Machine Learning on Miller

February 7, 2021

0.1 Predicting Diabetes

[20]:
```
import pandas as pd #data frame library
import numpy as np #data manipulation and analysis
from matplotlib import pyplot as plt #plotting dataset
```

0.1.1 Load and review data

[21]:
```
df=pd.read_csv('pima-data.csv', delimiter=',')  #load Pima data. Adjust path as␣
↪necesary
df.shape
```

[21]:
```
(768, 10)
```

[22]:
```
df.head()   #to show the beginning row of our data set
```

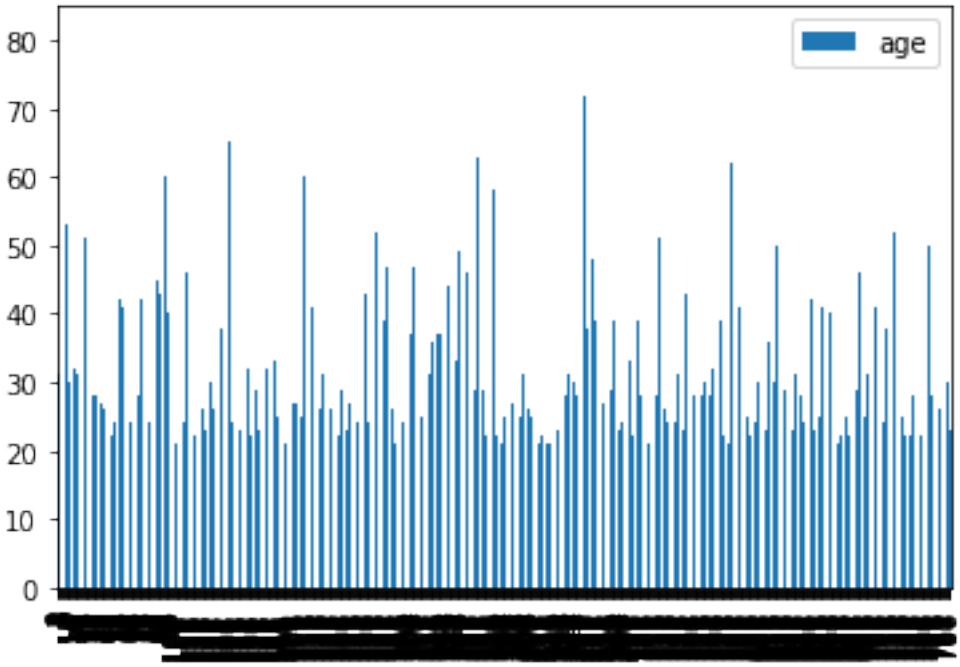
[22]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	\
0	6	148	72	35	0	33.6	0.627	
1	1	85	66	29	0	26.6	0.351	
2	8	183	64	0	0	23.3	0.672	
3	1	89	66	23	94	28.1	0.167	
4	0	137	40	35	168	43.1	2.288	

	age	skin	diabetes
0	50	1.3790	True
1	31	1.1426	False
2	32	0.0000	True
3	21	0.9062	False
4	33	1.3790	True

[23]:
```
df.plot(y="age",kind="bar")
```

[23]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x19416077788>
```



[24]:
```
# Find missing values
print('Missing values:{}'.format(df.isnull().any().sum()))
# Find duplicated records
print('\nNumber of duplicated records: {}'.format(df.duplicated().sum()))
```

```
Missing values:0

Number of duplicated records: 0
```

[25]:
```
df=pd.read_csv('pima-data - missing values.csv', delimiter=',')  #load Pima␣
 ↪data. Adjust path as necesary
df.head()
```

[25]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	\
0	6	?	72	35	0	33.6	0.627	
1	1	85	66	29	0	26.6	0.351	
2	8	183	64	0	0	23.3	0.672	
3	1	89	66	23	94	28.1	0.167	
4	0	137	40	35	168	43.1	2.288	

	age	skin	diabetes
0	?	1.3790	True
1	31	1.1426	False
2	32	0.0000	True
3	21	0.9062	False

```
4   33  1.3790      True
```

[26]:
```
# Find missing values
print('Missing values:{}'.format(df.isnull().any().sum()))
# Find duplicated records
print('\nNumber of duplicated records: {}'.format(df.duplicated().sum()))
```

```
Missing values:0

Number of duplicated records: 0
```

[27]:
```
print (df.astype(str) != '?')
```

```
     num_preg  glucose_conc  diastolic_bp  thickness  insulin   bmi  \
0        True         False          True       True     True  True
1        True          True          True       True     True  True
2        True          True          True       True     True  True
3        True          True          True       True     True  True
4        True          True          True       True     True  True
..        …             …             …          …        …     …
763      True          True          True       True     True  True
764      True          True          True       True     True  True
765      True          True          True       True     True  True
766      True          True          True       True     True  True
767      True          True          True       True     True  True

     diab_pred    age  skin  diabetes
0         True  False  True      True
1         True   True  True      True
2         True   True  True      True
3         True   True  True      True
4         True   True  True      True
..         …     …   …       …
763       True   True  True      True
764       True   True  True      True
765       True   True  True      True
766       True   True  True      True
767       True   True  True      True

