# Mushrooms

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## 1 Mushrooms

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### 1.1 Contents

### 1.2 Introduction

All mushrooms are edible, some of them are edible once.

Eating wild mushrooms can be a treat; they are one of the few plant foods which contain vitamin D and some other benefits for the human beings [3], however, adverse reactions can occur after eating a wild mushroom. Some of those negative reactions include serious respiratory symptoms, with nauseas and vomiting. As consecuence vital organs could be damaged, which can result in death. [1] Thus, the objective for this research is to analyze and predict whether a mushroom is edible or poisonous based on certain characteristics.

### 1.3 State of art

It is very difficult to distinguish between edible and poisonous mushrooms. Based on the experience of many scientist, there are some observations, which may help to identify the poisonous mushrooms: bright color, pink spores, a hot burning taste or acidic flavor, growing on wooden pieces in hidden places, difficult to break and bear a cup like structure (volva) at the base. Some of the poisonous mushrooms when taken orally produce hallucinations. These include toadstools of the genera Amanita, Psilocybe and Conocybe [5].

In the literature, many authors have worked on solve this problem using new techniques such as trained algorithms, predictors and so on. One of them was presented by Glockner [2], who used a deep learning algorithm to solve the problem even when there are few information about mushrooms. Glockner found almost 1200 pictures about edible and poisonous mushrooms. Using a TensorFlow based network to train the algorithm. To test the program, each image has a score for poison and for edible (0..1), with an accuracy of almost ~97%.

Other projects such as the present by Garziano [4], who creates a huge domain knowledge about the mushrooms. His study includes the feature analysis such as the structure, color, shape and size of a mushroom. Each feature gives a importance to determine if the mushroom is edible or not. The feature analysis gives some interesting facts to solve the problem, i.e "only poisonous mushrooms have convex cap-shape or "only edible mushrooms have sunken cap-shape" Also, the analysis provided the importance level for each feature compared with the others ones. Finally, the author were able to estimate if a mushroom was edible or not based on certain characteristics.

## 1.4 Mushrooms

Mushrooms are a type of fungus. They are non-flowering and can grow in a variety of habitats. Mushrooms and other fungi reproduce by small dust-like particles called spores. Typically produced above ground on soil or on its food source.

They have a long history, both in folklore and in the kitchen. where we can cook many species of them. Also, mushrooms have served humans as medecine and psychoactive drugs, religious symbols and helpful tools.

Identifying mushrooms requires a basic understanding of their structure. They have spores which are produced on the gills (under the cap). The ring which surround the stem or stalk is present in some species. The base is called volva (in the bottom).

An important factor to the identification is the color, this is used to help classify mushrooms and it can help to identify them. Spore print colors include white (most common), brown, black, purple-brown, pink, yellow, and creamy, but almost never blue, green, or red.

In the literature, there are some clasifications for the Mushrooms. The fungi society of Saskatchewan created a glossary to help to understand the mushrooms [7].

### 1.4.1 Mushroom Features Glossary

The cap can be found on different presentations such as the convex, or conical and even flat. This is the upper parte of the mushroom. We can see some examples in the following image.

Under the cap there is a region called the Gills, which is a series of radially surfaces. The spores depends by the gills.

The stalk, also known as stem is the main support of the mushroom. It is topped by the cap.

The mushrooms also have a ring, which is a surface circligng the stem. It is present of mature mushroms. The ring is also a tissue that connects the stem and the caps before the gills are exposed and the fruiting body develops. It is present in some species of mushrooms, not in all.

In the base of the mushroom exists the volva, which is a cup rounded. It is present befor the fruiting body appears.

Based on this research we would like analyze the mushroom to determine whether they are edible or not.

### 1.5 Analysis

All the libraries needed for the project are in the `sllab.py` file.

[1]:
```python
from sllab import *
```

```
Packages:
    numpy as np
    matplotlib.pyplot as plt
    pandas as pd

Functions:
    plotXY
    plot_frontiere
```

The `MultiColumnLabelEncoder` class was added to help, analyze and manage the data. The reason to use it was to reshape the information into a numerical values.

