IS624 - Assignment 1

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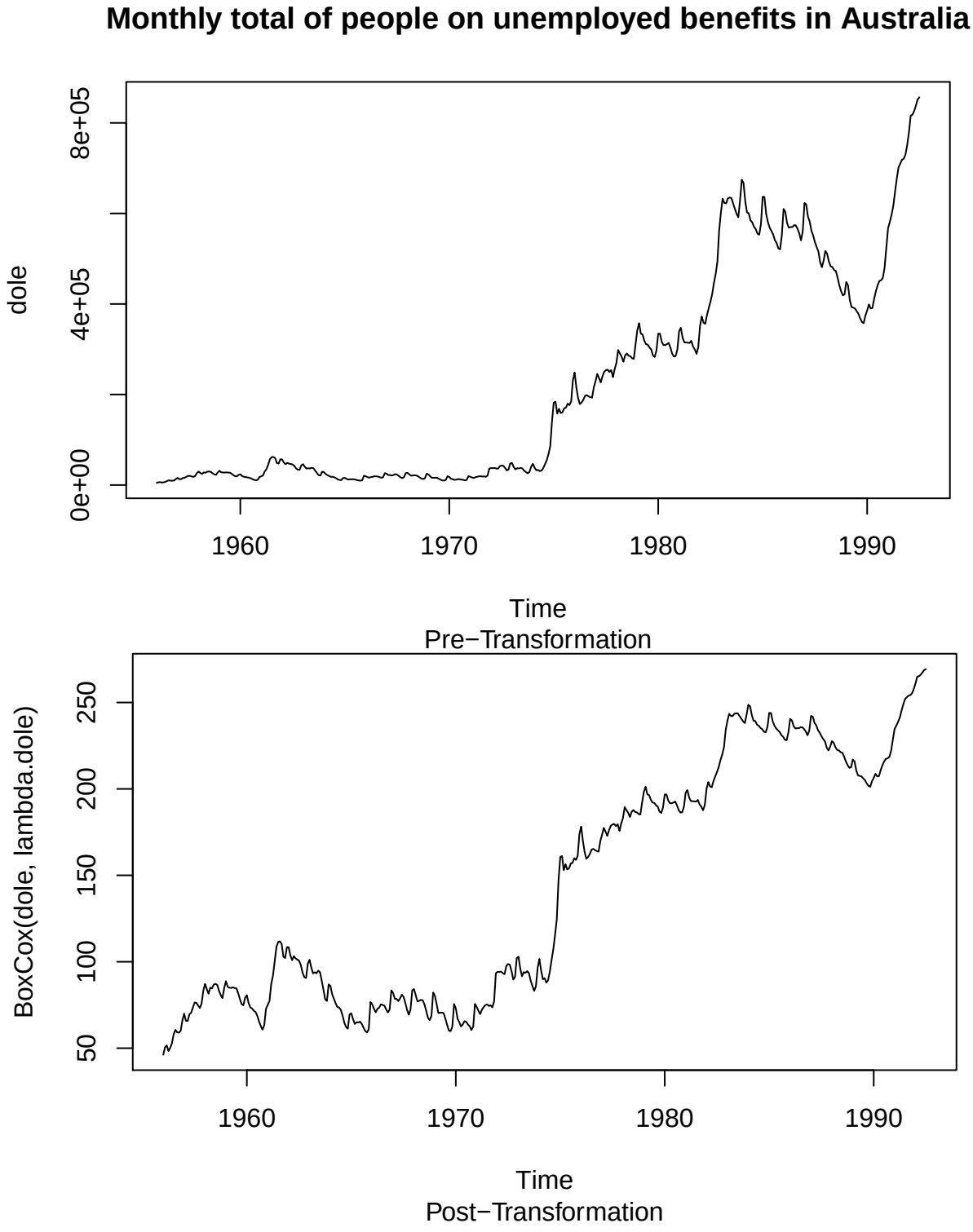
Code

The official R code for this homework is located on github.com. All the code below is copied from the problem functions in that file.

Question 2.1a)

The following code produces two graphs of the pre and post transformation of the monthly total of people on unemployed benefits in Australia. The data looks skewed to me, and by recommendation of the first textbook, I would apply this transformation. Note that the y-scale is a lot smaller with the transform, which is true across all problems in this question.

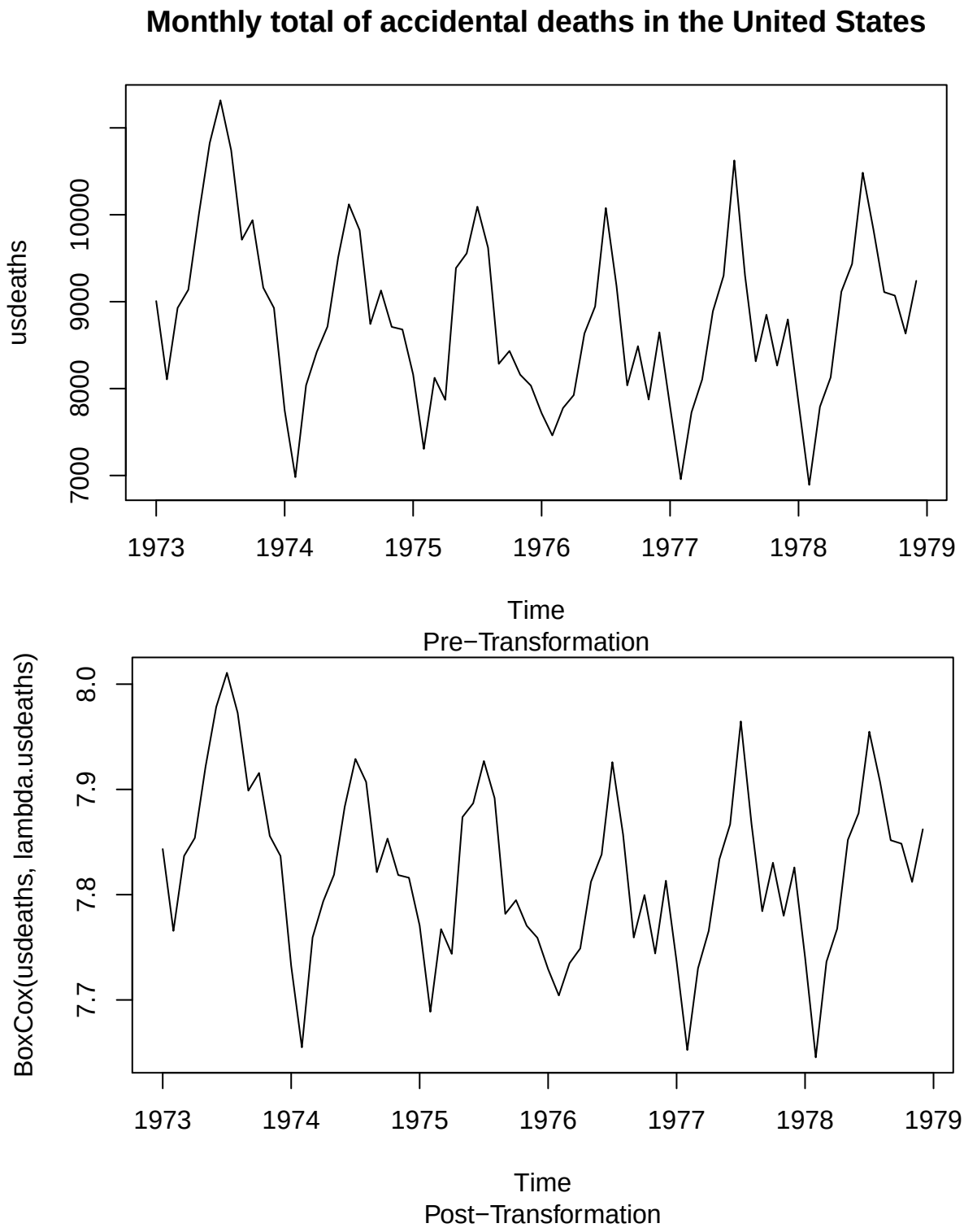
```
#' Plot the Monthly total of people on unemployed benefits in Australia (January 1956-July 1992).
lambda.dole <- BoxCox.lambda(dole)  # 0.3290922
plot(dole, main="Monthly total of people on unemployed benefits in Australia", sub="Pre-Transformation")
plot(BoxCox(dole, lambda.dole), sub="Post-Transformation")
```


