Random Forest Routines

Classification Trees

Classification trees are a tree-based model and are used to predict a qualitative response. The variables that go into these classification trees can be numerical or categorical. We predict that "each observation belongs to the most commonly occuring class (or category) of training observations in the region to which it belongs" (James, 2013). They are useful because they provide predictors in situations where there are many variables that interact in complicated, non-linear ways. In interpreting these classification trees, we are often "interested in both the class prediction corresponding to a particular terminal node region, and in the class proportions among the training observations that fall into that region" (James, 2013).

So, in simpler terms, a classification tree consists of a set of true/false decision rules. It is kind of like a game of 20 questions, where we ask different questions based on the answers to previous questions, and then at the end we make a guess based on all the answers. We can visualize a decision tree as a set of nodes (corresponding to true/false questions), each of which has two branches depending on the answer to the question. Unlike real trees, we usually draw them with their "root" at the top, and the "leaves" at the bottom. In order to make predictions with the tree, we start at the top (the "root" node), and ask questions, traveling left or right in the tree based on what the answer is (left for true and right for false). At each step, we reach a new node, with a new question. Once we reach the bottom (a leaf node), we make a prediction based on the set of answers, just like 20 questions. But unlike 20 questions, the number of questions in a decision tree is not always 20, but can vary (Corso, 2013). XXXXX**This was adapted from a lecture PPT of James Corso from SUNY at Buffalo CSE 555 course.**

Shall we look at an example of a classification tree?

We are using a data set from a survey taken in the MAT 111 class (Elementary Probability and Statistics). This data set has 71 rows and 12 variables. The survey includes variables such as sex, height, GPA, sleep, and the fastest speed ever driven. The names of some of the variables may seem a little odd, such as weight_feel, love_first, and extra_life. The weight_feel variable is how the participant feels about their weight. They could have answered underweight ("a"), about right ("b"), or overweight ("c"). The love_feel variable is whether or not the participant believes in love at first sight and the extra_life variable is whether or not the participant believes in extraterrestrial life. The seat variable is where the participant sits in a classroom. The letter "a" corresponds to sitting in the front, "b" corresponds sitting in the middle rows, and "c" corresponds to sitting in the back rows.

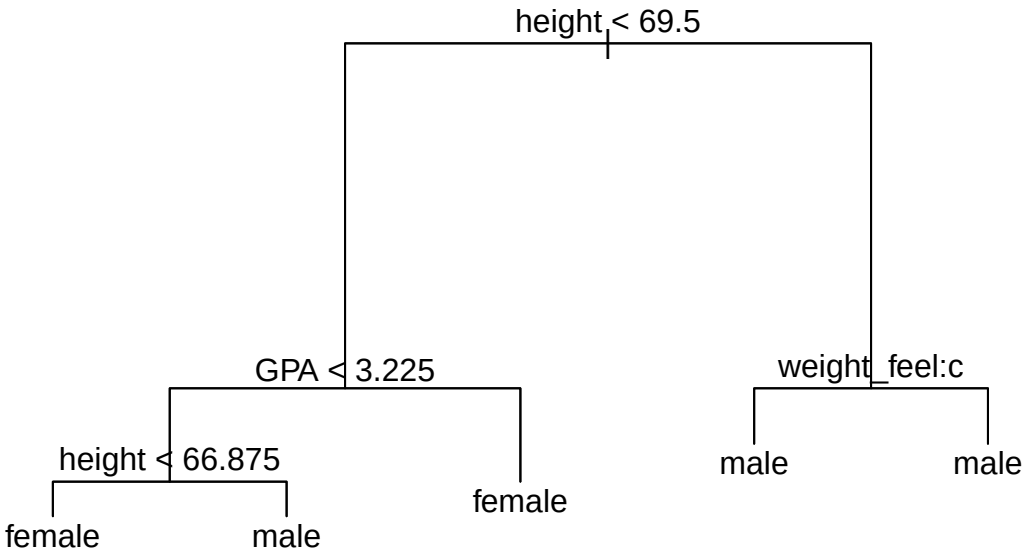
```
set.seed(2020)

m111s.tr <- tree(sex~fastest+GPA+height+sleep+weight_feel+love_first,
                 data=m111survey)

m111s.tr
```

```
## node), split, n, deviance, yval, (yprob)
##       * denotes terminal node
##
## 1) root 70 96.120 female ( 0.5571 0.4429 )
##   2) height < 69.5 42 34.450 female ( 0.8571 0.1429 )
##     4) GPA < 3.225 18 22.910 female ( 0.6667 0.3333 )
##       8) height < 66.875 9  6.279 female ( 0.8889 0.1111 ) *
##       9) height > 66.875 9 12.370 male ( 0.4444 0.5556 ) *
##     5) GPA > 3.225 24  0.000 female ( 1.0000 0.0000 ) *
##   3) height > 69.5 28 19.070 male ( 0.1071 0.8929 )
##     6) weight_feel: 3_overweight 10 12.220 male ( 0.3000 0.7000 ) *
```

```
##     7) weight_feel: 1_underweight,2_about_right 18  0.000 male ( 0.0000 1.0000 ) *
```

