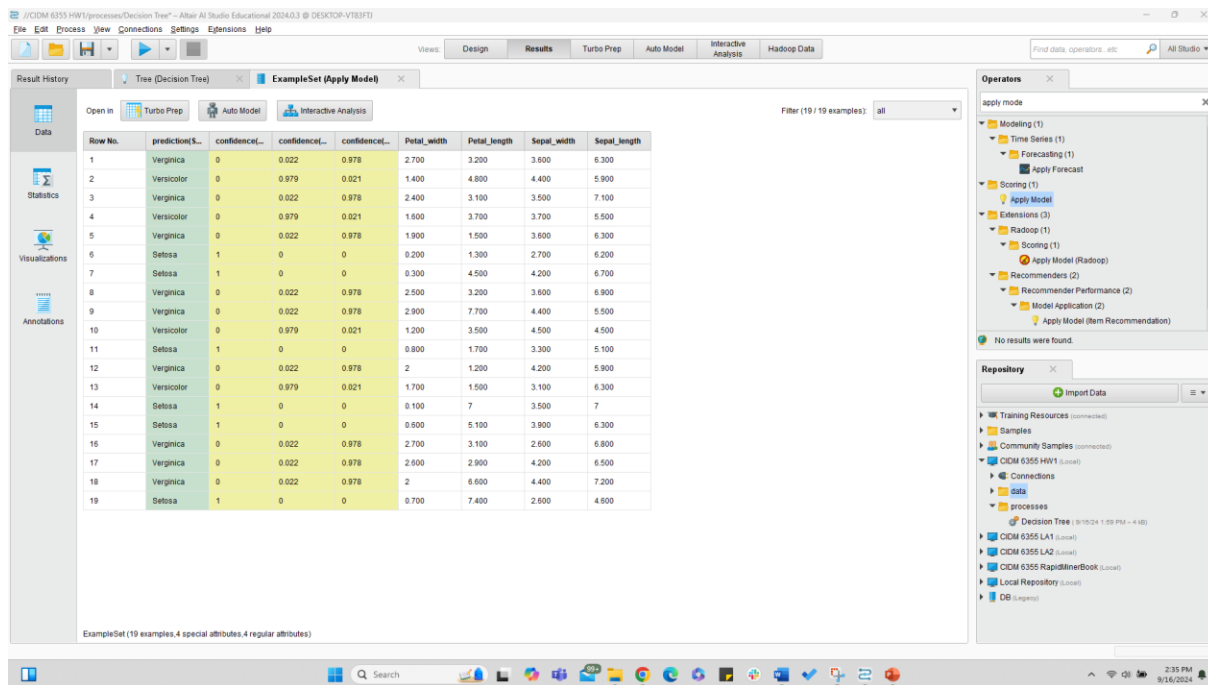


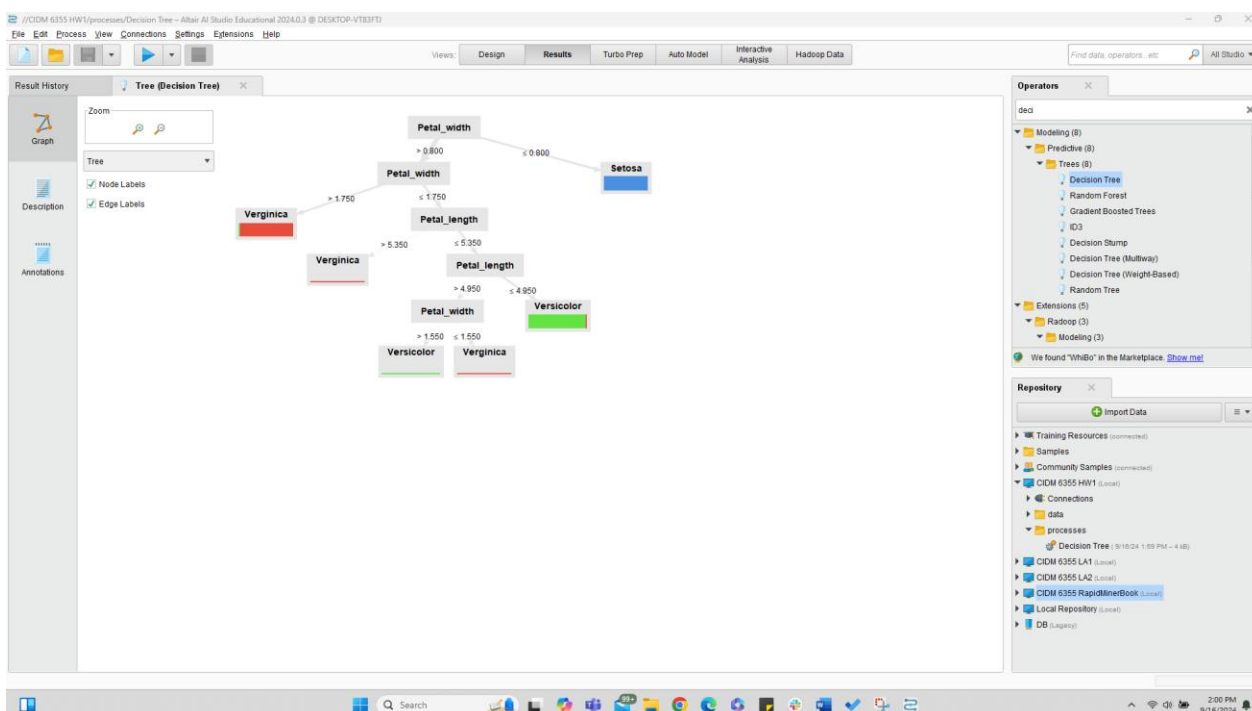
1) Screenshots in RapidMiner Lab (10 points)