Monthly total of people on unemployed benefits in Australia
dole
0e+00
4e+05
8e+05
1960
1970
1980
1990
Time
Pre−Transformation
BoxCox(dole, lambda.dole)
50
100
150
200
250
1960
1970
1980
1990
Time
Post−Transformation

Question 2.1b)

The following code produces two graphs of the pre and post transformation of the monthly total of accidental deaths in the United States. The lambda value is small, and according to the text, since the seasonality already looks to be the same across the data, this transformation is probably not needed ("A good value of lambda is one which makes the size of the seasonal variation about the same across the whole series"). I have plotted both either way.

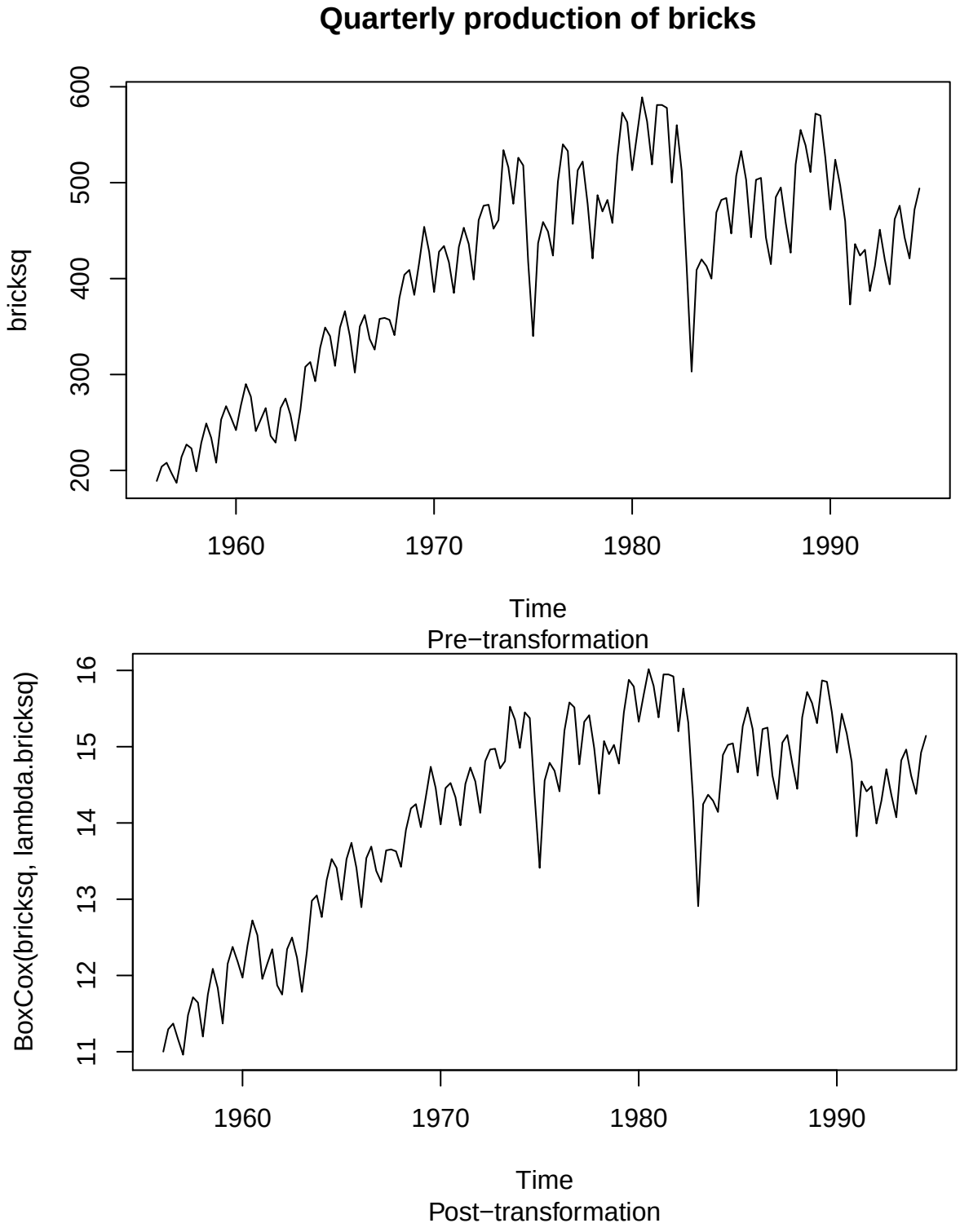
```
#' Monthly total of accidental deaths in the United States (January 1973-December 1978).
lambda.usdeaths <- BoxCox.lambda(usdeaths)  # -0.03363775
plot(usdeaths, main="Monthly total of accidental deaths in the United States", sub="Pre-Transformation")
plot(BoxCox(usdeaths, lambda.usdeaths), sub="Post-Transformation")
```


Monthly total of accidental deaths in the United States
usdeaths
7000
8000
9000
10000
1973
1974
1975
1976
1977
1978
1979
Time
Pre−Transformation
BoxCox(usdeaths, lambda.usdeaths)
7.7
7.8
7.9
8.0
1973
1974
1975
1976
1977
1978
1979
Time
Post−Transformation

Question 2.1c)

The following code produces two graphs of the pre and post transformation of the Quarterly production of bricks. The shape of the data does not change signicificantly, but like previous portions of the question, the y-scale is smaller.

```
#' Quarterly production of bricks (in millions of units) at Portland, Australia (March 1956-September 1
lambda.bricksq <- BoxCox.lambda(bricksq)  # 0.2548929
plot(bricksq, main="Quarterly production of bricks", sub="Pre-transformation")
plot(BoxCox(bricksq, lambda.bricksq), sub="Post-transformation")
```