[2]:
```python
# A utility from https://stackoverflow.com/questions/24458645/label-encoding-across-multiple-columns-in-scikit-learn
# Adapted and changed to Labelbonarizer that fits with the whole dataframe.
class MultiColumnLabelEncoder:
    def __init__(self,columns = None):
        self.columns = columns # array of column names to encode
        self.lb = pp.LabelEncoder()

    def fit(self,X,y=None):
        self.lb.fit(np.concatenate(X.to_numpy(), axis=0))
        return self

    def transform(self,X):
        output = X.copy()
        if self.columns is None:
            self.columns = output.columns

        for col_id, col in enumerate(self.columns):
            output[col] = self.lb.transform(output[col])

        return output

    def fit_transform(self,X,y=None):
        return self.fit(X,y).transform(X)
```

The mushroom dataset, provide different files where the information was classified by `short-names` and `expanded`. Both contains information about more than 1 thousand of studied species and their characteristics. In terms of the project, the caracteristics are called features. In the expanded file, we could find the whole dataset with the full name for each feature, however in the `agaricus-lepiota.data` or short name file, only the first letter for each feature name is stored. This is an optimization in terms of use of hardware resources.

[3]:
```
data_names = pd.read_csv("expanded",
                        skiprows=9,
                        skipfooter=1)
```

[4]:
```
data_names.head()
```

[4]:
```
   EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW  \
0  EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW
1  EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW
2  EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW
3  EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW
4  EDIBLE  CONVEX  SMOOTH  WHITE  BRUISES  ALMOND  FREE  CROWDED  NARROW

  WHITE.1  … SMOOTH.2 WHITE.2 WHITE.3  PARTIAL WHITE.4  ONE  PENDANT  \
0   WHITE  …   SMOOTH   WHITE   WHITE  PARTIAL   WHITE  ONE  PENDANT
1    PINK  …   SMOOTH   WHITE   WHITE  PARTIAL   WHITE  ONE  PENDANT
2    PINK  …   SMOOTH   WHITE   WHITE  PARTIAL   WHITE  ONE  PENDANT
3   BROWN  …   SMOOTH   WHITE   WHITE  PARTIAL   WHITE  ONE  PENDANT
4   BROWN  …   SMOOTH   WHITE   WHITE  PARTIAL   WHITE  ONE  PENDANT

   PURPLE  SEVERAL  WOODS
0   BROWN  SEVERAL  WOODS
1  PURPLE  SEVERAL  WOODS
2   BROWN  SEVERAL  WOODS
3  PURPLE  SEVERAL  WOODS
4   BROWN  SEVERAL  WOODS

[5 rows x 23 columns]
```

[5]:
```
dataset = pd.read_csv("agaricus-lepiota.data",
                        skiprows=9,
                        skipfooter=1)
```

[6]:
```
dataset.head()
```

[6]:
```
   e  b  s  y  t  a  f  c b.1  g  … s.2  w w.1  p w.2  o p.1  k s.3  m
0  e  x  y  y  t  l  f  c   b  g  …   s  w   w  p   w  o   p  n   n  g
1  e  x  y  y  t  a  f  c   b  n  …   s  w   w  p   w  o   p  k   s  m
2  e  b  s  y  t  a  f  c   b  w  …   s  w   w  p   w  o   p  n   s  g
3  p  x  y  w  t  p  f  c   n  k  …   s  w   w  p   w  o   p  n   v  u
4  e  x  f  n  f  n  f  w   b  n  …   f  w   w  p   w  o   e  k   a  g

[5 rows x 23 columns]
```

### 1.6 Feature selection

This data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). Each species is identified as definitely edible, definitely poisonous, or of unknown edibility and not recommended. This latter class was combined with the poisonous one. The Guide clearly states that there is no simple rule for determining the edibility of a mushroom; no rule like “leaflets three, let it be” for Poisonous Oak and Ivy.

