Mushrooms

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Introduction

The primary goal of this project is to best predict whether or not a mushroom is poisonous depending on various physical characteristics, rarity, and habitat of the fungus. The data set consists of 8124 hypothetical samples, constructed from the Audobon Society Field Guide. The samples correspond to 23 species of mushrooms from the Agaricus and Lepiota Families. Each mushroom is categorized as either poisonous or edible, with mushrooms 'not reccomended for eating' or of unknown edibility counted as poisonous. Though the observations are hypothetical mushrooms, analyzing them can still provide beneficial results that can be applied to help identify the edibility of the near 14,000 existing species of mushrooms.

Some light data cleaning was done, including just changing the "poisonous" variable from p/e to 1/0 for ease of fitting with models like logistic regression models. The veil-type variable was removed because all mushrooms in the data set had the same characteristic for this attribute.

```
 1. cap-shape:                bell=b,conical=c,convex=x,flat=f, knobbed=k,sunken=s
 2. cap-surface:              fibrous=f,grooves=g,scaly=y,smooth=s
 3. cap-color:                brown=n,buff=b,cinnamon=c,gray=g,green=r,
                              pink=p,purple=u,red=e,white=w,yellow=y

 4. bruises?:                 bruises=t,no=f
 5. odor:                     almond=a,anise=l,creosote=c,fishy=y,foul=f,
                              musty=m,none=n,pungent=p,spicy=s

 6. gill-attachment:          attached=a,descending=d,free=f,notched=n
 7. gill-spacing:             close=c,crowded=w,distant=d
 8. gill-size:                broad=b,narrow=n
 9. gill-color:               black=k,brown=n,buff=b,chocolate=h,gray=g,
                              green=r,orange=o,pink=p,purple=u,red=e, white=w,yellow=y

10. stalk-shape:              enlarging=e,tapering=t
```

```
11. stalk-root:               bulbous=b,club=c,cup=u,equal=e, rhizomorphs=z,rooted=r,missing=
12. stalk-surface-above-ring: fibrous=f,scaly=y,silky=k,smooth=s
13. stalk-surface-below-ring: fibrous=f,scaly=y,silky=k,smooth=s
14. stalk-color-above-ring:   brown=n,buff=b,cinnamon=c,gray=g,orange=o,
                              pink=p,red=e,white=w,yellow=y
15. stalk-color-below-ring:   brown=n,buff=b,cinnamon=c,gray=g,orange=o,
                              pink=p,red=e,white=w,yellow=y
16. veil-type:                partial=p,universal=u
17. veil-color:               brown=n,orange=o,white=w,yellow=y
18. ring-number:              none=n,one=o,two=t
19. ring-type:                cobwebby=c,evanescent=e,flaring=f,large=l,
                              none=n,pendant=p,sheathing=s,zone=z
20. spore-print-color:        black=k,brown=n,buff=b,chocolate=h,green=r,
                              orange=o,purple=u,white=w,yellow=y
21. population:               abundant=a,clustered=c,numerous=n, scattered=s,several=v,solita
22. habitat:                  grasses=g,leaves=l,meadows=m,paths=p, urban=u,waste=w,woods=d
```

Citations Mushroom. (1987). UCI Machine Learning Repository. https://doi.org/10.24432/C5959T.

Certain variables appear to be much more indicative of mushroom edibility than others.

```
library(ggplot2)
mushrooms <- read.csv("Mushrooms - Sheet1.csv")
mushrooms$poisonous[mushrooms$poisonous == 'p'] <- 'Poisonous'
mushrooms$poisonous[mushrooms$poisonous == 'e'] <- 'Edible'

no_veil <- subset(mushrooms, select = -c(veil))
no_veil$poisonous[no_veil$poisonous == 'Poisonous'] <- 1
no_veil$poisonous[no_veil$poisonous == 'Edible'] <- 0
no_veil$poisonous <- as.numeric((no_veil$poisonous))
```

