

A Python Companion to ISLR

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1 Introduction

Figure 1 shows graphs of Wage versus three variables.

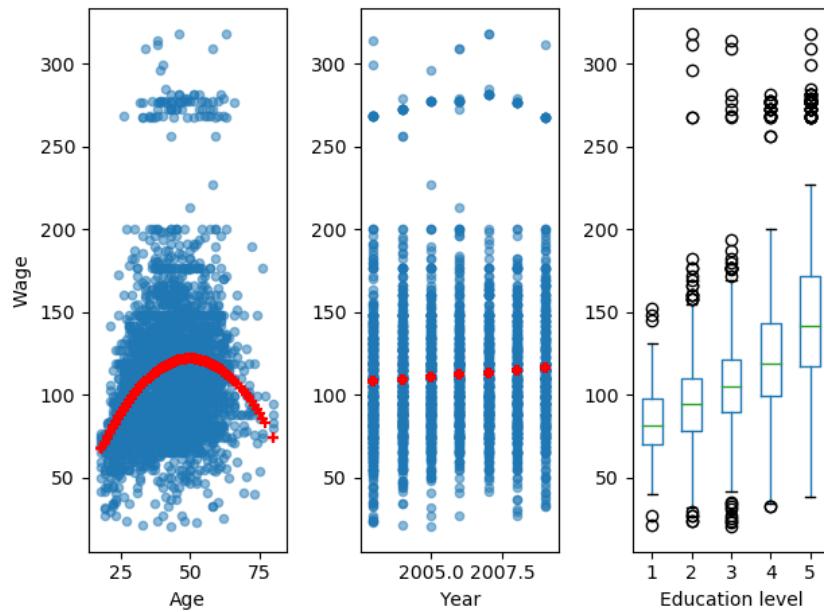


Figure 1: `Wage` data, which contains income survey information for males from the central Atlantic region of the United States. Left: `wage` as a function of `age`. On average, `wage` increases with `age` until about 60 years of age, at which point it begins to decline. Center: `wage` as a function of `year`. There is a slow but steady increase of approximately \$10,000 in the average `wage` between 2003 and 2009. Right: Boxplots displaying `wage` as a function of `education`, with 1 indicating the lowest level (no highschool diploma) and 5 the highest level (an advanced graduate degree). On average, `wage` increases with the level of `education`.

Figure 2 shows boxplots of previous days' percentage changes in S&P 500 grouped according to today's change Up or Down.

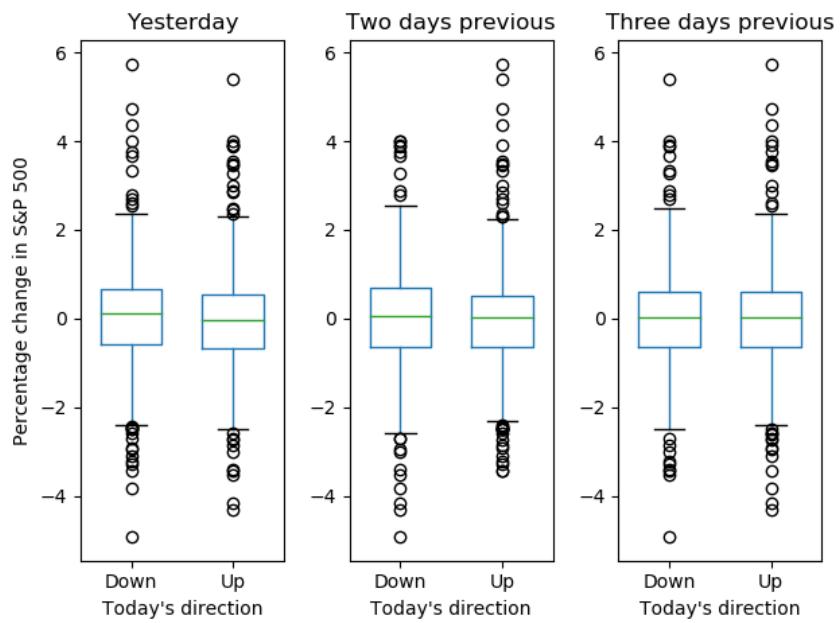


Figure 2: Left: Boxplots of the previous day's percentage change in the S&P 500 index for the days for which the market increased or decreased, obtained from the `Smarket` data. Center and Right: Same as left panel, but the percentage changes for two and three days previous are shown.

2 Statistical Learning

2.1 What is Statistical Learning?

Figure 3 shows scatter plots of `sales` versus `TV`, `radio`, and `newspaper` advertising. In each panel, the figure also includes an OLS regression line.

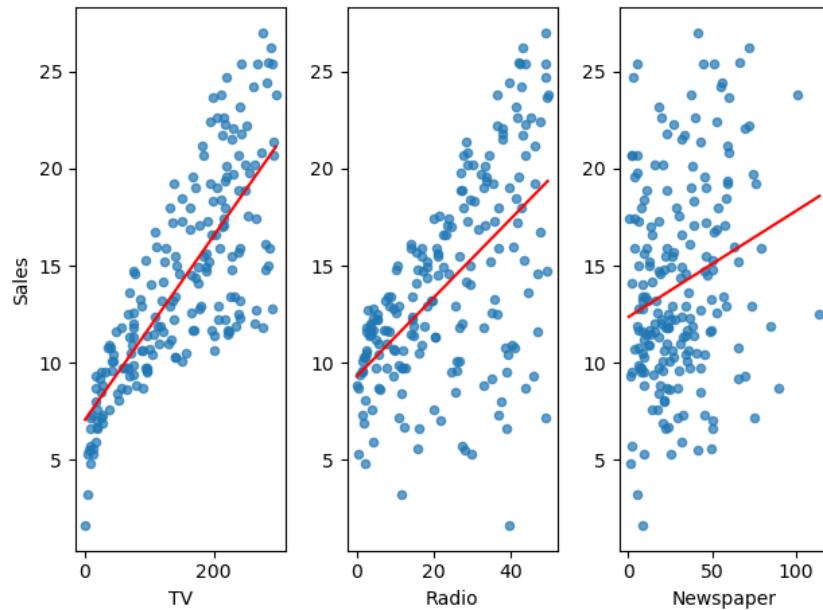


Figure 3: The Advertising data set. The plot displays `sales`, in thousands of units, as a function of `TV`, `radio`, and `newspaper` budgets, in thousands of dollars, for 200 different markets. In each plot we show the simple least squares fit of `sales` to that variable. In other words, each red line represents a simple model that can be used to predict `sales` using `TV`, `radio`, and `newspaper`, respectively.

Figure 4 is a plot of `Income` versus `Years of Education` from the `Income` data set. In the left panel, the “true” function (given by blue line) is actually my guess.

Figure 5 is a plot of `Income` versus `Years of Education` and `Seniority` from the `Income` data set. Since the book does not provide the true values of `Income`, “true” values shown in the plot are actually third order polynomial fit.

Figure 6 shows an example of the parametric approach applied to the

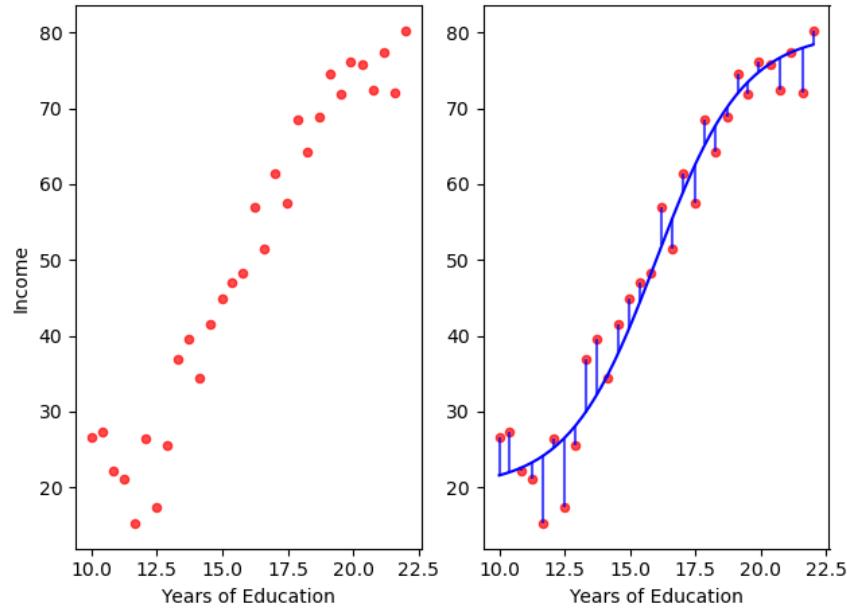


Figure 4: The `Income` data set. Left: The red dots are the observed values of `income` (in tens of thousands of dollars) and `years of education` for 30 individuals. Right: The blue curve represents the true underlying relationship between `income` and `years of education`, which is generally unknown (but is known in this case because the data are simulated). The vertical lines represent the error associated with each observation. Note that some of the errors are positive (when an observation lies above the blue curve) and some are negative (when an observation lies below the curve). Overall, these errors have approximately mean zero.

2.1 What is Statistical Learning?

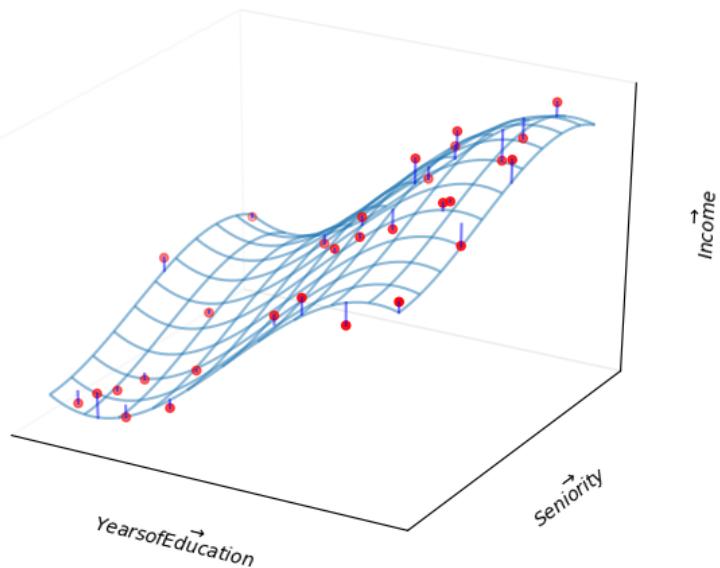


Figure 5: The plot displays `income` as a function of `years of education` and `seniority` in the `Income` data set. The blue surface represents the true underlying relationship between `income` and `years of education` and `seniority`, which is known since the data are simulated. The red dots indicate the observed values of these quantities for 30 individuals.

2.2 Assessing Model Accuracy

Income data from previous figure.

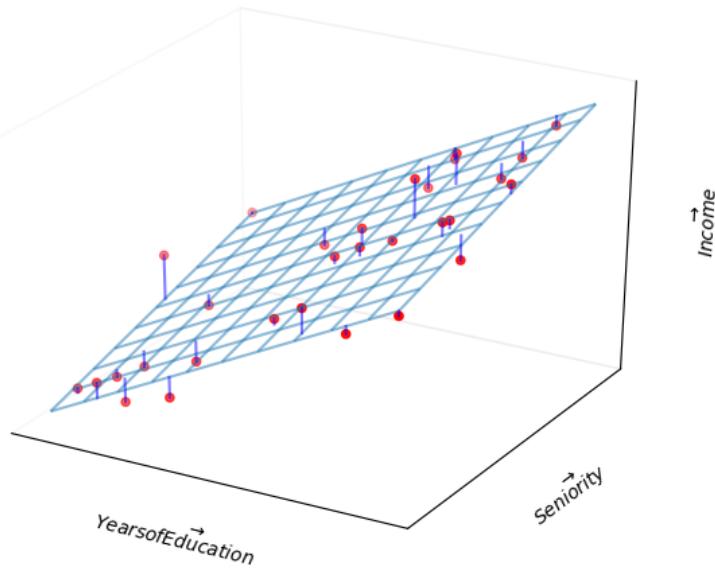


Figure 6: A linear model fit by least squares to the Income data from figure 5. The observations are shown in red, and the blue plane indicates the least squares fit to the data.

Figure 7 provides an illustration of the trade-off between flexibility and interpretability for some of the methods covered in this book.

Figure 8 provides a simple illustration of the clustering problem.

2.2 Assessing Model Accuracy

Figure 9 illustrates the tradeoff between training MSE and test MSE. We select a “true function” whose shape is similar to that shown in the book. In the left panel, the orange, blue, and green curves illustrate three possible estimates for f given by the black curve. The orange line is the linear regression fit, which is relatively inflexible. The blue and green curves were produced using *smoothing splines* from `UnivariateSpline` function in `scipy` package. We obtain different levels of flexibility by varying the parameter s , which affects the number of knots.

For the right panel, we have chosen polynomial fits. The degree of polynomial represents the level of flexibility. This is because the function

2.2 Assessing Model Accuracy

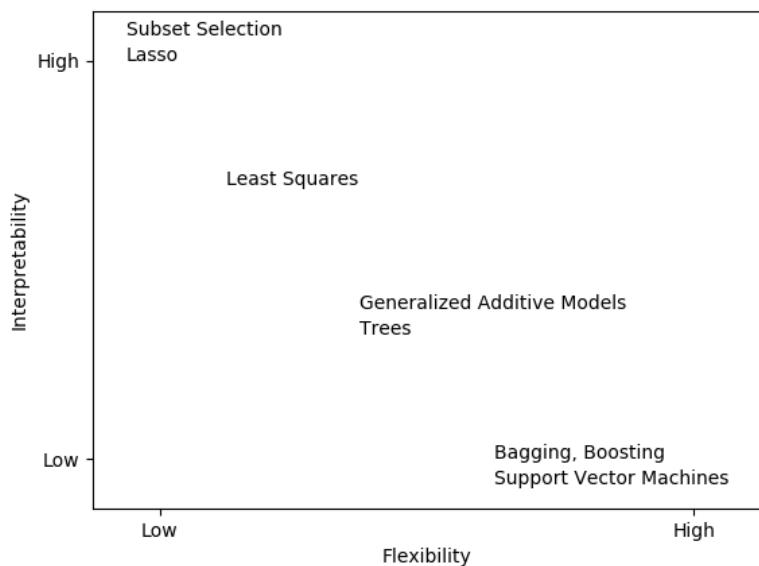


Figure 7: A representation of the tradeoff between flexibility and interpretability, using different statistical learning methods. In general, as the flexibility of a method increases, its interpretability decreases.

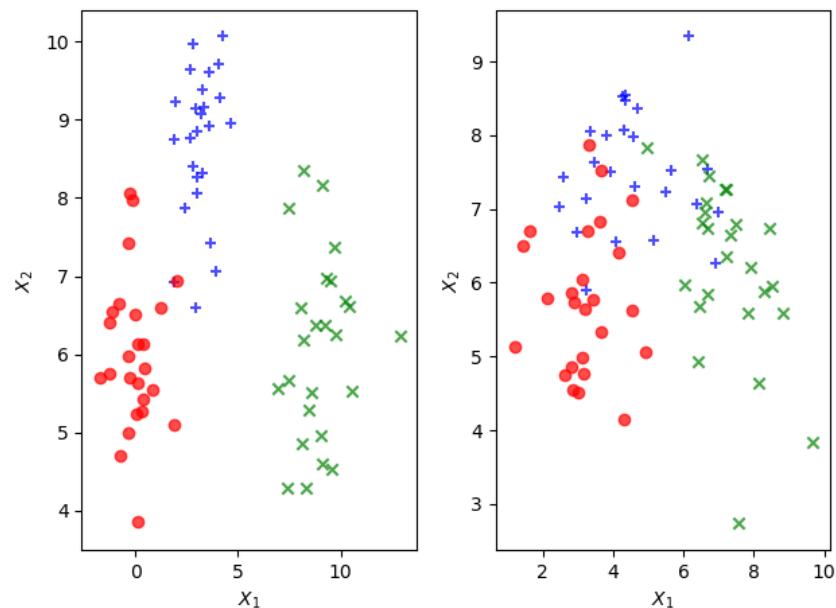


Figure 8: A clustering data set involving three groups. Each group is shown using a different colored symbol. Left: The three groups are well-separated. In this setting, a clustering approach should successfully identify the three groups. Right: There is some overlap among the groups. Now the clustering task is more challenging.

2.2 Assessing Model Accuracy

`UnivariateSpline` does not more than five degrees of freedom.

When we repeat the simulations for figure 9, we see considerable variation in the right panel MSE plots. But the overall conclusion remains the same.

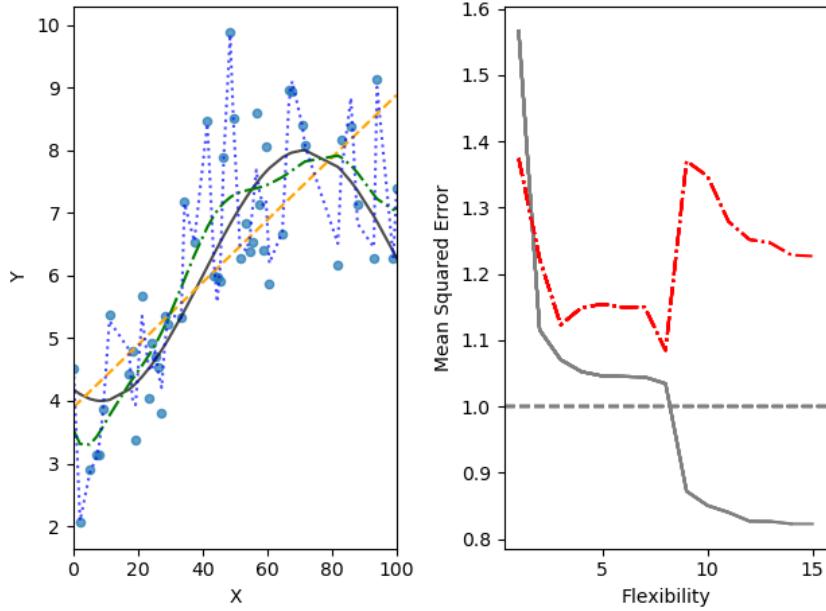


Figure 9: Left: Data simulated from f , shown in black. Three estimates of f are shown: the linear regression line (orange curve), and two smoothing spline fits (blue and green curves). Right: Training MSE (grey curve), test MSE (red curve), and minimum possible test MSE over all methods (dashed grey line).

Figure 10 provides another example in which the true f is approximately linear.

Figure 11 displays an example in which f is highly non-linear. The training and test MSE curves still exhibit the same general patterns.

Figure 12 displays the relationship between bias, variance, and test MSE. This relationship is referred to as *bias-variance trade-off*. When simulations are repeated, we see considerable variation in different graphs, especially for MSE lines. But overall shape remains the same.

Figure 13 provides an example using a simulated data set in two-dimensional space consisting of predictors X_1 and X_2 .

Figure 14 displays the KNN decision boundary, using $K = 10$, when

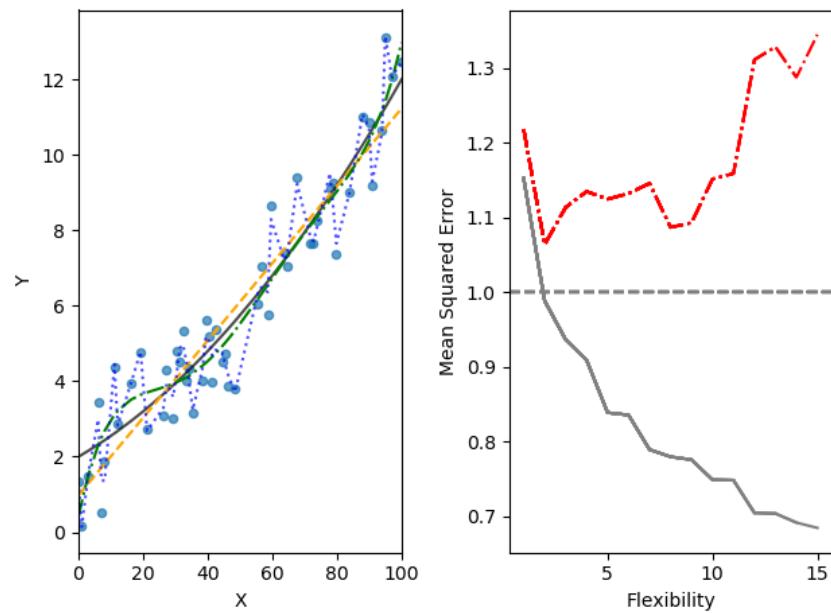


Figure 10: Details are as in figure 9 using a different true f that is much closer to linear. In this setting, linear regression provides a very good fit to the data.

2.2 Assessing Model Accuracy

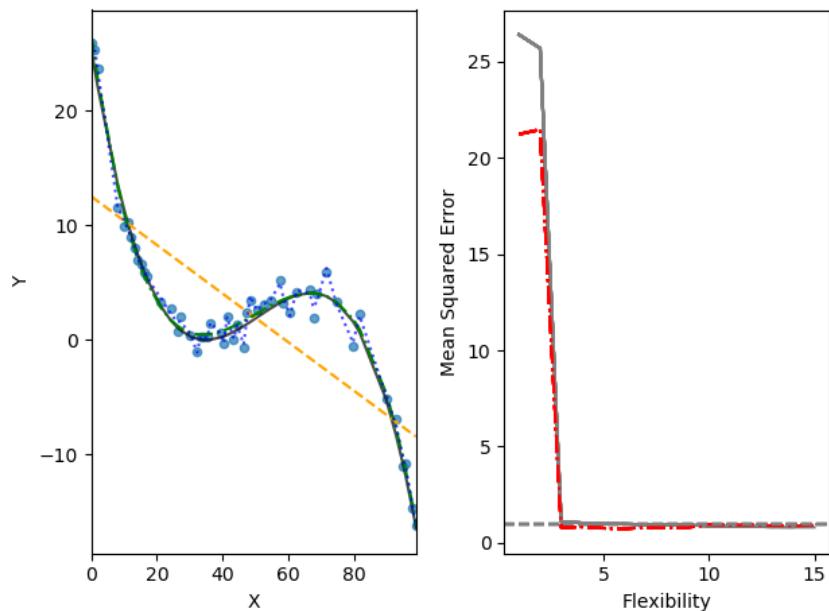


Figure 11: Details are as in figure 9, using a different f that is far from linear. In this setting, linear regression provides a very poor fit to the data.

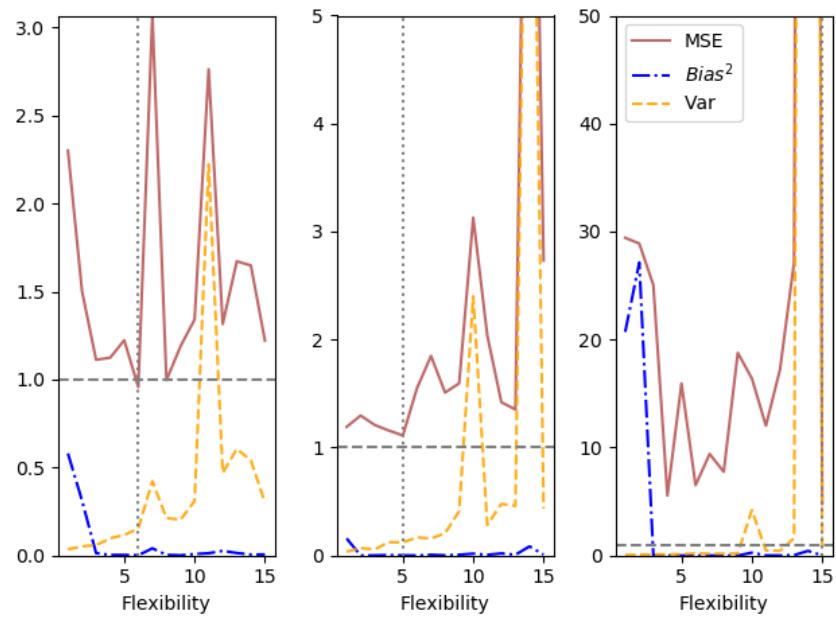


Figure 12: Squared bias (blue curve), variance (orange curve), $Var(\epsilon)$ (dashed line), and test MSE (red curve) for the three data sets in figures 9 - 11. The vertical dotted line indicates the flexibility level corresponding to the smallest test MSE.

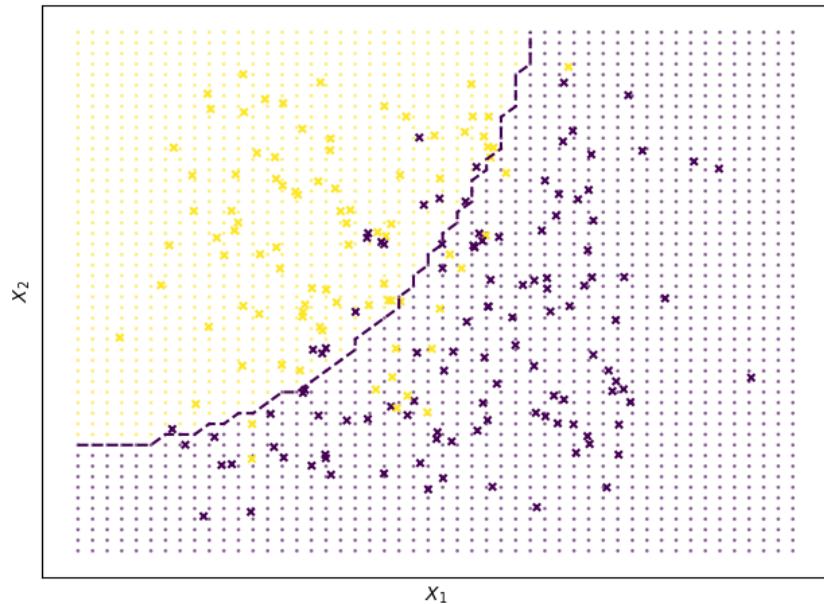


Figure 13: A simulated data set consisting of 200 observations in two groups, indicated in blue and orange. The dashed line represents the Bayes decision boundary. The orange background grid indicates the region in which a test observation will be assigned to the orange class, and blue background grid indicates the region in which a test observation will be assigned to the blue class.

2.2 Assessing Model Accuracy

applied to the simulated data set from figure 13. Even though the true distribution is not known by the KNN classifier, the KNN decision making boundary is very close to that of the Bayes classifier.

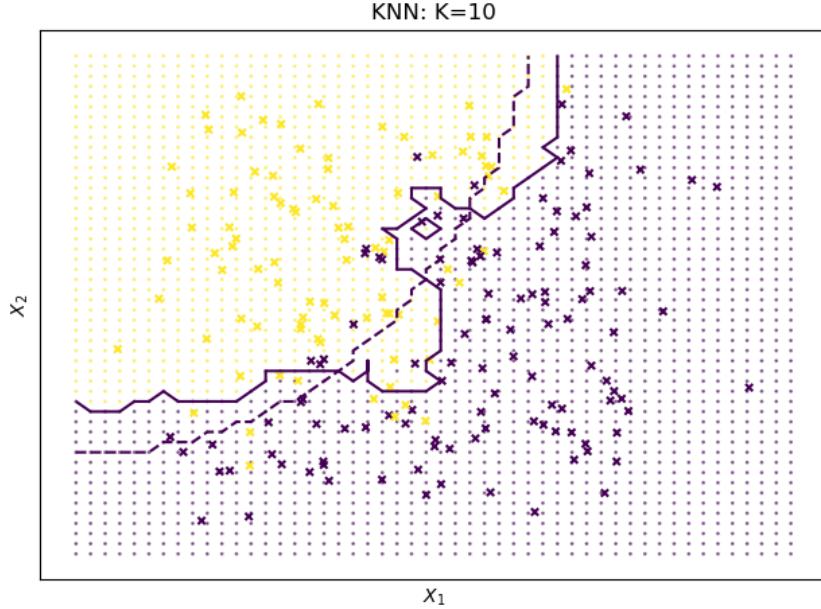


Figure 14: The firm line indicates the KNN decision boundary on the data from figure 13, using $K = 10$. The Bayes decision boundary is shown as a dashed line. The KNN and Bayes decision boundaries are very similar.

In figure 16 we have plotted the KNN test and training errors as a function of $\frac{1}{K}$. As $\frac{1}{K}$ increases, the method becomes more flexible. As in the regression setting, the training error rate consistently declines as the flexibility increases. However, the test error exhibits the characteristic U-shape, declining at first (with a minimum at approximately $K = 10$) before increasing again when the method becomes excessively flexible and overfits.

2.2 Assessing Model Accuracy

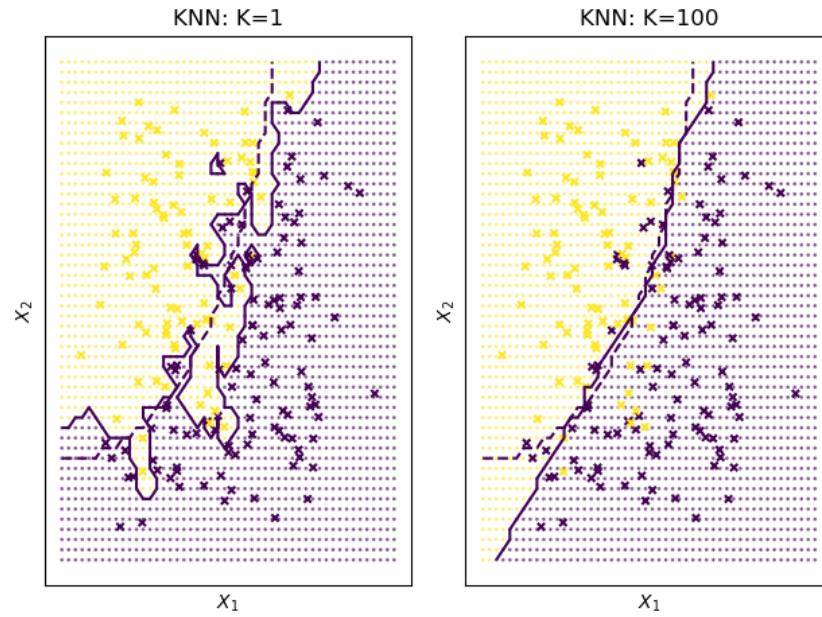


Figure 15: A comparison of the KNN decision boundaries (solid curves) obtained using $K = 1$ and $K = 100$ on the data from figure 13. With $K = 1$, the decision boundary is overly flexible, while with $K = 100$ it is not sufficiently flexible. The Bayes decision boundary is shown as dashed line.

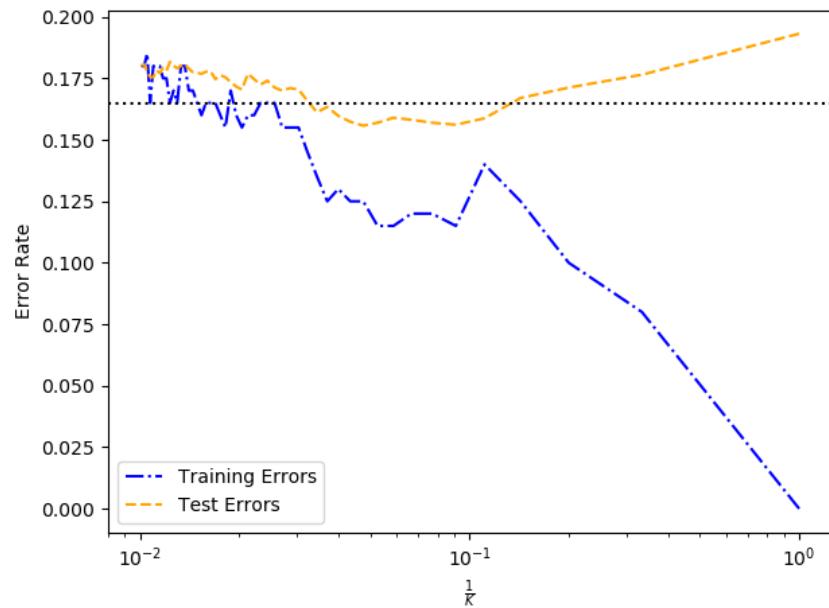


Figure 16: The KNN training error rate (blue, 200 observations) and test error rate (orange, 5,000 observations) on the data from figure 13 as the level of flexibility (assessed using $\frac{1}{K}$) increases, or equivalently as the number of neighbors K decreases. The black dashed line indicates the Bayes error rate.

2.3 Lab: Introduction to Python

2.3.1 Basic Commands

In Python a list can be created by enclosing comma-separated elements by square brackets. Length of a list can be obtained using `len` function.

```
x = [1, 3, 2, 5]
print(len(x))
y = 3
z = 5
print(y + z)
```

4

8

To create an array of numbers, use `array` function in `numpy` library. `numpy` functions can be used to perform element-wise operations on arrays.

```
import numpy as np
x = np.array([[1, 2], [3, 4]])
y = np.array([6, 7, 8, 9]).reshape((2, 2))
print(x)
print(y)
print(x ** 2)
print(np.sqrt(y))
```

```
[[1 2]
 [3 4]]
[[6 7]
 [8 9]]
[[ 1  4]
 [ 9 16]]
[[2.44948974 2.64575131]
 [2.82842712 3.]]
```

`numpy.random` has a number of functions to generate random variables that follow a given distribution. Here we create two correlated sets of numbers, `x` and `y`, and use `numpy.corrcoef` to calculate correlation between them.

```
import numpy as np
np.random.seed(911)
x = np.random.normal(size=50)
```

2.3 Lab: Introduction to Python

```
y = x + np.random.normal(loc=50, scale=0.1, size=50)
print(np.corrcoef(x, y))
print(np.corrcoef(x, y)[0, 1])
print(np.mean(x))
print(np.var(y))
print(np.std(y) ** 2)
```

```
[[1.          0.99374931]
 [0.99374931 1.          ]]
0.9937493134584551
-0.020219724397254404
0.9330621750073689
0.9330621750073688
```

2.3.2 Graphics

`matplotlib` library has a number of functions to plot data in Python. It is possible to view graphs on screen or save them in file for inclusion in a document.

```
import numpy as np
import matplotlib           # only if we need to save
    figure in file
matplotlib.use('Agg')      # only to save figure in file
import matplotlib.pyplot as plt

x = np.random.normal(size=100)
y = np.random.normal(size=100)
plt.plot(x, y)
plt.xlabel('This is x-axis')
plt.ylabel('This is y-axis')
plt.title('Plot of X vs Y')

plt.savefig('xyPlot.png')      # only to save figure in a file
```

`numpy` function `linspace` can be used to create a sequence between a start and an end of a given length.

```
import numpy as np
import matplotlib.pyplot as plt

x = np.linspace(-np.pi, np.pi, num=50)
y = x
xx, yy = np.meshgrid(x, y)
zz = np.cos(yy) / (1 + xx ** 2)
```

```
plt.contour(xx, yy, zz)

fig, ax = plt.subplots()
zsa = (zz - zz.T) / 2.0
CS = ax.contour(xx, yy, zsa)
ax.clabel(CS, inline=1)
```

2.3.3 Indexing Data

To access elements of an array, specify indexes inside square brackets. It is possible to access multiple rows and columns. `shape` method gives number of rows followed by number of columns.

```
import numpy as np

A = np.array(np.arange(1, 17))
A = A.reshape(4, 4, order='F') # column first, Fortran style
print(A)
print(A[1, 2])
print(A[(0,2), :][:, (1,3)])
print(A[range(0,3), :][:, range(1,4)])
print(A[range(0, 2), :])
print(A[:, range(0, 2)])
print(A[0,:])
print(A.shape)
```

```
[[ 1  5  9 13]
 [ 2  6 10 14]
 [ 3  7 11 15]
 [ 4  8 12 16]]
10
[ 5 15]
[ 5 10 15]
[[ 1  5  9 13]
 [ 2  6 10 14]]
[[1 5]
 [2 6]
 [3 7]
 [4 8]]
(4, 4)
```

2.3.4 Loading Data

pandas library provides `read_csv` function to read files with data in rectangular shape.

```
import pandas as pd
Auto = pd.read_csv('data/Auto.csv')
print(Auto.head())
print(Auto.shape)
print(Auto.columns)
```

	mpg	cylinders	displacement	...	year	origin	name
0	18.0	8	307.0	...	70	1	chevrolet chevelle malibu
1	15.0	8	350.0	...	70	1	buick skylark 320
2	18.0	8	318.0	...	70	1	plymouth satellite
3	16.0	8	304.0	...	70	1	amc rebel sst
4	17.0	8	302.0	...	70	1	ford torino

[5 rows x 9 columns]
(397, 9)
Index(['mpg', 'cylinders', 'displacement', 'horsepower', 'weight',
 'acceleration', 'year', 'origin', 'name'],
 dtype='object')

To load data from an R library, use `get_rdataset` function from `statsmodels`. This function seems to work only if the computer is connected to the internet.

```
from statsmodels import datasets
carseats = datasets.get_rdataset('Carseats', package='ISLR').
    data
print(carseats.shape)
print(carseats.columns)
```

(400, 11)
Index(['Sales', 'CompPrice', 'Income', 'Advertising', 'Population', 'Price',
 'ShelveLoc', 'Age', 'Education', 'Urban', 'US'],
 dtype='object')

2.3.5 Additional Graphical and Numerical Summaries

`plot` method can be directly applied to a `pandas` dataframe.

2.3 Lab: Introduction to Python

```
import pandas as pd
Auto = pd.read_csv('data/Auto.csv')
Auto.boxplot(column='mpg', by='cylinders', grid=False)
```

hist method can be applied to plot a histogram.

```
import pandas as pd
Auto = pd.read_csv('data/Auto.csv')
Auto.hist(column='mpg')
Auto.hist(column='mpg', color='red')
Auto.hist(column='mpg', color='red', bins=15)
```

For pairs plot, use scatter_matrix method in pandas.plotting.

```
import pandas as pd
from pandas import plotting
Auto = pd.read_csv('data/Auto.csv')
plotting.scatter_matrix(Auto[['mpg', 'displacement',
    'horsepower', 'weight',
    'acceleration']])
```

On pandas dataframes, describe method produces a summary of each variable.

```
import pandas as pd
Auto = pd.read_csv('data/Auto.csv')
print(Auto.describe())
```

	mpg	cylinders	...	year	origin
count	397.000000	397.000000	...	397.000000	397.000000
mean	23.515869	5.458438	...	75.994962	1.574307
std	7.825804	1.701577	...	3.690005	0.802549
min	9.000000	3.000000	...	70.000000	1.000000
25%	17.500000	4.000000	...	73.000000	1.000000
50%	23.000000	4.000000	...	76.000000	1.000000
75%	29.000000	8.000000	...	79.000000	2.000000
max	46.600000	8.000000	...	82.000000	3.000000

[8 rows x 7 columns]

3 Linear Regression

3.1 Simple Linear Regression

Figure 17 displays the simple linear regression fit to the `Advertising` data, where $\hat{\beta}_0 = 0.0475$ and $\hat{\beta}_1 = 7.0326$.

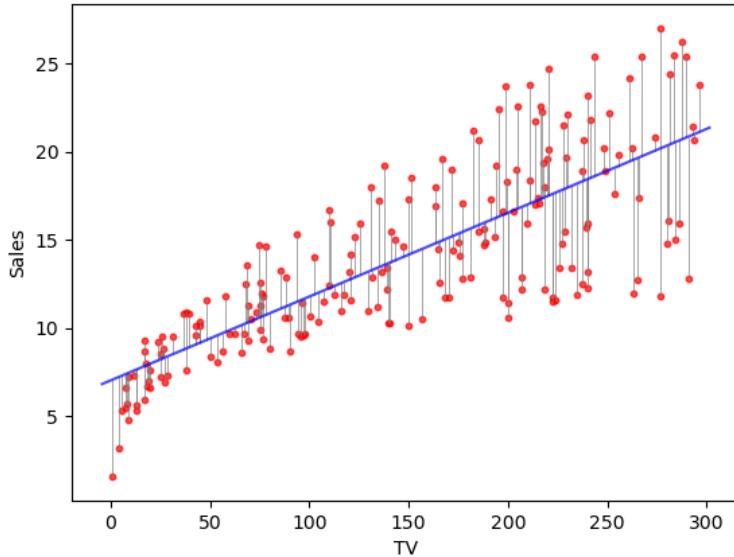


Figure 17: For the `Advertising` data, the least squares fit for the regression of `sales` onto `TV` is shown. The fit is found by minimizing the sum of squared errors. Each grey line represents an error, and the fit makes a compromise by averaging their squares. In this case a linear fit captures the essence of the relationship, although it is somewhat deficient in the left of the plot.

In figure 18, we have computed RSS for a number of values of β_0 and β_1 , using the advertising data with `sales` as the response and `TV` as the predictor.

The left-hand panel of figure 19 displays *population regression line* and *least squares line* for a simple simulated example. The red line in the left-hand panel displays the *true* relationship, $f(X) = 2 + 3X$, while the blue line is the least squares estimate based on observed data. In the right-hand panel of figure 19 we have generated five different data sets from the model $Y = 2 + 3X + \epsilon$ and plotted the corresponding five least squares lines.

3.1 Simple Linear Regression

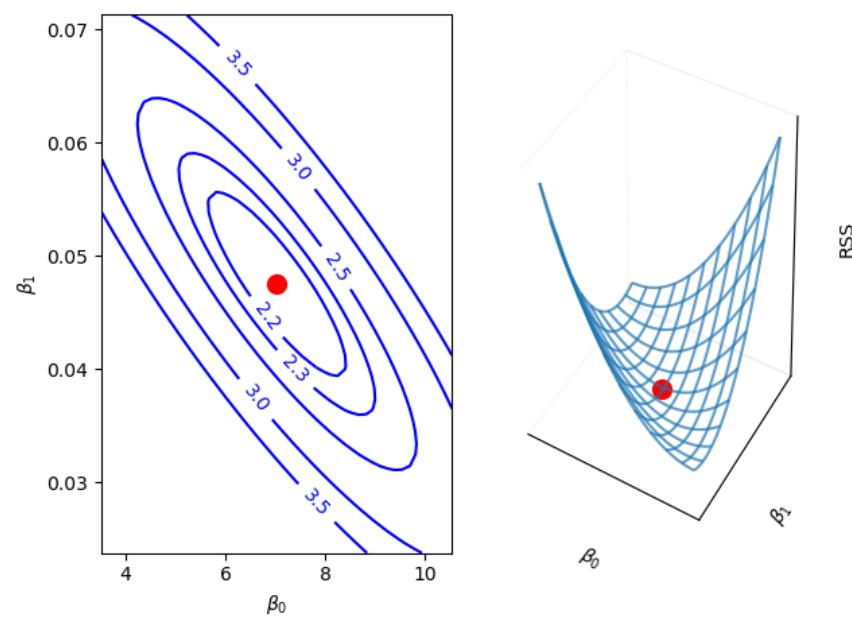


Figure 18: Contour and three-dimensional plots of the RSS on the `Advertising` data, using `sales` as the response and `TV` as the predictor. The red dots correspond to the least squares estimates $\hat{\beta}_0$ and $\hat{\beta}_1$.

