Results

December 15, 2016

1 Sepsis scoring system and mortality prediction

This analysis has two main goals (phases as Byron specified in his requirements)

In the first phase we are deploying a battery of machine learning algorithm to understand the data generated in the lab. There are several points of interests and questions to answer to, may be the more important ones are :

- Is it possible to predict mortality ? and if yes, can we do it accurately ?
- What are the most important features from the dataset ?
- Is the scoring system objective enough in predicting the outcome

In the second phase we focus back on the data to dig for cutoffs. This phase make sense only if we reduce the number of features to the most important ones, AND if the features have a direct effect on the outcome.

In this report, we will go through the details of the methodology as well as the results generated.

Details about the fundamental differences between the different algorithms used will not be discussed here, to make this report as intuitive as possible, if there is need for algorithmic explanation I will be happy to provide this

2 Datasets

We had initially two types of datasets in this study, **horizontal** data set, with mice per row and visit per columns, and a **vertical** dataset with each visit/mouse per row. In order to use machine learning approaches to study these datasets we need data, more data. With this in mind, the usage of the horizontal dataset will be constraining as we will end up with very few instances to work with. We will be using the vertical dataset to increase the predictive power of our models. We will make an **assumption** that each row is independent, even if it is a different visit for the same mouse. The purpose especially for the first phase is to study the combination of different features on the final outcome, which makes this assumption reasonable. Besides, the dataset contains a lot of **missing records** which forces us to handle these missing data either by removing entirely the rows having missing data as they will not be useful for the model, or do what we call **imputation** replacing these missing values by the average of a particular feature.

> spoiler : I played with the data and realized there is a lot of data to be imputed, which introduces a bias to the final model, thus I removed the rows with one or more missing data, the reduction in size is not dramatic in some cases

3 Phase 1 : predicting mortality

3.1 Methodology

The approach we adopted for the analysis of this dataset follows a standard methodology used in machine learning. We first begin by looking at the data, from a descriptive perspective, then we try to visualize the dataset in order to have a general idea on the trends if any.

In order to apply any machine learning algorithm, we need to transform the data into a format that will minimize the error propagation due to the difference in the way different features were measured and reported. We apply several techniques like rescaling and normalization. This step is necessary to make sure our models are accurate and **generalizable.**

> a model is generalizable when it predicts accurately on a new and unknown dataset

We then need to take a look at our features one by one. We need to know what feature combination impacts the most the performance of our models. To do that, several techniques for feature selection exist, and we will apply some of them to our dataset in order to pick the most important ones to use in our models.

> Feature selection by itself is a research field. CHosing the right feature selection algorithm is very important. There are 3 types classes of feature selection approaches : **filter methods** that consider all features independent and apply statistical tests and methods to assign a scoring to each feature, **wrapper methods** that consider the selection of a set of features as a search problem, and evalustae feature importance based on a model accuracy and finally **embedded methods** that learns feature importance while building the model

We will mainly be doing classification in this analysis, but we might do some regression as well. We will be applying different approaches to our data and measure the accuracy of our models to pick the winning solution.

It is an optimization analysis as we study different types of features reduction combined with different classification algorithms to benchmark and pick the most accurate combination.

The general approach in this notebook is summarized in the figure below:

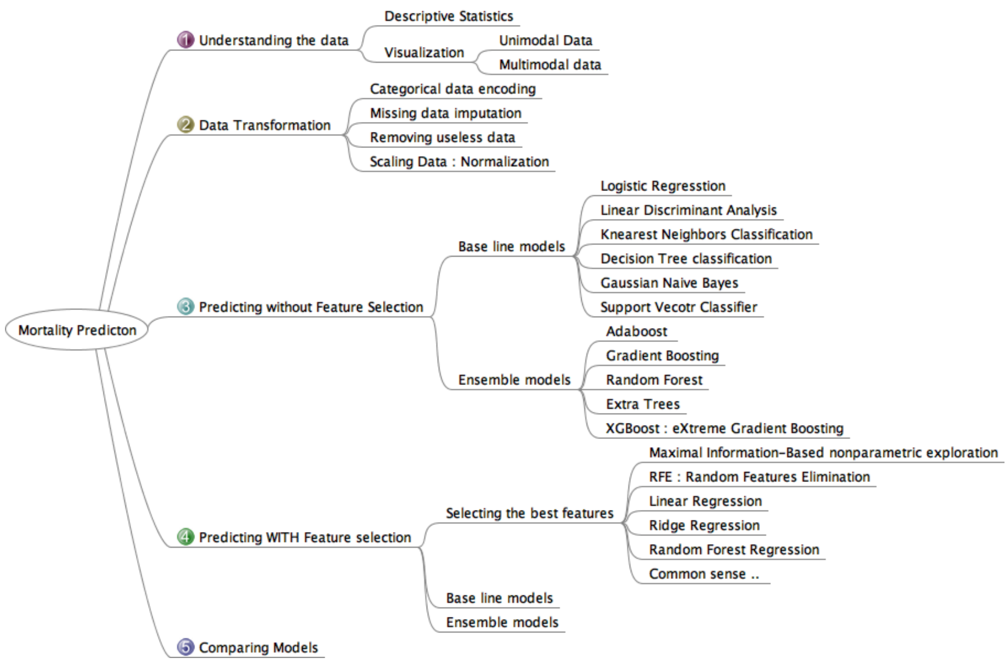
There are 4 notebooks that are exactely similar with this report, only data and results change. We will be using in this report the first dataset with full data, and no BCG as a template to explain the different steps of the analysis, **a section at the end will summarize all the results we had with all the datasets**

3.2 Analysis Environment

This analysis was done using open source tools mainly.

- Python Anaconda
- Jupyter Notebook

I also used Tableau free edition for some visualizations.



approach

3.3 Understand the data

3.3.1 Descriptive Statistics

Let's start first by importing all libraries we need for the analysis, for reading the files, creating plots, performaing machine learning data analysis etc ..

```
In [1]: %matplotlib inline
        # Load libraries
        import numpy as np
        from numpy import arange
        from numpy import set_printoptions
        from matplotlib import pyplot as plt
        import seaborn as sns
        import pandas as pd
        from pandas import read_csv
        from pandas import set_option
        from pandas.tools.plotting import scatter_matrix
        from sklearn import preprocessing
        from sklearn.preprocessing import Imputer
        from sklearn.decomposition import PCA
        from sklearn.preprocessing import StandardScaler, MinMaxScaler, Normalizer
        from sklearn.model_selection import train_test_split
        from sklearn.model_selection import KFold
        from sklearn.model_selection import cross_val_score
        from sklearn.model_selection import GridSearchCV
        from sklearn.feature_selection import SelectKBest
        from sklearn.feature_selection import chi2
```

```python
from sklearn.feature_selection import RFE
from sklearn.feature_selection import f_regression
from sklearn.linear_model import LinearRegression
from sklearn.linear_model import Lasso
from sklearn.linear_model import ElasticNet
from sklearn.linear_model import Ridge
from sklearn.linear_model import Lasso
from sklearn.linear_model import RandomizedLasso
from sklearn.tree import DecisionTreeRegressor
from sklearn.ensemble import RandomForestRegressor
from sklearn.neighbors import KNeighborsRegressor
from sklearn.svm import SVR
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score, roc_curve, auc
from sklearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestRegressor
from sklearn.ensemble import GradientBoostingRegressor
from sklearn.ensemble import ExtraTreesRegressor
from sklearn.ensemble import AdaBoostRegressor
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import mean_squared_error
from string import letters
from sklearn.cross_validation import ShuffleSplit
from sklearn.metrics import r2_score
from collections import defaultdict
import pprint
from minepy import MINE

from sklearn import cross_validation
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.grid_search import GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
from sklearn.ensemble import AdaBoostClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import ExtraTreesClassifier
import xgboost

sns.set(style="white")
plt.rcParams['figure.figsize'] = (20.0, 10.0)
```

```
/Users/Rad/anaconda2/lib/python2.7/site-packages/matplotlib/font_manager.py:273: UserWarning: Ma
  warnings.warn('Matplotlib is building the font cache using fc-list. This may take a moment.')
/Users/Rad/anaconda2/lib/python2.7/site-packages/sklearn/cross_validation.py:44: DeprecationWarn
  "This module will be removed in 0.20.", DeprecationWarning)
/Users/Rad/anaconda2/lib/python2.7/site-packages/sklearn/grid_search.py:43: DeprecationWarning:
  DeprecationWarning)
```

Now let's create the function to read and load the data

```
In [2]: # Load the data set into a dataframe
        df = pd.read_csv('../data/excel_updates_danny/cs.mortality.vertical.full.nobcg.leftvrigh
```

```
In [3]: # Print dataset
        df.shape
```

```
Out[3]: (585, 44)
```