This tree is used to predict the sex of an individual based on the variables of fastest speed ever driven, GPA, height, the amount of sleep the participant got the night before, how the participant feels about their weight, and if the participant believes in love at first sight. The summary given shows the variables actually used in constructing the classification tree, the number of terminal nodes, the residual mean deviance, and the misclassification error rate.

```
plot(m111s.tr)
text(m111s.tr)
```



Looking at this tree, we can see that the first division is set when height is less than 69.5 inches. If the height of an observation is less than 69.5 inches they are put into the left region and those with a height equal to or above 69.5 inches are put into the right region. Those in the left hand region are divided by GPA. If the GPA is greater than or equal to 3.225, the prediction is female. If the GPA is less than 3.225, then a further division by height is made. If the height is less than 66.875 inches, then female is predicted. Otherwise, the sex is predicted as male. Those in the right region are divided by how they feel about their weight. Notice that the division is by "weight_feel:c". This means that the left region feel underweight or about right and the right region feel overweight. Instead of using the full name of the variable, this tree made shorter version. The letter "a" corresponds to feeling underweight, the letter "b" corresponds to feeling about right, and the letter "c" corresponds to feeling overweight. Looking at the two terminal nodes, it appears that it doesn't matter how they feel about their weight; the prediction will still be male.

Now, it may seem odd that the classification tree made a split that ended up in two nodes with the same prediction. Why bother making another division? This split was made because it led to increased *node purity*. This means that the region could be further subdivided into 2 regions where each was more purely

male or female. After the division, one node is completely male and the other is 70% male. If the height is greater than 69.5 inches and they feel overweight, then male is absolutely certain. If they feel just right or underweight, 70% of the node are male. Even though we are less certain of this classification (compared to 89% male before the division), it improves the deviance. We want the deviance as close to 0 as possible and the deviance improved from 19.070 to 12.220. The sum of the deviances from the post-division nodes is closer to 0 than the pre-division node.

The deviance formula used for the classification trees is:

-2 $\sum_k n_{ik} log_e(p_{ik})$

where n_ik is the number of a certain type in the node and p_ik is the proportion of the proportion of a certain type in the node.

So using the classification tree example, let's look at how the deviance was found for the final height split (height < 66.875).

Talk about deviance tree.control- governs how finely tree will be made. Find Dr. White's email with dev. formula. Talk about default tree control. When do RF, trees are larger and makes fewer errors, but doesn't mean it will do well; chance error as patterns

```
summary(m111s.tr)
```

```
##
## Classification tree:
## tree(formula = sex ~ fastest + GPA + height + sleep + weight_feel +
##     love_first, data = m111survey)
## Variables actually used in tree construction:
## [1] "height"      "GPA"         "weight_feel"
## Number of terminal nodes:  5
## Residual mean deviance:  0.4748 = 30.86 / 65
## Misclassification error rate: 0.1143 = 8 / 70
```

As you can see from this example, classification trees are easy to interpret and fairly good predictions can be made from them. In this example the misclassification error rate is about 11.4%, or 8 out of 70 observations were misclassified.

Random forests

Random forests are more advanced learning models that are capable of creating more complex decision boundaries than logistic regression. The "forest" part of the name means that it is made up of multiple decision trees (in general, the more trees, the better). Usually in a random forest instead of building a tree using all the features, we use only a random subset of features and use bagging to create the trees. That means different trees will consider different features when asking questions. But in a forest, other trees would include this feature, so it would still influence the overall prediction by the random forest.

XXXXX**Step by step process of how RF is built**

Random forests have low bias (just like individual decision trees), and by adding more trees, we reduce variance. XXXXX**Do I need to talk about variance and bias in this section?**

Here is an example of a random forest:

```
set.seed(1010)
rf.sexm111 <- randomForest(sex~fastest+GPA+height+sleep+weight_feel+
                             love_first+extra_life+ideal_ht+seat+
                             enough_Sleep+diff.ideal.act., data=m111surv2)
rf.sexm111
```

```
##
## Call:
##  randomForest(formula = sex ~ fastest + GPA + height + sleep +      weight_feel + love_first + extra
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 3
##
##         OOB estimate of  error rate: 4.41%
## Confusion matrix:
##        female male class.error
## female     37    1  0.02631579
## male        2   28  0.06666667
```

XXXXX**Talk about results of random forest At 50th stage, looking at each of the items in training set, can tree vote on that item? The ones that didn't use item (individual in random resample) have a vote. Majority vote wins- either right or wrong. OOB is the percentage of time the group of 50 trees got it wrong. Females = 1 only wrong 2.6% of time, males= 2 wrong 10% of time.**

