Chapter 5

Conceptual

1. Using basic statistical properties of the variance, as well as single variable calculus, derive

$$\alpha = \frac{\sigma_Y^2 - \sigma_{XY}}{\sigma_X^2 + \sigma_Y^2 - 2\sigma_{XY}}. (1)$$

In other words, prove that α given by the above formula does indeed minimize $Var(\alpha X + (1 - \alpha)Y)$.

Proof. Let X and Y be random variables and define $f(\alpha) = \operatorname{Var}(\alpha X + (1 - \alpha)Y)$. We first note that $\operatorname{Var}(\alpha X + (1 - \alpha)Y) = \alpha^2 \operatorname{Var}(X) + (1 - \alpha)^2 \operatorname{Var}(Y) + 2\alpha(1 - \alpha) \operatorname{Cov}(X, Y) = \alpha^2(\sigma_X^2 + \sigma_Y^2 - 2\sigma_{XY}) - 2\alpha(\sigma_Y^2 - \sigma_{XY}) + \sigma_Y^2$ for each $\alpha \in \mathbb{R}$. Thus f is quadratic in α with positive leading coefficient and hence has a minimum which must occur at its unique critical point. Now $\frac{d}{d\alpha}f = 2\alpha(\sigma_X^2 + \sigma_Y^2 - 2\sigma_{XY}) - 2(\sigma_Y^2 - \sigma_{XY})$ and hence f is critical at $\alpha = \frac{\sigma_Y^2 - \sigma_{XY}}{\sigma_X^2 + \sigma_Y^2 - 2\sigma_{XY}}$. Therefore, f has a (unique) minimum at $\alpha = \frac{\sigma_Y^2 - \sigma_{XY}}{\sigma_X^2 + \sigma_Y^2 - 2\sigma_{XY}}$.

- 2. We will now derive the probability that a given observation is part of a bootstrap sample. Suppose that we obtain a bootstrap sample from a set of n observations.
 - (a) What is the probability that the first bootstrap observation is not the jth observation from the original sample? Justify your answer. Since the first bootstrap observation is chosen uniformly from a population of n objects, the probability that the first observation is any given observation is $\frac{1}{n}$. Thus the probability that the first observation is not the jth element is $1 - \frac{1}{n}$.
 - (b) What is the probability that the second bootstrap observation is not the jth observation from the original sample?

 The probability is again $1 \frac{1}{n}$ for the same reasons as above.

 - (c) Argue that the probability that the jth observation is not in the bootstrap sample is $(1-\frac{1}{n})^n$. Since each observation has a probability of $1-\frac{1}{n}$ of not picking the jth element and the n bootstrap observations are made independently and with replacement the probability that the bootstrap sample does not contain the j observation is $(1-\frac{1}{n})^n$.
 - (d) When n=5, what is the probability that the jth observation is in the bootstrap sample? $P(j \in B) = 1 (1 \frac{1}{5})^5 \approx 0.672$
 - (e) When n = 100, what is the probability that the jth observation is in the bootstrap sample?

1

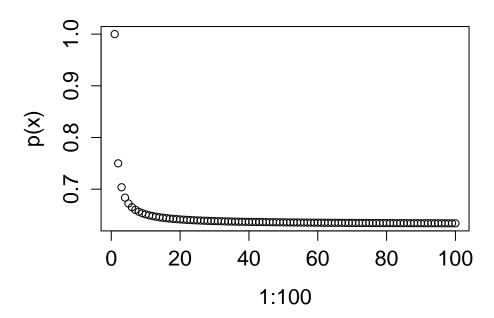
$$P(j \in B) = (1 - \frac{1}{100})^{100} \approx 0.634$$

(f) When n = 10,000, what is the probability that the jth observation is in the bootstrap sample?

$$P(j \in B) = (1 - \frac{1}{10000})^{10000} \approx 0.632$$

(g) Create a plot that displays, for each integer value of n from 1 to 100,000, the probability that the jth observation is in the bootstrap sample. Comment on what you observe.

```
> p=function(n){return(1-(1-1/n)^n)}
> plot(x=1:100,p(x))
```



The graph rapidly decreases to an asymptote $p(x) = \frac{e-1}{e}$.

(h) We will now investigate numerically the probability that a bootstrap sample of size n = 100 contains the jth observation. Here j = 4. We repeatedly create bootstrap samples, and each time we record whether or not the fourth observation is contained in the bootstrap sample.

```
> store=rep(NA,10000)
> for(i in 1:10000){
    store[i]=sum(sample(1:100), rep=TRUE)==4)>0
    }
> mean(store)
```

Comment on the results obtained.

