Q-1 Select a dataset or datasets of your choice.

- Apply a classification algorithm and then evaluate the classification model as it is done in "classification_metrics.ipynb".

source: http://archive.ics.uci.edu/ml/datasets/Wine+Quality (http://archive.ics.uci.edu/ml/datasets/Wine+Quality)

clas·si·fi·ca·tion

The action or process of classifying something according to shared qualities or characteristics.

More »

In [58]:

```
#from IPython.core.interactiveshell
#InteractiveShell.ast_node_interact
```

In [59]:

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn import metrics

% matplotlib inline

from IPython.core.display import display, HTML
display(HTML("<style>.container { width:90% !important; }</style
>"))
pd.set_option('display.max_columns', 100)
```

In [60]:

```
df = pd.read_csv('winequality-red.csv')
```

In [61]:

```
df.sample(5)
```

Out[61]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH
715	7.2	0.49	0.18	2.7	0.069	13.0	34.0	0.99670	3.29
27	7.9	0.43	0.21	1.6	0.106	10.0	37.0	0.99660	3.17
1028	7.2	0.34	0.21	2.5	0.075	41.0	68.0	0.99586	3.37
1160	10.6	0.36	0.57	2.3	0.087	6.0	20.0	0.99676	3.14
431	7.8	0.55	0.35	2.2	0.074	21.0	66.0	0.99740	3.25

In [62]:

```
# quality over 5, normalizing quality to binary
df['overfive'] = (df.quality > 5).astype(int)
```

In [63]:
```
df.sample(5)
```

Out[63]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH
262	8.0	0.520	0.03	1.7	0.070	10.0	35.0	0.99575	3.34
44	6.8	0.670	0.02	1.8	0.050	5.0	11.0	0.99620	3.48
710	10.6	1.025	0.43	2.8	0.080	21.0	84.0	0.99850	3.06
388	7.8	0.460	0.26	1.9	0.088	23.0	53.0	0.99810	3.43
1528	7.9	0.290	0.49	2.2	0.096	21.0	59.0	0.99714	3.31

In [64]:
```
X = df.iloc[:,0:-2]
y = df.iloc[:,-1]
```

In [65]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, random
_state=0)
```

In [66]:
```
from sklearn.linear_model import LogisticRegression
logreg = LogisticRegression()
logreg.fit(X_train, y_train)
y_pred_class = logreg.predict(X_test)
#y_pred_class predicts 1 and 0
```

Out[66]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_i
ntercept=True,
          intercept_scaling=1, max_iter=100, multi_class='ov
r', n_jobs=1,
          penalty='l2', random_state=None, solver='liblinear',
tol=0.0001,
          verbose=0, warm_start=False)
```

In [67]:
```
from sklearn import metrics
print(metrics.accuracy_score(y_test, y_pred_class))
```

```
0.7575
```

In [68]:
```
y_test.value_counts()

max(y_test.mean(), 1-y_test.mean())

# calculating null accuracy
y_test.value_counts().head(1)/len(y_test)
```

Out[68]:
```
1    215
0    185
Name: overfive, dtype: int64
```

Out[68]:
```
0.5375
```

Out[68]:
```
1    0.5375
Name: overfive, dtype: float64
```

confusion matrix

In [69]:
```
confusion = metrics.confusion_matrix(y_test, y_pred_class)
TP = confusion[1, 1]
TN = confusion[0, 0]
FP = confusion[0, 1]
FN = confusion[1, 0]

# TN FP  - (T)specificity  (F) false positive
# FN TP  - (T)sensitivity
#     * precision

print(confusion)
```

```
[[134  51]
 [ 46 169]]
```

In [70]:
```
# classification error = Total false / Total true
print((FP + FN) / float(TP + TN + FP + FN))
print(1 - metrics.accuracy_score(y_test, y_pred_class))
```

```
0.2425
0.2425
```

In [71]:
```
# sensitivity (aka: true positive rate)
print(TP / float(TP + FN))
print(metrics.recall_score(y_test, y_pred_class))
```

```
0.786046511628
0.786046511628
```

In [72]:
```
# specificity (true negative)
print(TN / float(TN + FP))
```

```
0.724324324324
```

In [73]:
```
# false positive rate
print(FP / float(TN + FP))
```

```
0.275675675676
```

In [74]:
```
# precision
print(TP / float(TP + FP))
print(metrics.precision_score(y_test, y_pred_class))
```

