Classification and Regression Trees

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Math 243: Stat Learning

November 12th, 2021

Outline

In today's class, we will...

- Discuss classification trees for classification problems.
- Build handmade classification tree models

Section 1

Classification Trees

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- The most natural choice is to use *Classification Error Rate E* (i.e. proportion of obs. in region not in most common class)

$$E = 1 - \max_k(p_{mk}) \quad \text{where } \hat{p}_{mk} = \text{prop. obs. in region m in class k}$$

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  - But because of the greedy algorithm used to split trees, E tends to overfit to noise in the training data

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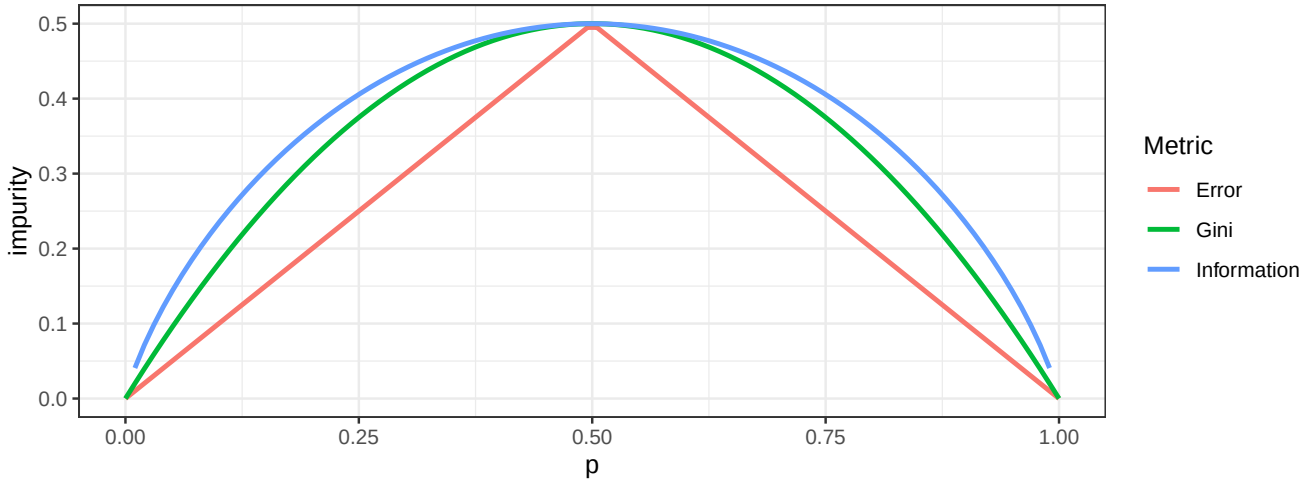
Metrics

- The following plot demonstrates sensitivity of metrics E, G, D to changes in class proportion p.



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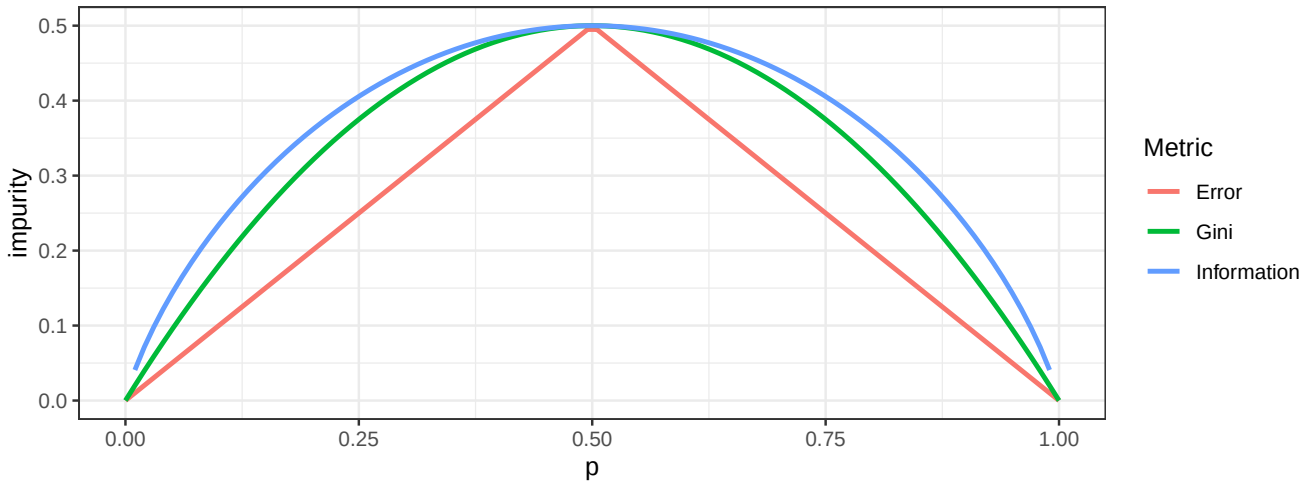

