Data Science: Capstone CYO Project - Mushroom

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Introduction

In this report, our goal is to predict the edibility (class: edible / poisonous) of mushroom basing on attribution information. Data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). The reason of selecting this dataset is that this problem is related to classification which is a large part of application in data science. And, it is also a complement to project – MovieLens that we can cover each part of what we have learnt from the course.

The mushroom dataset has already been well formatted. Process of data cleaning is only removing 2 attributes prior to splitting the data to training set and test set. 10 algorithms are applied and an ensemble model combining the prior 10 different algorithms to see if it can provide improvement to our predictions.

1. Data Cleaning

Mushroom data set contains 23 columns of 1 class and 22 attributes related to cap, bruises, odor, gill, stalk, veil, ring, spore color, population and habitat of 8,124 observations.

```
## 'data.frame':    8124 obs. of  23 variables:
##  $ class                    : Factor w/ 2 levels "e","p": 2 1 1 2 1 1 1 1 2 1 ...
##  $ cap_shape                : Factor w/ 6 levels "b","c","f","k",..: 6 6 1 6 6 6 1 1 6 1 ...
##  $ cap_surface              : Factor w/ 4 levels "f","g","s","y": 3 3 3 4 3 4 3 4 4 3 ...
##  $ cap_color                : Factor w/ 10 levels "b","c","e","g",..: 5 10 9 9 4 10 9 9 9 10 ...
##  $ bruises                  : Factor w/ 2 levels "f","t": 2 2 2 2 1 2 2 2 2 2 ...
##  $ odor                     : Factor w/ 9 levels "a","c","f","l",..: 7 1 4 7 6 1 1 4 7 1 ...
##  $ gill_attachment          : Factor w/ 2 levels "a","f": 2 2 2 2 2 2 2 2 2 2 ...
##  $ gill_spacing             : Factor w/ 2 levels "c","w": 1 1 1 1 2 1 1 1 1 1 ...
##  $ gill_size                : Factor w/ 2 levels "b","n": 2 1 1 2 1 1 1 1 2 1 ...
##  $ gill_color               : Factor w/ 12 levels "b","e","g","h",..: 5 5 6 6 5 6 3 6 8 3 ...
##  $ stalk_shape              : Factor w/ 2 levels "e","t": 1 1 1 1 2 1 1 1 1 1 ...
##  $ stalk_root               : Factor w/ 5 levels "?","b","c","e",..: 4 3 3 4 4 3 3 3 4 3 ...
##  $ stalk_surface_above_ring: Factor w/ 4 levels "f","k","s","y": 3 3 3 3 3 3 3 3 3 3 ...
##  $ stalk_surface_below_ring: Factor w/ 4 levels "f","k","s","y": 3 3 3 3 3 3 3 3 3 3 ...
##  $ stalk_color_above_ring  : Factor w/ 9 levels "b","c","e","g",..: 8 8 8 8 8 8 8 8 8 8 ...
##  $ stalk_color_below_ring  : Factor w/ 9 levels "b","c","e","g",..: 8 8 8 8 8 8 8 8 8 8 ...
##  $ veil_type                : Factor w/ 1 level "p": 1 1 1 1 1 1 1 1 1 1 ...
##  $ veil_color               : Factor w/ 4 levels "n","o","w","y": 3 3 3 3 3 3 3 3 3 3 ...
##  $ ring_number              : Factor w/ 3 levels "n","o","t": 2 2 2 2 2 2 2 2 2 2 ...
##  $ ring_type                : Factor w/ 5 levels "e","f","l","n",..: 5 5 5 5 1 5 5 5 5 5 ...
##  $ spore_print_color        : Factor w/ 9 levels "b","h","k","n",..: 3 4 4 3 4 3 3 4 3 3 ...
##  $ population               : Factor w/ 6 levels "a","c","n","s",..: 4 3 3 4 1 3 3 4 5 4 ...
##  $ habitat                  : Factor w/ 7 levels "d","g","l","m",..: 6 2 4 6 2 2 4 4 2 4 ...
```

```
##  class    cap_shape cap_surface   cap_color    bruises       odor
##  e:4208   b: 452    f:2320      n      :2284   f:4748   n      :3528
##  p:3916   c:   4    g:   4      g      :1840   t:3376   f      :2160
##           f:3152    s:2556      e      :1500            s      : 576
##           k: 828    y:3244      y      :1072            y      : 576
##           s:  32                w      :1040            a      : 400
##           x:3656                b      : 168            l      : 400
##                                 (Other): 220            (Other): 484
##  gill_attachment gill_spacing gill_size   gill_color   stalk_shape stalk_root
##  a: 210          c:6812       b:5612    b      :1728   e:3516      ?:2480
##  f:7914          w:1312       n:2512    p      :1492   t:4608      b:3776
```

```
##                                     w      :1202              c: 556
##                                     n      :1048              e:1120
##                                     g      : 752              r: 192
##                                     h      : 732
##                                     (Other):1170
##  stalk_surface_above_ring stalk_surface_below_ring stalk_color_above_ring
##  f: 552                   f: 600                   w      :4464
##  k:2372                   k:2304                   p      :1872
##  s:5176                   s:4936                   g      : 576
##  y:  24                   y: 284                   n      : 448
##                                                    b      : 432
##                                                    o      : 192
##                                                    (Other): 140
##  stalk_color_below_ring veil_type veil_color ring_number ring_type
##  w      :4384           p:8124    n:  96     n:  36      e:2776
##  p      :1872                     o:  96     o:7488      f:  48
##  g      : 576                     w:7924     t: 600      l:1296
##  n      : 512                     y:   8                 n:  36
##  b      : 432                                            p:3968
##  o      : 192
##  (Other): 156
##  spore_print_color population habitat
##  w      :2388      a: 384     d:3148
##  n      :1968      c: 340     g:2148
##  k      :1872      n: 400     l: 832
##  h      :1632      s:1248     m: 292
##  r      :  72      v:4040     p:1144
##  b      :  48      y:1712     u: 368
##  (Other): 144                 w: 192
```