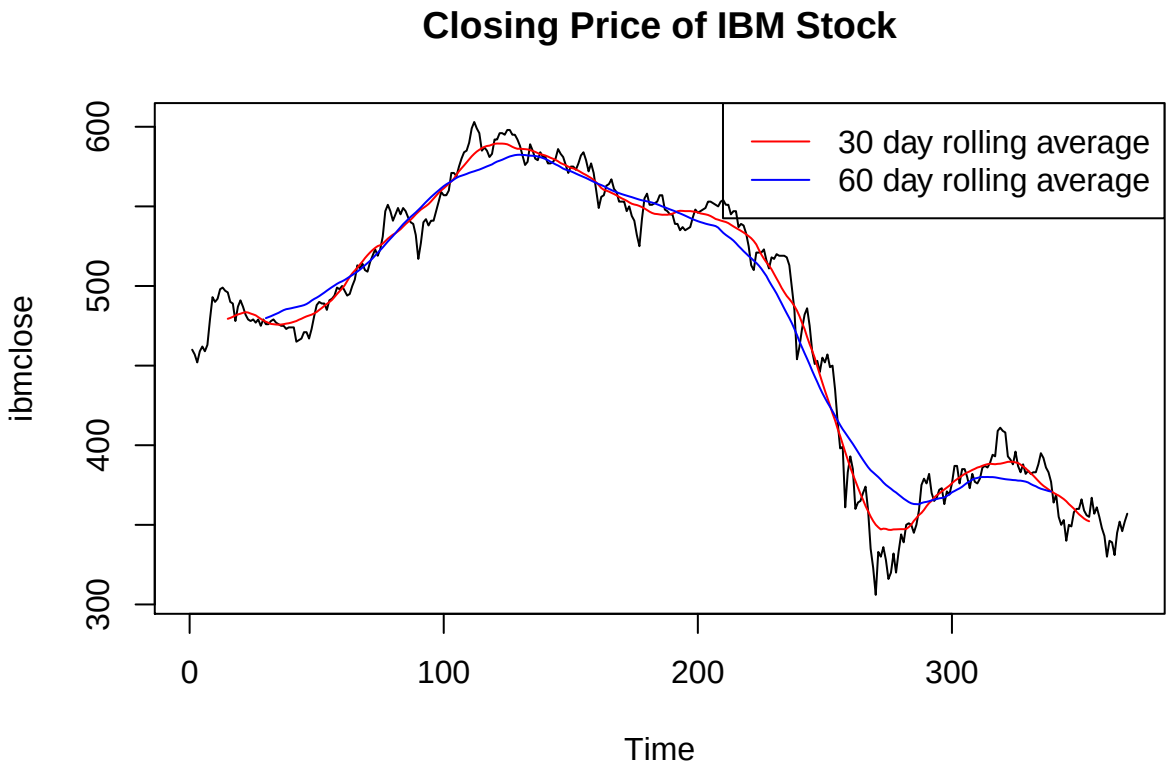

Quarterly production of bricks
bricksq
200
300
400
500
600
1960
1970
1980
1990
Time
Pre−transformation
BoxCox(bricksq, lambda.bricksq)
11
12
13
14
15
16
1960
1970
1980
1990
Time
Post−transformation

Question 2.3

Question 2.3a)

To become familiar with the ibmclose data set, here we plot the time series with some running averages. The big dip in price is going to give us trouble with our simplistic forcasting. The data is not in the right format for doing seasonal or month graphs (see next question).

```
#' Produce some plots of the data in order to become familiar with it.
plot(ibmclose, main="Closing Price of IBM Stock")
lines(rollmean(ibmclose, k=30, fill=NA), col="red")
lines(rollmean(ibmclose, k=60, fill=NA), col="blue")
legend("topright", lty=1, col=c("red", "blue"), legend=c("30 day rolling average","60 day rolling averag
```



Question 2.3b)

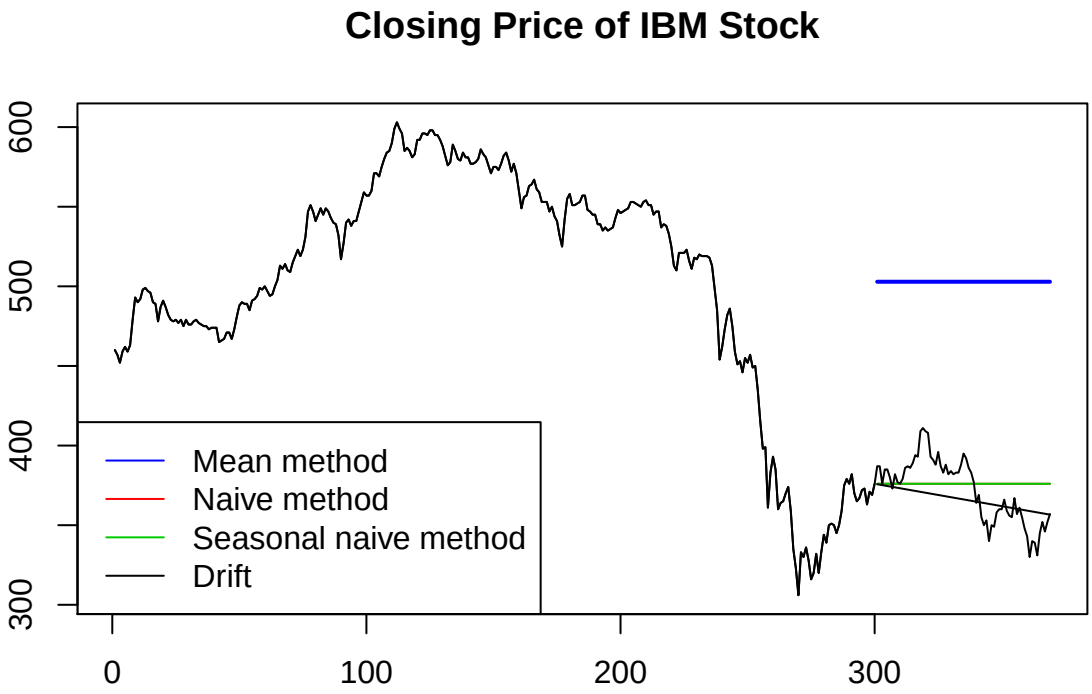
The ibmclose data is split into a 300-day training set and a 69-day test set:

```
ibmclose.training <- window(ibmclose, start=1, end=300)
ibmclose.test <- window(ibmclose, start=301)
```

Question 2.3c)

