Mushroom Classification Using K-Nearest Neighbors (KNN), Support Vector Machine, and Random Forest Algorithms

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There are countless types of mushrooms in the world. The biggest problem with mushrooms to date is which mushrooms are edible and which are poisonous.The aim of our project is to create a model that shows which mushrooms are edible and which are poisonous by analyzing some properties of edible and poisonous mushrooms, ultimately, using this model to discover whether an unknown mushroom is edible or not.

1 - Importing Mushroom Dataset

First, we start by importing the most essential libraries that we will need to import and analyze the dataset.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

We will important the mushroom data. The source of the data is UCI Machine Learning Repository. We downloaded the *.csv* file from Kaggle due to easier usage.

```
dataset = pd.read_csv('mushrooms.csv')
```

Now, the mushrooms.csv dataset is imported to the environment.

2 - Understanding the data

Now, we should analyze the dataset from various aspects to understand its structure better. Let's see the first 5 rows of the data:

```
dataset.head()
```

```
  class cap-shape cap-surface cap-color bruises odor gill-
attachment  \
0     p         x           s         n       t    p               f

1     e         x           s         y       t    a               f

2     e         b           s         w       t    l               f

3     p         x           y         w       t    p               f

4     e         x           s         g       f    n               f
```

```
  gill-spacing gill-size gill-color  ... stalk-surface-below-ring  \
0            c         n          k  ...                        s
1            c         b          k  ...                        s
2            c         b          n  ...                        s
3            c         n          n  ...                        s
4            w         b          k  ...                        s

  stalk-color-above-ring stalk-color-below-ring veil-type veil-
color  \
0                      w                      w         p          w

1                      w                      w         p          w

2                      w                      w         p          w

3                      w                      w         p          w

4                      w                      w         p          w


  ring-number ring-type spore-print-color population habitat
0           o         p                 k          s       u
1           o         p                 n          n       g
2           o         p                 n          n       m
3           o         p                 k          s       u
4           o         e                 n          a       g

[5 rows x 23 columns]
```

As it can be seen on the above table, values are single letters in this dataset where each letter corresponds to a specific meaning (e.g. in the "cap-shape" column, b=bell, c=conical, f=flat, s=sunken).

Since the most important and targeted column of this data is the "class" column, we should know that;

- p = poisonous
- e = edible

Let's check the columns and see if there is any *null* variable in the data:

```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
```

```
 0   class                     8124 non-null   object
 1   cap-shape                 8124 non-null   object
 2   cap-surface               8124 non-null   object
 3   cap-color                 8124 non-null   object
 4   bruises                   8124 non-null   object
 5   odor                      8124 non-null   object
 6   gill-attachment           8124 non-null   object
 7   gill-spacing              8124 non-null   object
 8   gill-size                 8124 non-null   object
 9   gill-color                8124 non-null   object
 10  stalk-shape               8124 non-null   object
 11  stalk-root                8124 non-null   object
 12  stalk-surface-above-ring  8124 non-null   object
 13  stalk-surface-below-ring  8124 non-null   object
 14  stalk-color-above-ring    8124 non-null   object
 15  stalk-color-below-ring    8124 non-null   object
 16  veil-type                 8124 non-null   object
 17  veil-color                8124 non-null   object
 18  ring-number               8124 non-null   object
 19  ring-type                 8124 non-null   object
 20  spore-print-color         8124 non-null   object
 21  population                8124 non-null   object
 22  habitat                   8124 non-null   object
dtypes: object(23)
memory usage: 1.4+ MB
```

```
dataset.isna().sum().sum()
```

```
0
```

There is no *null* variables in this data. Now, let's check if there is any other class than "poisonous" and "edible":

```
dataset["class"].unique()
```

```
array(['p', 'e'], dtype=object)
```

There are only 2 classes as expected. Let's check the unique values of all columns:

```
for col in dataset.columns:
  print(dataset[col].unique())
```

```
['p' 'e']
['x' 'b' 's' 'f' 'k' 'c']
['s' 'y' 'f' 'g']
['n' 'y' 'w' 'g' 'e' 'p' 'b' 'u' 'c' 'r']
['t' 'f']
['p' 'a' 'l' 'n' 'f' 'c' 'y' 's' 'm']
['f' 'a']
['c' 'w']
['n' 'b']
['k' 'n' 'g' 'p' 'w' 'h' 'u' 'e' 'b' 'r' 'y' 'o']
```

```
['e' 't']
['e' 'c' 'b' 'r' '?']
['s' 'f' 'k' 'y']
['s' 'f' 'y' 'k']
['w' 'g' 'p' 'n' 'b' 'e' 'o' 'c' 'y']
['w' 'p' 'g' 'b' 'n' 'e' 'y' 'o' 'c']
['p']
['w' 'n' 'o' 'y']
['o' 't' 'n']
['p' 'e' 'l' 'f' 'n']
['k' 'n' 'u' 'h' 'w' 'r' 'o' 'y' 'b']
['s' 'n' 'a' 'v' 'y' 'c']
['u' 'g' 'm' 'd' 'p' 'w' 'l']
```

There are many unique values in different features. The description of these values are given in the source of the data as;

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,solitary=y

22. habitat: grasses=g,leaves=l,meadows=m,paths=p, urban=u,waste=w,woods=d

```
dataset.shape
```

```
(8124, 23)
```

There are 8124 samples with 23 features where one of the features represent the class of the mushroom. Hence, we can say that the data has 22 independent variable where the class variable is the dependent variable. Now, let's analyze the columns in detail:

```
dataset.describe()
```

```
       class cap-shape cap-surface cap-color bruises  odor gill-
attachment  \
count   8124      8124        8124      8124    8124  8124
8124
unique     2         6           4        10       2     9
2
top        e         x           y         n       f     n
f
freq    4208      3656        3244      2284    4748  3528
7914

       gill-spacing gill-size gill-color  ... stalk-surface-below-ring
\
count          8124      8124       8124  ...                      8124

unique            2         2         12  ...                         4

top               c         b          b  ...                         s

freq           6812      5612       1728  ...                      4936


       stalk-color-above-ring stalk-color-below-ring veil-type veil-
color  \
count                    8124                    8124      8124
8124
unique                      9                       9         1
4
top                         w                       w         p
w
freq                     4464                    4384      8124
7924

       ring-number ring-type spore-print-color population habitat
count         8124      8124              8124       8124    8124
unique           3         5                 9          6       7
top              o         p                 w          v       d
freq          7488      3968              2388       4040    3148
```

```
[4 rows x 23 columns]
```

The detailed analysis clearly shows that the 51.8% of the mushrooms are **edible** (4208 out of 8124 samples).

