STA130: Week 10 R Demo

Palmer Penguins

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.4     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(palmerpenguins)
```

Goal: We want to try to predict the species of a penguin, based on the information we know about them

```
library(rpart)
library(partykit)
```

```
## Loading required package: grid
```

```
## Loading required package: libcoin
```

```
## Loading required package: mvtnorm
```

```
# First, we'll restrict attention to observations that don't have any missing values
summary(penguins) ## New function to give a quick overview of each of the variables in a tibble
```

```
##       species          island    bill_length_mm  bill_depth_mm
##  Adelie   :152   Biscoe   :168   Min.   :32.10   Min.   :13.10
##  Chinstrap: 68   Dream    :124   1st Qu.:39.23   1st Qu.:15.60
##  Gentoo   :124   Torgersen: 52   Median :44.45   Median :17.30
##                                  Mean   :43.92   Mean   :17.15
##                                  3rd Qu.:48.50   3rd Qu.:18.70
##                                  Max.   :59.60   Max.   :21.50
##                                  NA's   :2       NA's   :2
##  flipper_length_mm  body_mass_g       sex           year
##  Min.   :172.0     Min.   :2700   female:165   Min.   :2007
##  1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007
##  Median :197.0     Median :4050   NA's  : 11   Median :2008
##  Mean   :200.9     Mean   :4202                Mean   :2008
##  3rd Qu.:213.0     3rd Qu.:4750                3rd Qu.:2009
##  Max.   :231.0     Max.   :6300                Max.   :2009
##  NA's   :2         NA's   :2
```

```
penguins_clean <- penguins %>%
  filter(!is.na(bill_length_mm) & !is.na(bill_depth_mm) & !is.na(flipper_length_mm) & !is.na(body_mass_g
```

```r
summary(penguins_clean)
```

```
##       species          island    bill_length_mm  bill_depth_mm
##  Adelie   :151   Biscoe   :167   Min.   :32.10   Min.   :13.10
##  Chinstrap: 68   Dream    :124   1st Qu.:39.23   1st Qu.:15.60
##  Gentoo   :123   Torgersen: 51   Median :44.45   Median :17.30
##                                  Mean   :43.92   Mean   :17.15
##                                  3rd Qu.:48.50   3rd Qu.:18.70
##                                  Max.   :59.60   Max.   :21.50
##  flipper_length_mm  body_mass_g       sex           year
##  Min.   :172.0     Min.   :2700   female:165   Min.   :2007
##  1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007
##  Median :197.0     Median :4050   NA's  :  9   Median :2008
##  Mean   :200.9     Mean   :4202                Mean   :2008
##  3rd Qu.:213.0     3rd Qu.:4750                3rd Qu.:2009
##  Max.   :231.0     Max.   :6300                Max.   :2009
```

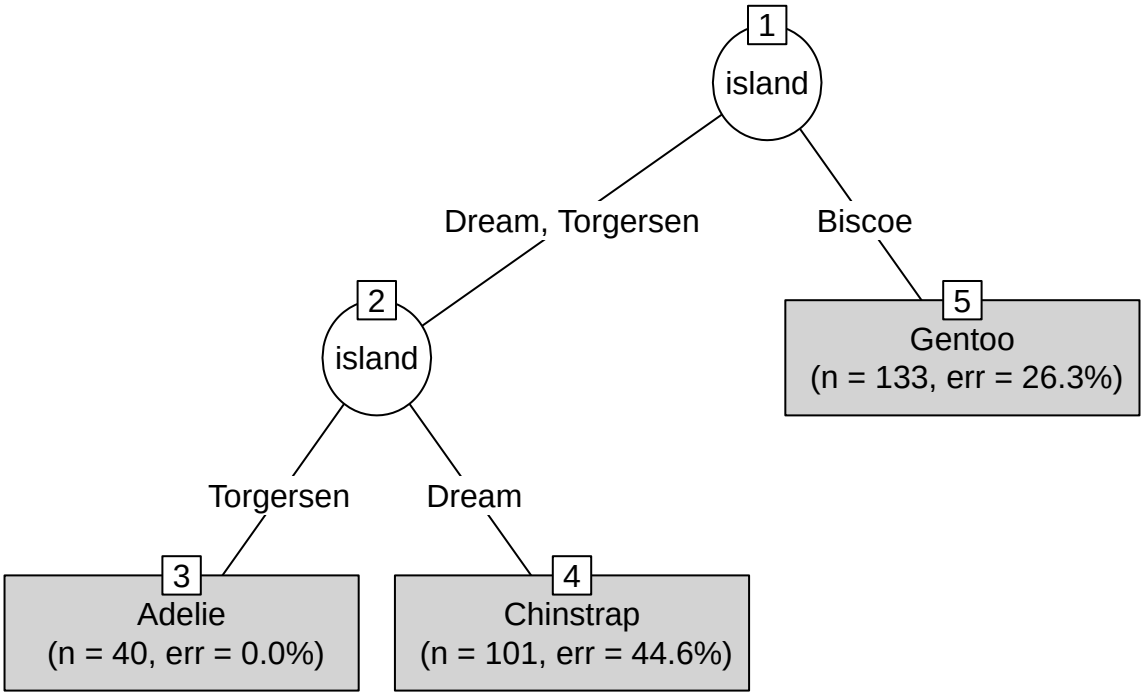
```r
# Now, we'll divide our data into training/testing datasets
# Set up
set.seed(17);
n <- nrow(penguins_clean)
training_indices <- sample(1:n, size=round(0.8*n))