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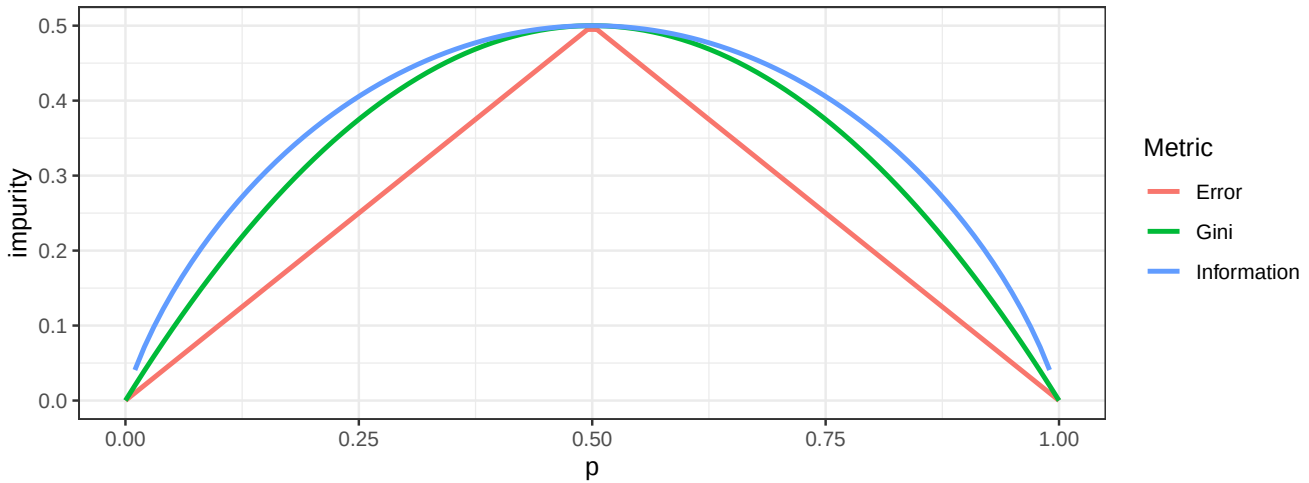

- The Gini Index and Information are both more sensitive to changes in node purity than Error (represented by convexity of curves)
  - Suppose we have an initial class balance of [300, 500] and make a single split into nodes [0,100] and [300,400]
  - The misclassification rate is constant, although node purity has increased

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- An alternative is to allow the model algorithm to lump together values as necessary at each node (order levels in increasing frequency, then make appropriate cut)
  - But this generally leads to less interpretable models

Section 2

Classification Trees in R

Mushroom Hunting

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Can I eat this?