3 - Data Preparation

Since the values are letters and we need quantitative data to pass it through the machine learning models, we need to convert these values into quantitative versions using label encoders.

```
from sklearn.preprocessing import LabelEncoder
data_encoded = dataset.copy()
le = LabelEncoder()
for col in data_encoded.columns:
  data_encoded[col] = le.fit_transform(data_encoded[col])

data_encoded.head()
```

```
   class  cap-shape  cap-surface  cap-color  bruises  odor  gill-
attachment  \
0      1          5            2          4        1     6
1
1      0          5            2          9        1     0
1
2      0          0            2          8        1     3
1
3      1          5            3          8        1     6
1
4      0          5            2          3        0     5
1

   gill-spacing  gill-size  gill-color  ...  stalk-surface-below-ring
\
0             0          1           4  ...                         2

1             0          0           4  ...                         2

2             0          0           5  ...                         2

3             0          1           5  ...                         2

4             1          0           4  ...                         2


   stalk-color-above-ring  stalk-color-below-ring  veil-type  veil-
color  \
0                       7                       7          0
2
```

```
1                       7                       7          0
2
2                       7                       7          0
2
3                       7                       7          0
2
4                       7                       7          0
2

   ring-number  ring-type  spore-print-color  population  habitat
0            1          4                  2           3        5
1            1          4                  3           2        1
2            1          4                  3           2        3
3            1          4                  2           3        5
4            1          0                  3           0        1

[5 rows x 23 columns]
```

The values are quantitative and can be used in the models now. For the "class" column, the corresponding values are as follow;

- *1* = poisonous
- *0* = edible

We can analyze the dataset again to see if we need feature scaling (normalization in range 0 to 1).

```
data_encoded.describe()

             class    cap-shape  cap-surface    cap-color      bruises
\
count  8124.000000  8124.000000  8124.000000  8124.000000  8124.000000

mean      0.482029     3.348104     1.827671     4.504677     0.415559

std       0.499708     1.604329     1.229873     2.545821     0.492848

min       0.000000     0.000000     0.000000     0.000000     0.000000

25%       0.000000     2.000000     0.000000     3.000000     0.000000

50%       0.000000     3.000000     2.000000     4.000000     0.000000

75%       1.000000     5.000000     3.000000     8.000000     1.000000

max       1.000000     5.000000     3.000000     9.000000     1.000000


              odor  gill-attachment  gill-spacing    gill-size   gill-
color  \
```

```
count  8124.000000      8124.000000   8124.000000  8124.000000
8124.000000
mean      4.144756         0.974151      0.161497     0.309207
4.810684
std       2.103729         0.158695      0.368011     0.462195
3.540359
min       0.000000         0.000000      0.000000     0.000000
0.000000
25%       2.000000         1.000000      0.000000     0.000000
2.000000
50%       5.000000         1.000000      0.000000     0.000000
5.000000
75%       5.000000         1.000000      0.000000     1.000000
7.000000
max       8.000000         1.000000      1.000000     1.000000
11.000000

       ...  stalk-surface-below-ring  stalk-color-above-ring  \
count  ...                8124.000000             8124.000000
mean   ...                   1.603644                5.816347
std    ...                   0.675974                1.901747
min    ...                   0.000000                0.000000
25%    ...                   1.000000                6.000000
50%    ...                   2.000000                7.000000
75%    ...                   2.000000                7.000000
max    ...                   3.000000                8.000000

       stalk-color-below-ring  veil-type   veil-color  ring-number  \
count             8124.000000     8124.0  8124.000000  8124.000000
mean                 5.794682        0.0     1.965534     1.069424
std                  1.907291        0.0     0.242669     0.271064
min                  0.000000        0.0     0.000000     0.000000
25%                  6.000000        0.0     2.000000     1.000000
50%                  7.000000        0.0     2.000000     1.000000
75%                  7.000000        0.0     2.000000     1.000000
max                  8.000000        0.0     3.000000     2.000000

         ring-type  spore-print-color   population      habitat
count  8124.000000        8124.000000  8124.000000  8124.000000
mean      2.291974           3.596750     3.644018     1.508616
std       1.801672           2.382663     1.252082     1.719975
min       0.000000           0.000000     0.000000     0.000000
25%       0.000000           2.000000     3.000000     0.000000
50%       2.000000           3.000000     4.000000     1.000000
75%       4.000000           7.000000     4.000000     2.000000
max       4.000000           8.000000     5.000000     6.000000

[8 rows x 23 columns]
```

Since the data range is not extreme and the variance is low enough, we do **not** need to normalize the values

The machine learning models need to be trained first and then tested for checking their accuracies. For this purpose, we need to prepare an X and a Y variable where;

- X = independent variable (input): It keeps the 22 independent features of the mushrooms in n **mxn** matrix where m is the number of mushroom samples (8124) and n is the number of features (22).
- Y = dependent variable (output): It keeps the class of the mushrooms in an **n** sized vector where n is the number of mushrooms (8124).

```
x = data_encoded.drop(["class"],axis=1)
y = data_encoded["class"].to_numpy()
```

```
x.head()
```

```
   cap-shape  cap-surface  cap-color  bruises  odor  gill-
attachment  \
0          5            2          4        1     6                1

1          5            2          9        1     0                1

2          0            2          8        1     3                1

3          5            3          8        1     6                1

4          5            2          3        0     5                1


   gill-spacing  gill-size  gill-color  stalk-shape  ...  \
0             0          1           4            0  ...
1             0          0           4            0  ...
2             0          0           5            0  ...
3             0          1           5            0  ...
4             1          0           4            1  ...

   stalk-surface-below-ring  stalk-color-above-ring  stalk-color-
below-ring  \
0                         2                       7
7
1                         2                       7
7
2                         2                       7
7
3                         2                       7
7
4                         2                       7
7
```

```
   veil-type  veil-color  ring-number  ring-type  spore-print-color  \
0          0           2            1          4                  2
1          0           2            1          4                  3
2          0           2            1          4                  3
3          0           2            1          4                  2
4          0           2            1          0                  3

   population  habitat
0           3        5
1           2        1
2           2        3
3           3        5
4           0        1

[5 rows x 22 columns]
```

```
y
```

```
array([1, 0, 0, ..., 0, 1, 0])
```