We have a dataset with 585 instances and 44 features
Let's take a look at the types of each attribute

```
In [4]: # Print data types for attributes

        pd.set_option('display.max_rows', 600)
        df.dtypes
```

```
Out[4]: pupID                                               object
        litter                                               int64
        sex                                                 object
        outcome                                             object
        challenge.time                                      object
        weight.challenge                                   float64
        weight                                             float64
        ch.weight                                          float64
        pch.weight                                         float64
        time                                                object
        hr.post.challenge                                  float64
        visit                                               object
        score.overall                                       object
        score.left                                          object
        score.right                                         object
        rights.mobile.overall                                int64
        rights.shakey.overall                                int64
        rights.lethargic.overall                             int64
        rights.nonmobile.overall                             int64
        fail_to_right.one.side.overall                       int64
        fail_to_right.mobile.hips.over                       int64
        fail_to_right.lethargic.hips.overall                 int64
        fail_to_right.lethargic.two.visits.overall           int64
```

```
fail_to_right.nonmobile.hips.overall            int64
rights.mobile.left                            float64
rights.shakey.left                            float64
rights.lethargic.left                         float64
rights.nonmobile.left                         float64
rights.only.left                              float64
fail_to_right.mobile.hips.left                float64
fail_to_right.lethargic.hips.left             float64
fail_to_right.lethargic.two.visits.left       float64
fail_to_right.nonmobile.hips.left             float64
rights.mobile.right                           float64
rights.shakey.right                           float64
rights.lethargic.right                        float64
rights.nonmobile.right                        float64
rightss.only.right                            float64
fail_to_right.mobile.hips.right               float64
fail_to_right.lethargic.hips.right            float64
fail_to_right.lethargic.two.visits.right      float64
fail_to_right.nonmobile.hips.right            float64
obs.found.dead                                  int64
observations                                   object
dtype: object
```

Let's take a look at the 20 first rows of the dataset

In [5]:
```
#print first 20 rows
df.head(20)
```

Out[5]:
```
                                      pupID  litter sex outcome challenge.time  \
0      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
1      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
2      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
3      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
4      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
5      2015.07.31_F1_M7 (M)_saline_old.0.8       1   M    live            NaN
6      2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
7      2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
8      2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
9      2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
10     2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
11     2015.07.31_F1_M8 (F)_saline_old.0.8       1   F    live            NaN
12     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
13     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
14     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
15     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
16     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
17     2015.07.31_F1_M9 (F)_saline_old.0.8       1   F    live            NaN
18  2015.07.31_G2.F2_M1 (M)_saline_old.1.1       2   M     die            NaN
```

```
19  2015.07.31_G2.F2_M1 (M)_saline_old.1.1       2   M     die            NaN

    weight.challenge  weight  ch.weight  pch.weight time       ...        \
0                NaN     NaN        NaN         NaN  NaN       ...
1                NaN     NaN        NaN         NaN  NaN       ...
2                NaN     NaN        NaN         NaN  NaN       ...
3                NaN     NaN        NaN         NaN  NaN       ...
4                NaN     NaN        NaN         NaN  NaN       ...
5                NaN     NaN        NaN         NaN  NaN       ...
6                NaN     NaN        NaN         NaN  NaN       ...
7                NaN     NaN        NaN         NaN  NaN       ...
8                NaN     NaN        NaN         NaN  NaN       ...
9                NaN     NaN        NaN         NaN  NaN       ...
10               NaN     NaN        NaN         NaN  NaN       ...
11               NaN     NaN        NaN         NaN  NaN       ...
12               NaN     NaN        NaN         NaN  NaN       ...
13               NaN     NaN        NaN         NaN  NaN       ...
14               NaN     NaN        NaN         NaN  NaN       ...
15               NaN     NaN        NaN         NaN  NaN       ...
16               NaN     NaN        NaN         NaN  NaN       ...
17               NaN     NaN        NaN         NaN  NaN       ...
18               NaN     NaN        NaN         NaN  NaN       ...
19               NaN     NaN        NaN         NaN  NaN       ...

    rights.shakey.right rights.lethargic.right rights.nonmobile.right  \
0                   NaN                    NaN                    NaN
1                   NaN                    NaN                    NaN
2                   NaN                    NaN                    NaN
3                   NaN                    NaN                    NaN
4                   NaN                    NaN                    NaN
5                   NaN                    NaN                    NaN
6                   NaN                    NaN                    NaN
7                   NaN                    NaN                    NaN
8                   NaN                    NaN                    NaN
9                   NaN                    NaN                    NaN
10                  NaN                    NaN                    NaN
11                  NaN                    NaN                    NaN
12                  NaN                    NaN                    NaN
13                  NaN                    NaN                    NaN
14                  NaN                    NaN                    NaN
15                  NaN                    NaN                    NaN
16                  NaN                    NaN                    NaN
17                  NaN                    NaN                    NaN
18                  NaN                    NaN                    NaN
19                  NaN                    NaN                    NaN

   rightss.only.right fail_to_right.mobile.hips.right  \
0                 NaN                             NaN
```

```
1                  NaN                                 NaN
2                  NaN                                 NaN
3                  NaN                                 NaN
4                  NaN                                 NaN
5                  NaN                                 NaN
6                  NaN                                 NaN
7                  NaN                                 NaN
8                  NaN                                 NaN
9                  NaN                                 NaN
10                 NaN                                 NaN
11                 NaN                                 NaN
12                 NaN                                 NaN
13                 NaN                                 NaN
14                 NaN                                 NaN
15                 NaN                                 NaN
16                 NaN                                 NaN
17                 NaN                                 NaN
18                 NaN                                 NaN
19                 NaN                                 NaN

    fail_to_right.lethargic.hips.right  \
0                                  NaN
1                                  NaN
2                                  NaN
3                                  NaN
4                                  NaN
5                                  NaN
6                                  NaN
7                                  NaN
8                                  NaN
9                                  NaN
10                                 NaN
11                                 NaN
12                                 NaN
13                                 NaN
14                                 NaN
15                                 NaN
16                                 NaN
17                                 NaN
18                                 NaN
19                                 NaN

    fail_to_right.lethargic.two.visits.right  \
0                                        NaN
1                                        NaN
2                                        NaN
3                                        NaN
4                                        NaN
```

```
5                                          NaN
6                                          NaN
7                                          NaN
8                                          NaN
9                                          NaN
10                                         NaN
11                                         NaN
12                                         NaN
13                                         NaN
14                                         NaN
15                                         NaN
16                                         NaN
17                                         NaN
18                                         NaN
19                                         NaN

    fail_to_right.nonmobile.hips.right  obs.found.dead  observations
0                                  NaN               0           NaN
1                                  NaN               0           NaN
2                                  NaN               0           NaN
3                                  NaN               0           NaN
4                                  NaN               0           NaN
5                                  NaN               0           NaN
6                                  NaN               0           NaN
7                                  NaN               0           NaN
8                                  NaN               0           NaN
9                                  NaN               0           NaN
10                                 NaN               0           NaN
11                                 NaN               0           NaN
12                                 NaN               0           NaN
13                                 NaN               0           NaN
14                                 NaN               0           NaN
15                                 NaN               0           NaN
16                                 NaN               0           NaN
17                                 NaN               0           NaN
18                                 NaN               0           NaN
19                                 NaN               0           NaN

[20 rows x 44 columns]
```

As we can see a lot of data is missing, we will deal with this later in our analysis
For now let's summarize the distribution of each attribute, not all of this is informative, as some text data is transformed automatically into numerical data, but we are more interested in the distribution of the attributes (features)

```
In [7]: pd.set_option('precision', 3)
        df.describe()
```

```
/Users/Rad/anaconda2/lib/python2.7/site-packages/numpy/lib/function_base.py:3834: RuntimeWarning
```

```
RuntimeWarning)
```

Out[7]:

```
        litter  weight.challenge   weight  ch.weight  pch.weight  \
count  585.000           553.000  406.000    406.000     406.000
mean    11.191             4.302    4.123     -0.053      -0.829
std      6.634             0.748    0.690      0.352       8.527
min      1.000             2.510    2.430     -1.960     -35.701
25%      4.000               NaN      NaN        NaN         NaN
50%     12.000               NaN      NaN        NaN         NaN
75%     17.000               NaN      NaN        NaN         NaN
max     25.000             5.930    5.930      0.890      32.271

       hr.post.challenge  rights.mobile.overall  rights.shakey.overall  \
count            585.000                585.000                585.000
mean              33.096                  0.256                  0.099
std               20.112                  0.437                  0.299
min               12.083                  0.000                  0.000
25%               18.167                  0.000                  0.000
50%               25.333                  0.000                  0.000
75%               42.417                  1.000                  0.000
max               96.000                  1.000                  1.000

       rights.lethargic.overall  rights.nonmobile.overall       ...         \
count                   585.000                   585.000       ...
mean                      0.229                     0.051       ...
std                       0.421                     0.221       ...
min                       0.000                     0.000       ...
25%                       0.000                     0.000       ...
50%                       0.000                     0.000       ...
75%                       0.000                     0.000       ...
max                       1.000                     1.000       ...

       rights.mobile.right  rights.shakey.right  rights.lethargic.right  \
count              532.000              532.000                 532.000
mean                 0.244                0.117                   0.250
std                  0.430                0.321                   0.433
min                  0.000                0.000                   0.000
25%                    NaN                  NaN                     NaN
50%                    NaN                  NaN                     NaN
75%                    NaN                  NaN                     NaN
max                  1.000                1.000                   1.000

       rights.nonmobile.right  rightss.only.right  \
count                 532.000             532.000
mean                    0.086               0.064
std                     0.281               0.245
min                     0.000               0.000
```

```
25%                         NaN                   NaN
50%                         NaN                   NaN
75%                         NaN                   NaN
max                       1.000                 1.000

       fail_to_right.mobile.hips.right  fail_to_right.lethargic.hips.right  \
count                          532.000                             532.000
mean                             0.107                               0.085
std                              0.310                               0.279
min                              0.000                               0.000
25%                                NaN                                 NaN
50%                                NaN                                 NaN
75%                                NaN                                 NaN
max                              1.000                               1.000

       fail_to_right.lethargic.two.visits.right  \
count                                   532.000
mean                                      0.011
std                                       0.106
min                                       0.000
25%                                         NaN
50%                                         NaN
75%                                         NaN
max                                       1.000

       fail_to_right.nonmobile.hips.right  obs.found.dead
count                             532.000         585.000
mean                                0.060           0.034
std                                 0.238           0.182
min                                 0.000           0.000
25%                                   NaN           0.000
50%                                   NaN           0.000
75%                                   NaN           0.000
max                                 1.000           1.000

[8 rows x 34 columns]
```

