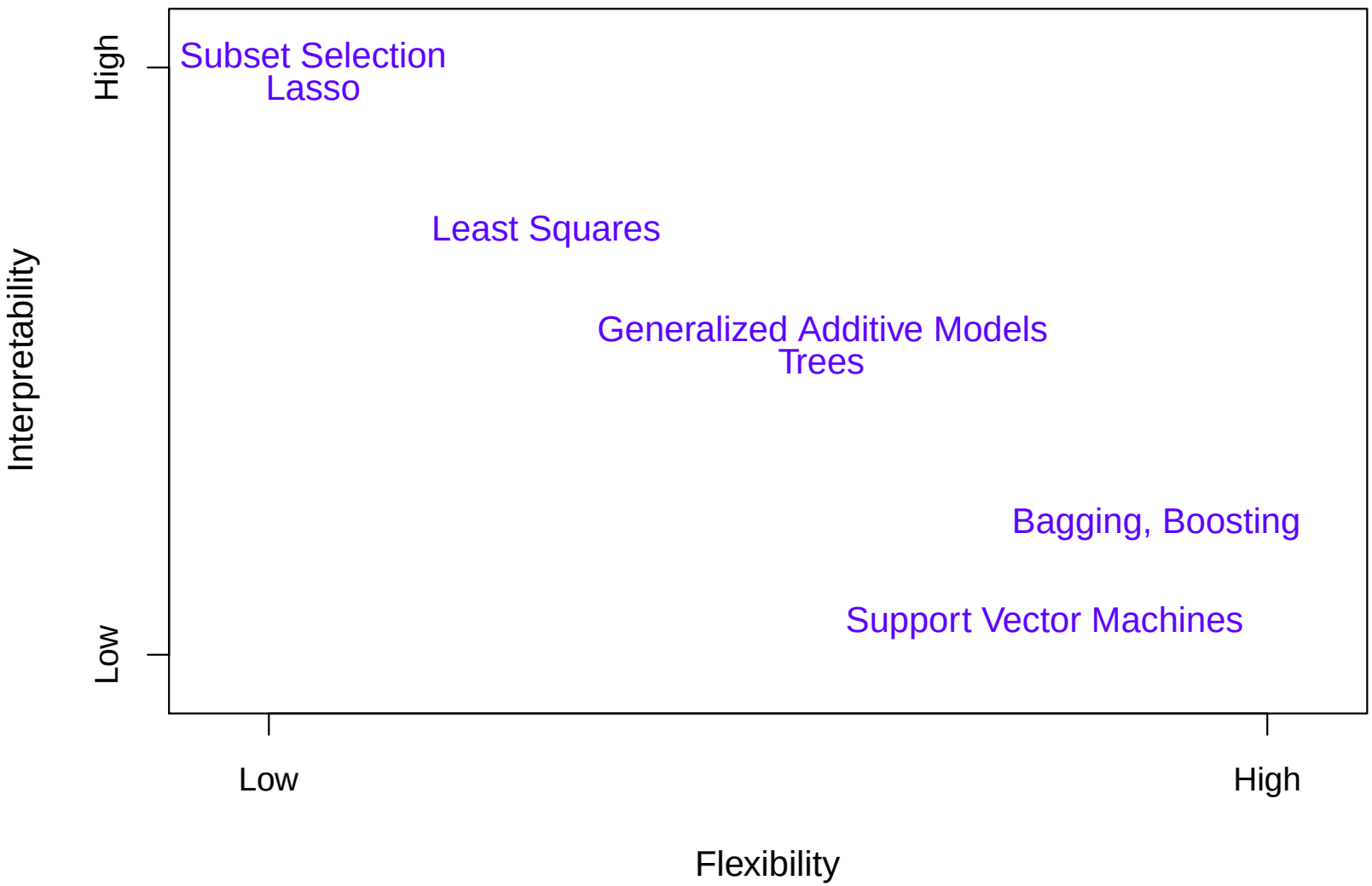
The *linear* model is an important example of a parametric model:

$$f_L(X) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots \beta_p X_p.$$

- A linear model is specified in terms of $p + 1$ parameters $\beta_0, \beta_1, \ldots, \beta_p$.
- We estimate the parameters by fitting the model to training data.
- Although it is *almost never correct*, a linear model often serves as a good and interpretable approximation to the unknown true function $f(X)$.

Some trade-offs

- Prediction accuracy versus interpretability.
  — Linear models are easy to interpret; thin-plate splines are not.
- Good fit versus over-fit or under-fit.
  — How do we know when the fit is just right?
- Parsimony versus black-box.
  — We often prefer a simpler model involving fewer variables over a black-box predictor involving them all.


Subset Selection
Lasso
Least Squares
Generalized Additive Models
Trees
Bagging, Boosting
Support Vector Machines
High
Low
Interpretability
Low
High
Flexibility

Assessing Model Accuracy

Suppose we fit a model $\hat{f}(x)$ to some training data $\mathsf{Tr} = \{x_i, y_i\}_1^N$, and we wish to see how well it performs.