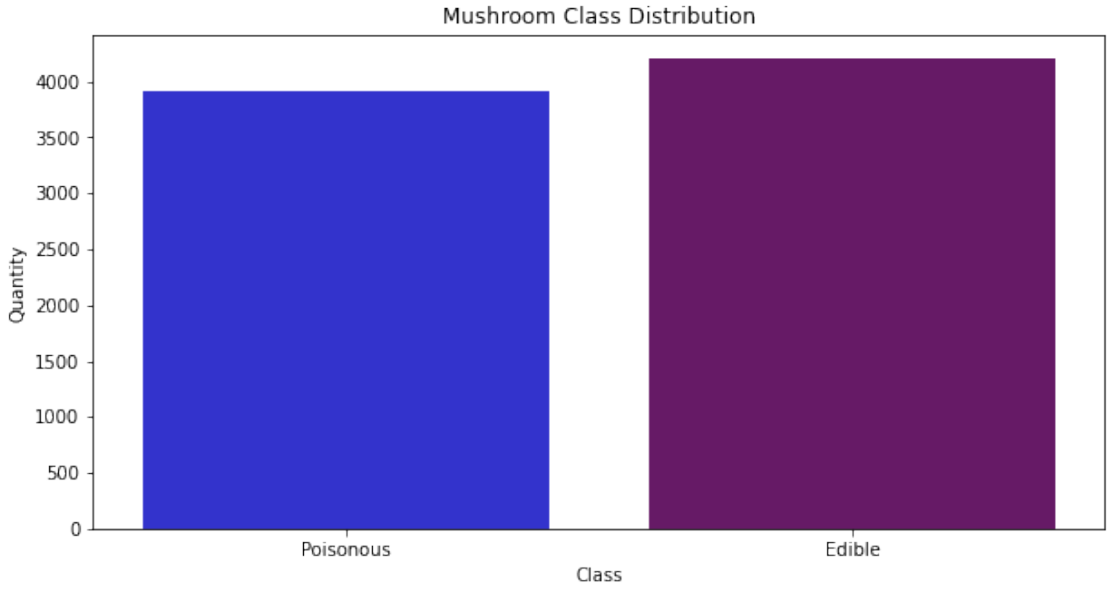
Dataset splitted into 2 parts which are train and test sets.

```
from sklearn.model_selection import train_test_split

x_train, x_test, y_train, y_test = train_test_split(x, y, test_size =
0.2)
```

4 - Data Visualization

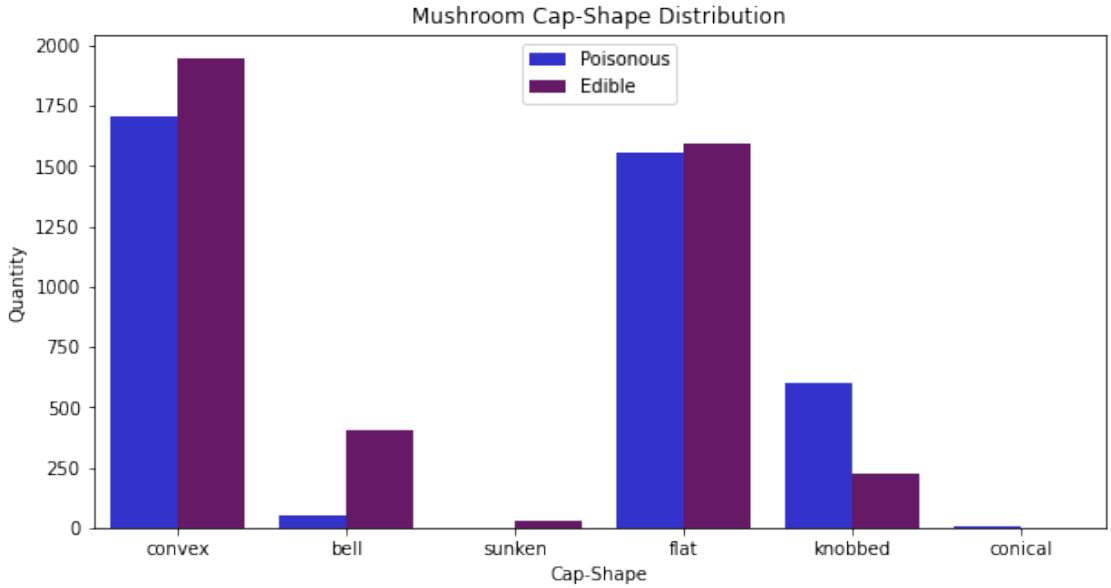
One of the best ways to understand a data is to see it visually. We can plot some aspects of the data for better understanding. Let's see the class distribution first:

```
import matplotlib.pylab as pylab
import seaborn as sns

def column_plot(column, hue=None, color=["blue", "purple"],
labels=None):
    fig, ax = plt.subplots(figsize=(10, 5))
    sns.countplot(x=column, hue=hue, palette=color, saturation=0.6,
data=dataset, dodge=True, ax=ax)
    ax.set(title = f"Mushroom {column.title()} Distribution",
xlabel=f"{column.title()}", ylabel="Quantity")
    if labels!=None:
        ax.set_xticklabels(labels)
    if hue!=None:
        ax.legend(("Poisonous", "Edible"), loc=0)

class_dict = ("Poisonous", "Edible")
column_plot(column="class", labels=class_dict)
```



To make a classification regarding the independent variables, classification algorithms check the relation of these independent variables with the dependent one(s). For instance, conical shaped mushrooms are tend to be poisonous slightly more than edible. To prove it, we can visualize the "cap-shape" column regarding the class of the mushrooms:

```
shape_dict = {"bell":"b","conical":"c","convex":"x","flat":"f",
"knobbed":"k","sunken":"s"}
labels = ("convex", "bell", "sunken", "flat", "knobbed", "conical")
column_plot(column="cap-shape", hue="class", labels=labels)
```