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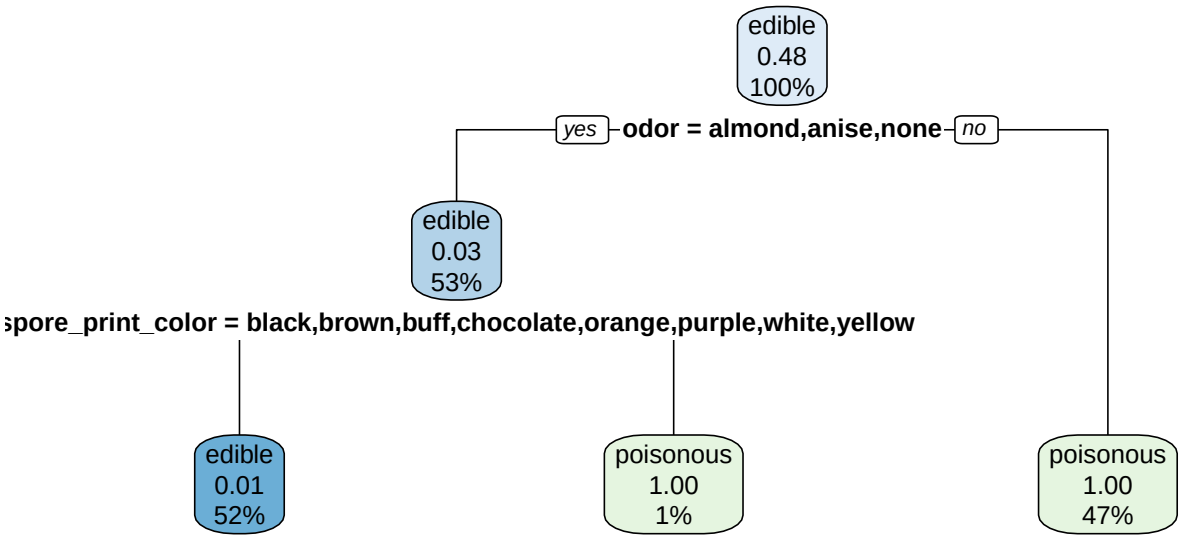
```
## Rows: 6,498
## Columns: 23
## $ edibility                <fct> edible, edible, edible, edible, edible, edibl~
## $ cap_shape                <fct> convex, bell, convex, convex, bell, bell, bel~
## $ cap_surface              <fct> scaly, scaly, scaly, smooth, scaly, smooth, s~
## $ cap_color                <fct> yellow, white, gray, yellow, white, white, ye~
## $ bruises                  <fct> yes, yes, no, yes, yes, yes, yes, yes, yes, y~
## $ odor                     <fct> almond, anise, none, almond, almond, anise, a~
## $ gill_attachement         <fct> free, free, free, free, free, free, free, fre~
## $ gill_spacing             <fct> close, close, crowded, close, close, close, c~
## $ gill_size                <fct> broad, broad, broad, broad, broad, broad, bro~
## $ gill_color               <fct> black, brown, black, brown, gray, brown, gray~
## $ stalk_shape              <fct> enlarging, enlarging, tapering, enlarging, en~
## $ stalk_root               <fct> club, club, equal, club, club, club, club, cl~
## $ stalk_surface_above_ring <fct> smooth, smooth, smooth, smooth, smooth, smoot~
## $ stalk_surface_below_ring <fct> smooth, smooth, smooth, smooth, smooth, smoot~
## $ stalk_color_above_ring   <fct> purple, purple, purple, purple, purple, purpl~
## $ stalk_color_below_ring   <fct> purple, purple, purple, purple, purple, purpl~
## $ veil_type                <fct> partial, partial, partial, partial, partial, ~
## $ veil_color               <fct> white, white, white, white, white, white, whi~
## $ ring_number              <fct> one, one, one, one, one, one, one, one, one, ~
## $ ring_type                <fct> pendant, pendant, evanescent, pendant, pendan~
## $ spore_print_color        <fct> brown, brown, brown, black, black, brown, bla~
## $ population               <fct> numerous, numerous, abundant, numerous, numer~
## $ habitat                  <fct> grasses, meadows, grasses, grasses, meadows, ~
```

Implementing classfication trees in R

As with regression trees, we use the ‘rpart“ package.

```
library(rpart)
library(rpart.plot)
mushroom_tree<-rpart(edibility ~ ., data = mushrooms_train)
rpart.plot(mushroom_tree)
```