3.1 Simple Linear Regression

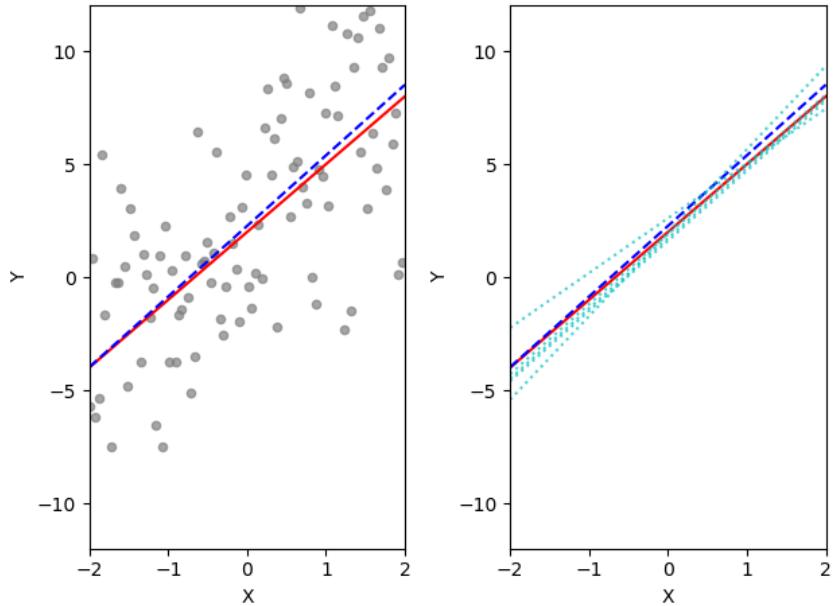


Figure 19: A simulated data set. Left: The red line represents the true relationship, $f(X) = 2 + 3X$, which is known as the population regression line. The blue line is the least squares line; it is the least squares estimate for $f(X)$ based on the observed data, shown in grey circles. Right: The population regression line is again shown in red, and the least squares line in blue. In cyan, five least squares lines are shown, each computed on the basis of a separate random set of observations. Each least squares line is different, but on average, the least squares lines are quite close to the population regression line.

3.2 Multiple Linear Regression

For **Advertising** data, table 1 provides details of the least squares model for the regression of number of units sold on TV advertising budget.

	Coef.	Std.Err.	t	P > t
Intercept	7.0326	0.4578	15.3603	0.0
TV	0.0475	0.0027	17.6676	0.0

Table 1: For **Advertising** data, the coefficients of the least squares model for the regression of number of units sold on TV advertising budget. An increase of \$1,000 on the TV advertising budget is associated with an increase in sales by around 50 units.

Next, in table 2, we report more information about the least squares model.

Quantity	Value
Residual standard error	3.259
R ²	0.612
F-statistic	312.145

Table 2: For the **Advertising** data, more information about the least squares model for the regression of number of units sold on TV advertising budget.

3.2 Multiple Linear Regression

Table 3 shows results of two simple linear regressions, each of which uses a different advertising medium as a predictor. We find that a \$1,000 increase in spending on radio advertising is associated with an increase in sales by around 202 units. A \$1,000 increase in advertising spending on newspapers increases sales by approximately 55 units.

3.2 Multiple Linear Regression

	Coef.	Std.Err.	t	$P > t $
Intercept	9.312	0.563	16.542	0.0
radio	0.202	0.02	9.921	0.0
Intercept	12.351	0.621	19.876	0.0
newspaper	0.055	0.017	3.3	0.001

Table 3: More simple linear regression models for **Advertising** data. Coefficients of the simple linear regression model for number of units sold on Top: radio advertising budget and Bottom: newspaper advertising budget. A \$1,000 increase in spending on radio advertising is associated with an average increase sales by around 202 units, while the same increase in spending on newspaper advertising is associated with an average increase of around 55 units. **Sales** variable is in thousands of units, and the **radio** and **newspaper** variables are in thousands of dollars..

Figure 20 illustrates an example of the least squares fit to a toy data set with $p = 2$ predictors.

Table 4 displays multiple regression coefficient estimates when TV, radio, and newspaper advertising budgets are used to predict product sales using **Advertising** data.

	Coef.	Std.Err.	t	$P > t $
Intercept	2.939	0.312	9.422	0.0
TV	0.046	0.001	32.809	0.0
radio	0.189	0.009	21.893	0.0
newspaper	-0.001	0.006	-0.177	0.86

Table 4: For the **Advertising** data, least squares coefficient estimates of the multiple linear regression of number of units sold on radio, TV, and newspaper advertising budgets.

Table 5 shows the correlation matrix for the three predictor variables and response variable in table 4.

Figure 21 displays a three-dimensional plot of TV and **radio** versus **sales**.

3.2 Multiple Linear Regression

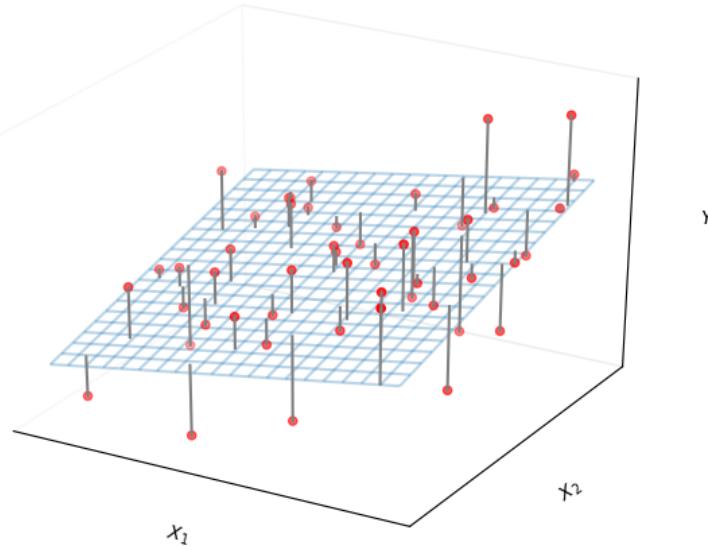


Figure 20: In a three-dimensional setting, with two predictors and one response, the least squares regression line becomes a plane. The plane is chosen to minimize the sum of the squared vertical distances between each observation (shown in red) and the plane.

	TV	radio	newspaper	sales
TV	1.0	0.0548	0.0566	0.7822
radio	0.0548	1.0	0.3541	0.5762
newspaper	0.0566	0.3541	1.0	0.2283
sales	0.7822	0.5762	0.2283	1.0

Table 5: Correlation matrix for TV, `radio`, and `sales` for the `Advertising` data.

Quantity	Value
Residual standard error	1.69
R^2	0.897
F-statistic	570.0

Table 6: More information about the least squares model for the regression of number of units sold on TV, newspaper, and radio advertising budgets in the `Advertising` data. Other information about this model was displayed in table 4.

3.2 Multiple Linear Regression

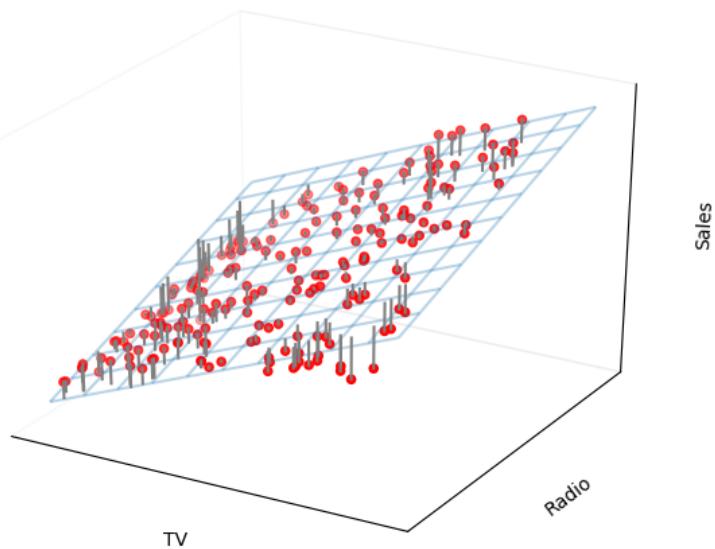


Figure 21: For the `Advertising` data, a linear regression fit to `sales` using `TV` and `radio` as predictors. From the pattern of the residuals, we can see that there is a pronounced non-linear relationship in the data. The positive residuals tend to lie along the 45-degree line, where `TV` and `Radio` budgets are split evenly. The negative residuals tend to lie away from this line, where budgets are more lopsided.

3.3 Other Considerations in the Regression Model

3.3 Other Considerations in the Regression Model

Credit data set displayed in figure 22 records **balance** (average credit card debt for a number of individuals) as well as several quantitative predictors: **age**, **cards** (number of credit cards), **education** and **rating** (credit rating).

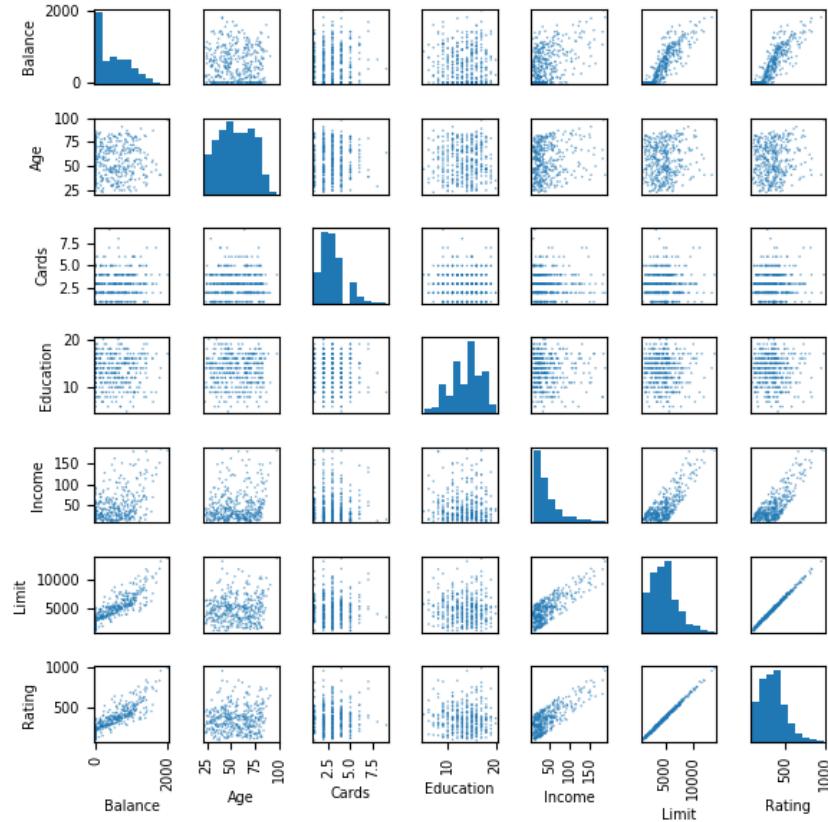


Figure 22: The Credit dataset contains information about **balance**, **age**, **cards**, **education**, **income**, **limit**, and **rating** for a number of potential customers.

Table 7 displays the coefficient estimates and other information associated with the model where **gender** is the only explanatory variable.

From table 8 we see that the estimated **balance** for the baseline, African American, is \$531.0. It is estimated that the Asian category will have an additional \$-18.7 debt, and that the Caucasian category will have an additional \$-12.5 debt compared to African American category.

3.3 Other Considerations in the Regression Model

	Coef.	Std.Err.	t	$P > t $
Intercept	509.803	33.128	15.389	0.0
Gender[T.Female]	19.733	46.051	0.429	0.669

Table 7: Least squares coefficient estimates associated with the regression of `balance` onto `gender` in the `Credit` data set.

	Coef.	Std.Err.	t	$P > t $
Intercept	531.0	46.319	11.464	0.0
Ethnicity[T.Asian]	-18.686	65.021	-0.287	0.774
Ethnicity[T.Caucasian]	-12.503	56.681	-0.221	0.826

Table 8: Least squares coefficient estimates associated with the regression of `balance` onto `ethnicity` in the `Credit` data set.

Table 9 shows results of regressing `sales` and `TV` and `radio` when an interaction term is included. Coefficient of interaction term `TV:radio` is highly significant.

In figure 23, the left panel shows least squares lines when we predict `balance` using `income` (quantitative) and `student` (qualitative variables). There is no interaction term between `income` and `student`. The right panel shows least squares lines when an interaction term is included.

	Coef.	Std.Err.	t	$P > t $
Intercept	6.75	0.248	27.233	0.0
TV	0.019	0.002	12.699	0.0
radio	0.029	0.009	3.241	0.001
TV:radio	0.001	0.0	20.727	0.0

Table 9: For `Advertising` data, least squares coefficient estimates associated with the regression of `sales` onto `TV` and `radio`, with an interaction term.

Figure 24 shows a scatter plot of `mpg` (gas mileage in miles per gallon) versus `horsepower` in the `Auto` data set. The figure also includes least squares fit line for linear, second degree, and fifth degree polynomials in `horsepower`.

Table 10 shows regression results of a quadratic fit to explain `mpg` as a function of `horsepower` and `horsepower`².

The left panel of figure 25 displays a residual plot from the linear regression of `mpg` onto `horsepower` on the `Auto` data set. The red line is a smooth

3.3 Other Considerations in the Regression Model

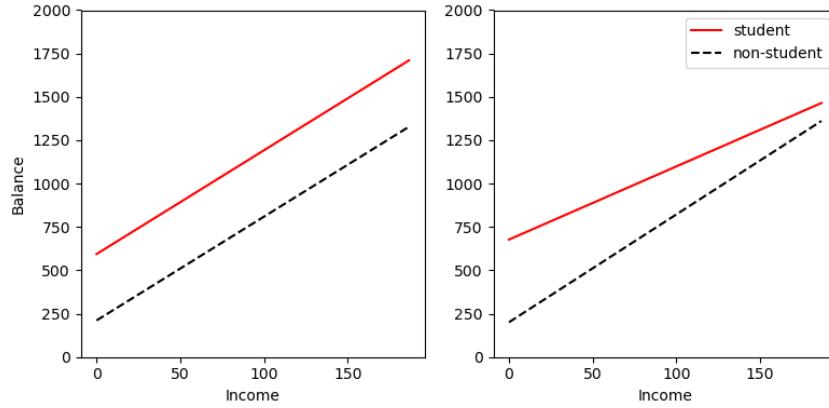


Figure 23: For the `Credit` data, the least squares lines are shown for prediction of `balance` from `income` for students and non-students. Left: There is no interaction between `income` and `student`. Right: There is an interaction term between `income` and `students`.

	Coef.	Std.Err.	<i>t</i>	<i>P</i> > <i>t</i>
Intercept	56.9001	1.8004	31.6037	0.0
horsepower	-0.4662	0.0311	-14.9782	0.0
<i>horsepower</i> ²	0.0012	0.0001	10.0801	0.0

Table 10: For the `Auto` data set, least squares coefficient estimates associated with the regression of `mpg` onto `horsepower` and

3.3 Other Considerations in the Regression Model

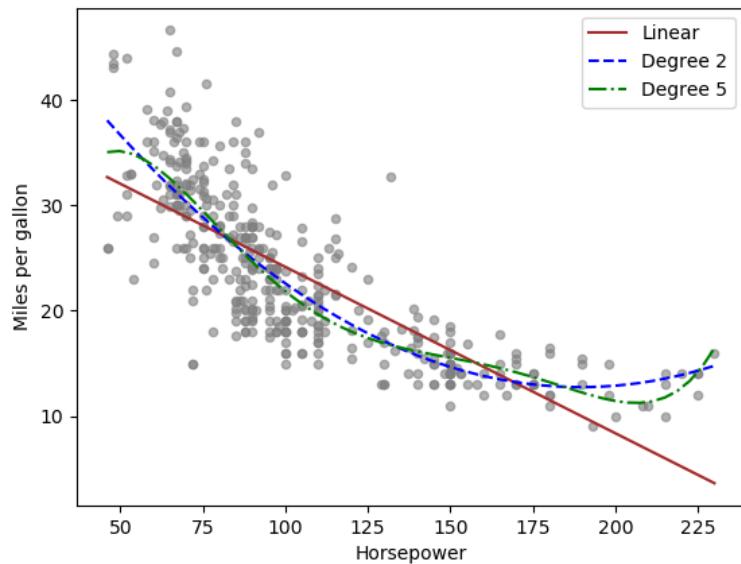


Figure 24: The `Auto` data set. For a number of cars, `mpg` and `horsepower` are shown. The linear regression fit is shown in orange. The linear regression fit for a model that includes first- and second-order terms of `horsepower` is shown as blue curve. The linear regression fit for a model that includes all polynomials of `horsepower` up to fifth-degree is shown in green.

3.3 Other Considerations in the Regression Model

fit to the residuals, which is displayed in order to make it easier to identify any trends. The residuals exhibit a clear U-shape, which strongly suggests non-linearity in the data. In contrast, the right hand panel of figure 25 displays the residual plot results from the model which contains a quadratic term in `horsepower`. Now there is little pattern in residuals, suggesting that the quadratic term improves the fit to the data.

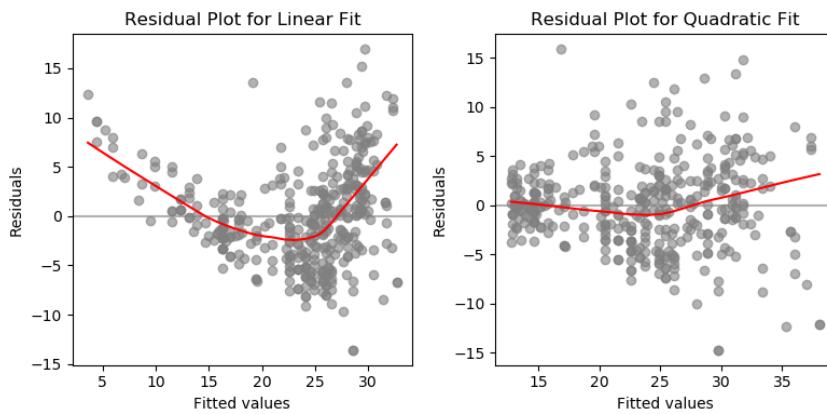


Figure 25: Plots of residuals versus predicted (or fitted) values for the `Auto` data set. In each plot, the red line is a smooth fit to the residuals, intended to make it easier to identify a trend. Left: A linear regression of `mpg` on `horsepower`. A strong pattern in the residuals indicates non-linearity in the data. Right: A linear regression of `mpg` on `horsepower` and square of `horsepower`. Now there is little pattern in the residuals.

Figure 26 provides an illustration of correlations among residuals. In the top panel, we see the residuals from a linear regression fit to data generated with uncorrelated errors. There is no evidence of time-related trend in the residuals. In contrast, the residuals in the bottom panel are from a data set in which adjacent errors had a correlation of 0.9. Now there is a clear pattern in the residuals - adjacent residuals tend to take on similar values. Finally, the center panel illustrates a more moderate case in which the residuals had a correlation of 0.5. There is still evidence of tracking, but the pattern is less pronounced.

In the left-hand panel of figure 27, the magnitude of the residuals tends to increase with the fitted values. The right hand panel displays residual plot after transforming the response using $\log(Y)$. The residuals now appear to have constant variance, although there is some evidence of a non-linear

3.3 Other Considerations in the Regression Model

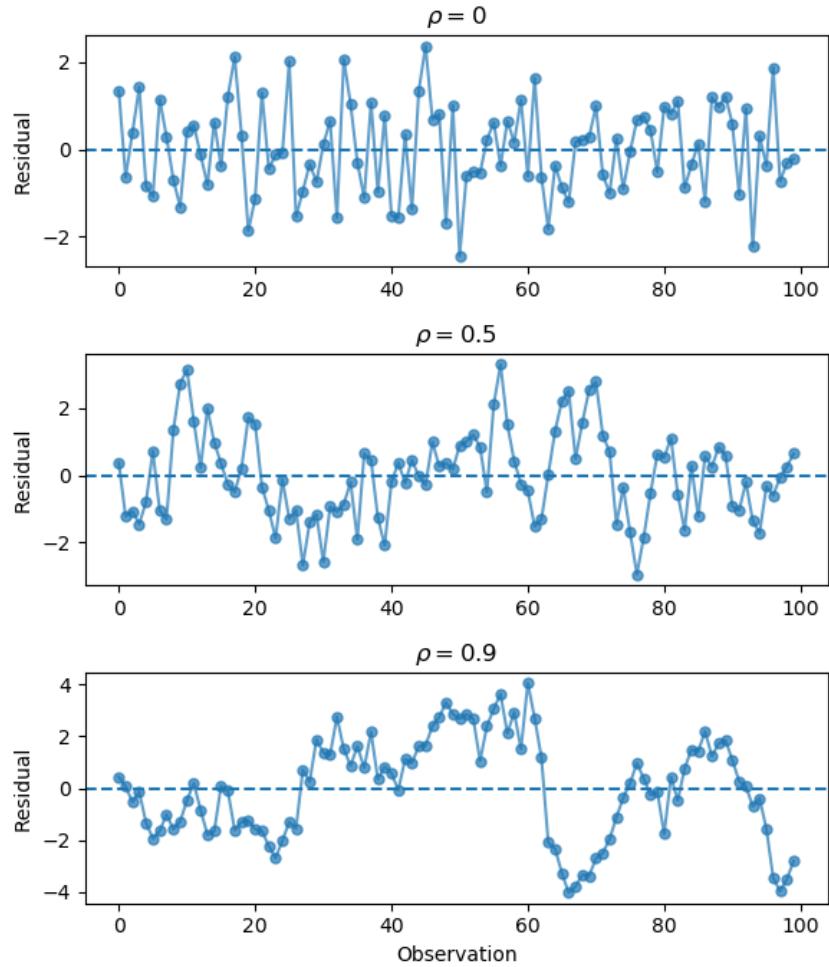


Figure 26: Plots of residuals from simulated time series data sets generated with differing levels of correlation ρ between error terms for adjacent time points.

3.3 Other Considerations in the Regression Model

relationship in the data.

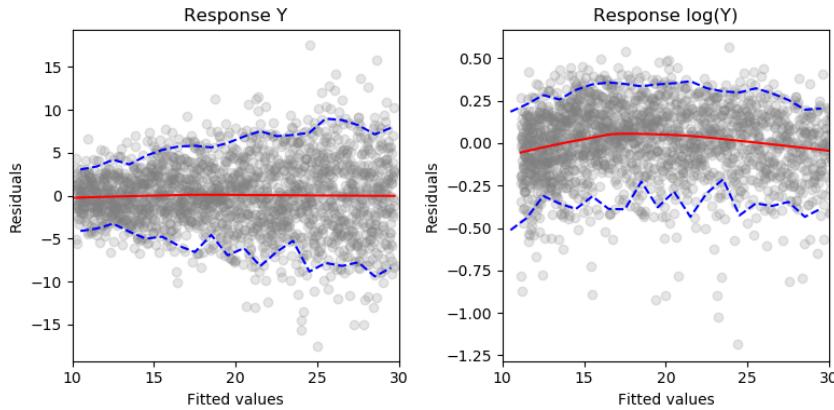


Figure 27: Residual plots. The red line, a smooth fit to the residuals, is intended to make it easier to identify a trend. The blue lines track 5th and 95th percentiles of the residuals, and emphasize patterns. Left: The funnel shape indicates heteroscedasticity. Right: the response has been log transformed, and now there is no evidence of heteroscedasticity.

The red point (observation 20) in the left hand panel of figure 28 illustrates a typical outlier. The red solid line is the least squares regression fit, while the blue dashed line is the least squares fit after removal of the outlier. In this case, removal of outlier has little effect on the least squares line. In the center panel of figure 28, the outlier is clearly visible. In practice, to decide if the outlier is sufficiently big to be considered an outlier, we can plot *studentized residuals*, computed by dividing each residual ϵ_i by its estimated standard error. These are shown in the right hand panel.

Observation 41 in the left-hand panel in figure 29 has high leverage, in that the predictor value for this observation is large relative to the other observations. The data displayed in figure 29 are the same as the data displayed in figure 28, except for the addition of a single high leverage observation¹. The red solid line is the least squares fit to the data, while the blue dashed line is the fit produced when observation 41 is removed. Comparing the left-hand panels of figures 28 and 29, we observe that removing the high leverage observation has a much more substantial impact on least squares line than removing the outlier. The center panel of figure 29, for a data set with two predictors X_1 and X_2 . While most of the observations' predictor values fall

¹The middle panel is from a different data set.

3.3 Other Considerations in the Regression Model

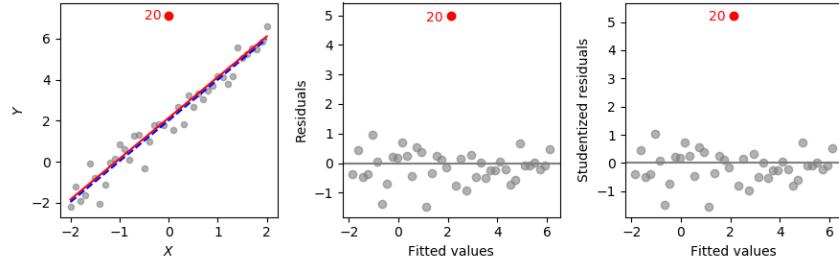


Figure 28: Left: The least squares regression line is shown in red. The regression line after removing the outlier is shown in blue. Center: The residual plot clearly identifies the outlier. Right: The outlier has a studentized residual of 6; typically we expect values between -3 and 3.

within the region of blue dashed lines, the red observation is well outside this range. But neither the value for X_1 nor the value for X_2 is unusual. So if we examine just X_1 or X_2 , we will not notice this high leverage point. The right-panel of figure 29 provides a plot of studentized residuals versus h_i for the data in the left hand panel. Observation 41 stands out as having a very high leverage statistic as well as a high studentized residual.

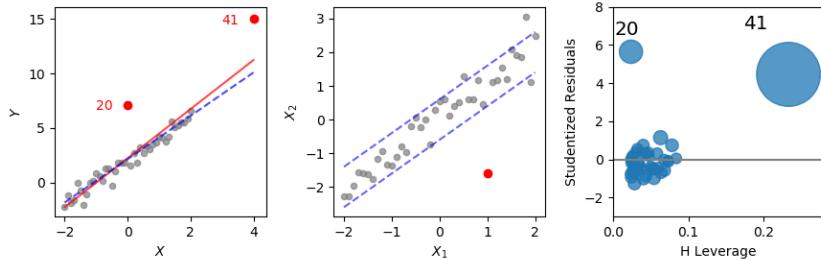


Figure 29: Left: Observation 41 is a high leverage point, while 20 is not. The red line is the fit to all the data, and the blue line is the fit with observation 41 removed. Center: The red observation is not unusual in terms of its X_1 value or its X_2 value, but still falls outside the bulk of the data, and hence has high leverage. Right: Observation 41 has a high leverage and a high residual.

Figure 30 illustrates the concept of collinearity.

Figure 31 illustrates some of the difficulties that can result from collinearity. The left panel is a contour plot of the RSS associated with different pos-

3.3 Other Considerations in the Regression Model

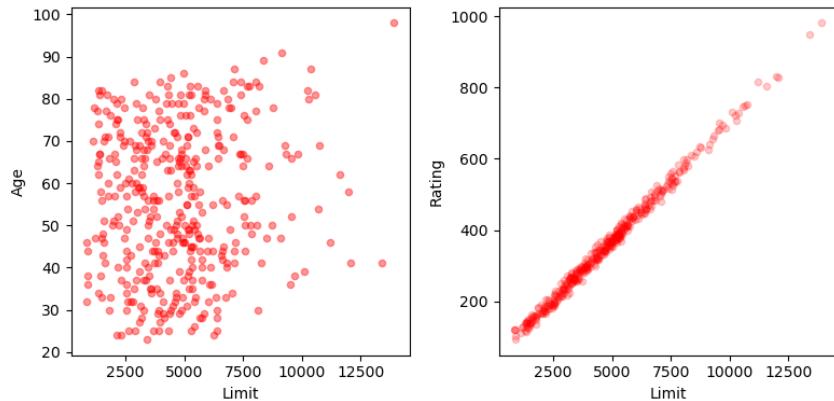


Figure 30: Scatter plots of the observations from the `Credit` data set. Left: A plot of `age` versus `limit`. These two variables not collinear. Right: A plot of `rating` versus `limit`. There is high collinearity.

sible coefficient estimates for the regression of `balance` on `limit` and `age`. Each ellipse represents a set of coefficients that correspond to the same RSS, with ellipses nearest to the center taking on the lowest values of RSS. The black dot and the associated dashed lines represent the coefficient estimates that result in the smallest possible RSS. The axes for `limit` and `age` have been scaled so that the plot includes possible coefficients that are up to four standard errors on either side of the least squares estimates. We see that the true `limit` coefficient is almost certainly between 0.15 and 0.20.

In contrast, the right hand panel of figure 31 displays contour plots of the RSS associated with possible coefficient estimates for the regression of `balance` onto `limit` and `rating`, which we know to be highly collinear. Now the contours run along a narrow valley; there is a broad range of values for the coefficient estimates that result in equal values for RSS.

Table 11 compares the coefficient estimates obtained from two separate multiple regression models. The first is a regression of `balance` on `age` and `limit`. The second is a regression of `balance` on `rating` and `limit`. In the first regression, both `age` and `limit` are highly significant with very small p-values. In the second, the collinearity between `limit` and `rating` has caused the standard error for the `limit` coefficient to increase by a factor of 12 and the p-value to increase to 0.701. In other words, the importance of the `limit` variable has been masked due to the presence of collinearity.

3.3 Other Considerations in the Regression Model

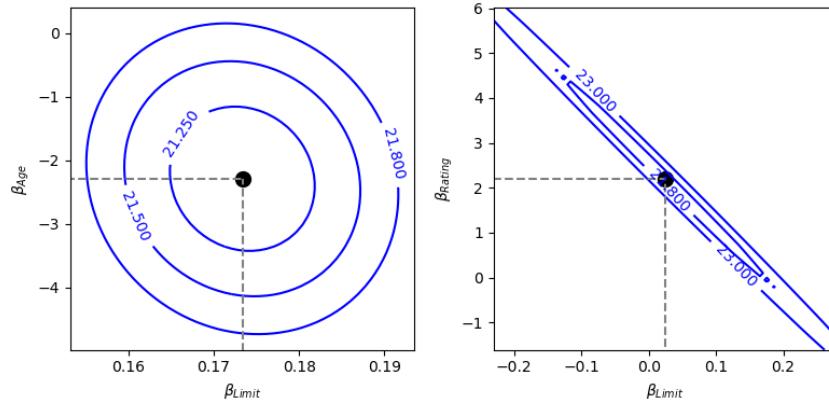


Figure 31: Contour plots for the RSS values as a function of the parameters β for various regressions involving the `Credit` data set. In each plot, the black dots represent the coefficient values corresponding to the minimum RSS. Left: A contour plot of RSS for the regression of `balance` onto `age` and `limit`. The minimum value is well defined. Right: A contour plot of RSS for the regression of `balance` onto `rating` and `limit`. Because of the collinearity, there are many pairs $(\beta_{Limit}, \beta_{Rating})$ with a similar value for RSS.

	Coef.	Std.Err.	t	$P > t $
Intercept	-173.411	43.828	-3.957	0.0
Age	-2.291	0.672	-3.407	0.001
Limit	0.173	0.005	34.496	0.0
Intercept	-377.537	45.254	-8.343	0.0
Rating	2.202	0.952	2.312	0.021
Limit	0.025	0.064	0.384	0.701

Table 11: The results for two multiple regression models involving the `Credit` data set. The top panel is a regression of `balance` on `age` and `limit`. The bottom panel is a regression of `balance` on `rating` and `limit`. The standard error of $\hat{\beta}_{Limit}$ increases 12-fold in the second regression, due to collinearity.

3.4 The Marketing Plan

3.5 Comparison of Linear Regression with K-Nearest Neighbors

Figure 32 illustrates two KNN fits on a data set with $p = 2$ predictors. The fit with $K = 1$ is shown in the left-hand panel, while the right-hand panel displays the fit with $K = 9$. When $K = 1$, the KNN fit perfectly interpolates the training observations, and consequently takes the form of a step function. When $K = 9$, the KNN fit is still a step function, but averaging over nine observations results in much smaller regions of constant prediction, and consequently a smoother fit.

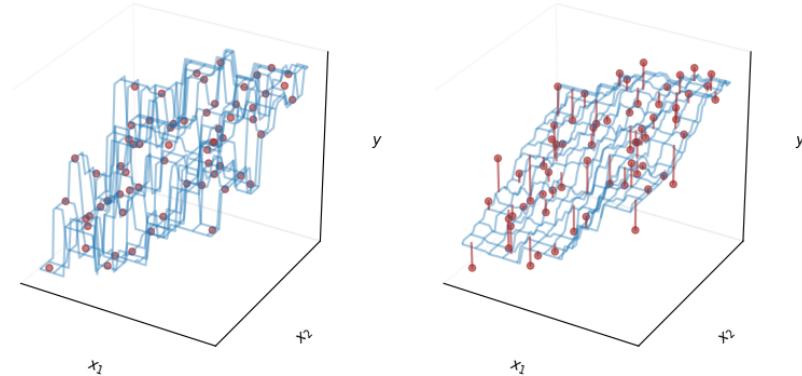


Figure 32: Plots of $\hat{f}(X)$ using KNN regression on two-dimensional data set with 64 observations (brown dots). Left: $K = 1$ results in a rough step function fit. Right: $K = 9$ produces a much smoother fit.

Figure 33 provides an example of KNN regression with data generated from a one-dimensional regression model. the black dashed lines represent $f(X)$, while the blue curves correspond to the KNN fits using $K = 1$ and $K = 9$. In this case, the $K = 1$ predictions are far too variable, while the smoother $K = 9$ fit is much closer to $f(X)$.

Figure 34 represents the linear regression fit to the same data. It is almost perfect. The right hand panel of figure 34 reveals that linear regression outperforms KNN for this data. The green line, plotted as a function of $\frac{1}{K}$, represents the test set mean squared error (MSE) for KNN. The KNN errors are well above the horizontal dashed line, which is the test MSE for linear regression.

3.5 Comparison of Linear Regression with K-Nearest Neighbors

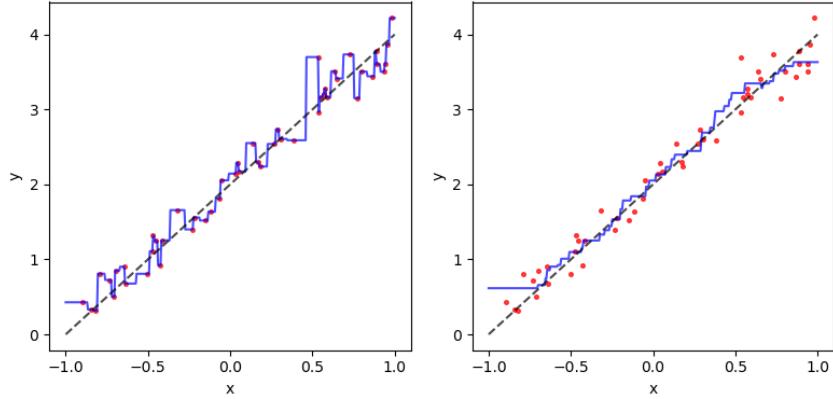


Figure 33: Plots of $\hat{f}(X)$ using KNN regression on a one-dimensional data set with 50 observations. The true relationship is given by the black dashed line. Left: The blue curve corresponds to $K = 1$ and interpolates (i.e., passes directly through) training data. Right: The blue curve corresponds to $K = 9$, and represents a smoother fit.

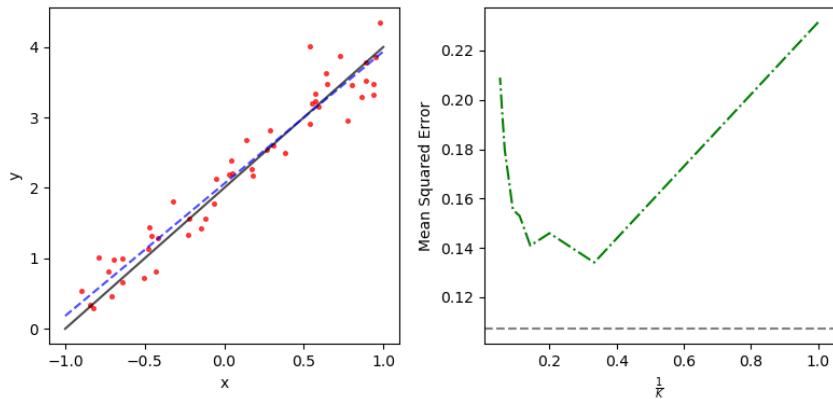


Figure 34: The same data set shown in figure 33 is investigated further. Left: The blue dashed line is the least squares fit to the data. Since $f(X)$ is in fact linear (displayed in black line), the least squares regression line provides a very good estimate of $f(X)$. Right: The dashed horizontal line represents the least squares test set MSE, while the green line corresponds to the MSE for KNN as a function of $\frac{1}{K}$. Linear regression achieves a lower test MSE than does KNN regression, since $f(X)$ is in fact linear.

3.5 Comparison of Linear Regression with K-Nearest Neighbors

Figure 35 examines the relative performances of least squares regression and KNN under increasing levels of non-linearity in the relationship between X and Y . In the top row, the true relationship is nearly linear. In this case, we see that the test MSE for linear regression is still superior to that of KNN for low values of K (far right). However, as K increases, KNN outperforms linear regression. The second row illustrates a more substantial deviation from linearity. In this situation, KNN substantially outperforms linear regression for all values of K .

Figure 36 considers the same strongly non-linear situation as in the lower panel of figure 35, except that we have added additional *noise* predictors that are not associated with the response. When $p = 1$ or $p = 2$, KNN outperforms linear regression. But as we increase p , linear regression becomes superior to KNN. In fact, increase in dimensionality has only caused a small increase in linear regression test set MSE, but it has caused a much bigger increase in the MSE for KNN.

3.5 Comparison of Linear Regression with K-Nearest Neighbors

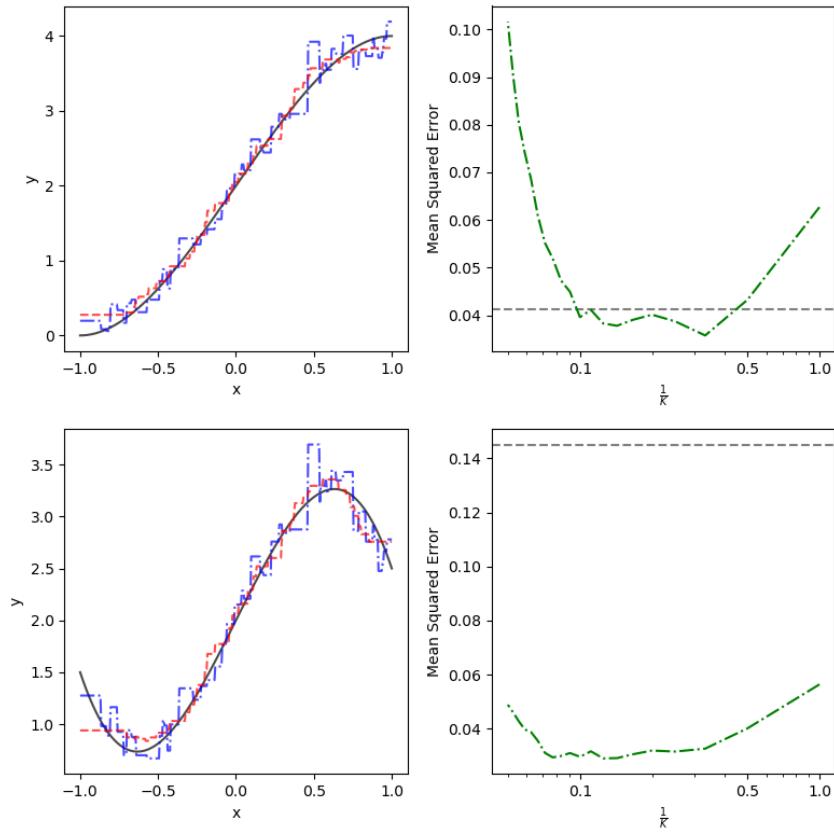


Figure 35: Top Left: In a setting with a slightly non-linear relationship between X and Y (solid black line), the KNN fits with $K = 1$ (blue) and $K = 9$ (red) are displayed. Top Right: For the slightly non-linear data, the test set MSE for least squares regression (horizontal) and KNN with various values of $\frac{1}{K}$ (green) are displayed. Bottom Left and Bottom Right: As in the top panel, but with a strongly non-linear relationship between X and Y .

3.5 Comparison of Linear Regression with K-Nearest Neighbors

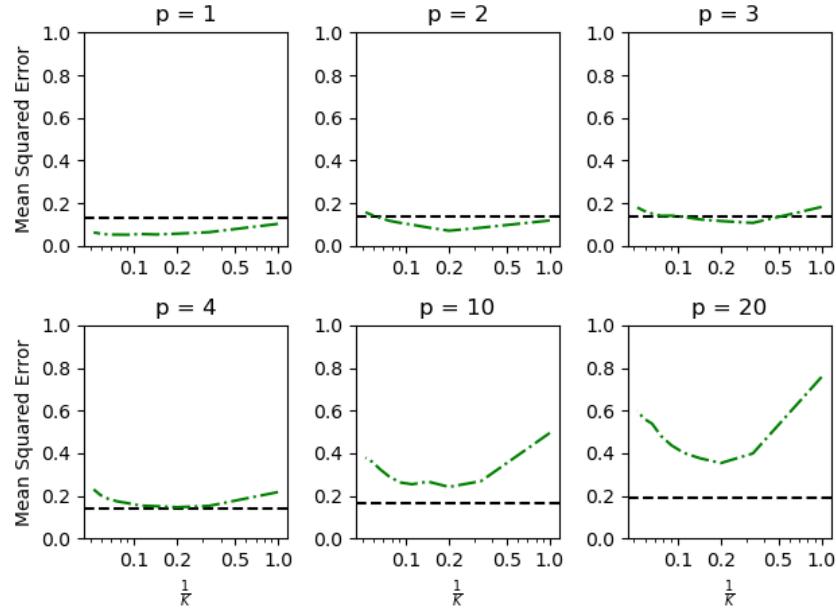


Figure 36: Test MSE for linear regressions (black horizontal lines) and KNN (green curves) as the number of variables p increases. The true function is non-linear in the first variable, as in the lower panel in figure 35, and does not depend upon the additional variables. The performance of linear regression deteriorates slowly in the presence of these additional variables, whereas KNN's performance degrades more quickly as p increases.

3.6 Lab: Linear Regression

3.6.1 Libraries

The `import` function, along with an optional `as`, is used to load *libraries*. Before a library can be loaded, it must be installed on the system.

```
import numpy as np
import statsmodels.formula.api as smf
```

3.6.2 Simple Linear Regression

We load Boston data set from R library MASS. Then we use `ols` function from `statsmodels.formula.api` to fit simple linear regression model, with `medv` as response and `lstat` as the predictor.