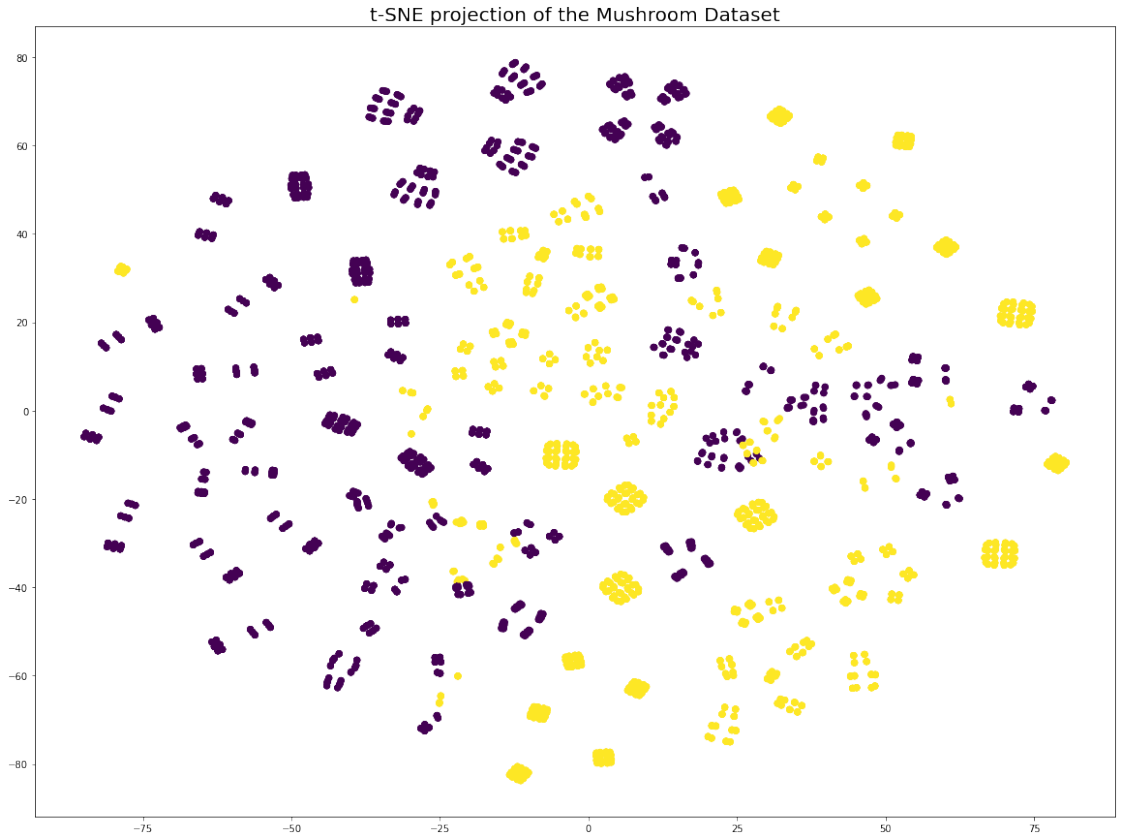


We used the t-SNE statistical method in order to visually observe which mushrooms are poisonous or non-poisonous according to what. Thus, we were able to examine our high-dimensional data in a 2-dimensional way.

```
from sklearn.manifold import TSNE
model = TSNE(learning_rate = 100)
transformed = model.fit_transform(x)
```

```
c:\Users\Atahan\Anaconda3\lib\site-packages\sklearn\manifold\
_t_sne.py:780: FutureWarning: The default initialization in TSNE will
change from 'random' to 'pca' in 1.2.
  warnings.warn(
```

```
xs = transformed[:,0]
ys = transformed[:,1]
plt.scatter(xs, ys, c=y)
plt.title('t-SNE projection of the Mushroom Dataset', fontsize=20)
plt.rcParams["figure.figsize"] = (20,15)
plt.show()
```

