Logistic Regression Project INSE 6220

April 14, 2018

1 Logistic Regression

In this project we will be working with a The Breast Dataset, indicating whether a patient has breat cancer or not. Thus, we will try to create a logistic regression model that will make the classification of future patients.

This data set contains the following features:

- 'Sample code number': id number
- 'Clump Thickness': 1 - 10
- 'Uniformity of Cell Shape': 1 - 10
- 'Marginal Adhesion': 1 - 10
- 'Single Epithelial Cell Size': 1 - 10
- 'Bare Nuclei': 1 - 10
- 'Bland Chromatin': 1 - 10
- 'Normal Nucleoli': 1 - 10
- 'Mitoses': 1 - 10
- 'Class': (2 for benign, 4 for malignant)

1.1 Import Libraries

Import a few libraries you think you'll need (Or just import them as you go along!)

```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        import seaborn as sns

        %matplotlib inline
```

1.2 Get the Data

Read in the Breast.xlsx file and set it to a data frame called ad_data.

```
In [2]: ad_data = pd.read_excel('Breast.xlsx')
```

Check the head of ad_data

```
In [3]: ad_data.head()
```

```
Out[3]:         ID  X1  X3  X4  X5  X6  X7  X8  Class
        0  1000025   5   1   1   2   1   3   1      2
        1  1015425   3   1   1   2   2   3   1      2
        2  1016277   6   8   1   3   4   3   7      2
        3  1017023   4   1   3   2   1   3   1      2
        4  1017122   8  10   8   7  10   9   7      4
```

** Use info and describe() on ad_data**

```
In [4]: ad_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 629 entries, 0 to 628
Data columns (total 9 columns):
ID       629 non-null int64
X1       629 non-null int64
X3       629 non-null int64
X4       629 non-null int64
X5       629 non-null int64
X6       629 non-null int64
X7       629 non-null int64
X8       629 non-null int64
Class    629 non-null int64
dtypes: int64(9)
memory usage: 44.3 KB
```

```
In [8]: ad_data[['X1', 'X3', 'X4','X5', 'X6','X7', 'X8', 'Class']].describe()
```

```
Out[8]:              X1          X3          X4          X5          X6          X7  \
        count  629.000000  629.000000  629.000000  629.000000  629.000000  629.000000
        mean     4.496025    3.275040    2.914149    3.289348    3.610493    3.507154
        std      2.864576    3.005149    2.928382    2.252860    3.663291    2.471886
        min      1.000000    1.000000    1.000000    1.000000    1.000000    1.000000
        25%      2.000000    1.000000    1.000000    2.000000    1.000000    2.000000
        50%      4.000000    2.000000    1.000000    2.000000    1.000000    3.000000
        75%      6.000000    5.000000    4.000000    4.000000    7.000000    5.000000
        max     10.000000   10.000000   10.000000   10.000000   10.000000   10.000000

                     X8       Class
        count  629.000000  629.000000
        mean     2.958665    2.731320
        std      3.121970    0.963996
        min      1.000000    2.000000
        25%      1.000000    2.000000
        50%      1.000000    2.000000
        75%      4.000000    4.000000
        max     10.000000    4.000000
```

1.3 Exploratory Data Analysis

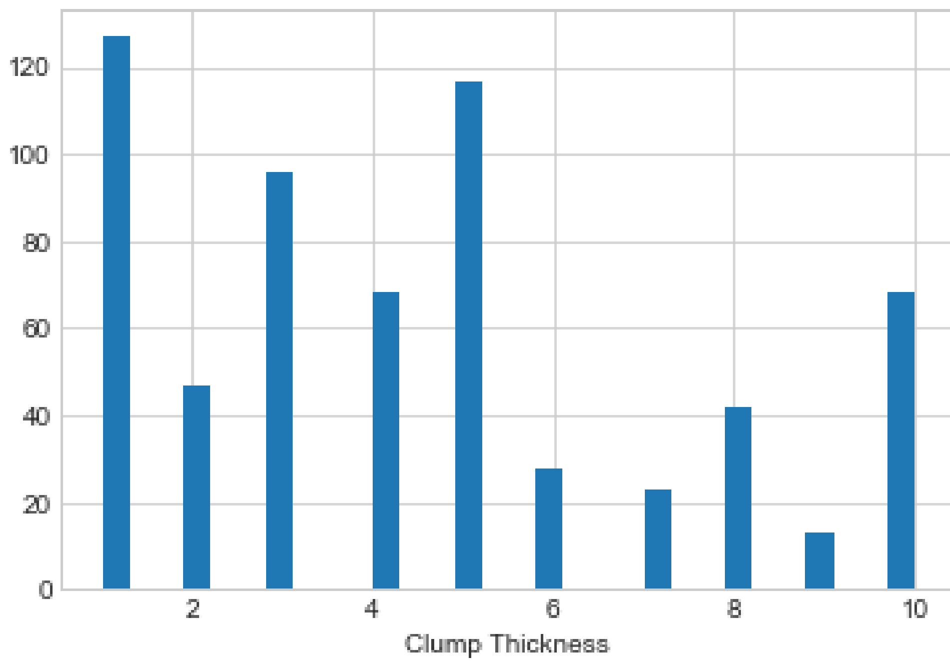
Let's use seaborn to explore the data!