```
0.768181818182
0.768181818182
```

Logistic regression - adjusting classificiation threshold

In [75]:
```
y_pred_class[0:10]
logreg.predict(X_test)[0:10]
```

Out[75]:
```
array([1, 0, 1, 0, 1, 0, 0, 1, 0, 0])
```

Out[75]:
```
array([1, 0, 1, 0, 1, 0, 0, 1, 0, 0])
```

In [76]:
```
logreg.predict_proba(X_test)[0:10,:]
```

Out[76]:
```
array([[ 0.31610978,  0.68389022],
       [ 0.73174635,  0.26825365],
       [ 0.06517001,  0.93482999],
       [ 0.59212302,  0.40787698],
       [ 0.28622327,  0.71377673],
       [ 0.84859946,  0.15140054],
       [ 0.56828991,  0.43171009],
       [ 0.2291421 ,  0.7708579 ],
       [ 0.83836126,  0.16163874],
       [ 0.85135368,  0.14864632]])
```

In [77]:
```
y_pred_prob = logreg.predict_proba(X_test)[:, 1]
y_pred_prob[0:10]
```

Out[77]:
```
array([ 0.68389022,  0.26825365,  0.93482999,  0.40787698,  0.
71377673,
        0.15140054,  0.43171009,  0.7708579 ,  0.16163874,  0.
14864632])
```

In [78]:
```
# histogram of predicted probabilities
plt.hist(y_pred_prob, bins=8)
plt.xlim(0, 1)
plt.title('Histogram of predicted probabilities')
plt.xlabel('Predicted probability of diabetes')
plt.ylabel('Frequency')
```

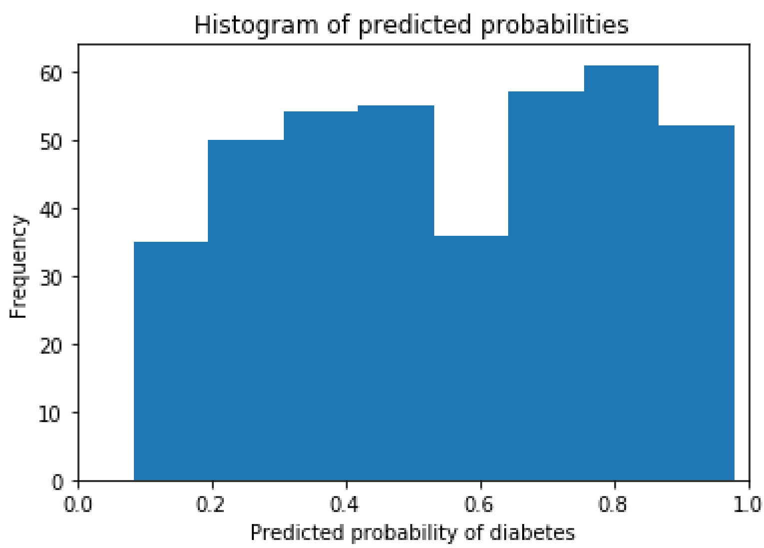
Out[78]:
```
(array([ 35.,  50.,  54.,  55.,  36.,  57.,  61.,  52.]),
 array([ 0.08312215,  0.19512717,  0.30713219,  0.41913722,
0.53114224,
        0.64314726,  0.75515229,  0.86715731,  0.97916233]),
 <a list of 8 Patch objects>)
```

Out[78]:
```
(0, 1)
```

Out[78]:
```
Text(0.5,1,'Histogram of predicted probabilities')
```

Out[78]:
```
Text(0.5,0,'Predicted probability of diabetes')
```

Out[78]:
```
Text(0,0.5,'Frequency')
```



In [79]:
```
from sklearn.preprocessing import binarize
y_pred_class = binarize([y_pred_prob], 0.3)[0]
```

In [80]:
```
print(confusion)
```

```
[[134  51]
 [ 46 169]]
```

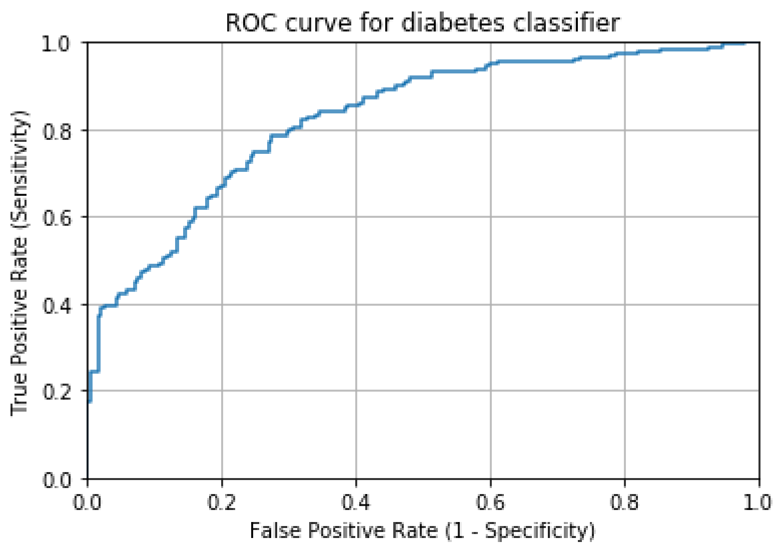
In [81]:
```
# new confusion matrix based on 0.3
print(metrics.confusion_matrix(y_test, y_pred_class))
```

```
[[ 73 112]
 [ 11 204]]
```

ROC Curve

In [82]:
```
fpr, tpr, thresholds = metrics.roc_curve(y_test, y_pred_prob)
plt.plot(fpr, tpr)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.0])
plt.title('ROC curve for diabetes classifier')
plt.xlabel('False Positive Rate (1 - Specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')
plt.grid(True)
```

```
Out[82]: [<matplotlib.lines.Line2D at 0x114fd69e8>]
Out[82]: (0.0, 1.0)
Out[82]: (0.0, 1.0)
Out[82]: Text(0.5,1,'ROC curve for diabetes classifier')
Out[82]: Text(0.5,0,'False Positive Rate (1 - Specificity)')
Out[82]: Text(0,0.5,'True Positive Rate (Sensitivity)')
```



In [83]:
```
# define a function that accepts a threshold and prints sensitiv
ity and specificity
def evaluate_threshold(threshold):
    print('Sensitivity:', tpr[thresholds > threshold][-1])
    print('Specificity:', 1 - fpr[thresholds > threshold][-1])
```

In [84]:
```
evaluate_threshold(0.5)
```

```
Sensitivity: 0.786046511628
Specificity: 0.724324324324
```

In [85]:
```
print(metrics.roc_auc_score(y_test, y_pred_prob))
```

```
0.824915147706
```

In [86]:
```
from sklearn.cross_validation import cross_val_score
cross_val_score(logreg, X, y, cv=10, scoring='roc_auc').mean()
```

```
Out[86]: 0.81084804229674268
```