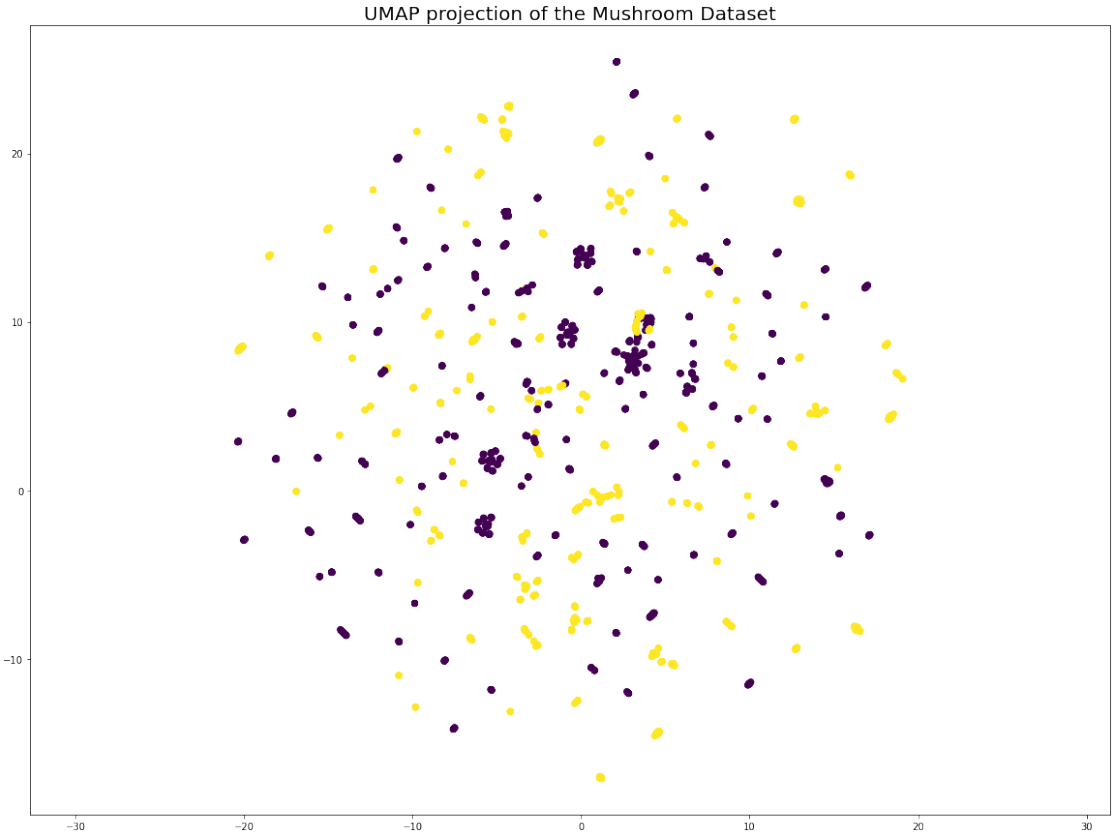


We visualized our data with another method which is UMAP. While t-SNE moves the high dimensional graph to a lower dimensional space points by points, UMAP compresses that graph.

```
#pip install umap-learn
import umap.umap_ as umap
```

```
reducer = umap.UMAP()
embedding = reducer.fit_transform(x)
plt.scatter(embedding[:, 0],embedding[:, 1],c=y)
```

```
plt.gca().set_aspect('equal', 'datalim')
plt.title('UMAP projection of the Mushroom Dataset', fontsize=20)
plt.rcParams["figure.figsize"] = (20,15)
plt.show()
```



Although it is not so obvious on the UMAP graph, we observed that our mushrooms can be easily distinguished from each other on the t-SNE graph.

5 - Classification of the Mushrooms

5.1 - k-Fold Cross Validation

We now have the train and test data. For the validation process, we will use only the train data which corresponds to 80% of the dataset.

Splitting a dataset into training and testing set is an essential and basic task when comes to getting a machine learning model ready for training. To determine if our model is overfitting or not, we need to test it on unseen data (validation set).

We will use k-Fold Cross-Validation method with k=5 as it is the most popular usage. In this case, data will be divided into k=5 pieces, and iteratively, each of the piece will be used as the validation data while the other ones are train data as a whole. At the end, we will have a k sized vector that contains the accuracy for each trial.

```
from sklearn.model_selection import KFold
from sklearn.metrics import accuracy_score

k_fold_split = 5

def model_validation(model):
  k_fold = KFold(n_splits=k_fold_split)
  acc_score = []

  for training_index , validation_index in k_fold.split(x_train):
      x_training, x_validation = x_train.iloc[training_index,:],
x_train.iloc[validation_index,:]
      y_training, y_validation = y_train[training_index] ,
y_train[validation_index]

      model.fit(x_training, y_training)
      pred_values = model.predict(x_validation)

      acc = accuracy_score(pred_values , y_validation)
      acc_score.append(acc)

  return acc_score
```

5.2 - Classification via KNN, SVM, and RF

We understood the data and prepared to be passed through classification algorithms in the previous sections. It is time to use the models over the data.

As expected in the project, we will use 3 different classification algorithms; K-Nearest Neighbors (KNN), Suppor Vector Machine (SVM), and Random Forest. Furhermore, we will use these algorithms with different possible hyperparameters and try to find the best settings by measuring the accuracies.

Scikit-learn library will be used for the implementation of the algorithms.

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
import sklearn #to use sklearn.base.clone for cloning the best models
import itertools #used for creating all of the element-combinations of
the given list of lists
from tqdm import tqdm #used for printing the progress of the for loop
```

5.2.1 - K-Nearest Neighbors (KNN)

In the KNN classifier, these possible parameters values will be combined with each other (Parameters and possible inputs are taken from the official website of the Scikit-learn library):

- *n_neighbors* = Number of neighbors to use. This the k value:

    - From 1 to 15
- *weights* = Weight function used in prediction
    - ["uniform", "distance"]
- *algorithm* = Algorithm used to compute the nearest neighbors
    - "auto" will be left as default since it is already optimized.
- *leaf_size* = Leaf size passed to BallTree or KDTree. This can affect the speed of the construction and query, as well as the memory required to store the tree.
    - from 30 to 35
- *p* = Power parameter for the Minkowski metric
    - from 1 to 3

All of the possible combinations of these values will be applied and the best accuracy will be printed with parameters.

```
best_knn_avg_acc = 0
best_knn_acc_list = []
best_knn_params = None
best_knn_model = None

n_neighbors = range(1, 16)
weights = ["uniform", "distance"]
leaf_size = range(30, 36)
p = range(1, 4)

param_combination = [n_neighbors, weights, leaf_size, p]

k_avg_accuracies = {} #this dictionary will collect the average
accuries of different k valued models. Those accuracies' average will
be reported
for i in n_neighbors:
    k_avg_accuracies[i] = []

print(f"{len(list(itertools.product(*param_combination)))} different
combinations of the parameters will be tested using k-Fold Cross
Validation.\n")

for comb in tqdm(itertools.product(*param_combination)):
    knn = KNeighborsClassifier(n_neighbors=comb[0], weights=comb[1],
leaf_size=comb[2], p=comb[3])

    knn_accuracies = model_validation(knn)
    knn_avg_accuracy = sum(knn_accuracies)/k_fold_split

    k_avg_accuracies[comb[0]].append(knn_avg_accuracy)

    if knn_avg_accuracy > best_knn_avg_acc:
      best_knn_avg_acc = knn_avg_accuracy
      best_knn_params = comb
```

```
            best_knn_model = knn
            best_knn_acc_list = knn_accuracies

best_knn_model = sklearn.base.clone(best_knn_model) # deep copying the
best model(untrained) to train again with the entire training data
best_knn_model.fit(x_train, y_train) # training the copied best model
with the training data
test_pred_values = best_knn_model.predict(x_test)
test_acc = accuracy_score(test_pred_values , y_test)

print(f"\n---\nResult:\n\nBest model's parameters:\n\tk =
{best_knn_params[0]}\n\tweights = {best_knn_params[1]}\n\tleaf_size =
{best_knn_params[2]}\n\tp = {best_knn_params[3]}\n\n---\nTrain
Results:\n\nBest model's average accuracy = {best_knn_avg_acc}\nBest
model's accuracy for each fold = {best_knn_acc_list}\n\n---\nTest
Results:\n\nBest model's accuracy = {test_acc}")
print("***\n***\n[Extra] Average accuracies for each k value with
every combination during validation process:\n")
for i in n_neighbors:
    print(f"\tk = {i}, average accuracy =
{np.mean(np.array(k_avg_accuracies[i]))}")
```

```
540 different combinations of the parameters will be tested using k-
Fold Cross Validation.