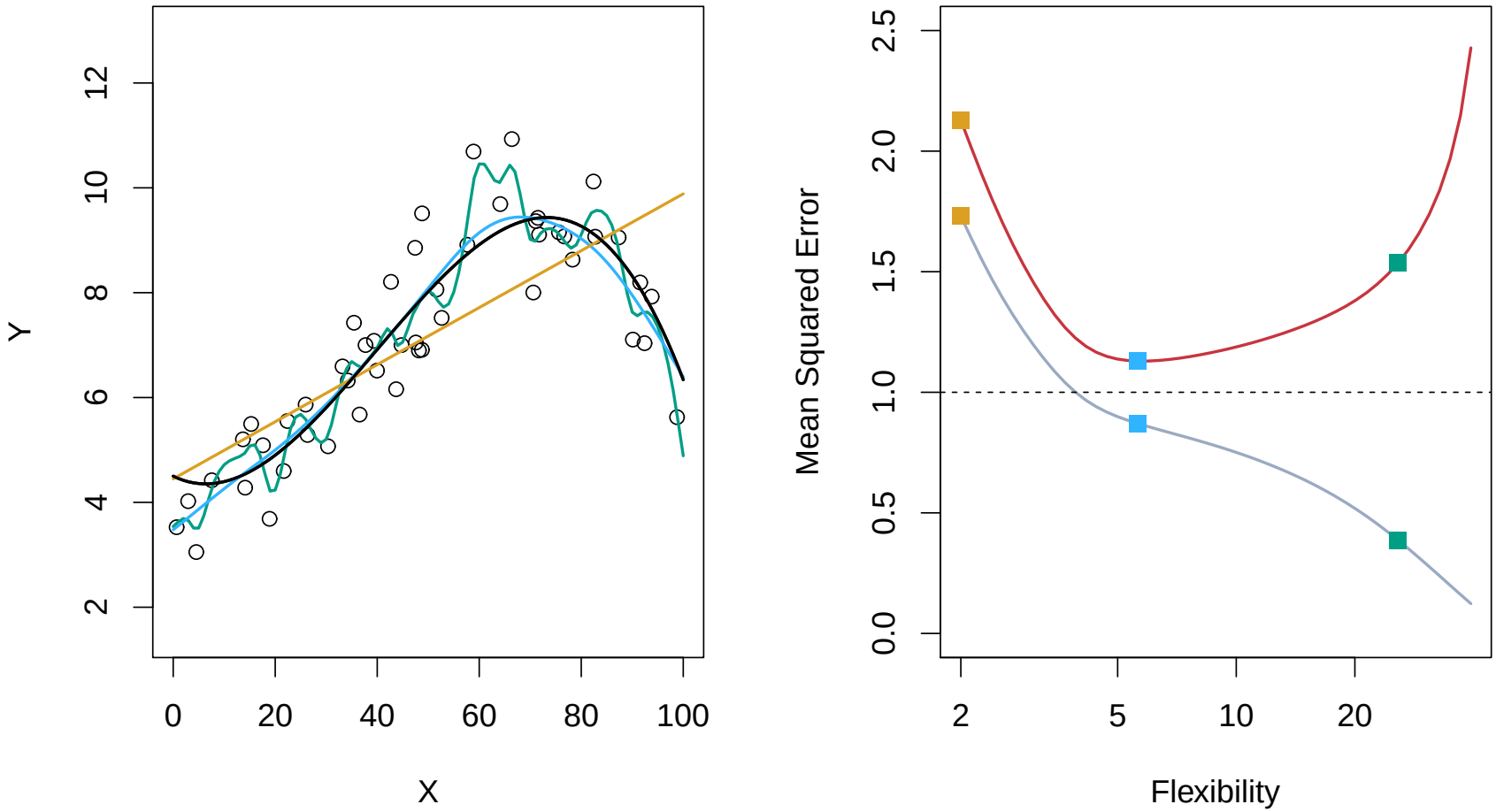
- We could compute the average squared prediction error over Tr:

$$\text{MSE}_{\mathsf{Tr}} = \text{Ave}_{i \in \mathsf{Tr}}[y_i - \hat{f}(x_i)]^2$$

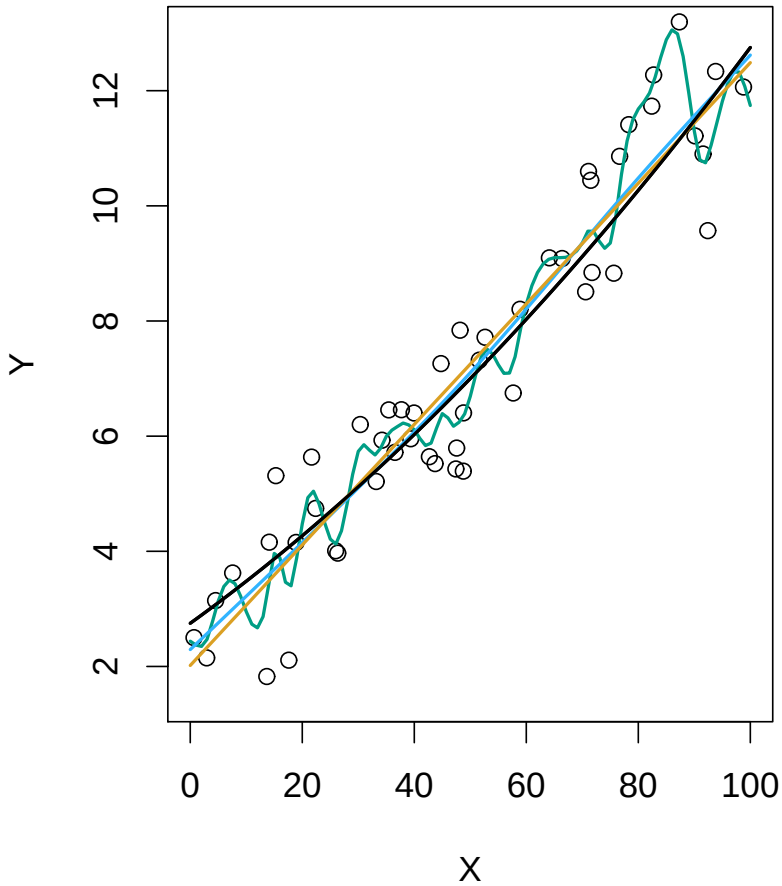
This may be biased toward more overfit models.

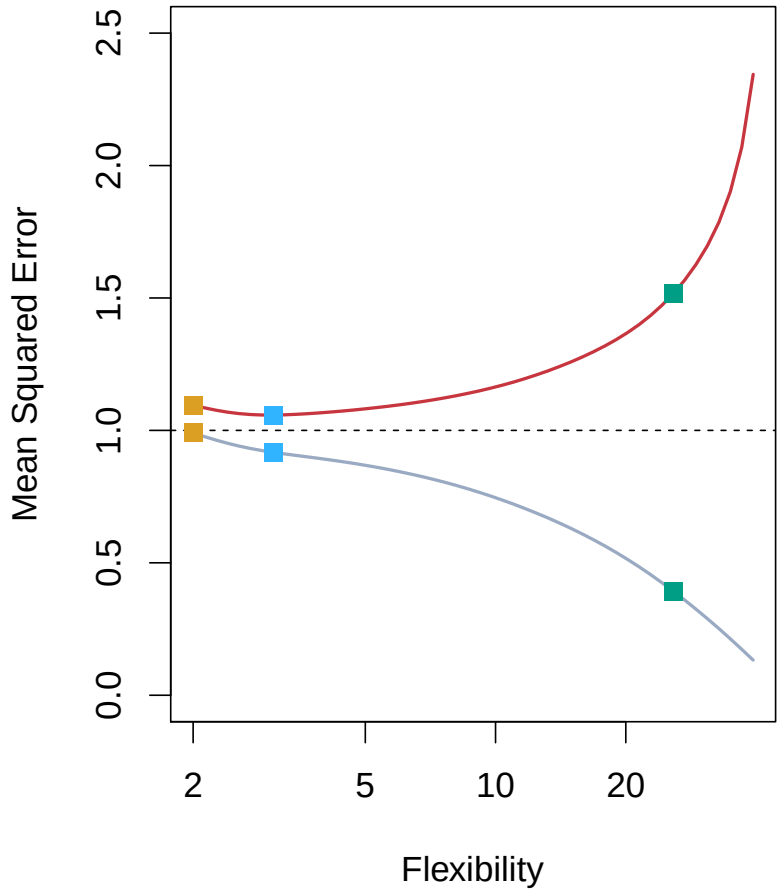
- Instead we should, if possible, compute it using fresh *test* data $\mathsf{Te} = \{x_i, y_i\}_1^M$:

$$\text{MSE}_{\mathsf{Te}} = \text{Ave}_{i \in \mathsf{Te}}[y_i - \hat{f}(x_i)]^2$$