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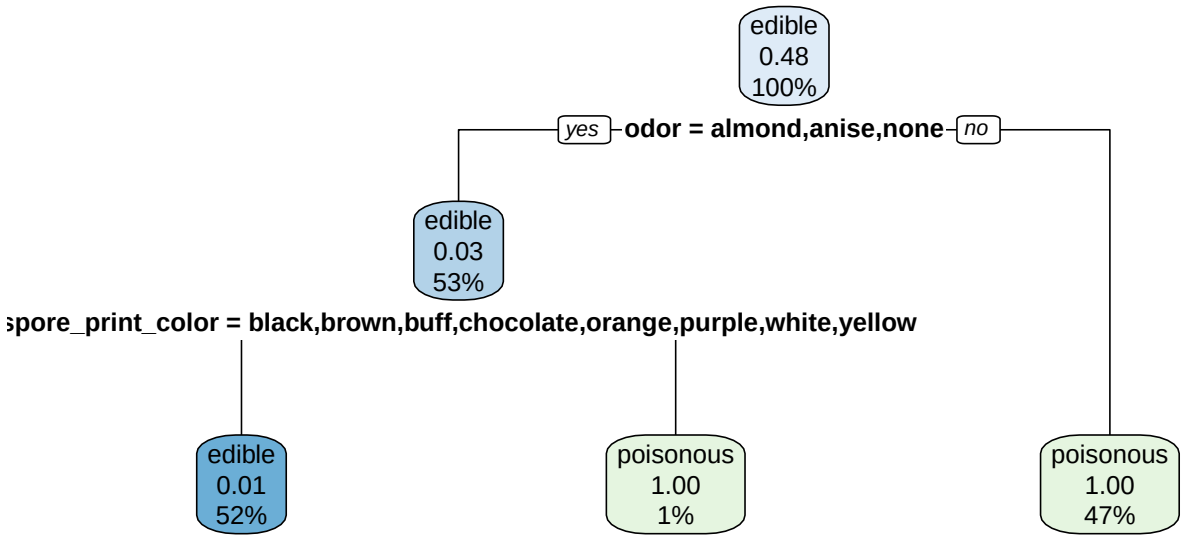

- The default parameters created data with relatively few terminal nodes.
  - And it seems like we obtained good class purity!

Model Accuracy

- How well did we do on test data?

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```
library(yardstick)
mushroom_preds <- predict(mushroom_tree, mushrooms_test, type = "class")
mushroom_probs <- predict(mushroom_tree, mushrooms_test, type = "prob")[,"edible"]

results <- data.frame(obs = mushrooms_test$edibility,preds = mushroom_preds,
                      probs = mushroom_probs)

accuracy(results, truth = obs, estimate = preds)
```

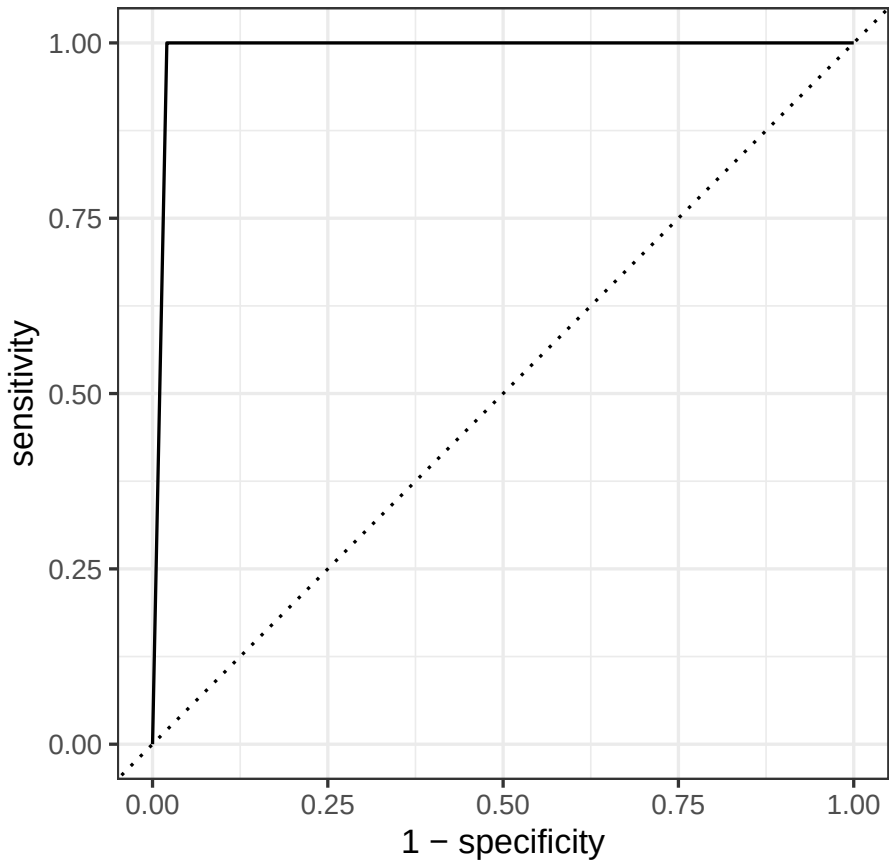
```
## # A tibble: 1 x 3
##   .metric  .estimator .estimate
##   <chr>    <chr>          <dbl>
## 1 accuracy binary         0.990
```

- Looks like we have fantastic accuracy!

ROC Curve

Look at that ROC curve!