The table above is not that informative, there are a lot of missing values, and also categorical attributes that need to be converted

The most important thing we want to see here prior to starting any analysis is how balanced this dataset is, so we will try to take a look at the dsitribution of the outcome, which is the class we want to predict with the score

In [6]:
```
# class distribution
df.groupby('outcome').size()
```

Out[6]:
```
outcome
die              160
```

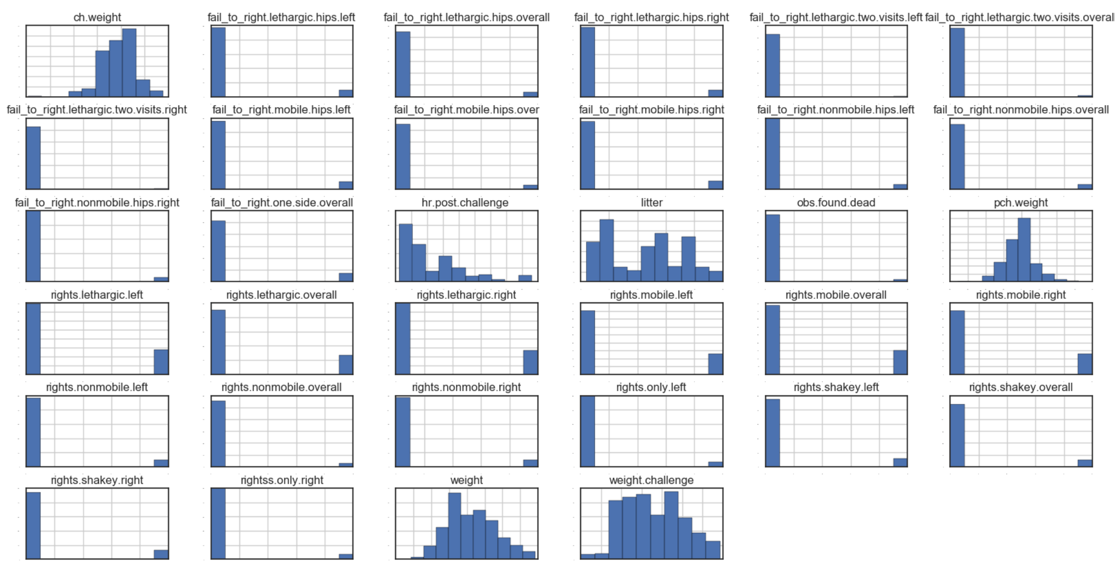
```
found.dead     93
live          332
dtype: int64
```

As we can see the class `live` is higher than the two other, but when we merge `found.dead` with `die` we can have a dataset that is more or less balanced. That said this is a general observation, things can change later when we transform the data.

3.3.2 Visualization

Unimodal Data Visualization Let's look at how the data looks like before any transformation. It is always useful to lok how different attributes are distributed.

```
In [8]: # histograms
        df.hist(sharex=False, sharey=False, xlabelsize=1, ylabelsize=1)
        plt.show()
```



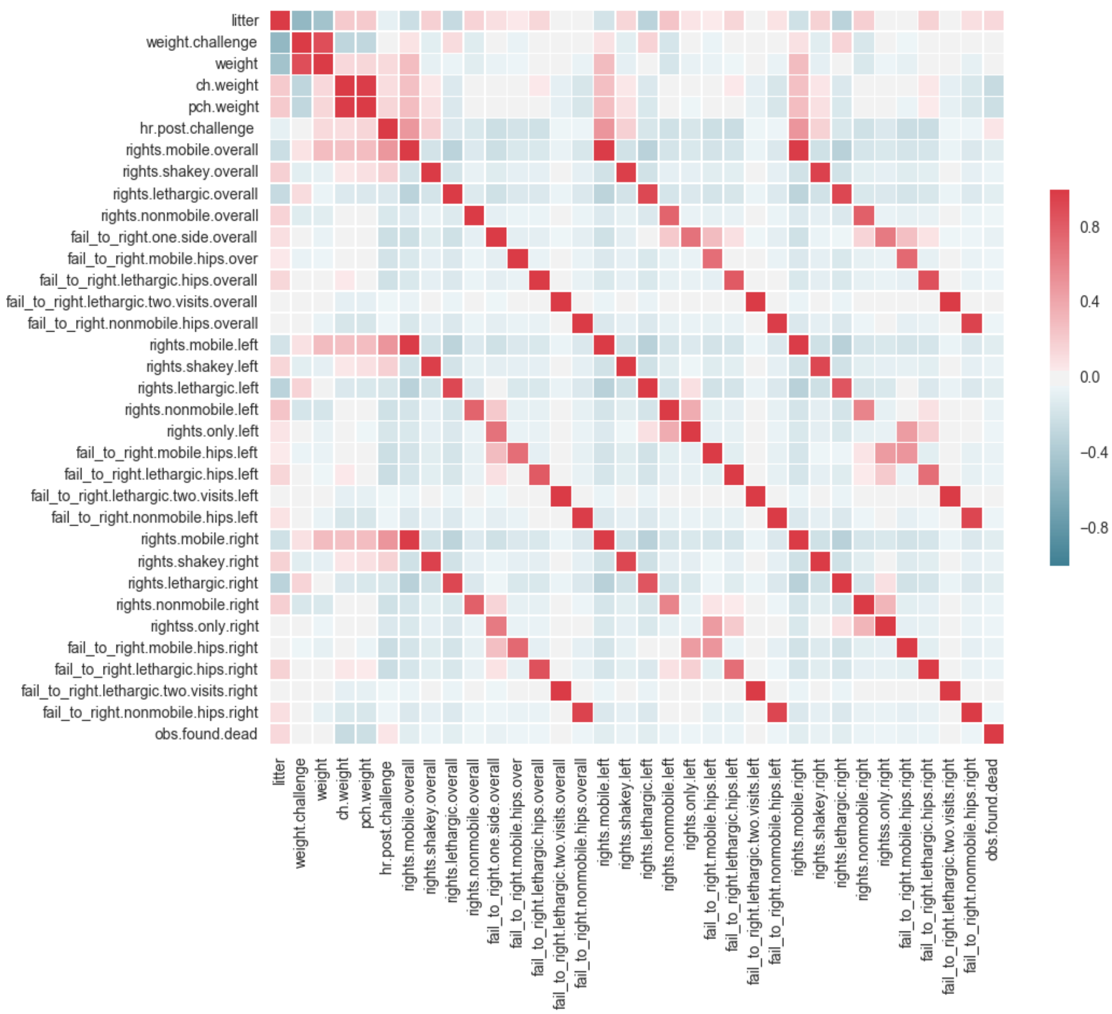
Because we have a lot of features that are 0/1 we don't get much out of this plot, except that all features/attributes related to `weight` seem to have a gaussian like distribution

Multimodal Data Visualization Let's see if we have attributes that correlate

```
In [9]: correlations = df.corr(method='pearson')
        correlations

        # Plot Correlations
        corr = df.corr()
        # Generate a mask for the upper triangle
        mask = np.zeros_like(corr, dtype=np.bool)
        mask[np.triu_indices_from(mask)] = False
```

```python
# Set up the matplotlib figure
f, ax = plt.subplots(figsize=(11, 9))
cmap = sns.diverging_palette(220, 10, as_cmap=True)
#for tick in ax.get_xticklabels():
#    tick.set_rotation(90)
# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr, mask=mask, cmap=cmap, vmax=1,
            square=True,
            linewidths=.5, cbar_kws={"shrink": .5}, ax=ax)
```

```
Out[9]: <matplotlib.axes._subplots.AxesSubplot at 0x11c02ab90>
```



As we can see we have a lot of diagonals in this dataset, which means not all these features are going to be included in the dataset when building the final model as we have a lot of correlations

We can already spot some positive correlation between the weight and the hours post challenges even if it is a slightly positive (not a strong correlation judging by the colors). There is also a correlation between the different weights features which makes sense, and also between the scores (left, right, overall)

The top left corner seems to have some useful information

Not all the algorithms deal with correlated features equally. Some algorithms like Naive Bayes assumes attributes independence, so it may behaves in an unexpected way, some other approaches like Support Vector Machines care about it much less.

One thing we can do here, is to take the decision to reduce the number of attributes by doing a **Principal Component Aanalysis**, squeezing features that are part of the same components, transform the original dataset and see what this will give us. This will make the part 2 hard to do, we have a small dataset, we will stick with the feature selection approach.