Now, we can look at individual trees from this forest to see the differences:

```
st1 <- getTree(rf.sexm111, k=1, labelVar = TRUE)
names(st1)[1:2] <- c("LD", "RD")
st1
```

```
##    LD RD   split var split point status prediction
## 1   2  3         GPA       3.715      1       <NA>
## 2   4  5    ideal_ht      71.000      1       <NA>
## 3   0  0        <NA>       0.000     -1     female
## 4   6  7      height      66.875      1       <NA>
## 5   8  9      height      77.000      1       <NA>
## 6   0  0        <NA>       0.000     -1     female
## 7  10 11 weight_feel       1.000      1       <NA>
## 8   0  0        <NA>       0.000     -1       male
## 9  12 13 weight_feel       2.000      1       <NA>
## 10  0  0        <NA>       0.000     -1       male
## 11 14 15        seat       1.000      1       <NA>
## 12  0  0        <NA>       0.000     -1       male
## 13  0  0        <NA>       0.000     -1     female
## 14  0  0        <NA>       0.000     -1       male
## 15  0  0        <NA>       0.000     -1     female
```

XXXXX**Do this for all trees**

```
st2 <- getTree(rf.sexm111, k=250, labelVar = TRUE)
names(st2)[1:2] <- c("LD", "RD")
st2
```

```
##    LD RD       split var split point status prediction
## 1   2  3          height      66.875      1       <NA>
## 2   4  5        ideal_ht      72.500      1       <NA>
## 3   6  7 diff.ideal.act.       1.750      1       <NA>
## 4   0  0            <NA>       0.000     -1     female
```

```
## 5   0  0            <NA>       0.000     -1       male
## 6   8  9     weight_feel       1.000      1       <NA>
## 7   0  0            <NA>       0.000     -1       male
## 8   0  0            <NA>       0.000     -1       male
## 9  10 11          height      72.500      1       <NA>
## 10  0  0            <NA>       0.000     -1     female
## 11  0  0            <NA>       0.000     -1       male
```

```
st3 <- getTree(rf.sexm111, k=499, labelVar = TRUE)
names(st3)[1:2] <- c("LD", "RD")
st3
```

```
##    LD RD       split var split point status prediction
## 1   2  3        ideal_ht       70.75      1       <NA>
## 2   4  5      extra_life        1.00      1       <NA>
## 3   6  7 diff.ideal.act.       -1.50      1       <NA>
## 4   0  0            <NA>        0.00     -1     female
## 5   8  9         fastest       97.50      1       <NA>
## 6   0  0            <NA>        0.00     -1     female
## 7   0  0            <NA>        0.00     -1       male
## 8   0  0            <NA>        0.00     -1     female
## 9  10 11            seat        2.00      1       <NA>
## 10  0  0            <NA>        0.00     -1       male
## 11  0  0            <NA>        0.00     -1     female
```

```
st4 <- getTree(rf.sexm111, k=96, labelVar = TRUE)
names(st4)[1:2] <- c("LD", "RD")
st4
```

```
##    LD RD   split var split point status prediction
## 1   2  3         GPA      3.1335      1       <NA>
## 2   4  5       sleep      7.7500      1       <NA>
## 3   6  7 weight_feel      3.0000      1       <NA>
## 4   8  9       sleep      6.5000      1       <NA>
## 5  10 11       sleep      8.2500      1       <NA>
## 6  12 13    ideal_ht     70.0000      1       <NA>
## 7  14 15      height     72.0000      1       <NA>
## 8   0  0        <NA>      0.0000     -1       male
## 9  16 17        seat      3.0000      1       <NA>
## 10 18 19     fastest    115.0000      1       <NA>
## 11  0  0        <NA>      0.0000     -1     female
## 12  0  0        <NA>      0.0000     -1     female
## 13  0  0        <NA>      0.0000     -1       male
## 14  0  0        <NA>      0.0000     -1     female
## 15 20 21       sleep      6.0000      1       <NA>
## 16 22 23      height     64.8750      1       <NA>
## 17  0  0        <NA>      0.0000     -1     female
## 18  0  0        <NA>      0.0000     -1       male
## 19  0  0        <NA>      0.0000     -1     female
## 20  0  0        <NA>      0.0000     -1       male
## 21  0  0        <NA>      0.0000     -1     female
## 22  0  0        <NA>      0.0000     -1     female
## 23  0  0        <NA>      0.0000     -1       male
```

```r
st5 <- getTree(rf.sexm111, k=153, labelVar = TRUE)
names(st5)[1:2] <- c("LD", "RD")
st5
```

```
##    LD RD   split var split point status prediction
## 1   2  3         GPA        2.75      1       <NA>
## 2   4  5 weight_feel        3.00      1       <NA>
## 3   6  7    ideal_ht       71.00      1       <NA>
## 4   0  0        <NA>        0.00     -1       male
## 5   8  9        seat        1.00      1       <NA>
## 6   0  0        <NA>        0.00     -1     female
## 7  10 11      height       77.00      1       <NA>
## 8   0  0        <NA>        0.00     -1     female
## 9   0  0        <NA>        0.00     -1       male
## 10  0  0        <NA>        0.00     -1       male
## 11  0  0        <NA>        0.00     -1     female
```

XXXXX**Probably need to talk about what each tree means, since it is not in a neat visual form**