[1] 0.6467

These results are in line with the exact result in (e).

- 3. We now review k-fold cross-validation.
 - (a) Explain how k-fold cross-validation is implemented.

k-fold cross-validation is implemented by first partitioning the sample into k subset. Then for each of the k subsets the desired model is fit to the union of the remaining k-1 subsets. An error statistic (MSE in the case of regression and error rate in the case of classification) is then computed using the held out subset. Finally, the overall error statistic and its standard error are estimated using the mean and standard deviation, resp., of the k subset error statistics.

- (b) What are the advantages and disadvantages of k-fold cross-validation relative to:
 - i. The validation set approach? k-fold cross-validation is more computationally expensive than the validation set approach. It is however more accurate, since the error statistic is estimated using multiple fit models each of which utilizes more of the training data. In particular, k-fold cross-validation will have much lower bias.

ii. LOOCV?

k-fold cross-validation is less computationally expensive than LOOCV since it fits fewer models to the data (assuming k < n). LOOCV has the benefit of producing a deterministic estimate of the error statistic, whereas the k-fold cross-validation estimate will depend on the choice of partition. LOOCV will have lower bias, but a higher variance.

4. Suppose that we use some statistical learning method to make a prediction for the response Y for a particular value of the predictor X. Carefully describe how we might estimate the standard deviation of our prediction.

We can use the bootstrap to estimate the standard deviation of our prediction. From our training data we repeatedly generate new training sets by sampling from the original training set with replacement. For each of these bootstrap samples we fit our desired learning method to generate a prediction for Y for the given X. We can then estimate the standard error in our prediction by using the standard deviation of the collection of resampled predictions.

Applied

- 5. In Chapter 4, we used logistic regression to predict the probability of **default** using **income** and **balance** on the **Default** data set. We will now estimate the test error of this logistic regression model using the validation set approach. Do not forget to set a random seed before beginning your analysis.
 - (a) Fit a logistic regression model that uses income and balance to predict default.

```
> library(ISLR)
> attach(Default)
> set.seed(1)
> glm.fit=glm(default~income+balance, data=Default, family=binomial)
> summary(glm.fit)
Call:
glm(formula = default ~ income + balance, family = binomial,
   data = Default)
Deviance Residuals:
            10 Median
                             30
                                    Max
-2.4725 -0.1444 -0.0574 -0.0211 3.7245
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.154e+01 4.348e-01 -26.545 < 2e-16 ***
           2.081e-05 4.985e-06 4.174 2.99e-05 ***
balance
           5.647e-03 2.274e-04 24.836 < 2e-16 ***
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 2920.6 on 9999 degrees of freedom
Residual deviance: 1579.0 on 9997 degrees of freedom
AIC: 1585
Number of Fisher Scoring iterations: 8
```

- (b) Using the validation set approach, estimate the test error of this model. In order to do this, you must perform the following steps:
 - i. Split the sample set into a training set and a validation set.
 - ii. Fit a multiple logistic regression model using only the training observations.
 - iii. Obtain a prediction of default status for each individual in the validation set by computing the posterior probability of default for that individual, and classifying the individual to the **default** category if the posterior probability is greater than 0.5.
 - iv. Compute the validation set error, which is the fraction of the observations in the validation set that are misclassified.

```
> estimateError=function(){
+    train=sample(length(default),length(default)/2)
+    glm.fit=glm(default~income+balance, data=Default, family=binomial,
    subset=train)
+    fit.probs=predict(glm.fit, Default[-train,], type="response")
+    fit.pred=rep("No", length(default)/2)
+    fit.pred[fit.probs>0.5]="Yes"
```

```
+ return(mean(fit.pred!=Default[-train,][1]))
+ }
> estimateError()
[1] 0.0286
```

(c) Repeat the process in (b) three times, using three different splits of the observations into training and validation sets. Comment on the results obtained.

```
> estimateError()
[1] 0.0236
> estimateError()
[1] 0.028
> estimateError()
[1] 0.0268
```

The estimates are comparable and vary by less than 0.1%.