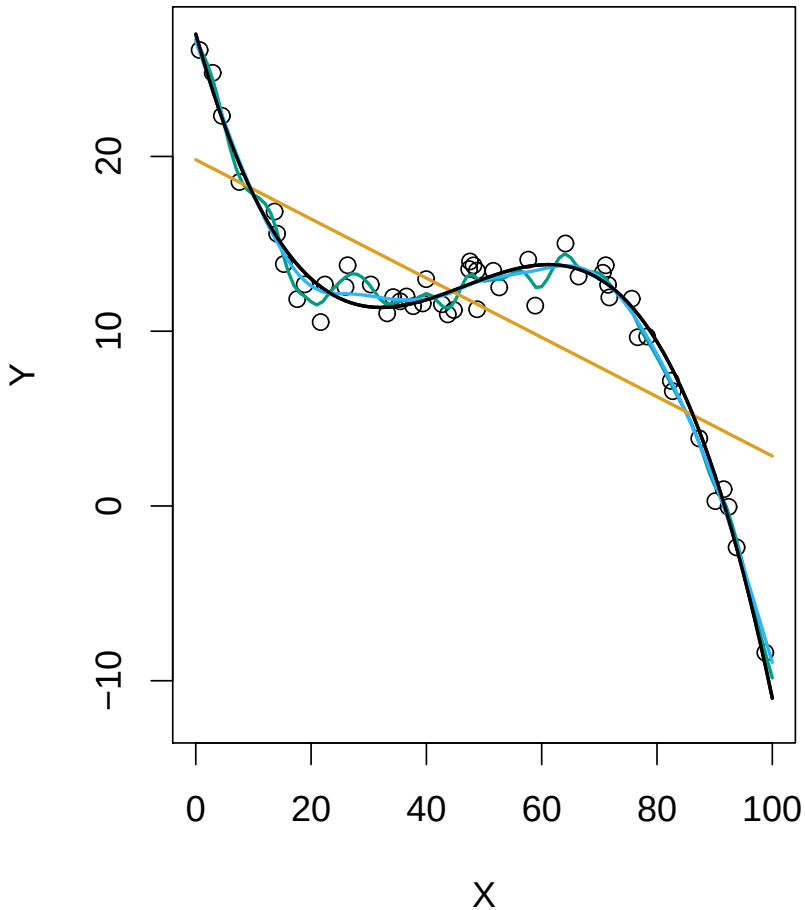


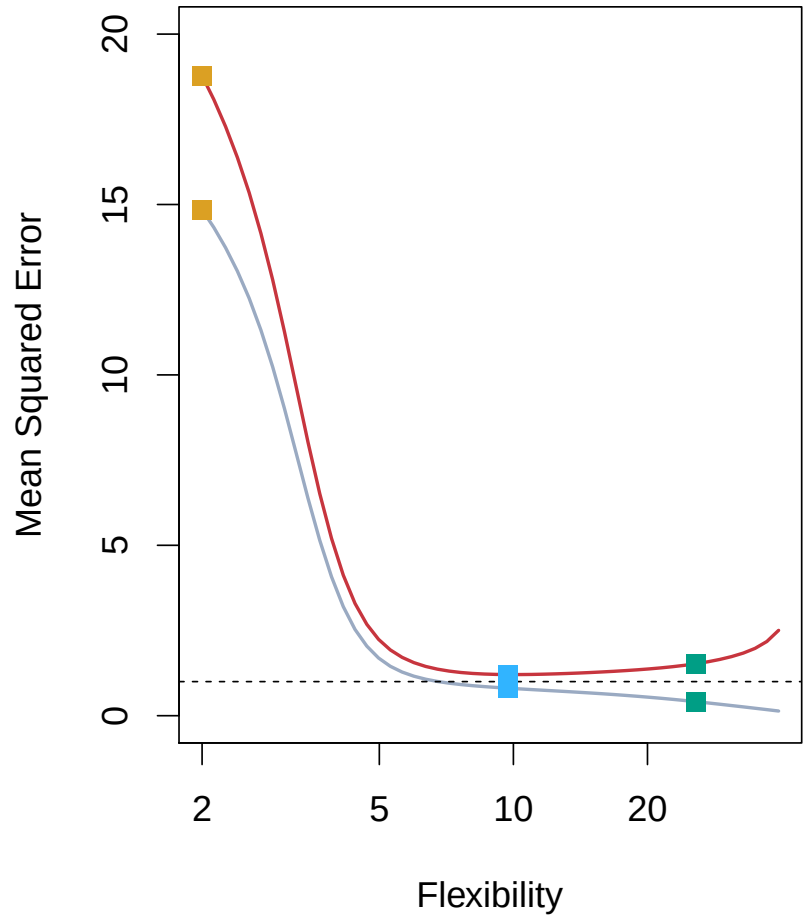
Black curve is truth. Red curve on right is MSE_{Te}, grey curve is MSE_{Tr}. Orange, blue and green curves/squares correspond to fits of different flexibility.





Here the truth is smoother, so the smoother fit and linear model do really well.





Here the truth is wiggly and the noise is low, so the more flexible fits do the best.

Estimation
Model Bias-Variance Trade-off

Suppose we have fit a model $\hat{f}(x)$ to some training data Tr, and let (x_0, y_0) be a test observation drawn from the population. If the true model is $Y = f(X) + \epsilon$ (with $f(x) = E(Y|X = x)$), then

$$E\left(y_0 - \hat{f}(x_0)\right)^2 = \text{Var}(\hat{f}(x_0)) + [\text{Bias}(\hat{f}(x_0))]^2 + \text{Var}(\epsilon).$$

The expectation averages over the variability of y_0 as well as the variability in Tr. Note that $\text{Bias}(\hat{f}(x_0))] = E[\hat{f}(x_0)] - f(x_0)$.