Function `summary2()` gives some basic information about the model. We can use `dir()` to find out what other pieces of information are stored in `lm_fit`. The `predict()` function can be used to produce prediction of `medv` for a given value of `lstat`.

```
import statsmodels.formula.api as smf
from statsmodels import datasets

boston = datasets.get_rdataset('Boston', 'MASS').data
print(boston.columns)
print('-----')

lm_reg = smf.ols(formula='medv ~ lstat', data=boston)
lm_fit = lm_reg.fit()
print(lm_fit.summary2())
print('-----')

print(dir(lm_fit))
print('-----')

print(lm_fit.predict(exog=dict(lstat=[5, 10, 15])))
```

```
Index(['crim', 'zn', 'indus', 'chas', 'nox', 'rm', 'age', 'dis', 'rad', 'tax',
       'ptratio', 'black', 'lstat', 'medv'],
      dtype='object')
-----
```

```
Results: Ordinary least squares
```

```
=====
Model:          OLS           Adj. R-squared:   0.543
```

3.6 Lab: Linear Regression

```

Dependent Variable: medv                  AIC:            3286.9750
Date:          2019-05-28 14:10  BIC:            3295.4280
No. Observations: 506                  Log-Likelihood: -1641.5
Df Model:       1                   F-statistic:      601.6
Df Residuals:   504                  Prob (F-statistic): 5.08e-88
R-squared:      0.544                Scale:           38.636
-----
Coef.        Std.Err.        t      P>|t|    [0.025    0.975]
-----
Intercept     34.5538     0.5626    61.4151  0.0000  33.4485  35.6592
lstat        -0.9500     0.0387   -24.5279  0.0000 -1.0261 -0.8740
-----
Omnibus:      137.043     Durbin-Watson: 0.892
Prob(Omnibus): 0.000      Jarque-Bera (JB): 291.373
Skew:          1.453      Prob(JB):      0.000
Kurtosis:     5.319      Condition No.: 30
=====
-----
['HC0_se', 'HC1_se', 'HC2_se', 'HC3_se', '_HCCM', '__class__', '__delattr__',
 '__dict__', '__dir__', '__doc__', '__eq__', '__format__', '__ge__',
 '__getattribute__', '__gt__', '__hash__', '__init__', '__init_subclass__',
 '__le__', '__lt__', '__module__', '__ne__', '__new__', '__reduce__',
 '__reduce_ex__', '__repr__', '__setattr__', '__sizeof__', '__str__',
 '__subclasshook__', '__weakref__', '_cache', '_data_attr',
 '_get_robustcov_results', '_is_nested', '_wexog_singular_values', 'aic',
 'bic', 'bse', 'centered_tss', 'compare_f_test', 'compare_lm_test',
 'compare_lr_test', 'condition_number', 'conf_int', 'conf_int_el', 'cov_HC0',
 'cov_HC1', 'cov_HC2', 'cov_HC3', 'cov_kwds', 'cov_params', 'cov_type',
 'df_model', 'df_resid', 'eigenvals', 'el_test', 'ess', 'f_pvalue', 'f_test',
 'fittedvalues', 'fvalue', 'get_influence', 'get_prediction',
 'get_robustcov_results', 'initialize', 'k_constant', 'llf', 'load', 'model',
 'mse_model', 'mse_resid', 'mse_total', 'nobs', 'normalized_cov_params',
 'outlier_test', 'params', 'predict', 'pvalues', 'remove_data', 'resid',
 'resid_pearson', 'rsquared', 'rsquared_adj', 'save', 'scale', 'ssr',
 'summary', 'summary2', 't_test', 't_test_pairwise', 'tvalues',
 'uncentered_tss', 'use_t', 'wald_test', 'wald_test_terms', 'wresid']
-----
0      29.803594
1      25.053347

```

3.6 Lab: Linear Regression

```
2    20.303101
dtype: float64
```

We will now plot `medv` and `lstat` along with least squares regression line.

```
import statsmodels.formula.api as smf
from statsmodels import datasets

boston = datasets.get_rdataset('Boston', 'MASS').data
print(boston.columns)
print('-----')

lm_reg = smf.ols(formula='medv ~ lstat', data=boston)
lm_fit = lm_reg.fit()
print(lm_fit.summary2())
print('-----')

print(dir(lm_fit))
print('-----')

print(lm_fit.predict(exog=dict(lstat=[5, 10, 15])))
import statsmodels.api as sm
import matplotlib.pyplot as plt

fig = plt.figure()
ax = fig.add_subplot(111)
boston.plot(x='lstat', y='medv', alpha=0.7, ax=ax)
sm.graphics.abline_plot(model_results=lm_fit, ax=ax, c='r')
```

Next we examine some diagnostic plots.

```
import statsmodels.formula.api as smf
from statsmodels import datasets

boston = datasets.get_rdataset('Boston', 'MASS').data
print(boston.columns)
print('-----')

lm_reg = smf.ols(formula='medv ~ lstat', data=boston)
lm_fit = lm_reg.fit()
print(lm_fit.summary2())
print('-----')

print(dir(lm_fit))
print('-----')

print(lm_fit.predict(exog=dict(lstat=[5, 10, 15])))
import statsmodels.api as sm
```

3.6 Lab: Linear Regression

```
from statsmodels.nonparametric.smoothers_lowess import lowess
import matplotlib.pyplot as plt
import numpy as np

fig = plt.figure()
ax1 = fig.add_subplot(221)
ax1.scatter(lm_fit.fittedvalues, lm_fit.resid, s=5, c='b',
            alpha=0.6)
ax1.axhline(y=0, linestyle='--', c='r')
# resid_lowess_fit = lowess(endog=lm_fit.resid, exog=lm_fit.
#                             fittedvalues,
#                             is_sorted=True)
# ax1.plot(resid_lowess_fit[:,0], resid_lowess_fit[:,1])
ax1.set_xlabel('Fitted values')
ax1.set_ylabel('Residuals')
ax1.set_title('Residuals vs Fitted')

ax2=fig.add_subplot(222)
sm.graphics.qqplot(lm_fit.resid, ax=ax2, markersize=3, line='s',
                   ,
                   linestyle='--', fit=True, alpha=0.4)
ax2.set_ylabel('Standardized residuals')
ax2.set_title('Normal Q-Q')

influence = lm_fit.get_influence()
standardized_resid = influence.resid_studentized_internal
ax3 = fig.add_subplot(223)
ax3.scatter(lm_fit.fittedvalues, np.sqrt(np.abs(
    standardized_resid)), s=5,
            alpha=0.4, c='b')
ax3.set_xlabel('Fitted values')
ax3.set_ylabel(r'$\sqrt{|Standardized|; residuals |mid} $')
ax3.set_title('Scale-Location')

ax4 = fig.add_subplot(224)
sm.graphics.influence_plot(lm_fit, size=2, alpha=0.4, c='b',
                           ax=ax4)
ax4.xaxis.label.set_size(10)
ax4.yaxis.label.set_size(10)
ax4.title.set_size(12)
ax4.set_xlim(0, 0.03)
for txt in ax4.texts:
    txt.set_visible(False)
ax4.axhline(y=0, linestyle='--', color='grey')

fig.tight_layout()
```

3.6.3 Multiple Linear Regression

In order to fit a multiple regression model using least squares, we again use the `ols` and `fit` functions. The syntax `ols(formula='y ~ x1 + x2 + x3')` is used to fit a model with three predictors, `x1`, `x2`, and `x3`. The `summary2()` now outputs the regression coefficients for all three predictors.

`statsmodels` does not seem to have R like facility to include all variables using the formula `y ~ ..`. To include all variables, we either write them individually, or use code to create a formula.

```
import statsmodels.formula.api as smf
from statsmodels import datasets

boston = datasets.get_rdataset('Boston', 'MASS').data

lm_reg = smf.ols(formula='medv ~ lstat + age', data=boston)
lm_fit = lm_reg.fit()

print(lm_fit.summary2())
print('-----')

# Create formula to include all variables
all_columns = list(boston.columns)
all_columns.remove('medv')
my_formula = 'medv ~ ' + ' + '.join(all_columns)
print(my_formula)
print('-----')

all_reg = smf.ols(formula=my_formula, data=boston)
all_fit = all_reg.fit()
print(all_fit.summary2())
print('-----')
```

Results: Ordinary least squares

Model:	OLS	Adj. R-squared:	0.549
Dependent Variable:	medv	AIC:	3281.0064
Date:	2019-05-29 10:07	BIC:	3293.6860
No. Observations:	506	Log-Likelihood:	-1637.5
Df Model:	2	F-statistic:	309.0
Df Residuals:	503	Prob (F-statistic):	2.98e-88
R-squared:	0.551	Scale:	38.108
Coef.	Std.Err.	t	P> t [0.025 0.975]

3.6 Lab: Linear Regression

```

Intercept      33.2228    0.7308   45.4579  0.0000  31.7869  34.6586
lstat        -1.0321    0.0482  -21.4163  0.0000  -1.1267  -0.9374
age          0.0345    0.0122    2.8256  0.0049   0.0105   0.0586
-----
Omnibus:            124.288    Durbin-Watson:       0.945
Prob(Omnibus):     0.000      Jarque-Bera (JB): 244.026
Skew:              1.362      Prob(JB):           0.000
Kurtosis:           5.038      Condition No.: 201
=====
-----
medv ~ crim + zn + indus + chas + nox + rm + age + dis + rad + tax +
ptratio + black + lstat
-----
Results: Ordinary least squares
=====
Model:             OLS          Adj. R-squared: 0.734
Dependent Variable: medv        AIC:            3025.6086
Date:              2019-05-29 10:07 BIC:            3084.7801
No. Observations: 506          Log-Likelihood: -1498.8
Df Model:          13          F-statistic:       108.1
Df Residuals:      492          Prob (F-statistic): 6.72e-135
R-squared:          0.741        Scale:            22.518
-----
          Coef.    Std.Err.      t    P>|t|    [0.025    0.975]
-----
Intercept  36.4595    5.1035   7.1441  0.0000  26.4322  46.4868
crim      -0.1080    0.0329  -3.2865  0.0011  -0.1726  -0.0434
zn         0.0464    0.0137   3.3816  0.0008   0.0194   0.0734
indus     0.0206    0.0615   0.3343  0.7383  -0.1003   0.1414
chas      2.6867    0.8616   3.1184  0.0019   0.9939   4.3796
nox       -17.7666   3.8197  -4.6513  0.0000  -25.2716 -10.2616
rm         3.8099    0.4179   9.1161  0.0000   2.9887   4.6310
age       0.0007    0.0132   0.0524  0.9582  -0.0253   0.0266
dis       -1.4756    0.1995  -7.3980  0.0000  -1.8675  -1.0837
rad        0.3060    0.0663   4.6129  0.0000   0.1757   0.4364
tax       -0.0123    0.0038  -3.2800  0.0011  -0.0197  -0.0049
ptratio   -0.9527    0.1308  -7.2825  0.0000  -1.2098  -0.6957
black     0.0093    0.0027   3.4668  0.0006   0.0040   0.0146
lstat     -0.5248    0.0507 -10.3471 0.0000  -0.6244  -0.4251

```

3.6 Lab: Linear Regression

```
-----  
Omnibus:            178.041        Durbin-Watson:      1.078  
Prob(Omnibus):      0.000          Jarque-Bera (JB): 783.126  
Skew:               1.521          Prob(JB):         0.000  
Kurtosis:            8.281          Condition No.:   15114  
===== * The condition number is large (2e+04). This might indicate  
       strong multicollinearity or other numerical problems.  
=====
```

3.6.4 Interaction Terms

The syntax `lstat:black` tells `ols` to include an interaction term between `lstat` and `black`. The syntax `lstat*age` simultaneously includes `lstat`, `age`, and the interaction term `lstat × age` as predictors. It is a shorthand for `lstat + age + lstat:age`.

```
import statsmodels.formula.api as smf  
from statsmodels import datasets  
  
boston = datasets.get_rdataset('Boston', 'MASS').data  
  
my_reg = smf.ols(formula='medv ~ lstat * age', data=boston)  
my_fit = my_reg.fit()  
print(my_fit.summary2())
```

```
Results: Ordinary least squares  
=====  
Model:                 OLS           Adj. R-squared:    0.553  
Dependent Variable: medv          AIC:             3277.9547  
Date:                  2019-05-29 11:48 BIC:             3294.8609  
No. Observations:     506           Log-Likelihood: -1635.0  
Df Model:              3             F-statistic:      209.3  
Df Residuals:         502           Prob (F-statistic): 4.86e-88  
R-squared:             0.556          Scale:            37.804  
=====  
Coef.      Std.Err.      t      P>|t|      [0.025      0.975]  
-----  
Intercept  36.0885   1.4698  24.5528  0.0000  33.2007  38.9763  
lstat      -1.3921   0.1675  -8.3134  0.0000 -1.7211  -1.0631  
age        -0.0007   0.0199  -0.0363  0.9711 -0.0398  0.0383  
lstat:age   0.0042   0.0019   2.2443  0.0252  0.0005  0.0078
```

Omnibus:	135.601	Durbin-Watson:	0.965
Prob(Omnibus):	0.000	Jarque-Bera (JB):	296.955
Skew:	1.417	Prob(JB):	0.000
Kurtosis:	5.461	Condition No.:	6878

* The condition number is large (7e+03). This might indicate strong multicollinearity or other numerical problems.

3.6.5 Non-linear Transformations of the Predictors

The `ols` function can also accommodate non-linear transformations of the predictors. For example, given a predictor X , we can create predictor X^2 using `I(X ** 2)`. We now perform a regression of `medv` onto `lstat` and `lstat2`.

The near-zero p-value associated with the quadratic term suggests that it leads to an improve model. We use `anova_lm()` function to further quantify the extent to which the quadratic fit is superior to the linear fit. The null hypothesis is that the two models fit the data equally well. The alternative hypothesis is that the full model is superior. Given the large F-statistic and zero p-value, this provides very clear evidence that the model with quadratic term is superior. A plot of residuals versus fitted values shows that, with quadratic term included, there is no discernible pattern in residuals.

```

import statsmodels.formula.api as smf
from statsmodels import datasets
import statsmodels.api as sm
lowess = sm.nonparametric.lowess
import matplotlib.pyplot as plt

boston = datasets.get_rdataset('Boston', 'MASS').data

my_reg = smf.ols(formula='medv ~ lstat', data=boston)
my_fit = my_reg.fit()

my_reg2 = smf.ols(formula='medv ~ lstat + I(lstat ** 2)', data=
                  boston)
my_fit2 = my_reg2.fit()
print(my_fit.summary2())
print('-----')

print(sm.stats.anova_lm(my_fit2))
print('-----')

print(sm.stats.anova_lm(my_fit, my_fit2))

```

3.6 Lab: Linear Regression

```
my_regs = (my_reg, my_reg2)

fig = plt.figure(figsize=(8,4))
i_reg = 1
for reg in my_regs:
    ax = fig.add_subplot(1, 2, i_reg)
    fit = reg.fit()
    ax.scatter(fit.fittedvalues, fit.resid, s=7, alpha=0.6)
    lowess_fit = lowess(fit.resid, fit.fittedvalues)
    ax.plot(lowess_fit[:,0], lowess_fit[:,1], c='r')
    ax.axhline(y=0, linestyle='--', color='grey')
    ax.set_xlabel('Fitted values')
    ax.set_ylabel('Residuals')
    ax.set_title(reg.formula)
    i_reg += 1

fig.tight_layout()
```

```
Results: Ordinary least squares
=====
Model:                 OLS          Adj. R-squared:  0.543
Dependent Variable: medv          AIC:            3286.9750
Date:                  2019-05-29 12:41 BIC:            3295.4280
No. Observations:   506          Log-Likelihood: -1641.5
Df Model:                1          F-statistic:     601.6
Df Residuals:           504          Prob (F-statistic): 5.08e-88
R-squared:              0.544          Scale:           38.636
-----
          Coef.    Std.Err.      t    P>|t|    [0.025  0.975]
-----
Intercept    34.5538    0.5626   61.4151  0.0000  33.4485  35.6592
lstat       -0.9500    0.0387  -24.5279  0.0000 -1.0261 -0.8740
-----
Omnibus:        137.043      Durbin-Watson:  0.892
Prob(Omnibus):  0.000      Jarque-Bera (JB): 291.373
Skew:           1.453      Prob(JB):        0.000
Kurtosis:        5.319      Condition No.:   30
-----
          df      sum_sq      mean_sq          F      PR(>F)
lstat      1.0  23243.913997  23243.913997  761.810354  8.819026e-103
```

3.6 Lab: Linear Regression

```
I(lstat ** 2)      1.0    4125.138260    4125.138260  135.199822    7.630116e-28
Residual          503.0   15347.243158     30.511418      NaN           NaN
-----
df_resid          ssr   df_diff      ss_diff         F       Pr(>F)
0      504.0  19472.381418      0.0        NaN        NaN        NaN
1      503.0   15347.243158      1.0  4125.13826  135.199822  7.630116e-28
```

3.6.6 Qualitative Predictors

We will now examine `Carseats` data, which is part of the `ISLR` library. We will attempt to predict `Sales` (child car seat sales) based on a number of predictors. `statsmodels` automatically converts string variables into categorical variables. If we want `statsmodels` to treat a numerical variable `x` as qualitative predictor, the formula should be `y ~ C(x)`. Here `C()` stands for categorical.

```
import statsmodels.formula.api as smf
from statsmodels import datasets

carseats = datasets.get_rdataset('Carseats', 'ISLR').data
print(carseats.columns)
print('-----')

all_columns = list(carseats.columns)
all_columns.remove('Sales')
my_formula = 'Sales ~ ' + ' + '.join(all_columns)
my_formula += ' + Income:Advertising + Price:Age'

print(my_formula)
print('-----')

my_reg = smf.ols(formula=my_formula, data=carseats)
my_fit = my_reg.fit()
print(my_fit.summary2())

Index(['Sales', 'CompPrice', 'Income', 'Advertising', 'Population', 'Price',
       'ShelveLoc', 'Age', 'Education', 'Urban', 'US'],
      dtype='object')
-----
Sales ~ CompPrice + Income + Advertising + Population + Price + ShelveLoc +
Age + Education + Urban + US + Income:Advertising + Price:Age
-----
Results: Ordinary least squares
=====
```

3.6 Lab: Linear Regression

Model:	OLS	Adj. R-squared:	0.872			
Dependent Variable:	Sales	AIC:	1157.3378			
Date:	2019-05-29 12:53	BIC:	1213.2183			
No. Observations:	400	Log-Likelihood:	-564.67			
Df Model:	13	F-statistic:	210.0			
Df Residuals:	386	Prob (F-statistic):	6.14e-166			
R-squared:	0.876	Scale:	1.0213			
<hr/>						
	Coef.	Std.Err.	t	P> t	[0.025	0.975]
<hr/>						
Intercept	6.5756	1.0087	6.5185	0.0000	4.5922	8.5589
ShelveLoc[T.Good]	4.8487	0.1528	31.7243	0.0000	4.5482	5.1492
ShelveLoc[T.Medium]	1.9533	0.1258	15.5307	0.0000	1.7060	2.2005
Urban[T.Yes]	0.1402	0.1124	1.2470	0.2132	-0.0808	0.3612
US[T.Yes]	-0.1576	0.1489	-1.0580	0.2907	-0.4504	0.1352
CompPrice	0.0929	0.0041	22.5668	0.0000	0.0848	0.1010
Income	0.0109	0.0026	4.1828	0.0000	0.0058	0.0160
Advertising	0.0702	0.0226	3.1070	0.0020	0.0258	0.1147
Population	0.0002	0.0004	0.4329	0.6653	-0.0006	0.0009
Price	-0.1008	0.0074	-13.5494	0.0000	-0.1154	-0.0862
Age	-0.0579	0.0160	-3.6329	0.0003	-0.0893	-0.0266
Education	-0.0209	0.0196	-1.0632	0.2884	-0.0594	0.0177
Income:Advertising	0.0008	0.0003	2.6976	0.0073	0.0002	0.0013
Price:Age	0.0001	0.0001	0.8007	0.4238	-0.0002	0.0004
<hr/>						
Omnibus:	1.281	Durbin-Watson:	2.047			
Prob(Omnibus):	0.527	Jarque-Bera (JB):	1.147			
Skew:	0.129	Prob(JB):	0.564			
Kurtosis:	3.050	Condition No.:	130576			
<hr/>						

* The condition number is large (1e+05). This might indicate strong multicollinearity or other numerical problems.

3.6.7 Calling R from Python

4 Classification

4.1 An Overview of Classification

In figure 37, we have plotted annual `income` and monthly credit card `balance` for a subset of individuals in `Credit` data set. The left hand panel displays individuals who defaulted in brown, and those who did not in blue. We have plotted only a fraction of individuals who did not default. It appears that individuals who defaulted tended to have higher credit card balances than those who did not. In the right hand panel, we show two pairs of boxplots. The first shows the distribution of `balance` split by the binary `default` variable; the second is a similar plot for `income`.

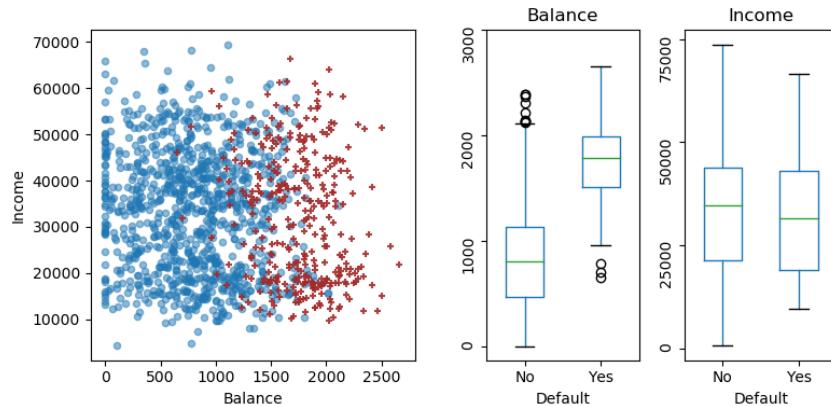


Figure 37: The `Default` data set. Left: The annual income and monthly credit card balances of a number of individuals. The individuals who defaulted on their credit card debt are shown in brown, and those who did not default are shown in blue. Center: Boxplots of `balance` as a function of `default` status. Right: Boxplots of `income` as a function of `default` status.

4.2 Why Not Linear Regression?

4.3 Logistic Regression

Using `Default` data set, in figure 38 we show probability of default as a function of `balance`. The left panel shows a model fitted using linear regression. Some of the probabilities estimates (for low balance) are outside

4.3 Logistic Regression

the $[0, 1]$ interval. The right panel shows a model fitted using logistic regression, which models the probability of default as a function of `balance`. Now all probability estimates are in the $[0, 1]$ interval.

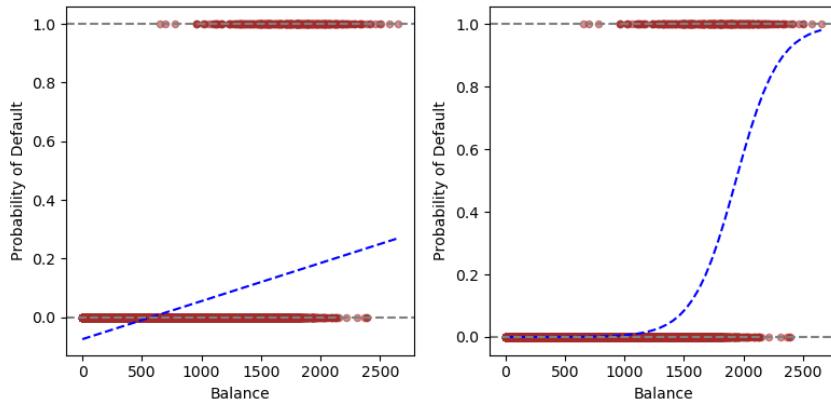


Figure 38: Classification using `Default` data. Left: Estimated probability of `default` using linear regression. Some estimated probabilities are negative! The brown ticks indicate the 0/1 values coded for `default` (`No` or `Yes`). Right: Predicted probabilities of `default` using logistic regression. All probabilities lie between 0 and 1.

Table 12 shows the coefficient estimates and related information that result from fitting a logistic regression model on the `Default` data in order to predict the probability of `default = Yes` using `balance`.

	Coef.	Std.Err.	z	$P > z $
Intercept	-10.6513	0.3612	-29.4913	0.0
balance	0.0055	0.0002	24.9524	0.0

Table 12: For the `Default` data, estimated coefficients of the logistic regression model that predicts the probability of `default` using `balance`. A one-unit increase in `balance` is associated with an increase in the log odds of `default` by 0.0055 units.

Table 13 shows the results of logistic model where `default` is a function of the qualitative variable `student`.

Table 14 shows the coefficient estimates for a logistic regression model that uses `balance`, `income` (in thousands of dollars), and `student` status to predict probability of `default`.

4.4 Linear Discriminant Analysis

	Coef.	Std.Err.	z	$P > z $
Intercept	-3.5041	0.0707	-49.5541	0.0
student[T.Yes]	0.4049	0.115	3.5202	0.0004

Table 13: For the `Default` data, estimated coefficients of the logistic regression model that predicts the probability of `default` using student status.

	Coef.	Std.Err.	z	$P > z $
Intercept	-10.869	0.4923	-22.0793	0.0
student[T.Yes]	-0.6468	0.2363	-2.7376	0.0062
balance	0.0057	0.0002	24.7365	0.0
income	0.003	0.0082	0.3698	0.7115

Table 14: For the `Default` data, estimated coefficients of the logistic regression model that predicts the probability of `default` using `balance`, `income`, and `student` status. In fitting this model, `income` was measured in thousands of dollars.

The left hand panel of figure 39 shows average default rates for students and non-students, respectively, as a function of credit card balance. *For a fixed value of `balance` and `income`, a student is less likely to default than a non-student.* This is true for all values of balance. This is consistent with negative coefficient of `student` in table 14. But the horizontal lines near the base of the plot, which show the default rates for students and non-students averaged over all values of `balance` and `income`, suggest the opposite effect: the overall student default rate is higher than non-student default rate. Consequently, there is a positive coefficient for `student` in the single variable logistic regression output shown in table 13.

4.4 Linear Discriminant Analysis

In the left panel of figure 40, two normal density functions that are displayed, $f_1(x)$ and $f_2(x)$, represent two distinct classes. The Bayes classifier boundary, shown as vertical dashed line, is estimated using the function `GaussianNB()`. The right hand panel displays a histogram of a random sample of 20 observations from each class. The LDA decision boundary is shown as firm vertical line.

Two examples of multivariate Gaussian distributions with $p = 2$ are shown in figure 41. In the upper panel, the height of the surface at any particular point represents the probability that both X_1 and X_2 fall in the small region around that point. If the surface is cut along the X_1 axis or along the

4.4 Linear Discriminant Analysis

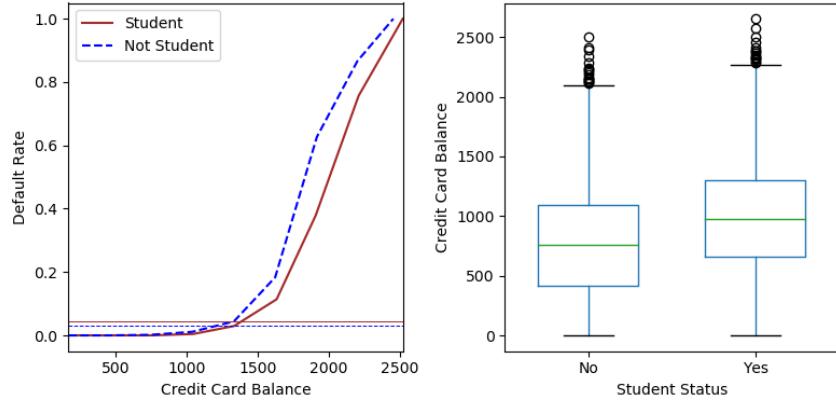


Figure 39: Confounding in the `Default` data. Left: Default rates are shown for students (brown) and non-students (blue). The solid lines display default rate as a function of `balance`, while the horizontal lines display the overall default rates. Right: Boxplots of `balance` for students and non-students are shown.

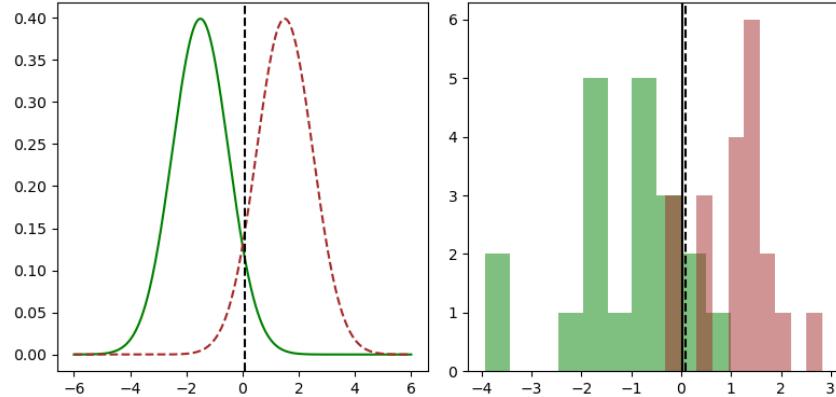


Figure 40: Left: Two one-dimensional normal density functions are shown. The dashed vertical line represents the Bayes decision boundary. Right: 20 observations were drawn from each of the two classes, and are shown as histograms. The Bayes decision boundary is again shown as a dashed vertical line. The solid vertical line represents the LDA decision boundary estimated from the training data.

X_2 axis, the resulting cross-section will have the shape of a one-dimensional normal distribution. The left-hand panel illustrates an example in which $\text{var}(X_1) = \text{var}(X_2)$ and $\text{cor}(X_1, X_2) = 0$; this surface has a characteristic *bell shape*. However, the bell shape will be distorted if the predictors are correlated or have unequal variances, as is illustrated in the right-hand panel of figure 41. In this situation, the base of the bell will have an elliptical, rather than circular, shape. The contour plots in the lower panel are not in the book.

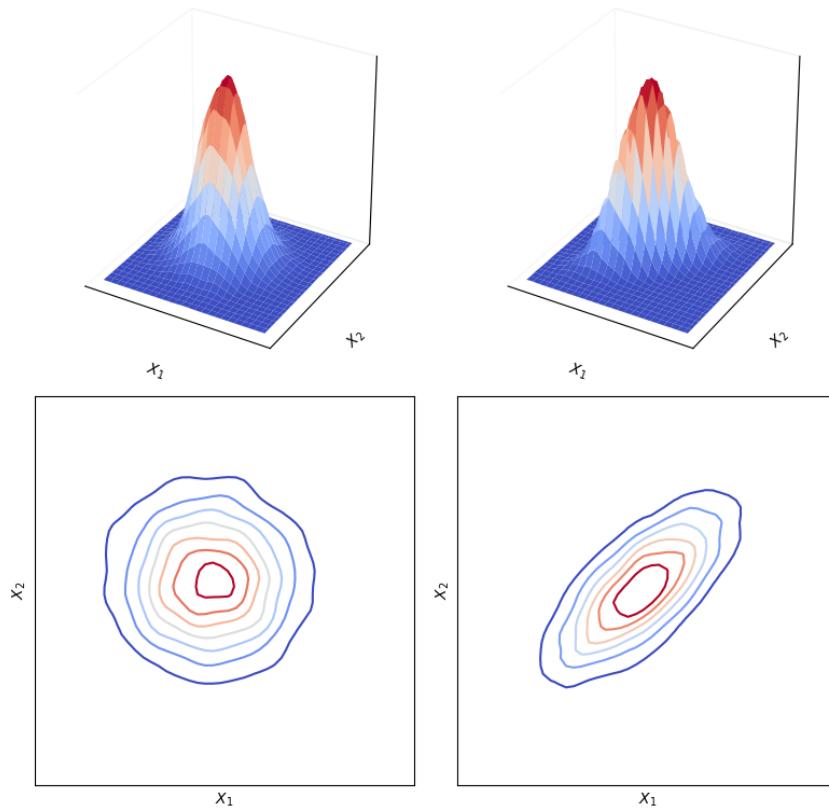


Figure 41: Two multivariate Gaussian density functions are shown, with $p = 2$. Left: The two predictors are uncorrelated. Right: The two predictors have a correlation of 0.7. The lower panel shows contour plots of the surfaces drawn in the upper panel. Here the correlations can be easily seen.

Figure 42 shows an example of three equally sized Gaussian classes with

4.4 Linear Discriminant Analysis

class-specific mean vectors and a common covariance matrix. The dashed lines are the Bayes decision boundaries.

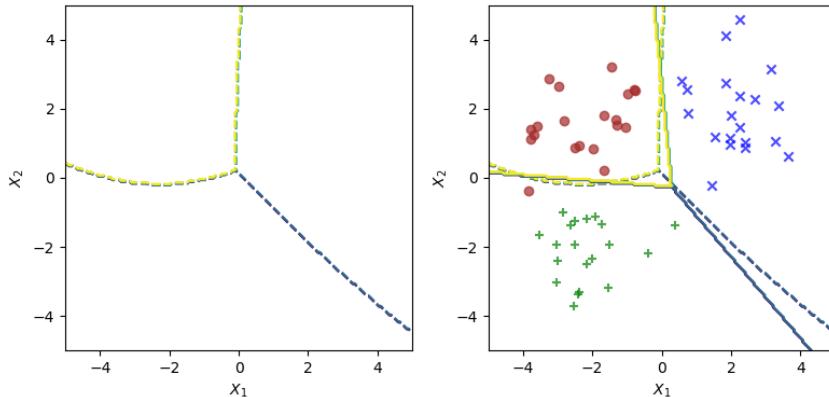


Figure 42: An example with three classes. The observation from each class are drawn from a multivariate Gaussian distribution with $p = 2$, with a class-specific mean vector and a common covariance matrix. Left: The dashed lines are the Bayes decision boundaries. Right: 20 observations were generated from each class, and the corresponding LDA decision boundaries are indicated using solid black lines. The Bayes decision boundaries are once again shown as dashed lines.

A *confusion matrix*, shown for the **Default** data in table 15, is a convenient way to display prediction of default in comparison to true default. Table 16 shows the error rates that result when we label any customer with a posterior probability of default above 20% to the *default* class.

Figure 43 illustrates the trade-off that results from modifying the threshold value for the posterior probability of default. Various error rates are shown as a function of the threshold value. Using a threshold of 0.5 minimizes the overall error rate, shown as a black line. But when a threshold of 0.5 is used, the error rate among the individuals who default is quite high (blue dashed line). As the threshold is reduced, the error rate among individuals who default decreases steadily, but the error rate among individuals who do not default increases.

Figure 44 displays the ROC curve for the LDA classifier on the **Default** data set.

Table 17 shows the possible results when applying a classifier (or diagnostic test) to a population.

4.4 Linear Discriminant Analysis

	true No	true Yes	Total
predict No	9645	254	9899
predict Yes	22	79	101
Total	9667	333	10000

Table 15: A confusion matrix compares the LDA predictions to the true default statuses for the training observations in the `Default` data set. Elements of the diagonal matrix represent individuals whose default statuses were correctly predicted, while off-diagonal elements represent individuals that were missclassified.

	true No	true Yes	Total
predict No	9435	140	9575
predict Yes	232	193	425
Total	9667	333	10000

Table 16: A confusion matrix compares LDA predictions to the true default statuses for the training observations in the `Default` data set, using a modified threshold value that predicts default for any individuals whose posterior default probability exceeds 20%.

Predicted class	True class		Total
	- or Null	+ or Non-null	
- or Null	True Negative (TN)	False Negative (FN)	N*
	False Positive (FP)	True Positive (TP)	P*
Total		N	P

Table 17: Possible results when applying a classifier or diagnostic test to a population.

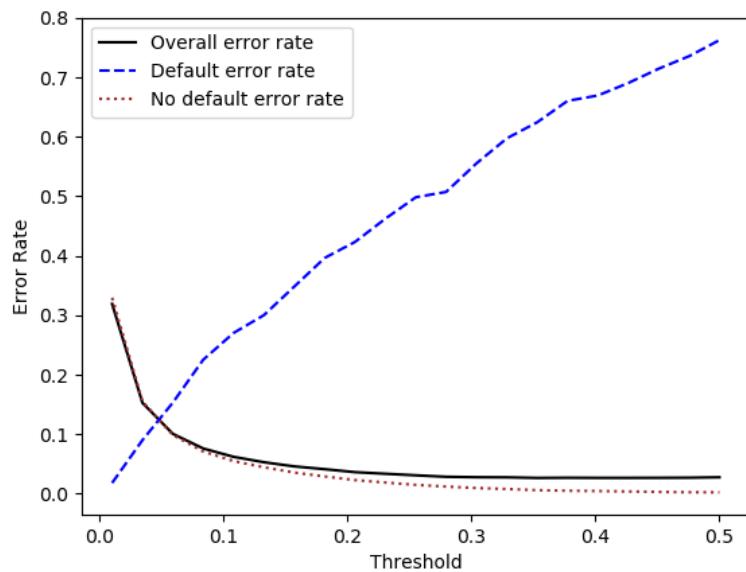


Figure 43: For the `Default` data set, error rates are shown as a function of the threshold value for the posterior probability that is used to perform the assignment of default. The black solid line displays the overall error rate. The blue dashed line represents the fraction of defaulting customers that are incorrectly classified, and the orange dotted line indicates the fraction of errors among the non-defaulting customers.

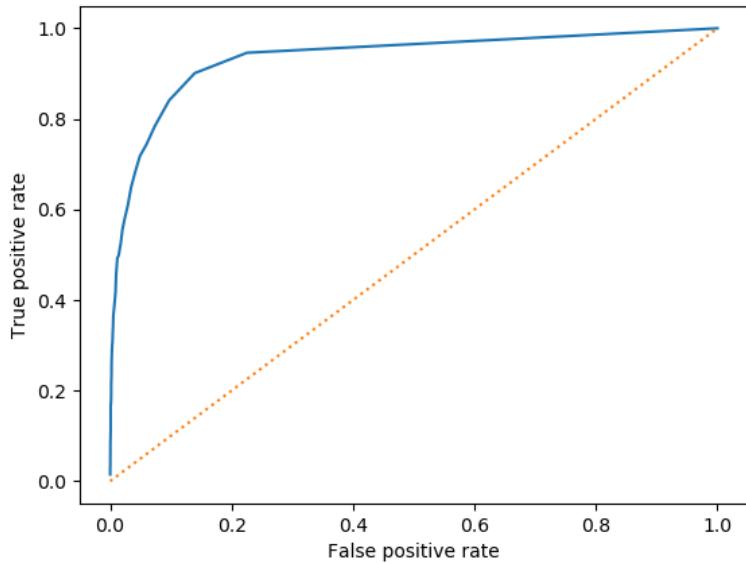


Figure 44: A ROC curve for the LDA classifier on the `Default` data. It traces two types of error as we vary the threshold value for the posterior probability of default. The actual thresholds are not shown. The true positive rate is the sensitivity: the fraction of defaulters that are correctly identified using a given threshold value. The false positive rate is the fraction of non-defaulters we incorrectly specify as defaulters, using the same threshold value. The ideal ROC curve hugs the top left corner, indicating a high true positive rate and a low false positive rate. The dotted line represents the “no information” classifier; this is what we would expect if student status and credit card balance are not associated with the probability of default.

4.5 A Comparison of Classification Methods

Table 18 lists many of the popular performance measures that are used in this context.

Name	Definition	Synonyms
False Positive rate	FP / N	Type I error, $1 - \text{specificity}$
True Positive rate	TP / P	$1 - \text{Type II error}$, power, sensitivity, recall
Positive Predicted value	TP / P^*	Precision, $1 - \text{false discovery proportion}$
Negative Predicted value	TN / N^*	

Table 18: Important measures for classification and diagnostic testing, derived from quantities in table 17.

Figure 45 illustrates the performances of LDA and QDA in two scenarios. In the left-hand panel, the two Gaussian classes have a common correlation of 0.7 between X_1 and X_2 . As a result, the Bayes decision boundary is nearly linear and is accurately approximated by the LDA decision boundary. In contrast, the right-hand panel displays a situation in which the orange class has a correlation of 0.7 between the variables and blue class has a correlation of -0.7.

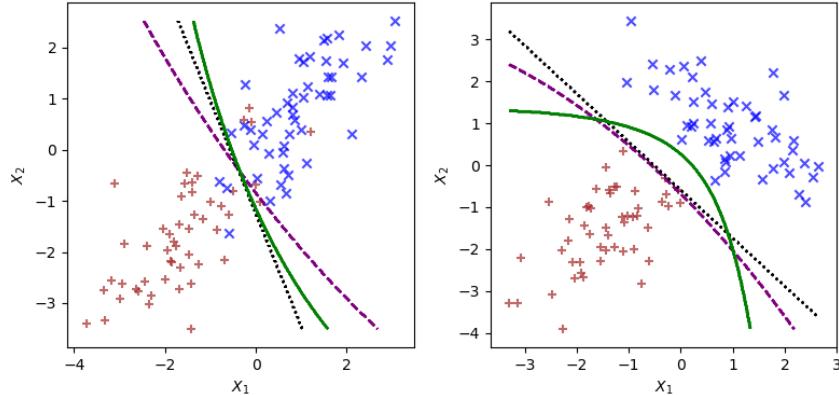


Figure 45: Left: The Bayes (purple dashed), LDA (black dotted), and QDA (green solid) decision boundaries for a two-class problem with $\Sigma_1 = \Sigma_2$. Right: Details are as given in the left-hand panel, except that $\Sigma_1 \neq \Sigma_2$.

4.5 A Comparison of Classification Methods

Figure 46 illustrates the performances of the four classification approaches (KNN, LDA, Logistic, and QDA) when Bayes decision boundary is linear.

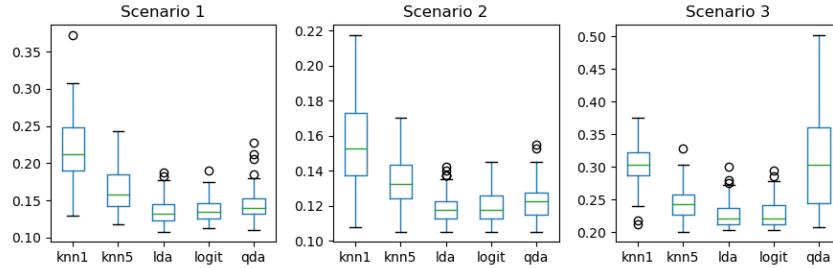


Figure 46: Boxplots of the test error rates for each of the linear scenarios described in the main text.

4.6 Lab: Logistic Regression, LDA, QDA, and KNN

4.6.1 The Stock Market Data

We will begin by examining some numerical and graphical summaries of the Smarket data, which is part of the ISLR library.

```
from statsmodels import datasets
import pandas as pd

smarket = datasets.get_rdataset('Smarket', 'ISLR').data

print(smarket.columns)
print('-----')
print(smarket.shape)
print('-----')
print(smarket.describe())
print('-----')
print(smarket.iloc[:, 1:8].corr())
print('-----')
smarket.boxplot(column='Volume', by='Year', grid=False)
```

```
Index(['Year', 'Lag1', 'Lag2', 'Lag3', 'Lag4', 'Lag5', 'Volume', 'Today',
       'Direction'],
      dtype='object')
-----
```

```
(1250, 9)
-----
```

	Year	Lag1	...	Volume	Today
count	1250.000000	1250.000000	...	1250.000000	1250.000000
mean	2003.016000	0.003834	...	1.478305	0.003138

4.6 Lab: Logistic Regression, LDA, QDA, and KNN

```
      std      1.409018    1.136299    ...      0.360357    1.136334  
      min     2001.000000   -4.922000    ...      0.356070   -4.922000  
      25%    2002.000000   -0.639500    ...      1.257400   -0.639500  
      50%    2003.000000    0.039000    ...      1.422950    0.038500  
      75%    2004.000000    0.596750    ...      1.641675    0.596750  
      max     2005.000000    5.733000    ...      3.152470    5.733000  
  
[8 rows x 8 columns]  
-----  
      Lag1      Lag2      Lag3      Lag4      Lag5      Volume      Today  
Lag1    1.000000  -0.026294  -0.010803  -0.002986  -0.005675  0.040910  -0.026155  
Lag2   -0.026294   1.000000  -0.025897  -0.010854  -0.003558  -0.043383  -0.010250  
Lag3   -0.010803  -0.025897   1.000000  -0.024051  -0.018808  -0.041824  -0.002448  
Lag4   -0.002986  -0.010854  -0.024051   1.000000  -0.027084  -0.048414  -0.006900  
Lag5   -0.005675  -0.003558  -0.018808  -0.027084   1.000000  -0.022002  -0.034860  
Volume  0.040910  -0.043383  -0.041824  -0.048414  -0.022002   1.000000  0.014592  
Today   -0.026155  -0.010250  -0.002448  -0.006900  -0.034860   0.014592  1.000000  
-----
```

4.6.2 Logistic Regression

Next, we will fit a logistic regression model to predict `Direction` using `Lag1` through `Lag5` and `Volume`.

```
from statsmodels import datasets  
import statsmodels.formula.api as smf  
import numpy as np  
import pandas as pd  
  
smarket = datasets.get_rdataset('Smarket', 'ISLR').data  
smarket['direction_cat'] = smarket['Direction'].apply(lambda x:  
    int(x=='Up'))  
  
logit_model = smf.logit(  
    formula='direction_cat ~ Lag1 + Lag2 + Lag3 + Lag4 + Lag5 +  
    Volume',  
    data=smarket)  
logit_fit = logit_model.fit()  
  
print(logit_fit.summary2())  
print('-----')  
print(dir(logit_fit))          # see what information is  
                             # available from fit  
print('-----')  
print(logit_fit.params)        # coefficients estimates
```

4.6 Lab: Logistic Regression, LDA, QDA, and KNN

```

print('-----')
print(logit_fit.summary2().tables[1]) # coefficients estimates,
    std error, and z
print('-----')
print(logit_fit.summary2().tables[1].iloc[:,3]) # P > |z|
    column only
print('-----')
print(logit_fit.predict()[:10]) # probabilities for training
    data
print('-----')
smarket['predict_direction'] = np.vectorize(
    lambda x: 'Up' if x > 0.5 else 'Down')(logit_fit.predict())
print(pd.crosstab(smarket['predict_direction'], smarket['
    Direction']))

```

Optimization terminated successfully.