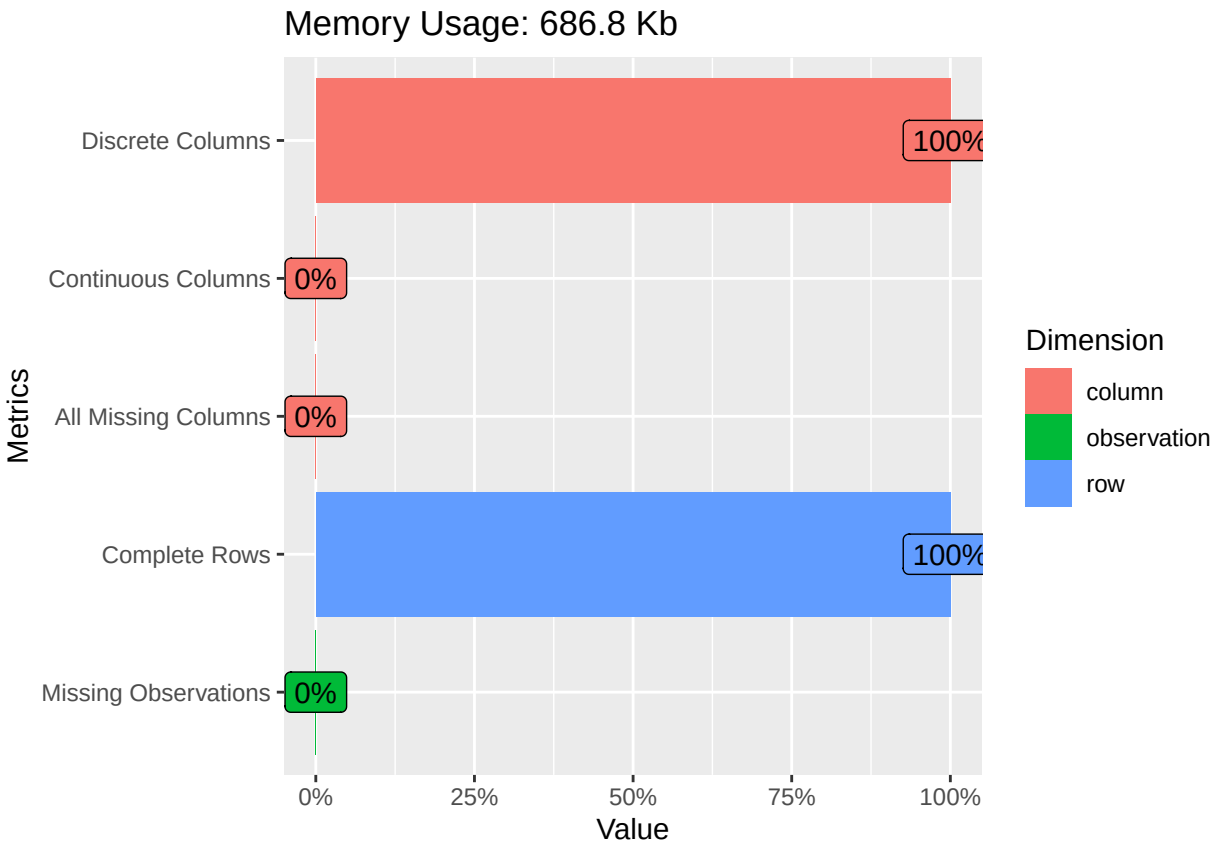
According to description from the source, there is data missing in the attribute of stalk_root. The missing data point is marked "?" from the source already. On the other hand, veil_type is a constant. Both stalk_root and veil_type are removed before we start data exploration & modeling.