Typically as the *flexibility* of $\hat{f}$ increases, its variance increases, and its bias decreases. So choosing the flexibility based on average test error amounts to a *bias-variance trade-off.*

Bias-Variance Trade-Off

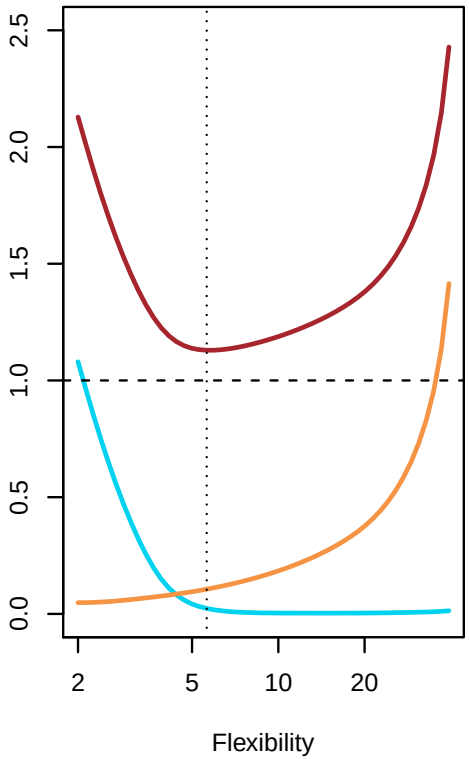
$$
\begin{aligned}
E_{Te}\left(y_0 - \widehat{f}\left(x_0\right)\right)^2 &= E\left(f\left(x_0\right) + \epsilon - \widehat{f}\left(x_0\right) + \overline{\widehat{f}}\left(x_0\right) - \overline{\widehat{f}}\left(x_0\right)\right)^2 \\
&= E\left(\left(f\left(x_0\right) - \overline{\widehat{f}}\left(x_0\right)\right) + \epsilon + \left(\overline{\widehat{f}}\left(x_0\right) - \widehat{f}\left(x_0\right)\right)\right)^2 \\
&= \left(f\left(x_0\right) - \overline{\widehat{f}}\left(x_0\right)\right)^2 + E\left(\overline{\widehat{f}}\left(x_0\right) - \widehat{f}\left(x_0\right)\right)^2 + E\left(\epsilon\right)^2 \\
&\quad \left[\text{Bias}\left(\widehat{f}\left(x_0\right)\right)\right]^2 + \text{Var}\left(\widehat{f}\left(x_0\right)\right) + \text{Var}\left(\epsilon\right)
\end{aligned}
$$

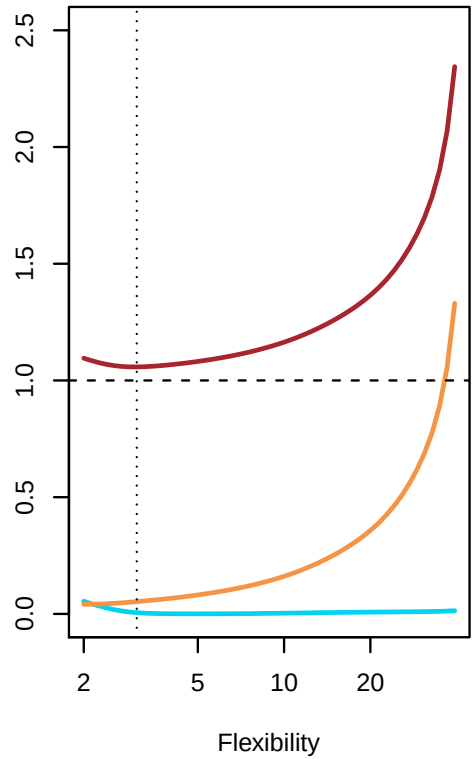
Where $\overline{\widehat{f}}\left(x_0\right)$ denotes $E\left(\widehat{f}\left(x_0\right)\right)$.

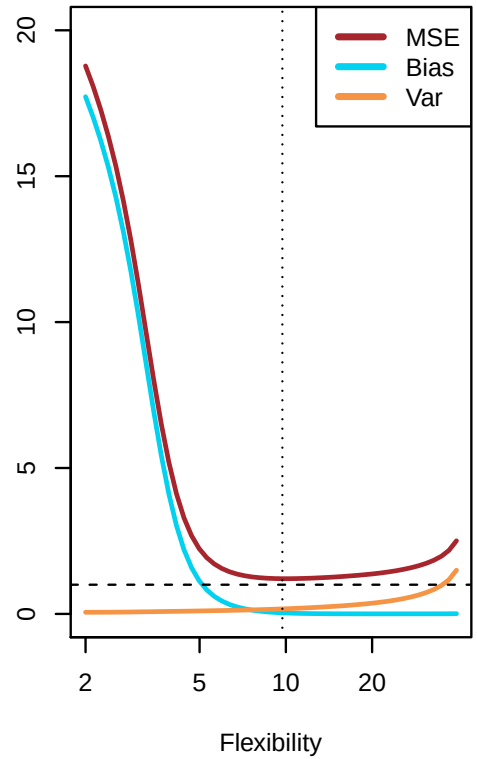
Second equality: $f\left(x_0\right)$ and $\overline{\widehat{f}}\left(x_0\right)$ are constants,
ϵ independent of $\widehat{f}\left(x_0\right)$ since ϵ is from *test* data and $\widehat{f}\left(x_0\right)$ constructed from *training* data.

- OLS with redundant variables is unbiased but high variance.
  Across many randomly drawn samples, $\overline{\widehat{f}}\left(x_0\right) = f\left(x_0\right)$.
  The variance of $\widehat{f}\left(x_0\right)$ across samples is large because of the variance in the estimated coefficient on redundant variables.

Bias-variance trade-off for the three examples







More on prediction-error estimates

- Best solution: a large designated test set. Often not available
- Some methods make a *mathematical adjustment* to the training error rate in order to estimate the test error rate. These include the *Cp statistic*, *AIC* and *BIC*. They are discussed elsewhere in this course
- Here we instead consider a class of methods that estimate the test error by *holding out* a subset of the training observations from the fitting process, and then applying the statistical learning method to those held out observations

Adjusted R^2

- For a least squares model with d variables, the adjusted R^2 statistic is calculated as

$$\text{Adjusted } R^2 = 1 - \frac{\text{RSS}/(n-d-1)}{\text{TSS}/(n-1)}.$$

  where TSS is the total sum of squares.
- Unlike C_p, AIC, and BIC, for which a *small* value indicates a model with a low test error, a *large* value of adjusted R^2 indicates a model with a small test error.
- Maximizing the adjusted R^2 is equivalent to minimizing $\frac{\text{RSS}}{n-d-1}$. While RSS always decreases as the number of variables in the model increases, $\frac{\text{RSS}}{n-d-1}$ may increase or decrease, due to the presence of d in the denominator.
- Unlike the R^2 statistic, the adjusted R^2 statistic *pays a price* for the inclusion of unnecessary variables in the model. See Figure on slide 19.