penguins_clean <- penguins_clean %>% rowid_to_column() # adds a new ID column

# Create training and testing datasets
train <- penguins_clean %>% filter(rowid %in% training_indices)
test <- penguins_clean %>% filter(!rowid %in% training_indices)

# How many observations are there in each of the training and testing datasets?
nrow(train)
```

```
## [1] 274
```

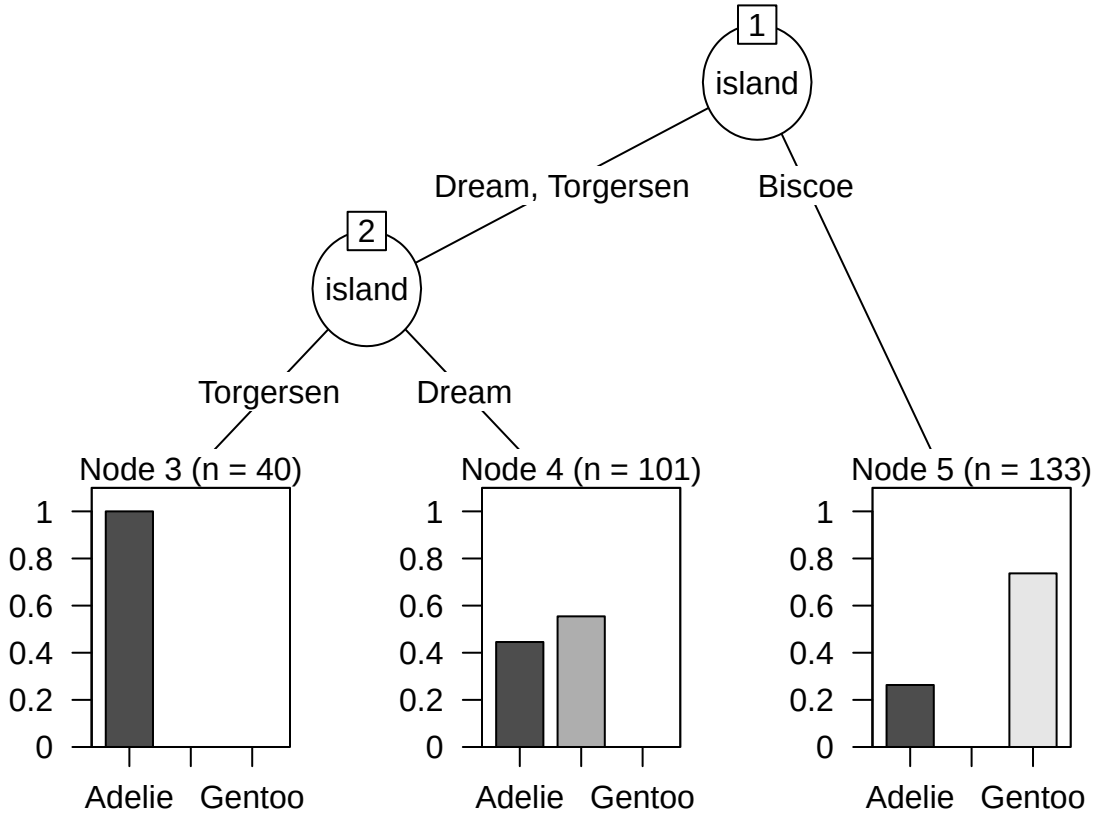
```r
nrow(test)
```

```
## [1] 68
```

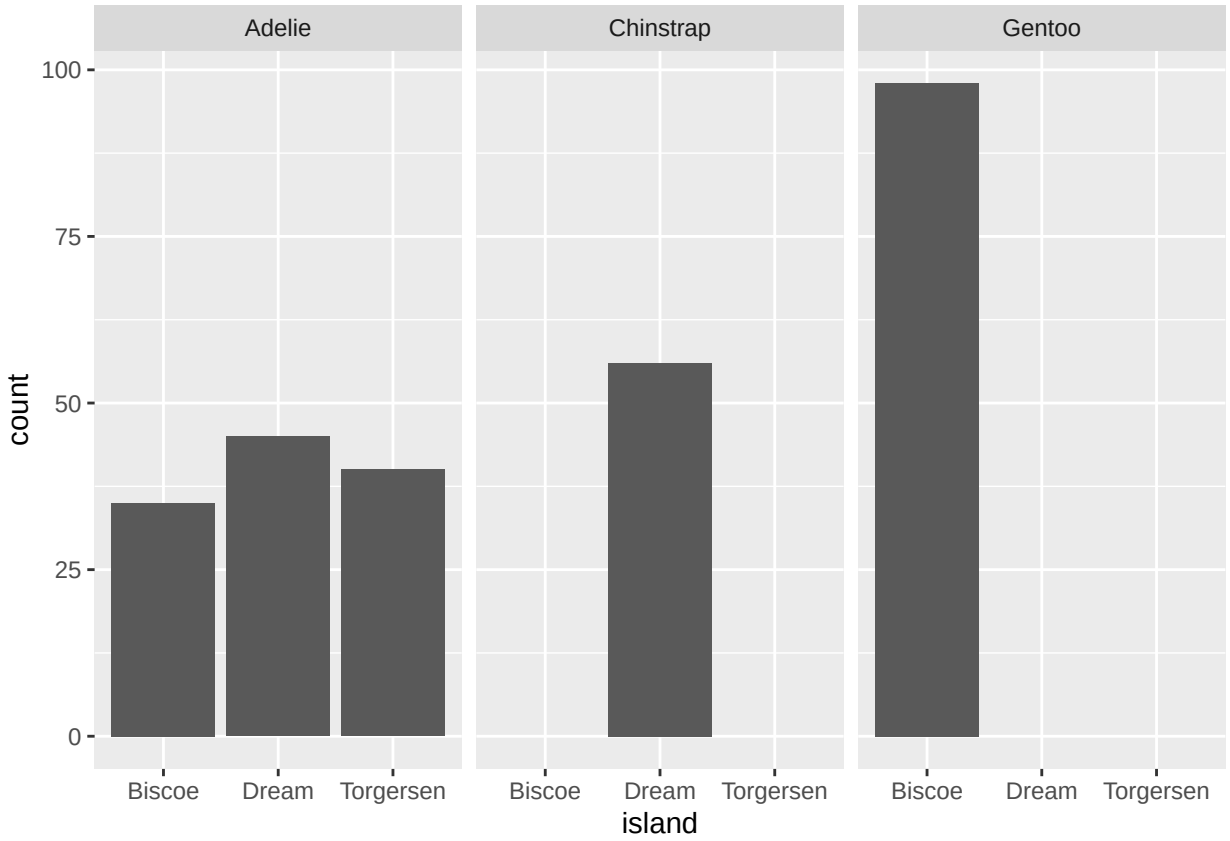
