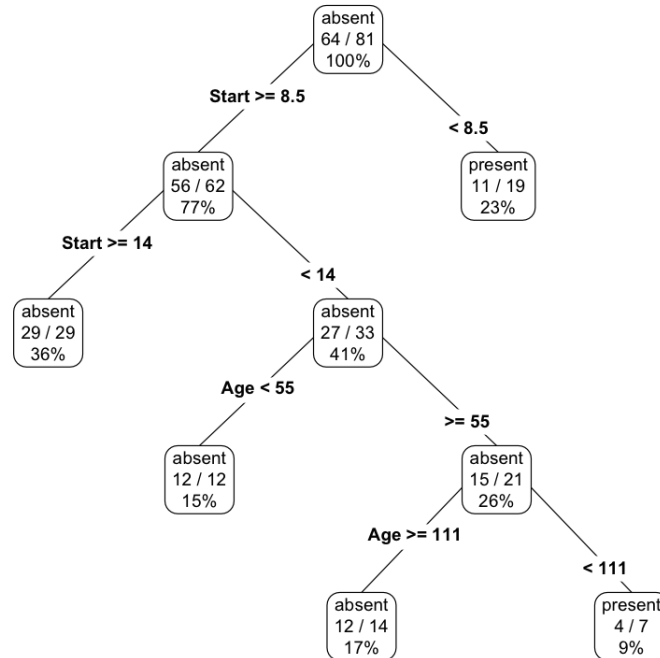


1. The **kyphosis** data set in R contains information about children who have had corrective spinal surgery.

The data is stored for 81 subjects, with 4 columns for each. The columns are Kyphosis which takes values 'absent' or 'present', Age (in months), Number, which gives the number of vertebrae involved and Start, which is the topmost vertebra number operated on.

2. the tree for predicting Kyphosis based upon the other variables in the data set is shown below.



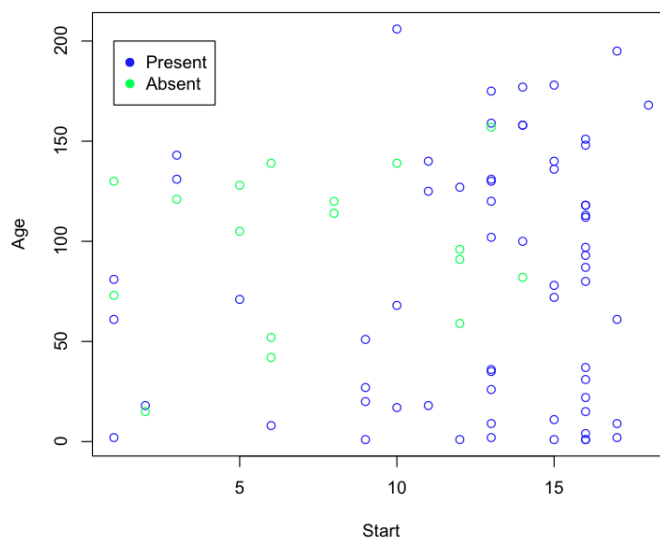
The confusion matrix is shown below.

		predicted kyphosis	
		absent	present
Kyphosis	absent	53	11
	present	2	15

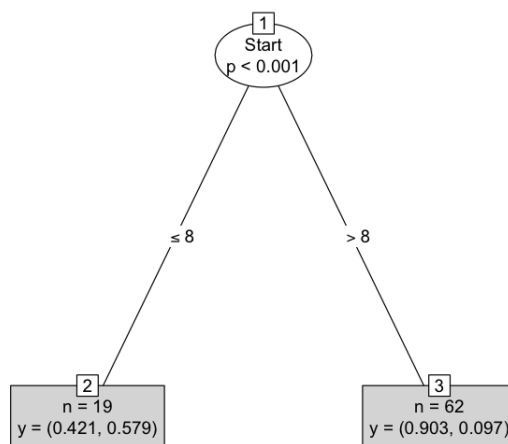
The accuracy is the sum of the diagonal entries of the decision matrix (in other words, the number of accurate predicted results) divided by the total number. For this case, $\text{accuracy} = 0.8395062$

The error is $\text{error} = 1 - \text{accuracy} = 0.1604938$

3. According to the tree, the most important variables for predicting kyphosis are Start, which is the vertebra being operated on and the Age of the patient. These two variables partition the data most effectively.