But first of all we will need to start doing some transformation to make sure we have all the features included, not only the numerical ones, so we will have to do some transformations.

Let's list all the features we have so far.

3.3.3 Data Transformation

Categorical Data Encoding

```
In [10]: list(df)
```

```
Out[10]: ['pupID',
          'litter',
          'sex',
          'outcome',
          'challenge.time',
          'weight.challenge',
          'weight',
          'ch.weight',
          'pch.weight',
          'time',
          'hr.post.challenge ',
          'visit',
          'score.overall',
          'score.left',
          'score.right',
          'rights.mobile.overall',
          'rights.shakey.overall',
          'rights.lethargic.overall',
          'rights.nonmobile.overall',
          'fail_to_right.one.side.overall',
          'fail_to_right.mobile.hips.over',
          'fail_to_right.lethargic.hips.overall',
          'fail_to_right.lethargic.two.visits.overall',
          'fail_to_right.nonmobile.hips.overall',
          'rights.mobile.left',
          'rights.shakey.left',
          'rights.lethargic.left',
          'rights.nonmobile.left',
          'rights.only.left',
          'fail_to_right.mobile.hips.left',
          'fail_to_right.lethargic.hips.left',
```

```
 'fail_to_right.lethargic.two.visits.left',
 'fail_to_right.nonmobile.hips.left',
 'rights.mobile.right',
 'rights.shakey.right',
 'rights.lethargic.right',
 'rights.nonmobile.right',
 'rightss.only.right',
 'fail_to_right.mobile.hips.right',
 'fail_to_right.lethargic.hips.right',
 'fail_to_right.lethargic.two.visits.right',
 'fail_to_right.nonmobile.hips.right',
 'obs.found.dead',
 'observations']
```

The features that we need to transform to numerical ones are : - sex - outcome
The ones we will drop that are not useful here are - pupId - Litter - observations

```
In [11]: df_clean = df.drop(['litter', 'pupID', 'visit', 'observations'], axis=1)
```

Let's now merge the **outcome** values corresponding to `die` and `found dead` to make a binary classification instead of having three classes

```
In [12]: df_clean.outcome = df_clean.outcome.str.replace("found.dead","die")
         df_clean.groupby('outcome').size()

Out[12]: outcome
         die     253
         live    332
         dtype: int64
```

This is a **balanced** enough dataset.
Now we need to codify the classes `live` and `die` with `0` and `1`

```
In [17]: # Verify code for the outcome
         zip(df_clean.outcome, pd.factorize(df_clean.outcome)[0])[15:20]

Out[17]: [('live', 0), ('live', 0), ('live', 0), ('die', 1), ('die', 1)]

In [18]: transformed_outcome = pd.factorize(df_clean.outcome)
         df_clean['outcome'] = transformed_outcome[0].astype(float)
```

Now we will do the same with `sex` attribute

```
In [20]: zip(df_clean.sex, pd.factorize(df_clean.sex)[0])
         transformed_sex = pd.factorize(df_clean.sex)
         df_clean['sex'] = transformed_sex[0].astype(float)
```

Now let's remove the time related attributes as we are not doing any time series analysis here

```
In [21]: df_clean = df_clean.drop(['challenge.time', 'time'], axis=1)
```

Three columns remain having `string` values while a number is expected, we will fix that by changing `FD == Found Dead` values into `0`

```
In [23]: df_clean['score.left'] = df_clean['score.left'].str.replace("FD","0").astype(float)
         df_clean['score.right'] = df_clean['score.right'].str.replace("FD","0").astype(float)
         df_clean['score.overall'] = df_clean['score.overall'].str.replace("FD","0").astype(floa
```

Missing Data Imputation As explained in the begining of this document, we decided to drop all rows with at least a missing value. I tested the imputation method with the mean value per column but it altered the shape of the format introducing a bias that can be dangerous for the final model

```
In [24]: #fill_NaN = Imputer(missing_values=np.nan, strategy='mean', axis=1)
         #imputed_DF = pd.DataFrame(fill_NaN.fit_transform(df_clean))
         #imputed_DF.columns = df_clean.columns
         #imputed_DF.index = df_clean.index

         imputed_DF = df_clean.dropna()
         imputed_DF.columns = df_clean.columns
         #imputed_DF.index = df_clean.index
```

```
In [25]: imputed_DF.head()
```

```
Out[25]:     sex  outcome  weight.challenge  weight  ch.weight  pch.weight  \
         32  0.0      1.0              4.31    3.56      -0.75     -17.401
         33  0.0      1.0              4.31    4.05      -0.26      -6.032
         35  0.0      1.0              4.31    4.33      -0.02      -0.464
         38  0.0      1.0              4.80    4.91      -0.11      -2.292
         39  0.0      1.0              4.80    4.24      -0.56     -11.667

             hr.post.challenge  score.overall  score.left  score.right  \
         32             35.150            0.0         0.0          0.0
         33             26.167            1.0         1.0          1.0
         35             12.333            6.0         6.0          6.0
         38             12.333            8.0         6.0          3.0
         39             35.150            0.0         0.0          5.0

                    ...          rights.mobile.right  rights.shakey.right  \
         32         ...                          0.0                  0.0
         33         ...                          0.0                  0.0
         35         ...                          0.0                  0.0
         38         ...                          0.0                  0.0
         39         ...                          0.0                  0.0

             rights.lethargic.right  rights.nonmobile.right  rightss.only.right  \
         32                     0.0                     0.0                 0.0
         33                     0.0                     0.0                 0.0
         35                     1.0                     0.0                 0.0
```

```
38                     0.0                      0.0                   0.0
39                     0.0                      1.0                   1.0

    fail_to_right.mobile.hips.right  fail_to_right.lethargic.hips.right  \
32                              0.0                                 0.0
33                              0.0                                 0.0
35                              0.0                                 0.0
38                              1.0                                 0.0
39                              0.0                                 0.0

    fail_to_right.lethargic.two.visits.right  \
32                                       0.0
33                                       1.0
35                                       0.0
38                                       0.0
39                                       0.0

    fail_to_right.nonmobile.hips.right  obs.found.dead
32                                 1.0               0
33                                 0.0               0
35                                 0.0               0
38                                 0.0               0
39                                 0.0               0

[5 rows x 38 columns]
```

In [26]:
```
#df_clean_no_nas = df_clean.dropna()
#0df_clean_no_nas.head()
df_clean_2 = imputed_DF
```

In [27]:
```
df_clean_2.groupby('outcome').size()
```

Out[27]:
```
outcome
0.0    228
1.0    164
dtype: int64
```

The drop of the missing value didnt affect the balance in the dataset with a slightly higher number of mice that lived

Now let's drop the outcome column as we will not be counting it as feature

In [28]:
```
df_final = df_clean_2.drop(['outcome', 'obs.found.dead'], axis=1)
```

Scaling Data : Normalization Now we need to compare apples to apples, we have different features with different scales we will reduce all the features to the same one by doing a data normalization

In [31]:
```
#df_scaled = preprocessing.scale(df_final)
scaler = StandardScaler().fit(df_final)
```

```
normalized_df = scaler.transform(df_final)
df_scaled_df = pd.DataFrame(normalized_df, columns = df_final.columns)
df_scaled_df.head()
```

```
Out[31]:      sex  weight.challenge  weight  ch.weight  pch.weight  hr.post.challenge  \
0 -1.047             0.103  -0.837     -1.959      -1.924              0.104
1 -1.047             0.103  -0.122     -0.586      -0.610             -0.368
2 -1.047             0.103   0.287      0.087       0.034             -1.095
3 -1.047             0.771   1.133     -0.165      -0.177             -1.095
4 -1.047             0.771   0.155     -1.427      -1.261              0.104

   score.overall  score.left  score.right  rights.mobile.overall  \
0         -1.994      -1.949       -1.956                 -0.589
1         -1.609      -1.573       -1.580                 -0.589
2          0.315       0.309        0.303                 -0.589
3          1.085       0.309       -0.827                  1.697
4         -1.994      -1.949       -0.074                 -0.589

                 ...                  fail_to_right.nonmobile.hips.left  \
0                ...                                              3.606
1                ...                                             -0.277
2                ...                                             -0.277
3                ...                                             -0.277
4                ...                                              3.606

   rights.mobile.right  rights.shakey.right  rights.lethargic.right  \
0               -0.585               -0.395                  -0.522
1               -0.585               -0.395                  -0.522
2               -0.585               -0.395                   1.915
3               -0.585               -0.395                  -0.522
4               -0.585               -0.395                  -0.522

   rights.nonmobile.right  rightss.only.right  \
0                  -0.303              -0.261
1                  -0.303              -0.261
2                  -0.303              -0.261
3                  -0.303              -0.261
4                   3.298               3.831

   fail_to_right.mobile.hips.right  fail_to_right.lethargic.hips.right  \
0                           -0.328                              -0.323
1                           -0.328                              -0.323
2                           -0.328                              -0.323
3                            3.052                              -0.323
4                           -0.328                              -0.323

   fail_to_right.lethargic.two.visits.right  \
0                                    -0.125
```

```
1                                     8.021
2                                    -0.125
3                                    -0.125
4                                    -0.125

   fail_to_right.nonmobile.hips.right
0                              3.606
1                             -0.277
2                             -0.277
3                             -0.277
4                             -0.277

[5 rows x 36 columns]
```