Try recreating the plots shown below!

** Create a histogram of the Clump Thickness**

```
In [6]: sns.set_style('whitegrid')
        ad_data['X1'].hist(bins=30)
        plt.xlabel('Clump Thickness')
```

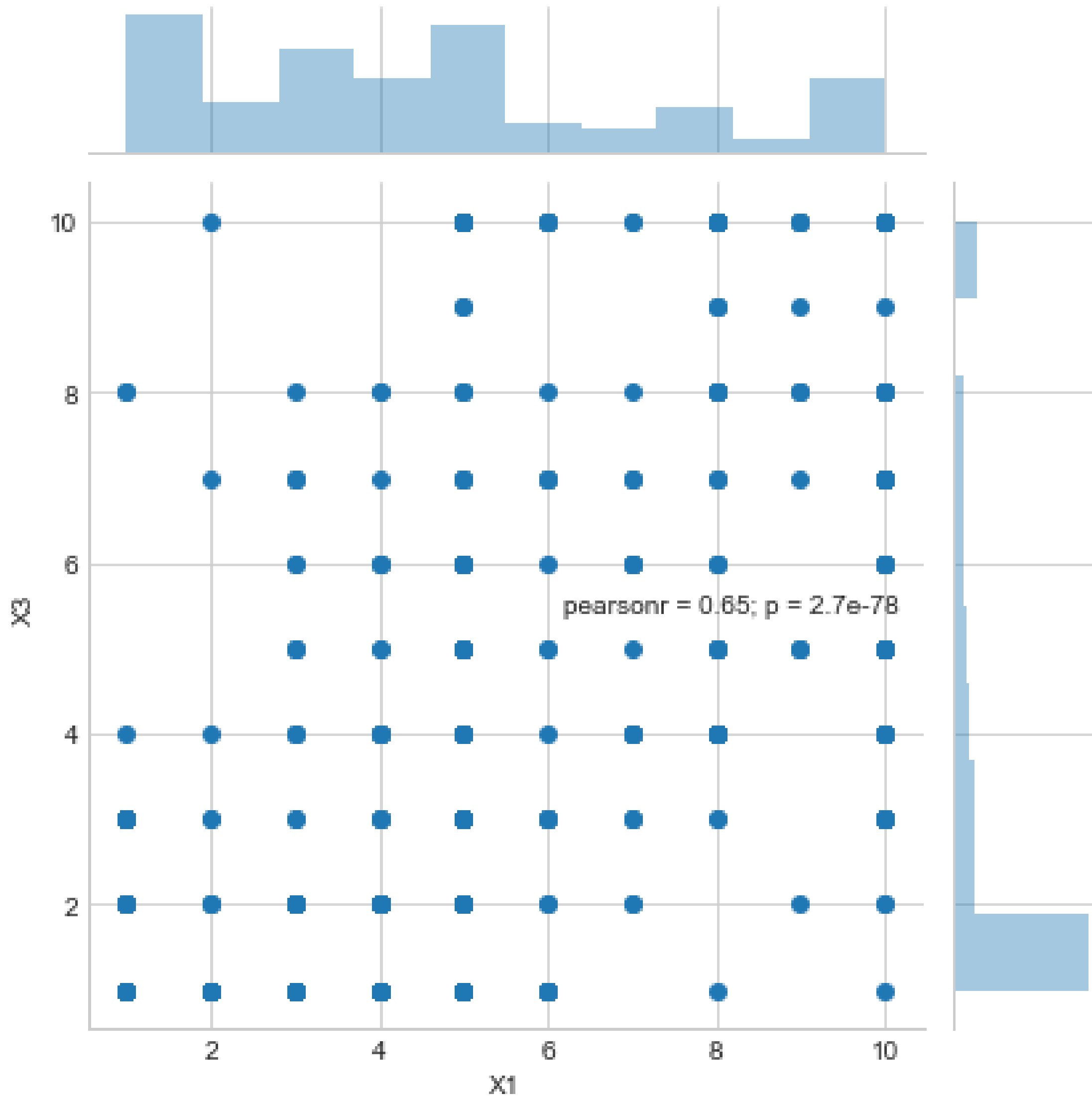
```
Out[6]: Text(0.5,0,'Clump Thickness')
```