Current function value: 0.691034

Iterations 4

Results: Logit

```
=====
Model:           Logit          Pseudo R-squared: 0.002
Dependent Variable: direction_cat      AIC:            1741.5841
Date:             2019-06-06 18:56  BIC:            1777.5004
No. Observations: 1250          Log-Likelihood:   -863.79
Df Model:          6            LL-Null:         -865.59
Df Residuals:     1243          LLR p-value:     0.73187
Converged:        1.0000        Scale:           1.0000
No. Iterations:   4.0000
=====
```

	Coef.	Std.Err.	z	P> z	[0.025	0.975]
Intercept	-0.1260	0.2407	-0.5234	0.6007	-0.5978	0.3458
Lag1	-0.0731	0.0502	-1.4566	0.1452	-0.1714	0.0253
Lag2	-0.0423	0.0501	-0.8446	0.3984	-0.1405	0.0559
Lag3	0.0111	0.0499	0.2220	0.8243	-0.0868	0.1090
Lag4	0.0094	0.0500	0.1873	0.8514	-0.0886	0.1073
Lag5	0.0103	0.0495	0.2083	0.8350	-0.0867	0.1074
Volume	0.1354	0.1584	0.8553	0.3924	-0.1749	0.4458

```
-----
['__class__', '__delattr__', '__dict__', '__dir__', '__doc__', '__eq__',

```

```

'__format__', '__ge__', '__getattribute__', '__getstate__', '__gt__',
'__hash__', '__init__', '__init_subclass__', '__le__', '__lt__',
'__module__', '__ne__', '__new__', '__reduce__', '__reduce_ex__', '__repr__',
'__setattr__', '__sizeof__', '__str__', '__subclasshook__', '__weakref__',
'_cache', '_data_attr', '_get_endog_name', '_get_robustcov_results', 'aic',
'bic', 'bse', 'conf_int', 'cov_kwds', 'cov_params', 'cov_type', 'df_model',
'df_resid', 'f_test', 'fittedvalues', 'get_margeff', 'initialize',
'k_constant', 'llf', 'llnull', 'llr', 'llr_pvalue', 'load', 'mle_retvals',
'mle_settings', 'model', 'nobs', 'normalized_cov_params', 'params',
'pred_table', 'predict', 'prsqared', 'pvalues', 'remove_data', 'resid_dev',
'resid_generalized', 'resid_pearson', 'resid_response', 'save', 'scale',
'set_null_options', 'summary', 'summary2', 't_test', 't_test_pairwise',
'tvalues', 'use_t', 'wald_test', 'wald_test_terms']
-----
Intercept -0.126000
Lag1 -0.073074
Lag2 -0.042301
Lag3 0.011085
Lag4 0.009359
Lag5 0.010313
Volume 0.135441
dtype: float64
-----
            Coef.  Std.Err.      z   P>|z|      [0.025      0.975]
Intercept -0.126000 0.240737 -0.523394 0.600700 -0.597836 0.345836
Lag1      -0.073074 0.050168 -1.456583 0.145232 -0.171401 0.025254
Lag2      -0.042301 0.050086 -0.844568 0.398352 -0.140469 0.055866
Lag3       0.011085 0.049939  0.221974 0.824334 -0.086793 0.108963
Lag4       0.009359 0.049974  0.187275 0.851445 -0.088589 0.107307
Lag5       0.010313 0.049512  0.208296 0.834998 -0.086728 0.107354
Volume    0.135441 0.158361  0.855266 0.392404 -0.174941 0.445822
-----
Intercept 0.600700
Lag1      0.145232
Lag2      0.398352
Lag3      0.824334
Lag4      0.851445
Lag5      0.834998
Volume   0.392404
Name: P>|z|, dtype: float64

```

```
-----
[0.50708413 0.48146788 0.48113883 0.51522236 0.51078116 0.50695646
 0.49265087 0.50922916 0.51761353 0.48883778]
-----
Direction      Down   Up
predict_direction
Down           145  141
Up             457  507
```

We now use data for years 2001 through 2004 to train the model, then use data for year 2005 to test the model.

```
from statsmodels import datasets
import statsmodels.formula.api as smf
import pandas as pd
import numpy as np

smarket = datasets.get_rdataset('Smarket', 'ISLR').data
smarket['direction_cat'] = smarket['Direction'].apply(lambda x:
    int(x == 'Up'))
smarket_train = smarket.loc[smarket['Year'] < 2005]
smarket_test = smarket.loc[smarket['Year'] == 2005].copy()

logit_model = smf.logit(
    formula='direction_cat ~ Lag1 + Lag2 + Lag3 + Lag4 + Lag5 +
    Volume',
    data=smarket_train)
logit_fit = logit_model.fit()

prob_up_test = logit_fit.predict(smarket_test)
smarket_test.loc[:, 'direction_predict'] = np.vectorize(
    lambda x: 'Up' if x > 0.5 else 'Down')(prob_up_test)

confusion_test = \
    pd.crosstab(smarket_test['direction_predict'], smarket_test
        ['Direction'])
print(confusion_test)
print('-----')
print(np.mean(np.mean(smarket_test['direction_predict']) ==
    smarket_test['Direction'])))
print('-----')

# Refit logistic regression with only Lag1 and Lag2
logit_model = smf.logit('direction_cat ~ Lag1 + Lag2', data=
    smarket_train)
logit_fit = logit_model.fit()
prob_up_test = logit_fit.predict(smarket_test)
```

```
smarket_test['direction_pred_2var'] = np.vectorize(
    lambda x: 'Up' if x > 0.5 else 'Down')(prob_up_test)

print(pd.crosstab(smarket_test['direction_pred_2var'],
                  smarket_test['Direction']))
print('-----')

print(np.mean(smarket_test['direction_pred_2var'] ==
              smarket_test['Direction']))
print('-----')

print(logit_fit.predict(exog=dict(Lag1=[1.2, 1.5], Lag2
                                   =[1.1, -0.8])))

Optimization terminated successfully.
    Current function value: 0.691936
    Iterations 4
    Direction      Down   Up
    direction_predict
    Down           77   97
    Up             34   44
    -----
    0.4801587301587302
    -----
    Optimization terminated successfully.
    Current function value: 0.692085
    Iterations 3
    Direction      Down   Up
    direction_pred_2var
    Down           35   35
    Up             76  106
    -----
    0.5595238095238095
    -----
    0      0.479146
    1      0.496094
    dtype: float64
```

4.6.3 Linear Discriminant Analysis

Now we will perform LDA on Smarket data.

```
from sklearn.discriminant_analysis import
    LinearDiscriminantAnalysis as LDA
from statsmodels import datasets
import pandas as pd
import numpy as np

smarket = datasets.get_rdataset('Smarket', 'ISLR').data
smarket_train = smarket.loc[smarket['Year'] < 2005]
smarket_test = smarket.loc[smarket['Year'] == 2005].copy()

lda_model = LDA()
lda_fit = lda_model.fit(smarket_train[['Lag1', 'Lag2']],
    smarket_train['Direction'])

print(lda_fit.priors_)                      # Prior probabilities of groups
print('-----')
print(lda_fit.means_)                       # Group means
print('-----')
print(lda_fit.scalings_)                     # Coefficients of linear
                                              discriminants
print('-----')
lda_predict_2005 = lda_fit.predict(smarket_test[['Lag1', 'Lag2']])
print(pd.crosstab(lda_predict_2005, smarket_test['Direction']))
print('-----')
print(np.mean(lda_predict_2005 == smarket_test['Direction']))
print('-----')
lda_predict_prob2005 = lda_fit.predict_proba(smarket_test[['
    Lag1', 'Lag2']])
print(np.sum(lda_predict_prob2005[:,0] >= 0.5))
print(np.sum(lda_predict_prob2005[:,0] < 0.5))
```

```
[0.49198397 0.50801603]
-----
[[ 0.04279022  0.03389409]
 [-0.03954635 -0.03132544]]
-----
[[-0.64201904]
 [-0.51352928]]
-----
Direction  Down     Up
row_0
Down        35     35
Up          76   106
-----
```

```
0.5595238095238095
```

```
-----
```

```
70
```

```
182
```

4.6.4 Quadratic Discriminant Analysis

We will now fit a QDA model to the Smarket data.

```
from statsmodels import datasets
from sklearn.discriminant_analysis import
    QuadraticDiscriminantAnalysis as QDA
import pandas as pd
import numpy as np

smarket = datasets.get_rdataset('Smarket', 'ISLR').data
smarket_train = smarket.loc[smarket['Year'] < 2005]
smarket_test = smarket.loc[smarket['Year'] == 2005].copy()

qdf = QDA()
qdf.fit(smarket_train[['Lag1', 'Lag2']], smarket_train['
    Direction'])

print(qdf.priors_)                      # Prior probabilities of groups
print('-----')
print(qdf.means_)                      # Group means
print('-----')
predict_direction2005 = qdf.predict(smarket_test[['Lag1', 'Lag2
   ']])
print(pd.crosstab(predict_direction2005, smarket_test['
    Direction']))
print('-----')
print(np.mean(predict_direction2005 == smarket_test['Direction'
    ]))
```

```
[0.49198397 0.50801603]
```

```
-----
```

```
[[ 0.04279022  0.03389409]
 [-0.03954635 -0.03132544]]
```

```
-----
```

Direction	Down	Up
row_0		
Down	30	20
Up	81	121

```
-----
```

0.5992063492063492

4.6.5 K-Nearest Neighbors

We will now perform KNN, also on the Smarket data.

```
from statsmodels import datasets
from sklearn.neighbors import KNeighborsClassifier
import pandas as pd
import numpy as np

smarket = datasets.get_rdataset('Smarket', 'ISLR').data
smarket_train = smarket.loc[smarket['Year'] < 2005]
smarket_test = smarket.loc[smarket['Year'] == 2005].copy()

knn1 = KNeighborsClassifier(n_neighbors=1)
knn1.fit(smarket_train[['Lag1', 'Lag2']], smarket_train['Direction'])
smarket_test['predict_dir_knn1'] = knn1.predict(smarket_test[['Lag1', 'Lag2']])
print(pd.crosstab(smarket_test['predict_dir_knn1'],
                   smarket_test['Direction']))
print('-----')
print(np.mean(smarket_test['predict_dir_knn1'] == smarket_test['Direction']))
print('-----')

knn3 = KNeighborsClassifier(n_neighbors=3)
knn3.fit(smarket_train[['Lag1', 'Lag2']], smarket_train['Direction'])
smarket_test['predict_dir_knn3'] = knn3.predict(smarket_test[['Lag1', 'Lag2']])
print(pd.crosstab(smarket_test['predict_dir_knn3'],
                   smarket_test['Direction']))
print('-----')
print(np.mean(smarket_test['predict_dir_knn3'] == smarket_test['Direction']))
```

Direction	Down	Up
predict_dir_knn1		
Down	43	58
Up	68	83

0.5		

Direction	Down	Up

```
predict_dir_knn3
Down           48  55
Up            63  86
-----
0.5317460317460317
```

4.6.6 An Application to Caravan Insurance Data

Finally, we will apply the KNN approach to the `Caravan` data set in the `ISLR` library.

```
from statsmodels import datasets
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
import pandas as pd
import numpy as np

caravan = datasets.get_rdataset('Caravan', 'ISLR').data
print(caravan['Purchase'].value_counts())
print('-----')

caravan_scale = caravan.iloc[:, :-1]
caravan_scale = (caravan_scale - caravan_scale.mean()) /
    caravan_scale.std()

caravan_test = caravan_scale.iloc[:1000]
purchase_test = caravan.iloc[:1000]['Purchase']

caravan_train = caravan_scale.iloc[1000:]
purchase_train = caravan.iloc[1000:]['Purchase']

# Fit KNN with 1, 3, and 5 neighbors
knn1 = KNeighborsClassifier(n_neighbors=1)
knn1.fit(caravan_train, purchase_train)
purchase_predict_knn1 = knn1.predict(caravan_test)

print(np.mean(purchase_test != purchase_predict_knn1))
print('-----')
print(np.mean(purchase_test == 'Yes'))
print('-----')
print(pd.crosstab(purchase_predict_knn1, purchase_test))
print('-----')

knn3 = KNeighborsClassifier(n_neighbors=3)
knn3.fit(caravan_train, purchase_train)
purchase_predict_knn3 = knn3.predict(caravan_test)

print(np.mean(purchase_test != purchase_predict_knn3))
```

4.6 Lab: Logistic Regression, LDA, QDA, and KNN

```
print('-----')
print(np.mean(purchase_test == 'Yes'))
print('-----')
print(pd.crosstab(purchase_predict_knn3, purchase_test))
print('-----')

knn5 = KNeighborsClassifier(n_neighbors=5)
knn5.fit(caravan_train, purchase_train)
purchase_predict_knn5 = knn5.predict(caravan_test)

print(np.mean(purchase_test != purchase_predict_knn5))
print('-----')
print(np.mean(purchase_test == 'Yes'))
print('-----')
print(pd.crosstab(purchase_predict_knn5, purchase_test))
print('-----')

# Now fit logistic regression
logit_model = LogisticRegression(solver='lbfgs', max_iter=1000)
logit_model.fit(caravan_train, purchase_train)
purchase_predict_logit = logit_model.predict(caravan_test)
print(pd.crosstab(purchase_predict_logit, purchase_test))
print('-----')

purchase_predict_prob_logit = logit_model.predict_proba(
    caravan_test)
purchase_predict_logit_prob25 = np.vectorize(
    lambda x: 'Yes' if x > 0.25 else 'No')(
    purchase_predict_prob_logit[:,1])
print(pd.crosstab(purchase_predict_logit_prob25, purchase_test))
)
```

```
No      5474
Yes     348
Name: Purchase, dtype: int64
-----
0.118
-----
0.059
-----
Purchase   No  Yes
row_0
No        873   50
Yes       68    9
-----
```

```

0.074
-----
0.059
-----
Purchase  No  Yes
row_0
No        921   54
Yes       20    5
-----
0.066
-----
0.059
-----
Purchase  No  Yes
row_0
No        930   55
Yes       11    4
-----
Purchase  No  Yes
row_0
No        934   59
Yes       7     0
-----
Purchase  No  Yes
row_0
No        917   48
Yes       24   11

```

5 Resampling Methods

5.1 Cross-Validation

Figure 47 displays the *validation set approach*, a simple strategy to estimate the test error associated with fitting a particular statistical learning method on a set of observations.

In figure 48, the left-hand panel shows validation sample MSE as a function of polynomial order for which a regression model was fit on training sample. The two samples are obtained by randomly splitting `Auto` data set into two data sets of 196 observations each. The right-hand panel shows the results of repeating this exercise 10 times, each time with a different ran-

5.1 Cross-Validation

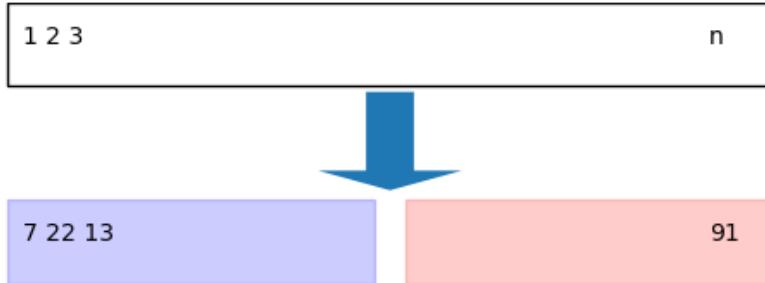


Figure 47: A schematic display of the validation set approach. A set of n observations are randomly split into a training set (shown in blue, containing observations 7, 22, and 13, among others) and a validation set (shown in red, and containing observation 91, among others). The statistical learning method is fit on the training set, and its performance is evaluated on the validation set.

dom split of the observations into training and validation sets. The model with a quadratic term has a lower MSE compared to the model with only a linear term. There is not much benefit from adding cubic or higher order polynomial terms in the regression model.

Figure 49 displays the Leave One Out Cross Validation (LOOCV) approach.

The left-hand panel of figure 50 shows test set MSE as a function of polynomial degree when LOOCV is used on the `Auto` data set. We fit linear regression models to predict `mpg` using polynomial functions of `horsepower`. The right-hand panel of figure 50 shows nine different 10-fold CV estimates for the `Auto` data set, each resulting from a different random split of the observations into ten folds.

Figure 51 illustrates the k -fold CV approach.

In figure 52, we plot the cross-validation estimates and true test error rates that result from fitting least squares polynomials to the simulated data sets illustrated in figures 9, 10, and 11 of chapter 2. In all three plots, the two cross validation errors are very similar.

Figure 53 shows Bayesian decision boundary (blue dashed line) and logistic regression decision boundary (black line) for 1- to 4-degree polynomials on X_1 and X_2 .

The left-hand panel of figure 54 displays in black 10-fold CV error rates that result from fitting ten logistic regression models to the data, using

5.1 Cross-Validation

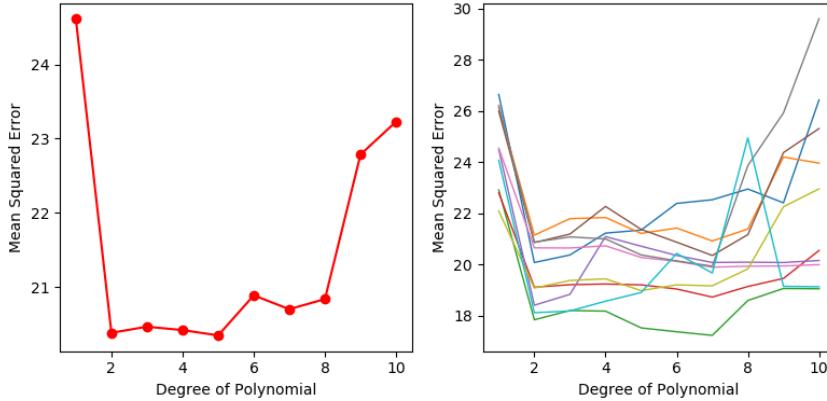


Figure 48: The validation set approach was used in the `Auto` data set in order to estimate the test error that results from predicting `mpg` using polynomial functions of `horsepower`. Left: Validation error estimates for a single split into training and validation data sets. Right: The validation method was repeated ten times, each time using a different random split of the observations into a training set and a validation set. This illustrates the variability of the estimated test MSE that results from this approach.

polynomial functions of the predictors up to tenth order. The true test errors are shown in red, and the training errors are shown in blue. The training error tends to decrease as the flexibility of the fit increases. The test error is higher than training error. The 10-fold CV error rate is a close approximation to the test error rate.

The right-hand panel of figure 54 displays the same three curves using the KNN approach for classification, as a function of the value of K (the number of neighbors used in the KNN classifier). Again, the training error rate declines as the method becomes more flexible, and so we see that the training error rate cannot be used to select the optimal value of K .

5.1 Cross-Validation

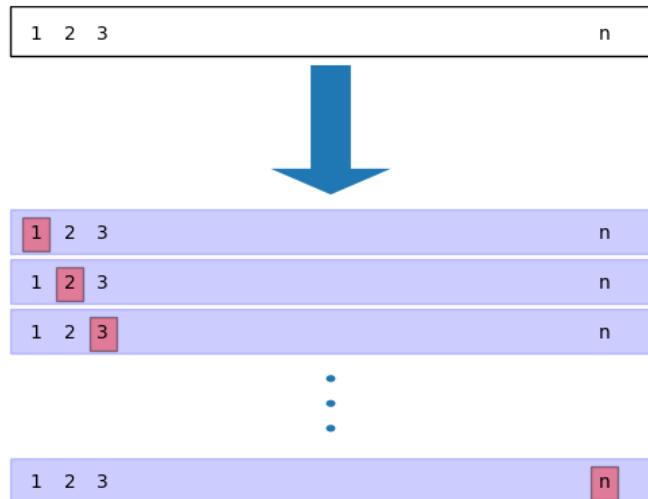


Figure 49: A schematic display of LOOCV. A set of n data points is repeatedly split into a training set (shown in blue) containing all but one observation, and a validation set that contains only that observation (shown in red). The test error is then estimated by averaging the n resulting MSE's. The first training set contains all but observation 1, the second training set contains all but observation 2, and so on.

5.1 Cross-Validation

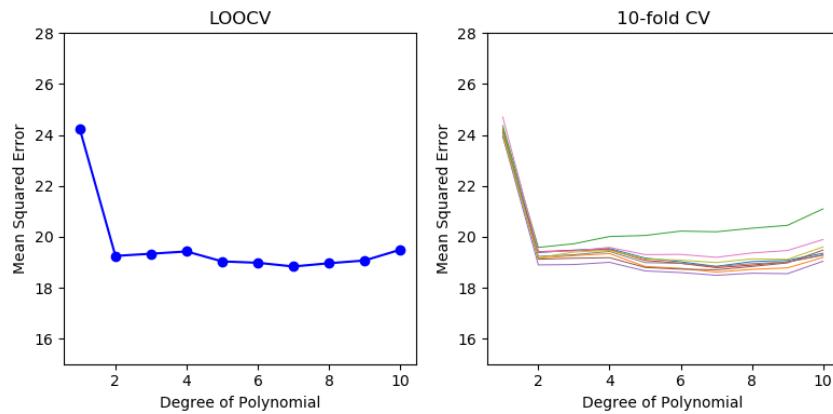


Figure 50: Cross-validation was used in the `Auto` data set in order to estimate the test error that results from predicting `mpg` using polynomial functions of `horsepower`. Left: The LOOCV error curve. Right: 10-fold CV was run nine separate times, each with a different random split of the data into ten parts. The figure shows the nine slightly different CV error curves.

5.1 Cross-Validation

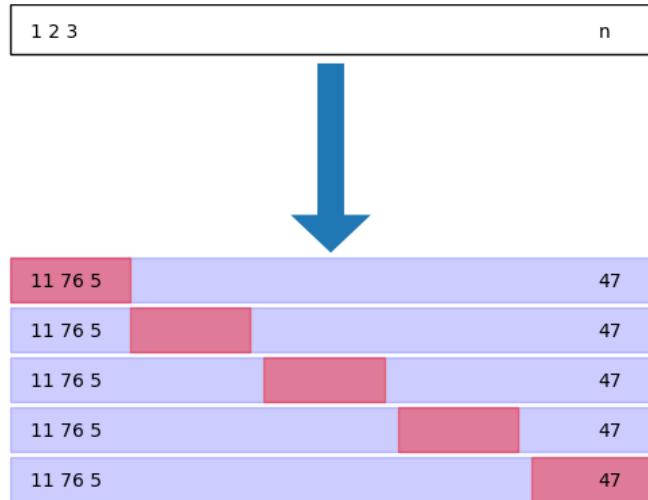


Figure 51: A schematic display of 5-fold CV. A set of n observations is randomly split into five non-overlapping groups. Each of these fifths acts as a validation set (shown in red), and the remainder as a training set (shown in blue). The test error is estimated by averaging the five resulting MSE estimates.

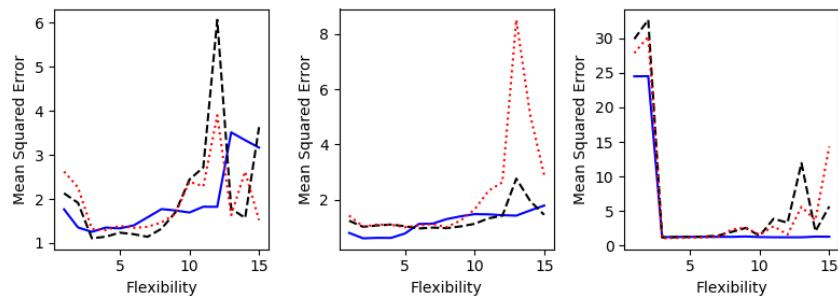


Figure 52: True and estimated test MSE for the simulated data sets in Figures 9 (left), 10 (center), and 11 (right). The true test MSE is shown in blue, the LOOCV estimate is shown in black dashed line, and the 10-fold CV estimate is shown in red dotted line.

5.1 Cross-Validation

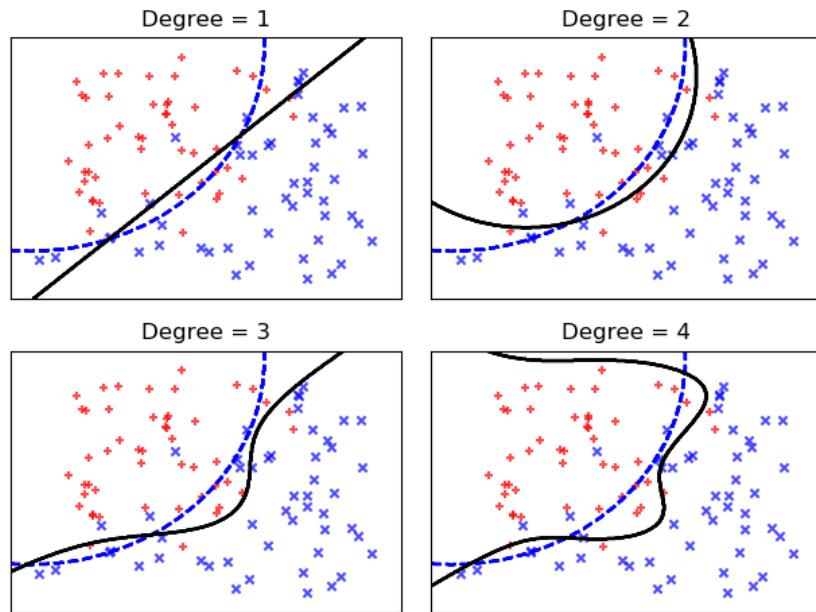


Figure 53: Logistic regression fits on the two-dimensional classification data displayed in figure 13. The Bayes decision boundary is represented using a blue dashed line. Estimated decision boundaries from linear, quadratic, cubic, and quartic (degrees 1-4) logistic regressions are displayed in black.

5.1 Cross-Validation

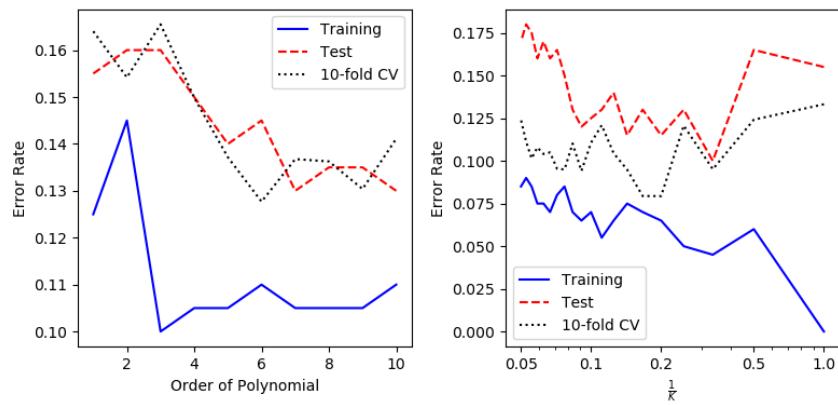


Figure 54: Test error (red), training error(blue), and 10-fold CV error (black) on the two-dimensional classification data displayed in 53. Left: Logistic regression using polynomial functions of the predictors. The order of the polynomials used is displayed on the x-axis. Right: The KNN classifier with different values of K , the number of neighbors used in the KNN classifier.

5.2 The Bootstrap

Figure 55 illustrates the approach for estimating α by repeated simulation of data. In each panel, we simulated 100 pairs of returns for the investments X and Y . We used these returns to estimate σ_X^2 , σ_Y^2 and σ_{XY} , which are then used to estimate α .

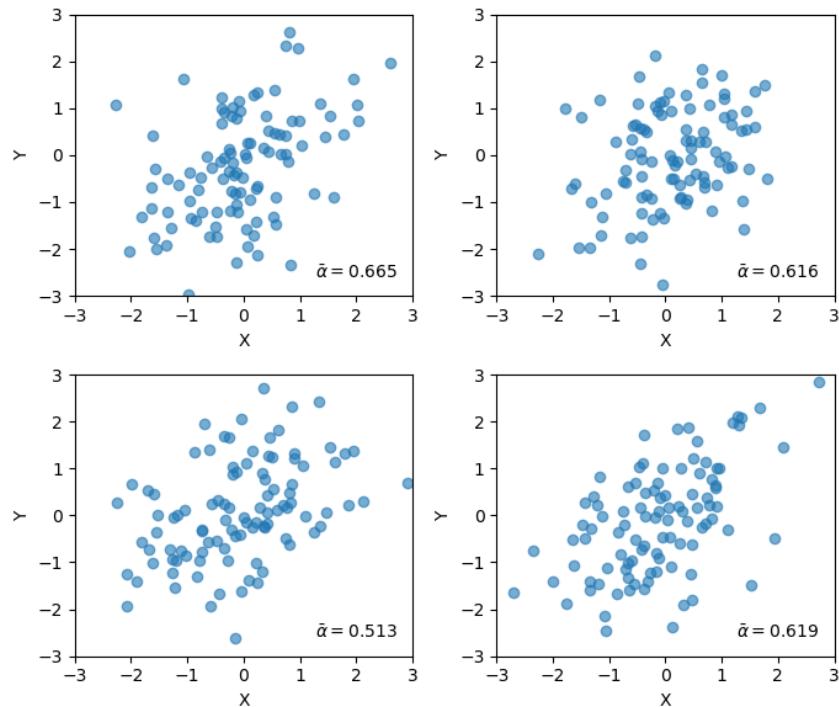


Figure 55: Each panel displays 100 simulated returns for investments X and Y . The resulting estimates of α are displayed in bottom right corner.

It is natural to wish to quantify the accuracy of our estimate of α . To estimate the standard deviation of $\hat{\alpha}$, we repeated the process of simulating 100 paired observations of X and Y , and estimating α 1000 times. We thereby obtain 1000 estimates of α , which we can call $\hat{\alpha}_1, \hat{\alpha}_2, \dots, \hat{\alpha}_{1000}$. The left-hand panel of figure 56 displays a histogram of the resulting estimates. The mean over all 1000 estimates for α is 0.599, which is very close to $\alpha = 0.6$. The standard deviation of the estimates is 0.08.

The bootstrap approach is illustrated in the center panel of figure 56, which displays a histogram of 1000 bootstrap estimates of α , each computed

using a distinct bootstrap data set. The panel was constructed on the basis of a single data set, and hence could be created using real data. The right-hand panel displays the information in the center and left panels in a different way, via boxplots of the estimates of α obtained by generating 1000 simulated data sets from the true population and using the bootstrap approach.

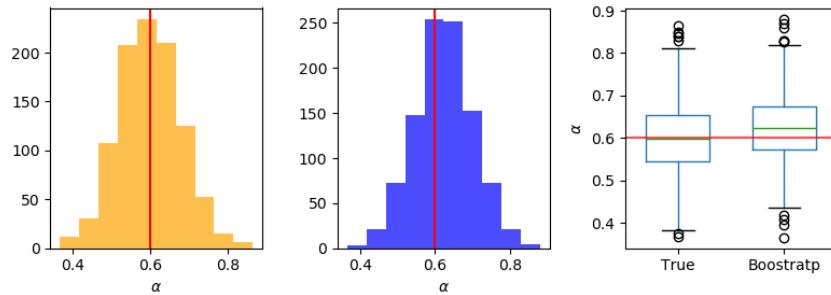


Figure 56: Left: A histogram of the estimates of α obtained by generating 1000 simulated data sets from the true population. Center: A histogram of the estimates of α obtained from 1000 bootstrap samples from a single data set. Right: The estimates of α displayed in the left and center panels are shown as boxplots. In each panel, the red line indicates the true value of α .

5.3 Lab: Cross-Validation and the Bootstrap

5.3.1 The Validation Set Approach

We use the function `choice` in `numpy.random` library to split the set of observations in `Auto` data set into two subsets of 196 observations. Then we fit regression models on the training data set and calculate validation error on the validation set.

These results show that a model that predicts `mpg` using a quadratic function of `horsepower` performs better than a model that predicts `mpg` using a linear function of horsepower. There is little evidence that a cubic function of `horsepower` is better than the quadratic function.

```

import numpy as np
from statsmodels import datasets
import statsmodels.formula.api as smf

auto = datasets.get_rdataset('Auto', 'ISLR').data
    
```

```
np.random.seed(911)
train_ind = np.random.choice(auto.shape[0], size=int(auto.shape[0]/2),
                             replace=False)
all_ind = np.arange(auto.shape[0])
test_ind = set(all_ind).difference(set(train_ind))
test_ind = list(test_ind)
auto_train = auto.iloc[train_ind]
auto_test = auto.iloc[test_ind]

# Fit first linear model
lm_model = smf.ols(formula='mpg ~ horsepower', data=auto_train)
lm_fit = lm_model.fit()
mse_train = np.sum((lm_fit.predict(auto_train) - auto_train['mpg']) ** 2) / \
            (auto_train.shape[0] - 2)
print(mse_train)
print(lm_fit.mse_resid)           # same value
print('-----')

mse_test = np.sum((lm_fit.predict(auto_test) - auto_test['mpg']) ** 2) / \
            (auto_test.shape[0] - 2)
print(mse_test)
print('-----')

# Fit quadratic model
lm_model2 = smf.ols('mpg ~ horsepower + I(horsepower ** 2)', data=auto_train)
lm_fit2 = lm_model2.fit()
mse_test2 = np.sum((lm_fit2.predict(auto_test) - auto_test['mpg']) ** 2) / \
            (auto_test.shape[0] - 3)
print(mse_test2)
print('-----')

# Fit third order polynomial model
lm_model3 = smf.ols('mpg ~ horsepower + I(horsepower ** 2) + I(horsepower ** 3)', data=auto_train)
lm_fit3 = lm_model3.fit()
mse_test3 = np.sum((lm_fit3.predict(auto_test) - auto_test['mpg']) ** 2) / \
            (auto_test.shape[0] - 4)
print(mse_test3)
```

23.61593457249045

23.615934572490445

```
-----
24.868027221207488
-----
20.701029881139203
-----
20.893010200297326
```

5.3.2 Leave-One-Out Cross-Validation

Using first principles, it is straightforward to implement leave-one-out cross-validation.

```
# mseLOOCV.py

import numpy as np
from statsmodels import datasets
import statsmodels.formula.api as smf

auto = datasets.get_rdataset('Auto', 'ISLR').data
all_ind = np.arange(auto.shape[0])

my_formula = 'mpg ~ horsepower'

mse_loocv = []
degree = []
for i_degree in range(1, 6):
    mse = []
    for i_obs in range(auto.shape[0]):
        # auto_train = auto.loc[all_ind != i_obs]
        auto_train = auto.drop(auto.index[i_obs])
        auto_test = auto.iloc[i_obs]
        lm_model = smf.ols(my_formula, data=auto_train)
        lm_fit = lm_model.fit()
        hp_predict = lm_fit.predict(
            exog=dict(horsepower=auto_test['horsepower']))
        mse.append((hp_predict - auto_test['mpg']) ** 2)

    mse_loocv.append(np.mean(mse))
    degree.append(i_degree)
    my_formula += ' + I(horsepower **' + str(i_degree + 1) + ')'
    ,

for i_degree, mse in zip(degree, mse_loocv):
    print('degree: ', i_degree, ', mse_loocv:', round(mse, 3))

import sys
sys.path.append('code/chap5/')
```

```
import mseLOOCV

---

  
degree: 1 , mse_loocv: 24.232  
degree: 2 , mse_loocv: 19.248  
degree: 3 , mse_loocv: 19.335  
degree: 4 , mse_loocv: 19.424  
degree: 5 , mse_loocv: 19.033
```

5.3.3 k-Fold Cross-Validation

Using first principles, it is straightforward to implement k -fold CV. Once again, we see little evidence that using cubic or higher order polynomial terms leads to lower test error than simply using a quadratic fit.

```
# mse_kFoldCV.py  
  
import numpy as np  
import statsmodels.formula.api as smf  
from statsmodels import datasets  
  
auto = datasets.get_rdataset('Auto', 'ISLR').data  
  
n_folds = 10  
max_degree = 10  
  
np.random.seed(911)  
fold_ind = np.random.choice(n_folds, auto.shape[0])  
all_ind = np.arange(auto.shape[0])  
degree = []  
mse_folds = {}  
  
my_formula = 'mpg ~ horsepower'  
for i_degree in range(1, max_degree + 1):  
    mse_folds[i_degree] = []  
    for i_fold in range(n_folds):  
        train_df = auto.loc[i_fold != fold_ind]  
        test_df = auto.loc[i_fold == fold_ind]  
        lm_model = smf.ols(my_formula, data=train_df)  
        lm_fit = lm_model.fit()  
        mse = np.mean((lm_fit.predict(test_df) - test_df['mpg']) **  
                     2)  
        mse_folds[i_degree].append(mse)  
  
    degree.append(i_degree)  
    my_formula += ' + I(horsepower ** ' + str(i_degree + 1) + ' )'
```

```
mse_degree = []
for i_degree in mse_folds.keys():
    mse_degree.append(np.mean(mse_folds[i_degree]))

for i_degree, mse_kfold in zip(degree, mse_degree):
    print('degree: ', i_degree, ', mse_kfold: ', round(
        mse_kfold, 3))



---


import sys
sys.path.append('cnodee/chap5/')

import mse_kFoldCV


---


degree:  1 , mse_kfold:  24.213
degree:  2 , mse_kfold:  19.378
degree:  3 , mse_kfold:  19.477
degree:  4 , mse_kfold:  19.538
degree:  5 , mse_kfold:  19.166
degree:  6 , mse_kfold:  19.183
degree:  7 , mse_kfold:  19.157
degree:  8 , mse_kfold:  23.247
degree:  9 , mse_kfold:  23.258
degree:  10 , mse_kfold:  65.251
```

5.3.4 The Bootstrap

1. Estimating the Accuracy of a Statistic of Interest We will first write a function that takes two inputs, data and index, and calculates the desired statistic α . Then we will repeatedly call this function and store the estimates of α .

```
# alphaBootstrap.py

import numpy as np
import pandas as pd
# from statsmodels import datasets
import statsmodels.formula.api as smf

def alphaEst(returns_df, row_index):
    '''Assumes returns_df is a return dataframe with two
       columns of stock returns,
       row_index is a list of row indexes to be used in
       calculation.
```

```
    Returns alpha estimate using subset of data defined by
    row_index.'''
```

```
    cov_xy = np.cov(returns_df.iloc[row_index], rowvar=
                     False)
    return (cov_xy[1, 1] - cov_xy[0, 1]) / \
(cov_xy[0, 0] + cov_xy[1, 1] - 2 * cov_xy[0, 1])
```

```
def bootStrap(my_df, myFunc, sample_size, n_bootstrap,
all_res=False):
    ''' Assumes my_df is a dataframe and myFunc is a
        function that can
        estimate a statistic on my_df. Estimate statistic
        n_bootstrap times,
        each with a sample of size sample_size.
        Return mean and standard error of statistic.'''
    my_stat = []
    for i in range(n_bootstrap):
        index = np.random.choice(my_df.shape[0], sample_size)
        my_stat.append(myFunc(my_df, index))

        if isinstance(my_stat[0], float):
            my_res = {'mean': np.mean(my_stat), 'std. error': np.std
                      (my_stat)}
        if all_res:
            my_res['stats'] = my_stat

    elif isinstance(my_stat[0], pd.core.series.Series):
        my_stat_dict = {}
        for ind in my_stat[0].index:
            my_stat_dict[ind] = []
        for i in range(len(my_stat)):
            for key in my_stat_dict.keys():
                my_stat_dict[key].append(my_stat[i][key])
        my_res = {}
        for key in my_stat_dict.keys():
            my_res[key] = {}
            my_res[key]['mean'] = np.mean(my_stat_dict[key])
            my_res[key]['std. error'] = np.std(my_stat_dict[key]
                                              [])
        if all_res:
            my_res['stats'] = my_stat

    return my_res
```

```
def autoDataCoef(auto_df, row_index):
    '''Assumes auto_df is a dataframe which includes 'mpg'
```

5.3 Lab: Cross-Validation and the Bootstrap

```
        and
'horsepower' columns. Fit a linear regression model
on auto_df.
Use row_index to create a subset of auto_df. Return
regression
coefficients estimated from subset of auto_df.''
lm_model = smf.ols('mpg ~ horsepower', data=auto_df.
    iloc[row_index])
lm_fit = lm_model.fit()
return lm_fit.params

def autoDataCoef2(auto_df, row_index):
    '''Assumes auto_df is a dataframe which has columns ,
       mpg' and
'horsepower'. Fit an OLS regression model with mpg as
       a
quadratic function of horsepower. Use subset of
       auto_df defined
by row_index. Return regression coefficient estimates
       .'''
    lm_model = smf.ols('mpg ~ horsepower + I(horsepower **
        2)',

                     data=auto_df.iloc[row_index])
    lm_fit = lm_model.fit()
    return lm_fit.params


---


from statsmodels import datasets
import numpy as np
import sys
sys.path.append('code/chap5/')
from alphaBootstrap import alphaEst, bootStrap

portfolio = datasets.get_rdataset('Portfolio', 'ISLR').
    data

np.random.seed(911)
alpha_boot = bootStrap(portfolio, alphaEst, sample_size
    =100, n_bootstrap=1000)
print(alpha_boot)


---


{'mean': 0.5753949845303641, 'std. error': 0.08938513622277834}
```

2. Estimating the Accuracy of a Linear Regression Model We now use bootstrap method to assess the variability of the estimates for β_0 and β_1 , the intercept and slope terms for the linear regression model that

5.3 Lab: Cross-Validation and the Bootstrap

uses `horsepower` to predict `mpg` in the `Auto` data set. We will compare the estimates obtained using the bootstrap to those obtained using the standard formulas for $SE(\hat{\beta}_0)$ and $SE(\hat{\beta}_1)$.

```
from statsmodels import datasets
import statsmodels.formula.api as smf
import numpy as np
import sys
sys.path.append('code/chap5/')
from alphaBootstrap import autoDataCoef, bootStrap

auto = datasets.get_rdataset('Auto', 'ISLR').data

np.random.seed(911)
mpg_hp_boot = bootStrap(auto, autoDataCoef, sample_size
=392, n_bootstrap=1000)
print('Bootstrap results:')
for key in mpg_hp_boot.keys():
    print(key, ':', mpg_hp_boot[key])
print('-----')

lm_model = smf.ols('mpg ~ horsepower', data=auto)
lm_fit = lm_model.fit()
print('Regression results:')
print(lm_fit.summary2().tables[1].iloc[:, :4])
```

Bootstrap results:

```
Intercept : {'mean': 39.94234375950751, 'std. error': 0.8748453071088308}
horsepower : {'mean': -0.15796112230552348, 'std. error': 0.007526082860287968}
-----
Regression results:
      Coef.  Std.Err.          t      P>|t|
Intercept  39.935861  0.717499  55.659841  1.220362e-187
horsepower -0.157845  0.006446 -24.489135  7.031989e-81
```

Finally, we compute the bootstrap standard error estimates and the standard linear regression estimates that result from fitting the quadratic model to the `Auto` data.