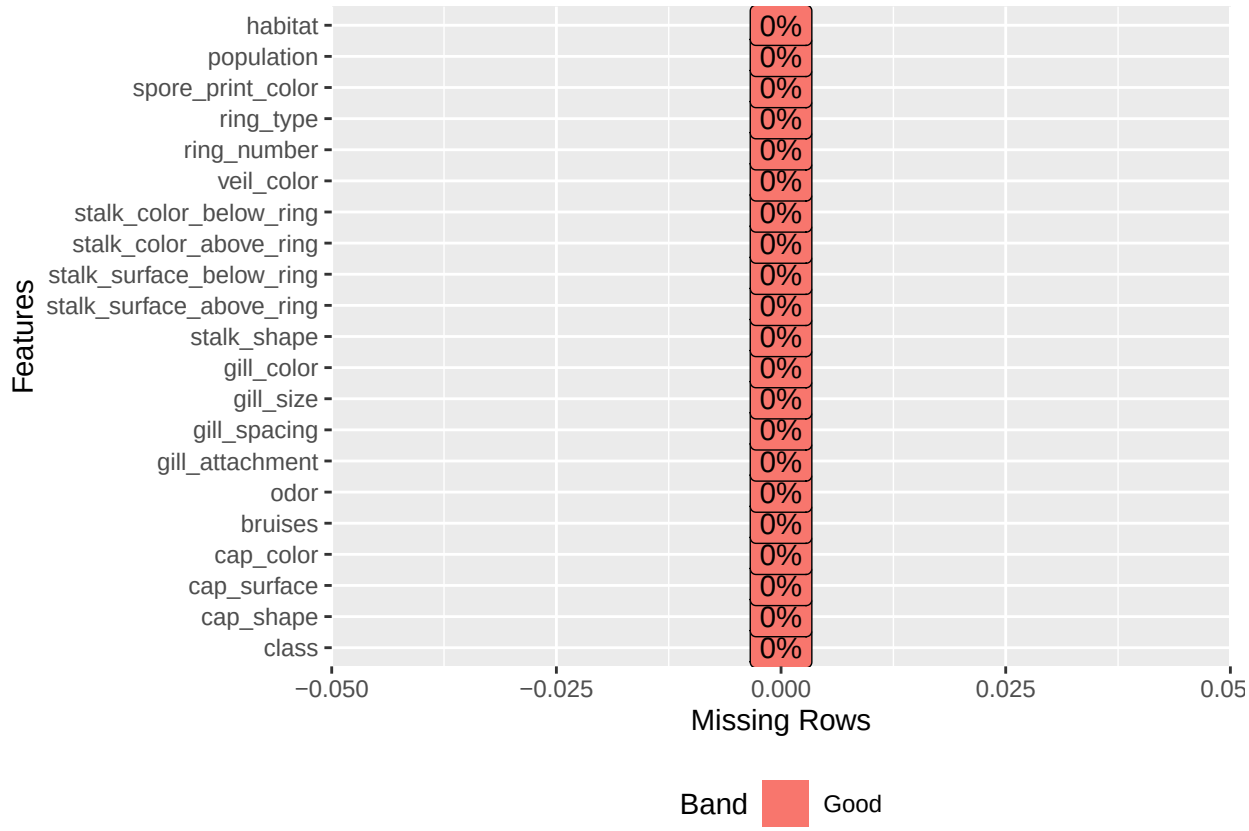
```
mushroom <- mushroom %>% select(-veil_type, -stalk_root)
```

