Bar chart wine

May 1, 2022

[ ]:

```python
from sklearn.datasets import load_wine
d = load_wine()
print(d)

x=d.data
y=d.target
```

```
{'data': array([[1.423e+01, 1.710e+00, 2.430e+00, …, 1.040e+00, 3.920e+00,
        1.065e+03],
       [1.320e+01, 1.780e+00, 2.140e+00, …, 1.050e+00, 3.400e+00,
        1.050e+03],
       [1.316e+01, 2.360e+00, 2.670e+00, …, 1.030e+00, 3.170e+00,
        1.185e+03],
       …,
       [1.327e+01, 4.280e+00, 2.260e+00, …, 5.900e-01, 1.560e+00,
        8.350e+02],
       [1.317e+01, 2.590e+00, 2.370e+00, …, 6.000e-01, 1.620e+00,
        8.400e+02],
       [1.413e+01, 4.100e+00, 2.740e+00, …, 6.100e-01, 1.600e+00,
        5.600e+02]]), 'target': array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2]), 'frame': None, 'target_names': array(['class_0', 'class_1',
'class_2'], dtype='<U7'), 'DESCR': '.. _wine_dataset:\n\nWine recognition
dataset\n------------------------\n\n**Data Set Characteristics:**\n\n
:Number of Instances: 178 (50 in each of three classes)\n    :Number of
Attributes: 13 numeric, predictive attributes and the class\n    :Attribute
Information:\n \t\t- Alcohol\n \t\t- Malic acid\n \t\t- Ash\n\t\t- Alcalinity of
ash  \n \t\t- Magnesium\n\t\t- Total phenols\n \t\t- Flavanoids\n \t\t-
Nonflavanoid phenols\n \t\t- Proanthocyanins\n\t\t- Color intensity\n \t\t-
Hue\n \t\t- OD280/OD315 of diluted wines\n \t\t- Proline\n\n    - class:\n
- class_0\n            - class_1\n            - class_2\n\t\t\n    :Summary
Statistics:\n    \n    ============================ ==== ===== ======= =====\n
Min   Max   Mean     SD\n    ============================ ==== ===== =======
=====\n    Alcohol:                      11.0  14.8    13.0   0.8\n    Malic
Acid:                    0.74  5.80    2.34  1.12\n    Ash:
1.36  3.23    2.36  0.27\n    Alcalinity of Ash:            10.6  30.0    19.5
3.3\n    Magnesium:                    70.0 162.0    99.7  14.3\n    Total
Phenols:                 0.98  3.88    2.29  0.63\n    Flavanoids:
0.34  5.08    2.03  1.00\n    Nonflavanoid Phenols:         0.13  0.66    0.36
0.12\n    Proanthocyanins:              0.41  3.58    1.59  0.57\n    Colour
Intensity:               1.3  13.0     5.1   2.3\n    Hue:
0.48  1.71    0.96  0.23\n    OD280/OD315 of diluted wines: 1.27  4.00    2.61
0.71\n    Proline:                      278  1680     746   315\n
============================ ==== ===== ======= =====\n\n    :Missing Attribute
Values: None\n    :Class Distribution: class_0 (59), class_1 (71), class_2
(48)\n    :Creator: R.A. Fisher\n    :Donor: Michael Marshall
(MARSHALL%PLU@io.arc.nasa.gov)\n    :Date: July, 1988\n\nThis is a copy of UCI
ML Wine recognition datasets.\nhttps://archive.ics.uci.edu/ml/machine-learning-
databases/wine/wine.data\n\nThe data is the results of a chemical analysis of
wines grown in the same\nregion in Italy by three different cultivators. There
are thirteen different\nmeasurements taken for different constituents found in
the three types of\nwine.\n\nOriginal Owners: \n\nForina, M. et al, PARVUS -
\nAn Extendible Package for Data Exploration, Classification and Correlation.
\nInstitute of Pharmaceutical and Food Analysis and Technologies,\nVia Brigata
Salerno, 16147 Genoa, Italy.\n\nCitation:\n\nLichman, M. (2013). UCI Machine
Learning Repository\n[https://archive.ics.uci.edu/ml]. Irvine, CA: University of
California,\nSchool of Information and Computer Science. \n\n.. topic::
References\n\n  (1) S. Aeberhard, D. Coomans and O. de Vel, \n  Comparison of
Classifiers in High Dimensional Settings, \n  Tech. Rep. no. 92-02, (1992),
Dept. of Computer Science and Dept. of  \n  Mathematics and Statistics, James
Cook University of North Queensland. \n  (Also submitted to Technometrics). \n\n
The data was used with many others for comparing various \n  classifiers. The
classes are separable, though only RDA \n  has achieved 100% correct
classification. \n  (RDA : 100%, QDA 99.4%, LDA 98.9%, 1NN 96.1% (z-transformed
data)) \n  (All results using the leave-one-out technique) \n\n  (2) S.
Aeberhard, D. Coomans and O. de Vel, \n  "THE CLASSIFICATION PERFORMANCE OF RDA"
\n  Tech. Rep. no. 92-01, (1992), Dept. of Computer Science and Dept. of \n
Mathematics and Statistics, James Cook University of North Queensland. \n  (Also
submitted to Journal of Chemometrics).\n', 'feature_names': ['alcohol',
'malic_acid', 'ash', 'alcalinity_of_ash', 'magnesium', 'total_phenols',
'flavanoids', 'nonflavanoid_phenols', 'proanthocyanins', 'color_intensity',
'hue', 'od280/od315_of_diluted_wines', 'proline']}
```