Bootstrap results:

```
Intercept : {'mean': 57.02549325815686, 'std. error': 2.012215071375403}
horsepower : {'mean': -0.46840037414346225, 'std. error': 0.03187991112044731}
I(horsepower ** 2) : {'mean': 0.0012391590913923556, 'std. error': 0.00011523595}
```

```
-----
Regression results:
            Coef.    Std.Err.      t      P>|t|
Intercept      56.900100  1.800427  31.603673  1.740911e-109
horsepower     -0.466190  0.031125 -14.978164  2.289429e-40
I(horsepower ** 2)  0.001231  0.000122  10.080093  2.196340e-21
```

6 Linear Model Selection and Regularization

6.1 Subset Selection

An application of best subset selection is shown in figure 57. Each plotted point corresponds to a least squares regression model fit using a different subset of the 10 predictors in the `Credit` data set. We have plotted the RSS and R^2 statistics for each model, as a function of the number of variables. The red curve connects the best models for each model size, according to RSS or R^2 . Initially, these quantities improve as the number of variables increases. However, from the three-variable model on, there is little improvement in RSS and R^2 when more predictors are included.

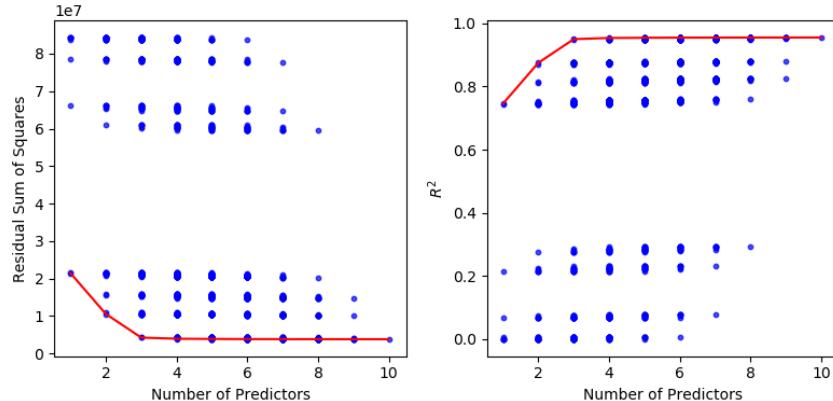


Figure 57: For each possible model containing a subset of the ten predictors in the `Credit` data set, the RSS and R^2 are displayed. The red frontier tracks the *best* model for a given number of predictors, according to RSS and R^2 .

Table 19 shows first four selected models for the best subset and forward subset selection on the `Credit` data set. Both best subset selection and forward stepwise selection choose `Rating` for the best one-variable model and

6.1 Subset Selection

then include **Income** and **Student** for the two- and three-variable models. However, best subset selection replaces **Rating** by **Cards** in the four-variable model. On the other hand forward stepwise selection must maintain **Rating** in its four-variable model.

Count	Best subset	Forward stepwise
1	Rating	Rating
2	Income, Rating	Rating, Income
3	Income, Rating, Student	Rating, Income, Student
4	Income, Limit, Cards, Student	Rating, Income, Student, Limit

Table 19: The first four selected models for best subset selection and forward stepwise selection on the **Credit** data set. The first three models are identical, but the fourth models differ.

Figure 58 displays C_p , BIC, and adjusted R^2 for the best model of each size produced by best subset selection on the **Credit** data set.

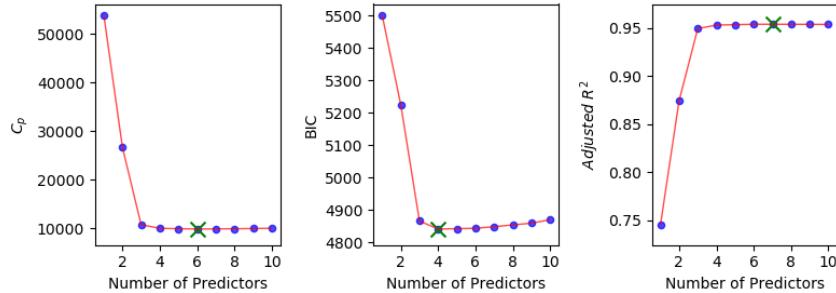


Figure 58: C_p , BIC, and adjusted R^2 are shown for the best models of each size for the **Credit** data set (the lower frontier in figure 57). C_p and BIC are estimates of test MSE. In the middle panel we see that the BIC estimate of test error shows an increase after four variables are selected. The other two plots are rather flat after four variables are selected.

Figure 59 displays, as a function of d , the BIC, validation set errors, and cross-validation errors on the **Credit** data set, for the best d -variable model. The validation errors were calculated by randomly selecting two-thirds of the observations as the training set, and the remainder as the validation set. The cross-validation errors were computed using $k = 10$ folds. Depending upon the choice of the random seed, validation errors may be minimized by six or seven predictors.

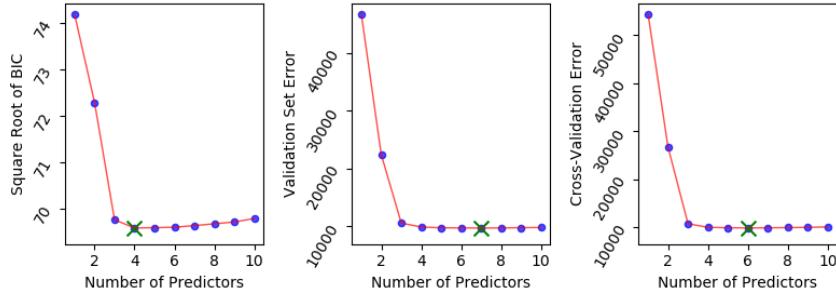


Figure 59: For the `Credit` data set, three quantities are displayed for the best model containing predictors, for d ranging from 1 to 10. The overall *best* model, based on each of these quantities, is shown as a green cross. Left: Square root of BIC. Center: Validation set errors. Right: Cross-validation errors.

6.2 Shrinkage Methods

In figure 60 the ridge regression coefficient estimates for the `Credit` data set are displayed. In the left-hand panel, each curve corresponds to the ridge regression coefficient estimate for one of the four important variables, plotted as a function of λ . At the extreme left side of the plot, λ is essentially zero, and so the corresponding ridge coefficients estimates are the same as the usual least square estimates. But as λ increases, the ridge coefficients shrink towards zero.

The right-hand panel of figure 60 displays the same ridge coefficient estimates as the left-hand panel. But instead of displaying λ on the x -axis, we now display $\|\hat{\beta}_\lambda^R\|_2/\|\hat{\beta}\|_2$, where $\hat{\beta}$ denotes the vector of least squares coefficient estimates. The notation $\|\beta\|_2$ denotes the ℓ_2 norm of a vector. This norm is defined as $\|\beta\|_2 = \sqrt{\sum_{j=1}^p \beta_j^2}$. It measures the distance of β from zero.

Ridge regression's advantage over least squares is rooted in *bias-variance tradeoff*. As λ increases, the flexibility of ridge regression fit decreases, leading to decreased variance but increased bias. We use a simulated data set with $p = 30$ features and $n = 50$ observations. Figure 61 shows the bias-variance tradeoff on this simulated data set.

In figure 62, coefficient plots are generated from applying the lasso to the `Credit` data set. When $\lambda = 0$, then the lasso simply gives the least squares fit. When λ becomes sufficiently large, the lasso gives the null model in which all coefficient estimates equal zero. However, in between these two extremes,

6.2 Shrinkage Methods

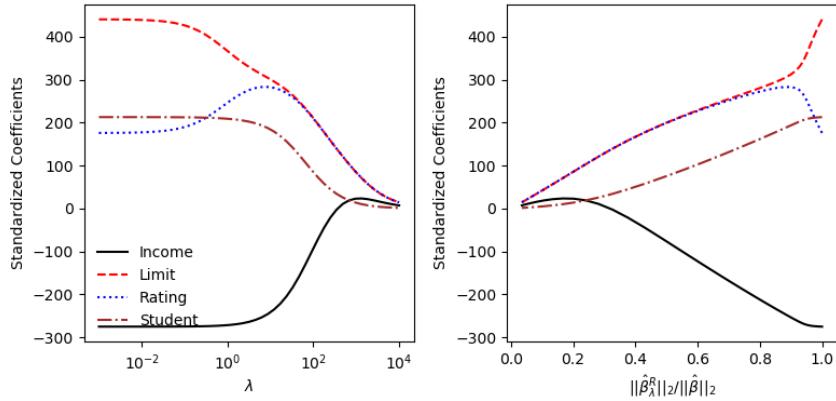


Figure 60: The standardized ridge regression coefficients are displayed for the `Credit` data set, as a function of λ and $\|\hat{\beta}_\lambda^R\|_2 / \|\hat{\beta}\|_2$.

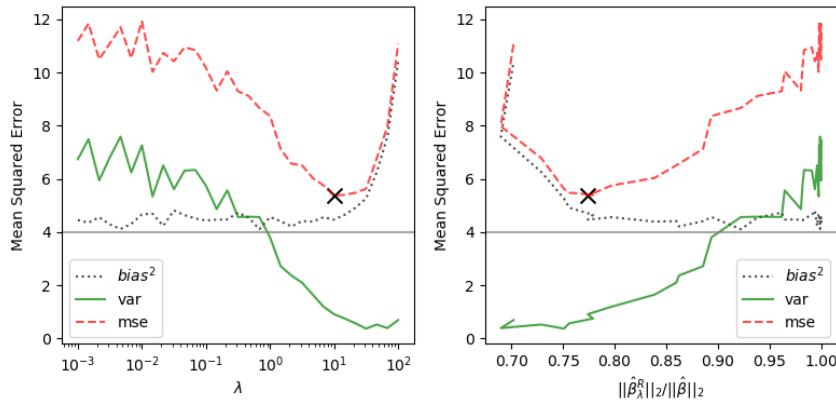


Figure 61: Squared bias, variance, and test mean squared error for the ridge regression predictions on a simulated data set, as a function of λ (left-hand panel) and $\|\hat{\beta}_\lambda^R\|_2 / \|\hat{\beta}\|_2$. The horizontal lines show the minimum possible MSE. The crosses show the ridge regression models for which the MSE is the smallest.

6.2 Shrinkage Methods

the ridge regression and the lasso regression models are quite different. In the right-hand panel of figure 62, as we move from left to right, at first the lasso model only contains the `Rating` predictor. Then `Student` and `Limit` enter the model, shortly followed by `Income`. Depending upon the value of λ , the lasso can produce a model involving any number of variables. In contrast, although the magnitude of the estimates will depend upon λ , ridge regression will always include all of the variables in the model.

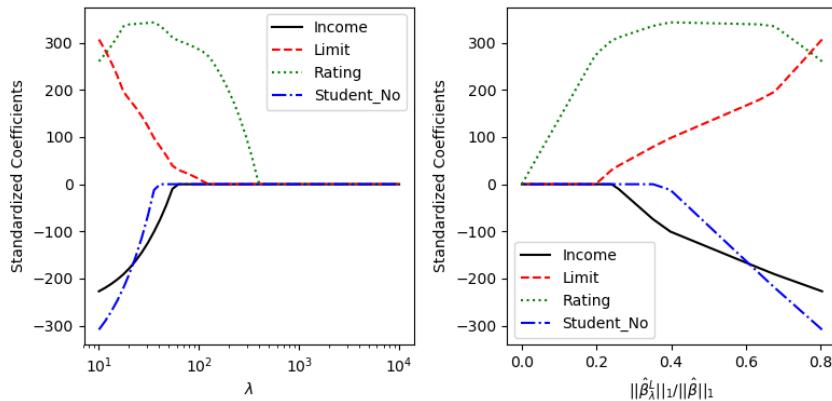


Figure 62: The standardized lasso coefficients on the `Credit` data set are shown as a function of λ and $\|\hat{\beta}_\lambda^L\|_1/\|\hat{\beta}\|_1$.

Figure 63 illustrates why lasso, unlike ridge regression, results in coefficient estimates that are exactly zero. In the left-hand panel, lasso coefficient constraint region is represented by solid blue diamond. In the right-hand panel, ridge regression coefficient constraint region is represented by solid blue circle. The ellipses centered around represent regions of constant RSS. As ellipses expand outward from the least squares coefficient estimates, RSS increases. Lasso and ridge regression coefficient estimates are given by the first point at which an ellipse touches the constraint region. Since lasso constraint has *corners* at each of the axes, the ellipse will often intersect the constraint region on an axis. When this occurs, one of the coefficients will equal zero. On the other hand, since ridge regression constraint has no sharp edges, the intersection will generally not occur on an axis. Therefore ridge regression coefficients will usually be non-zero.

Figure 64 displays the choice of λ that results from performing leave-one-out cross-validation on the ridge regression fits from the `Credit` data set. The dashed vertical lines indicate the selected value of λ .

6.2 Shrinkage Methods

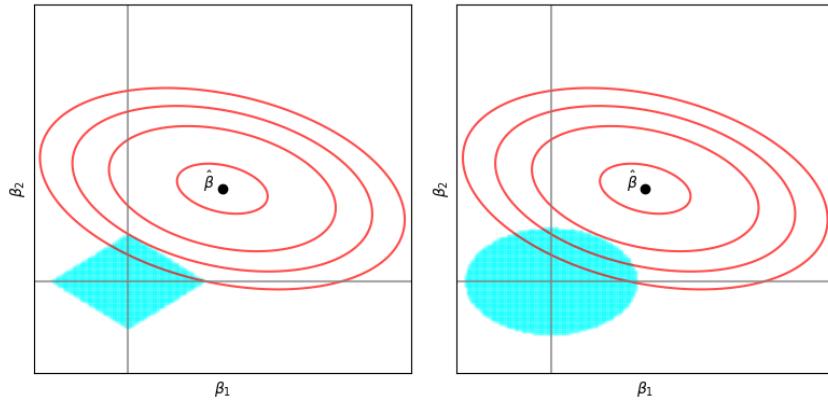


Figure 63: Contours of the error and constraint functions for the lasso (left) and ridge regression (right). The solid blue areas are constraint regions, $\|\beta_1\| + \|\beta_2\| \leq s$ and $\beta_1^2 + \beta_2^2 \leq s$, while the red ellipses are the contours of the RSS.

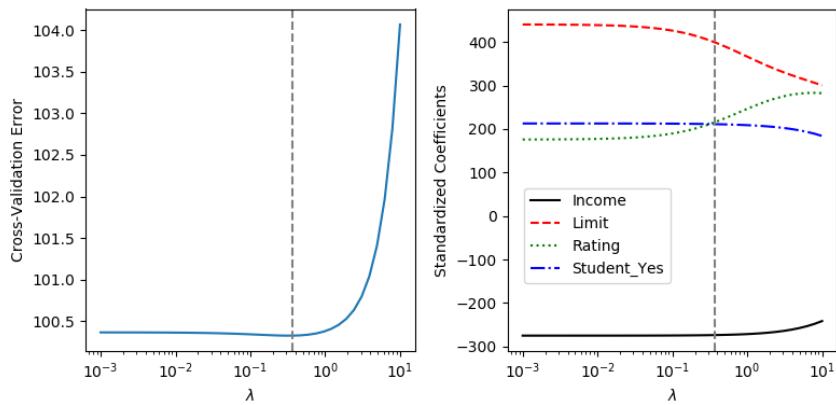


Figure 64: Left: For various values of λ , cross-validation errors that result from applying ridge regression to the Credit data set. Right: The coefficient estimates as a function of λ . The vertical dashed lines indicate the value of λ selected by cross-validation.

6.3 Dimension Reduction Methods

Figure 65 shows daily changes in 10-year Treasury note yield (10 YR) and 2-year Treasury note yield (2 YR) in year 2018. The green solid line represents the first principal component direction of the data. We can see by eye that this is the direction along which there is the greatest variability in the data.

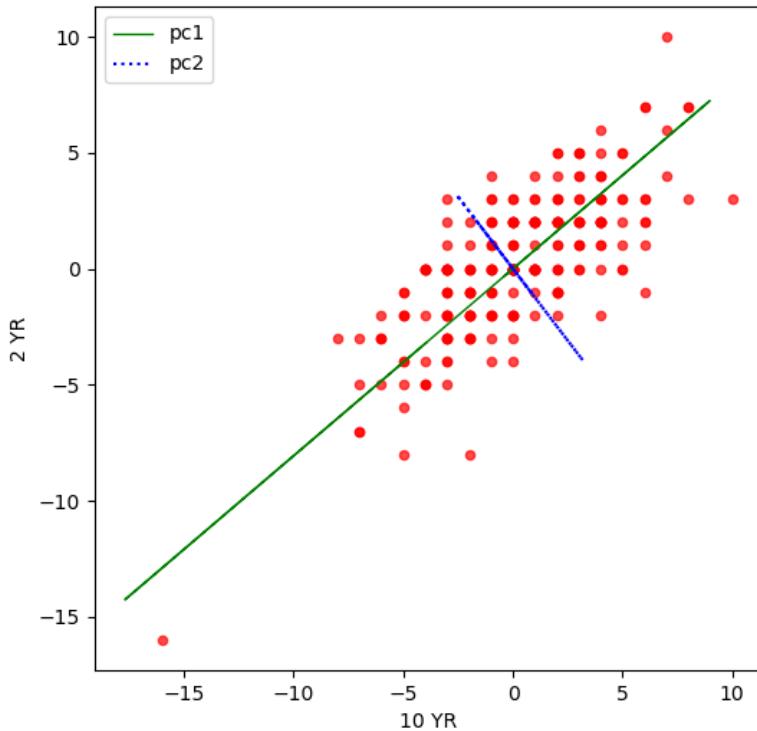


Figure 65: Daily changes in 10-year Treasury note yield (10 YR) and 2-year Treasury note yield (2 YR) in year 2018 are shown as red circles. The green solid line indicates the first principal component, and the blue dashed line indicates the second principal component.

In another interpretation of PCA, the first principal component vector defines the line that is *as close as possible* to the data. In figure 66, the left-hand panel shows the distances between data points and the first principal component. The first principal component has been chosen so that the

6.3 Dimension Reduction Methods

projected observations are *as close as possible* to the original observations.

In the right-hand panel of figure 66, the left-hand panel has been rotated so that the first principal component direction coincides with the x -axis.

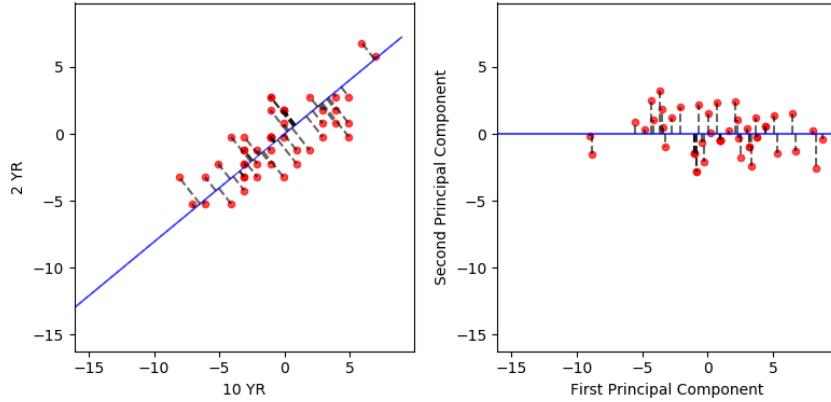


Figure 66: A subset of the Treasury yield data. Left: The first principal component direction is shown in blue. It is the dimension along which the data vary the most, and it also defines the line that is closest to all n of the observations. The distances from each observation to the principal component are represented in using black dashed line segments. Right: The left-hand panel has been rotated so that the first principal component direction coincides with the x-axis.

Figure 67 displays 10 YR and 2 YR versus first principal component scores. The plots show a strong relationship between the first principal component and the two features. In other words, the first principal component appears to capture most of the information contained in 10 YR and 2 YR.

Figure 68 displays 10 YR and 2 YR versus second principal component scores. The plots show a weak relationship between the second principal component and the two features. In other words, one only needs the first principal component to accurately represent 10 YR and 2 YR.

6.3 Dimension Reduction Methods

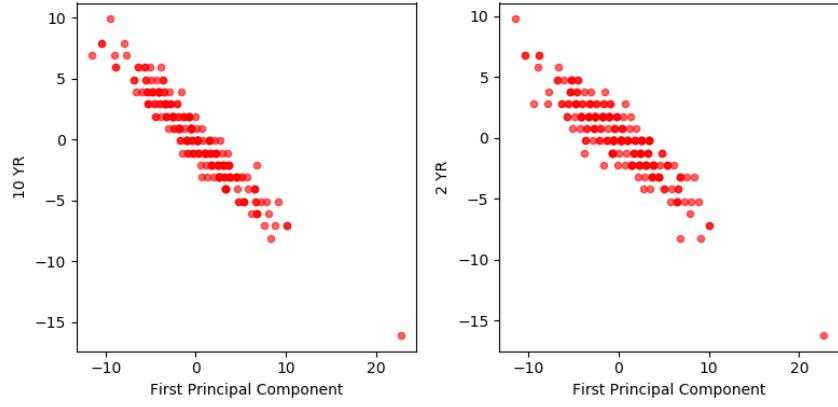


Figure 67: Plots of 10 YR and 2 YR versus first principal component scores. The relationships are strong.

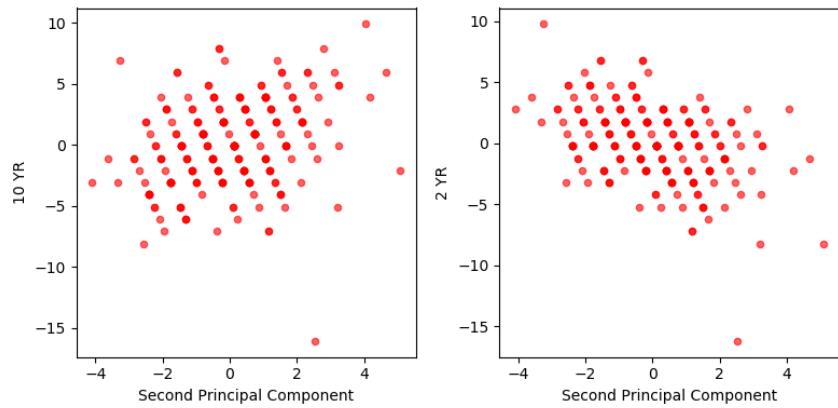


Figure 68: Plots of 10 YR and 2 YR versus second principal component scores. The relationships are weak.

6.4 Considerations in High Dimensions

Figure 69 shows $p = 1$ feature (plus an intercept) in two cases: when there are 20 observations (left-hand panel), and when there are only two observations (right-hand panel). When there are 20 observations, $n > p$ and the least squares regression line does not perfectly fit the data; instead, the regression line seeks to approximate the 20 observations as well as possible. On the other hand, when there are only two observations, then regardless of the values of those two observations, the regression line will fit the data exactly.

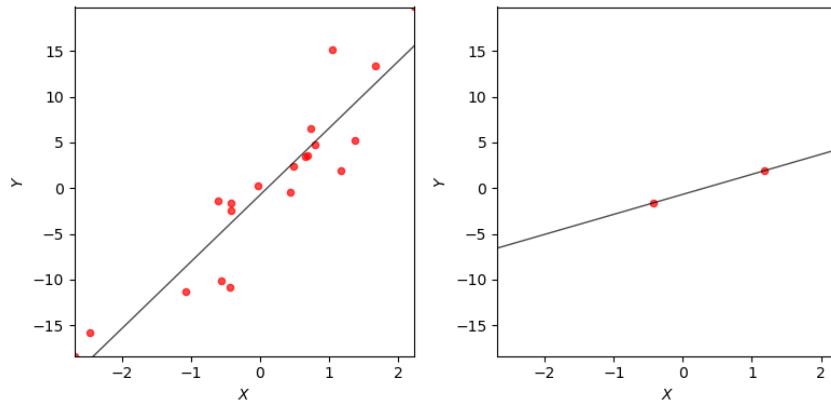


Figure 69: Left: Least squares regression in the low-dimensional setting. Right: Least squares regression with $n = 2$ observations and two parameters to be estimated (an intercept and a coefficient).

Figure 70 further illustrates the risk of carelessly applying least squares when the number of features p is large. Data were simulated with $n = 20$ observations, and regression was performed with between 1 and 20 features, each of which was completely unrelated to the response. As the number of features included increases, R^2 increases to 1, and correspondingly training set MSE decreases to zero. On the other hand, as the number features included increases, MSE on an *independent test set* becomes extremely large.

Figure 71 illustrates the performance of the lasso in a simple simulated example. There are $p = 20, 50$, or 2000 features, of which 20 are truly associated with the outcome.

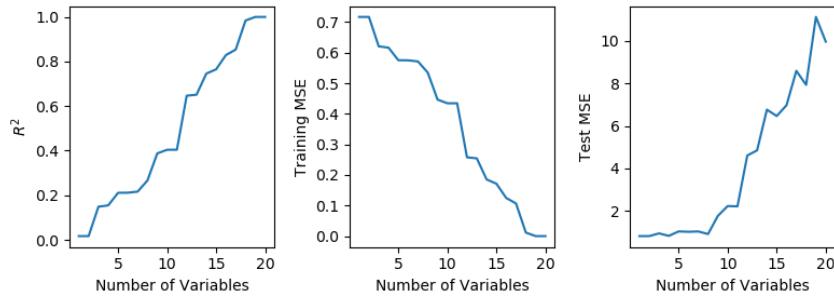


Figure 70: On a simulated example with $n = 20$ training observations, features that are completely unrelated to the outcome are added to the model. Left: As more features are included, the training R^2 increases to 1. Center: As more features are added, the training set MSE decreases to zero. Right: As more features are included, the test set MSE increases.

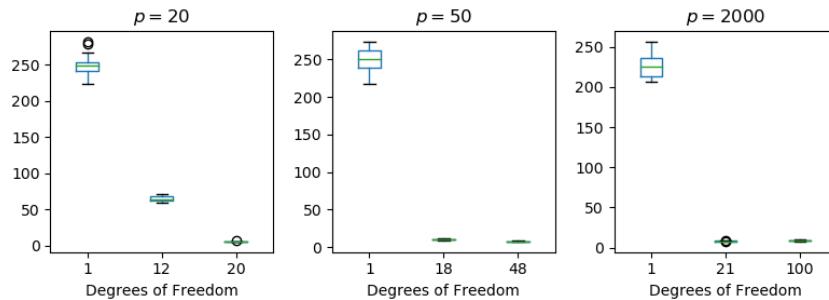


Figure 71: The lasso was performed with $n = 100$ observations and three values of p , the number of features. Of the p features, 20 were associated with the response. The boxplots show the test MSEs that result using four different values of the tuning parameter λ . For ease of interpretation, rather than reporting λ , the degrees of freedom are reported; for the lasso, this turns out to be simply the number of estimated non-zero coefficients. When $p = 20$, the lowest test MSE was obtained with the smallest amount of regularization. When $p = 50$, the lowest test MSE was achieved when there was a substantial amount of regularization. When $p = 2000$, we see results similar to $p = 50$, with very slight increase in test MSE with degrees of freedom.

6.5 Lab 1: Subset Selection Methods

6.5.1 Best Subset Selection

Here we apply the best subset selection approach to the `Hitters` data. We wish to predict a baseball player's `Salary` on the basis of various statistics associated with performance in the previous year.

We note that the `Salary` variable is missing for some of the players. The `dropna()` function in `pandas` module can be used to remove all the rows that have missing values in any variable.

It is straightforward to consider subsets of different sizes and, given a criterion, identify best model for each size. Program `subsetSelection.py` includes a function for this purpose. Using a given criterion, `bestModel` uses exhaustive enumeration to find the best model for a given size.

```
from statsmodels import datasets
# import pandas as pd
import numpy as np
import sys
sys.path.append('code/chap6/')
from subsetSelection import bestModel, C_p
from itertools import combinations
from operator import attrgetter
import matplotlib.pyplot as plt

hitters = datasets.get_rdataset('Hitters', 'ISLR').data
print(hitters.columns)
print('-----')
print(hitters.shape)
print('-----')
print(np.sum(hitters['Salary'].isna()))
print('-----')
hitters.dropna(inplace=True)
print(hitters.shape)
print('-----')

# Prepare inputs for allSubsets function
y_var = 'Salary'
x_vars = list(hitters.columns)
x_vars.remove(y_var)

# Select best model for a given subset size
# Use smallest RSS as the criterion to find best model
best_models = {}
for p in range(1, 7):
    best_models[p] = bestModel(y_var, x_vars, hitters,
                               subset_size=p,
```

6.5 Lab 1: Subset Selection Methods

```

        metric='ssr', metric_max=False)

for p in best_models.keys():
    print('Number of variables: ' + str(p))
    best_vars = list(best_models[p]['model_vars'])
    best_vars.sort()
    print(best_vars)
    print('-----')

# Print r-squared and adjusted r-squared
for p in best_models.keys():
    print('Num vars: ' + str(p) + ', R-squared: ' +
          str(round(best_models[p]['model'].rsquared, 3)) +
          ', adjusted R-squared: ' +
          str(round(best_models[p]['model'].rsquared_adj, 3)))

# Plot R-squared, adjusted R-squared, Cp, and BIC versus number
# of variables
fig = plt.figure(figsize=(8, 8))
ax1 = fig.add_subplot(221)
rsq = [best_models[k]['model'].rsquared for k in best_models.
       keys()]
ax1.plot(best_models.keys(), rsq)
ax1.set_ylabel(r'$R^2$')

ax2 = fig.add_subplot(222)
adj_rsq = [best_models[k]['model'].rsquared_adj for k in
           best_models.keys()]
ax2.plot(best_models.keys(), adj_rsq)
ax2.set_ylabel(r'Adjusted $R^2$')

ax3 = fig.add_subplot(223)
Cp = [C_p(best_models[k]['model']) for k in best_models.keys()]
ax3.plot(best_models.keys(), Cp)
ax3.set_ylabel(r'$C_p$')

ax4 = fig.add_subplot(224)
bic = [best_models[k]['model'].bic for k in best_models.keys()]
ax4.plot(best_models.keys(), bic)
ax4.set_ylabel('BIC')

for ax in fig.axes:
    ax.set_xlabel('Number of variables')
fig.tight_layout()

```

Index(['AtBat', 'Hits', 'HmRun', 'Runs', 'RBI', 'Walks', 'Years', 'CAtBat',
 'CHits', 'CHmRun', 'CRuns', 'CRBI', 'CWalks', 'League', 'Division',
 'PutOuts', 'Assists', 'Errors', 'Salary', 'NewLeague'],

```
        dtype='object')
-----
(322, 20)
-----
59
-----
(263, 20)
-----
Number of variables: 1
['CRBI']
Number of variables: 2
['CRBI', 'Hits']
Number of variables: 3
['CRBI', 'Hits', 'PutOuts']
Number of variables: 4
['CRBI', 'Division', 'Hits', 'PutOuts']
Number of variables: 5
['AtBat', 'CRBI', 'Division', 'Hits', 'PutOuts']
Number of variables: 6
['AtBat', 'CRBI', 'Division', 'Hits', 'PutOuts', 'Walks']
-----
Num vars: 1, R-squared: 0.321, adjusted R-squared: 0.319
Num vars: 2, R-squared: 0.425, adjusted R-squared: 0.421
Num vars: 3, R-squared: 0.451, adjusted R-squared: 0.445
Num vars: 4, R-squared: 0.475, adjusted R-squared: 0.467
Num vars: 5, R-squared: 0.491, adjusted R-squared: 0.481
Num vars: 6, R-squared: 0.509, adjusted R-squared: 0.497
```

The above results are output of program `subsetSelection.py`, which uses `statsmodels`. An advantage of using `statsmodels` is that a number of metrics (e.g., RSS, R-squared, adjusted R-squared, BIC, AIC, etc.) are built-in. Therefore, any of these can be used as the criterion to select the “best” model. But, when number of variables is large, `statsmodels` can be slow. The program `subsetSelectionSklearn.py` implements best subset selection using `sklearn`, which is faster than `statsmodels`. A disadvantage of using `sklearn` is that most of the metrics are not implemented. These can be implemented in a straightforward fashion.

In the next code block, we use `subsetSelectionSklearn.py` to find best models using exhaustive enumeration. As before, for any given subset size, best model is defined as the model which minimizes RSS.

6.5 Lab 1: Subset Selection Methods

```
from statsmodels import datasets
import pandas as pd
import sys
sys.path.append('code/chap6/')
from subsetSelectionSklearn import getVarLookup, bestSubset,
    testStats

hitters = datasets.get_rdataset('Hitters', 'ISLR').data
hitters = hitters.dropna()

# Prepare inputs for sklearn LinearRegression()
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']

var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)
X_numeric = hitters[var_numeric]

X_categorical = hitters[var_categorical]
X_categorical_dummies = pd.get_dummies(X_categorical)
var_categorical_dummies = list(X_categorical_dummies.columns)

X = pd.concat((X_numeric, X_categorical_dummies), axis=1)
y = hitters[y_var]

x_var_names = list(hitters.columns)
x_var_names.remove(y_var)

# Select best model for a given subset size
# Best model is defined as model with the lowest RSS
best_models = {}
best_model_stats = {}
for p in range(1, 19):
    best_models[p] = bestSubset(y, var_numeric, var_categorical,
        var_categorical_dummies, X, subset_size=p)
    best_model_stats[p] = testStats(X, y, best_models[p])
for p in best_models.keys():
    print('Subset size: ' + str(p) + ', ' +
        best_models[p]['metric_name'] + ': ' +
        str(round(best_models[p]['metric'])))
    print(best_models[p]['x_var_names'])
    print('Adjusted R-squared: ' +
        str(round(best_model_stats[p]['adj_rsq'], 3)) +
        ', Cp: ' + str(round(best_model_stats[p]['C_p'])) +
        ', AIC: ' + str(round(best_model_stats[p]['AIC'])) +
        ', BIC: ' + str(round(best_model_stats[p]['BIC'])))
```

6.5 Lab 1: Subset Selection Methods

```
Subset size: 1, RSS: 36179679.0
('CRBI',)
Adjusted R-squared: 0.319, Cp: 138323.0, AIC: 3862.0, BIC: 3869.0
Subset size: 2, RSS: 30646560.0
('Hits', 'CRBI')
Adjusted R-squared: 0.421, Cp: 118042.0, AIC: 3820.0, BIC: 3831.0
Subset size: 3, RSS: 29249297.0
('Hits', 'CRBI', 'PutOuts')
Adjusted R-squared: 0.445, Cp: 113486.0, AIC: 3810.0, BIC: 3825.0
Subset size: 4, RSS: 27970852.0
('Hits', 'CRBI', 'PutOuts', 'Division')
Adjusted R-squared: 0.467, Cp: 109382.0, AIC: 3800.0, BIC: 3818.0
Subset size: 5, RSS: 27149899.0
('AtBat', 'Hits', 'CRBI', 'PutOuts', 'Division')
Adjusted R-squared: 0.481, Cp: 107018.0, AIC: 3795.0, BIC: 3816.0
Subset size: 6, RSS: 26194904.0
('AtBat', 'Hits', 'Walks', 'CRBI', 'PutOuts', 'Division')
Adjusted R-squared: 0.497, Cp: 104144.0, AIC: 3787.0, BIC: 3812.0
Subset size: 7, RSS: 25906548.0
('Hits', 'Walks', 'CAtBat', 'CHits', 'CHmRun', 'PutOuts', 'Division')
Adjusted R-squared: 0.501, Cp: 103805.0, AIC: 3786.0, BIC: 3815.0
Subset size: 8, RSS: 25136930.0
('AtBat', 'Hits', 'Walks', 'CHmRun', 'CRuns', 'CWalks', 'PutOuts', 'Division')
Adjusted R-squared: 0.514, Cp: 101636.0, AIC: 3780.0, BIC: 3813.0
Subset size: 9, RSS: 24814051.0
('AtBat', 'Hits', 'Walks', 'CAtBat', 'CRuns', 'CRBI', 'CWalks', 'PutOuts',
'Division')
Adjusted R-squared: 0.518, Cp: 101166.0, AIC: 3779.0, BIC: 3815.0
Subset size: 10, RSS: 24500402.0
('AtBat', 'Hits', 'Walks', 'CAtBat', 'CRuns', 'CRBI', 'CWalks', 'PutOuts',
'Assists', 'Division')
Adjusted R-squared: 0.522, Cp: 100731.0, AIC: 3778.0, BIC: 3817.0
Subset size: 11, RSS: 24387345.0
('AtBat', 'Hits', 'Walks', 'CAtBat', 'CRuns', 'CRBI', 'CWalks', 'PutOuts',
'Assists', 'League', 'Division')
Adjusted R-squared: 0.523, Cp: 101058.0, AIC: 3778.0, BIC: 3821.0
Subset size: 12, RSS: 24333232.0
('AtBat', 'Hits', 'Runs', 'Walks', 'CAtBat', 'CRuns', 'CRBI', 'CWalks',
'PutOuts', 'Assists', 'League', 'Division')
Adjusted R-squared: 0.522, Cp: 101610.0, AIC: 3780.0, BIC: 3826.0
```

```

Subset size: 13, RSS: 24289148.0
('AtBat', 'Hits', 'Runs', 'Walks', 'CAtBat', 'CRuns', 'CRBI', 'CWalks',
'PutOuts', 'Assists', 'Errors', 'League', 'Division')
Adjusted R-squared: 0.521, Cp: 102200.0, AIC: 3781.0, BIC: 3831.0
Subset size: 14, RSS: 24248660.0
('AtBat', 'Hits', 'HmRun', 'Runs', 'Walks', 'CAtBat', 'CRuns', 'CRBI',
'CWALKS', 'PutOuts', 'Assists', 'Errors', 'League', 'Division')
Adjusted R-squared: 0.52, Cp: 102803.0, AIC: 3783.0, BIC: 3836.0
Subset size: 15, RSS: 24235177.0
('AtBat', 'Hits', 'HmRun', 'Runs', 'Walks', 'CAtBat', 'CHits', 'CRuns', 'CRBI',
'CWALKS', 'PutOuts', 'Assists', 'Errors', 'League', 'Division')
Adjusted R-squared: 0.518, Cp: 103509.0, AIC: 3785.0, BIC: 3842.0
Subset size: 16, RSS: 24219377.0
('AtBat', 'Hits', 'HmRun', 'Runs', 'RBI', 'Walks', 'CAtBat', 'CHits', 'CRuns',
'CRBI', 'CWALKS', 'PutOuts', 'Assists', 'Errors', 'League', 'Division')
Adjusted R-squared: 0.516, Cp: 104206.0, AIC: 3787.0, BIC: 3847.0
Subset size: 17, RSS: 24209447.0
('AtBat', 'Hits', 'HmRun', 'Runs', 'RBI', 'Walks', 'CAtBat', 'CHits', 'CRuns',
'CRBI', 'CWALKS', 'PutOuts', 'Assists', 'Errors', 'League', 'Division', 'NewLeague')
Adjusted R-squared: 0.514, Cp: 104926.0, AIC: 3788.0, BIC: 3853.0
Subset size: 18, RSS: 24201837.0
('AtBat', 'Hits', 'HmRun', 'Runs', 'RBI', 'Walks', 'Years', 'CAtBat', 'CHits',
'CRuns', 'CRBI', 'CWALKS', 'PutOuts', 'Assists', 'Errors', 'League', 'Division', 'NewLeague')
Adjusted R-squared: 0.513, Cp: 105654.0, AIC: 3790.0, BIC: 3858.0

```

Using BIC, the best subset has six variables. Using AIC or C_p , the best subset has 10 variables. Finally, using adjusted R-squared, the best subset has 11 variables.