- Screenshot 1: A screenshot of the decision tree graph with date and time at Step 1.8 (5 points)



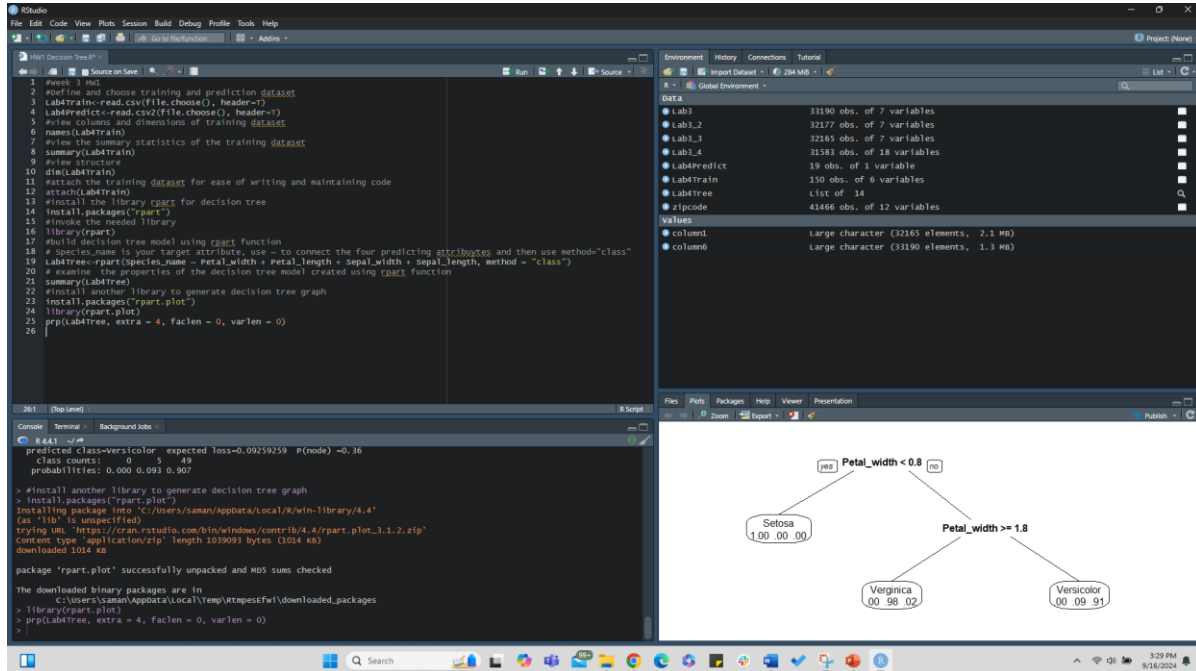
- Screenshot 2: A screenshot of prediction results for the 19 observations with date and time in Step 2.2 (5 points)