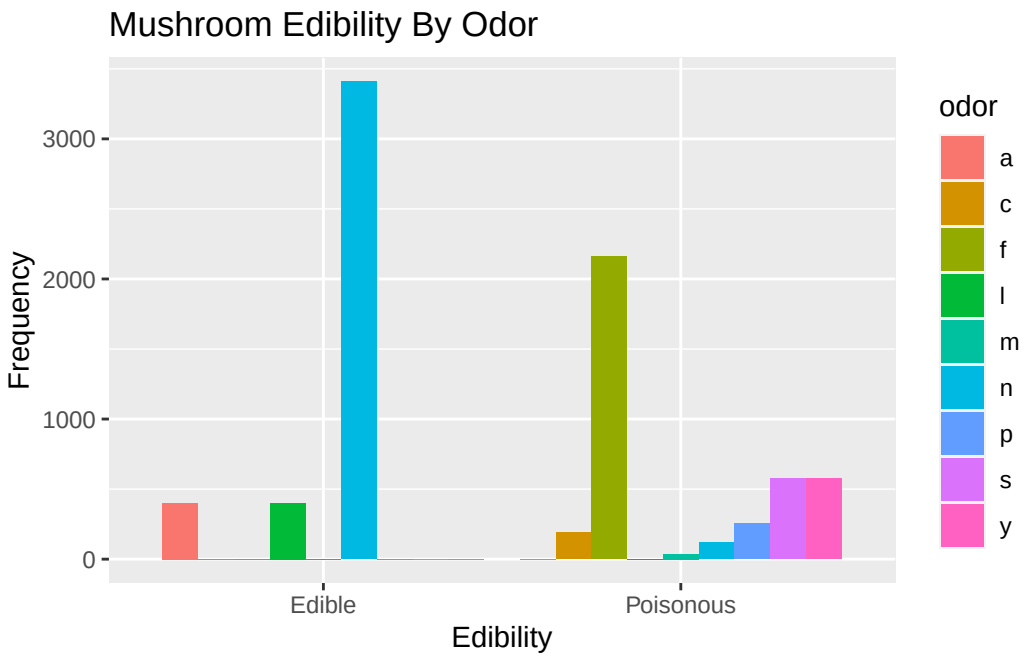
```
table(no_veil$poisonous)
```

```
   0    1
4208 3916
```

Roughly half (48.2%) of the mushrooms in the data set are poisonous, providing motivation for our model as otherwise the chances of predicting correctly would be roughly a 50/50 draw.

Certain variables are much more indicative of mushroom edibility than others.

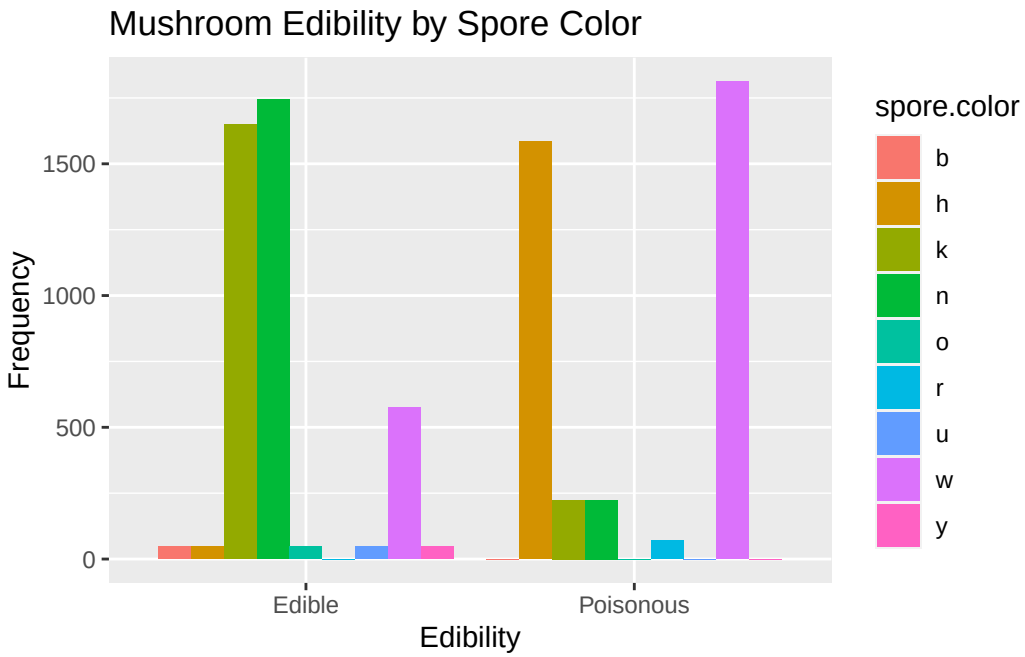
```
odor <- with(mushrooms, table(odor, poisonous))
ggplot(as.data.frame(odor), aes(factor(poisonous), Freq, fill = odor)) +
  geom_col(position = 'dodge') +
  labs(title = "Mushroom Edibility By Odor", x="Edibility",y="Frequency")
```