540it [55:57,  6.22s/it]


---
Result:

Best model's parameters:
      k = 1
      weights = uniform
      leaf_size = 30
      p = 1

---
Train Results:

Best model's average accuracy = 1.0
Best model's accuracy for each fold = [1.0, 1.0, 1.0, 1.0, 1.0]

---
Test Results:

Best model's accuracy = 1.0
***
***
```

```
[Extra] Average accuracies for each k value with every combination
during validation process:

      k = 1, average accuracy = 0.9992306507964707
      k = 2, average accuracy = 0.9988203746471643
      k = 3, average accuracy = 0.9982560549535147
      k = 4, average accuracy = 0.9979484416020212
      k = 5, average accuracy = 0.9980253252008447
      k = 6, average accuracy = 0.9975380864965161
      k = 7, average accuracy = 0.9978714987860484
      k = 8, average accuracy = 0.9967942204062297
      k = 9, average accuracy = 0.9968967845087939
      k = 10, average accuracy = 0.9958453445451136
      k = 11, average accuracy = 0.9956144766190957
      k = 12, average accuracy = 0.9947426422692013
      k = 13, average accuracy = 0.9943835494759283
      k = 14, average accuracy = 0.9935629379601666
      k = 15, average accuracy = 0.9934859951441936
```

540 different parameter combinations are trained with 5 folded Cross Validation so that in total, 2700 different training processes have been done.

5.2.2 - Support Vector Machine (SVM)

In the SVM classifier, these possible parameters values will be combined with each other (Parameters and possible inputs are taken from the official website of the Scikit-learn library):

- *C* = Regularization parameter. The strength of the regularization is inversely proportional to C. Must be strictly positive. The penalty is a squared l2 penalty.
  - from 1 to 3
- *kernel* = Specifies the kernel type to be used in the algorithm.
  - ["rbf", "poly", "sigmoid"]
- *gamma* = Kernel coefficient for ‘rbf’, ‘poly’ and ‘sigmoid’.
  - ["scale", "auto"]
- *shrinking* = Whether to use the shrinking heuristic.
  - [True, False]
- *decision_function_shape* = Whether to return a one-vs-rest (‘ovr’) decision function of shape (n_samples, n_classes) as all other classifiers, or the original one-vs-one (‘ovo’) decision function of libsvm which has shape (n_samples, n_classes * (n_classes - 1) / 2)
  - ["ovo", "ovr"]

All of the possible combinations of these values will be applied and the best accuracy will be printed with parameters.

```
best_svm_avg_acc = 0
best_svm_acc_list = []
```

```
best_svm_params = None
best_svm_model = None

C = range(1, 4)
kernel = ['rbf', 'poly', 'sigmoid']
gamma = ['scale', 'auto']
shrinking = [True, False]
decision_function_shape = ["ovo", "ovr"]

param_combination = [C, kernel, gamma, shrinking,
decision_function_shape]

print(f"{len(list(itertools.product(*param_combination)))} different
combinations of the parameters will be tested using k-Fold Cross
Validation.\n")

for comb in tqdm(itertools.product(*param_combination)):
    svm = SVC(C = comb[0], kernel = comb[1], gamma = comb[2],
shrinking = comb[3], decision_function_shape = comb[4])

    svm_accuracies = model_validation(svm)
    svm_avg_accuracy = sum(svm_accuracies)/k_fold_split

    if svm_avg_accuracy > best_svm_avg_acc:
      best_svm_avg_acc = svm_avg_accuracy
      best_svm_params = comb
      best_svm_model = svm
      best_svm_acc_list = svm_accuracies

best_svm_model = sklearn.base.clone(best_svm_model) # deep copying the
best model(untrained) to train again with the entire training data
best_svm_model.fit(x_train, y_train) # training the copied best model
with the training data
test_pred_values = best_svm_model.predict(x_test)
test_acc = accuracy_score(test_pred_values , y_test)

print(f"\n---\nResult:\n\nBest model's parameters:\n\tC =
{best_svm_params[0]}\n\tkernel = {best_svm_params[1]}\n\tgamma =
{best_svm_params[2]}\n\tshrinking = {best_svm_params[3]}\n\
tdecision_function_shape = {best_svm_params[4]}\n\n---\nTrain
Results:\n\nBest model's average accuracy = {best_svm_avg_acc}\nBest
model's accuracy for each fold = {best_svm_acc_list}\n\n---\nTest
Results:\n\nBest model's accuracy = {test_acc}")
```

```
72 different combinations of the parameters will be tested using k-
Fold Cross Validation.


72it [05:29,  4.58s/it]
```

```
---
Result:

Best model's parameters:
      C = 1
      kernel = poly
      gamma = auto
      shrinking = True
      decision_function_shape = ovo

---
Train Results:

Best model's average accuracy = 1.0
Best model's accuracy for each fold = [1.0, 1.0, 1.0, 1.0, 1.0]

---
Test Results:

Best model's accuracy = 1.0
```

72 different parameter combinations are trained with 5 folded Cross Validation so that in total, 360 different training processes have been done.

5.2.3 - Random Forest

In the Random Forest classifier, these possible parameters values will be combined with each other (Parameters and possible inputs are taken from the official website of the Scikit-learn library):

- *n_estimators* = The number of trees in the forest. This the tree count:
  - [100, 200, 300, 400, 500]
- *criterion* = The function to measure the quality of a split.
  - "gini" will be used because it's default value.
- *max_depth* = The maximum depth of the tree.
  - [10, 20, 30, 40, 50, None]
- *min_samples_split* = The minimum number of samples required to split an internal node.
  - [2, 4]
- *min_samples_leaf* = The minimum number of samples required to be at a leaf node.
  - [1, 2]
- *min_weight_fraction_leaf* = The minimum weighted fraction of the sum total of weights (of all the input samples) required to be at a leaf node.
  - default = 0.0 value is used.
- *max_features* = The number of features to consider when looking for the best split.
  - ["log2", "sqrt"]

- *max_leaf_nodes* = Grow trees with max_leaf_nodes in best-first fashion.
  - default = None value is used.
- *min_impurity_decrease* = A node will be split if this split induces a decrease of the impurity greater than or equal to this value.
  - default = 0.0 value is used.
- *bootstrap* = Whether bootstrap samples are used when building trees.
  - [True, False]
- *oob_score* = Whether to use out-of-bag samples to estimate the generalization score. Only available if bootstrap=True.
  - default = False value is used.
- *n_jobs* = The number of jobs to run in parallel.
  - default = None value is used.
- *random_state* = Controls both the randomness of the bootstrapping of the samples used when building trees (if bootstrap=True) and the sampling of the features to consider when looking for the best split at each node (if max_features < n_features).
  - default = None value is used.
- *verbose* = Controls the verbosity when fitting and predicting.
  - default = 0 value is used.
- *warm_start* = When set to True, reuse the solution of the previous call to fit and add more estimators to the ensemble, otherwise, just fit a whole new forest.
  - default = False value is used.
- *class_weight* = Weights associated with classes in the form {class_label: weight}. If not given, all classes are supposed to have weight one.
  - default = None value is used.
- *ccp_alpha* = Complexity parameter used for Minimal Cost-Complexity Pruning.
  - default = 0.0 value is used.
- *max_samples* = If bootstrap is True, the number of samples to draw from X to train each base estimator.
  - default = None value is used.

All of the possible combinations of these values will be applied and the best accuracy will be printed with parameters.