In [32]:

```
df_scaled_df.describe()
```

Out[32]:

```
             sex  weight.challenge     weight  ch.weight  pch.weight  \
count  3.920e+02         3.920e+02  3.920e+02  3.920e+02   3.920e+02
mean  -1.722e-16         1.071e-16  1.163e-15 -6.330e-17  -7.746e-17
std    1.001e+00         1.001e+00  1.001e+00  1.001e+00   1.001e+00
min   -1.047e+00        -2.351e+00 -2.487e+00 -5.350e+00  -4.041e+00
25%   -1.047e+00        -6.505e-01 -7.389e-01 -6.418e-01  -6.907e-01
50%    9.551e-01        -1.019e-01 -7.839e-02  1.429e-01   8.794e-02
75%    9.551e-01         7.705e-01  6.807e-01  5.633e-01   5.121e-01
max    9.551e-01         2.311e+00  2.622e+00  2.637e+00   3.820e+00

       hr.post.challenge  score.overall  score.left  score.right  \
count          3.920e+02      3.920e+02   3.920e+02    3.920e+02
mean          -8.836e-17      5.098e-18   1.257e-16    3.863e-16
std            1.001e+00      1.001e+00   1.001e+00    1.001e+00
min           -1.095e+00     -1.994e+00  -1.949e+00   -1.956e+00
25%           -7.884e-01     -5.508e-01  -8.199e-01   -8.269e-01
50%           -3.459e-01      3.152e-01   3.091e-01    3.025e-01
75%            5.249e-01      1.085e+00   1.062e+00    1.055e+00
max            3.303e+00      1.085e+00   1.062e+00    1.055e+00

       rights.mobile.overall                 ...                 \
count              3.920e+02                 ...
mean              -5.715e-16                 ...
std                1.001e+00                 ...
min               -5.891e-01                 ...
25%               -5.891e-01                 ...
50%               -5.891e-01                 ...
75%                1.697e+00                 ...
max                1.697e+00                 ...

       fail_to_right.nonmobile.hips.left  rights.mobile.right  \
count                          3.920e+02            3.920e+02
```

mean	-1.881e-16	1.994e-16
std	1.001e+00	1.001e+00
min	-2.774e-01	-5.852e-01
25%	-2.774e-01	-5.852e-01
50%	-2.774e-01	-5.852e-01
75%	-2.774e-01	1.709e+00
max	3.606e+00	1.709e+00

	rights.shakey.right	rights.lethargic.right	rights.nonmobile.right \
count	3.920e+02	3.920e+02	3.920e+02
mean	2.068e-17	1.069e-15	4.871e-16
std	1.001e+00	1.001e+00	1.001e+00
min	-3.954e-01	-5.222e-01	-3.032e-01
25%	-3.954e-01	-5.222e-01	-3.032e-01
50%	-3.954e-01	-5.222e-01	-3.032e-01
75%	-3.954e-01	-5.222e-01	-3.032e-01
max	2.529e+00	1.915e+00	3.298e+00

	rightss.only.right	fail_to_right.mobile.hips.right \
count	3.920e+02	3.920e+02
mean	-3.512e-17	2.368e-16
std	1.001e+00	1.001e+00
min	-2.610e-01	-3.276e-01
25%	-2.610e-01	-3.276e-01
50%	-2.610e-01	-3.276e-01
75%	-2.610e-01	-3.276e-01
max	3.831e+00	3.052e+00

	fail_to_right.lethargic.hips.right \
count	3.920e+02
mean	1.835e-16
std	1.001e+00
min	-3.228e-01
25%	-3.228e-01
50%	-3.228e-01
75%	-3.228e-01
max	3.098e+00

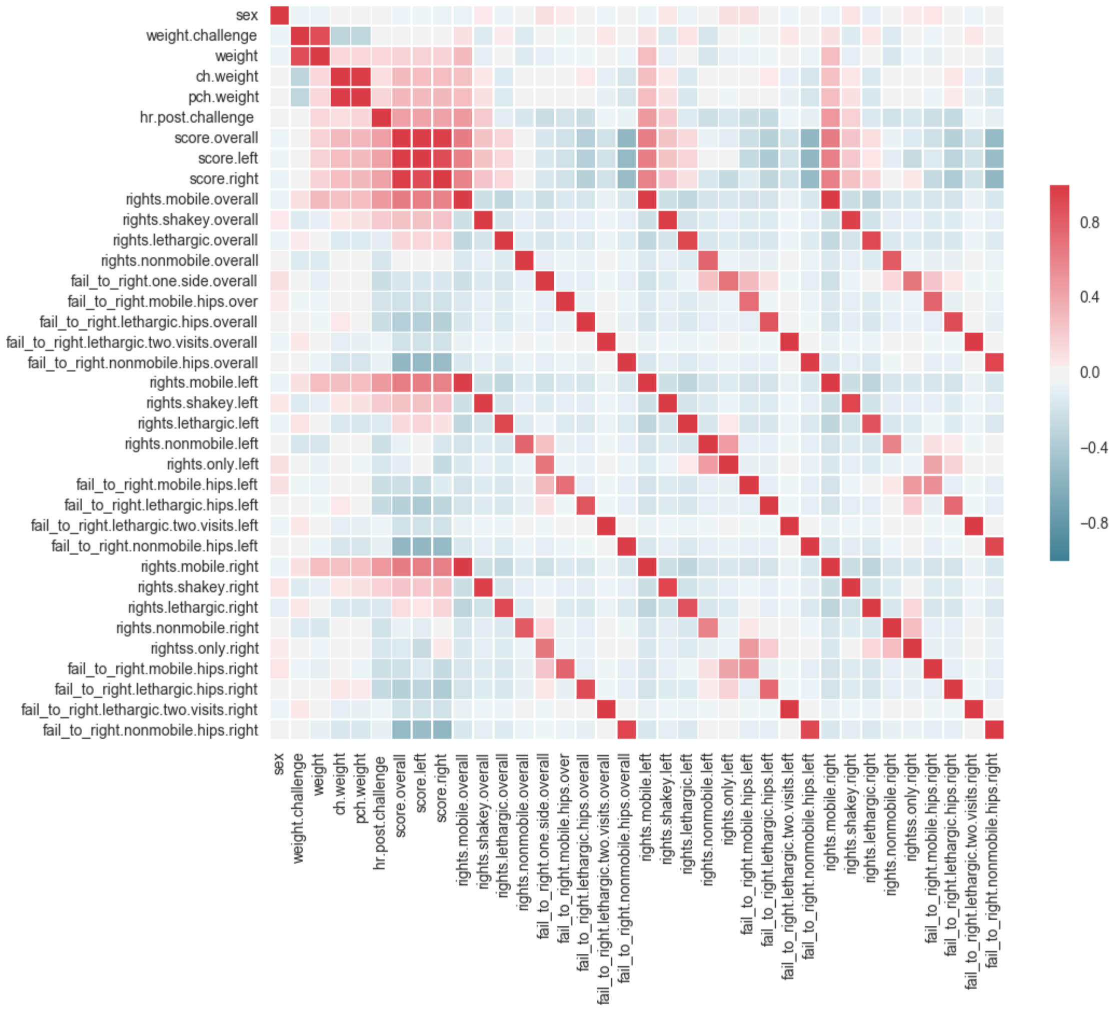
	fail_to_right.lethargic.two.visits.right \
count	3.920e+02
mean	-3.171e-16
std	1.001e+00
min	-1.247e-01
25%	-1.247e-01
50%	-1.247e-01
75%	-1.247e-01
max	8.021e+00

```
       fail_to_right.nonmobile.hips.right
count                           3.920e+02
mean                            1.385e-16
std                             1.001e+00
min                            -2.774e-01
25%                            -2.774e-01
50%                            -2.774e-01
75%                            -2.774e-01
max                             3.606e+00

[8 rows x 36 columns]
```

Let's see the effect of this standardization on the correlation between features !