6.5.2 Forward and Backward Stepwise Selection

Forward and backward stepwise selection are implemented in functions `forwardStepSelect` and `backwardStepSelect`. Given a data set and a metric, these functions add or eliminate a variable at every step.

```

from statsmodels import datasets
import pandas as pd
import sys
sys.path.append('code/chap6/')
from subsetSelection import forwardStepSelect,
                           backwardStepSelect
from subsetSelectionSklearn import getVarLookup, bestSubset

```

```
hitters = datasets.get_rdataset('Hitters', 'ISLR').data
hitters = hitters.dropna()

# Prepare inputs for subsetSelectionSklearn
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']

var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)
X_numeric = hitters[var_numeric]

X_categorical = hitters[var_categorical]
X_categorical_dummies = pd.get_dummies(X_categorical)
var_categorical_dummies = list(X_categorical_dummies.columns)

X = pd.concat((X_numeric, X_categorical_dummies), axis=1)
y = hitters[y_var]

x_var_names = list(hitters.columns)
x_var_names.remove(y_var)

# Select best model for a given subset size
# Best model is defined as model with the lowest RSS
best_model7 = bestSubset(y, var_numeric, var_categorical,
    var_categorical_dummies, X, subset_size=7)

print('Best models for subset size 7')
print('-----')
print('Best model from exhaustive enumeration')
best_model7_res = pd.DataFrame({'variable': ['intercept'],
    'coef': [best_model7['model'].intercept_]})
best_model7_res = pd.concat((best_model7_res, pd.DataFrame(
    {'variable': best_model7['var_numeric_dummies'],
     'coef': best_model7['model'].coef_}), axis=0,
    ignore_index=True))
print(best_model7_res)
print('-----')

# Prepare inputs for forward step or backward step
y_var = 'Salary'
x_vars = list(hitters.columns)
x_vars.remove(y_var)

# Forward step select
fwd_best_models = forwardStepSelect(y_var, x_vars, hitters,
    'ssr',
```

```
        metric_max=False)
print('Best model using forward step select')
print(fwd_best_models[7]['model'].params)
print('-----')

# Backward step select
bkwd_best_models = backwardStepSelect(y_var, x_vars, hitters,
                                       ssr,
                                       metric_max=False)
print('Best model using backward step select')
print(bkwd_best_models[7]['model'].params)
```

```
Best models for subset size 7
-----
Best model from exhaustive enumeration
      variable      coef
0   intercept  14.457626
1       Hits    1.283351
2      Walks    3.227426
3     CAtBat   -0.375235
4      CHits    1.495707
5     CHmRun    1.442054
6     PutOuts    0.236681
7  Division_E  64.993322
8  Division_W -64.993322
-----
Best model using forward step select
Intercept      109.787306
Division[T.W] -127.122393
CRBI          0.853762
Hits          7.449877
PutOuts       0.253340
AtBat         -1.958885
Walks         4.913140
CWalks        -0.305307
dtype: float64
-----
Best model using backward step select
Intercept      105.648749
Division[T.W] -116.169217
AtBat         -1.976284
```

```
Hits           6.757491
Walks          6.055869
CRuns          1.129309
CWalks         -0.716335
PutOuts        0.302885
dtype: float64
```

6.5.3 Choosing Among Models Using the Validation Set Approach and Cross-Validation

We now split the `Hitters` data set into two groups: training and test. We use training group to estimate regression coefficients. Then we use these coefficients to estimate RSS on test group. By repeating this procedure on subsets of all sizes, we find the optimal subset size (which results in the smallest RSS). For this subset size, we find the best model using the *entire* data set. Note that the last step has already been done in the previous section.

```
from statsmodels import datasets
import numpy as np
import pandas as pd
# from sklearn import LinearRegression
import sys
sys.path.append('code/chap6/')
from subsetSelectionSklearn import bestSubsetTest, getVarLookup
    , bestSubset

hitters = datasets.get_rdataset('Hitters', 'ISLR').data
hitters = hitters.dropna()

# Create indexes to split data between training and test groups
np.random.seed(911)
train_ind = np.random.choice([True, False], hitters.shape[0])
test_ind = (train_ind == False)

# Prepare inputs for LinearRegression
y_var = 'Salary'
var_categoric = ['League', 'Division', 'NewLeague']

var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categoric:
    var_numeric.remove(name)
X_numeric = hitters[var_numeric]

X_categoric = hitters[var_categoric]
```

6.5 Lab 1: Subset Selection Methods

```
X_categorical_dummies = pd.get_dummies(X_categorical)
var_categorical_dummies = list(X_categorical_dummies.columns)

X = pd.concat((X_numeric, X_categorical_dummies), axis=1)
y = hitters[y_var]

x_var_names = list(hitters.columns)
x_var_names.remove(y_var)

# Select best model for given subset size
# Estimate coefficients using training data
# Best model minimizes test RSS
best_models = {}
for p in range(1, 19):
    best_models[p] = bestSubsetTest(y, var_numeric,
                                    var_categorical,
                                    var_categorical_dummies, X, train_ind,
                                    test_ind, subset_size=p)

RSS = [best_models[k]['metric'] for k in best_models.keys()]
best_ind = np.argmin(RSS)
best_subset_size = list(best_models.keys())[best_ind]

print('Best model from cross-validation')
print('subset size: ' + str(best_subset_size) + ', RSS: ' +
      str(round(best_models[best_ind]['metric'], 0)))
coef_df = pd.DataFrame({'variable': ['intercept'], 'coefficient':
                           :
                           best_models[best_ind]['model'].intercept_})
coef_df = pd.concat((coef_df, pd.DataFrame(
    {'variable': best_models[best_ind]['var_numeric_dummies'],
     'coefficient': best_models[best_ind]['model'].coef_}),
    axis=0, ignore_index=True))

print(coef_df)
print('-----')

# Use full dataset to reestimate model for best subset size
best_model_alldata = bestSubset(y, var_numeric, var_categorical,
                                 var_categorical_dummies, X,
                                 best_subset_size)
coef_alldata = pd.DataFrame({'variable': ['intercept'],
                             'coefficient':
                               best_model_alldata['model'].intercept_})
coef_alldata = pd.concat(
    (coef_alldata, pd.DataFrame(
        {'variable': best_model_alldata['var_numeric_dummies'],
         'coefficient': best_model_alldata['model'].coef_})), axis=0,
    ignore_index=True)
```

```
print('Best subset size from cross validation')
print('Best model coefficients reestimated using all data')
print(coef_alldata)
```

```
Best model from cross-validation
subset size: 10, RSS: 15473294.0
      variable coefficient
0     intercept    80.226817
1        AtBat   -1.961614
2         Hits    7.665752
3        Walks    4.392214
4       CHmRun    0.780084
5        CRuns    0.655072
6       CWalks   -0.334012
7        Errors    0.739688
8   Division_E    60.649902
9   Division_W   -60.649902
10  NewLeague_A  -18.555935
11  NewLeague_N   18.555935
-----
Best subset size from cross validation
Best model coefficients reestimated using all data
      variable coefficient
0     intercept   106.345413
1        AtBat   -2.168650
2         Hits    6.918017
3        Walks    5.773225
4       CAtBat   -0.130080
5        CRuns    1.408249
6        CRBI     0.774312
7       CWalks   -0.830826
8        PutOuts   0.297373
9        Assists   0.283168
10  Division_E    56.190029
11  Division_W   -56.190029
```

We see that the best ten-variable model on the full data set has a different set of variables than the best ten-variable model on the training set. Moreover, the best ten-variable model on the training set is different from

the result in the book. In fact, it can change with the choice of seed used to partition the data set between training and test groups.

We now use 10-fold cross-validation to find best model (which minimizes test error) for each subset size. To speed up calculations, we use `multiprocessing` package.

```
from statsmodels import datasets
import numpy as np
import pandas as pd
import sys
sys.path.append('code/chap6/')
from subsetSelectionSklearn import bestSubsetCrossVal,
    bestSubset, getVarLookup
from multiprocessing import Pool

hitters = datasets.get_rdataset('Hitters', 'ISLR').data
hitters.dropna(inplace=True)

# Prepare inputs for LinearRegression
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']

var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)
X_numeric = hitters[var_numeric]

X_categorical = hitters[var_categorical]
X_categorical_dummies = pd.get_dummies(X_categorical)
var_categorical_dummies = list(X_categorical_dummies.columns)

X = pd.concat((X_numeric, X_categorical_dummies), axis=1)
y = hitters[y_var]

x_var_names = list(hitters.columns)
x_var_names.remove(y_var)

def bestSubsetMP(s):
    return bestSubsetCrossVal(y, var_numeric, var_categorical,
        var_categorical_dummies, X, subset_size=s)

size_list = np.arange(1, 19)
with Pool() as p:
    best_model_list = p.map(bestSubsetMP, size_list)

mse = [round(model['metric']) for model in best_model_list]
```

6.5 Lab 1: Subset Selection Methods

```
print('Cross validation MSE')
print(mse)
print('-----')

best_ind = np.argmin(mse)
best_size = size_list[best_ind]
print('Best subset size: ' + str(best_size))
best_model_cv = bestSubset(y, var_numeric, var_categorical,
                           var_categorical_dummies, X,
                           subset_size=best_size)

coef_df = pd.DataFrame({'variable': ['intercept'],
                        'coefficient': best_model_cv['model'].intercept_})
coef_df = pd.concat(
    (coef_df, pd.DataFrame({'variable': best_model_cv['var_numeric_dummies'],
                           'coefficient': best_model_cv['model'].coef_})),
    axis=0, ignore_index=True)
print('Best model coefficients')
print(coef_df)
```

```
Cross validation MSE
[139557.0, 119654.0, 115384.0, 111173.0, 108374.0, 104886.0, 104685.0, 102869.0,
 101997.0, 101760.0, 101805.0, 102509.0, 103381.0, 104389.0, 105478.0, 107019.0,
 108827.0, 110783.0]
-----
Best subset size: 10
Best model coefficients
      variable   coefficient
0     intercept  106.345413
1        AtBat    -2.168650
2         Hits     6.918017
3        Walks     5.773225
4       CAtBat    -0.130080
5        CRuns     1.408249
6         CRBI     0.774312
7       CWalks    -0.830826
8        PutOuts    0.297373
9        Assists    0.283168
10      Division_E   56.190029
11      Division_W  -56.190029
```

In the reported results, cross-validation selects a 10-variable model. Depending upon the choice of seed, a 9-, 10- or 11-variable model may be

selected.

6.6 Lab 2: Ridge Regression and the Lasso

From `sklearn` library, we will use `Ridge` and `Lasso` functions to perform ridge regression and the lasso.

6.6.1 Ridge Regression

In the `Ridge()` function of `sklearn` library, `alpha` input is similar to λ in the book. The `Ridge()` function minimizes $\|y - Xw\|_2^2 + \alpha\|w\|_2^2$. On the other hand, for ridge regression, `glmnet` used in the book minimizes $\frac{1}{N}\|y - X\beta\|_2^2 + \frac{\lambda}{2}\|\beta\|_2^2$. Therefore, to obtain comparable results similar to the book, we need to use in $\alpha_{Ridge} = \lambda_{book}N/2$.

We see that the ℓ_2 norms of ridge coefficients are different from those reported in the book. But, consistent with the book, as penalty decreases, ℓ_2 norm of coefficients increases.

Fitting a ridge regression model with $\lambda = 4$ leads to a much lower test MSE than than fitting a model with just an intercept. However, unlike the book, test MSE from ordinary least squares regression is lower than test MSE from ridge regression. These results change with the choice of seed.

```
from sklearn.linear_model import Ridge, RidgeCV
from sklearn.metrics import make_scorer, mean_squared_error
import numpy as np
import pandas as pd

hitters = pd.read_csv('data/Hitters.csv', index_col=0)
hitters.dropna(inplace=True)

# Prepare data for input to sklearn
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']
var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)

y = hitters[y_var]
X_numeric = hitters[var_numeric]
X_numeric_std = X_numeric / X_numeric.std()
X_categorical = hitters[var_categorical]
X_cat_dummies = pd.get_dummies(X_categorical)
X = pd.concat((X_numeric_std, X_cat_dummies), axis=1)
```

```
# lambda = 11498
ridge11k = Ridge(alpha=11498 * X.shape[0] / 2)
ridge11k.fit(X, y)
print('e12 norm when lambda is 11498')
print(np.sqrt(np.sum(ridge11k.coef_ ** 2)))

# lambda = 705
ridge700 = Ridge(alpha=705 * X.shape[0] / 2)
ridge700.fit(X, y)
print('e12 norm when lambda is 705')
print(np.sqrt(np.sum(ridge700.coef_ ** 2)))
print('-----')

# Split data into training and test groups
np.random.seed(911)
shuffle_ind = np.arange(X.shape[0])
np.random.shuffle(shuffle_ind)
train_ind = shuffle_ind[:int(X.shape[0] / 2.0)]
test_ind = shuffle_ind[int(X.shape[0] / 2.0):]
X_train = X.iloc[train_ind]
y_train = y[train_ind]
X_test = X.iloc[test_ind]
y_test = y[test_ind]

# lambda = 4
ridge4 = Ridge(alpha=4 * X.shape[0] / 2)
ridge4.fit(X_train, y_train)
y_predict = ridge4.predict(X_test)
print('Test MSE with lambda = 4')
print(round(np.mean((y_predict - y_test) ** 2)))

y_predict_train = ridge4.predict(X_train)
print('Test MSE when only an intercept is fit')
print(round(np.mean((y_test - np.mean(y_predict_train)) ** 2)))

# Very large lambda
ridge_inf = Ridge(alpha=1e10)
ridge_inf.fit(X_train, y_train)
y_predict = ridge_inf.predict(X_test)
print('Test MSE with very large lambda')
print(round(np.mean((y_predict - y_test) ** 2)))

# lambda = 0, equivalent to OLS
ridge_zero = Ridge(alpha=0)
ridge_zero.fit(X_train, y_train)
y_predict = ridge_zero.predict(X_test)
print('Test MSE with zero lambda')
print(round(np.mean((y_predict - y_test) ** 2)))
print('-----')
```

```
# Select best alpha using cross-validation
alpha_vals = np.logspace(-2, 5)
negative_mse = make_scorer(mean_squared_error,
    greater_is_better=False)
ridge_cv = RidgeCV(alphas=alpha_vals, scoring=negative_mse)
ridge_cv.fit(X_train, y_train)
print('Best lambda: ' + str(round(ridge_cv.alpha_ * 2 / X_train
    .shape[0], 3)))

ridge_best = Ridge(alpha=ridge_cv.alpha_)
ridge_best.fit(X_train, y_train)
y_predict = ridge_best.predict(X_test)
print('Test MSE with best lambda')
print(round(np.mean((y_predict - y_test) ** 2)))
```

```
el2 norm when lambda is 11498
0.1361967493538057
el2 norm when lambda is 705
2.1801333373772005
-----
Test MSE with lambda = 4
123619.0
Test MSE when only an intercept is fit
202378.0
Test MSE with very large lambda
202378.0
Test MSE with zero lambda
103859.0
-----
Best lambda: 2.121
Test MSE with best lambda
108007.0
```

6.6.2 The Lasso

We now ask whether the lasso can yield either a more accurate or a more interpretable model than ridge regression. We find that test MSE is much lower than the test MSE from a model with no coefficients. Test MSE from best fit lasso model is comparable to test MSE from best fit ridge model. Note that, for the chosen seeds, test MSE is slightly *lower* than training MSE. For other seeds, we find that test MSE is higher than training MSE.

Using the alpha of the best lasso model, we fit a lasso on the entire data set. Some of the variables have zero coefficients. Although the test MSE is very similar to test MSE reported in the book, the coefficients are quite different.

```
from sklearn.linear_model import Lasso, LassoCV
import numpy as np
import pandas as pd

hitters = pd.read_csv('data/Hitters.csv', index_col=0)
hitters.dropna(inplace=True)

# Prepare data for input to sklearn
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']
var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)

y = hitters[y_var]
X_numeric = hitters[var_numeric]
X_numeric_std = (X_numeric - X_numeric.mean()) / X_numeric.std()
X_categorical = hitters[var_categorical]
X_cat_dummies = pd.get_dummies(X_categorical)
X = pd.concat((X_numeric_std, X_cat_dummies), axis=1)

# Split data into training and test groups
np.random.seed(911)
shuffle_ind = np.arange(X.shape[0])
np.random.shuffle(shuffle_ind)
train_ind = shuffle_ind[:int(X.shape[0] / 2.0)]
test_ind = shuffle_ind[int(X.shape[0] / 2.0):]
X_train = X.iloc[train_ind]
y_train = y[train_ind]
X_test = X.iloc[test_ind]
y_test = y[test_ind]

# Find best alpha, calculate MSE
alpha_vals = np.logspace(-3, 3)
lasso_cv = LassoCV(alphas=alpha_vals, max_iter=10000, cv=10,
                    random_state=211)
lasso_cv.fit(X_train, y_train)

y_predict = lasso_cv.predict(X_train)
print('Train MSE with best lambda')
print(round(np.mean((y_predict - y_train) ** 2)))
```

```
y_predict = lasso_cv.predict(X_test)
print('Test MSE with best lambda')
print(round(np.mean((y_predict - y_test) ** 2)))
print('-----')

# Use best alpha to fit lasso on full data set
lasso = Lasso(alpha=lasso_cv.alpha_)
lasso.fit(X, y)
best_coef = pd.Series(lasso.coef_, index=X.columns)
best_coef = best_coef[np.abs(best_coef) > 1e-5]
best_coef = pd.concat((pd.Series(lasso.intercept_, index=[],
    Intercept]), best_coef))
print('Coefficients of best lasso fit')
print(best_coef)
```

```
Train MSE with best lambda
116129.0
Test MSE with best lambda
102605.0
-----
Coefficients of best lasso fit
Intercept      506.569249
Hits           84.392705
Walks          48.147509
CRuns          71.418900
CRBI           128.901955
PutOuts        60.083757
Division_E     59.851120
dtype: float64
```

6.7 Lab 3: PCR and PLS Regression

6.7.1 Principal Components Regression

We first run PCA on `Hitters` data. Then we use principal components as explanatory variables in linear regression.

```
from sklearn.decomposition import PCA
from sklearn.linear_model import LinearRegression
import pandas as pd
import numpy as np
from sklearn.model_selection import cross_val_score, KFold
from sklearn.metrics import mean_squared_error
```

6.7 Lab 3: PCR and PLS Regression

```
hitters = pd.read_csv('data/Hitters.csv', index_col=0)
hitters.dropna(inplace=True)

# Prepare data for use in sklearn
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']
var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)

X_numeric = hitters[var_numeric]
X_categorical = hitters[var_categorical]
X_cat_dummies = pd.get_dummies(X_categorical)
# An alternative method of including dummy variables
# Use this method to tie out with results in the book
X_cat_dummies.drop(columns=['League_A', 'Division_E',
    'NewLeague_A'],
    inplace=True)
X = pd.concat((X_numeric, X_cat_dummies), axis=1)
X = (X - X.mean()) / X.std()
y = hitters[y_var]

# Run PCA on explanatory variables
pca = PCA()
pca.fit(X)

# Run OLS regression using 1, 2, ..., all principal components
# Calculate percent variance of y explained (r-squared) using
cross validation
X_transform = pca.transform(X)
k_fold10 = KFold(n_splits=10, shuffle=True, random_state=911)
lm_model = LinearRegression()
r_sq = []# on training data
r_sq_cv = []# in cross validation
mse = []# on training data
mse_cv = []# in cross validation
for i_components in np.arange(1, X_transform.shape[1] + 1):
    scores_mse = cross_val_score(lm_model, X_transform[:, :i_components],
        y, scoring='neg_mean_squared_error',
        cv=k_fold10)
    mse_cv.append(np.mean(scores_mse))

# For LinearRegression, score is r-squared
scores_rsq = cross_val_score(lm_model, X_transform[:, :i_components],
    y, cv=k_fold10)
r_sq_cv.append(np.mean(scores_rsq))
```

```
# Fit on all data
lm_model.fit(X_transform[:, :i_components], y)
r_sq.append(lm_model.score(X_transform[:, :i_components], y))
mse.append(mean_squared_error(y, lm_model.predict(
X_transform[:, :i_components])))
mse_cv = [-1 * mse for mse in mse_cv]

print('Training data variance explained by principal components')
explain_df = pd.DataFrame(
{'num_components': np.arange(1, X_transform.shape[1] + 1),
 'X': np.round(np.cumsum(pca.explained_variance_ratio_), 4),
 'y': r_sq})
explain_df.set_index('num_components', inplace=True)
print(explain_df.head(10))
print('-----')

n_best_train = np.argmin(mse) + 1
n_best_cv = np.argmin(mse_cv) + 1
print('On training data, lowest mse occurs when %0.0f
components are included' %
n_best_train)
print('In cross validation, lowest mse occurs when %0.0f
components are included'
% n_best_cv)
print('-----')

# Split data into training and test
np.random.seed(211)
train_ind = np.random.choice([True, False], X_transform.shape
[0])
test_ind = (train_ind == False)
X_train = X.loc[train_ind]
X_train = (X_train - X_train.mean()) / X_train.std()
y_train = y[train_ind]

X_test = X.loc[test_ind]
X_test = (X_test - X_test.mean()) / X_test.std()
y_test = y[test_ind]

pca = PCA()
pca.fit(X_train)
X_train_transform = pca.transform(X_train)[:, :n_best_cv]
lm_model = LinearRegression()
lm_model.fit(X_train_transform, y_train)
```

```
X_test_transform = pca.transform(X_test)[:, :n_best_cv]
rss = np.mean((y_test - lm_model.predict(X_test_transform)) ** 2)
print('Using number of components that results in lowest cv MSE')
print('Test RSS: %0.0f' % rss)
```

Training data variance explained by principal components

	X	y
num_components		
1	0.3831	0.406269
2	0.6016	0.415822
3	0.7084	0.421733
4	0.7903	0.432236
5	0.8429	0.449044
6	0.8863	0.464800
7	0.9226	0.466864
8	0.9496	0.467498
9	0.9628	0.468580
10	0.9726	0.477632

On training data, lowest mse occurs when 19 components are included
 In cross validation, lowest mse occurs when 6 components are included

 Using number of components that results in lowest cv MSE
 Test RSS: 110989

6.7.2 Partial Least Squares

To perform partial least squares regression, we use `PLSRegression` function in `sklearn` library. While the overall results are the same (for best model using training data, test MSE is comparable to best model using PCA, ridge, or lasso), actual results will vary based on the choice of seed.

```
import pandas as pd
import numpy as np
from sklearn.cross_decomposition import PLSRegression
from sklearn.model_selection import cross_val_score

hitters = pd.read_csv('data/Hitters.csv', index_col=0)
hitters.dropna(inplace=True)

# Prepare data for sklearn
```

6.7 Lab 3: PCR and PLS Regression

```
y_var = 'Salary'
var_categorical = ['League', 'Division', 'NewLeague']
var_numeric = list(hitters.columns)
var_numeric.remove(y_var)
for name in var_categorical:
    var_numeric.remove(name)

X_numeric = hitters[var_numeric]
X_categorical = hitters[var_categorical]
X_cat_dummies = pd.get_dummies(X_categorical)
X = pd.concat((X_numeric, X_cat_dummies), axis=1)
y = hitters[y_var]

# Split data between training and test groups
np.random.seed(911)
train_ind = np.random.choice([True, False], X.shape[0])
test_ind = np.vectorize(lambda x: not x)(train_ind)
X_train = X.loc[train_ind]
X_test = X.loc[test_ind]
X_train = (X_train - X_train.mean()) / X_train.std()
X_test = (X_test - X_test.mean()) / X_test.std()
y_train = y[train_ind]
y_test = y[test_ind]

mse_cv = []
for i_components in np.arange(1, 20):
    pls = PLSRegression(n_components=i_components)
    scores = cross_val_score(pls, X_train, y_train, cv=10,
                           scoring='neg_mean_squared_error')
    mse_cv.append(np.mean(scores))

mse_cv = [-1 * mse for mse in mse_cv]
best_comp_count = np.argmin(mse_cv) + 1
print('Lowest MSE obtained when number of components is %0.0f' %
      best_comp_count)

# Fit PLS on test data using best number of components
pls = PLSRegression(n_components=best_comp_count)
pls.fit(X_test, y_test)
mse_test = np.mean((pls.predict(X_test).ravel() - y_test) ** 2)
print('Using best number of components from training PLS')
print('Test MSE: %0.0f' % mse_test)
```

```
Lowest MSE obtained when number of components is 3
Using best number of components from training PLS
Test MSE: 109315
```

7 Moving Beyond Linearity

7.1 Polynomial Regression

The left-hand panel of figure 72 is a plot of `wage` against `age` for the `Wage` data set, which contains demographic information for males who reside in the central Atlantic region of the United States. The scatter plot shows individual data points. The firm line is regression fit of fourth order polynomial. The dotted lines show 95% confidence interval.

The right-hand panel shows fitted probabilities of $wage > 250$ from a logistic regression, also on fourth order polynomial of `age`. The grey marks on the top and bottom of the panel indicate the ages of the high earners and low earners.

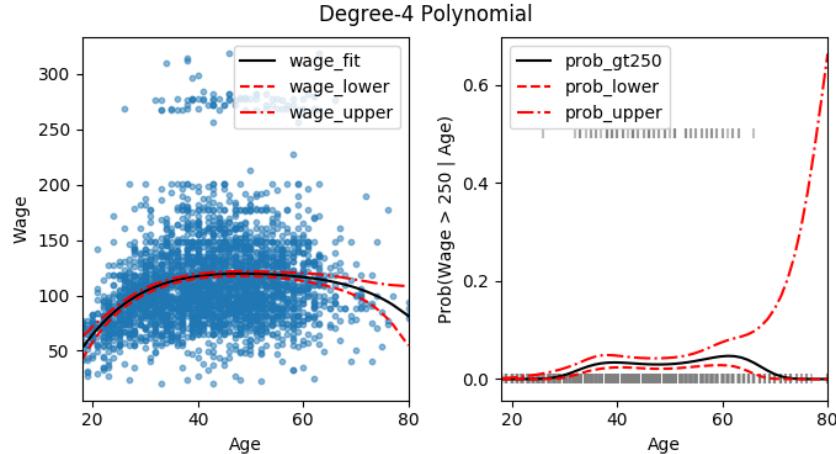


Figure 72: The `Wage` data. Left: The solid curve is a degree-4 polynomial of `wage` (in thousands of dollars) as a function of `age`, fit by least squares. The dotted curves indicate an estimated 95% confidence interval. Right: We model the binary event $wage > 250$ using logistic regression, again with a degree-4 polynomial. The fitted posterior probability of `wage` exceeding \$250,000 is shown in blue.

7.2 Step Functions

The left-hand panel of figure 73 shows a fit of step functions to the `Wage` data from figure 72. We also fit the logistic regression model to predict the

probability that an individual is a high earner based on `age`. The right-hand panel displays the fitted posterior probabilities.

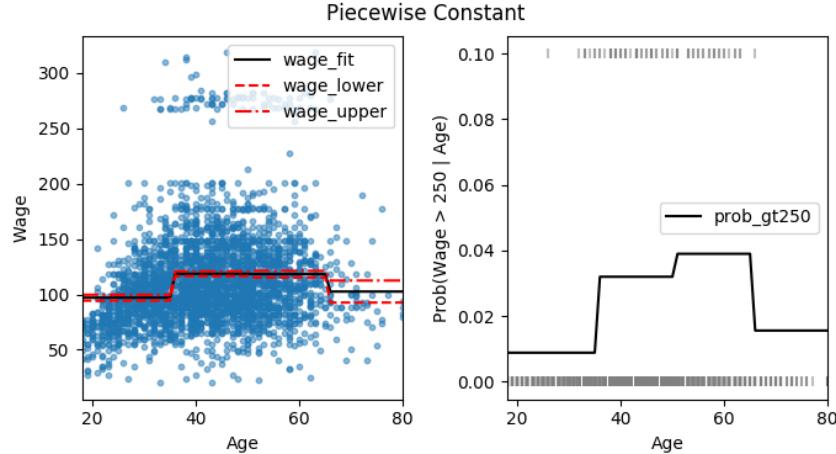


Figure 73: The `Wage` data. Left: The solid curve displays the fitted value from a least squares regression of `wage` (in thousands of dollars) using step functions of `age`. The dotted curves show an estimated 95% confidence interval. Right: We model the binary event `wage > 250` using logistic regression again using step functions of `age`. The fitted posterior probability of `wage` exceeding \$250,000 is shown.

7.3 Basis Functions

7.4 Regression Splines

7.5 Lab: Non-linear Modeling

7.5.1 Polynomial Regression and Step Functions

We define a simple function to replicate the output of `poly` function in R. We then fit `wage` as a fourth order orthogonal polynomial of `age`. Then we fit `wage` as a fourth order raw polynomial of `age`. Predicted values from both fits are very close to one another.

ANOVA analysis on nested models of upto five degree polynomials shows that first three degrees are highly significant. Fourth degree has a p-value just above 0.05. Fifth degree is not significant. Either a cubic or a quartic polynomial provide a reasonable fit.

With the fourth order polynomial as the chosen model, it is straightforward to plot fitted values and confidence intervals.

```
import pandas as pd
import numpy as np
import statsmodels.formula.api as smf
from statsmodels import datasets
from statsmodels.stats.api import anova_lm
import statsmodels.api as sm
import matplotlib.pyplot as plt

wage = datasets.get_rdataset('Wage', 'ISLR').data

# Replicate poly() function in R
# Based on an answer by K. A. Buhr on stackoverflow
def poly(x, p):
    x = np.array(x)
    X_mat = np.transpose(np.vstack([x ** k for k in range(p + 1)]))
    return np.linalg.qr(X_mat)[0][:, 1:]

# Fit wage as a function of orthogonal polynomial of age
X_wage = poly(wage['age'], 4)
X_wage = sm.add_constant(X_wage)

poly_model = sm.OLS(wage['wage'], X_wage)
poly_fit = poly_model.fit()

print('Coefficients of orthogonal polynomials upto 4 degrees')
print(poly_fit.summary2().tables[1].iloc[:, :4])
print('-----')

# Fit wage as a function of raw polynomials of age
model = smf.ols('wage ~ age + I(age ** 2) + I(age ** 3) + I(age ** 4)', data=wage)
fit = model.fit()
print('Coefficients of raw polynomials upto 4 degrees')
print(fit.summary2().tables[1].iloc[:, :4])
print('-----')

# Verify that both models produce identical fitted values
print('Orthogonal polynomials and raw polynomials fitted values nearly equal:')
print(np.all(np.abs(fit.fittedvalues - poly_fit.fittedvalues) < 1e-7))
print('-----')
```

7.5 Lab: Non-linear Modeling

```

# Fit models of degrees 1 to 5, then compare using ANOVA
fit1 = smf.ols('wage ~ age', data=wage).fit()
fit2 = smf.ols('wage ~ age + I(age ** 2)', data=wage).fit()
fit3 = smf.ols('wage ~ age + I(age ** 2) + I(age ** 3)', data=
    wage).fit()
fit4 = smf.ols('wage ~ age + I(age ** 2) + I(age ** 3) + I(age
    ** 4)',
    data=wage).fit()
fit5 = smf.ols('wage ~ age + I(age ** 2) + I(age ** 3) + I(age
    ** 4) + I(age ** 5)', data=wage).fit()

print('ANOVA on nested models upto 5 degrees')
print(anova_lm(fit1, fit2, fit3, fit4, fit5))
print('-----')

# For plotting, create age array, get prediction and confidence
# intervals
res_df = pd.DataFrame({'age': np.linspace(wage['age'].min(),
    wage['age'].max())})
res_df['wage_predict'] = fit.get_prediction(exog=res_df).
    predicted_mean
res_df['wage_low'] = fit.get_prediction(exog=res_df).conf_int()
[:, 0]
res_df['wage_high'] = fit.get_prediction(exog=res_df).conf_int()
[:, 1]

fig = plt.figure()
ax = fig.add_subplot()
wage.plot(x='age', y='wage', kind='scatter', alpha=0.5, ax=ax)
res_df.plot(x='age', y='wage_predict', c='r', ax=ax)
res_df.plot(x='age', y='wage_low', c='r', linestyle='--', ax=ax
    )
res_df.plot(x='age', y='wage_high', c='r', linestyle='-.', ax=
    ax)
ax.set_xlabel('Age')
ax.set_ylabel('Wage')
ax.set_title('Degree-4 Polynomial')

```

Coefficients of orthogonal polynomials upto 4 degrees

	Coef.	Std.Err.	t	P> t
const	111.703608	0.728741	153.283015	0.000000e+00
x1	447.067853	39.914785	11.200558	1.484604e-28
x2	-478.315806	39.914785	-11.983424	2.355831e-32
x3	-125.521686	39.914785	-3.144742	1.678622e-03
x4	77.911181	39.914785	1.951938	5.103865e-02

7.5 Lab: Non-linear Modeling

```

Coefficients of raw polynomials upto 4 degrees
      Coef.    Std.Err.      t    P>|t|
Intercept -184.154180  60.040377 -3.067172  0.002180
age         21.245521   5.886748  3.609042  0.000312
I(age ** 2) -0.563859   0.206108 -2.735743  0.006261
I(age ** 3)  0.006811   0.003066  2.221409  0.026398
I(age ** 4) -0.000032   0.000016 -1.951938  0.051039
-----
Orthogonal polynomials and raw polynomials fitted values nearly equal:
True
-----
ANOVA on nested models upto 5 degrees
      df_resid      ssr  df_diff      ss_diff        F    Pr(>F)
0     2998.0  5.022216e+06      0.0       NaN      NaN      NaN
1     2997.0  4.793430e+06      1.0  228786.010128  143.593107  2.363850e-32
2     2996.0  4.777674e+06      1.0   15755.693664   9.888756  1.679202e-03
3     2995.0  4.771604e+06      1.0    6070.152124   3.809813  5.104620e-02
4     2994.0  4.770322e+06      1.0   1282.563017   0.804976  3.696820e-01
-----
```

Next we consider the task of predicting whether an individual earns more than \$250,000 per year. The probability of wage greater than 250K is directly obtained from the `predict` method on `statsmodels` fit object. However, for logit models, `statsmodels` does not provide confidence intervals. We use the formula for confidence intervals.

```

from statsmodels import datasets
import statsmodels.formula.api as smf
from sklearn.preprocessing import PolynomialFeatures
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

wage = datasets.get_rdataset('Wage', 'ISLR').data

# Create dummy variable for wage > 250K
wage['wage_gt250K'] = wage['wage'].apply(lambda x: 1 if x > 250
                                           else 0)

model = smf.logit('wage_gt250K ~ age + I(age ** 2) + I(age **
3) + I(age ** 4)',
                  data=wage)
fit = model.fit()
```

7.5 Lab: Non-linear Modeling

```
# Predicted probability for plotting
res_df = pd.DataFrame({'age': np.linspace(wage['age'].min(),
                                             wage['age'].max())})
res_df['prob_wage_gt250'] = fit.predict(exog=res_df)

# Create X matrix for estimating confidence intervals
# Based on a suggestion from David Dale on stackoverflow
poly = PolynomialFeatures(degree=4)
X_mat = poly.fit_transform(res_df['age'][:, np.newaxis])

cov_beta = fit.cov_params()
predict_var = np.diag(np.dot(X_mat, np.dot(cov_beta, X_mat.T)))
predict_error = np.sqrt(predict_var)
Xb = np.dot(X_mat, fit.params)

predict_upper = Xb + 1.96 * predict_error
predict_lower = Xb - 1.96 * predict_error
res_df['prob_upper'] = np.exp(predict_upper) / (1 + np.exp(
    predict_upper))
res_df['prob_lower'] = np.exp(predict_lower) / (1 + np.exp(
    predict_lower))

fig = plt.figure()
ax = fig.add_subplot(111)
ax.scatter(wage['age'], wage['wage_gt250K']/2, marker='|',
           color='grey',
           alpha=0.5)
res_df.plot(x='age', y='prob_wage_gt250', c='b', ax=ax)
res_df.plot(x='age', y='prob_upper', c='r', linestyle='--', ax=
            ax)
res_df.plot(x='age', y='prob_lower', c='r', linestyle='-.', ax=
            ax)
ax.set_xlabel('Age')
ax.set_ylabel('Prob(Wage > 250 | Age)')
```

Optimization terminated successfully.

Current function value: 0.116870

Iterations 12

We now fit a step function of age.

```
from statsmodels import datasets
import statsmodels.formula.api as smf
import pandas as pd

wage = datasets.get_rdataset('Wage', 'ISLR').data
wage['age_grp'] = pd.cut(wage['age'], bins=[17, 33.5, 49, 64.5,
                                             81],
```

```
labels=['17to33', '33to49', '49to64', '64to80'])

step_model = smf.ols('wage ~ age_grp', data=wage)
step_fit = step_model.fit()

print('Coefficients of age groups')
print(step_fit.summary2().tables[1].iloc[:, :4])
```

```
Coefficients of age groups
      Coef.  Std.Err.      t      P>|t|
Intercept      94.158392  1.476069  63.789970  0.000000e+00
age_grp[T.33to49]  24.053491  1.829431  13.148074  1.982315e-38
age_grp[T.49to64]  23.664559  2.067958  11.443444  1.040750e-29
age_grp[T.64to80]   7.640592  4.987424   1.531972  1.256350e-01
```

8 Tree-Based Models

8.1 The Basics of Decision Trees

8.1.1 Regression Trees

Figure 74 shows a regression tree fit to `Hitters` data. We predict log of `Salary` based on `Years` (column 0 of `X` matrix) and `Hits` (column 1). The figure consists of a series of splitting rules. The top split assigns observations having `Years` < 4.5 to the left branch. Players with `Years` > 4.5 are assigned to the right branch, and then the group is further subdivided by `Hits`.

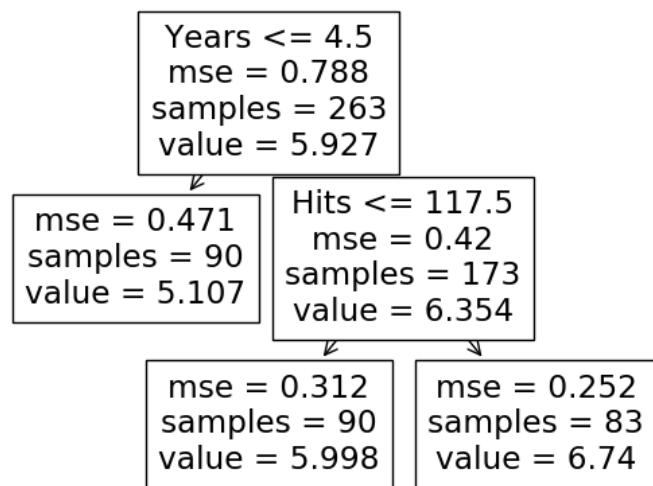


Figure 74: For the **Hitters** data, a regression tree for producing the log salary of a baseball player, based on the number of years that he has played in the major leagues and the number of hits that he made in the previous year.

8.1 The Basics of Decision Trees

Overall, the tree segments the players into four regions of predictor space: $R_1 = \{X | \text{Years} < 4.5, \text{Hits} < 15.5\}$, $R_2 = \{X | \text{Years} < 4.5, \text{Hits} > 15.5\}$, $R_3 = \{X | \text{Years} > 4.5, \text{Hits} < 117.5\}$, and $R_4 = \{X | \text{Years} > 4.5, \text{Hits} > 117.5\}$. Figure 75 illustrates the regions as a function of `Years` and `Hits`.

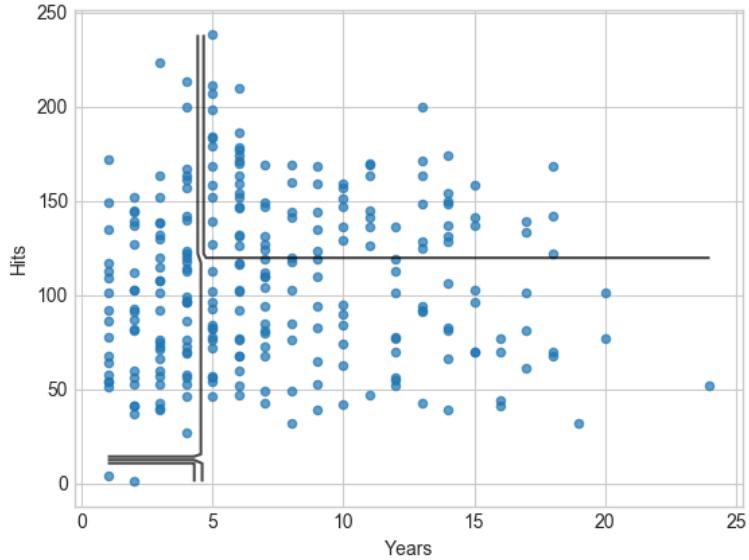


Figure 75: The four-region partition for the `Hitters` data set from the regression tree in Figure 74.

Figure 76 shows a five-region example of prediction via stratification of the feature space.

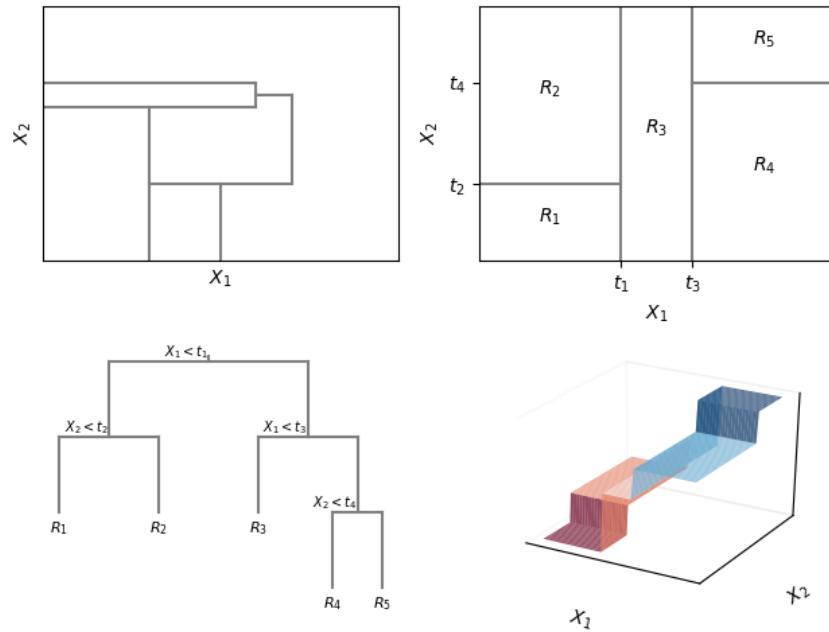


Figure 76: Top Left: A partition of two-dimensional space that could not result from recursive binary splitting. Top Right: The output of recursive binary splitting on a two-dimensional example. Bottom Left: A tree corresponding to the partition on the top right panel. Bottom Right: A perspective plot of the prediction surface corresponding to that tree.

8.1.2 Classification Trees

8.1.3 Trees versus Linear Models

Figure 77 is an example of when a linear model or a tree performs better. In the top row, the relationship between the features and responses is linear. A linear regression works well. In the bottom row, the relationship between the features and the responses is non-linear. A decision tree outperforms linear regression.

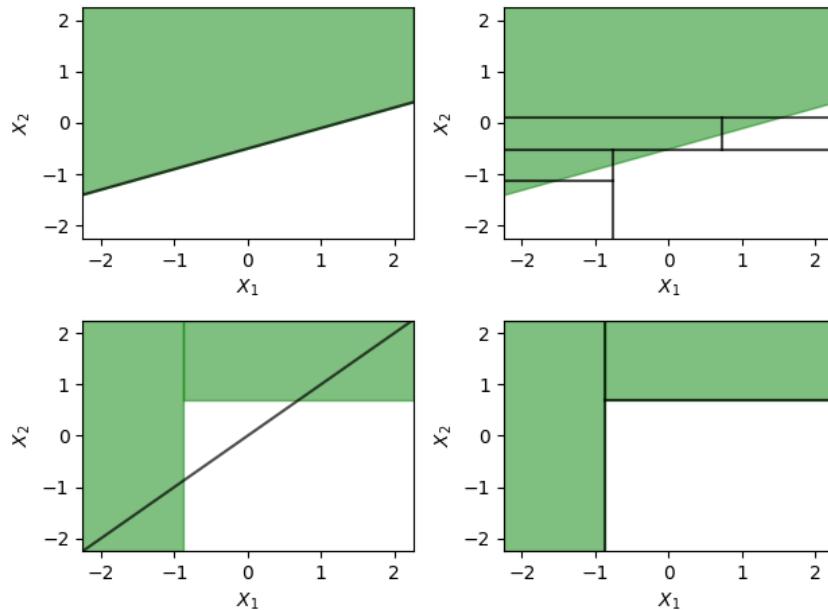


Figure 77: Top Row: A two-dimensional classification example in which the true decision boundary is linear, and is indicated by the shaded regions. A classical approach that assumes a linear boundary (left) will outperform a decision tree that performs splits parallel to the axes (right). Bottom Row: Here the true decision boundary is non-linear. A linear model is unable to capture the true decision boundary (left), whereas a decision tree is successful (right).

8.2 Bagging, Random Forests, Boosting

Figure 78 is a graphical representation of *variable importances* in the Heart data. We see the mean decrease in Gini index for each variable relative

to the largest. The variables with the largest mean decrease in Gini index are `Ca`, `Thal`, `HR`, and `Oldpeak`. When a categorical variable has more than two values, it appears in the figure more than once. For example, `Thal` has values `normal`, `reversable`, and `fixed`. In the figure, we see `Thal_normal` and `Thal_reversable`.