```r
# Let's build a tree using only geographic information to predict penguin species
tree1 <- rpart(species ~ island, data=train)
plot(as.party(tree1), type = "simple")
```



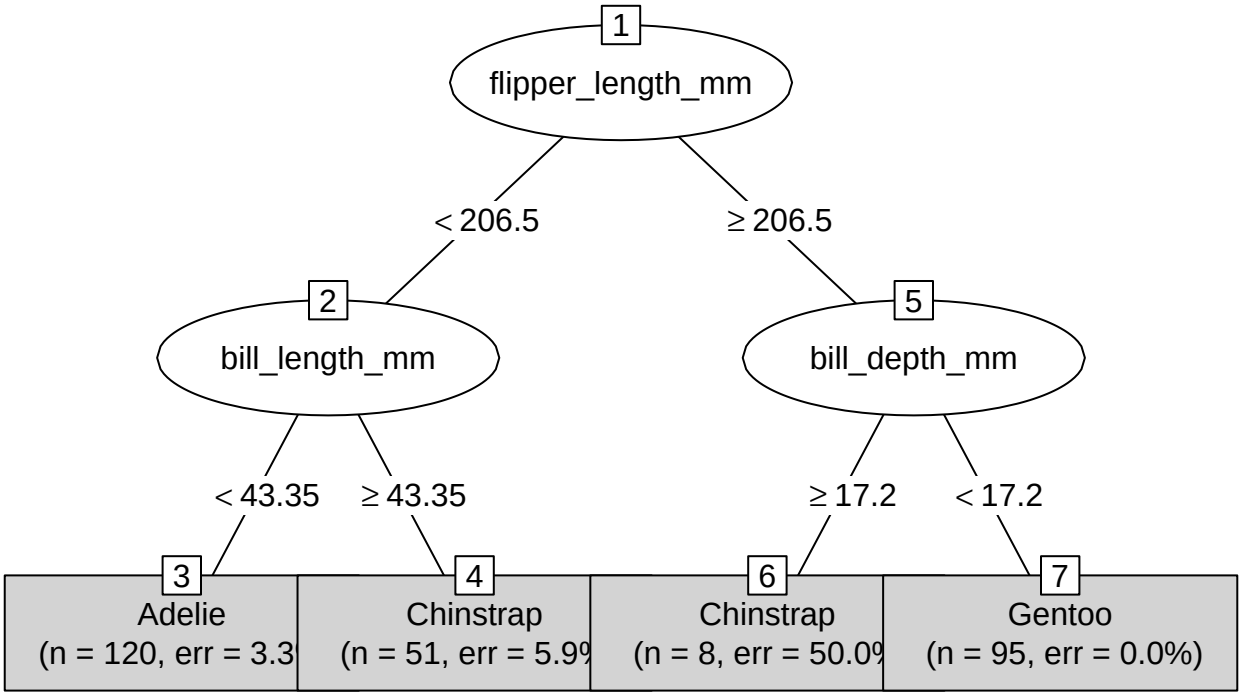