In [33]:
```
correlations = df_scaled_df.corr(method='pearson')
correlations

# Plot Correlations
corr = df_scaled_df.corr()
# Generate a mask for the upper triangle
mask = np.zeros_like(corr, dtype=np.bool)
mask[np.triu_indices_from(mask)] = False
# Set up the matplotlib figure
f, ax = plt.subplots(figsize=(11, 9))
cmap = sns.diverging_palette(220, 10, as_cmap=True)
#for tick in ax.get_xticklabels():
#    tick.set_rotation(90)
# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr, mask=mask, cmap=cmap, vmax=1,
            square=True,
            linewidths=.5, cbar_kws={"shrink": .5}, ax=ax)
```

Out[33]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x11d0a3050>
```



What we see here is the impact of data normalization on the extraction of meaningful information, here correlation, between different features, after standardizing the data we can clearly see a block on the top left corner of the correlation matrix that already tells something about the features that will impact mostly the outcome.

What we need to do now is proceed for feature selection applying different methods and test this process with different classifiers in order to study the best combination of feature selection and model accuracy (algorithm)

3.4 Predicting outcome WITHOUT feature selection

```
In [34]: X = df_scaled_df
         Y = df_clean_2["outcome"]
         names = df_scaled_df.columns
```

It is a good idea to use a validation hold-out set. This is a sample of the data that we hold back from our analysis and modeling. We use it right at the end of our project to confirm the accuracy of our final model. It is a smoke test that we can use to see if we messed up and to give us confidence on our estimates of accuracy on unseen data. We will use 80% of the dataset for modeling and hold back 20% for validation.

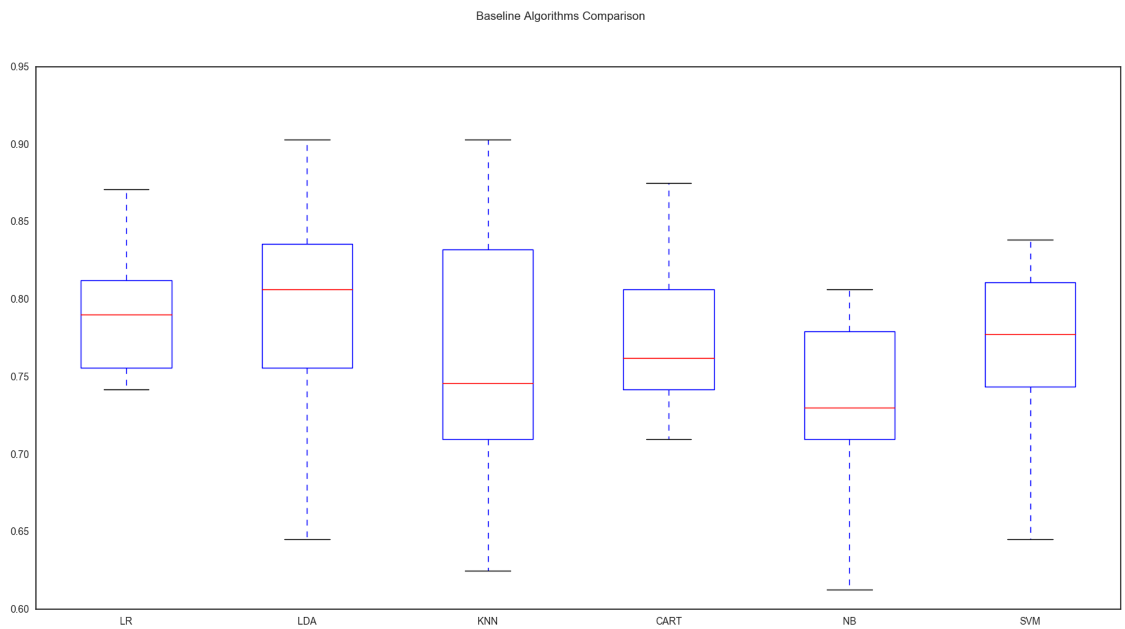
```
In [36]: # Validation dataset

         validation_size = 0.20
         seed = 7
         X_train, X_validation, Y_train, Y_validation = cross_validation.train_test_split(X, Y,t
```

3.4.1 Base Line Models

```
In [37]: def base_line_models(training_set, outcome):
             # Test options and evaluation metric
             num_folds = 10
             num_instances = len(training_set)
             seed = 7
             scoring = 'accuracy'

             # Spot-Check Algorithms
             models = []
             models.append(('LR', LogisticRegression()))
             models.append(('LDA', LinearDiscriminantAnalysis()))
             models.append(('KNN', KNeighborsClassifier()))
             models.append(('CART', DecisionTreeClassifier()))
             models.append(('NB', GaussianNB()))
             models.append(('SVM', SVC()))
             results = []
             names = []
             for name, model in models:
                 kfold = cross_validation.KFold(n=num_instances, n_folds=num_folds, random_state
                 cv_results = cross_validation.cross_val_score(model, training_set, outcome, cv=
                 results.append(cv_results)
                 names.append(name)
                 msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
                 print(msg)
             # Compare Algorithms
             fig = plt.figure()
             fig.suptitle('Baseline Algorithms Comparison')
             ax = fig.add_subplot(111)
             plt.boxplot(results)
             ax.set_xticklabels(names)
             plt.show()

         base_line_models(X_train, Y_train)
```

```
LR: 0.782661 (0.059212)
LDA: 0.795464 (0.069392)
KNN: 0.760685 (0.088701)
```

```
CART: 0.776310 (0.051248)


/Users/Rad/anaconda2/lib/python2.7/site-packages/sklearn/discriminant_analysis.py:389: UserWarni
  warnings.warn("Variables are collinear.")


NB: 0.734879 (0.057135)
SVM: 0.773085 (0.054942)
```

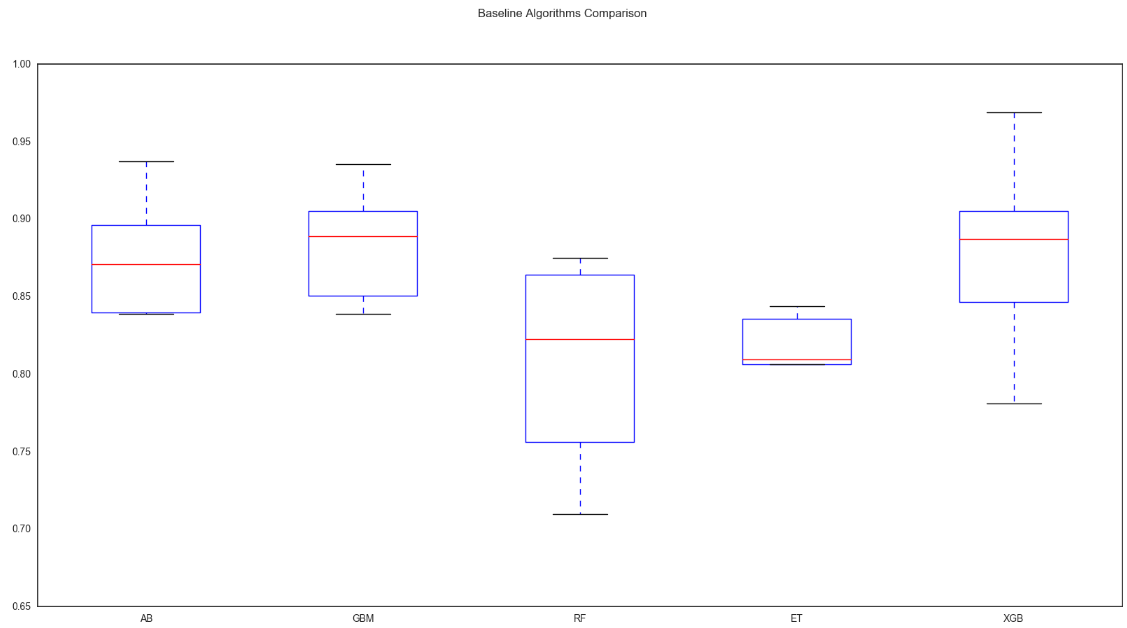


3.4.2 Ensemble Models

```
In [38]: def ensemble_models(training_set, outcome):
             # Test options and evaluation metric
             num_folds = 10
             num_instances = len(training_set)
             seed = 7
             scoring = 'accuracy'

             # ensembles
             ensembles = []
             ensembles.append(('AB', AdaBoostClassifier()))
             ensembles.append(('GBM', GradientBoostingClassifier()))
             ensembles.append(('RF', RandomForestClassifier()))
             ensembles.append(('ET', ExtraTreesClassifier()))
             ensembles.append(('XGB', xgboost.XGBClassifier()))
```

```
    results = []
    names = []
    for name, model in ensembles:
        kfold = cross_validation.KFold(n=num_instances, n_folds=num_folds, random_state
        cv_results = cross_validation.cross_val_score(model, training_set, outcome, cv=
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)
    # Compare Algorithms
    fig = plt.figure()
    fig.suptitle('Baseline Algorithms Comparison')
    ax = fig.add_subplot(111)
    plt.boxplot(results)
    ax.set_xticklabels(names)
    plt.show()