2. Data Exploration

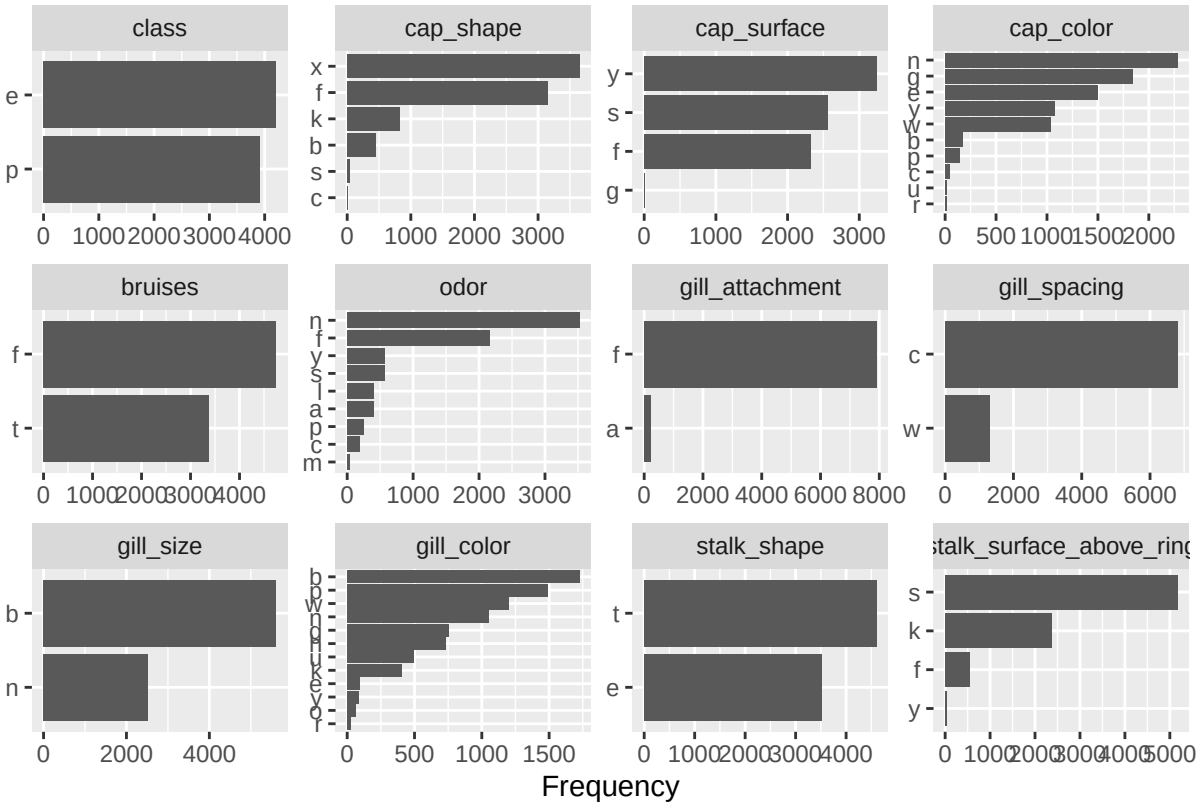
We will use Data Explorer package in the process of data exploration. By using this package, it provides a standardized method to get the insights from the dataset.