Now for some details

- *Mallow's C_p*:

$$C_p = \frac{1}{n}\left(\text{RSS} + 2d\hat{\sigma}^2\right),$$

  where d is the total # of parameters used and $\hat{\sigma}^2$ is an estimate of the variance of the error ϵ associated with each response measurement.
- The *AIC* criterion is defined for a large class of models fit by maximum likelihood:

$$\text{AIC} = -2\log L + 2 \cdot d$$

  where L is the maximized value of the likelihood function for the estimated model.
- In the case of the linear model with Gaussian errors, maximum likelihood and least squares are the same thing, and C_p and AIC are equivalent. *Prove this.*

Details on BIC

$$\text{BIC} = \frac{1}{n}\left(\text{RSS} + \log(n) d\hat{\sigma}^2\right).$$

- Like C_p, the BIC will tend to take on a small value for a model with a low test error, and so generally we select the model that has the lowest BIC value.
- Notice that BIC replaces the $2d\hat{\sigma}^2$ used by C_p with a $\log(n)d\hat{\sigma}^2$ term, where n is the number of observations.
- Since $\log n > 2$ for any $n > 7$, the BIC statistic generally places a heavier penalty on models with many variables, and hence results in the selection of smaller models than C_p. See Figure on slide 19.

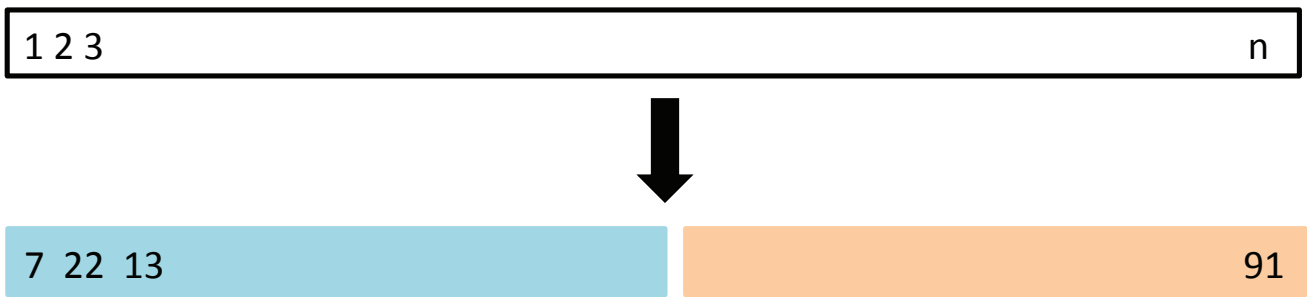
Cross-validation and the Bootstrap

- In the section we discuss two *resampling* methods: cross-validation and the bootstrap.
- These methods refit a model of interest to samples formed from the training set, in order to obtain additional information about the fitted model.
- For example, they provide estimates of test-set prediction error, and the standard deviation and bias of our parameter estimates

Validation-set approach

- Here we randomly divide the available set of samples into two parts: a *training set* and a *validation* or *hold-out set*.
- The model is fit on the training set, and the fitted model is used to predict the responses for the observations in the validation set.
- The resulting validation-set error provides an estimate of the test error. This is typically assessed using MSE in the case of a quantitative response and misclassification rate in the case of a qualitative (discrete) response.

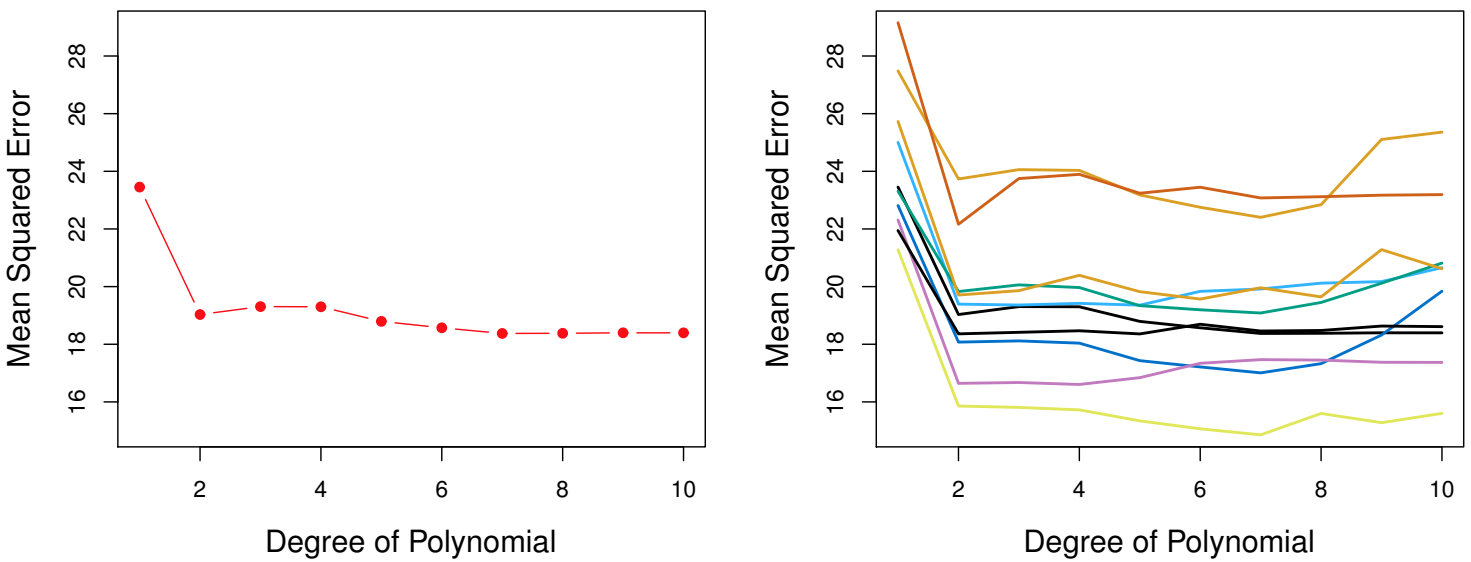
The Validation process



A random splitting into two halves: left part is training set, right part is validation set

Example: automobile data

- Want to compare linear vs higher-order polynomial terms in a linear regression
- We randomly split the 392 observations into two sets, a training set containing 196 of the data points, and a validation set containing the remaining 196 observations.



Left panel shows single split; right panel shows multiple splits

Drawbacks of validation set approach

- the validation estimate of the test error can be highly variable, depending on precisely which observations are included in the training set and which observations are included in the validation set.
- In the validation approach, only a subset of the observations — those that are included in the training set rather than in the validation set — are used to fit the model.
- This suggests that the validation set error may tend to *overestimate* the test error for the model fit on the entire data set. *Why?*

K-fold Cross-validation

- *Widely used approach* for estimating test error.
- Estimates can be used to select best model, and to give an idea of the test error of the final chosen model.
- Idea is to randomly divide the data into K equal-sized parts. We leave out part k, fit the model to the other $K-1$ parts (combined), and then obtain predictions for the left-out kth part.
- This is done in turn for each part $k = 1, 2, \ldots K$, and then the results are combined.