Create a jointplot showing Clump Thickness versus Uniformity of Cell Shape.

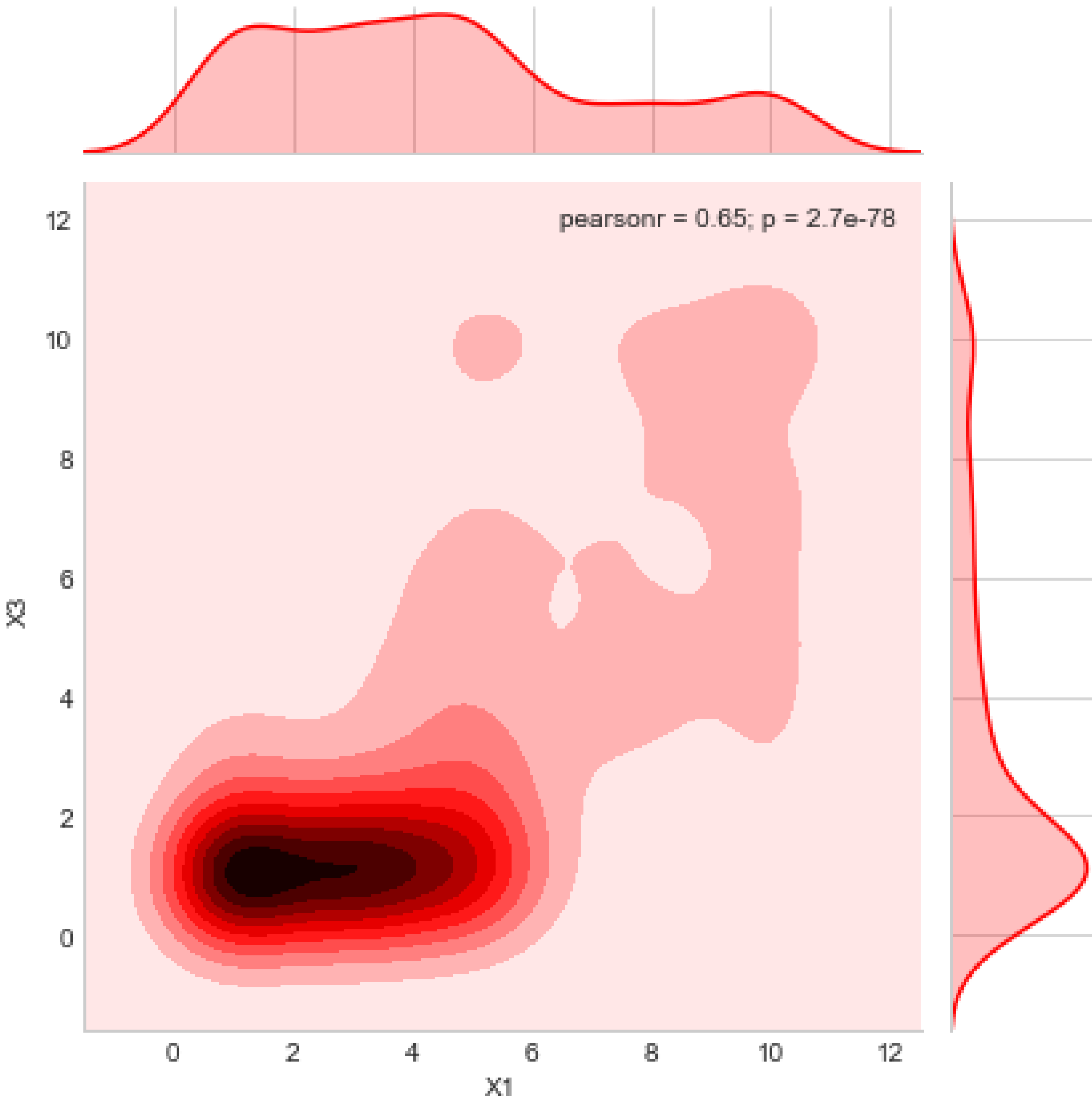
```
In [7]: sns.jointplot(x='X1',y='X3',data=ad_data)
```

```
Out[7]: <seaborn.axisgrid.JointGrid at 0x17c59772978>
```