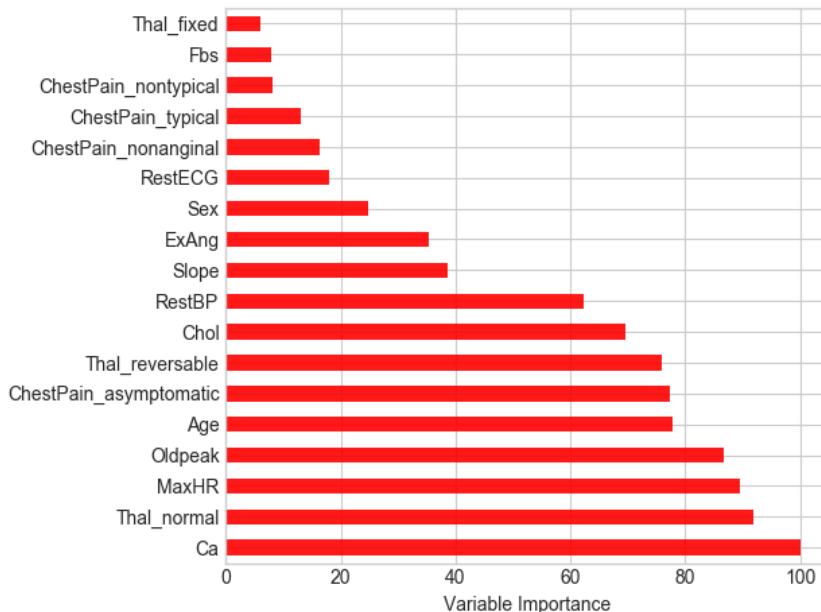


Figure 78: A variable importance plot for the `Heart` data. Variable importance is computed using the mean decrease in Gini index and expressed relative to the maximum.

8.3 Lab: Decision Trees

8.3.1 Fitting Classification Trees

In `scikit-learn` library, `tree` module implements classification and regression trees.

We first use classification trees to analyze the `Carseats` data set. In these data, `Sales` is a continuous variable, and so we begin by recoding it as a binary variable.

```
from statsmodels import datasets
```

8.3 Lab: Decision Trees

```
from sklearn.tree import DecisionTreeClassifier, export_text,
plot_tree
from sklearn.model_selection import train_test_split,
GridSearchCV

import pandas as pd

Carseats = datasets.get_rdataset('Carseats', 'ISLR').data

Carseats['High Sales'] = Carseats['Sales'].apply(
    lambda x: 'Yes' if x > 8 else 'No')

# Create dummy variables for qualitative data
X_numeric = Carseats[['CompPrice', 'Income', 'Advertising', ,
    'Population',
    'Price', 'Age', 'Education']]
X_cat = Carseats[['ShelveLoc', 'Urban', 'US']]
X_dummies = pd.get_dummies(X_cat, drop_first=True)
X = pd.concat([X_numeric, X_dummies], axis=1)
y = Carseats['High Sales']

# Fit model to all data
tree = DecisionTreeClassifier(ccp_alpha=0.02)
tree.fit(X, y)

print('Decision tree in text')
print(export_text(tree, feature_names=X.columns.to_list()))

# Split data between train and test sets
# Fit model to training data, then print prediction accuracy on
# test data
X_train, X_test, y_train, y_test = train_test_split(X, y,
    test_size=0.5,
    random_state=0)

model = DecisionTreeClassifier()
model.fit(X_train, y_train)

res_crosstab = pd.crosstab(y_test, model.predict(X_test))
res_crosstab.columns.name = 'High Sales Predict'
print('Prediction accuracy on test data')
print(res_crosstab)
print(str(round((96 + 48) / X_test.shape[0], 2)), 'of
    predictions are correct')

# Use grid search to find optimal level of tree complexity
param_grid = {'ccp_alpha': np.linspace(0, 0.02, 11)}
grid = GridSearchCV(DecisionTreeClassifier(), param_grid, cv=5,
    return_train_score=True)
```

```
grid.fit(X, y)

Decision tree in text
|--- ShelveLoc_Good <= 0.50
|   |--- Price <= 92.50
|   |   |--- class: Yes
|   |--- Price >  92.50
|   |   |--- Advertising <= 13.50
|   |   |   |--- class: No
|   |   |--- Advertising >  13.50
|   |   |   |--- class: Yes
|--- ShelveLoc_Good >  0.50
|   |--- class: Yes

Prediction accuracy on test data
High Sales Predict  No  Yes
High Sales
No          97  21
Yes         30  52
0.72  of predictions are correct
```

8.3.2 Fitting Regression Trees

Here we fit a regression tree to the Boston data set. First we create a training set, and fit the tree to the training data.

```
from statsmodels import datasets
from sklearn.model_selection import train_test_split,
    GridSearchCV
from sklearn.tree import DecisionTreeRegressor, export_text
import pandas as pd
import numpy as np

Boston = datasets.get_rdataset('Boston', package='MASS').data

X = Boston.drop(columns='medv')
y = Boston['medv']

X_train, X_test, y_train, y_test = train_test_split(X, y,
    test_size=0.5,
    random_state=0)

tree = DecisionTreeRegressor(max_leaf_nodes=40, random_state=0)
tree.fit(X_train, y_train)
```

8.3 Lab: Decision Trees

```
resid_mean_dev = np.mean(np.abs(y_test - tree.predict(X_test)))
resid_dist = pd.Series(np.quantile(y_test - tree.predict(X_test)
),
[0, 0.25, 0.5, 0.75, 1]),
index=['Min', '1st Qu', 'Median', '3rd Qu', 'Max'])

print('Residual mean deviance:', str(round(resid_mean_dev, 2)))
print('Distribution of residuals:')
print(resid_dist)
print('Mean squared error:', str(round(np.std(y_test - tree.
predict(X_test)),
2)))
print('-----')

# Use grid search to find best tree size
# Depending upon starting point, tree size can be very
# different
params_grid = {'max_leaf_nodes': np.arange(2, 21)}
grid = GridSearchCV(DecisionTreeRegressor(random_state=0),
param_grid=params_grid, cv=5)

grid.fit(X_train, y_train)

print('Best fitted tree')
print(export_text(grid.best_estimator_, feature_names=X.columns
.to_list()))

print('Mean squared error:',
str(np.round(np.std(y_test - grid.best_estimator_.predict
(X_test)), 2)))
```

```
Residual mean deviance: 3.07
Distribution of residuals:
Min      -16.675000
1st Qu    -2.118519
Median     -0.400000
3rd Qu     1.466667
Max       35.500000
dtype: float64
Mean squared error: 5.06
-----
Best fitted tree
|--- lstat <= 7.81
|   |--- rm <= 7.43
```

```
|   |   |--- dis <= 1.48
|   |   |   |--- value: [50.00]
|   |   |--- dis >  1.48
|   |   |   |--- rm <= 6.56
|   |   |   |   |--- value: [23.75]
|   |   |   |--- rm >  6.56
|   |   |   |   |--- value: [30.67]
|   |--- rm >  7.43
|   |   |--- ptratio <= 15.40
|   |   |   |--- value: [48.64]
|   |   |--- ptratio >  15.40
|   |   |   |--- value: [41.26]
|--- lstat >  7.81
|   |--- lstat <= 15.00
|   |   |--- rm <= 6.53
|   |   |   |--- value: [20.78]
|   |   |--- rm >  6.53
|   |   |   |--- value: [26.02]
|   |--- lstat >  15.00
|   |   |--- dis <= 1.92
|   |   |   |--- value: [11.67]
|   |   |--- dis >  1.92
|   |   |   |--- value: [16.83]
```

Mean squared error: 4.89

8.3.3 Bagging and Random Forests

```
from statsmodels import datasets
from sklearn.ensemble import RandomForestRegressor,
    BaggingRegressor
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeRegressor
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
plt.style.use('seaborn-whitegrid')

Boston = datasets.get_rdataset('Boston', package='MASS').data

X = Boston.drop(columns='medv').copy()
y = Boston['medv'].copy()
```

8.3 Lab: Decision Trees

```
X_train, X_test, y_train, y_test = train_test_split(X, y,
    random_state=0)

bag = BaggingRegressor(random_state=0)
bag.fit(X_train, y_train)

print('BaggingRegressor model')
print('Model performance on training data')
print('Mean of squared residuals: %0.2f' %
    np.mean((y_train - bag.predict(X_train)) ** 2))
print('Percent variance explained: %0.2f' % bag.score(X_train,
    y_train))

print('-----')
print('Model performance on test data')
print('Percent variance explained: %0.2f' %
    np.mean((y_test - bag.predict(X_test)) ** 2))

# plt.scatter(y_test, bag.predict(X_test), alpha=0.7)
# plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.
#     max()], linestyle='--',
#     alpha=0.7)
# plt.gca().set(xlabel='True price', ylabel='Predicted price')

forest = RandomForestRegressor(random_state=0)
forest.fit(X_train, y_train)

print('-----')
print('RandomForestRegressor model')
print('Mean of squared residuals: %0.2f' %
    np.mean((y_test - forest.predict(X_test)) ** 2))

feature_imp = pd.Series(forest.feature_importances_, index=X.
    columns.to_list())
feature_imp.sort_values(ascending=False, inplace=True)

print('-----')
print('Feature importance of variables')
print((feature_imp * 100).round(2))
```

```
BaggingRegressor model
Model performance on training data
Mean of squared residuals: 2.49
Percent variance explained: 0.97
-----
Model performance on test data
```

```
Percent variance explained: 22.79
-----
RandomForestRegressor model
Mean of squared residuals: 16.73
-----
Feature importance of variables
rm          41.65
lstat        40.75
dis           4.33
crim          4.15
ptratio       2.12
tax            1.80
nox            1.58
age            1.24
black          1.10
indus          0.69
rad             0.41
zn              0.11
chas            0.07
dtype: float64
```

8.3.4 Boosting

```
from statsmodels import datasets
import numpy as np
from sklearn.ensemble import AdaBoostRegressor
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeRegressor
import pandas as pd

Boston = datasets.get_rdataset('Boston', package='MASS').data

X = Boston.drop(columns='medv').copy()
y = Boston['medv'].copy()

X_train, X_test, y_train, y_test = train_test_split(X, y,
random_state=0)

tree = DecisionTreeRegressor(max_depth=4)
boost = AdaBoostRegressor(tree, n_estimators=5000, random_state
=0)

boost.fit(X_train, y_train)
```

8.3 Lab: Decision Trees

```
feature_imp = pd.Series(boost.feature_importances_, index=X_train.columns)
feature_imp.sort_values(ascending=False, inplace=True)

print('AdaBoostRegressor model')
print('Feature importances')
print((feature_imp * 100).round(2))
print('-----')

print('Model performance on training data')
print('Mean of squared residuals: %0.2f' % np.mean((y_train - boost.predict(X_train)) ** 2))
print('Percent of variance explained: %0.2f' % boost.score(X_train, y_train))
print('-----')

print('Model performance on test data')
print('Mean of squared residuals: %0.2f' % np.mean((y_test - boost.predict(X_test)) ** 2))
print('Percent of variance explained: %0.2f' % boost.score(X_test, y_test))
```

```
AdaBoostRegressor model
Feature importances
lstat      41.10
rm        31.69
dis        7.42
tax        4.69
ptratio    4.44
nox        2.32
crim       2.19
black      1.81
age        1.63
indus      1.60
rad         0.57
zn          0.27
chas        0.26
dtype: float64
-----
Model performance on training data
Mean of squared residuals: 3.37
Percent of variance explained: 0.96
-----
```

```
Model performance on test data
Mean of squared residuals: 21.91
Percent of variance explained: 0.73
```

9 Support Vector Machines

9.1 Maximal Margin Classifier

9.1.1 What is a Hyperplane?

Figure 79 shows a hyperplane in two-dimensional space.

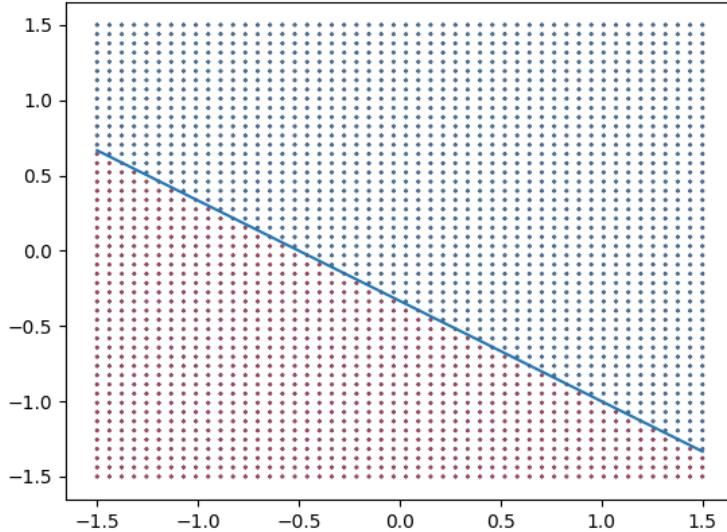


Figure 79: The hyperplane $1 + 2X_1 + 3X_2 = 0$ is shown. The blue region is the set of points for which $1 + 2X_1 + 3X_2 > 0$, and the red region is the set of points for which $1 + 2X_1 + 3X_2 < 0$.

9.1.2 Classification Using a Separating Hyperplane

Figure 80 shows an example of a separating hyperplane classifier.

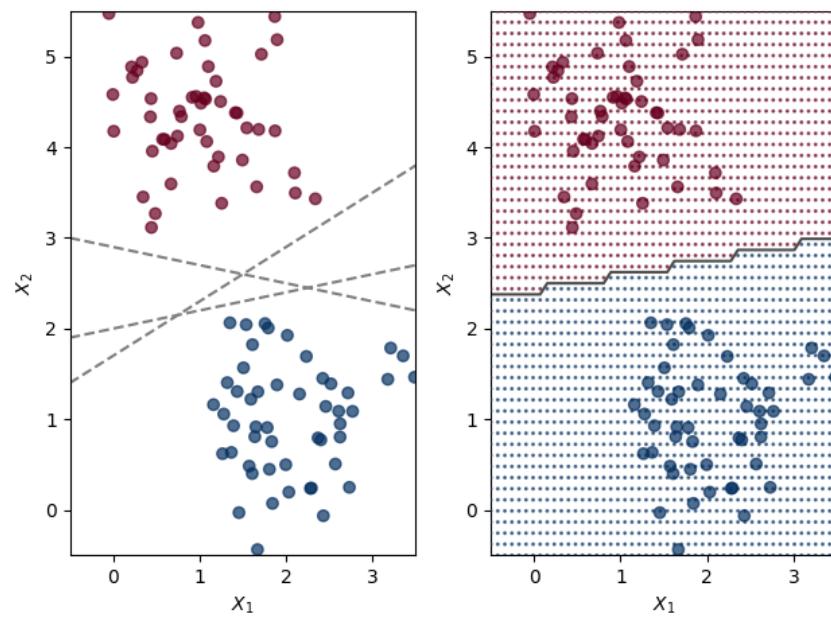


Figure 80: Left: There are two classes of observations, shown in red and blue, each of which has measurements on two variables. Three separating hyperplanes, out of many possible, are shown in gray. Right: A separating hyperplane is shown in black. The red and blue grid indicates the decision rule made by a classifier based on this separating hyperplane: a test observation that falls in the red portion of the grid will be assigned to the red class. A test observation that falls into the blue portion of the grid will be assigned to the blue class.

9.1.3 The Maximal Margin Classifier

Examining figure 81, we see that three training observations are equidistant from the maximal margin hyperplane and lie along the dashed lines indicating the width of the margin. The three observations are known as *support vectors*, since they are vectors in p -dimensional space (in figure 81, $p = 2$) and they “support” the maximal margin hyperplane. If these points were moved slightly, then the maximal margin hyperplane would move as well.

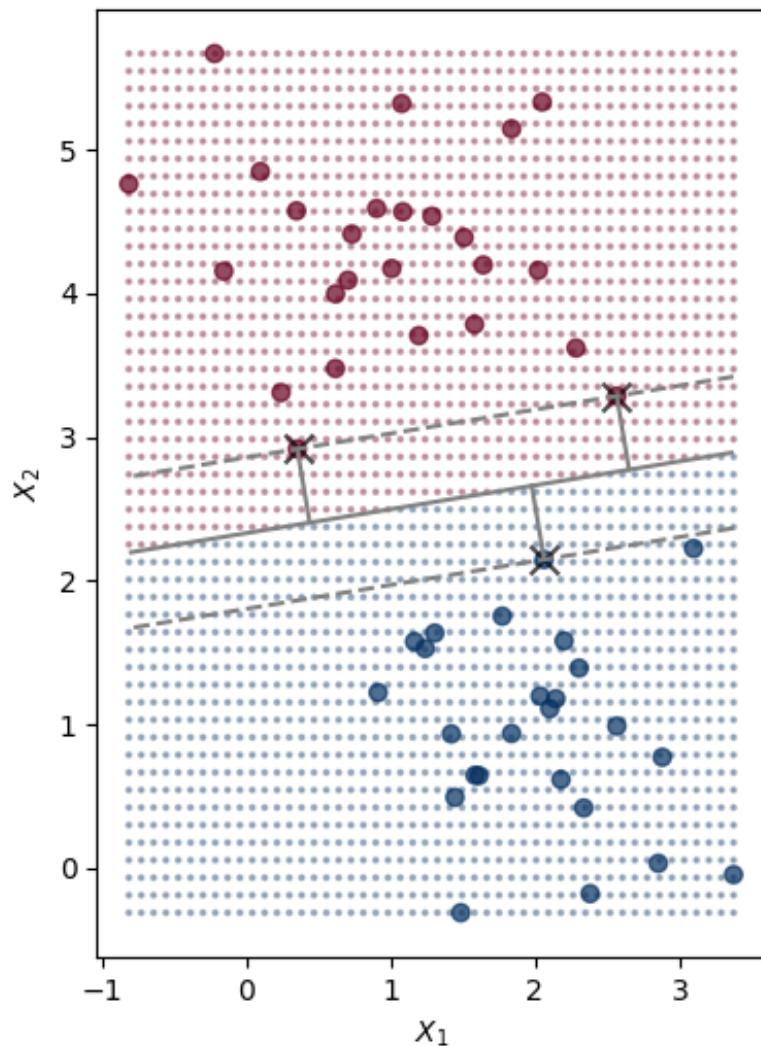


Figure 81: There are two classes of observations, shown in red and in blue. The maximal margin hyperplane is shown as a solid line. The margin is the distance from the solid line to either of the dashed lines. The two red points the blue point that lie on the dashed lines are support vectors. The red and blue grid indicates the decision rule made by a classifier based on this separating hyperplane.

9.1.4 Construction of the Maximal Margin Classifier

9.1.5 The Non-separable Case

Figure 82 shows an example where we cannot *exactly* separate the two classes. There is no maximal margin classifier.

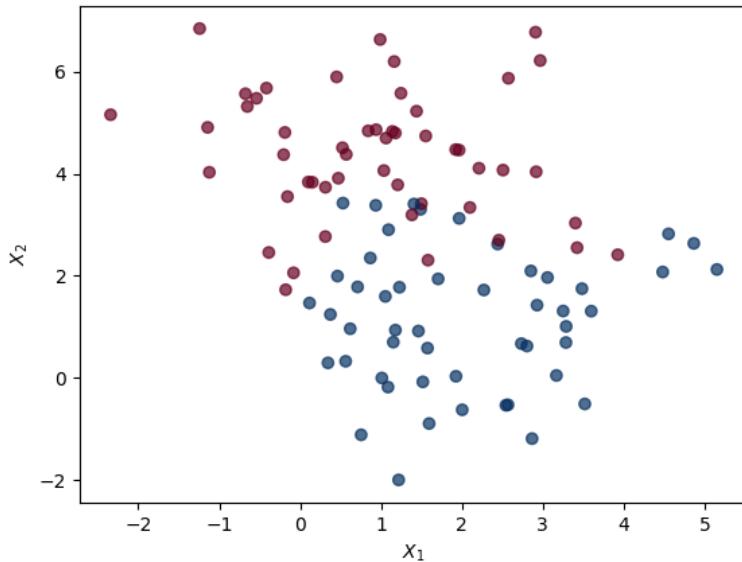


Figure 82: There are two classes of observations, shown in red and blue. In this case, the two classes are not separable by a hyperplane. Therefore, the maximal margin classifier cannot be used.

9.2 Support Vector Classifiers

9.2.1 Overview of the Support Vector Classifier

In figures 83, addition of a single observation in the right hand panel leads to a dramatic change in the maximal margin hyperplane.

Figure 84 is an example of a *support vector classifier*. Most of the observations are on the correct side of the margin. However, a small subset of observations are on the wrong side of the margin.

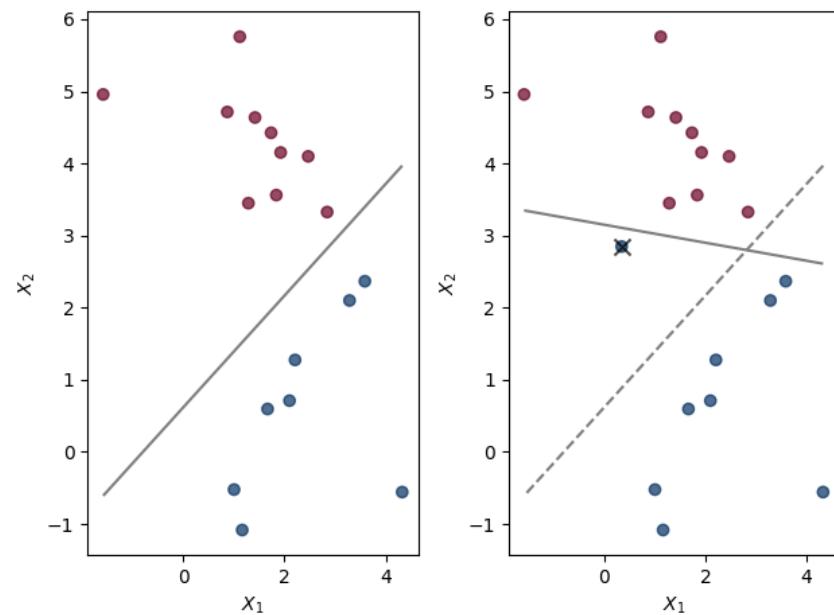


Figure 83: Left: Two classes of observations are shown in blue and in red, along with the maximal margin hyperplane. Right: An additional blue observation (marked with ‘x’) has been added, leading to a dramatic shift in the maximal margin hyperplane shown as a solid line. The dashed line indicates the maximal margin hyperplane that was obtained in the absence of this additional point.

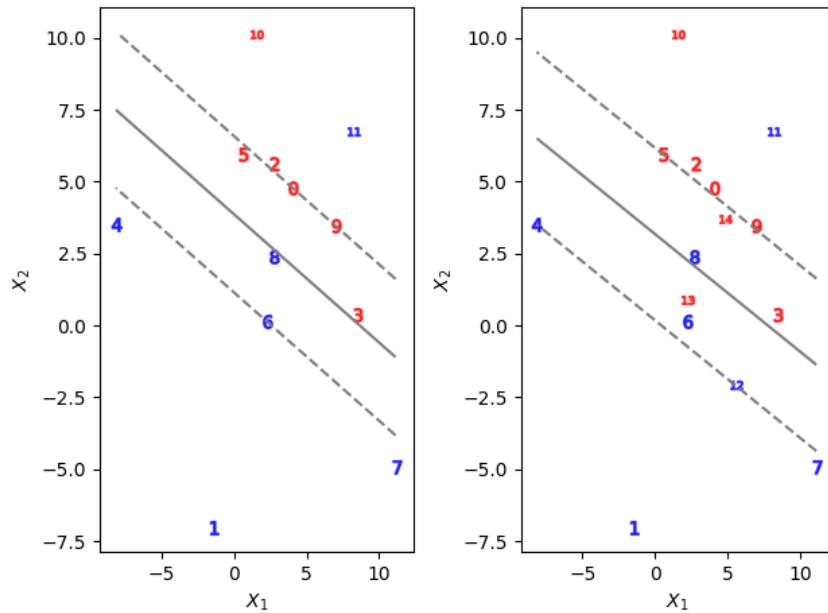


Figure 84: Left: A support vector classifier was fit to a small data set. The hyperplane is shown as a solid line and the margins are shown as dashed lines. Blue observations: Observations 1, 4, 7 are on the correct side of the margin. Observation 6 is on the margin. Observation 8 is on the wrong side of the margin. Observation 11 is on the wrong side of the hyperplane. Red observations: Observations 2, 10 are on the right side of the margin. Observations 0, 9 are on the margin. Observations 3, 5 are on the wrong side of the margin. No observation is on the wrong side of the hyperplane. Right: Same as right panel, with three additional points 12, 13, and 14. Observation 13 is on the wrong side of hyperplane. Now observation 8 is also on the wrong side of the hyperplane.

9.2.2 Details of the Support Vector Classifier

Figure 85 illustrates the width of margin for different values of regularization parameter C .

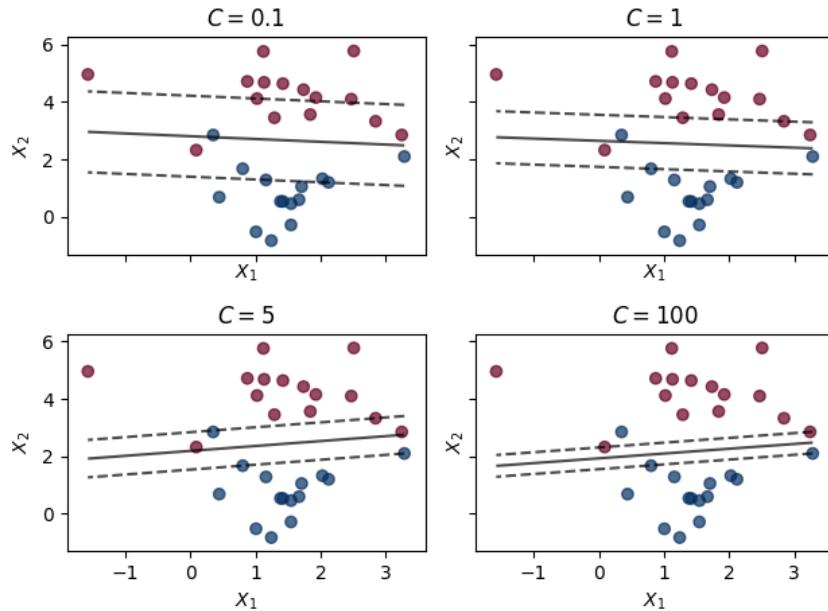


Figure 85: A support vector classifier was fit using four different values of the regularization parameter C (which is different from C , the non-negative tuning parameter, described in the book). The strength of the regularization is inversely proportional to C . When C is small, there is a high tolerance for observations being on the wrong side of the margin. Therefore, the margin is wide. As C increases, the tolerance for observations being on the wrong side of the margin decreases. Therefore, the margin narrows.

9.3 Support Vector Machines

9.3.1 Classification with Non-linear Decision Boundaries

In figure 86 consider the data shown in the left panel. It is clear that a support vector classifier or any linear classifier will perform poorly here. Indeed, the support vector classifier shown in the right panel is useless here.

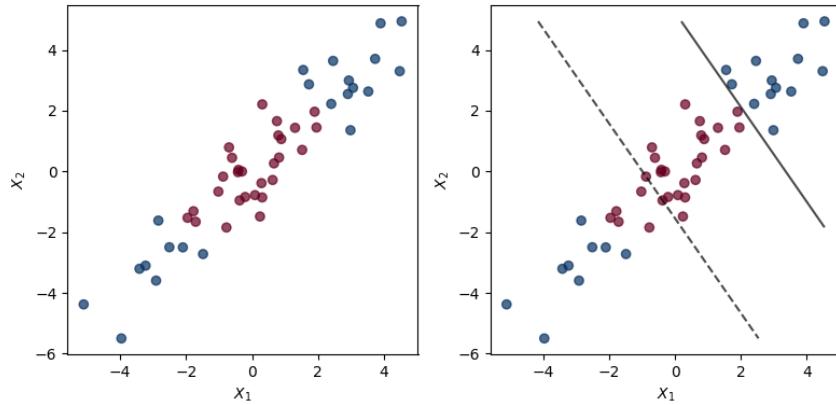


Figure 86: Left: The observations fall into two classes, with a non-linear boundary between them. Right: The support vector classifier seeks a linear boundary, and consequently performs poorly.

9.3.2 The Support Vector Machine

In figure 87, the left-hand panel shows an example of SVM with a polynomial kernel applied the non-linear data from figure 86. The fit is an improvement over the linear support vector classifier. The right-hannd panel show an example of an SVM with a radial kernel on this non-linear data. SVM does the best job of separating the two classes.

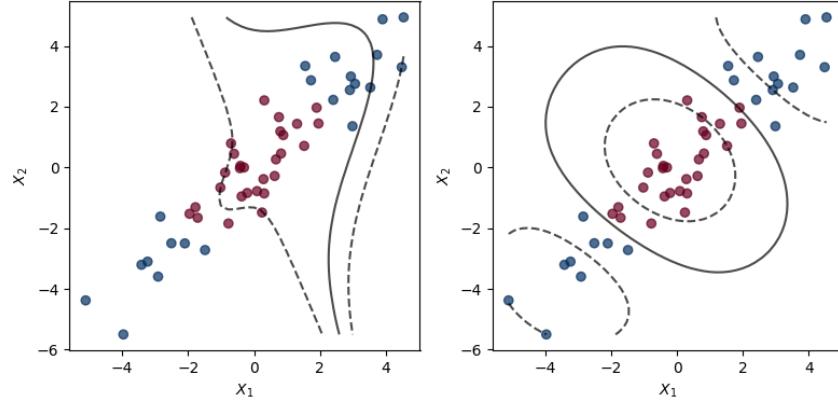


Figure 87: Left: An SVM with a polynomial kernel of degree 3 is applied to the non-linear data from figure 86, resulting in a more appropriate decision rule. Right: An SVM with a radial kernel is applied. In this example, radial kernel is the most capable of capturing the decision boundary.

9.3.3 An Application to the Heart Disease Data

In figure 88, the left-hand panel displays ROC curves for training set predictions for both LDA and the support vector classifier. The right-hand panel displays ROC curves for SVMs using a radial kernel, with two values of γ . As γ increases and the fit becomes more non-linear, the ROC improves.

Figure 89 compares ROC curves on test observations. Using default settings for all parameters other than γ , SVM model performance is worse than support vector classifier model performance. In the code, there is a commented section which shows how model parameters C and γ can be tuned to improve model performance.

9.3 Support Vector Machines

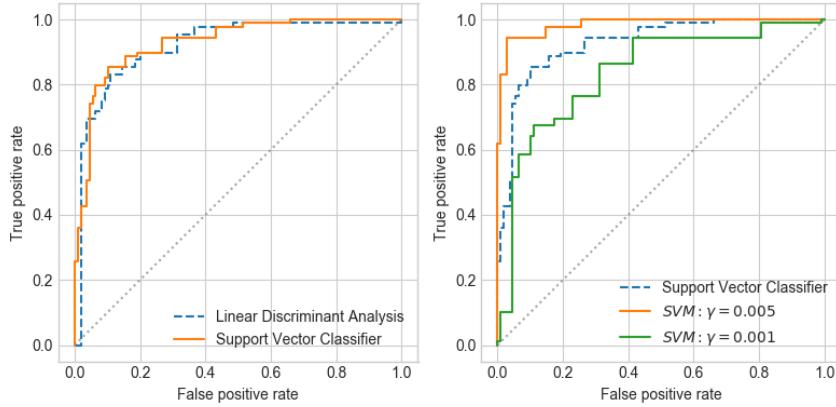


Figure 88: ROC curves for Heart data training set. Left: The support vector classifier and LDA are compared. Right: The support vector classifier is compared to an SVM using radial basis kernel with $\gamma = 0.005$ and $\gamma = 0.001$.

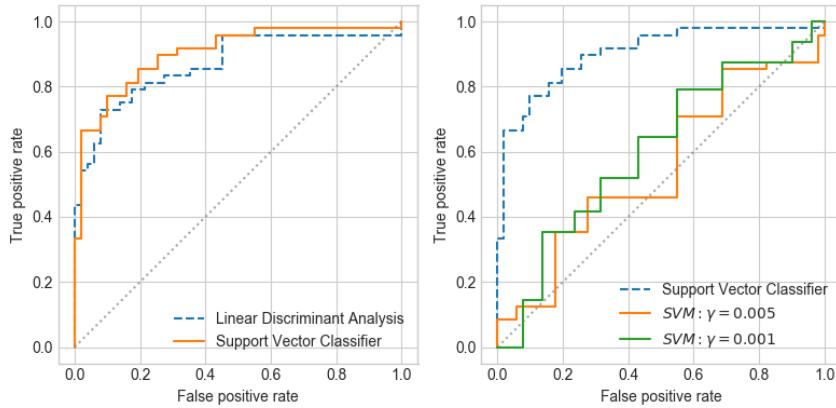


Figure 89: ROC curves for test set of the Heart data. Left: The support vector classifier and LDA are compared. Right: The support vector classifier is compared to an SVM using radial basis kernel with $\gamma = 0.005$ and $\gamma = 0.001$.

9.4 SVMs with More than Two Classes

9.4.1 One-Versus-One Classification

9.4.2 One-Versus-All Classification

9.5 Relationship with Logistic Regression

9.6 Lab: Support Vector Machines

We use `svm` module of `sklearn` library to demonstrate the support vector classifier and the SVM.

9.6.1 Support Vector Classifier

To fit a support vector classifier, we use `SVC` function with the argument `kernel` set to '`linear`'.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import rpy2.robjects as robjects
import sys
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import confusion_matrix
plt.style.use('seaborn-whitegrid')
sys.path.append('code/chap9')

from svm_funcs import svm_model_plot
# To replicate results, get data from R
X = robjects.r('''set.seed(1); x <- matrix(rnorm(20 * 2))''')
X = np.array(X).reshape((20, 2), order='F')
y = np.concatenate([np.ones(10) * -1, np.ones(10)])
y = y.astype(int)
X[y == 1, :] += 1

# Plot shows classes are not linearly separable
plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.get_cmap('RdBu',
2), alpha=0.7)

# Fit support vector classifier
svc = SVC(C=10, kernel='linear')
svc.fit(X, y)

svm_model_plot(svc, X, y)

# Support vector indices
# Remember python count begins at 0; R count begins at 1
```

```
print('Support vector indices:', svc.support_)

print('Parameters of support vector classifier:')
# print(svc.get_params())
for param_name in ['C', 'kernel']:
    print(' ', param_name, ':', svc.get_params()[param_name])
print('Number of support vectors:', svc.n_support_)
print('Number of classes:', svc.n_features_in_)
print('Classes:', svc.classes_)
print('-----')

# Use smaller value of cost to obtain larger number of support
vectors
svc = SVC(C=0.1, kernel='linear')
svc.fit(X, y)
svm_model_plot(svc, X, y)
print('Suport vector indices:', svc.support_)
print('-----')

# Use grid search to find the value of cost parameter C for
best fit
param_grid = {'C': [0.001, 0.01, 0.1, 1, 5, 10, 100]}
svc = SVC(kernel='linear')
grid = GridSearchCV(svc, param_grid=param_grid, cv=10)
grid.fit(X, y)

grid_res = pd.DataFrame(grid.cv_results_['params'])
grid_res['score'] = grid.cv_results_['mean_test_score']

print('Best parameter:', grid.best_params_)
print('Performance results:')
print(grid_res)
print('-----')

# Generate test data set
# First run code in book so that test set is identical to that
used in the book
# This does not produce results identical to those shown in the
book
# test_data = robjects.r('')
# get_x_test <- function(){
#   x <- matrix(rnorm(20 * 2), ncol = 2)
#   y <- c(rep(-1, 10), rep(1, 10))
#   x[y == 1, ] <- x[y == 1, ] + 1
#   dat <- data.frame(x = x, y = as.factor(y))
#   library(e1071)
#   svmfit <- svm(y ~ ., data = dat, kernel = 'linear', cost =
10, scale = FALSE)
#   set.seed(1)
```

```
# tune.out <- tune(svm, y ~ ., data = dat, kernel = 'linear',
#                   ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)))
# x_test <- matrix(rnorm(20 * 2))
# y_test <- sample(c(-1, 1), 20, rep = TRUE)
# c(x_test, y_test)
#
# get_x_test()
# ''')
# test_data = np.array(test_data)
# X_test = test_data[:20 * 2]
# X_test = np.array(X_test).reshape((20, 2), order='F')
# y_test = test_data[20 * 2:]
# y_test = np.array(y_test).astype(int)
# X_test[y_test == 1, :] += 1

np.random.seed(11)
X_test = np.random.normal(size=[20, 2])
y_test = np.random.choice([-1, 1], size=20, replace=True)
X_test[y_test == 1, :] += 1

model = grid.best_estimator_
y_predict = model.predict(X_test)

res_df = pd.DataFrame(confusion_matrix(y_test, y_predict),
                      columns=[-1, 1],
                      index=[-1, 1])
res_df.columns.name = 'Predict'
res_df.index.name = 'True'

print('Prediction on test data with best model (C=0.1):')
print(res_df)
print('-----')

# Fit support vector classifier with C = 0.01, then predict on
# test data
svc = SVC(C=0.01, kernel='linear')
svc.fit(X, y)
y_predict = svc.predict(X_test)
res_df_new = pd.DataFrame(confusion_matrix(y_test, y_predict),
                           columns=[-1, 1],
                           index=[-1, 1])
res_df_new.columns.name = 'Predict'
res_df_new.index.name = 'True'

print('Prediction on test data with model using C = 0.01:')
print(res_df_new)
print('-----')

# Separate the two classes so that they are linearly separable
```

9.6 Lab: Support Vector Machines

```
X[y == 1, :] += 0.5
plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.get_cmap('RdBu',
2), alpha=0.7)

X_test[y_test == 1, :] += 0.5

# Fit a support vector classifier with a high value of cost
svc = SVC(C=1e5, kernel='linear')
svc.fit(X, y)
svm_model_plot(svc, X, y)

print('Cost parameter:', svc.get_params()['C'])
print('Number of support vectors:', svc.n_support_)
print('Fraction of training observations correctly predicted:',
      svc.score(X, y))
print('Fraction of testing observations correctly predicted:',
      svc.score(X_test, y_test))
print('-----')

# Refit model with smaller value of cost parameter
svc = SVC(C=1, kernel='linear')
svc.fit(X, y)
svm_model_plot(svc, X, y)

print('Cost parameter:', svc.get_params()['C'])
print('Number of support vectors:', svc.n_support_)
print('Fraction of training observations correctly predicted:',
      svc.score(X, y))
print('Fraction of testing observations correctly predicted:',
      svc.score(X_test, y_test))
print('-----')
```

```
Support vector indices: [ 0  1  4  6 13 15 16]
Parameters of support vector classifier:
  C : 10
  kernel : linear
Number of support vectors: [4 3]
Number of classes: 2
Classes: [-1  1]
-----
Suport vector indices: [ 0  1  2  3  4  6  8  9 11 12 13 14 15 16 17 19]
-----
Best parameter: {'C': 0.1}
Performance results:
  C   score
```

```
0      0.001    0.75
1      0.010    0.75
2      0.100    0.95
3      1.000    0.90
4      5.000    0.85
5     10.000    0.85
6    100.000    0.85
-----
Prediction on test data with best model (C=0.1):
Predict -1    1
True
-1      11    2
1       2    5
-----
Prediction on test data with model using C = 0.01:
Predict -1    1
True
-1      12    1
1       4    3
-----
Cost parameter: 100000.0
Number of support vectors: [1 2]
Fraction of training observations correctly predicted: 1.0
Fraction of testing observations correctly predicted: 0.9
-----
Cost parameter: 1
Number of support vectors: [3 4]
Fraction of training observations correctly predicted: 0.95
Fraction of testing observations correctly predicted: 0.9
-----
```

9.6.2 Support Vector Machine

In order to fit an SVM using a non-linear kernel, we once again use the SVC function. We now set the parameter `kernel` to '`rbf`'.

```
import numpy as np
import rpy2.robj as robjects
import sys
import matplotlib.pyplot as plt
import pandas as pd
```

```
from sklearn.model_selection import train_test_split,
    GridSearchCV
from sklearn.svm import SVC

sys.path.append('code/chap9')

from svm_funcs import svm_model_plot

# To replicate results, get data from R
X = robjects.r('''set.seed(1); x <- matrix(rnorm(200 * 2), ncol
    = 2)''')
X = np.array(X).reshape(200, 2)
X[:100, :] += 2
X[100:150, :] -= 2
y = np.concatenate([np.ones(150), np.ones(50) * 2])

plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.get_cmap('RdBu',
    2), alpha=0.7)

# Split data between train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y,
    test_size=100,
    random_state=0)

# Fit training data set with a radial kernel
svm = SVC(kernel='rbf')
svm.fit(X_train, y_train)

svm_model_plot(svm, X_train, y_train)

print('SVM model fit with cost parameter:', svm.get_params()['C
    '])
print('Number of support vectors:', svm.n_support_)
print('Fraction of accurate predictions on training data:', 
    svm.score(X_train, y_train))
print('Fraction of accurate predictions on test data:', 
    svm.score(X_test, y_test))
print('-----')

# Fit training data set with a high value for cost parameter
svm = SVC(C=1e5, kernel='rbf')
svm.fit(X_train, y_train)

svm_model_plot(svm, X_train, y_train)

print('SVM model fit with cost parameter:', svm.get_params()['C
    '])
print('Number of support vectors:', svm.n_support_)
print('Fraction of accurate predictions on training data:',
```

```
    svm.score(X_train, y_train))
print('Fraction of accurate predictions on test data:',
      svm.score(X_test, y_test))
print('-----')

# Find best values of C and gamma using grid search
param_grid = {'C': [0.1, 1, 5], 'gamma': [0.1, 0.5, 1]}
svm = SVC(kernel='rbf')
grid = GridSearchCV(svm, param_grid=param_grid)
grid.fit(X_train, y_train)

res_df = pd.DataFrame(grid.cv_results_['params'])
res_df['test_score'] = grid.cv_results_['mean_test_score']

print('Grid search results:')
print(res_df)
print('Fraction of accurate predictions on test data:',
      grid.best_estimator_.score(X_test, y_test))
```

```
SVM model fit with cost parameter: 1.0
Number of support vectors: [15 14]
Fraction of accurate predictions on training data: 0.92
Fraction of accurate predictions on test data: 0.85
-----
SVM model fit with cost parameter: 100000.0
Number of support vectors: [11  8]
Fraction of accurate predictions on training data: 0.99
Fraction of accurate predictions on test data: 0.8
-----
Grid search results:
      C   gamma  test_score
0  0.1    0.1      0.75
1  0.1    0.5      0.74
2  0.1    1.0      0.75
3  1.0    0.1      0.92
4  1.0    0.5      0.93
5  1.0    1.0      0.92
6  5.0    0.1      0.92
7  5.0    0.5      0.92
8  5.0    1.0      0.88
Fraction of accurate predictions on test data: 0.86
```

9.6.3 ROC Curves

In `sklearn` library, `metrics` module provides functions `roc_curve` and `plot_roc_curve`.