almond=a creosote=c foul=f anise=l musty=m none=n pungent=p spicy=s fishy=y

Mushrooms with an almond, anise and no odor are nearly all edible, while mushrooms smelling of creosote, foul, pungent, spicy, or fishy are nearly all poisonous, making odor a pretty good solo predictor of edibility.

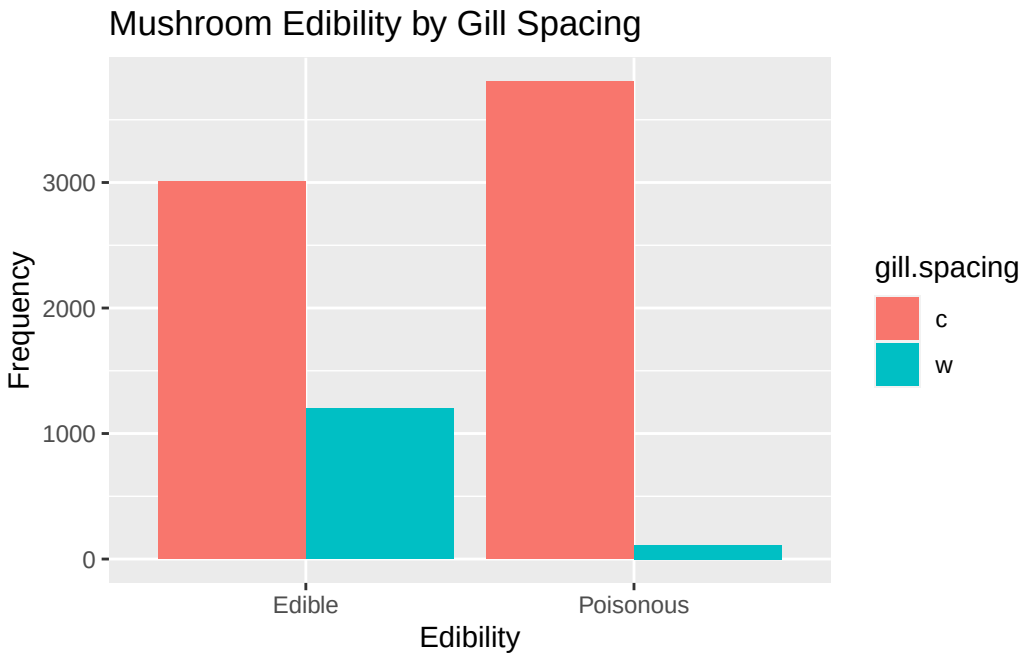
```
spore <- with(mushrooms, table(spore.color, poisonous))

ggplot(as.data.frame(spore), aes(factor(poisonous), Freq, fill = spore.color)) +
  geom_col(position = 'dodge') +
  labs(title="Mushroom Edibility by Spore Color", x="Edibility",y="Frequency")
```