K-fold Cross-validation in detail

Divide data into K roughly equal-sized parts ($K = 5$ here)

1	2	3	4	5
Validation	Train	Train	Train	Train

The details

- Let the K parts be $C_1, C_2, \ldots C_K$, where C_k denotes the indices of the observations in part k. There are n_k observations in part k: if N is a multiple of K, then $n_k = n/K$.
- Compute

$$\text{CV}_{(K)} = \sum_{k=1}^{K} \frac{n_k}{n} \text{MSE}_k$$

  where $\text{MSE}_k = \sum_{i \in C_k} (y_i - \hat{y}_i)^2 / n_k$, and $\hat{y}_i$ is the fit for observation i, obtained from the data with part k removed.
- Setting $K = n$ yields n-fold or *leave-one out cross-validation* (LOOCV).

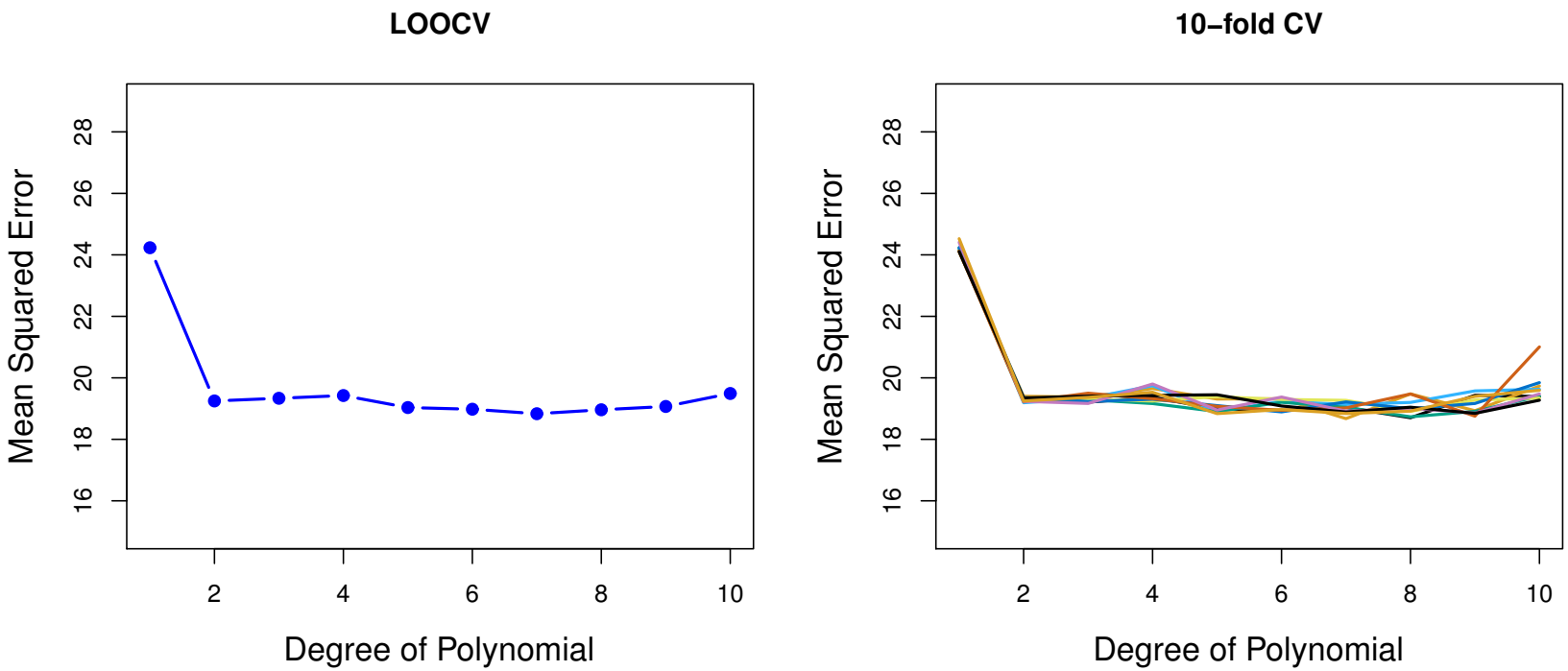
A nice special case!

- With least-squares linear or polynomial regression, an amazing shortcut makes the cost of LOOCV the same as that of a single model fit! The following formula holds:

$$\mathrm{CV}_{(n)} = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{y_i - \hat{y}_i}{1 - h_i}\right)^2,$$

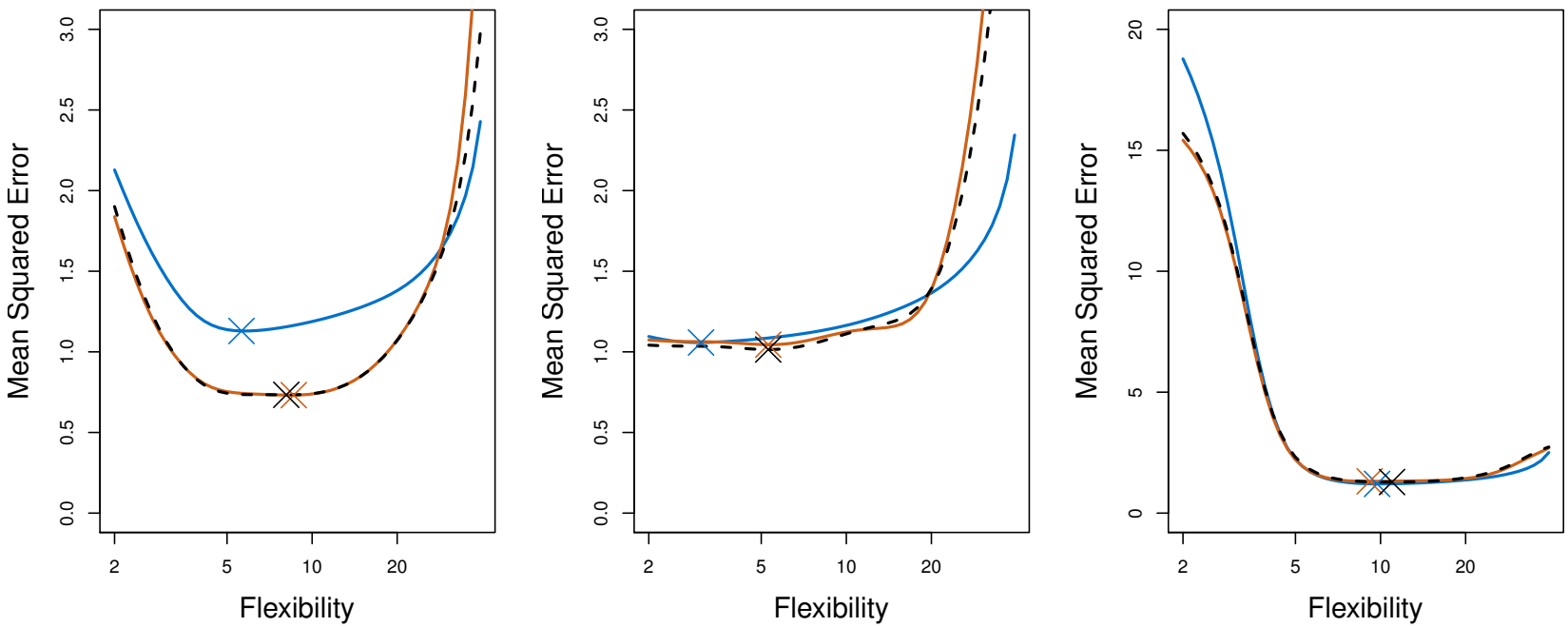
  where $\hat{y}_i$ is the ith fitted value from the original least squares fit, and h_i is the leverage (diagonal of the "hat" matrix; see book for details.) This is like the ordinary MSE, except the ith residual is divided by $1 - h_i$.
- LOOCV sometimes useful, but typically doesn't *shake up* the data enough. The estimates from each fold are highly correlated and hence their average can have high variance.
- a better choice is $K = 5$ or 10.