```
best_rf_avg_acc = 0
best_rf_acc_list = []
best_rf_params = None
best_rf_model = None

# Number of trees in random forest
n_estimators = [int(x) for x in np.linspace(start = 100, stop = 500,
num = 5)]
# Number of features to consider at every split
max_features = ['log2', 'sqrt']
# Maximum number of levels in tree
max_depth = [int(x) for x in np.linspace(10, 50, num = 5)]
```

```
max_depth.append(None)
# Minimum number of samples required to split a node
min_samples_split = [2, 4]
# Minimum number of samples required at each leaf node
min_samples_leaf = [1, 2]
# Method of selecting samples for training each tree
bootstrap = [True, False]

param_combination = [n_estimators, max_features, max_depth,
min_samples_split, min_samples_leaf, bootstrap]

print(f"{len(list(itertools.product(*param_combination)))} different
combinations of the parameters will be tested using k-Fold Cross
Validation.\n")

for comb in tqdm(itertools.product(*param_combination)):
    rf = RandomForestClassifier(n_estimators=comb[0],
max_features=comb[1],
                                max_depth=comb[2],
min_samples_split=comb[3],
                                min_samples_leaf=comb[4],
bootstrap=comb[5])

    rf_accuracies = model_validation(rf)
    rf_avg_accuracy = sum(rf_accuracies)/k_fold_split

    if rf_avg_accuracy > best_rf_avg_acc:
      best_rf_avg_acc = rf_avg_accuracy
      best_rf_params = comb
      best_rf_model = rf
      best_rf_acc_list = rf_accuracies

best_rf_model = sklearn.base.clone(best_rf_model) # deep copying the
best model(untrained) to train again with the entire training data
best_rf_model.fit(x_train, y_train) # training the copied best model
with the training data
test_pred_values = best_rf_model.predict(x_test)
test_acc = accuracy_score(test_pred_values , y_test)

print(f"\n---\nResult:\n\nBest model's parameters:\n\tn estimator =
{best_rf_params[0]}\n\tmax feature = {best_rf_params[1]}\n\tmax depth
= {best_rf_params[2]}\n\tmin samples split = {best_rf_params[3]}\n\
tmin samples leaf = {best_rf_params[4]}\n\tbootstrap=
{best_rf_params[5]}\n\n---\nTrain Results:\n\nBest model's average
accuracy = {best_rf_avg_acc}\nBest model's accuracy for each fold =
{best_rf_acc_list}\n\n---\nTest Results:\n\nBest model's accuracy =
{test_acc}")
```

```
480 different combinations of the parameters will be tested using k-
Fold Cross Validation.


480it [30:21,  3.80s/it]


---
Result:

Best model's parameters:
      n estimator = 100
      max feature = log2
      max depth = 10
      min samples split = 2
      min samples leaf = 1
      bootstrap= True

---
Train Results:

Best model's average accuracy = 1.0
Best model's accuracy for each fold = [1.0, 1.0, 1.0, 1.0, 1.0]

---
Test Results:

Best model's accuracy = 1.0
```

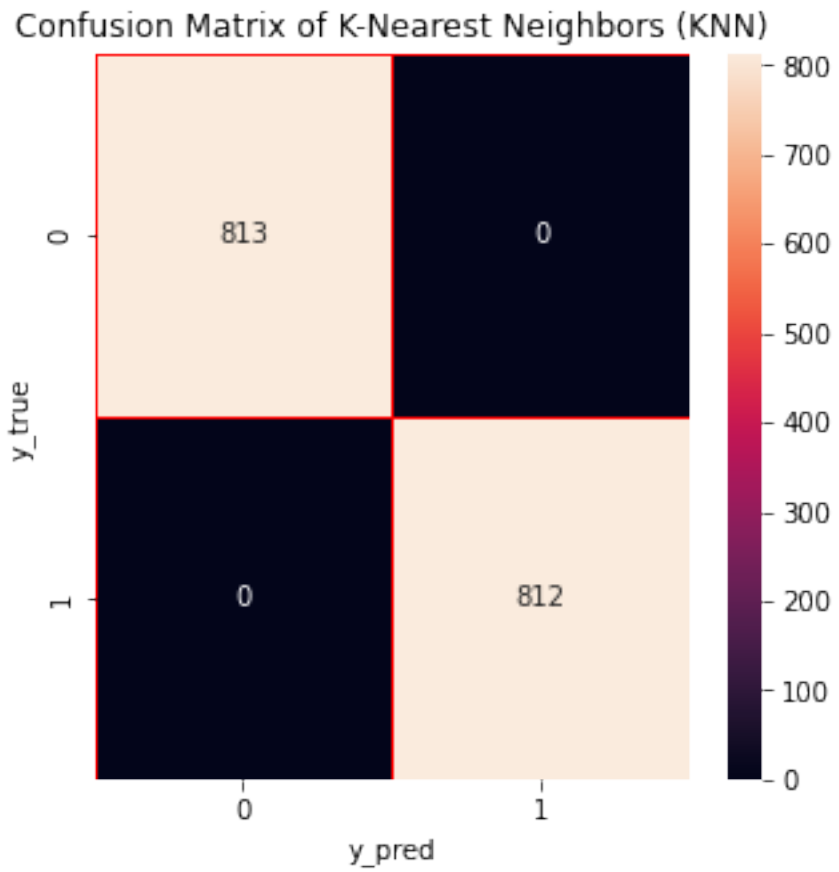
6 - Visual Results

To understand the performances of the model better, we can draw the confusion matrices of their predictions. Below function will take the models for each of the algorithms and draw their confusion matrix automatically.