2) Deliverables in R Lab (50 points)

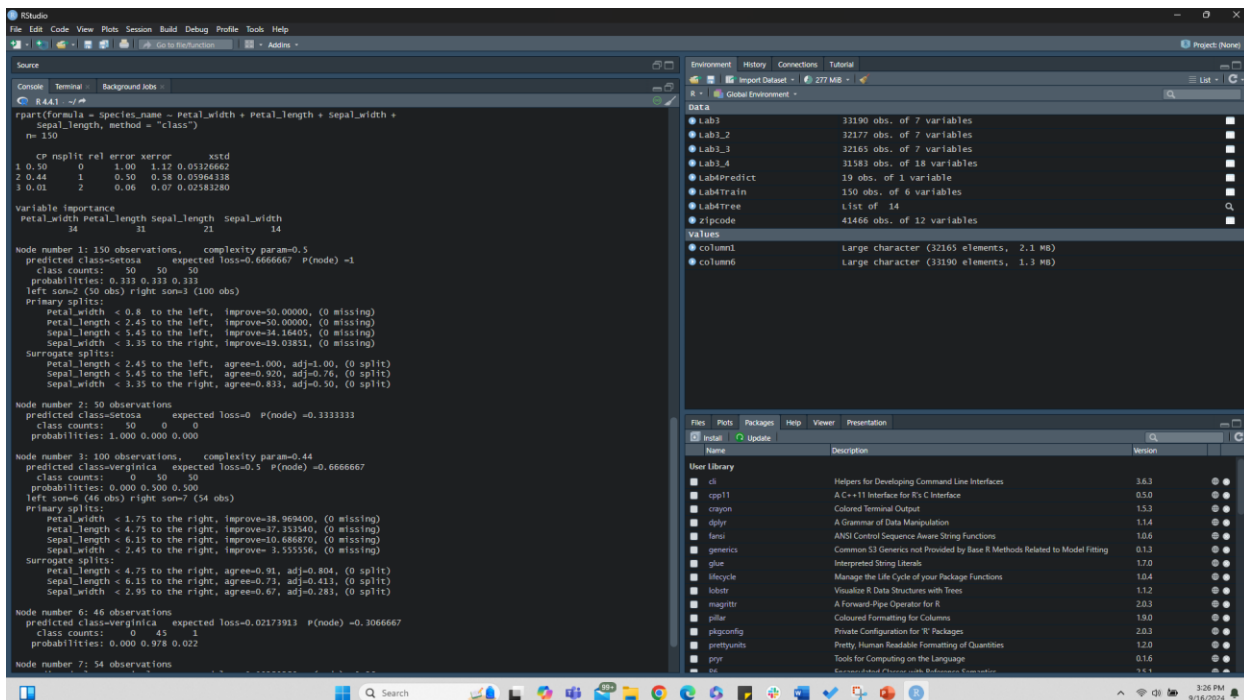


- Deliverable R1: take a screenshot of your decision tree model with date and time (5 points).

- **Deliverable R2:** take a screenshot of your decision tree graph with date and time and briefly describe it.



Your description must include the root node, split nodes, and leaf nodes. (10 points: 5 points for your screenshot and 5 points for your description).



The root node of this decision tree is `Petal_width < 0.8` at the top of the tree. There is only one other split node (not including the root node), which is `Petal_width >= 1.8`. The leaf nodes shown circled and are Setosa, Verginica, and Versicolor.

- **Deliverable R3:** after you apply the decision tree model to your prediction dataset, take a screenshot of the prediction result with date and time and briefly describe how the result help you determine the predicted class of each case. (10 points: 5 points for your screenshot and 5 points for your description).