(d) Now consider a logistic regression model that predicts the probability of **default** using **income**, **balance** and a dummy variable for **student**. Estimate the test error for this model using the validation set approach. Comment on whether or not including a dummy variable for **student** leads to a reduction in the test error rate.

```
> estimateError=function(){
+          train=sample(length(default),length(default)/2)
+          glm.fit=glm(default~income+balance+student, data=Default,
          family=binomial, subset=train)
+          fit.probs=predict(glm.fit, Default[-train,], type="response")
+          fit.pred=rep("No", length(default)/2)
+          fit.pred[fit.probs>0.5]="Yes"
+          return(mean(fit.pred!=Default[-train,][1]))
+ }
> estimateError()
[1] 0.0264
```

The inclusion of student in the model does not seem to reduce test error.

- 6. We continue to consider the use of a logistic regression model to predict the probability of default using income and balance on the Default data set. In particular, we will now compute estimates for the standard errors of the income and balance logistic regression coefficients in two different ways: (1) using the bootstrap, and (2) using the standard formula for computing the standard errors in the glm() function.
 - (a) Using the summary() and glm() functions, determine the estimated standard errors for the coefficients associated with income and balance in the multiple logistic regression model that uses both predictors.

```
> library(ISLR)
> attach(Default)
> set.seed(1)
```

```
> glm.fit=glm(default~income+balance, data=Default, family=binomial)
> summary(glm.fit)
Call:
glm(formula = default ~ income + balance, family = binomial,
   data = Default)
Deviance Residuals:
            10 Median
                            30
                                    Max
-2.4725 -0.1444 -0.0574 -0.0211 3.7245
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.154e+01 4.348e-01 -26.545 < 2e-16 ***
           2.081e-05 4.985e-06 4.174 2.99e-05 ***
balance
           5.647e-03 2.274e-04 24.836 < 2e-16 ***
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 2920.6 on 9999 degrees of freedom
Residual deviance: 1579.0 on 9997 degrees of freedom
AIC: 1585
Number of Fisher Scoring iterations: 8
```

(b) Write a function **boot.fn()**, that takes as input the **Default** data set as well as an index of the observations, and that outputs the coefficient estimates for **income** and **balance** in the multiple regression model.

```
> boot.fn=function(data,index){
+    glm.fit=glm(default~income+balance, data=data, family=binomial,
    subset=index)
+    return(glm.fit$coefficients[2:3])
+ }
> boot.fn(Default, rep(TRUE,length(balance)))
    income    balance
2.080898e-05 5.647103e-03
```

(c) Use the **boot()** function together with your **boot.fn()** function to estimate the standard errors of the logistic regression coefficients for **income** and **balance**.

```
> library(boot)
> boot(Default,boot.fn,50)

ORDINARY NONPARAMETRIC BOOTSTRAP

Call:
```

(d) Comment on the estimated standard errors obtained using the glm() function and using your bootstrap function.

The standard errors obtained from the bootstrap are roughly similar to those obtained from glm().

7. In Sections 5.3.2 and 5.3.3, we saw that the <code>cv.glm()</code> function can be used in order to compute the LOOCV test error estimate. Alternatively, one could compute those quantities using just the <code>glm()</code> and <code>predict.glm()</code> functions, and a for loop. You will now take this approach in order to compute the LOOCV error for a simple logistic regression model on the <code>Weekly</code> data set. Recall that in the context of classification problems, the LOOCV error is given by

$$CV_n = \frac{1}{n} \sum_{i=1}^n Err_i \tag{2}$$

(a) Fit a logistic regression model that predicts Direction using Lag1 and Lag2.

```
> attach(Weekly)
> glm.fit=glm(Direction~Lag1+Lag2, data=Weekly, family=binomial)
> summary(glm.fit)
Call:
glm(formula = Direction ~ Lag1 + Lag2, family = binomial, data = Weekly)
Deviance Residuals:
  Min
          10 Median
                         30
                               Max
-1.623 -1.261 1.001 1.083
                             1.506
Coefficients:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.22122 0.06147 3.599 0.000319 ***
Lag1
          -0.03872
                     0.02622 -1.477 0.139672
           0.06025
                     0.02655 2.270 0.023232 *
Lag2
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 1496.2 on 1088 degrees of freedom
Residual deviance: 1488.2 on 1086 degrees of freedom
AIC: 1494.2
```