1. Adding titles to organize the info

[7]:

```
classes = np.array([
    'class',
    'cap-shape',
    'cap-surface',
    'cap-color',
    'bruises?',
    'odor',
    'gill-attachment',
    'gill-spacing',
    'gill-size',
    'gill-color',
    'stalk-shape',
    'stalk-root',
    'stalk-surface-above-ring',
    'stalk-surface-below-ring',
    'stalk-color-above-ring',
    'stalk-color-below-ring',
    'veil-type',
    'veil-color',
    'ring-number',
    'ring-type',
    'spore-print-color',
    'population',
    'habitat'])

featured_classes = np.array([
    'cap-shape',
    'cap-surface',
    'cap-color',
    'bruises?',
    'odor',
    'gill-attachment',
    'gill-spacing',
    'gill-size',
    'gill-color',
    'stalk-shape',
    'stalk-root',
    'stalk-surface-above-ring',
    'stalk-surface-below-ring',
    'stalk-color-above-ring',
    'stalk-color-below-ring',
    'veil-type',
    'veil-color',
    'ring-number',
    'ring-type',
    'spore-print-color',
    'population',
    'habitat'])
```

The data is separated into features `X` and expected value `y`.

[8]:
```
dataset = pd.DataFrame(dataset.values, columns=classes)
X_data, y_data = pd.DataFrame(dataset, columns=featured_classes), pd.
 ↪DataFrame(dataset, columns=['class'])
```

2. Transform the data into a numerical values. Using the previous MultiColumnLabelEncoder function we can rebuild the information in terms of numbers to analyze them.

[9]:
```
from sklearn.preprocessing import StandardScaler

X = MultiColumnLabelEncoder().fit_transform(X_data)
y = MultiColumnLabelEncoder().fit_transform(y_data)
```

[10]:
```
X.shape
```

[10]:
```
(8113, 22)
```

[11]:
```
print("Data mean, and a standard deviation",np.mean(X),np.std(X))
```

```
Data mean, and a standard deviation cap-shape                   12.869839
cap-surface                 15.532109
cap-color                   11.708000
bruises?                    10.565142
odor                        10.606434
gill-attachment              5.871194
gill-spacing                 5.747073
gill-size                    5.092567
gill-color                  10.852582
stalk-shape                 11.814249
stalk-root                   2.177000
stalk-surface-above-ring    13.290768
stalk-surface-below-ring    13.482559
stalk-color-above-ring      15.876618
stalk-color-below-ring      15.817453
veil-type                   14.000000
```

```
veil-color                 19.825342
ring-number                13.291384
ring-type                  10.226427
spore-print-color          12.928017
population                 17.313078
habitat                     8.076174
dtype: float64 cap-shape                   7.496994
cap-surface                6.541714
cap-color                  6.217069
bruises?                   5.419967
odor                       4.901700
gill-attachment            0.792109
gill-spacing               6.257302
gill-size                  4.621872
gill-color                 6.184573
stalk-shape                5.944493
stalk-root                 2.548768
stalk-surface-above-ring   3.727814
stalk-surface-below-ring   4.029103
stalk-color-above-ring     5.402926
stalk-color-below-ring     5.404900
veil-type                  0.000000
veil-color                 1.142153
ring-number                1.050152
ring-type                  4.051910
spore-print-color          4.974655
population                 5.368198
habitat                    4.493485
dtype: float64
```

## 1.7 Model selection

We can translate the classes to numerical data. This way we could try linear regression methods or even correlation methods i.e. Pearsons Correlation to identify correlations between classes, this way we might find correlations that are not visible or more than 2-Dimensional. Also, we can use K-Nearest Neighbor Algorithm, which is a powerful classification model which can be used to classify labelled data points to make predictions on new data.

[12]:

```
# Parsing into a boolean values
y_labels = y.astype(int).values[:,-1]

seed = 42

# Split into train/test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,␣
 ↪stratify=y_labels, random_state=seed)
```

How do we define a good value for n_neighbors or k value? Using a square root of the data length and checking if it is an odd number!

[13]:

```
import math

if int(math.sqrt(len(y_test))) & 2 == 1:
    n_neighbors = int(math.sqrt(len(y_test))) - 1
else:
    n_neighbors = int(math.sqrt(len(y_test)))
```

[14]:

```
n_neighbors
```

[14]:

```
49
```

Our dataset is composed by 22 dimensions, where each one refers to the available feature. Our goal is to reduce the dimensions aiming to a high accuracy and effective time. To do that we compare over the dimensions how is the accuracy and the time.