Note that the blue prediction is for the mean predicition, and looks different due to using plot() versus lines(). Also note that both naive methods overlap their predicitions. Visually inspecting the predictions, drift is clearly the most accurate; the mean is so far away as it does not account well for the bug dip in value around t=250.

```
ibmclose.prediction_horizon <- length(ibmclose) - 300;

# Calc mean, naive, seasonal naive, drift predictions
ibmclose.fit.mean <- meanf(ibmclose.training, h=ibmclose.prediction_horizon)
ibmclose.fit.naive <- naive(ibmclose.training, h=ibmclose.prediction_horizon)
ibmclose.fit.seasonalNaive <- snaive(ibmclose.training, h=ibmclose.prediction_horizon)
ibmclose.fit.drift <- rwf(ibmclose.training, drift=TRUE, h=ibmclose.prediction_horizon)

# Plot data with predictions
#plot(ibmclose.training, main="Closing Price of IBM Stock")
plot(ibmclose.fit.mean, plot.conf=FALSE, main="Closing Price of IBM Stock")
lines(ibmclose.fit.naive$mean, col=2)
lines(ibmclose.fit.seasonalNaive$mean, col=3)
lines(ibmclose.fit.drift$mean, col=1)
lines(ibmclose)
legend("bottomleft", lty=1, col=c(4,2,3,1), legend=c("Mean method","Naive method","Seasonal naive metho
```



The various error rates are printed for mean, naive, seasonal naive and drift, respectively. Its clear that the mean error is too high compared to the rest. It seems that drift overall tends to have lower error values that the naive methods, but are generally pretty close. As said above, I think my tendency would be for the drift method.

```
# Look at error values from our predictions
accuracy(ibmclose.fit.mean, ibmclose.test)
accuracy(ibmclose.fit.naive, ibmclose.test)
accuracy(ibmclose.fit.seasonalNaive, ibmclose.test)
accuracy(ibmclose.fit.drift, ibmclose.test)
```

```
##                        ME      RMSE       MAE        MPE     MAPE
## Training set  1.660438e-14  73.61532  58.72231  -2.642058 13.03019
## Test set     -1.306180e+02 132.12557 130.61797 -35.478819 35.47882
```

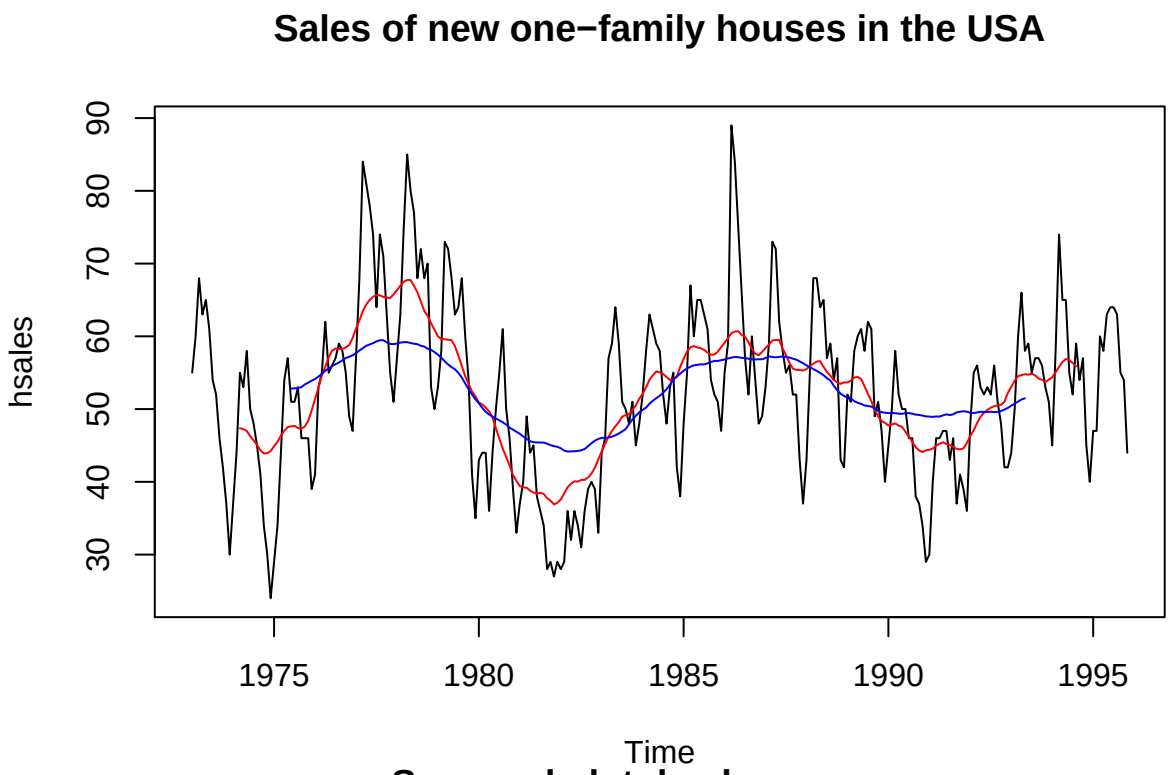
```
##                   MASE      ACF1 Theil's U
## Training set 11.52098 0.9895779        NA
## Test set     25.62649 0.9314689  19.05515
##                       ME      RMSE      MAE         MPE     MAPE     MASE
## Training set -0.2809365  7.302815  5.09699 -0.08262872 1.115844 1.000000
## Test set     -3.7246377 20.248099 17.02899 -1.29391743 4.668186 3.340989
##                    ACF1 Theil's U
## Training set 0.1351052        NA
## Test set     0.9314689  2.973486
##                       ME      RMSE      MAE         MPE     MAPE     MASE
## Training set -0.2809365  7.302815  5.09699 -0.08262872 1.115844 1.000000
## Test set     -3.7246377 20.248099 17.02899 -1.29391743 4.668186 3.340989
##                    ACF1 Theil's U
## Training set 0.1351052        NA
## Test set     0.9314689  2.973486
##                         ME      RMSE       MAE         MPE     MAPE
## Training set 2.870480e-14  7.297409  5.127996 -0.02530123 1.121650
## Test set     6.108138e+00 17.066963 13.974747  1.41920066 3.707888
##                    MASE      ACF1 Theil's U
## Training set 1.006083 0.1351052        NA
## Test set     2.741765 0.9045875  2.361092
```