ensemble_models(X_train, Y_train)
```

```
AB: 0.872077 (0.032209)
GBM: 0.872177 (0.062808)
RF: 0.804940 (0.061960)
ET: 0.811391 (0.072972)
XGB: 0.868851 (0.072187)
```

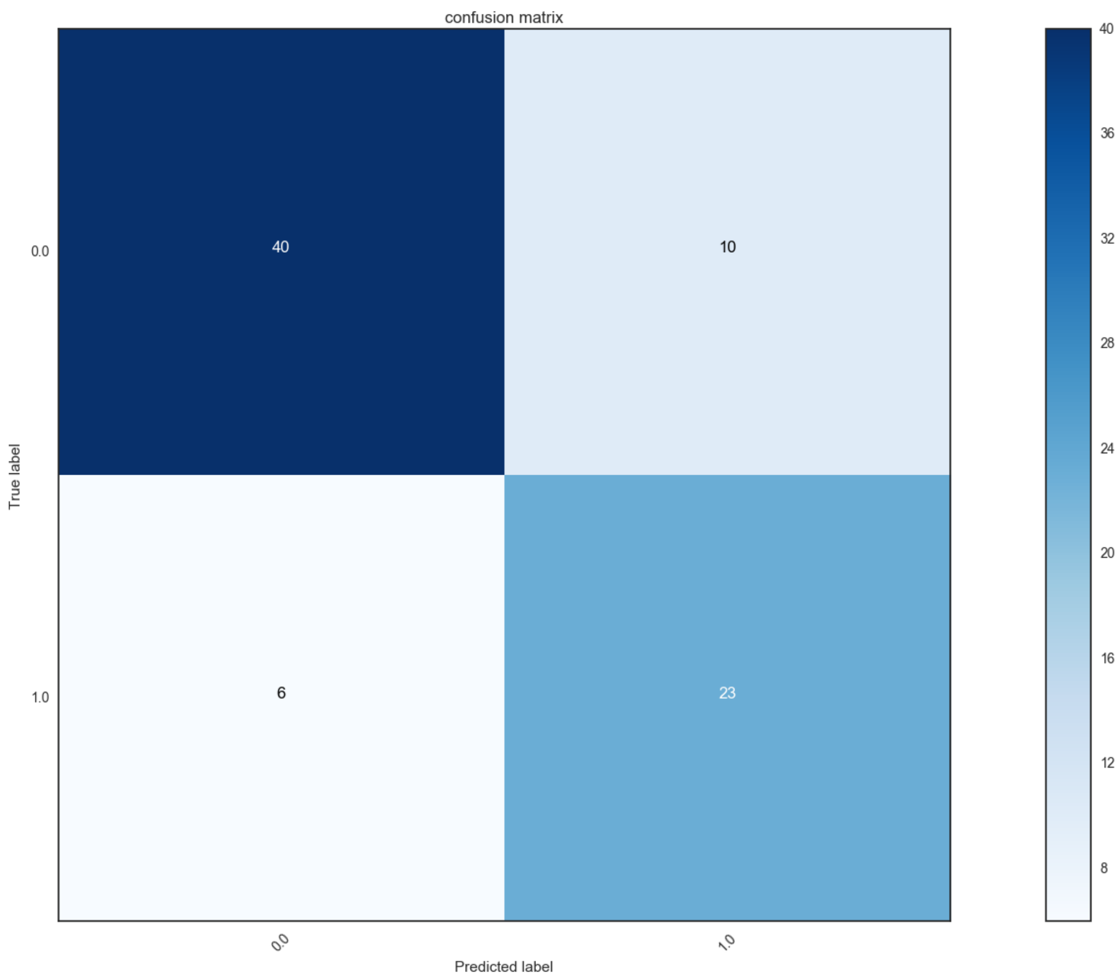


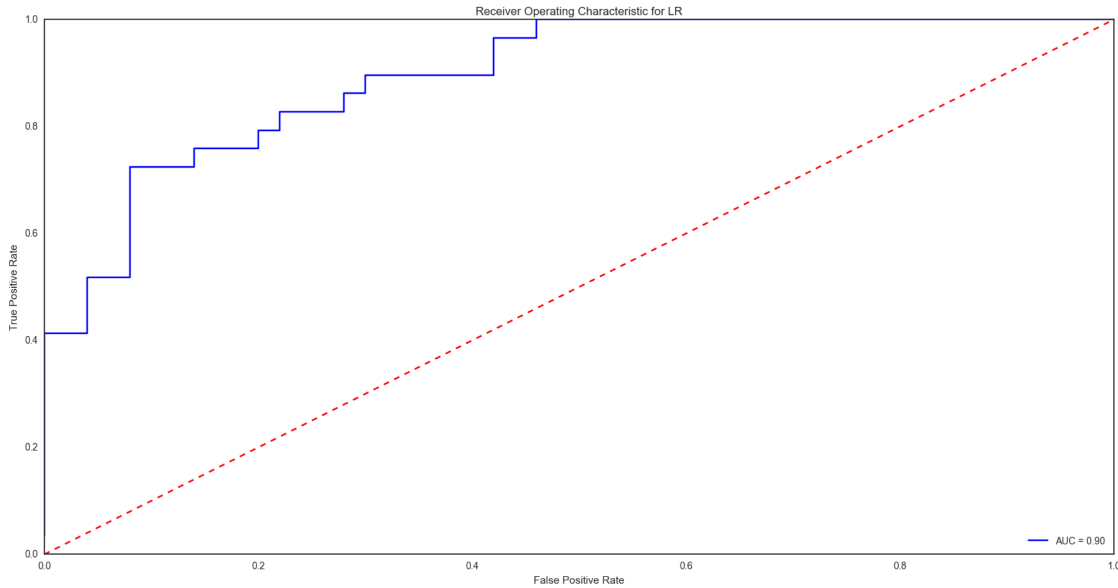
3.4.3 Model Validations

In [39]:
```
import itertools
import matplotlib.pyplot as plt


def plot_confusion_matrix(cm, classes,
                          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`.
    """
    plt.figure(1)
    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    #if normalize:
    #    cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
    #    print("Normalized confusion matrix")
    #else:
    #    print('Confusion matrix, without normalization')

    print(cm)

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

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


def validate_models(training_set, outcome, validation_data, validation_outcome):

    models = []

    #baselines

    models.append(('LR', LogisticRegression()))
```

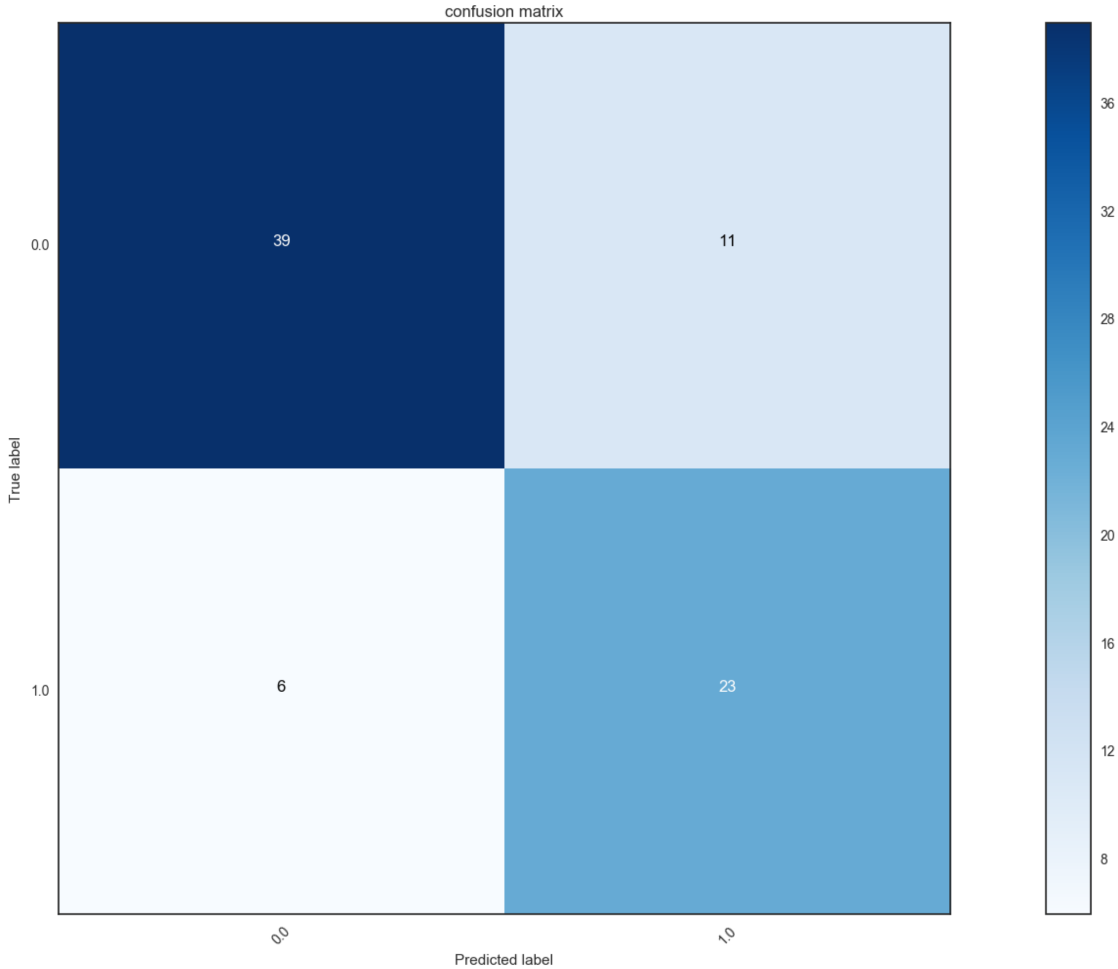
```python
    models.append(('LDA', LinearDiscriminantAnalysis()))
    models.append(('KNN', KNeighborsClassifier()))
    models.append(('CART', DecisionTreeClassifier()))
    models.append(('NB', GaussianNB()))
    models.append(('SVM', SVC(probability=True)))

    #ensemble

    models.append(('AB', AdaBoostClassifier()))
    models.append(('GBM', GradientBoostingClassifier()))
    models.append(('RF', RandomForestClassifier()))
    models.append(('ET', ExtraTreesClassifier()))
    models.append(('XGB', xgboost.XGBClassifier()))


    for name, model in models:
        mod = model
        mod.fit(training_set, outcome)
        # estimate accuracy on validation dataset
        predictions = mod.predict(validation_data)
        print "Validation based on " + name
        print(accuracy_score(validation_outcome, predictions))
        print(confusion_matrix(validation_outcome, predictions))
        cfmat = confusion_matrix(validation_outcome, predictions)
        plot_confusion_matrix(cfmat, classes=[0.0, 1.0] , title='confusion matrix')

        print(classification_report(validation_outcome, predictions))