(b) Fit a logistic regression model that predicts Direction using Lag1 and Lag2 using all but the first observation.

```
> glm.fit=glm(Direction~Lag1+Lag2, data=Weekly[-1,], family=binomial)
> summary(glm.fit)
Call:
glm(formula = Direction ~ Lag1 + Lag2, family = binomial, data = Weekly[-1,
Deviance Residuals:
   Min
            10 Median
                             3Q
                                    Max
-1.6258 -1.2617 0.9999 1.0819
                                 1.5071
Coefficients:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.22324
                    0.06150 3.630 0.000283 ***
          -0.03843
                     0.02622 -1.466 0.142683
Lag1
Lag2
           0.06085
                     0.02656 2.291 0.021971 *
Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 1494.6 on 1087 degrees of freedom
Residual deviance: 1486.5 on 1085 degrees of freedom
AIC: 1492.5
Number of Fisher Scoring iterations: 4
```

(c) Use the model from (b) to predict the direction of the first observation. You can do this by predicting that the first observation will go up if P(Direction=="Up"|Lag1,Lag2) > 0.5. Was this observation correctly classified?

```
> predict.glm(glm.fit, Weekly[1,], type="response")>0.5
    1
TRUE
> Direction[1]
[1] Down
Levels: Down Up
```

The model predicted that the first observation would be an Up. The true observation is Down.

- (d) Write a for loop from i = 1 to i = n, where n is the number of observations in the data set, that performs each of the following steps:
 - i. Fit a logistic regression model using all but the *i*th observation to predict Direction using Lag1 and Lag2.

- ii. Compute the posterior probability of the market moving up for the ith observation.
- iii. Use the posterior probability for the *i*th observation in order to predict whether or not the market moves up.
- iv. Determine whether or not an error was made in predicting the direction for the ith observation. If an error was made indicate this as a 1, and otherwise indicate it as a 0.

```
> for (i in 1:length(Direction)){
+    glm.fit=glm(Direction~Lag1+Lag2, data=Weekly[-i,], family=binomial)
+    pred_up=predict.glm(glm.fit, Weekly[i,], type="response")>0.5
+    if ((pred_up && Direction[i]!="Up")||(!pred_up && Direction[i]=="Up"))
+        results[i]=1
+ }
```

(e) Take the average of the n numbers obtained in (d) in order to obtain the LOOCV estimate for the test error. Comment on the results.

```
> mean(results)
[1] 0.4499541
```

LOOCV estimates the test error rate of the model is 45%.

- 8. We will now perform cross-validation on a simulated data set.
 - (a) Generate a simulated data set as follows:

```
> set.seed(1)
> y=rnorm(100)
> x=rnorm(100)
> y=x-2*x^2+rnorm(100)
```

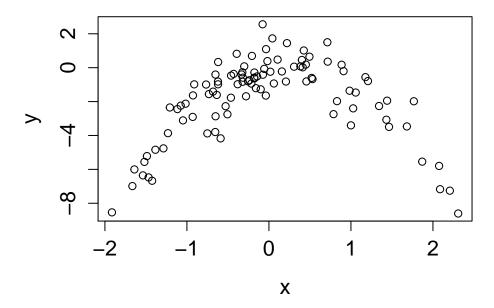
In this data set, what is n and what is p? Write out the model used to generate the data in equation form.

In this data set n = 100 and p = 2. The data are generated by

$$Y = X - 2X^2 + \epsilon,\tag{3}$$

where $X, \epsilon \sim N(0, 1)$.

(b) Create a scatterplot of X against Y. Comment on what you find.



As expected, the data appear quadratic in x.

(c) Set a random seed, and then compute the LOOCV errors that result from fitting the following four models using least squares:

i.
$$Y = \beta_0 + \beta_1 X + \epsilon$$

ii.
$$Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \epsilon$$

iii.
$$Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \epsilon$$

iv.
$$Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \beta_4 X^4 + \epsilon$$

Note you may find it helpful to use the $\mathtt{data.frame}()$ function to create a single data set containing both X and Y.

```
> library(boot)
> Data=data.frame(x,y)
> set.seed(1)
> glm.fit=glm(y~x)
> cv.glm(Data,glm.fit)$delta
[1] 5.890979 5.888812
```

```
> glm.fit=glm(y~poly(x,2))
> cv.glm(Data,glm.fit)$delta
[1] 1.086596 1.086326
```

```
> glm.fit=glm(y~poly(x,3))
> cv.glm(Data,glm.fit)$delta
```

```
> glm.fit=glm(y~poly(x,4))
> cv.glm(Data,glm.fit)$delta
[1] 1.114772 1.114334
```

(d) Repeat (c) using another random seed, report your results. Are your results the same as what you got in (c)? Why?

```
> set.seed(27)
> glm.fit=glm(y~x)
> cv.glm(Data,glm.fit)$delta
[1] 5.890979 5.888812
> glm.fit=glm(y~poly(x,2))
> cv.glm(Data,glm.fit)$delta
[1] 1.086596 1.086326
> glm.fit=glm(y~poly(x,3))
> cv.glm(Data,glm.fit)$delta
[1] 1.102585 1.102227
> glm.fit=glm(y~poly(x,4))
> cv.glm(Data,glm.fit)$delta
[1] 1.114772 1.114334
```

These results are identical to those obtained above. This is expected since LOOCV always trains the model on all training sets of a single fewer training example.