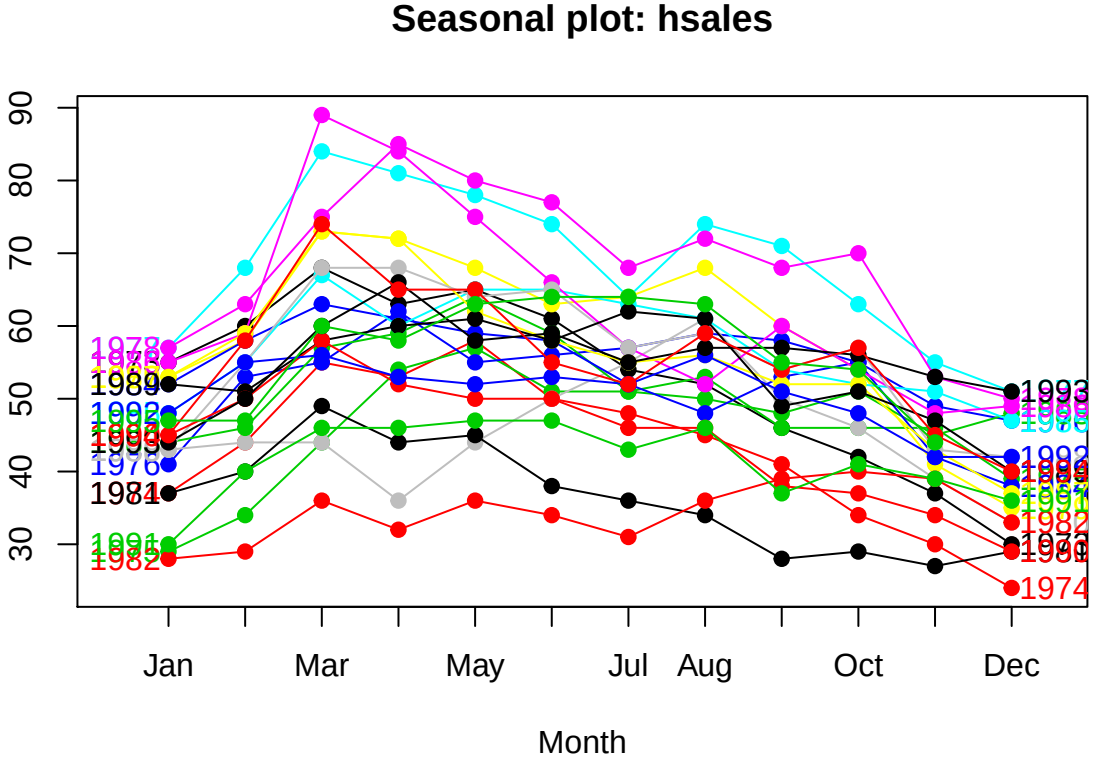
Question 2.4

Question 2.4a)

Here a simple ts plot, with a few moving averages is plotted, as well as a month and season plot, since the data is the right format (versus previous question).

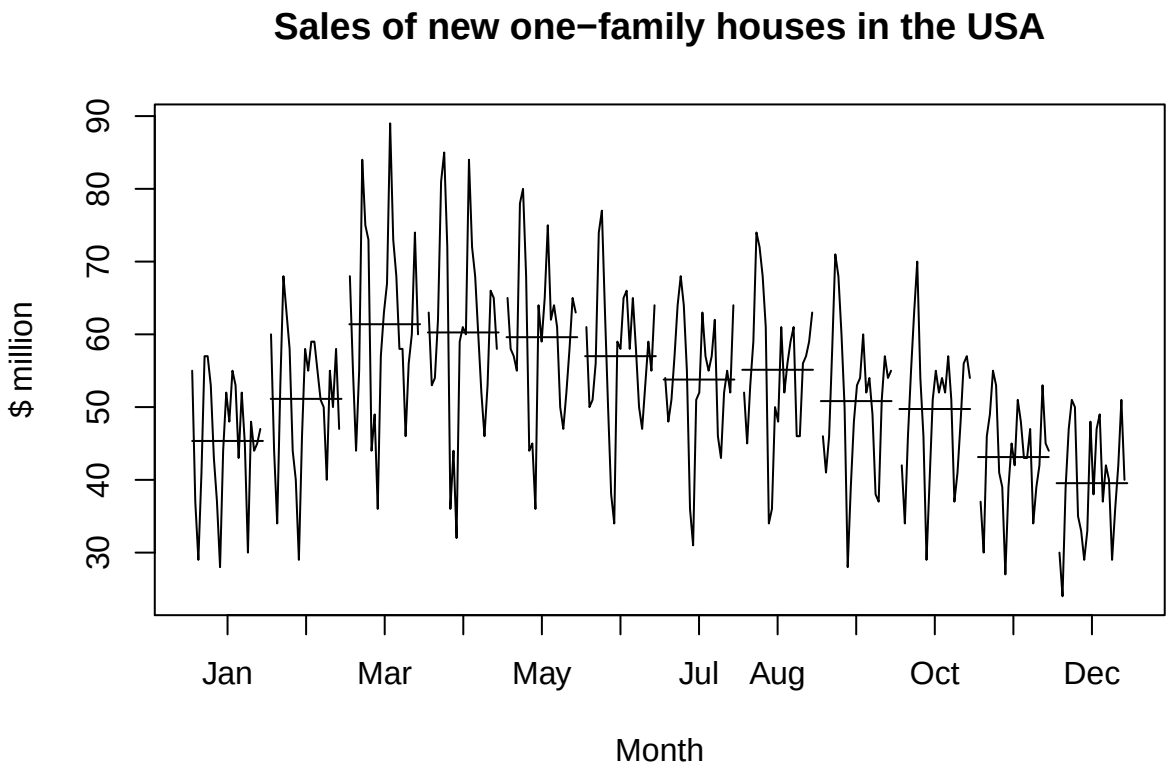
```
# Plot time series with some moving averages
plot(hsales, main="Sales of new one-family houses in the USA")
lines(rollmean(hsales, k=30, fill=NA), col="red")
lines(rollmean(hsales, k=60, fill=NA), col="blue")

# Show seasonal plot, which should a general downward trend from March onwards
seasonplot(hsales, col=1:20, pch=19, year.labels=TRUE, year.labels.left=TRUE)
```





Here are the sales by month, which emphasizes that there is a ramp up in sales from Jan to Mar, but declines for the rest of the year:

```
monthplot(hsales,ylab="$ million",xlab="Month",xaxt="n", main="Sales of new one-family houses in the US
axis(1,at=1:12,labels=month.abb,cex=0.8)
```



Question 2.4b)

Split the hsales data set into a training set and a test set, where the test set is the last two years of data.

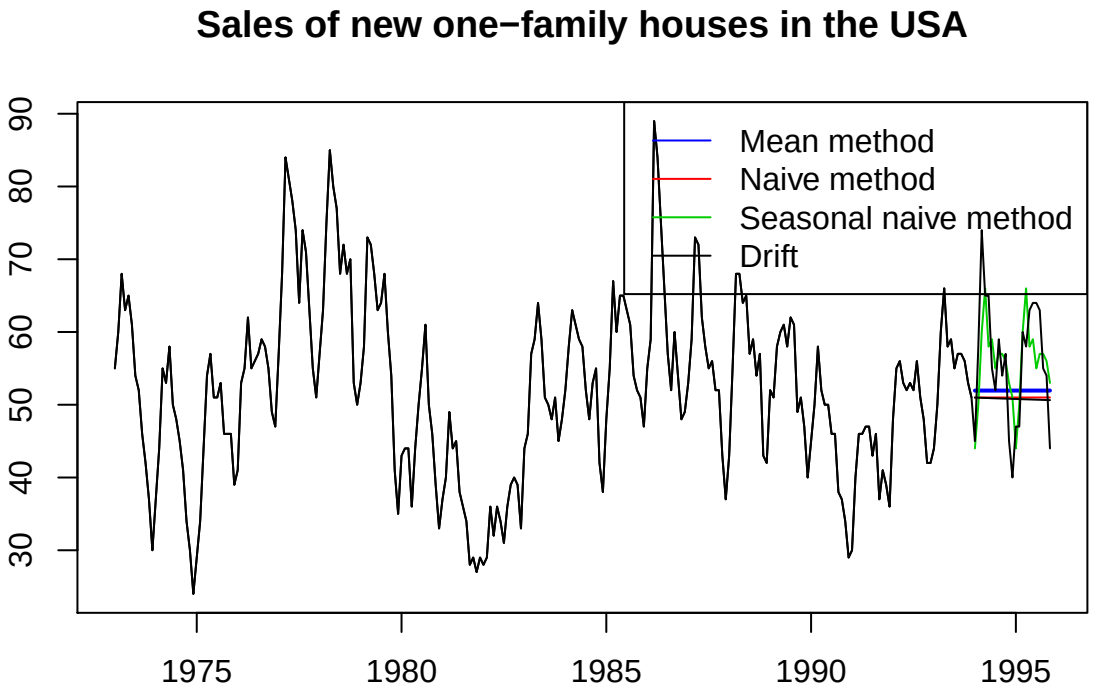
```
hsales.training <- window(hsales, start=c(1973, 1), end=c(1993, 12))
hsales.test <- window(hsales, start=c(1994, 1), end=c(1995, 11))
```