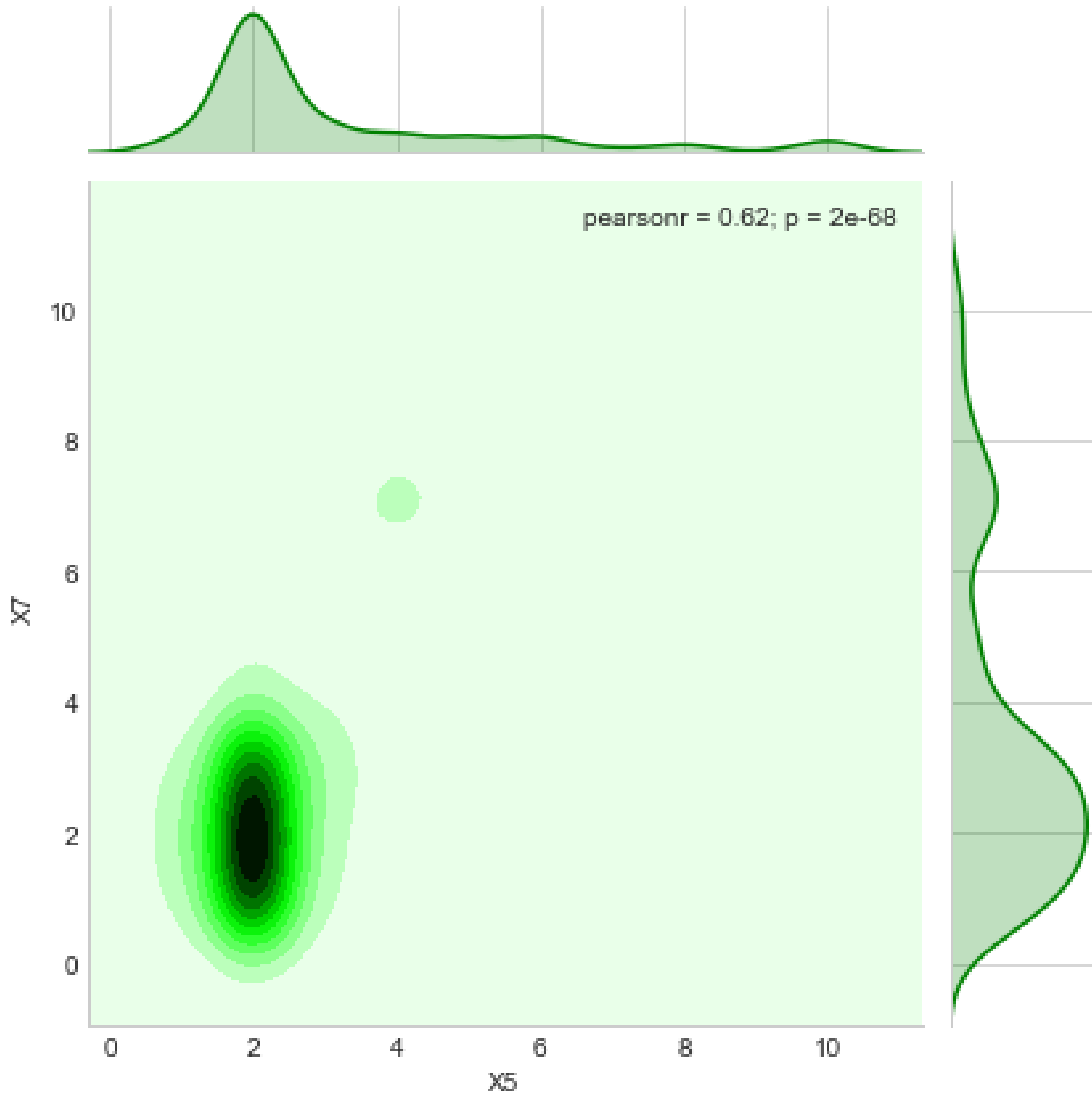
Create a jointplot showing the kde distributions of Clump Thickness on site vs. Uniformity of Cell Shape.

```
In [8]: sns.jointplot(x='X1',y='X3',data=ad_data,color='red',kind='kde');
```