```
from sklearn.metrics import confusion_matrix

def draw_conf_matrix(model, model_name):
  y_pred = model.predict(x_test)
  y_true = y_test
  cm = confusion_matrix(y_true, y_pred)
  f, ax = plt.subplots(figsize =(5,5))
  sns.heatmap(cm, annot = True, linewidths=0.5, linecolor="red", fmt =
".0f", ax=ax)
  plt.xlabel("y_pred")
  plt.ylabel("y_true")
  plt.title(f"Confusion Matrix of {model_name}")
  plt.show()
```

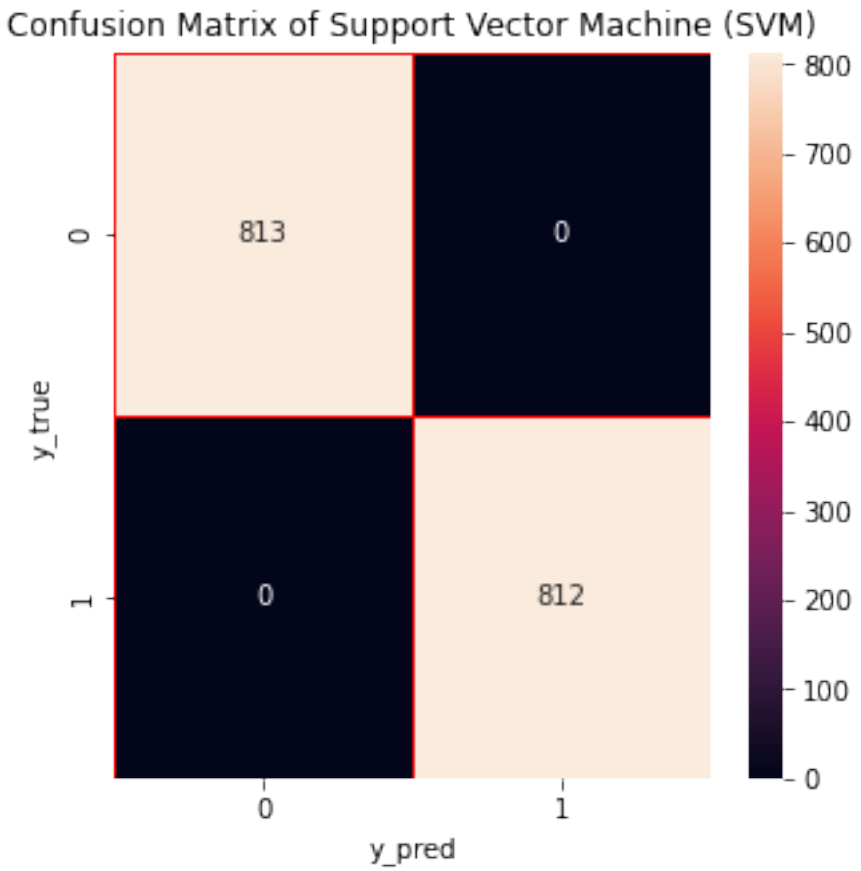
6.1 - K-Nearest Neighbors (KNN) Confusion Matrix

```
draw_conf_matrix(best_knn_model, "K-Nearest Neighbors (KNN)")
```



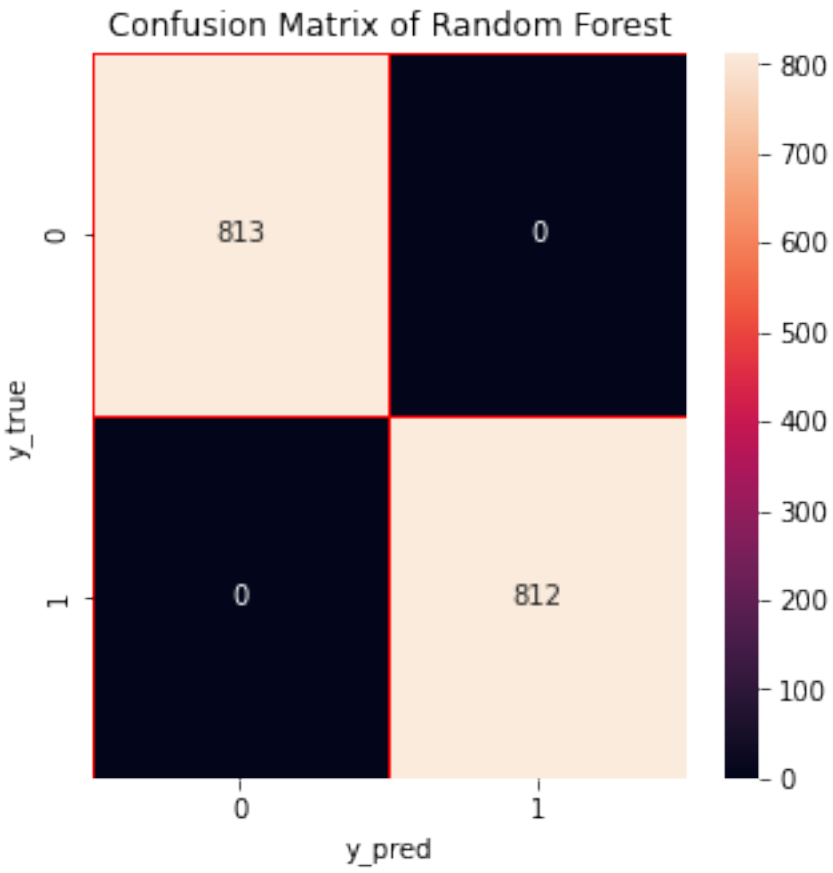
6.2 - Support Vector Machine (SVM) Confusion Matrix

```
draw_conf_matrix(best_svm_model, "Support Vector Machine (SVM)")
```



6.3 - Random Forest Confusion Matrix

```
draw_conf_matrix(best_rf_model, "Random Forest")
```


Confusion Matrix of Random Forest
813
0
0
812
y_true
y_pred
0
1
0
1
800
700
600
500
400
300
200
100
0