Question 2.4c)

Visual inspection shows that the seasonal naive method looks pretty accurate across the 23months of prediction, though the predicted value in 23months looks pretty off. None of the methods seem to predict the end drop-off in value towards the end of 1995.

```
hsales.prediction_horizon <- 23;

# Calculate the mean, naive, seasonal naive, drift predicitons
hsales.fit.mean <- meanf(hsales.training, h=hsales.prediction_horizon)
hsales.fit.naive <- naive(hsales.training, h=hsales.prediction_horizon)
hsales.fit.seasonalNaive <- snaive(hsales.training, h=hsales.prediction_horizon)
hsales.fit.drift <- rwf(hsales.training, drift=TRUE, h=hsales.prediction_horizon)

# Plot the data with our predicitons
#plot(hsales.training, main="Sales of new one-family houses in the USA w/ Forecasts")
plot(hsales.fit.mean, plot.conf=FALSE, main="Sales of new one-family houses in the USA")
lines(hsales.fit.naive$mean, col=2)
lines(hsales.fit.seasonalNaive$mean, col=3)
lines(hsales.fit.drift$mean, col=1)
```

```
lines(hsales)
legend("topright", lty=1, col=c(4,2,3,1), legend=c("Mean method","Naive method","Seasonal naive method"
```



Here are the error values for the mean, naive, seasonal naive and drift methods, respectively. The seasonal naive is a clear winner here. Visually, the seaonal naive method overlaps the test data very well, and generally has the least amount of error for any error metric.

```
# Look at error values from our predictions
accuracy(hsales.fit.mean, hsales.test)
accuracy(hsales.fit.naive, hsales.test)
accuracy(hsales.fit.seasonalNaive, hsales.test)
accuracy(hsales.fit.drift, hsales.test)
```

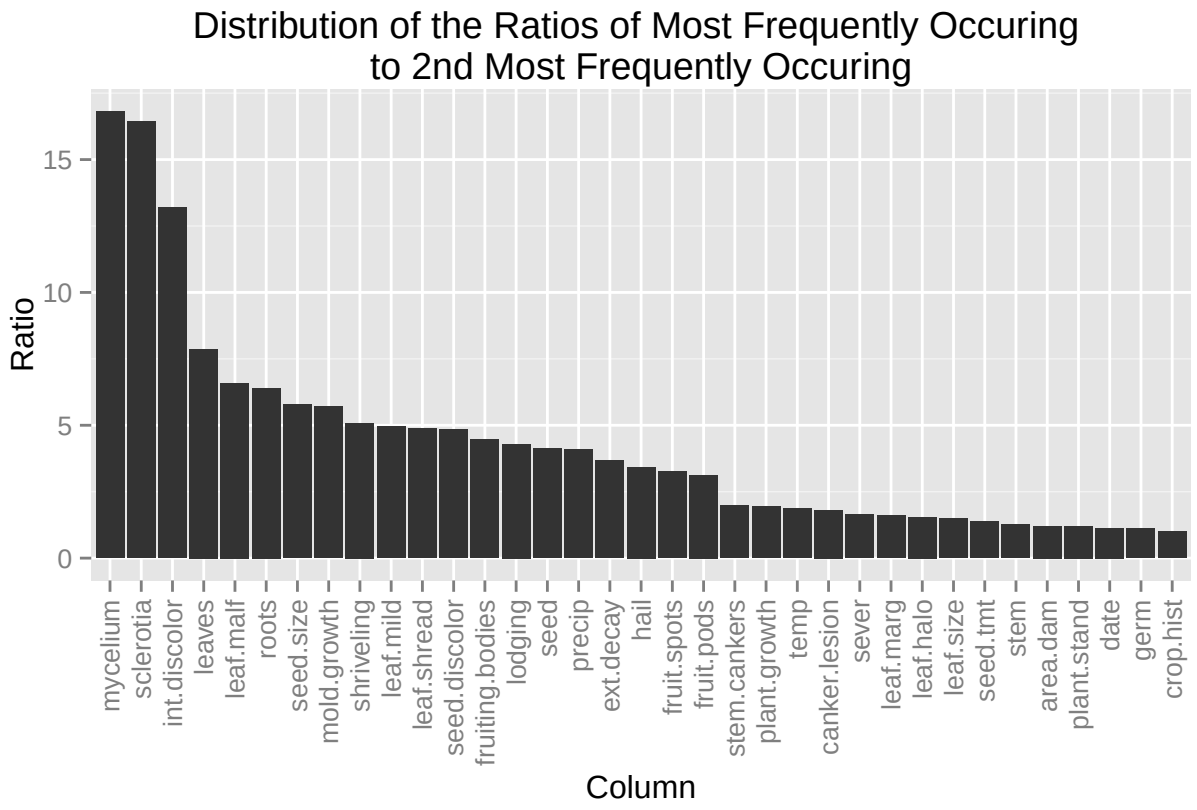
```
##                       ME      RMSE      MAE       MPE     MAPE     MASE
## Training set 2.480763e-15 12.138802 9.498898 -6.120182 20.30851 1.119163
## Test set     4.051587e+00  9.216133 7.850759  5.074990 13.75973 0.924979
##                   ACF1 Theil's U
## Training set 0.8661515        NA
## Test set     0.5095178   1.13105
##                       ME     RMSE      MAE        MPE      MAPE      MASE
## Training set -0.01593625 6.289813 4.988048 -0.7800232  9.880157 0.5876934
## Test set      5.00000000 9.670664 8.304348  6.8080182 14.381673 0.9784210
##                   ACF1 Theil's U
## Training set 0.1829708        NA
## Test set     0.5095178  1.179633
##                     ME      RMSE    MAE        MPE     MAPE      MASE
## Training set 0.1375000 10.576113 8.4875 -2.1016380 17.63375 1.0000000
## Test set     0.3043478  6.160886 5.0000 -0.7312374  9.12828 0.5891016
##                   ACF1 Theil's U
## Training set 0.838108        NA
## Test set     0.224307 0.8031005
```

```
##                        ME     RMSE      MAE        MPE     MAPE      MASE
## Training set 2.377739e-15 6.289793 4.987730 -0.7474544  9.87819 0.5876560
## Test set     5.191235e+00 9.761548 8.393037  7.1599507 14.50303 0.9888703
##                    ACF1 Theil's U
## Training set 0.1829708        NA
## Test set     0.5083059  1.188562
```