```
roc_curve(results, truth = obs, probs) %>%
autoplot()
```



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- Here, $L(i,j)$ is the loss occurred when predicting level j when the truth is level i.

Additional Parameters

- To incorporate loss, create a penalty matrix and add to the `parms` argument in `rpart`:

```
penalty_matrix <- matrix(c(0,1,20,0), byrow = T, nrow = 2)
penalty_matrix
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##      [,1] [,2]
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```
mushroom_no_poison <- rpart(edibility ~., data = mushrooms_train,
                            parms = list(loss = penalty_matrix))
rpart.plot(mushroom_no_poison)
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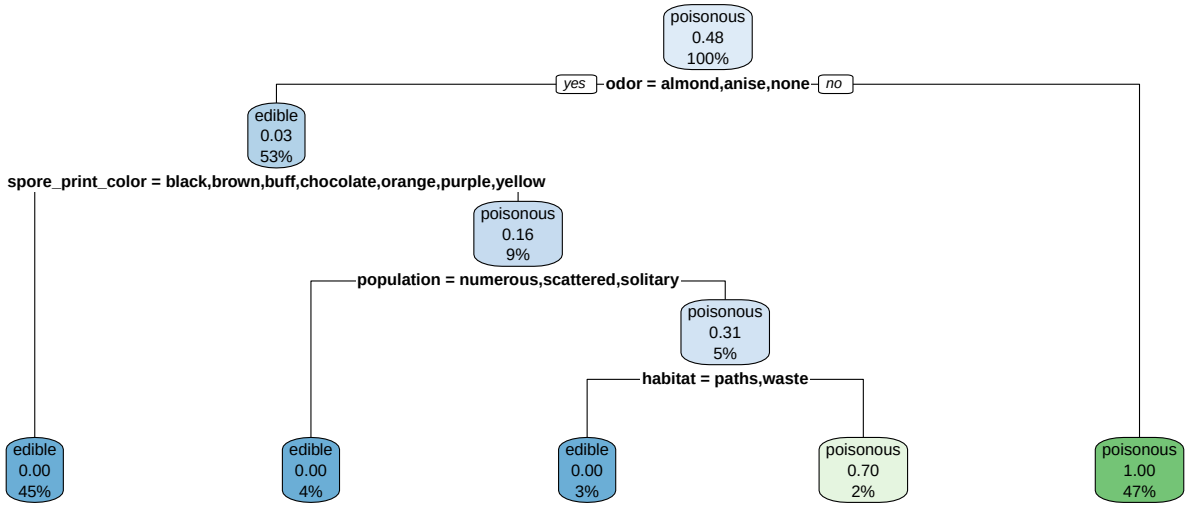

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results %>% group_by(model) %>% accuracy( truth = obs, estimate = preds)
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## # A tibble: 2 x 4
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```
results %>% filter(model == "with loss") %>% conf_mat(truth = obs, estimate = preds)
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##   edible       833         0
##   poisonous      9       784
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- But can we now improve that Type I error?
  - To reclaim some of those "poisonous" mushrooms, we'll need to build a deeper tree.