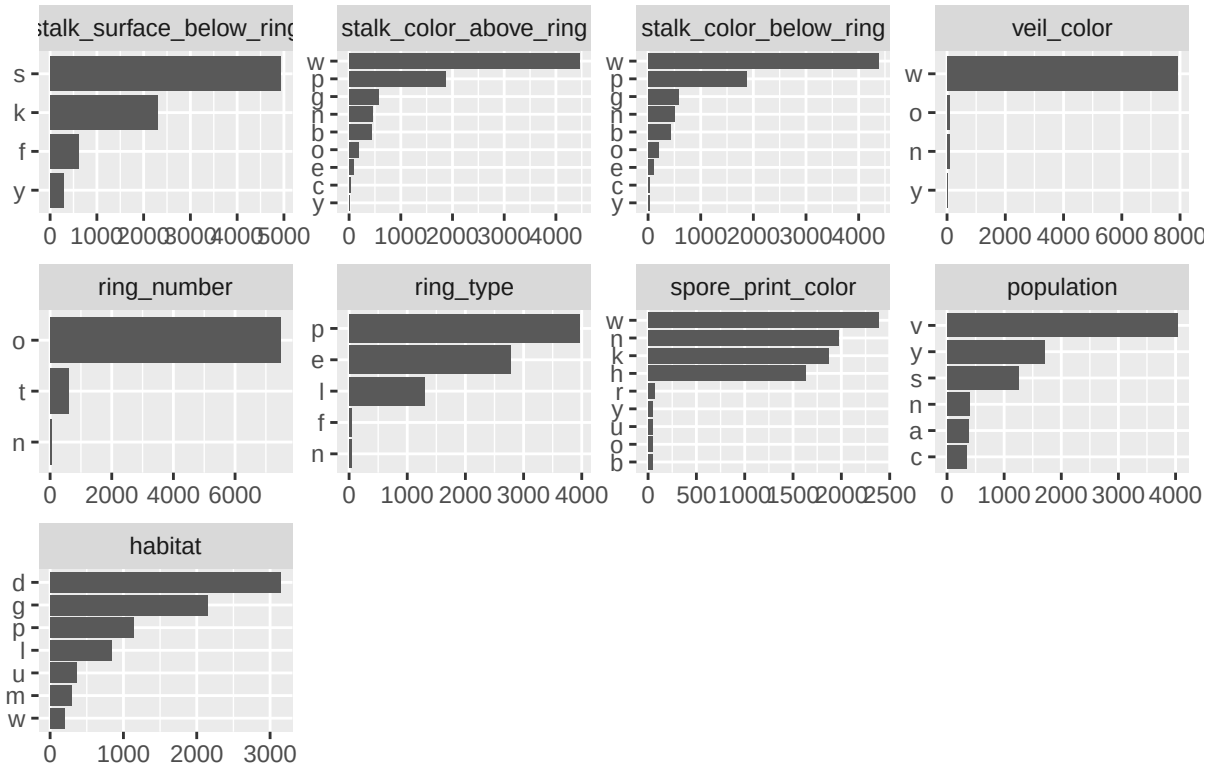
From below 2 charts, we can see that the mushroom data is discrete with no data missing.