buff=b chocolate=h black=k brown=n orange=o green=r purple=u white=w yellow=y

Similarly spore color is also a decent solo predictor of edibility. Mushrooms with buff, black, brown, orange, purple, and yellow spores are mostly edible while mushrooms with chocolate, green,and white spores are mostly poisonous.

```
tbl3 <- with(mushrooms, table(gill.spacing, poisonous))
ggplot(as.data.frame(tbl3), aes(factor(poisonous), Freq, fill = gill.spacing)) +
  geom_col(position = 'dodge') +
  labs(title="Mushroom Edibility by Gill Spacing", x = "Edibility", y="Frequency")
```



close=c crowded=w

While odor and spore color are both pretty good predictors of edibility all around, other variables like gill spacing were only edibility indicators for one of the levels. That is, mushrooms with wide gill spacing are a good indicator that a mushroom is edible, but knowing that a mushroom has close gill spacing is not really indicitive of the mushroom's edibility.

tbl <- with(mushrooms, table(bruises, poisonous)) ggplot(as.data.frame(tbl), aes(factor(poisonous), Freq, fill = bruises)) +
geom_col(position = 'dodge')

tbl4 <- with(no_veil, table(gill.size, poisonous))

ggplot(as.data.frame(tbl4), aes(factor(poisonous), Freq, fill = gill.size)) +
geom_col(position = 'dodge')

tbl5 <- with(no_veil, table(gill.color, poisonous))

ggplot(as.data.frame(tbl5), aes(factor(poisonous), Freq, fill = gill.color)) +
geom_col(position = 'dodge')

tbl6 <- with(no_veil, table(ss.above, poisonous))

ggplot(as.data.frame(tbl6), aes(factor(poisonous), Freq, fill = ss.above)) +
geom_col(position = 'dodge')

Methodology

Because this data set only contains categorical variables and no one attribute appeared immediately more important in categorizing a mushroom as poisonous or not, we were interested in including all the variables as predictors in our model. After some experimentation with LASSO and all subset variable selection models, there turned out to be so many variables and categories within each variable that it seemed better to just keep all variables in. Some light data cleaning was done, mainly removing the veil-type variable because all mushrooms in the set had the same veil-type ('partial').

The primary outcome of interest is whether or not a mushroom is poisonous or edible. Since this is a binary outcome (ambiguous or unknown edibilities were deemed poisonous in this data set) using either a logistical regression model or classification tree seemed the most fitting.

For creating and testing the classification tree, the original data set was split into two halves (one for training, and one for testing). With the training data set, multiple complexity parameter (cp) levels ranging from 0.01 to 0.0001 were tested. The cp level determines how "pruned" the classification tree is, where smaller cp levels render larger trees. cp levels between 0.04-0.07 seemed to render the most accurate classification trees, sensitivity of 0.48, specificity of 0.55, positive predictive value of 0.5, and negative predictive value of 0.53. Seeing as there are only two possible classifications, however, the outcomes of our classification tree are not all that better than just randomly categorizing a mushroom as poisonous or edible.

On the other hand, the log-odds model was able to predict mushroom edibility with 100% accuracy, and was the final model chosen. In terms of meeting assumptions, the notion of linearity does not really apply as all of our predictors are categorical. The independence assumption is also not necessarily met. While the exact process of which the hypothetical mushroom samples in the data set were created is unclear, we do know that the mushrooms were designed after 23 existing mushrooms. Based on this information, it is likely that mushrooms designed off of the same real mushroom likely have some similar attributes. Thus, there is reason to believe that the independence assumption is not met for the log-odds model. However, this violation of independence is not neccesarily a bad thing——the whole point of the model (to predict edibility) is based on the fact that similar mushrooms may have similar poisonous status', and it is likely that mushrooms based off the same mushroom will have the same poisonous/edible characteristic. No variable interactions or transformations were made in the final model.