Deliverable R3 description: For each row, the results show a confidence percentage of each species name. Where the highest confidence percentage is, is where I determine the prediction. For example, if we look at row 4, the confidence percentages are as follows: Setosa:0, Verginica: 0.09259259, and Versicolor: 0.90740741. Since Versicolor has the highest confidence percentage, we can conclude that Versicolor is the species name.

```

1 #HWY Decision tree party
2 # Define and choose training and prediction dataset
3 Lab4Train<-read.csv(file.choose(), header=T)
4 #View columns and dimensions of training dataset
5 names(Lab4Train)
6 #View the summary statistics of the training dataset
7 summary(Lab4Train)
8 #View structure
9 str(Lab4Train)
10 #Attach the training dataset for ease of writing and maintaining code
11 attach(Lab4Train)
12 #Install the library party for decision tree
13 install.packages("party")
14 #Load the needed library
15 library(party)
16 #Build decision tree model using ctree function
17 #Species_name is your target attribute, use ~ to connect the four predicting attributes
18 str(Lab4Train)
19 Lab4Train[,6]<-as.factor(Lab4Train[,6])
20 #Build decision tree model using ctree function
21 Lab4Tree<-ctree(Species_name ~ Petal_width + Petal_length + Sepal_width + Sepal_length, data = Lab4Train)
22 #Examine the properties of the decision tree model created
23 Lab4Tree
24
2561 (Top Level)

```

```

> # Species_name is your target attribute, use ~ to connect the four predicting attributes
> str(Lab4Train)
data.frame: 150 obs. of 6 variables:
 $ Species_name : fct 1 1 1 1 1 1 1 1 1 1 ...
 $ Petal_width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Petal_length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Sepal_width : num 3.5 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Sepal_length: num 5.1 4.9 4.7 4.8 5.5 4.6 5.4 4.4 4.9 ...
 $ Species_name: chr "Setosa" "Setosa" "Setosa" "Setosa" ...
> Lab4Train[,6]<-as.factor(Lab4Train[,6])
> Lab4Tree<-ctree(Species_name ~ Petal_width + Petal_length + Sepal_width + Sepal_length, data = Lab4Train)
> #Examine the properties of the decision tree model created
> Lab4Tree
Conditional inference tree with 4 terminal nodes

Response: Species_name
Inputs: petal_width, petal_length, sepal_width, sepal_length
Number of observations: 150

1) petal_length <= 1.9; criterion = 1, statistic = 140.264
  2) weights = 50
  1) petal_length > 1.9
    3) petal_width <= 1.7; criterion = 1, statistic = 67.894
      4) petal_length <= 4.8; criterion = 0.999, statistic = 13.865
        5)* weights = 46
        4) petal_length > 4.8
          6)* weights = 4
          3) petal_width <= 1.7
            7)* weights = 46

```

- **Deliverable R4:** take a screenshot of your decision tree model with date and time. Try to use the resources provided to understand its output (5 points).

```

1 #HWY Decision tree
2 # Define and choose training and prediction dataset
3 Lab4Train<-read.csv(file.choose(), header=T)
4 Lab4Predict<-read.csv(file.choose(), header=T)
5 #View columns and dimensions of training dataset
6 names(Lab4Train)
7 #View the summary statistics of the training dataset
8 summary(Lab4Train)
9 #View structure
10 str(Lab4Train)
11 #Attach the training dataset for ease of writing and maintaining code
12 attach(Lab4Train)
13 #Install the library rpart for decision tree
14 install.packages("rpart")
15 #Load the needed library
16 library(rpart)
17 #Build decision tree model using rpart function
18 #Species_name is your target attribute, use ~ to connect the four predicting attributes and then use method="class"
19 Lab4Tree<-rpart(Species_name ~ Petal_width + Petal_length + Sepal_width + Sepal_length, method = "class")
20 #Examine the properties of the decision tree model created using rpart function
21 summary(Lab4Tree)
22 #Install another library to generate decision tree graph
23 library("rpart.plot")
24 library(rpart.plot)
25 prp(Lab4Tree, extra = 4, facen ~ 0, varlen ~ 0)
26 #Apply the decision tree model to the prediction dataset to generate the value of target attribute in the prediction da
27 Lab4Score<-predict(Lab4Tree, Lab4Predict)
28 Lab4Score
29
291 (Top Level)

```

```

> Lab4Score<-predict(Lab4Tree, Lab4Predict)
> Lab4Score
Setosa Versinica Versicolor
1 0 0.97826087 0.02173913
2 0 0.09259259 0.90740741
3 0 0.97826087 0.02173913
4 0 0.09259259 0.90740741
5 0 0.97826087 0.02173913
6 1 0.00000000 0.00000000
7 1 0.00000000 0.00000000
8 0 0.97826087 0.02173913
9 0 0.97826087 0.02173913
10 0 0.09259259 0.90740741
11 0 0.09259259 0.90740741
12 0 0.97826087 0.02173913
13 0 0.09259259 0.90740741
14 1 0.00000000 0.00000000
15 1 0.00000000 0.00000000
16 0 0.97826087 0.02173913
17 0 0.97826087 0.02173913
18 0 0.97826087 0.02173913
19 1 0.00000000 0.00000000