Question 3.2a

It seems that only three columns come close (but don't quite hit the threshold) to matching the rules of thumb for degenerate categorical data as described in the book. Those columns are mycelium, int.discolor, and sclerotia (see output):

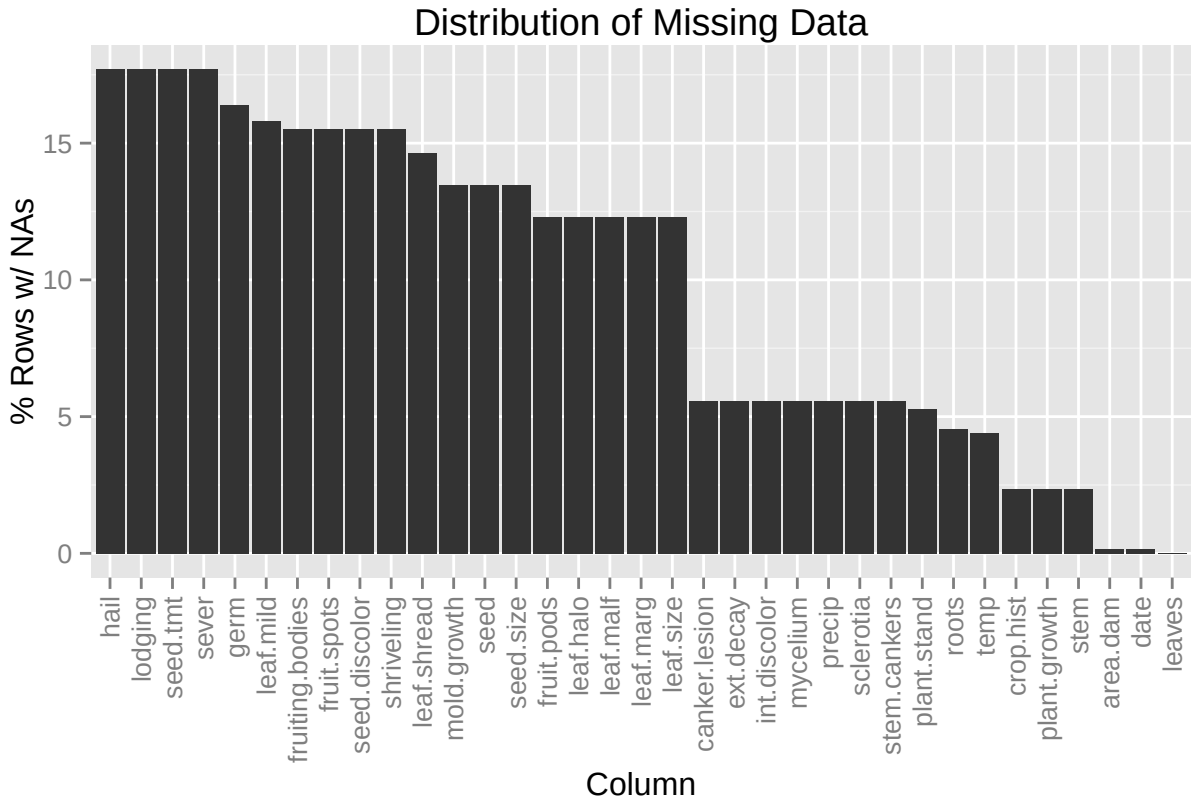
```
nrows <- nrow(Soybean);
i <- 1;
ratios <- c()
for (column in colnames(Soybean)[2:length(colnames(Soybean))]) {
  t <- count(Soybean, column)
  sorted_t <- t[order(-t['freq']), 'freq']

  ratios[i] <- (sorted_t[1] / sorted_t[2]);
  i <- i + 1;
}

ratios.dist <- data.frame(y=ratios, x=colnames(Soybean)[2:length(colnames(Soybean))])
ratios.dist$x <-reorder(ratios.dist$x,-ratios.dist$y)
ggplot(ratios.dist) +
  geom_bar(aes(x=x, y=y), stat="identity") +
  theme(axis.text.x=element_text(angle=90,hjust=1,vjust=0.5)) +
  ggtitle("Distribution of the Ratios of Most Frequently Occuring \nto 2nd Most Frequently Occuring") +
  ylab("Ratio") + xlab("Column")
```



Question 3.2b

Looking at the histogram, it seems that quite a few predictors have signifcant number of NAs. There is a dropoff in NA level from around 12% to 5% (highest being almost 20% missing data). Also, the columns herbicide-injury, cyst-nematode, 2-4-d-injury, diaporthe-pod-&-stem-blight have no instances / rows that do not have a NA in them. The class phytophthora-rot has 68 NAs, but all other classes have complete cases:

```
i <- 1;
nas <- c()
for (column in colnames(Soybean)[2:length(colnames(Soybean))]) {
  t <- count(Soybean, column)
  nas[i] <- ifelse(length(t[is.na(t[column]), 'freq']), t[is.na(t[column]), 'freq'] * 100 / nrows, 0)
  i <- i + 1;
}

# Display histogram of distrubtion of NAs
nas.dist <- data.frame(y=nas, x=colnames(Soybean)[2:length(colnames(Soybean))])
nas.dist$x <-reorder(nas.dist$x,-nas.dist$y)
ggplot(nas.dist) +
  geom_bar(aes(x=x, y=y), stat="identity") +
  theme(axis.text.x=element_text(angle=90,hjust=1,vjust=0.5)) +
  ggtitle("Distribution of Missing Data") +
  ylab("% Rows w/ NAs") + xlab("Column")
```




```
# The columns herbicide-injury, cyst-nematode, 2-4-d-injury, diaporthe-pod-&-stem-blight
# have no instances / rows that do not have a NA in them
# The Class phytophthora-rot has 68  NAs, but all other classes have none
withnas <- count(Soybean$Class)
```

```
withoutnas <- count(Soybean[complete.cases(Soybean), 'Class'])
for (i in 1:nrow(withoutnas)) {
  classval <- withoutnas[i, 'x']
  diff <- withnas[withnas$x == classval, 'freq'] - withoutnas[withoutnas$x == classval, 'freq']
  if(diff > 0) {
    print(paste("Class", classval, "has", diff, " NAs"))
  }
}
```

```
## [1] "Class phytophthora-rot has 68  NAs"
```

Question 3.2c)

We should start by investigating the nature of the missing data for predictors with a large number of missing values as well as why some classes have a high occurance of NAs. Our predictive model is going to be biased if we do not have good observations for 4 or 5 of the 19 outcome classes.