Auto data revisited



Left: The LOOCV error curve. Right: 10-fold CV was run nine separate times, each with a different random split of the data into ten parts. The figure shows the nine slightly different CV error curves.

True and estimated test MSE for the simulated data



True and estimated test MSE for simulated data sets. The true test MSE is shown in blue, the LOOCV estimate is shown as a black dashed line, and the 10-fold CV estimate is shown in orange. The crosses indicate the minimum of each of the MSE curves. curves.

Other issues with Cross-validation

- Since each training set is only $(K-1)/K$ as big as the original training set, the estimates of prediction error will typically be biased upward. *Why?*
- This bias is minimized when $K = n$ (LOOCV), but this estimate has high variance, as noted earlier.
- $K = 5$ or 10 provides a good compromise for this bias-variance tradeoff.

Cross-validation: right and wrong

- Consider a simple classifier applied to some two-class data:
  1. Starting with 5000 predictors and 50 samples, find the 100 predictors having the largest correlation with the class labels.
  2. We then apply a classifier such as logistic regression, using only these 100 predictors.

  How do we estimate the test set performance of this classifier?

  Can we apply cross-validation in step 2, forgetting about step 1?

NO!

- This would ignore the fact that in Step 1, the procedure *has already seen the labels of the training data*, and made use of them. This is a form of training and must be included in the validation process.
- It is easy to simulate realistic data with the class labels independent of the outcome, so that true test error =50%, but the CV error estimate that ignores Step 1 is zero! *Try to do this yourself*
- We have seen this error made in many high profile genomics papers.

The Wrong and Right Way

- *Wrong:* Apply cross-validation in step 2.
- *Right:* Apply cross-validation to steps 1 and 2.

Pre-validation

- In microarray and other genomic studies, an important problem is to compare a predictor of disease outcome derived from a large number of "biomarkers" to standard clinical predictors.
- Comparing them on the same dataset that was used to derive the biomarker predictor can lead to results strongly biased in favor of the biomarker predictor.
- *Pre-validation* can be used to make a fairer comparison between the two sets of predictors.

Idea behind Pre-validation

- Designed for comparison of adaptively derived predictors to fixed, pre-defined predictors.
- The idea is to form a "pre-validated" version of the adaptive predictor: specifically, a "fairer" version that hasn't "seen" the response y.

Motivating example

An example of this problem arose in the paper of van't Veer *et al. Nature* (2002). Their microarray data has 4918 genes measured over 78 cases, taken from a study of breast cancer. There are 44 cases in the good prognosis group and 34 in the poor prognosis group. A "microarray" predictor was constructed as follows:

1. 70 genes were selected, having largest absolute correlation with the 78 class labels.
2. Using these 70 genes, a nearest-centroid classifier $C(x)$ was constructed.
3. Applying the classifier to the 78 microarrays gave a dichotomous predictor $z_i = C(x_i)$ for each case i.

Pre-validation in detail for this example

1. Divide the cases up into $K = 13$ equal-sized parts of 6 cases each.
2. Set aside one of parts. Using only the data from the other 12 parts, select the features having absolute correlation at least .3 with the class labels, and form a nearest centroid classification rule.
3. Use the rule to predict the class labels for the 13th part
4. Do steps 2 and 3 for each of the 13 parts, yielding a "pre-validated" microarray predictor $\tilde{z}_i$ for each of the 78 cases.
5. Fit a logistic regression model to the pre-validated microarray predictor and the 6 clinical predictors.

Results

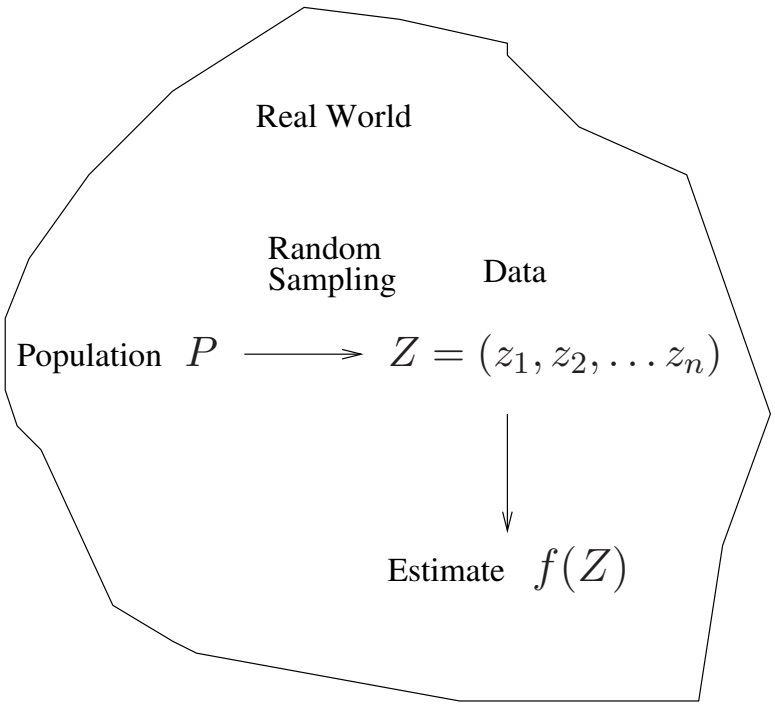
Comparison of the microarray predictor with some clinical predictors, using logistic regression with outcome `prognosis`:

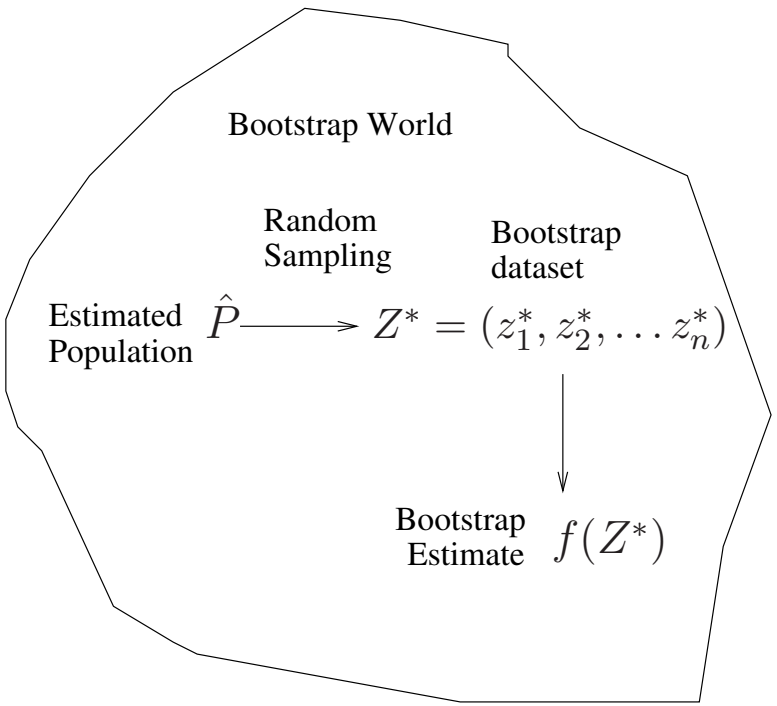
Model	Coef	Stand. Err.	Z score	p-value
		Re-use		
microarray	4.096	1.092	3.753	0.000
angio	1.208	0.816	1.482	0.069
er	-0.554	1.044	-0.530	0.298
grade	-0.697	1.003	-0.695	0.243
pr	1.214	1.057	1.149	0.125
age	-1.593	0.911	-1.748	0.040
size	1.483	0.732	2.026	0.021
		Pre-validated		
microarray	1.549	0.675	2.296	0.011
angio	1.589	0.682	2.329	0.010
er	-0.617	0.894	-0.690	0.245
grade	0.719	0.720	0.999	0.159
pr	0.537	0.863	0.622	0.267
age	-1.471	0.701	-2.099	0.018
size	0.998	0.594	1.681	0.046

The Bootstrap

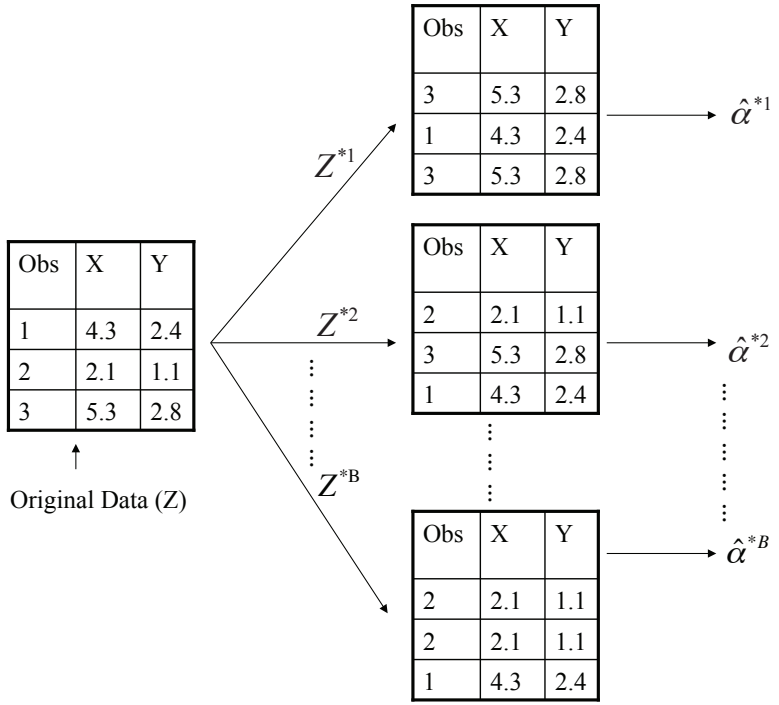
- The *bootstrap* is a flexible and powerful statistical tool that can be used to quantify the uncertainty associated with a given estimator or statistical learning method.
- For example, it can provide an estimate of the standard error of a coefficient, or a confidence interval for that coefficient.

A general picture for the bootstrap





Example with just 3 observations



A graphical illustration of the bootstrap approach on a small sample containing $n = 3$ observations. Each bootstrap data set contains n observations, sampled with replacement from the original data set. Each bootstrap data set is used to obtain an estimate of α

- Denoting the first bootstrap data set by Z^{*1}, we use Z^{*1} to produce a new bootstrap estimate for α, which we call $\hat{\alpha}^{*1}$
- This procedure is repeated B times for some large value of B (say 100 or 1000), in order to produce B different bootstrap data sets, $Z^{*1}, Z^{*2}, \ldots, Z^{*B}$, and B corresponding α estimates, $\hat{\alpha}^{*1}, \hat{\alpha}^{*2}, \ldots, \hat{\alpha}^{*B}$.
- We estimate the standard error of these bootstrap estimates using the formula

$$\mathrm{SE}_B(\hat{\alpha}) = \sqrt{\frac{1}{B-1}\sum_{r=1}^{B}\left(\hat{\alpha}^{*r} - \bar{\hat{\alpha}}^{*}\right)^2}.$$

- This serves as an estimate of the standard error of $\hat{\alpha}$ estimated from the original data set. See center and right panels of Figure on slide 29. Bootstrap results are in blue. For this example $\mathrm{SE}_B(\hat{\alpha}) = 0.087$.

The bootstrap in general

- In more complex data situations, figuring out the appropriate way to generate bootstrap samples can require some thought.
- For example, if the data is a time series, we can't simply sample the observations with replacement (*why not?*).
- We can instead create blocks of consecutive observations, and sample those with replacements. Then we paste together sampled blocks to obtain a bootstrap dataset.

Can the bootstrap estimate prediction error?

- In cross-validation, each of the K validation folds is distinct from the other $K-1$ folds used for training: *there is no overlap*. This is crucial for its success. *Why?*
- To estimate prediction error using the bootstrap, we could think about using each bootstrap dataset as our training sample, and the original sample as our validation sample.
- But each bootstrap sample has significant overlap with the original data. About two-thirds of the original data points appear in each bootstrap sample. *Can you prove this?*
- This will cause the bootstrap to seriously underestimate the true prediction error. *Why?*
- The other way around— with original sample = training sample, bootstrap dataset = validation sample— is worse!

Removing the overlap

- Can partly fix this problem by only using predictions for those observations that did not (by chance) occur in the current bootstrap sample.
- But the method gets complicated, and in the end, cross-validation provides a simpler, more attractive approach for estimating prediction error.