** Create a jointplot of 'Single Epithelial Cell Size' vs. 'Bland chromatin'**

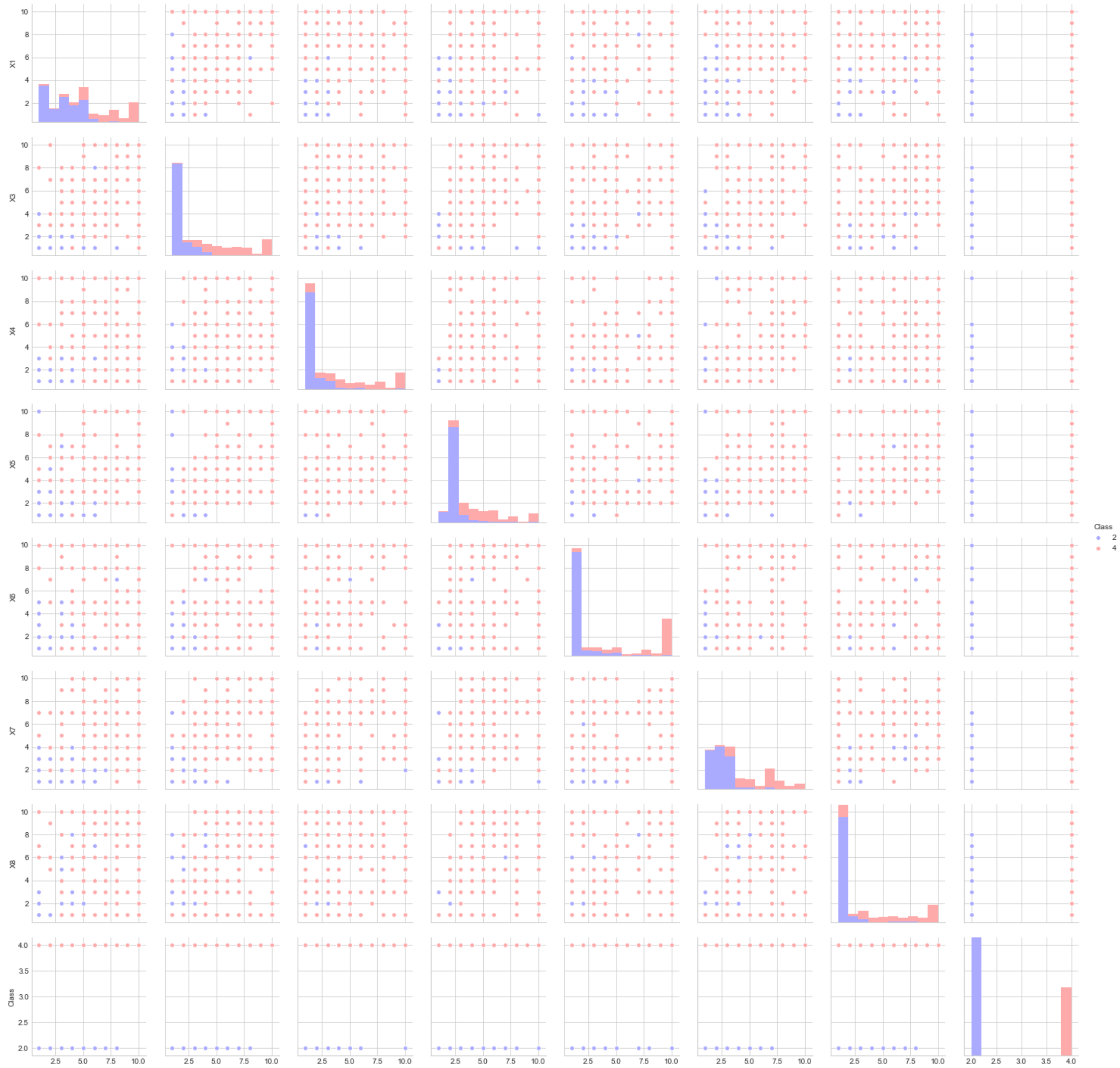
```
In [9]: sns.jointplot(x='X5',y='X7',data=ad_data,color='green',kind='kde')

Out[9]: <seaborn.axisgrid.JointGrid at 0x17c5ce3c668>
```