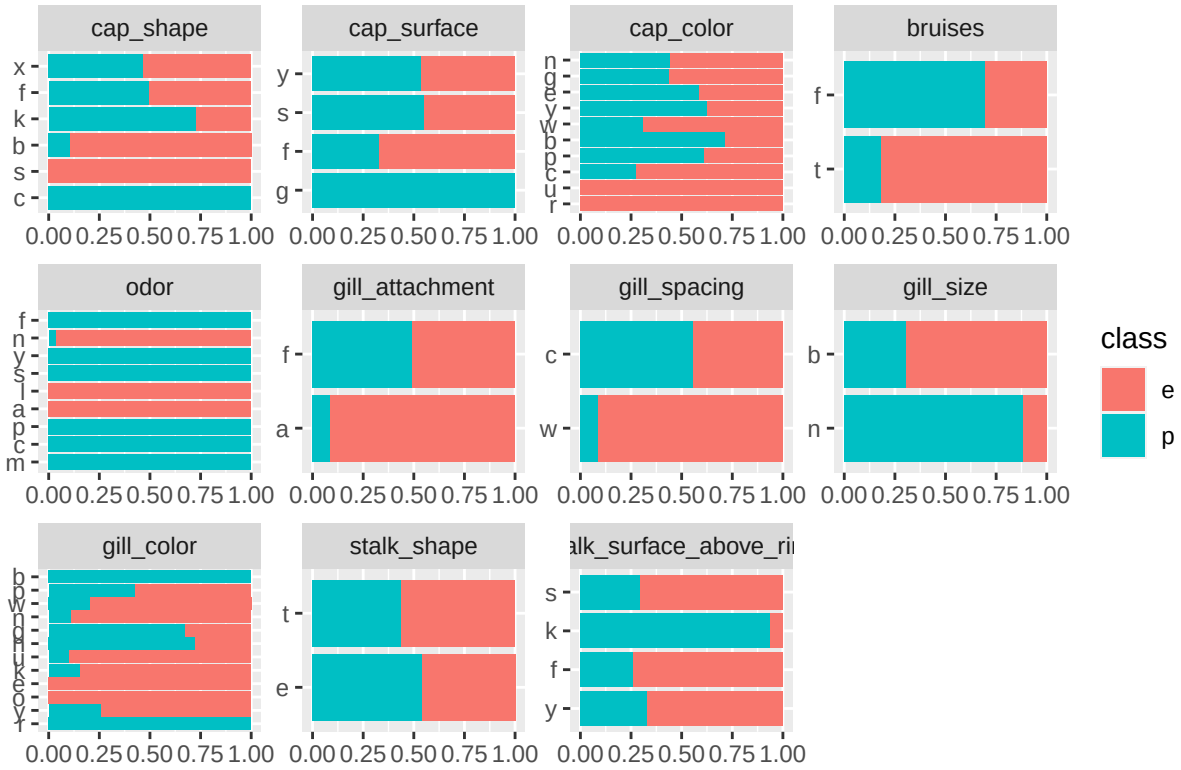

Memory Usage: 686.8 Kb
Discrete Columns
Continuous Columns
All Missing Columns
Complete Rows
Missing Observations
Metrics
100%
0%
0%
100%
0%
0%
25%
50%
75%
100%
Value
Dimension
column
observation
row



From below frequency and percentage charts, we can see how many observations belong to each category in each attribute and among those how many are edible or poisonous. In class which we are going to predict, we can say the feature is roughly equal distributed. However, observations are mainly clustered in one category in gill_attachment, gill_spacing, veil_color and ring_number.