Results

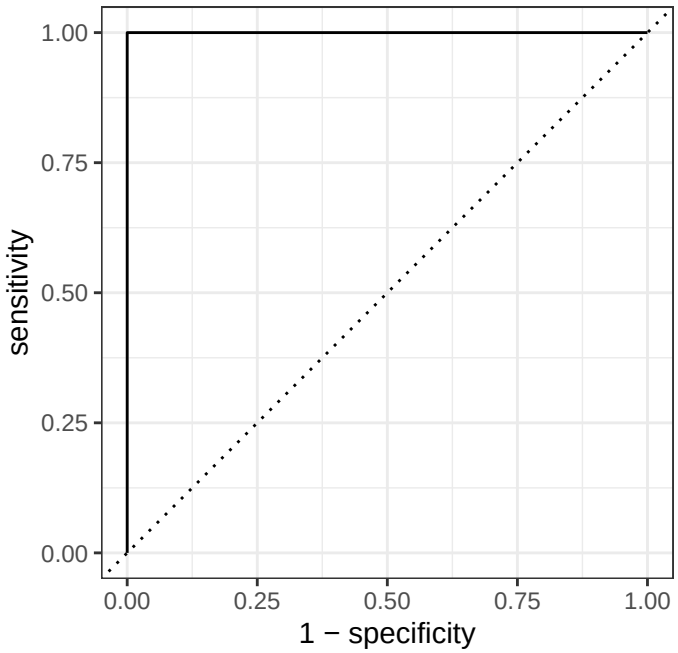
The following is our final logistical regression model that uses all variables in the data set as predictors (besides the veil-type variable, which as mentioned all mushrooms had the same characteristic for).

```r
library(tidymodels)
library(tidyverse)
library(leaps)
library(glmnet)
```

```r
m2 <- glm(poisonous ~ .,
          data = no_veil,
          family = "binomial")
m2_aug <- augment(m2)

m2_aug <- m2_aug %>%
  mutate(prob = exp(.fitted)/(1 + exp(.fitted)),
         pred_pois = ifelse(prob > 0.5, "Poisonous", "Edible")) %>%
  select(.fitted, prob, pred_pois, poisonous)

table(m2_aug$pred_pois, m2_aug$poisonous)
```

```
            0    1
Edible    4208    0
Poisonous    0 3916
```

```r
m2_aug %>%
  roc_curve(
    truth = as.factor(poisonous),
    prob,
    event_level = "second"
  ) %>%
  autoplot()
```




```
m2_aug %>%
  roc_auc(
    truth = as.factor(poisonous),
    prob,
    event_level = "second"
  )
```

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

Evident by both the table and ROC curve, our model can perfectly predict a mushroom's edibility. Consequently, the model's sensitivity, specificity, positive predictive value, and negative predictive value are all 1.

Discussion

It is likely that our model has 'perfect' predicting power due to the sheer number of predictors and characteristics where each mushroom essentially is unique. Given this, there is reason to

believe that by knowing a mushroom's physical characteristics, you can determine whether or not the mushrooms is poisonous or edible. There are, however, limitations to the conclusiosn that our model can make. For one, as discussed earlier the independence assumption for our data set is likely violated due to the fact that the mushrooms are all generated based on 23 species of real mushrooms. Given this, if mushrooms based off the same species have similar characterstic and have the same edibility, then this makes it extremely easy to predict the edibility of mushrooms in our dataset, and our model is more using the species of mushroom as a predictor as opposed to its specific physical characteristics. The fact that the data set only represents 23 species of mushrooms when there are believed to be over 27,000 species in total also makes our model not generalization to predict the edibility of all mushrooms.

Ideas for future work include further using a larger data set that either includes real mushrooms (as opposed to hypothetical ones) and more importantly a much wider range of mushroom species. If someone were truly wanting to reliably predict mushroom edibility with a model, they'd probably want a well-trained one. Using training and testing subsets would also be a way to test future models, to more accurately test the model with data that it does not have direct information on from the model creation process.