** Finally, create a pairplot with the hue defined by the 'Clicked on Ad' column feature.**

```
In [10]: sns.pairplot(ad_data[['X1', 'X3', 'X4','X5', 'X6','X7', 'X8', 'Class']],hue='Class',pal
```

```
Out[10]: <seaborn.axisgrid.PairGrid at 0x17c5d599908>
```



2 Logistic Regression

It's time to do a train test split, and train our model!

** Split the data into training set and testing set using train_test_split**

```
In [29]: from sklearn.model_selection import train_test_split
```

```
In [30]: X = ad_data[['X1', 'X3', 'X4','X5', 'X6','X7', 'X8']]
         y = ad_data['Class']
```

```
In [31]: X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=4
         X_test.head()
```

```
Out[31]:      X1  X3  X4  X5  X6  X7  X8
         494   2   1   1   1   1   1   1
         244   8   7   1   3  10   3   9
         551   5   1   1   2   1   1   1
         213   1   1   1   1   1   3   1
         532   5   1   1   2   1   1   1
```

** Train and fit a logistic regression model on the training set.**

```
In [32]: from sklearn.linear_model import LogisticRegressionCV
```

```
In [33]: logmodel = LogisticRegressionCV(cv=10)
         logmodel.fit(X_train,y_train)
```

```
Out[33]: LogisticRegressionCV(Cs=10, class_weight=None, cv=10, dual=False,
                    fit_intercept=True, intercept_scaling=1.0, max_iter=100,
                    multi_class='ovr', n_jobs=1, penalty='l2', random_state=None,
                    refit=True, scoring=None, solver='lbfgs', tol=0.0001, verbose=0)
```

2.1 Predictions and Evaluations

** Now predict values for the testing data.**

```
In [34]: predictions = logmodel.predict(X_test)
         logPred=logmodel.predict(X)
         logPred=logPred.tolist()
         y=y.tolist()
         #logmodel.score(logmodel.predict(X),y)
```

** Create a classification report for the model.**

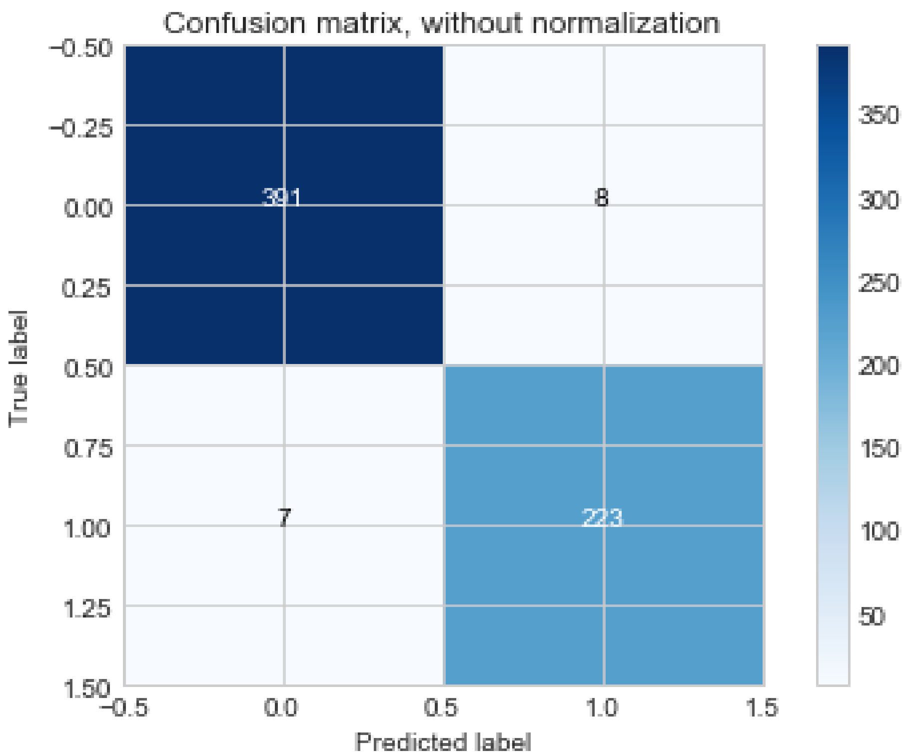
```
In [35]: from sklearn.metrics import classification_report
         from itertools import cycle
```

```
In [36]: print(classification_report(y_test,predictions))

             precision    recall  f1-score   support

          2       0.99      0.98      0.98       121
          4       0.96      0.99      0.97        68

avg / total       0.98      0.98      0.98       189
```

```
In [37]: ###Confusion matrix with sklearn
         import itertools
         from sklearn.metrics import confusion_matrix, roc_curve, roc_auc_score
         cnf_matrix = confusion_matrix(y,logPred)
```