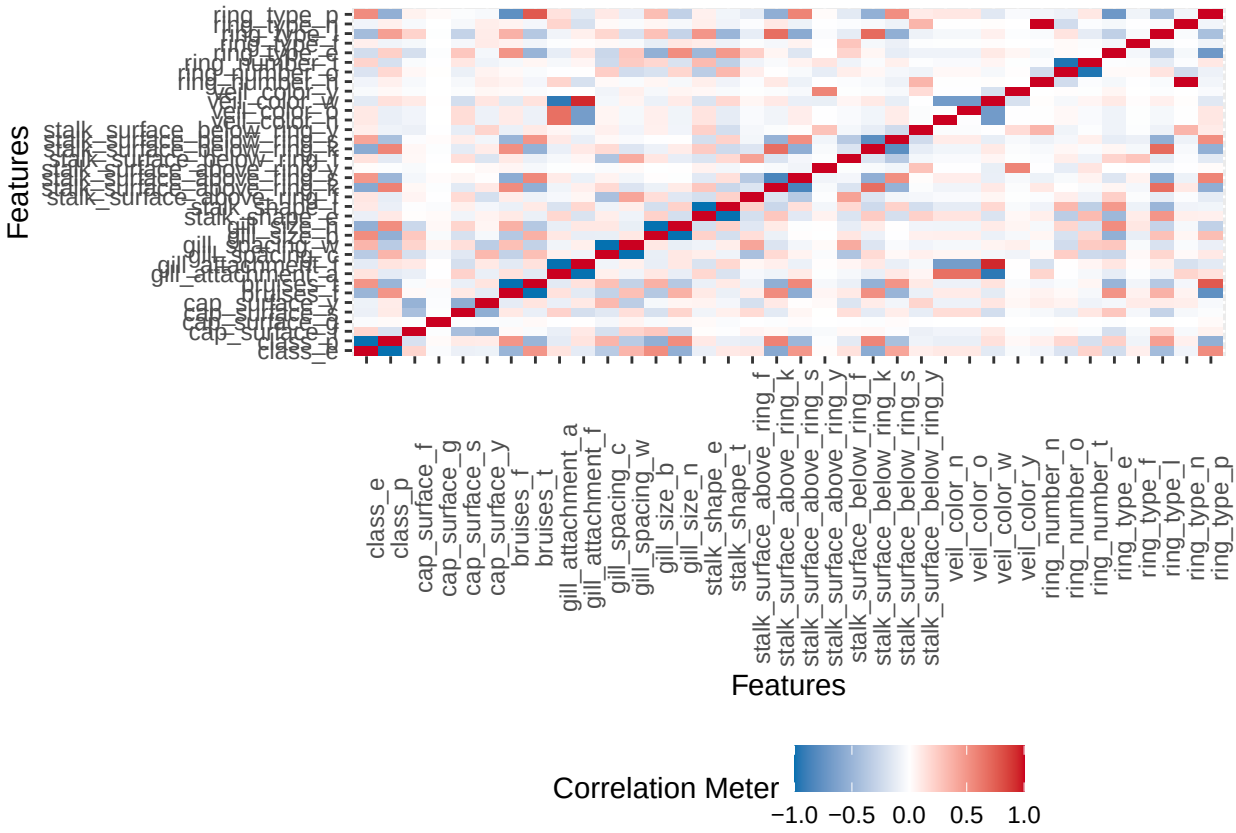

class
e
p
0 1000 2000 3000 4000
cap_shape
x
f
k
b
s
c
0 1000 2000 3000
cap_surface
y
s
f
g
0 1000 2000 3000
cap_color
n
g
e
y
w
b
p
c
u
r
0 500 1000 1500 2000
bruises
f
t
0 1000 2000 3000 4000
odor
n
f
y
s
l
a
p
c
m
0 1000 2000 3000
gill_attachment
f
a
0 2000 4000 6000 8000
gill_spacing
c
w
0 2000 4000 6000
gill_size
b
n
0 2000 4000
gill_color
b
p
w
n
g
h
u
k
e
y
o
r
0 500 1000 1500
stalk_shape
t
e
0 1000 2000 3000 4000
talk_surface_above_ring
s
k
f
y
0 1000 2000 3000 4000 5000
Frequency


stalk_surface_below_ring
stalk_color_above_ring
stalk_color_below_ring
veil_color
ring_number
ring_type
spore_print_color
population
habitat
Frequency


cap_shape
x
f
k
b
s
c
cap_surface
y
s
f
g
cap_color
n
g
e
y
w
b
p
c
u
r
bruises
f
t
odor
f
n
y
s
l
a
p
c
m
gill_attachment
f
a
gill_spacing
c
w
gill_size
b
n
gill_color
b
p
w
n
g
r
u
k
e
o
y
r
stalk_shape
t
e
alk_surface_above_ri
s
k
f
y
0.00 0.25 0.50 0.75 1.00
class
e
p

From correlation matrix (filtered category less than 5), there is high correlation between veil_color and gill_attachment, stalk_surface_above_ring and bruises.

```
## 9 features with more than 5 categories ignored!
## cap_shape: 6 categories
## cap_color: 10 categories
## odor: 9 categories
## gill_color: 12 categories
## stalk_color_above_ring: 9 categories
## stalk_color_below_ring: 9 categories
## spore_print_color: 9 categories
## population: 6 categories
## habitat: 7 categories
```



3. Modeling Approach

We will use 10 algorithms and 1 ensemble model to see if this can provide improvement to our predictions. Algorithms are listed below.

3-1. glm 3-2. lda 3-3. Naïve Bayes 3-4. svmLinear 3-5. classification 3-6. knn 3-7. gamLoess 3-8. multinom 3-9. rf 3-10. adaboost 3-11. ensemble

3-1. Generalized Linear Model (glm)

So among all classification model Random Forest Classification has highest accuracy score = 99.75%.

Result

a results section that presents the modeling results and discusses the model performance

Conclusion

a conclusion section that gives a brief summary of the report, its limitations and future work