```
import numpy as np
import matplotlib.pyplot as plt
import rpy2.robjects as robjects
from sklearn.svm import SVC
from sklearn.metrics import plot_roc_curve
from sklearn.model_selection import train_test_split

X = robjects.r('''set.seed(1); x <- matrix(rnorm(200 * 2), ncol
= 2)''')
X = np.array(X, order='F')
X[:100, :] += 2
X[100:150, :] -= 2
y = np.concatenate([np.ones(150), np.ones(50) * 2])

X_train, X_test, y_train, y_test = train_test_split(X, y)

svm = SVC(probability=True, random_state=0)
svm.fit(X_train, y_train)

fig, ax = plt.subplots()
plot_roc_curve(svm, X_train, y_train, label='Training data', ax
=ax)
plot_roc_curve(svm, X_test, y_test, label='Test data',
linestyle='--', ax=ax)
```

9.6.4 SVM with Multiple Classes

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn.svm import SVC
from sklearn.model_selection import train_test_split

np.random.seed(0)
X = np.random.normal(size=[200, 2])
X[:100, :] += 2
X[100:150, :] -= 2
y = np.concatenate([np.ones(150), np.ones(50) * 2])

X = np.vstack([X, np.random.normal(size=[50, 2])])
y = np.concatenate([y, np.zeros(50)])
y = y.astype(int)
X[y == 0, 1] += 2
```

9.6 Lab: Support Vector Machines

```
plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.get_cmap('viridis', 3),
            alpha=0.7)

X_train, X_test, y_train, y_test = train_test_split(X, y,
                                                    random_state=0)

svm = SVC()
svm.fit(X_train, y_train)

print('In training data, fraction of observations correctly
      classified:',
      round(svm.score(X_train, y_train), 2))
print('In test data, fraction of observations correctly
      classified:',
      round(svm.score(X_test, y_test), 2))
```

In training data, fraction of observations correctly classified: 0.81
In test data, fraction of observations correctly classified: 0.84

9.6.5 Application to Gene Expression Data

```
import numpy as np
import pandas as pd
from rpy2 import robjects
from sklearn.svm import SVC
from sklearn.metrics import confusion_matrix

khan = {}
khan['xtrain'] = robjects.r('library(ISLR); Khan$xtrain')
khan['xtest'] = robjects.r('Khan$xtest')
khan['ytrain'] = robjects.r('Khan$ytrain')
khan['ytest'] = robjects.r('Khan$ytest')

X_train = np.array(khan['xtrain'])
X_test = np.array(khan['xtest'])
y_train = np.array(khan['ytrain']).astype(int)
y_test = np.array(khan['ytest']).astype(int)

print('Shape of training data:', X_train.shape)
print(y_train.shape)
print('Shape of test data:', X_test.shape)
print(y_test.shape)

print('Count of tissue sample types in training data:')
print(pd.value_counts(y_train).sort_index())
print('In test data:')
```

```
print(pd.value_counts(y_test).sort_index())
print('-----')

# Fit linear kernel model
svc = SVC(kernel='linear')
svc.fit(X_train, y_train)

y_predict_train = svc.predict(X_train)
train_confusion = pd.DataFrame(confusion_matrix(y_train,
    y_predict_train))
y_predict_test = svc.predict(X_test)
test_confusion = pd.DataFrame(confusion_matrix(y_test,
    y_predict_test))

for df in [train_confusion, test_confusion]:
    df.columns = [1, 2, 3, 4]
    df.index = [1, 2, 3, 4]
    df.columns.name = 'Predicted'
    df.index.name = 'True'

print('Number of support vectors:', svc.n_support_)
print('Fraction of correct predictions on training data:',
    svc.score(X_train, y_train))
print('Confusion matrix on training data:')
print(train_confusion)
print('-----')

print('Fraction of correct predictions on test data:',
    svc.score(X_test, y_test))
print('Confusion matrix on test data:')
print(test_confusion)
```

```
Shape of training data: (63, 2308)
(63,)
Shape of test data: (20, 2308)
(20,)
Count of tissue sample types in training data:
1      8
2     23
3     12
4     20
dtype: int64
In test data:
1      3
2      6
3      6
```

```
4      5
dtype: int64
-----
Number of support vectors: [ 7 18  9 20]
Fraction of correct predictions on training data: 1.0
Confusion matrix on training data:
Predicted  1   2   3   4
True
1          8   0   0   0
2          0  23   0   0
3          0   0  12   0
4          0   0   0  20
-----
Fraction of correct predictions on test data: 0.9
Confusion matrix on test data:
Predicted  1   2   3   4
True
1          3   0   0   0
2          0   6   0   0
3          0   2   4   0
4          0   0   0   5
```

10 Unsupervised Learning

10.1 The Challenge of Unsupervised Learning

10.2 Principal Component Analysis

10.2.1 What are Principal Components?

We first normalize `USArrests` data so that every variable has mean 0 and standard deviation 1. Then we perform PCA on the normalized data set. Table 20 shows loadings of the first two principal components. Figure 90 plots the first two principal components of these data. The figure represents both the principal component scores and the loading vectors in a single *biplot* display.

10.2 Principal Component Analysis

	PC1	PC2
Murder	0.5358995	0.4181809
Assault	0.5831836	0.1879856
UrbanPop	0.2781909	-0.8728062
Rape	0.5434321	-0.1673186

Table 20: The principal component loading factors, ϕ_1 and ϕ_2 , for the `USArrests` data. These are also displayed in figure 90.

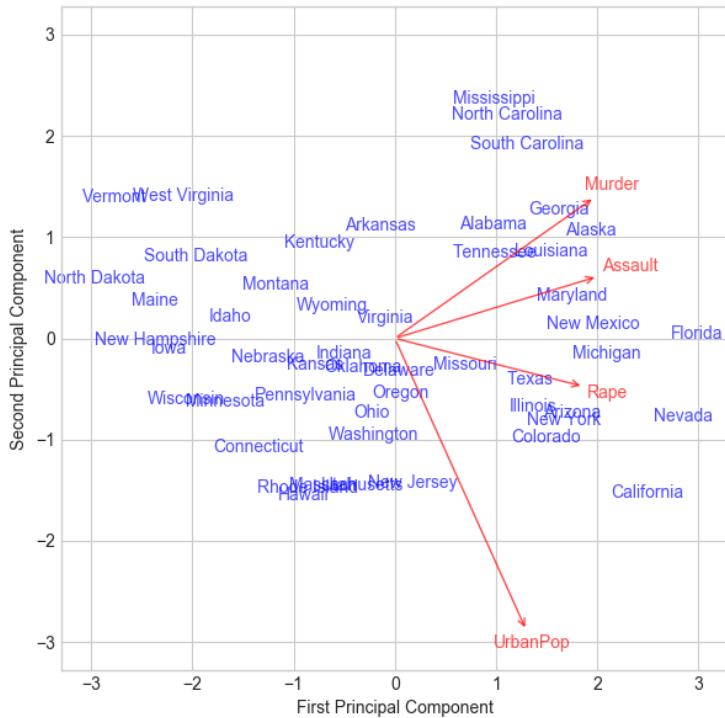


Figure 90: The first two principal components for the `USArrests` data. The blue state names represent the scores for the first two principal components. The red arrows indicate the first two principal components loading vectors. This figure is known as a biplot, because it displays both the principal component scores and the principal component loadings.

10.2.2 Another Interpretation of Principal Components

10.2.3 More on PCA

In figure 91, the left-hand panel is the same as figure 90, where each variable was first scaled to have mean zero and standard deviation one, then principal component analysis was performed. The right-hand panel displays the first two principal components on the raw data. Since variables were not scaled to have standard deviation one, the first principal component places almost all of its weight on **Assault**, while the second principal component places almost all of its weight on **UrbanPop**.

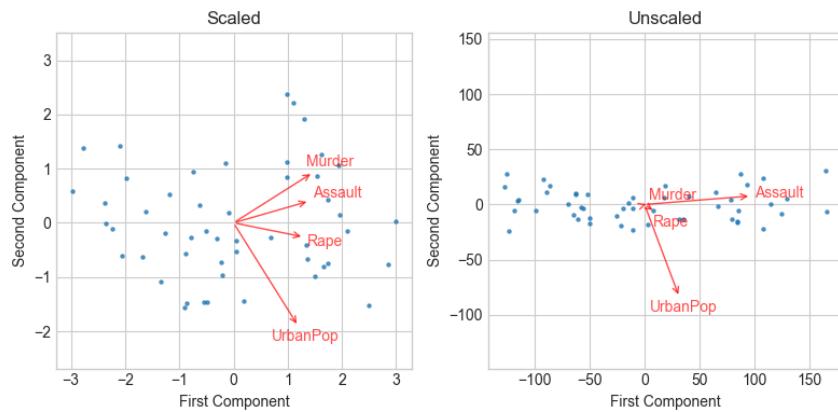


Figure 91: Two principal component biplots for **USArrests** data. Left: Same as figure 90, with variables scaled to have unit standard deviations. Right: Principal components using unscaled data. **Assault** has by far the largest loading on the first principal component because it has the largest variance among the four variables. In general, it is recommended to scale variables to have standard deviation one.

In Figure 92, the left-hand panel shows the proportion of variance explained (PVE) by each principal component of **USArrests** data. The right-hand panel shows the cumulative PVE.

10.3 Clustering Methods

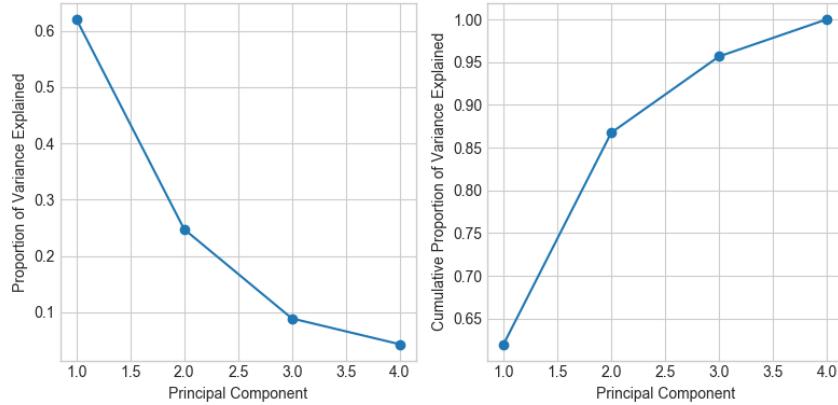


Figure 92: Left: A scree plot depicting the proportion of variance explained by each of the four principal components in the `USArrests` data. Right: The cumulative proportion of variance explained by the four principal components.

10.3 Clustering Methods

10.3.1 K-Means Clustering

Figure 93 shows the results obtained from performing K -means clustering on a simulated example consisting of 60 observations in two dimensions. Three different values of K are used.

10.3 Clustering Methods

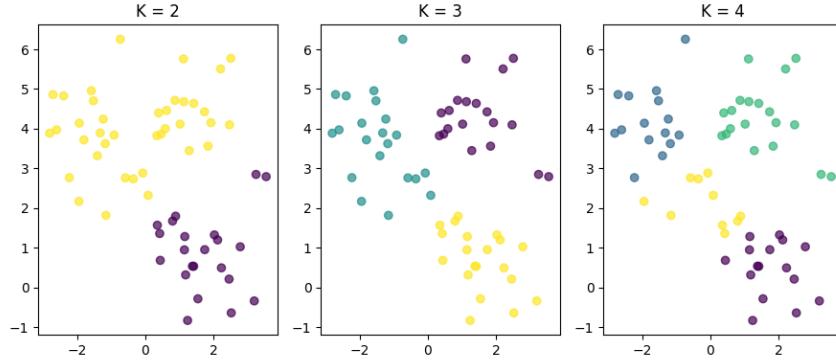


Figure 93: A simulated data set with 60 observations in two-dimensional space. Panels show the results of applying K -means clustering with different values of K , the number of clusters. The color of each observation indicates the cluster to which it was assigned using the K -means clustering algorithm. Since there is no ordering of clusters, the cluster coloring is arbitrary. The cluster labels are the outputs of the clustering procedure.

Figure 94 shows the progression of the K -Means Clustering Algorithm on the toy example from figure 93.

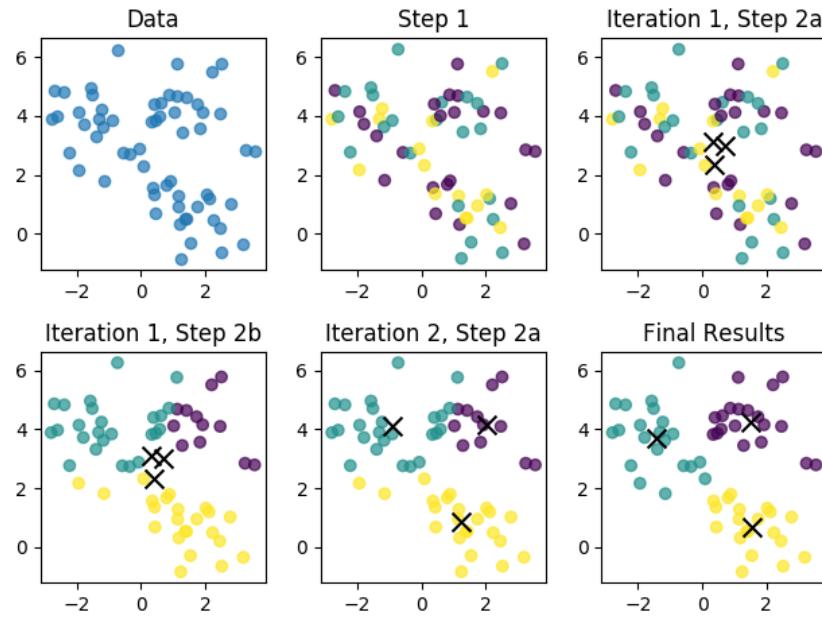


Figure 94: The progress of K -means algorithm on the example of figure 93 with $K = 3$. Top left: The observations are shown. Top center: In Step 1 of the algorithm, each observation is randomly assigned to a cluster. Top right: In Step 2(a), the cluster centroids are computed. These are shown as \times . Since the clusters were chosen at random, initially centroids are almost overlapping. Bottom left: In Step 2(b), each observation is assigned to the nearest centroid. Bottom center: Step 2(a) is once again performed, leading to new cluster centroids. Bottom right: The results obtained after five iterations.

Figure 95 shows the local optima obtained by running K -means clustering six times using six different initial cluster assignments, using toy data from figure 93.

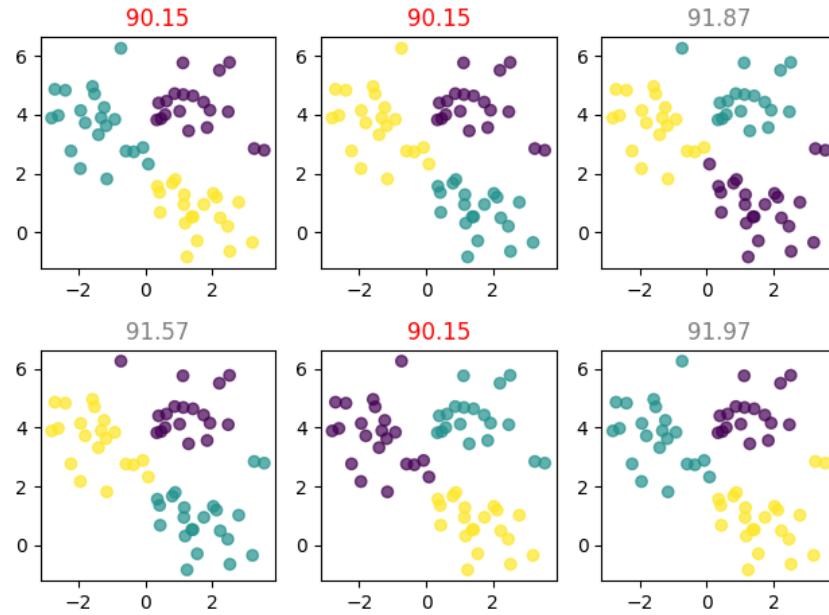


Figure 95: K -means clustering performed six times on the data from figure 93 with $K = 3$, each time with a different random assignment of the observations in Step 1 of the K -means algorithm. Above each plot is the value of the objective (sum of squares of distances from centroids). Three different local optima were obtained, one of which resulted in a smaller value of the objective and provides better separation between the clusters. Those labeled in red all achieved the same best solution.

10.3.2 Hierarchical Clustering

We begin with the simulated data set shown in figure 96, consisting of 45 observations in two-dimensional space. The data were generated from a three-class model; the true class labels for each observation are shown in distinct colors. However, suppose the data were observed without class labels, and that we wanted to perform hierarchical clustering of the data. Hierarchical clustering yields the results shown in the left-hand panel of figure 97. In the center-panel, cutting the dendrogram at a height of 15

results in two clusters. In the right-hand panel, cutting the dendrogram at a height of 10 results in three clusters.

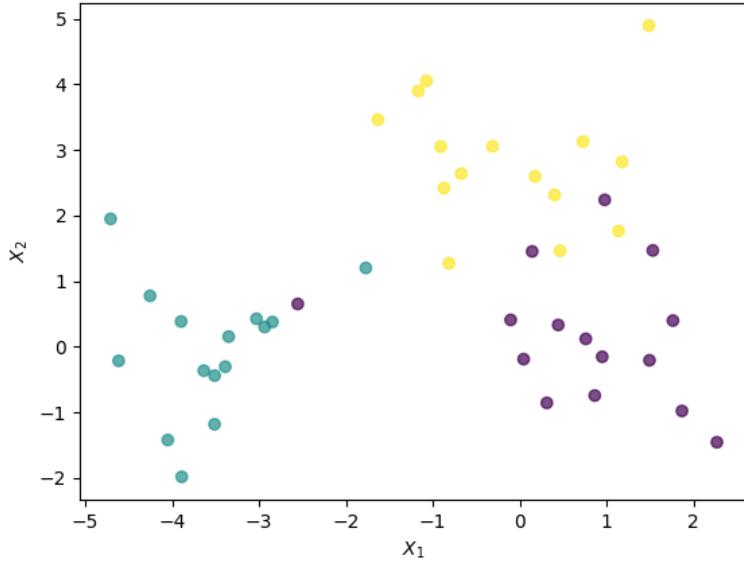


Figure 96: Forty five observations generated in two-dimensional space. In reality there are three distinct classes, shown in separate colors. However, we will treat these class labels as unknown. To discover the classes, we will seek to cluster the observations.

10.3 Clustering Methods

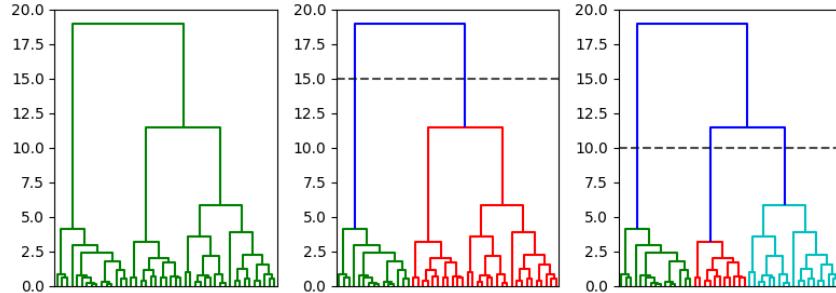


Figure 97: Left: Dendrogram obtained from hierarchically clustering the data from figure 96 with complete linkage and Euclidean distance. Center: Dendrogram from left-hand panel, cut at a height of 15 (indicated by dashed line). This cut results in two distinct clusters, shown in different colors. Right: Dendrogram from left-hand panel, now cut at a height of 10. This cut results in three distinct clusters, shown in different colors. The colors were not used in clustering, but are simply used for display purposes.

Consider the left-hand panel of figure 98, which shows a simple dendrogram obtained from hierarchically clustering nine observations. We can see that observations 2 and 4 are quite similar to each other, since they fuse at the lowest point on the dendrogram. Observations 1 and 7 are also quite similar to each other. However, while observations 9 and 8 are next to each other in the dendrogram, it is incorrect to conclude that these observations are similar to each other. In fact, based on information provided in the dendrogram, observation 9 is no more similar to observation 8 than it is to observations 2 and 4.

Figure 99 displays the first few steps in hierarchical clustering algorithm, for the data from figure 97

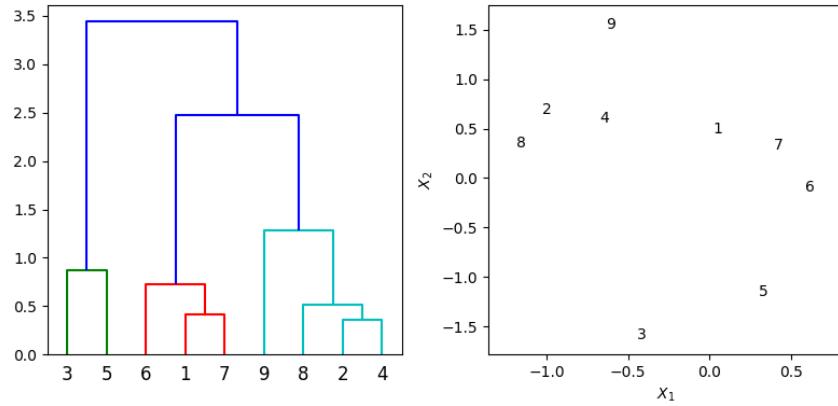


Figure 98: An illustration of how to properly interpret a dendrogram with nine observations in two-dimensional space. Left: A dendrogram generated using Euclidean distance and complete linkage. Observations 2 and 4 are quite similar to each other, as are observations 1 and 7. However, observation 9 is no more similar to observation 8 than it is to observations 2 and 4, even though observations 9 and 8 are closer together in terms of horizontal distance. This is because observations 8, 2, and 4 all fuse with observation 9 at the same height, approximately 1.3. Right: The raw data used to generate the dendrogram can be used to verify that indeed, observation 9 is no more similar to observation 8 than it is to observations 2 and 4.

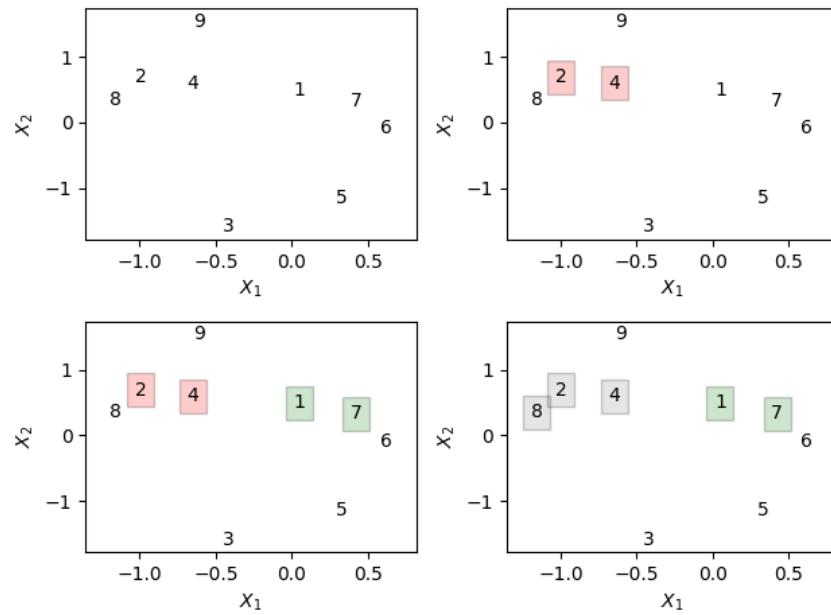


Figure 99: An illustration of the first few steps of the hierarchical clustering algorithm, using data from figure 98, with complete linkage and Euclidean distance. Top Left: Initially there are nine clusters, $\{1\}$, $\{2\}$, ..., $\{9\}$. Top Right: The two clusters that are closest together, $\{2\}$ and $\{4\}$, are fused into a single cluster. Bottom Left: The next two clusters that are closest together, $\{1\}$ and $\{7\}$, are fused into a single cluster. Bottom Right: The two clusters that are closest together using complete linkage, $\{8\}$ and $\{2, 4\}$, are fused into a single cluster.

10.3 Clustering Methods

Figure 100 illustrates dendograms resulting from the same data set when three different linkages are applied. Average and complete linkages tend to yield more balanced clusters.

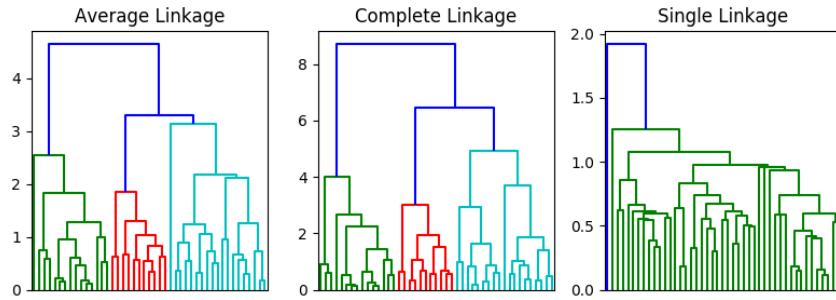


Figure 100: Average, complete, and single linkage applied to data set from figure 96. Average and complete linkages tend to yield more balanced results.

Figure 101 illustrates the difference between Euclidean and correlation-based distance.

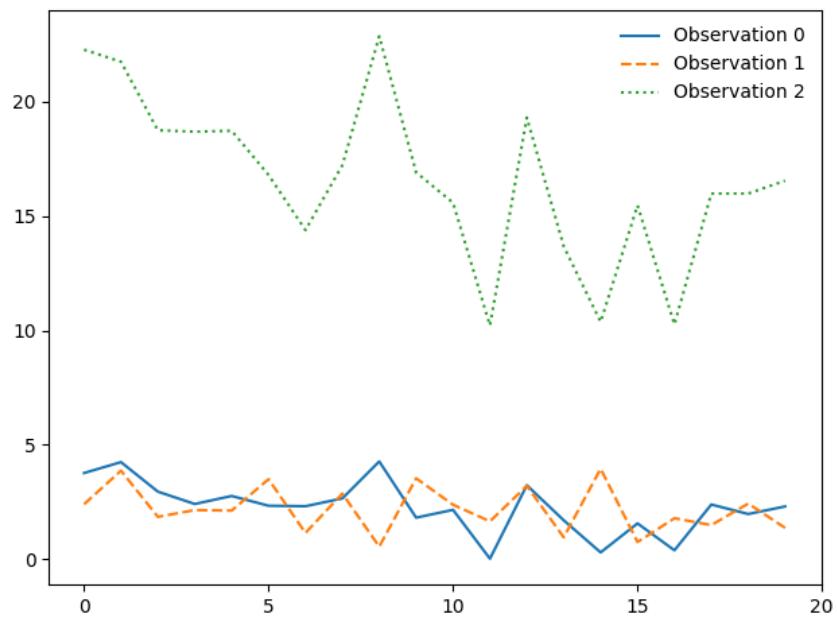


Figure 101: Three observations with measurements on 20 variables. Observations 0 and 1 have similar values for each variable. Therefore, there is a small distance between them. But since they are weakly correlated, they have a large correlation-based distance. On the other hand, observations 0 and 2 have quite different values for each variable, and so there is a large Euclidean distance between them. But since they are highly correlated, there is a small correlation-based distance between them.

10.4 Lab 1: Principal Components Analysis

```
from statsmodels.datasets import get_rdataset
import pandas as pd
from sklearn.decomposition import PCA

arrests = get_rdataset('USArrests').data

print('Variables in USArrests data:')
print(arrests.columns)
print('Means of variables:')
print(arrests.mean().round(2))
print('Variances of variables:')
print(arrests.var().round(2))
print('-----')

# Normalize data by subtracting mean and dividing by standard
# deviation
arrests_normalized = (arrests - arrests.mean()) / arrests.std()

# Calculate principal components
pca = PCA()
pca.fit(arrests_normalized)

arrests_pc = pd.DataFrame(pca.components_.T, index=
    arrests_normalized.columns)
print('Principal components of USArrests:')
print(arrests_pc)
print('-----')

# To plot Figure 10.1, see program code/chap10/arrest_pca.py
print('Variance explained by principal components:')
print(pca.explained_variance_.round(3))
print('Proportion of variance explained:')
print(pca.explained_variance_ratio_.round(4))
```

```
Variables in USArrests data:
Index(['Murder', 'Assault', 'UrbanPop', 'Rape'], dtype='object')
Means of variables:
Murder      7.79
Assault     170.76
UrbanPop     65.54
Rape        21.23
dtype: float64
Variances of variables:
Murder      18.97
```

```
Assault      6945.17
UrbanPop     209.52
Rape         87.73
dtype: float64
-----
Principal components of USArrests:
      0        1        2        3
Murder  0.535899  0.418181 -0.341233  0.649228
Assault  0.583184  0.187986 -0.268148 -0.743407
UrbanPop 0.278191 -0.872806 -0.378016  0.133878
Rape    0.543432 -0.167319  0.817778  0.089024
-----
Variance explained by principal components:
[2.48  0.99  0.357 0.173]
Proportion of variance explained:
[0.6201 0.2474 0.0891 0.0434]
```

10.5 Lab 2: Clustering

10.5.1 K-Means Clustering

```
from rpy2 import robjects
import numpy as np
from sklearn.cluster import KMeans

X = robjects.r('set.seed(2); x <- rnorm(50 * 2)')
X = np.array(X).reshape((50, 2), order='F')

X[:25, 0] += 3
X[:25, 1] -= 4

km = KMeans(n_clusters=2, random_state=0)
km.fit(X)

print('Predicted cluster assignments:')
print(km.predict(X))
print('-----')
# To plot clusters, see code/chap10/km_cluster.py

# K-means clusters with 3 clusters
km3 = KMeans(n_clusters=3, random_state=2)
km3.fit(X)

print('Cluster centers:')
print(km3.cluster_centers_)
```

```

y_predict = km3.predict(X)
within_clust_dist_sq = [((X[y_predict == i] - km3.
    cluster_centers_[i]) ** 2).sum()
    for i in range(3)]
total_dist_sq = ((X - X.mean(axis = 0)) ** 2).sum()
print('between_SS / total_SS =',
    round(1 - sum(within_clust_dist_sq) / total_dist_sq, 3) *
    100, '%')

# To select the number of times k-means algorithm will be run,
# assign a value to n_init

```

10.5.2 Hierarchical Clustering

```
from rpy2 import robjects
import numpy as np
from scipy.cluster.hierarchy import linkage, dendrogram,
    fcluster
import matplotlib.pyplot as plt

X = robjects.r('set.seed(2); x <- rnorm(50 * 2)')
X = np.array(X).reshape((50, 2), order='F')

X[:25, 0] += 3
X[:25, 1] -= 4

hc_complete = linkage(X, method='complete')
hc_average = linkage(X, method='average')
hc_single = linkage(X, method='single')
link_names = ['Complete', 'Average', 'Single']

fig = plt.figure(figsize=(8, 3))
for i, hc in enumerate([hc_complete, hc_average, hc_single]):
    axi = fig.add_subplot(1, 3, i + 1)
    dendrogram(hc, labels=link_names, color_threshold=0)
```

10.6 Lab 3: NCI60 Data Example

10.6 Lab 3: NCI60 Data Example

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

10.6 Lab 3: NCI60 Data Example

```
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data

print('Data dimensions:', nci_data.shape)
print('Counts of cancer types:')
print(nci_data['labs'].value_counts())
```

Data dimensions: (64, 6831)

Counts of cancer types:

RENAL	9
NSCLC	9
MELANOMA	8
COLON	7
BREAST	7
LEUKEMIA	6
OVARIAN	6
CNS	5
PROSTATE	2
K562B-repro	1
K562A-repro	1
MCF7A-repro	1
UNKNOWN	1
MCF7D-repro	1

Name: labs, dtype: int64

10.6.1 PCA on NCI60 Data

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data

from sklearn.decomposition import PCA

X = nci_data.iloc[:, :-1]          # do not include labs

pca = PCA(n_components=3)
pca.fit(X)
```

```
labs = nci_data['labs']
lab_names = nci_data['labs'].unique()
lab_names.sort()
lab_colors = labs.apply(lambda x: np.where(lab_names == x)
                       [0][0])

Z = pca.transform(X)

fig = plt.figure(figsize=(8, 4))
ax1 = fig.add_subplot(1, 2, 1)
ax1.scatter(Z[:, 0], Z[:, 1], c=lab_colors,
            cmap=plt.cm.get_cmap('rainbow', len(lab_names)), alpha
            =0.7)
ax1.set(xlabel=r'$Z_1$', ylabel=r'$Z_2$')

ax2 = fig.add_subplot(1, 2, 2)
ax2.scatter(Z[:, 0], Z[:, 2], c=lab_colors,
            cmap=plt.cm.get_cmap('rainbow', len(lab_names)), alpha
            =0.7)
ax2.set(xlabel=r'$Z_1$', ylabel=r'$Z_3$')

fig.tight_layout()
fig.savefig(fname)
return fname
```

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data

from sklearn.decomposition import PCA
import pandas as pd

X = nci_data.iloc[:, :-1]           # do not include labs
X_scaled = (X - X.mean()) / X.std()

pca = PCA(n_components=5)
pca.fit(X_scaled)

pca_res = np.vstack([np.sqrt(pca.explained_variance_),
                     pca.explained_variance_ratio_,
                     np.cumsum(pca.explained_variance_ratio_)])
```

```
pca_res_df = pd.DataFrame(
    pca_res, columns=['PC1', 'PC2', 'PC3', 'PC4', 'PC5'],
```

10.6 Lab 3: NCI60 Data Example

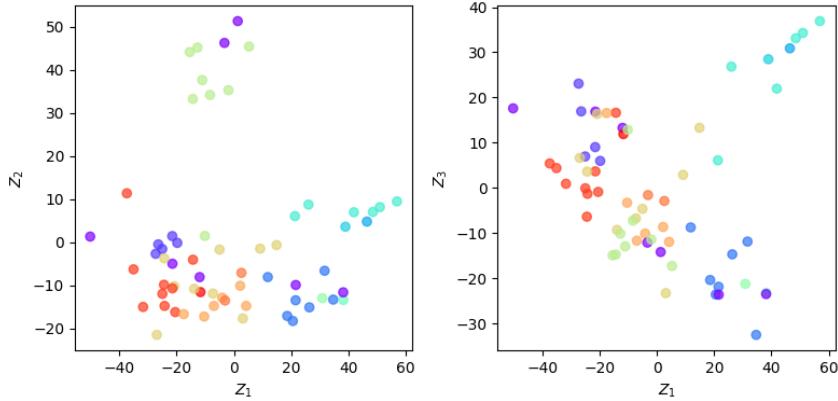


Figure 102: Projections of the NCI60 cancer cell lines onto the first three principal components. On the whole, in this low-dimensional space, observations belonging to a single cancer type tend to be near each other. It would not have been possible to visualize the data without using a dimension reduction method such as PCA. Based on the full data set, there are $\binom{6,830}{2}$ possible scatterplots, none of which would have been particularly informative.

```
index=[ 'Standard deviation', 'Proportion of variance',
       'Cumulative proportion'])

print('Proportion of variance explained (PVE) of first five
      principal components:')
print(pca_res_df.round(4))
```

	Proportion of variance explained (PVE) of first five principal components:				
	PC1	PC2	PC3	PC4	PC5
Standard deviation	27.8535	21.4814	19.8205	17.0326	15.9718
Proportion of variance	0.1136	0.0676	0.0575	0.0425	0.0373
Cumulative proportion	0.1136	0.1812	0.2387	0.2811	0.3185

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data
```

```

from sklearn.decomposition import PCA

X = nci_data.iloc[:, :-1]           # do not include labs
X_normalized = (X - X.mean()) / X.std()

pca = PCA()
pca.fit(X_normalized)

fig = plt.figure(figsize=(8, 4))
ax1 = fig.add_subplot(1, 2, 1)
ax1.plot(pca.explained_variance_ratio_)
ax1.set(xlabel='Principal Component', ylabel='PVE')

ax2 = fig.add_subplot(1, 2, 2)
ax2.plot(np.cumsum(pca.explained_variance_ratio_))
ax2.set(xlabel='Principal Component', ylabel='Cumulative PVE')

fig.tight_layout()
fig.savefig(fname)
return fname

```

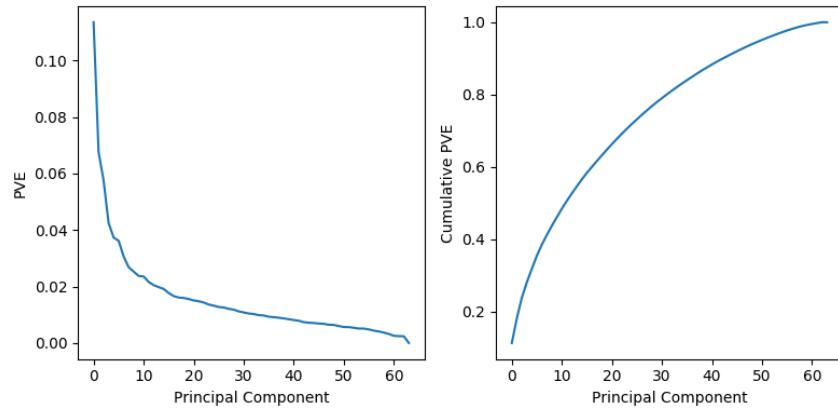


Figure 103: The PVE of principal components of the NCI60 cancer cell line microarray data set. Left: PVE of each principal component is shown. Right: Cumulative PVE of the principal components is shown. Together, all principal components explain all of the variance.

10.6.2 Clustering the Observations of the NCI60 Data

10.6 Lab 3: NCI60 Data Example

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data

from scipy.cluster.hierarchy import linkage, dendrogram

X = nci_data.iloc[:, :-1]           # do not include labs
X_scaled = (X - X.mean()) / X.std()

linkages = ['complete', 'average', 'single']

fig = plt.figure(figsize=(6, 8))
for i, link in enumerate(linkages):
    axi = fig.add_subplot(3, 1, i + 1)
    Z = linkage(X_scaled, method=link)
    dn = dendrogram(Z, labels=nci_data['labs'], leaf_rotation
                     =90, ax=axi)
    axi.set(title=link.capitalize() + ' Linkage')

fig.tight_layout()
fig.savefig(fname)
return fname



---


import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.datasets import get_rdataset

nci = get_rdataset('NCI60', package='ISLR')
nci_data = nci.data

from scipy.cluster.hierarchy import linkage, dendrogram,
    fcluster
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA

X = nci_data.iloc[:, :-1]
X_scaled = (X - X.mean()) / X.std()

Z = linkage(X_scaled, method='complete')
Z_labels = fcluster(Z, t=4, criterion='maxclust')

res_tab = pd.crosstab(nci_data['labs'], Z_labels)
res_tab.columns.name = 'predict_label'
print('Cross table when dendrogram is used to predict four
```

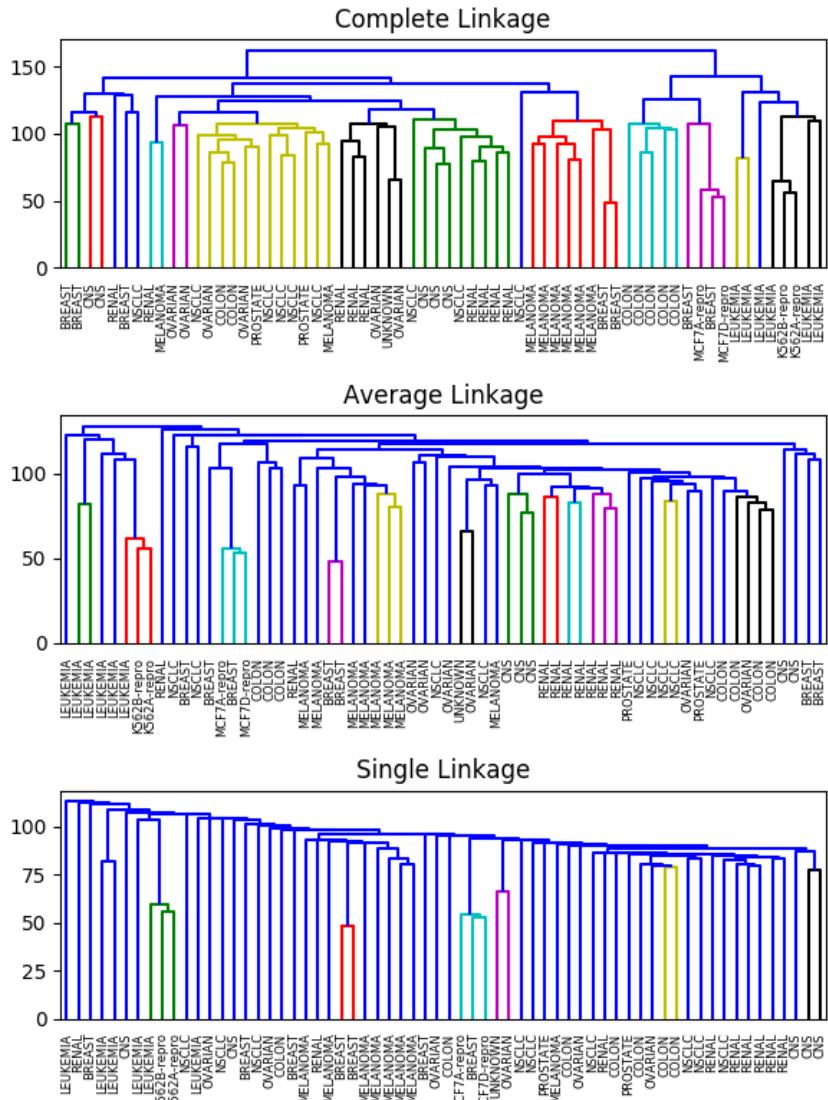


Figure 104: The NCI60 cancer cell line microarray data, clustered with average, complete, and single linkage, all using Euclidean distance as the dissimilarity measure. Complete and average linkages tend to yield evenly sized clusters. Single linkage tends to yield extended clusters to which single leaves are fused one by one.

```
        labels:')

print(res_tab)
print('-----')

# Plot the cut on the dendrogram that produces these four
# clusters
fig, ax = plt.subplots()
dn = dendrogram(Z, labels=nci_data['labs'], ax=ax)
ax.axhline(y=139, color='red', linestyle='--', alpha=0.7)
fig.tight_layout()

# Fit data to K-means clustering, compare results with
# hierarchical clustering
kmm = KMeans(n_clusters=4, random_state=0)
kmm.fit(X_scaled)

kmm_vs_hier = pd.crosstab(kmm.predict(X_scaled), Z_labels)
kmm_vs_hier.index.name = 'k-means clusters'
kmm_vs_hier.columns.name = 'hierarchical clusters'
print('Cross table of k-means clusters and hierarchical
      clusters:')

print(kmm_vs_hier)
print('-----')

# Hierarchical clustering on first five principal components
pca = PCA(n_components=5)

Z_pca = linkage(pca.fit_transform(X_scaled), method='complete')
dn_pca = dendrogram(Z_pca, labels=nci_data['labs'])
plt.tight_layout()

res_pca_hier_tab = pd.crosstab(nci_data['labs'],
                               fcluster(Z_pca, t=4, criterion='maxclust'))
res_pca_hier_tab.columns.name = 'predict_label'
print('Cross table when hierarchical clustering is performed on
      first five principal components:')

print(res_pca_hier_tab)
```

Cross table when dendrogram is used to predict four labels:

predict_label	1	2	3	4
labs				
BREAST	3	2	2	0
CNS	2	3	0	0
COLON	0	2	5	0
K562A-repro	0	0	0	1
K562B-repro	0	0	0	1

```
LEUKEMIA      0  0  0  6
MCF7A-repro   0  0  1  0
MCF7D-repro   0  0  1  0
MELANOMA      0  8  0  0
NSCLC         1  8  0  0
OVARIAN        0  6  0  0
PROSTATE       0  2  0  0
RENAL          1  8  0  0
UNKNOWN         0  1  0  0
-----
Cross table of k-means clusters and hierarchical clusters:
hierarchical clusters  1   2   3   4
k-means clusters
0                      0   2   9   0
1                      0   0   0   8
2                      0   9   0   0
3                     7  29   0   0
-----
Cross table when hierarchical clustering is performed on first five principal components
predict_label  1   2   3   4
labs
BREAST        0   5   2   0
CNS           2   3   0   0
COLON          7   0   0   0
K562A-repro   0   0   0   1
K562B-repro   0   0   0   1
LEUKEMIA       2   0   0   4
MCF7A-repro   0   0   1   0
MCF7D-repro   0   0   1   0
MELANOMA       1   7   0   0
NSCLC          8   1   0   0
OVARIAN        5   1   0   0
PROSTATE       2   0   0   0
RENAL          7   2   0   0
UNKNOWN         0   1   0   0
```