[768 rows x 10 columns]
```

[28]:
```
df = df.replace({'?': np.nan}).dropna()
```

[29]:
```
print (df.astype(str) != '?')
```

```
     num_preg  glucose_conc  diastolic_bp  thickness  insulin   bmi  \
1        True          True          True       True     True  True
2        True          True          True       True     True  True
```

```
3         True           True           True        True      True  True
4         True           True           True        True      True  True
5         True           True           True        True      True  True
..         …             …              …           …         …     …
763       True           True           True        True      True  True
764       True           True           True        True      True  True
765       True           True           True        True      True  True
766       True           True           True        True      True  True
767       True           True           True        True      True  True

     diab_pred   age  skin  diabetes
1         True  True  True      True
2         True  True  True      True
3         True  True  True      True
4         True  True  True      True
5         True  True  True      True
..         …    …     …          …
763       True  True  True      True
764       True  True  True      True
765       True  True  True      True
766       True  True  True      True
767       True  True  True      True

[767 rows x 10 columns]
```

Check Data Types

[31]:
```
df['diabetes']=df['diabetes'].map({True:1,False:0})
```

[32]:
```
df.head(5)
```

[32]:
```
   num_preg glucose_conc  diastolic_bp  thickness  insulin   bmi  diab_pred  \
1         1           85            66         29        0  26.6      0.351
2         8          183            64          0        0  23.3      0.672
3         1           89            66         23       94  28.1      0.167
4         0          137            40         35      168  43.1      2.288
5         5          116            74          0        0  25.6      0.201

  age    skin  diabetes
1  31  1.1426         0
2  32  0.0000         1
3  21  0.9062         0
4  33  1.3790         1
5  30  0.0000         0
```

[33]:
```
df.to_csv('Cleanning diabetes dataset.csv',sep=',',index=False)
```

[34]:
```
 #load Pima data. Adjust path as necesary
diabetes=pd.read_csv('Cleanning diabetes dataset.csv', delimiter=',')
diabetes.head()
```

[34]:

	num_preg	glucose_conc	diastolic_bp	thickness	insulin	bmi	diab_pred	age	skin	diabetes
0	1	85	66	29	0	26.6	0.351	31	1.1426	0
1	8	183	64	0	0	23.3	0.672	32	0.0000	1
2	1	89	66	23	94	28.1	0.167	21	0.9062	0
3	0	137	40	35	168	43.1	2.288	33	1.3790	1
4	5	116	74	0	0	25.6	0.201	30	0.0000	0

0.1.2 Data Split

[49]:
```
from sklearn.model_selection import train_test_split


X=df[['num_preg','glucose_conc','diastolic_bp','thickness','insulin','bmi','diab_pred','age']]
Y=df['diabetes']

X_train, X_test, y_train, y_test=train_test_split(X,Y, test_size=0.
 ↪20,random_state=0)
```

[50]:
```
from sklearn.preprocessing import StandardScaler
sc_X=StandardScaler()
X_train=sc_X.fit_transform(X_train)
X_test=sc_X.fit_transform(X_test)
```

[56]:
```
X_train
```

[56]:
```
array([[ 0.06649666,  1.92987383, -3.48834088, …, -0.47057917,
        -0.76640618,  0.23925174],
       [ 0.06649666, -0.69487691,  0.35552546, …, -1.13518625,
        -0.7345974 , -1.04800381],
       [ 1.5541774 ,  0.0862989 ,  0.05206233, …,  0.4240842 ,
        -0.56398668,  0.06761766],
       …,
       [ 0.9591051 , -0.22617143, -0.25140081, …, -0.59838823,
         0.73728155,  0.06761766],
       [ 0.66156896,  0.11754593,  0.35552546, …,  0.21958971,
        -1.02955153,  1.78395839],
```

```
       [-0.52857564,  0.24253406,  0.25437108, …,  0.14290428,
         0.32955084, -0.70473566]])
```

[113]:
```
from sklearn.svm import SVC
svm = SVC(C=4)
```

[114]:
```
svm.fit(X_train, y_train)
```

[114]:
```
SVC(C=4, break_ties=False, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='scale', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

[115]:
```
print('The accuracy on the training subset: {:.3f}'.format(svm.score(X_train,␣
 ↪y_train)))
print('The accuracy on the test subset: {:.3f}'.format(svm.score(X_test,␣
 ↪y_test)))
```

```
The accuracy on the training subset: 0.856
The accuracy on the test subset: 0.773
```

[102]:
```
from sklearn.externals import joblib
```

[103]:
```
joblib.dump(svm,'diabetes')
```

[103]:
```
['diabetes']
```

[42]:
```
clf=joblib.load('diabetes')
```

[44]:
```
data=clf.predict([[1,70,3,4,5,6,7,8]])
for i in range(1):
    if(data[i]==1):
        print("diabetes")

    elif(data[i]==0):
        print("Has No Diabetes")
```

```
has no diabetes
```