[15]:

```
## 22 is the max number of components given the available features
from time import time
acc = list()
tt = list()

for i in range(1,len(featured_classes)):
    #PIPELINE
    pca = make_pipeline(PCA(n_components=i, random_state=seed))
    knn = KNeighborsClassifier(n_neighbors=n_neighbors,p=2,metric='euclidean')
    pca.fit(X_train, y_train)
    knn.fit(pca.transform(X_train), y_train)
    start = time()
    acc_knn = knn.score(pca.transform(X_test), y_test)
    tt.append(time() - start)
    acc.append(acc_knn)
```

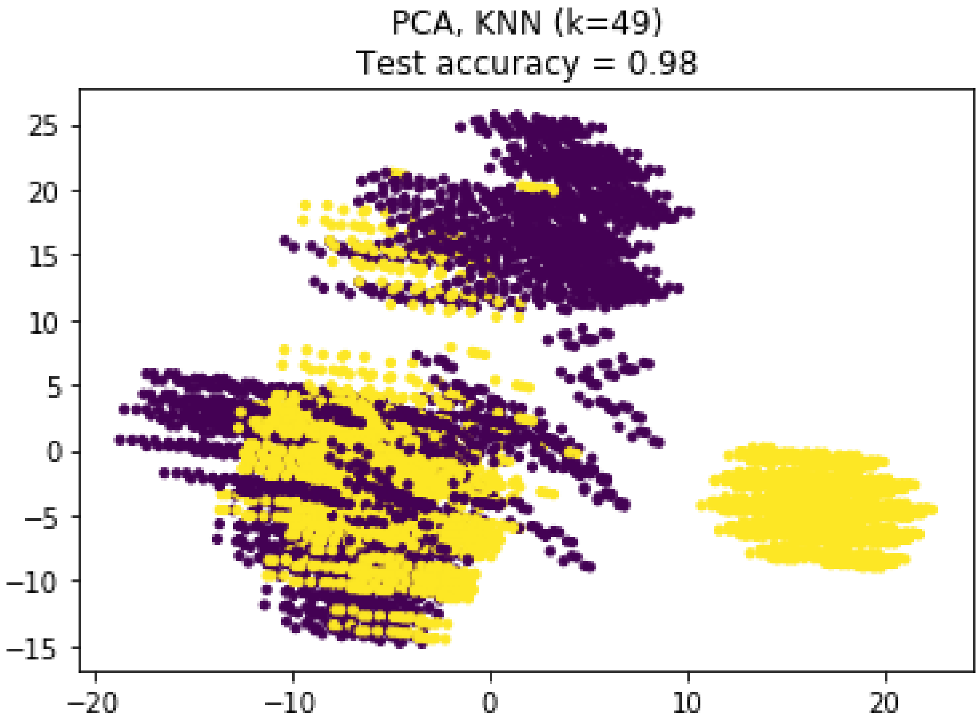
The results plotted in the Accuracy figure shows that starting from a component 10, the accuracy becomes really effective, also this value is constrained with the time, to prevent overfitting and more calculations.

The algorithm proposed uses a dimensional reduction with PCA, taking an optimal component, for this case `n_components=10`. As long we are looking to estimate whether a mushroom is edible or not, we classify the data using a K-NeighborhsClassifier.

[16]:

```
#PIPELINE
# Reduce dimension with PCA
# n_component=10 based on the accuracy test
pca = make_pipeline(PCA(n_components=10, random_state=seed))

# Use a nearest neighbor classifier to evaluate the methods
# p = 2 we are looking for Mushroom edible or not
knn = KNeighborsClassifier(n_neighbors=n_neighbors,p=2,metric='euclidean')
```