4. For the simple tree case using the ctree command, the tree was generated as shown.



The confusion matrix for this case is

		predicted kyphosis	
		absent	present
Kyphosis	absent	56	8
	present	6	11

The accuracy and error for this confusion matrix are: accuracy = 0.8271605 , and error = 1 - accuracy = 0.1728395

5. The main difference between the two trees is in the number and distribution in the end nodes. The simple tree has fewer terminal nodes, which gives a simpler categorization. In addition, the distribution in the right node is close to pure (roughly 90%). However, the distribution in the left node is very impure, closer to 50%. This is where the more complex tree is better. Therefore the answer to which is the better tree is problem dependent. The simple tree is best for quick categorization for when Start ≥ 8 , and the other tree for more detailed examination of the data.

The confusion matrices demonstrate a similar breakdown of effectiveness. Using the information to calculate error and accuracy shows that the rpart tree shows a slightly higher accuracy. However, the difference in accuracy is so small as to be negligible.

6. The overall entropy of the system is 0.7412467.

The rpart tree had a weighted entropy of 0.4177394.

The ctree had a weighted entropy of 0.5819756.

7. There is no great difference between the two trees. The maximum petal length for setosa flowers was recorded in the table as 1.9, and the minimum length petal for versicolor was recorded as 3.0.

Therefore the initial split requirement for the tree on page 28 (which is length ≤ 2.4) splits all of the setosa flowers into one branch. The p values in that branch show that neither virginica nor versicolor flowers are included in that branch, but are completely in the other. This is exactly the same condition in its effect upon the distribution as the condition on page 38 for length ≤ 1.9 , since all setosa petals are less than or equal to 1.9, and all other flower types have petals greater than 2.4.

The code used to calculate the minimum and maximum lengths of the respective flower types is shown below.

```

1  sindex=(iris$Species == "setosa")
2  largest_length = max(Petal.Length[sindex])
3  largest_length
4
5  vindex=(iris$Species == "versicolor")
6  shortest_length = min(Petal.Length[vindex])
7  shortest_length

```

The code for the kyphosis related questions is shown below.

```
1 # Data Mining hw 3
2
3 # problem 1
4 ##kyphosis {rpart}
5 #it is a data frame with 81 rows, 4 columns representing data on children
6 #who have had corrective spinal surgery.
7 #
8 #columns are as follows:
9 #+ Kyphosis
10 #+ + + A factor with levels 'absent' 'present' indicating if a kyphosis was
11 #+ + + present after the operation
12 #
13 #
14 #+ Age
15 #+ + + in months
16 #
17 #+ Number
18 #+ + + the number of vertebrae involved
19 #
20 #+ Start
21 #+ + + The number of the first (topmost) vertebra operated on.
22 #
23 library(rpart)
24 library(rpart.plot)
25 library(party)
26 library(treemap)
27 attach(kyphosis)
28
29 # problem number 2
30 #a)
31 ktree=rpart(Kyphosis~Age+Number+Start,data=kyphosis)
32 plot(ktree,main="Kyphosis~Age+Number+Start")
33 prp(ktree,type=2,extra=104)
34 #b)
35 predkyphos = predict(ktree,newdata=kyphosis,type="class")
36 confusionmatrix=table(Kyphosis,predkyphos)
37 #c)
38 accuracy = sum(diag(confusionmatrix))/sum(confusionmatrix)
39 error = 1 - accuracy
40
41 # problem number 4
42 #a)
43 ktree2=ctree(Kyphosis~.,data=kyphosis)
```

```
44 plot(ktree2,type='simple')
45 #b)
46 predkyphos2 = predict(ktree2,newdata=kyphosis)
47 confusionmatrix=table(Kyphosis,predkyphos2)
48 #c)
49 accuracy = sum(diag(confusionmatrix))/sum(confusionmatrix)
50 error = 1 - accuracy
```