[ ]:

```
acc=[]

from sklearn.neighbors import KNeighborsClassifier
c1f1 = KNeighborsClassifier(n_neighbors=3)
c1f1.fit(x, y)
```

```

from sklearn.model_selection import cross_val_score
scores1 = cross_val_score(c1f1,x,y,cv=10)
print(scores1)

import statistics
acc.append(statistics.mean(scores1))
print(acc)
```

```
[0.66666667 0.61111111 0.66666667 0.66666667 0.66666667 0.66666667
 0.72222222 0.77777778 0.88235294 0.88235294]
[0.7209150326797386]
```

[ ]:

```
from sklearn import svm
c1f2 = svm.SVC(kernel='linear')
c1f2.fit(x,y)

from sklearn.model_selection import cross_val_score
scores2 = cross_val_score(c1f2,x,y,cv=10)
print(scores2)

import statistics
acc.append(statistics.mean(scores2))
print(acc)
```

```
[0.88888889 0.94444444 0.88888889 0.94444444 0.94444444 0.94444444
 1.         1.         1.         1.        ]
[0.7209150326797386, 0.9555555555555555]
```

[ ]:

```
from sklearn.tree import DecisionTreeClassifier
c1f3 = DecisionTreeClassifier()
c1f3.fit(x,y)

from sklearn.model_selection import cross_val_score
scores3 = cross_val_score (c1f3, x,y,cv=10)
print(scores3)

import statistics
acc.append(statistics.mean(scores3))
print(acc)
```

```
[0.88888889 0.88888889 0.66666667 0.88888889 0.83333333 0.83333333
 1.         0.94444444 0.94117647 0.76470588]
[0.7209150326797386, 0.9555555555555555, 0.8650326797385621]
```

[ ]:

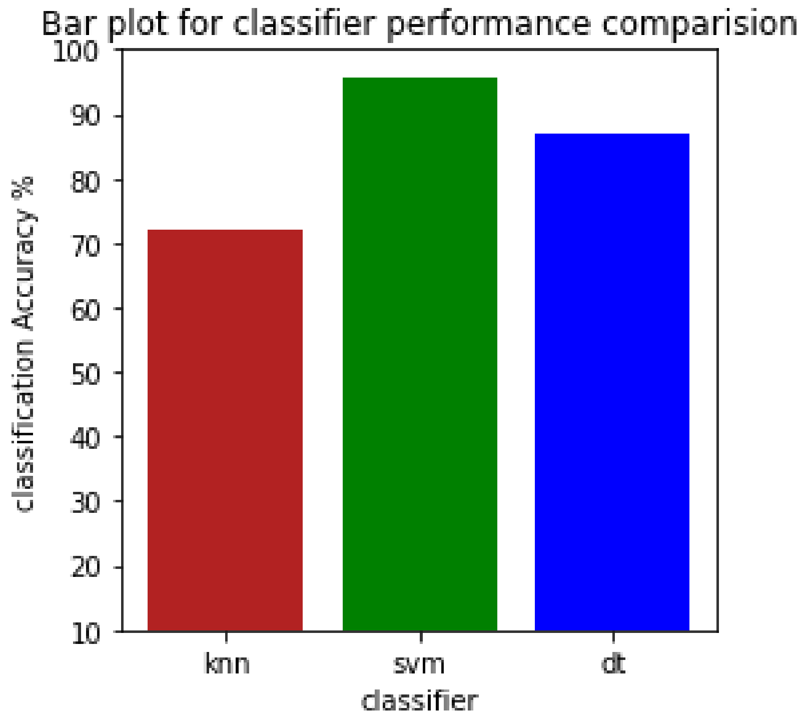
```
import matplotlib.pyplot as plt
```

```
data = {'knn':0.7209150326797386*100,'svm': 0.9555555555555555*100,'dt': 0.
 ↪8705882352941177*100}
classifiers = list(data.keys())
accuracy = list(data.values())

# creating the bar
plt.figure(figsize=(4,4))
plt.bar (classifiers, accuracy, color='maroon',width=0.6)

plt.
 ↪bar(classifiers,accuracy,color=['firebrick','green','blue','red','purple','skyblue'])
plt.ylim(10,100)

plt.ylabel('classification Accuracy %')
plt.xlabel('classifier')
plt.title("Bar plot for classifier performance comparision")
plt.show()
```



```
[ ]: from sklearn.linear_model import LogisticRegression
     c1f4=LogisticRegression(multi_class='multinomial',random_state=1)
     c1f4.fit(x,y)

     from sklearn.model_selection import cross_val_score
     from sklearn import metrics
     scores4 = cross_val_score(c1f4,x,y,cv=10)
     print(sorted(scores4))


     from sklearn.model_selection import cross_val_predict
     y_pred4=cross_val_predict(c1f4,x,y,cv=10)
     print(y_pred4)

     import statistics
     acc.append(statistics.mean(scores4))
     print(acc)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
/home/tg/Videos/silver-parakeet/Bar chart wine.ipynb Cell 6' in <cell line: 3>(
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000008?line=0'>1</a> from sklearn.linear_model␣
 ↪import LogisticRegression
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000008?line=1'>2</a>␣
 ↪c1f4=LogisticRegression(multi_class='multinomial',random_state=1)
----> <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000008?line=2'>3</a> c1f4.fit(x,y)
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000008?line=4'>5</a> from sklearn.model_selection␣
 ↪import cross_val_score
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000008?line=5'>6</a> from sklearn import metrics

NameError: name 'x' is not defined
```

[ ]:

```
from sklearn.naive_bayes import GaussianNB
clf5=GaussianNB()
clf5.fit(x, y)

from sklearn.model_selection import cross_val_score
from sklearn import metrics
scores5 = cross_val_score(clf5,x,y,cv=10)
print(scores5)

from sklearn.model_selection import cross_val_predict
y_pred5 = cross_val_predict(clf5, x, y, cv=10)
print(y_pred5)

import statistics
acc.append(statistics.mean(scores5))
```

```
print(acc)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
/home/tg/Videos/silver-parakeet/Bar chart wine.ipynb Cell 7' in <cell line: 3>(
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000009?line=0'>1</a> from sklearn.naive_bayes␣
 ↪import GaussianNB
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000009?line=1'>2</a> clf5=GaussianNB()
----> <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000009?line=2'>3</a> clf5.fit(x, y)
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000009?line=4'>5</a> from sklearn.model_selection
 ↪import cross_val_score
      <a href='vscode-notebook-cell:/home/tg/Videos/silver-parakeet/
 ↪Bar%20chart%20wine.ipynb#ch0000009?line=5'>6</a> from sklearn import metrics

NameError: name 'x' is not defined
```