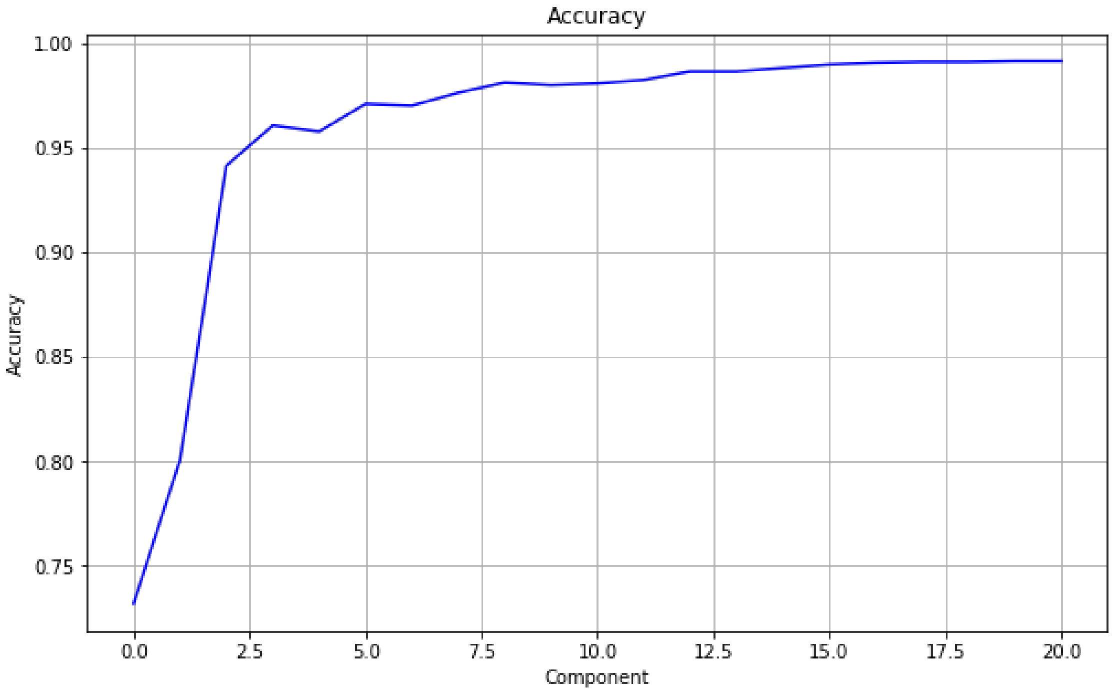
```
pca.fit(X_train, y_train)

# Fit a nearest neighbor classifier on the embedded training set
knn.fit(pca.transform(X_train), y_train)

# Compute the nearest neighbor accuracy on the embedded test set
acc_knn = knn.score(pca.transform(X_test), y_test)

# Embed the data set in 2 dimensions using the fitted model
X_embedded = pca.transform(X)

# Plot the projected points and show the evaluation score
plt.scatter(X_embedded[:, 0], X_embedded[:, 1], c=y_labels, s=10)
plt.title("{}, KNN (k={})\nTest accuracy = {:.2f}".format('PCA', n_neighbors,␣
 ↪acc_knn))
plt.show()
```



As we can see in the previous graph, our algorithm can estimate with a high accuracy if the mushroom is edible or not. To evaluate the algorithm we use two methods the knn score and the confusion matrix.