```

- The screenshot displays the RStudio environment with the following components:

 - Source Editor:** Contains R code for loading data, summarizing statistics, and building a decision tree model using the `party` package. The code includes comments and function calls like `read.csv`, `summary`, `attach`, `install.packages`, `library`, `model2tree`, and `predict`.
 - Environment Pane:** Shows the objects created in the R session:
 - `Lab4Predict`: 19 obs. of 5 variables
 - `Lab4Train`: 150 obs. of 6 variables
 - `Lab4Tree2`: Formal class 'RpartTree'
 - `Lab4score2`: Factor w/ 3 levels "setosa", "versicolosa", ...
 - Console:** Displays the output of the R code, showing the number of observations (150) and the results of the `summary` function for the `Lab4Tree2` model, including criteria and statistics for each variable.
 - Files Pane:** Shows the project files, including `R441.R`.
 - Package Pane:** Lists installed packages such as `tidyverse`, `ggplot2`, `dplyr`, `tidyr`, `stringr`, `readr`, `purrr`, `magrittr`, `matrixStats`, `modeltools`, `multcomp`, `mvtnorm`, `party`, and `rpart`.

- ```

RStudio: File Edit View Plots Session Build Debug Profile Tools Help
Lab4: Decision Tree

Load the library party to do decision tree
Define and choose training and prediction dataset
Lab4train<-read.csv(file.choose(), header=T)
Lab4predict<-read.csv(file.choose(), header=T)
View columns and dimensions of training dataset
names(Lab4train)
View the summary statistics of the training dataset
summary(Lab4train)
View structure
dim(Lab4train)
Attach the training dataset for ease of writing and maintaining code
attach(Lab4train)
Install the library party for decision tree
install.packages("party")
Invoke the needed library
library(party)
Build decision tree model using ctree function
Species.name is your target attribute, use ~ to connect the four predicting attributes
str(Lab4train)
Lab4train[,c(1)<-as.factor(Lab4train[,6])]
Lab4tree<-ctree(Species.name ~ Petal.Length + Petal.Length * sepal_width + sepal_length, data = Lab4train)
Examine the properties of the decision tree model created
Lab4tree2
Generate a decision tree graph
plot(Lab4tree2)

```

**Environment** | History | Connectors | Tutorial

Import Dataset - 420 MB

**Data**

|             |                         |
|-------------|-------------------------|
| Lab4Predict | 19 obs. of 5 variables  |
| Lab4train   | 150 obs. of 6 variables |
| Lab4tree2   | Formal class binarytree |

```

RStudio: File Edit View Plots Session Build Debug Profile Tools Help
Lab4: Decision Tree

Examine the properties of the decision tree model created
Lab4tree2

Conditional inference tree with 4 terminal nodes

Response: Species.name
Inputs: petal_width, petal_length, sepal_width, sepal_length
Number of observations: 150

1) Petal.Length > 1.9; criterion = 1, statistic = 140.264
2) ~ weights = 50
1) Petal.Length > 1.9
3) Petal.Width <= 1.7; criterion = 1, statistic = 67.894
4) Petal.Length <= 4.8; criterion = 0.999, statistic = 13.865
5) ~ weights = 46
4) Petal.Length <= 4.8
6) ~ weights = 8
3) Petal.Width <= 1.7
7) ~ weights = 46
Generate a decision tree graph
plot(Lab4tree2)

```

two models. When discussing each difference, please include both R and RM. For example, "R does ..., but RM does not ...." (10 points).

I am going to be comparing the RM decision tree and R library party decision tree. One of the first major differences I noticed was the structure of the decision tree itself. The decision tree in RM had more split nodes and leaf nodes than the one in R. Another difference between the two was the predictions. RM found the following predictions (in count): Setosa-6, Versicolor-4, and Virginica-9. While R found (in count): Setosa-5, Versicolor-4, and Virginica-10. We could say that there is not a major difference between these numbers, so either model still works. Lastly, back to the decision tree, the two models used different root nodes. RM used Petal\_width while R used Petal\_length. This could have led to the minor differences in the prediction results.