```
plot(as.party(tree1), type = "extended")
```



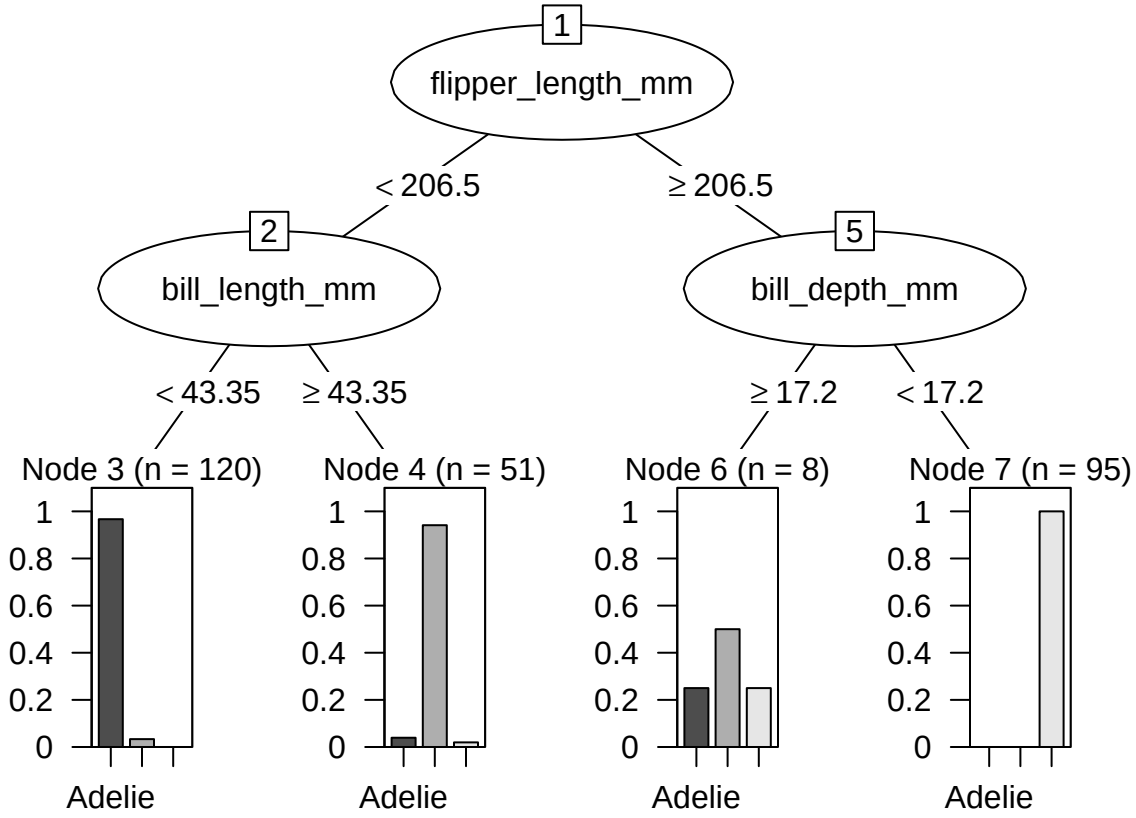

```
# What is the difference between type="simple" and type="extended" for visualizing a classification tre
# Both representing the same tree, just showing different info