For each predictor that has a high number of NAs (starting from the left in the question_3.2b histogram), we can determine if we can remove the predictor by checking if it has a high collinearity with any other predictor. If so, we can remove that preidctor and simply use the collinear predictor (presuming it has less instances of NAs). Imputing values would be difficult, since these are all categorical variables, and averaging those values would make no sense. We could impute a value using K-nearest neighbors, which would find the K rows that are closest to it by some definition of 'close', and then take a majority vote on what the categorical value should be.

Question 4.4a)

Th code below generates random samples of size 60 from oilType. The output shows how inconsistent the samples are with respect to the class frequencies, and vary far from the distribution from the full data.

```
#' (a) Use the sample function in base R to create a completely random sample
#' of 60 oils. How closely do the frequencies of the random sample match
#' the original samples? Repeat this procedure several times of understand
#' the variation in the sampling process.
print("Frequency from Data")
print(freq(oilType, plot = FALSE))

cat("\n")
print("Frequency from Sampling 60 items")
for (i in 1:5) {
  print(freq(sample(oilType, 60), plot = FALSE))
}
```

```
## [1] "Frequency from Data"
## oilType
##       Frequency Percent
## A            37  38.542
## B            26  27.083
## C             3   3.125
## D             7   7.292
## E            11  11.458
## F            10  10.417
## G             2   2.083
## Total        96 100.000
##
## [1] "Frequency from Sampling 60 items"
## sample(oilType, 60)
##       Frequency Percent
## A            21  35.000
## B            19  31.667
## C             1   1.667
## D             6  10.000
## E             5   8.333
## F             7  11.667
## G             1   1.667
## Total        60 100.000
## sample(oilType, 60)
##       Frequency Percent
## A            21   35.00
## B            16   26.67
## C             3    5.00
## D             6   10.00
## E             7   11.67
## F             7   11.67
## G             0    0.00
## Total        60  100.00
## sample(oilType, 60)
##       Frequency Percent
## A            21  35.000
```

```
## B            17  28.333
## C             2   3.333
## D             5   8.333
## E             9  15.000
## F             5   8.333
## G             1   1.667
## Total        60 100.000
## sample(oilType, 60)
##       Frequency Percent
## A            25  41.667
## B            14  23.333
## C             3   5.000
## D             4   6.667
## E             7  11.667
## F             6  10.000
## G             1   1.667
## Total        60 100.000
## sample(oilType, 60)
##       Frequency Percent
## A            25  41.667
## B            18  30.000
## C             0   0.000
## D             4   6.667
## E             6  10.000
## F             6  10.000
## G             1   1.667
## Total        60 100.000
```

Question 4.4b)

The createDataPartition is indeed giving back different numbers every time but table() output shows how it is very consistent in how it distributes samples across class values, and is very close to the ideal from the data itself. Much better than the previous approach.

```
#' (b) Use the caret package function createDataPartition to create a stratified
#' random sample. How does this compare to the completely random samples?
#' the variation in the sampling process.
print("Frequency from Data")
print(freq(oilType, plot = FALSE))

cat("\n")
print("Frequency from Sampling 60 items")
for (i in 1:5) {
  print(freq(oilType[createDataPartition(oilType, p=60 / length(oilType), list=FALSE)], plot = FALSE))
}
```

```
## [1] "Frequency from Data"
## oilType
##       Frequency Percent
## A            37  38.542
## B            26  27.083
## C             3   3.125
## D             7   7.292
```

```
## E            11  11.458
## F            10  10.417
## G             2   2.083
## Total        96 100.000
##
## [1] "Frequency from Sampling 60 items"
## oilType[createDataPartition(oilType, p = 60/length(oilType),      list = FALSE)]
##       Frequency Percent
## A            24  37.500
## B            17  26.562
## C             2   3.125
## D             5   7.812
## E             7  10.938
## F             7  10.938
## G             2   3.125
## Total        64 100.000
## oilType[createDataPartition(oilType, p = 60/length(oilType),      list = FALSE)]
##       Frequency Percent
## A            24  37.500
## B            17  26.562
## C             2   3.125
## D             5   7.812
## E             7  10.938
## F             7  10.938
## G             2   3.125
## Total        64 100.000
## oilType[createDataPartition(oilType, p = 60/length(oilType),      list = FALSE)]
##       Frequency Percent
## A            24  37.500
## B            17  26.562
## C             2   3.125
## D             5   7.812
## E             7  10.938
## F             7  10.938
## G             2   3.125
## Total        64 100.000
## oilType[createDataPartition(oilType, p = 60/length(oilType),      list = FALSE)]
##       Frequency Percent
## A            24  37.500
## B            17  26.562
## C             2   3.125
## D             5   7.812
## E             7  10.938
## F             7  10.938
## G             2   3.125
## Total        64 100.000
## oilType[createDataPartition(oilType, p = 60/length(oilType),      list = FALSE)]
##       Frequency Percent
## A            24  37.500
## B            17  26.562
## C             2   3.125
## D             5   7.812
## E             7  10.938
## F             7  10.938
```

```
## G             2   3.125
## Total        64 100.000
```

Question 4.4c)

When the number of samples is not large, a single test set should be avoided because we may need every sample during model building. We should use somekind of resampling technique, like k-fold cross-validation. The book recommends "If the samples size is small, we recommend repeated 10-fold cross-validation for several reasons: the bias and variance properties are good and, given the sample size, thecomputational costs are not large.

Question 4.4d)

The code following this shows the commands I used to come to the following conclusions.

By keeping the model performance steady, while changing the test sample size leads to a relationship where higher sample size means less uncertainity. This makes sense: we would expect us to be more certain if we have more samples to evaluate the model performance with.

If you keep the sample size steady, and vary the model performance leads to a relationship where: - the uncertainity maxes when performance is 50% (which makes sense since its binomial probability). - the uncertainity is less when model performace is near either extreme (partially due to clipping of the CI by the boundry)

```
spread <- function(obj) { conf <- obj$conf.int; return(conf[2] - conf[1]);}
spread(binom.test(16, 20)) # 0.37928
spread(binom.test(32, 40)) # 0.2659556
spread(binom.test(30, 40)) # 0.2850472
spread(binom.test(10, 40)) # 0.2850472
spread(binom.test(15, 40)) # 0.3147225
spread(binom.test(20, 40)) # 0.3239644
spread(binom.test(25, 40)) # 0.3147225
spread(binom.test(40, 40)) # 0.0880973
spread(binom.test(20, 40)) # 0.3239644
spread(binom.test(21, 40)) # 0.3236002
spread(binom.test(19, 40)) # 0.3236002
spread(binom.test(19, 20)) # 0.2474677
spread(binom.test(20, 20)) # 0.1684335
spread(binom.test(10, 20)) # 0.4560843
spread(binom.test(1, 20))  # 0.2474677
```