(e) Which of the models in (c) had the smallest LOOCV error? Is this what you expected? Explain your answer.

The quadratic fit has the smallest LOOCV error. This is expected as the simulated data are actually quadratic. The cubic and quartic fits do a much better job than the linear fit and are only slightly worse than the quadratic fit.

(f) Comment on the statistical significance of the coefficient estimates that results from fitting each of the models in (c) using least squares. Do these results agree with the conclusions drawn based on the cross-validation results?

In the full model the degree one and two terms are statistically significant, but the degree 3 and 4 terms are not. This is consistent with the conclusions drawn above from LOOCV. Inclusion of a degree 2 term significantly improves the model, but there is no need to include higher order terms.

- 9. We will now consider the Boston housing data set, from the MASS library.
 - (a) Based on this data set, provide an estimate for the population mean of medv. Call this estimate $\hat{\mu}$.

```
> library(MASS)
> attach(Boston)
> mean(medv)
[1] 22.53281
```

We estimate $\mu \approx \hat{\mu} = 22.53$.

(b) Provide an estimate of the standard error of $\hat{\mu}$. Interpret this result.

```
> sd(medv)/sqrt(length(medv))
[1] 0.4088611
```

We estimate $\sigma_{medv} \approx \hat{\sigma}_{medv} = 0.409$.

(c) Now estimate the standard error of $\hat{\mu}$ using the bootstrap. How does this compare to your answer from (b)?

```
> set.seed(1)
> boot.fn=function(data,index){return(mean(data[index]))}
> strap=boot(medv, boot.fn, 1000)
> strap

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```

```
Call:
boot(data = medv, statistic = boot.fn, R = 1000)

Bootstrap Statistics :
    original bias std. error
t1* 22.53281 0.008517589 0.4119374
```

The results are very similar, with a bootstrap estimate of 0.412 as compared to the value of 0.409 obtained from the formula.

(d) Based on your bootstrap estimate from (c), provide a 95% confidence interval for the mean of medv. Compare it to the results obtained using t.test(Boston\$medv).

```
> t.test(Boston$medv)
    One Sample t-test

data: Boston$medv
t = 55.1111, df = 505, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
    21.72953 23.33608
sample estimates:
mean of x
    22.53281

> c(strap$t0-2*0.4119374, strap$t0+2*0.4119374)
[1] 21.70893 23.35668
```

The bootstrap confidence interval is comparable but slightly wider than that obtained by the t-test.

(e) Based on this data set, provide an estimate, $\hat{\mu}_{med}$, for the median value of medv in the population.

```
> median(medv)
[1] 21.2
```

(f) We now would like to estimate the standard error of $\hat{\mu}_{med}$. Unfortunately, there is no simple formula for computing the standard error of the median. Instead, estimate the standard error of the median using the bootstrap. Comment on your findings.

```
> set.seed(1)
> boot.fn=function(data,index){return(median(data[index]))}
> strap=boot(medv, boot.fn, 1000)
> strap
```

```
ORDINARY NONPARAMETRIC BOOTSTRAP

Call:
boot(data = medv, statistic = boot.fn, R = 1000)

Bootstrap Statistics :
    original bias std. error
t1* 21.2 -0.01615 0.3801002
```

We find $\hat{\mu}_{med} = 21.2$ with a standard error of 0.380. The standard error is smaller than that of the mean estimate, and small relative to $\hat{\mu}$.

(g) Based on this data set, provide an estimate for the tenth percentile of **medv** in the Boston suburbs. Call this quantity $\hat{\mu}_{0.1}$.

```
> quantile(medv,0.1)
  10%
12.75
```

(h) Use the bootstrap to estimate the standard error of $\hat{\mu}_{0.1}$. Comment on your findings.

We find $\hat{\mu}_{0.1} = 12.75$ with a standard error of 0.511. The standard error is larger than that of the mean and median estimates, but still small relative to $\hat{\mu}_{0.1}$.