# How can we visualize what is going on behind the scenes?
train %>% ggplot(aes(x = island)) +
  geom_bar() +
  facet_wrap(~species)
```



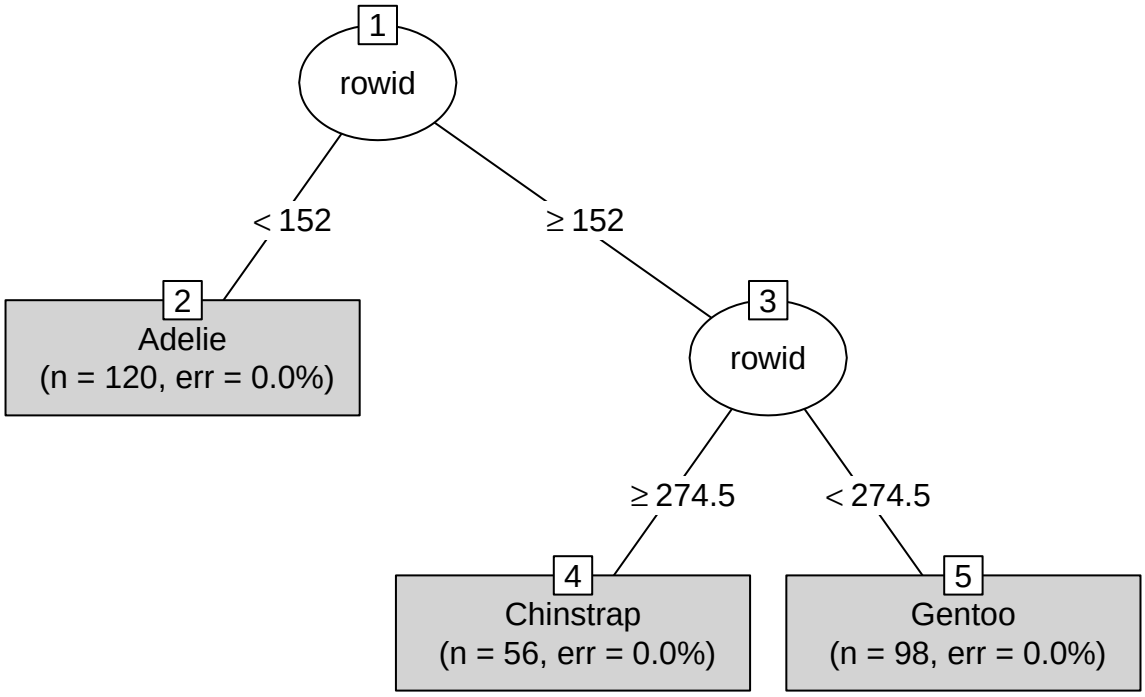

```
# Let's build a second tree using only physiological information to predict penguins species
tree2 <- rpart(species ~ bill_length_mm + bill_depth_mm + flipper_length_mm + body_mass_g, data = train
plot(as.party(tree2), type = "simple")
```



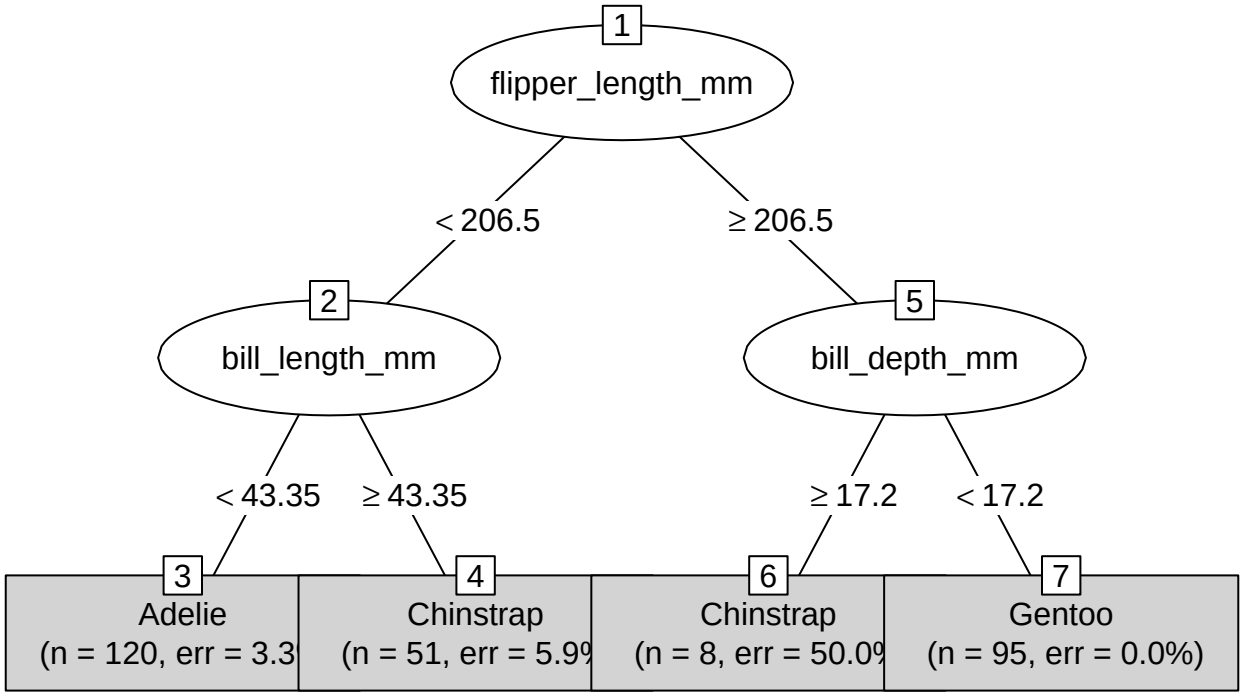