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  - Setting low values of cp lead to deeper trees

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mushroom_deep <- rpart(edibility ~., data = mushrooms_train,
                       parms = list(loss = penalty_matrix),
                       control = rpart.control(cp = .00001))
rpart.plot(mushroom_deep)
```

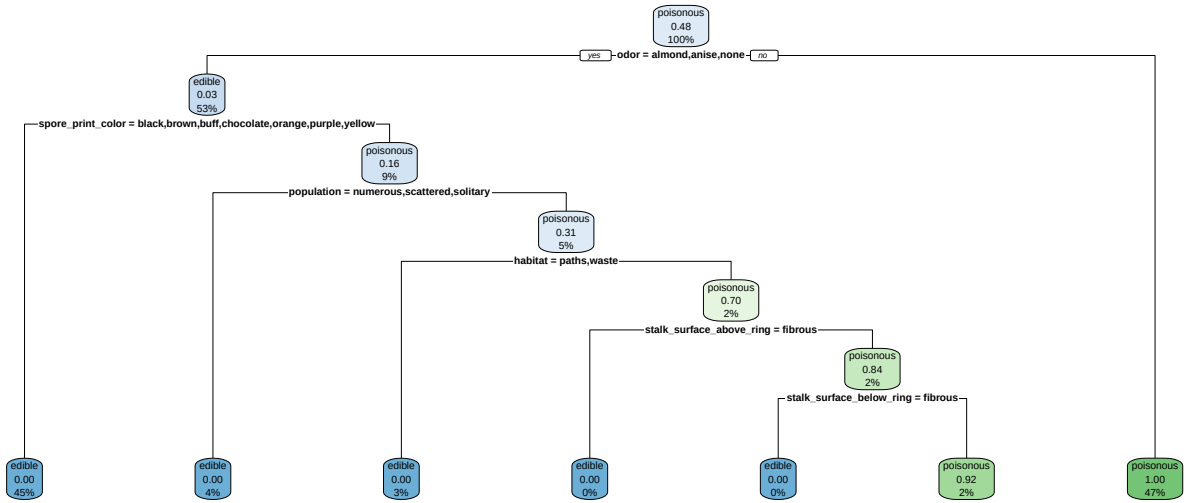

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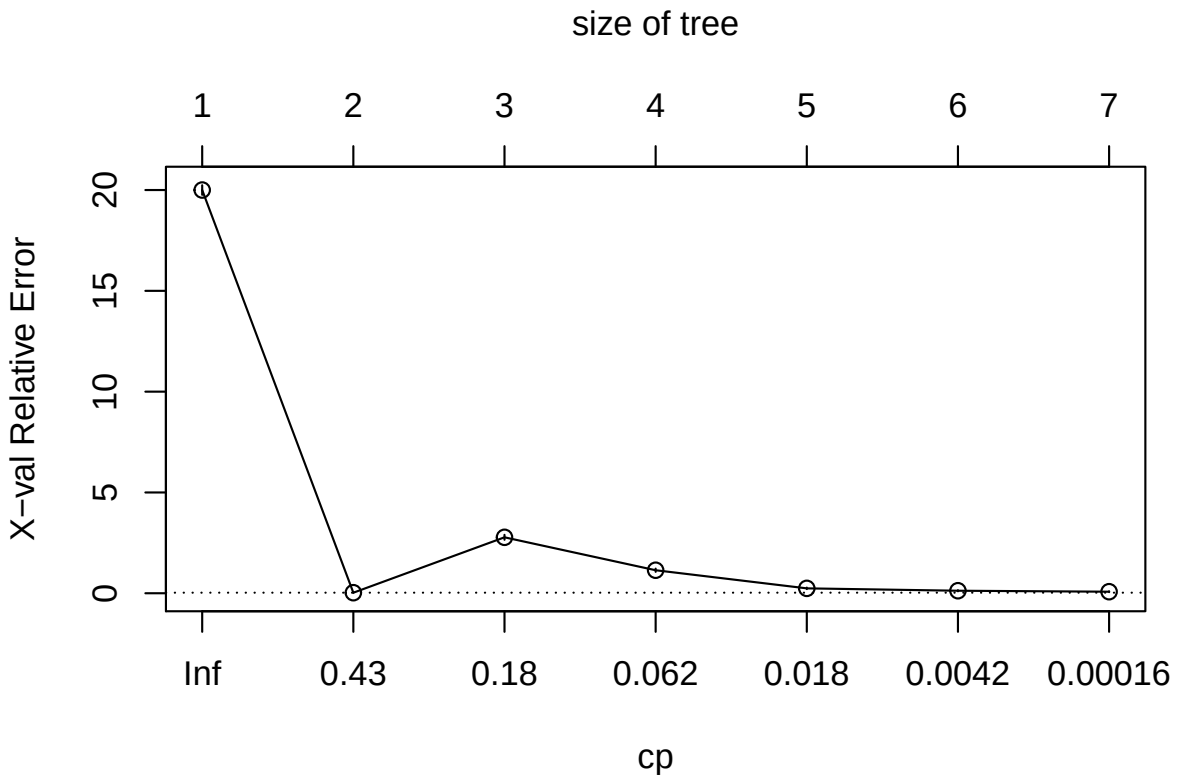