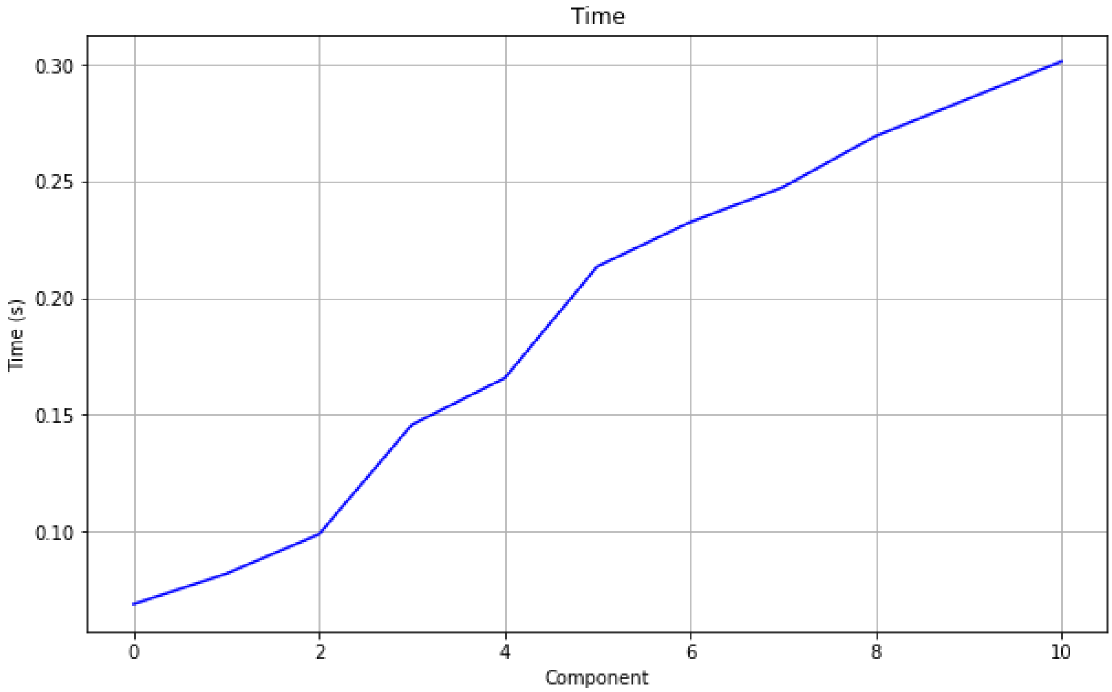
[17]:
```
plt.figure(figsize=(10,6))
plt.plot(range(len(acc)), acc,'b-')
plt.grid(True)
plt.title("Accuracy")
plt.xlabel("Component")
plt.ylabel("Accuracy")
```

```
[17]: Text(0, 0.5, 'Accuracy')
```



```
[18]: plt.figure(figsize=(10,6))
      plt.plot(tt[::2],'b-')
      plt.grid(True)
      plt.title("Time")
      plt.xlabel("Component")
      plt.ylabel("Time (s)")
```

```
[18]: Text(0, 0.5, 'Time (s)')
```



The previous graphs show the effectiveness how the algorithm can predict whether a mushroom is edible or not with an optimal time.

## 1.8 Evaluation

We measure our algorithm in different ways, using the `knn-score` and `confusion_matrix`. Both libraries provide us with a clear information about the evaluation made on the model.

[19]:

```
# Using a predictor for our test
y_pred = knn.predict(pca.transform(X_test))

print(len(y_pred), y_pred.shape,len(y_test), len(X_test), X_test.shape)
print(y_pred)
```

```
2434 (2434,) 2434 2434 (2434, 22)
[1 1 0 … 1 0 1]
```

The results show that the precision of our algorithm is quite effective with at least 98% of accuracy for each feature `edible` and `poisonous`.

[20]:

```
print("Results",classification_report(y_test, y_pred,␣
 ↪target_names=['edible','poisonous']))
```

```
Results              precision    recall  f1-score   support

      edible       0.98      0.98      0.98      1260
```

```
   poisonous       0.98      0.98      0.98      1174

    accuracy                           0.98      2434
   macro avg       0.98      0.98      0.98      2434
weighted avg       0.98      0.98      0.98      2434
```

An important thing to analize is whether our information is true positive or true negative, this means if we found edible or poisonous mushrooms with a high accuracy. The following table shows the way how the confusion matrix give us the information.

[21]:

```
confusion_matrix(y_test,y_pred)
```

[21]:

```
array([[1234,   26],
       [  23, 1151]], dtype=int64)
```

- As result we have `1234` mushroom species which are edibles.
- `1151` poisonous mushrooms.
- `26` false positives.
- `23` false negatives.

The number for **`false positives`** or **`false negatives`** is low compared the whol dataset, that means there is a percentage of `0.98%` to find an edible mushroom which in reality is poisonous. Also, the probability to find a mushroom poisonous which in reality is edible is the `0.94%`.

[22]:

```
accuracy_score(y_test,y_pred)
```

[22]:

```
0.9798685291700904
```

## 1.9 Conclusion

we created a exploratory analysis over the Mushrooms characteristics. We presented an algorithm which was trained with a dataset composed by 22 features of mushrooms, with the advantage of PCA we reduce the dimensions and we created a model using K-NeighborhsClassifier with an accuracy of ~97%.

## 1.10 References

(1) Metzler S. Metzler V. Orson K. Texas Mushrooms. University of Texas Press. Austin. https://books.google.cz/books?id=HRtfvVigMmsC&pg=PA37&redir_esc=y#v=onepage&q&f=false
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(7) https://www.usask.ca/biology/fungi/home_%20page.shtml