```
plot(as.party(tree2), type = "extended")
```




```
# Were all of the candidate predictors used to make splits in tree2?
# No! Body_mass_g is not used to make a split

# Now let's build a third tree which allows for all variables (apart from species) to be used to predic
tree3 <- rpart(species ~ ., data = train)
plot(as.party(tree3), type = "simple")
```




```r
# What's weird/wrong with the tree above?
# Rowid is an arbitrary label, which we shouldn't use to make predictions!

# Let's try that again
tree3 <- rpart(species ~ ., data = train %>% select(-rowid))
plot(as.party(tree3), type = "simple")
```



Now let's compare our three trees!

```
# Make predictions for test observations based on tree1
test_preds_1 <- predict(tree1, newdata=test, type="class")
head(test_preds_1)
```

```
##      1      2      3      4      5      6
## Adelie Adelie Adelie Adelie Adelie Gentoo
## Levels: Adelie Chinstrap Gentoo
```

```
m1.test <- table(test_preds_1, test$species)
m1.test
```

```
##
## test_preds_1 Adelie Chinstrap Gentoo
##    Adelie        11         0      0
##    Chinstrap     11        12      0
##    Gentoo         9         0     25
```

```
# What is the accuracy for tree1 based on testing data?
sum(diag(m1.test)) / sum(m1.test)
```

```
## [1] 0.7058824
```

```
# Can we calculate the sensitivity/specificity for this tree?
# No!
```

```r
# Which type of penguins are hardest to classify based on this tree?
# - Almost 2/3 of Adelie penguins in the testing data are misclassified
# - All of the Chinstrap and Gentoo penguins in the testing data are correctly classified!


# Make predictions for test observations based on tree2
test_preds_2 <- predict(tree2, newdata=test, type="class")
head(test_preds_2)
```

```
##      1      2      3      4      5      6
## Adelie Adelie Adelie Adelie Adelie Adelie
## Levels: Adelie Chinstrap Gentoo
```

```r
m2.test <- table(test_preds_2, test$species)
m2.test
```

```
##
## test_preds_2 Adelie Chinstrap Gentoo
##    Adelie        29         1      0
##    Chinstrap      2        11      0
##    Gentoo         0         0     25
```

```r
# What is the accuracy for tree1 based on testing data?
sum(diag(m2.test)) / sum(m2.test)
```

```
## [1] 0.9558824
```

```r
# Make predictions for test observations based on tree3
test_preds_3 <- predict(tree3, newdata=test, type="class")
head(test_preds_3)
```

```
##      1      2      3      4      5      6
## Adelie Adelie Adelie Adelie Adelie Adelie
## Levels: Adelie Chinstrap Gentoo
```

```r
m3.test <- table(test_preds_3, test$species)
m3.test
```

```
##
## test_preds_3 Adelie Chinstrap Gentoo
##    Adelie        29         1      0
##    Chinstrap      2        11      0
##    Gentoo         0         0     25
```

```r
# What is the accuracy for tree1 based on testing data?
sum(diag(m3.test)) / sum(m3.test)
```

```
## [1] 0.9558824
```

```r
# What do you notice about the confusion matrices for trees 2 and 3?
# They are the same!
# If we look at the trees more closely, we see that although one of the splits involves a different var

# Which tree would you prefer to use: tree1 or tree2/3?
# In this case, both trees have very similar complexity (similar number of splits/terminal nodes), but
```