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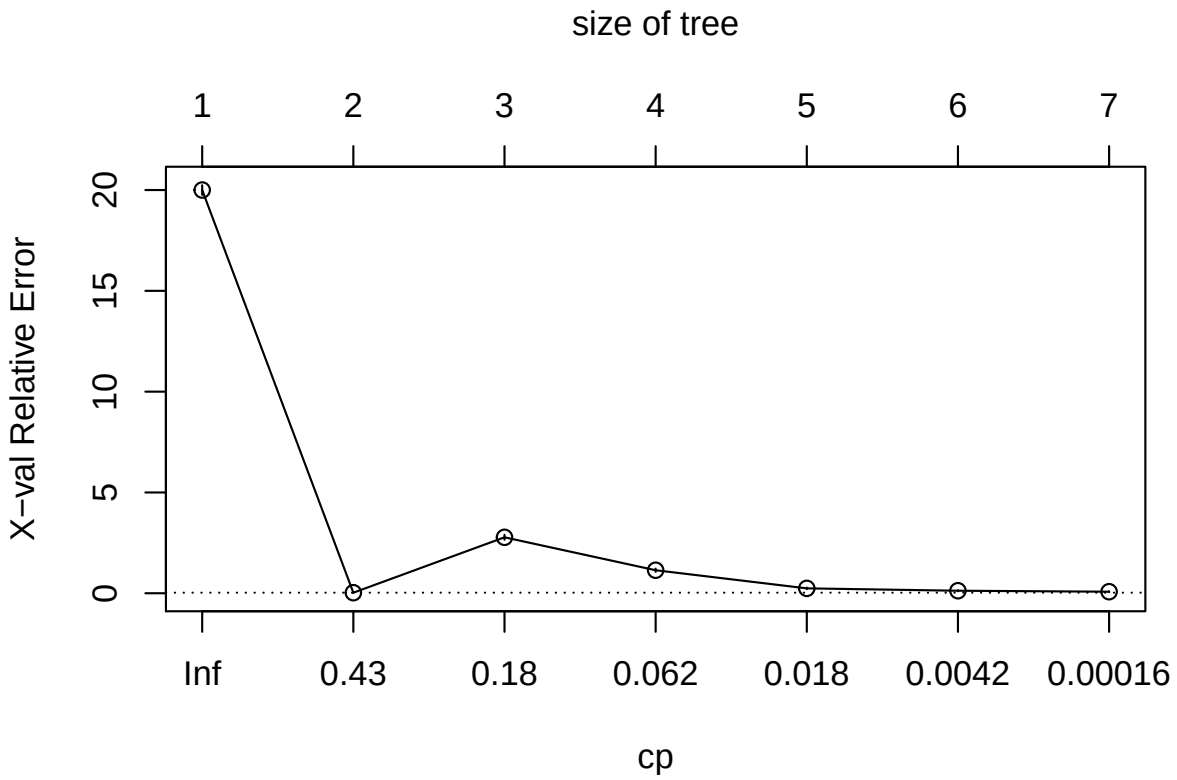

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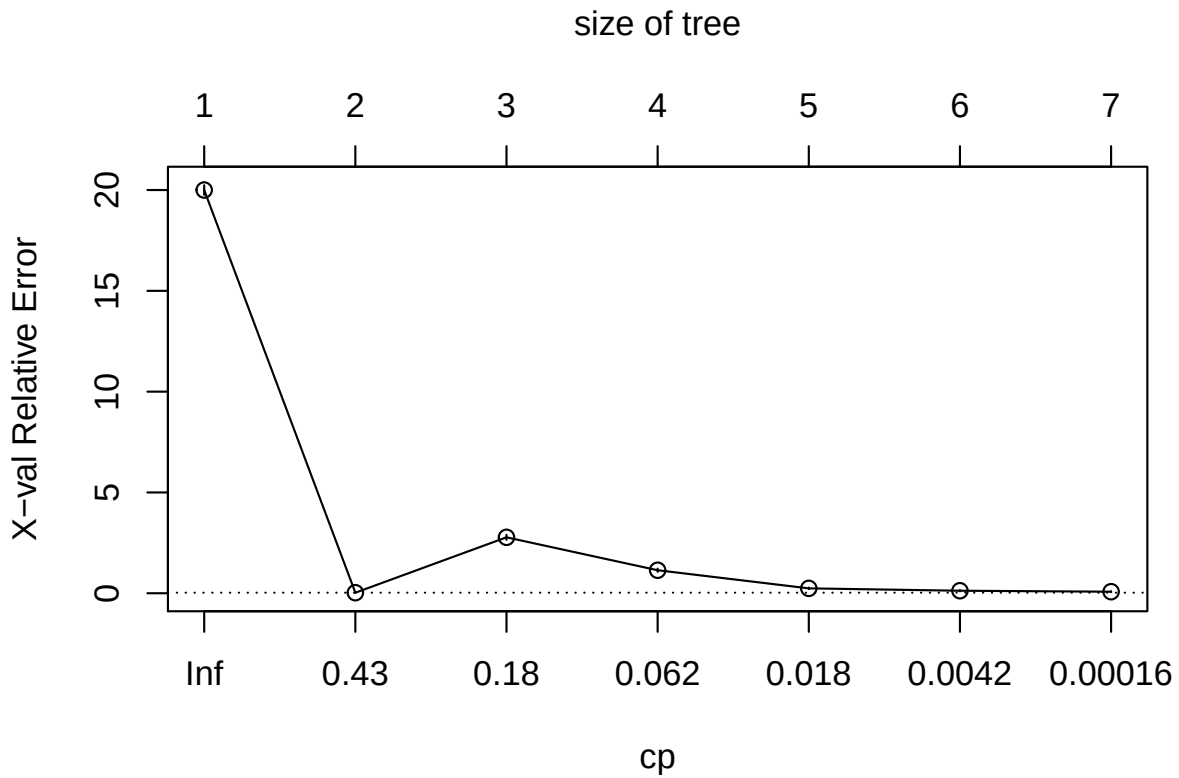

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```
mushroom_prune <- prune(mushroom_deep, cp = 0.0042)
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```

```
## # A tibble: 4 x 4
##   model        .metric  .estimator .estimate
##   <chr>        <chr>    <chr>          <dbl>
## 1 deep         accuracy binary         0.998
## 2 pruned       accuracy binary         0.996
## 3 with loss    accuracy binary         0.994
## 4 without loss accuracy binary         0.990
```

```
results %>% filter(model == "deep") %>% conf_mat(truth = obs, estimate = preds)
```

```
##            Truth
## Prediction  edible poisonous
##   edible       838         0
##   poisonous      4       784
```

```
results %>% filter(model == "pruned") %>% conf_mat(truth = obs, estimate = preds)
```

```
##            Truth
## Prediction  edible poisonous
##   edible       835         0
##   poisonous      7       784
```