In [38]:
```python
## Confusion matrix plot
def plot_confusion_matrix(cm,normalize=False,
                          title='Confusion matrix',
                          cmap=plt.cm.Blues):
    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """
    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")
    else:
        print('Confusion matrix, without normalization')

    print(cm)

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()

    fmt = '.2f' if normalize else 'd'
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.tight_layout()
    plt.ylabel('True label')
    plt.xlabel('Predicted label')

## Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix,
                      title='Confusion matrix, without normalization')
```

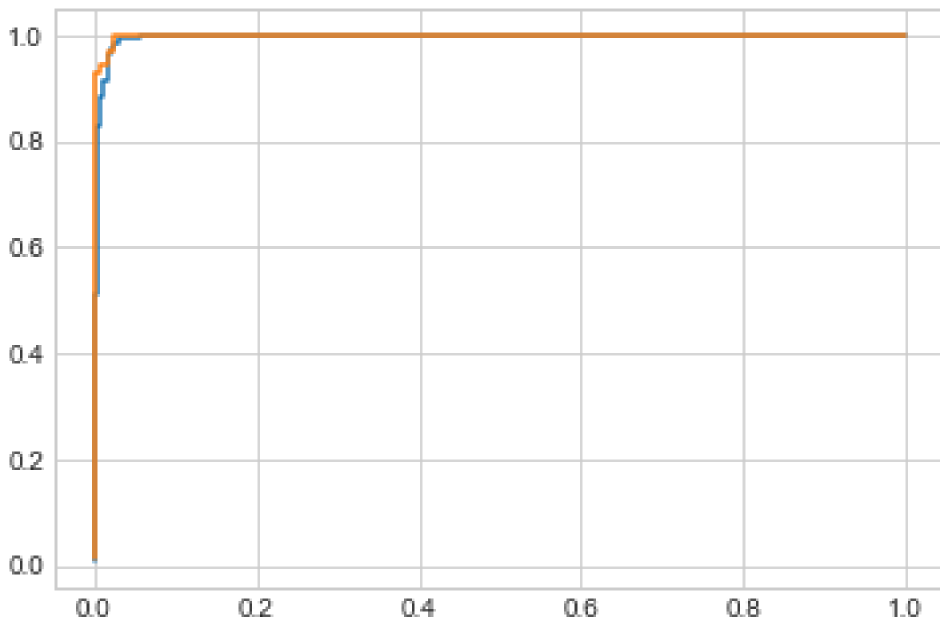
```
Confusion matrix, without normalization
[[391   8]
 [  7 223]]
```



In [48]:
```
from sklearn import preprocessing
##Computing false and true positive rates

lb = preprocessing.LabelBinarizer()
y_train = np.asarray(y_train)
y_train=lb.fit_transform(y_train)
y_test = np.asarray(y_test)
y_test=lb.fit_transform(y_test)


train_probs = logmodel.predict_proba(X_train)[:,1]
test_probs = logmodel.predict_proba(X_test)[:,1]


train_probs
auc_train = roc_auc_score(y_train, train_probs)
auc_test = roc_auc_score(y_test, test_probs)

print('Auc_train: {}'.format(auc_train))
print('Auc_test: {}'.format(auc_test))

roc_train = roc_curve(y_train, train_probs)
```

```
roc_test = roc_curve(y_test, test_probs)

plt.plot(roc_train[0], roc_train[1])

plt.plot(roc_test[0], roc_test[1])
plt.show()
```

```
Auc_train: 0.9961142197353229
Auc_test: 0.9986631016042781
```



2.2 End!