        # calculate the fpr and tpr for all thresholds of the classification
        probs = mod.predict_proba(validation_data)
        preds = probs[:,1]
        fpr, tpr, threshold = roc_curve(validation_outcome, preds)
        roc_auc = auc(fpr, tpr)

        # method I: plt
        plt.figure(2)
        plt.title('Receiver Operating Characteristic for ' + name)
        plt.plot(fpr, tpr, 'b', label = 'AUC = %0.2f' % roc_auc)
        plt.legend(loc = 'lower right')
        plt.plot([0, 1], [0, 1],'r--')
        plt.xlim([0, 1])
        plt.ylim([0, 1])
        plt.ylabel('True Positive Rate')
        plt.xlabel('False Positive Rate')
        plt.show()

validate_models(X_train, Y_train, X_validation, Y_validation)
```

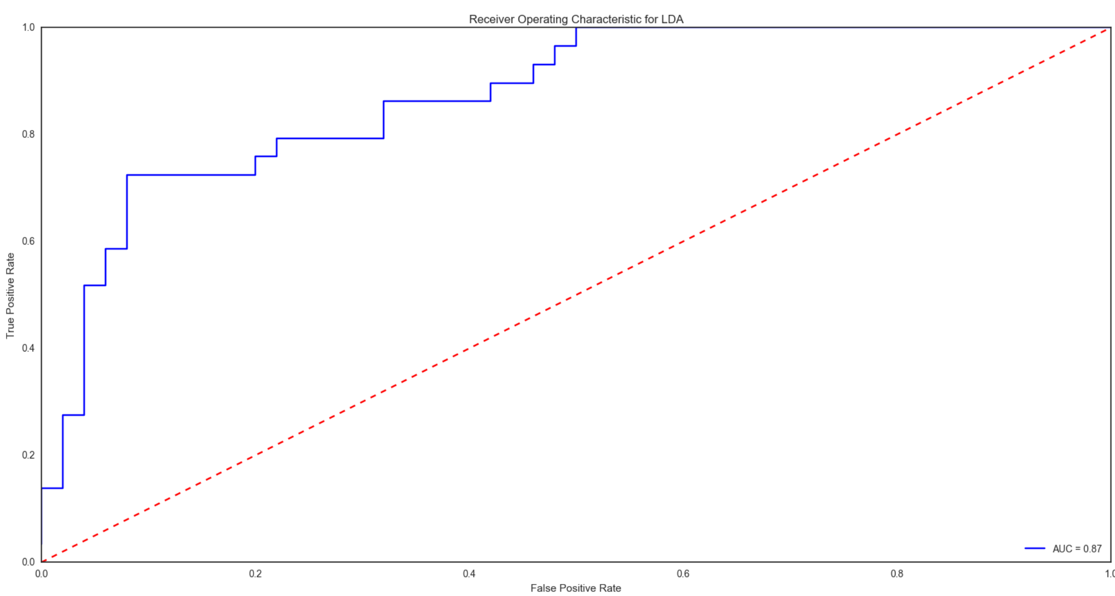
```
Validation based on LR
0.79746835443
[[40 10]
 [ 6 23]]
[[40 10]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.80      0.83        50
        1.0       0.70      0.79      0.74        29

avg / total       0.81      0.80      0.80        79
```



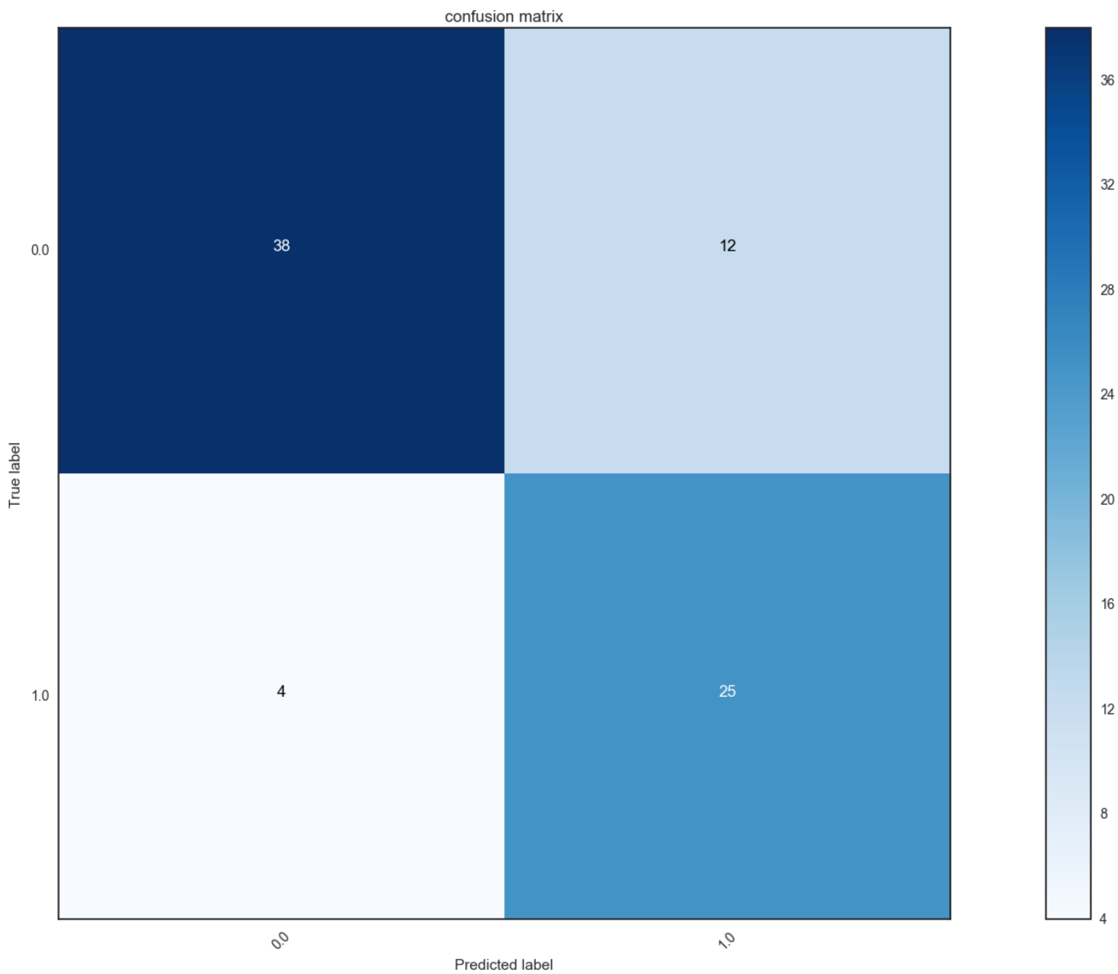


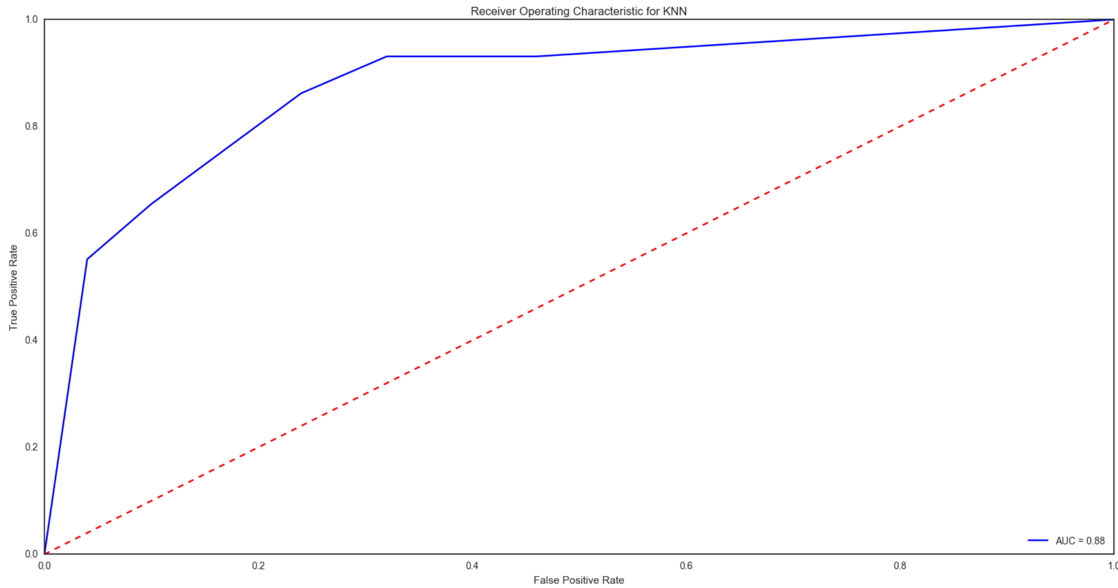

```
Validation based on LDA
0.784810126582
[[39 11]
 [ 6 23]]
[[39 11]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.78      0.82        50
        1.0       0.68      0.79      0.73        29

avg / total       0.80      0.78      0.79        79
```


confusion matrix
0.0
1.0
True label
39
11
6
23
0.0
1.0
Predicted label
36
32
28
24
20
16
12
8

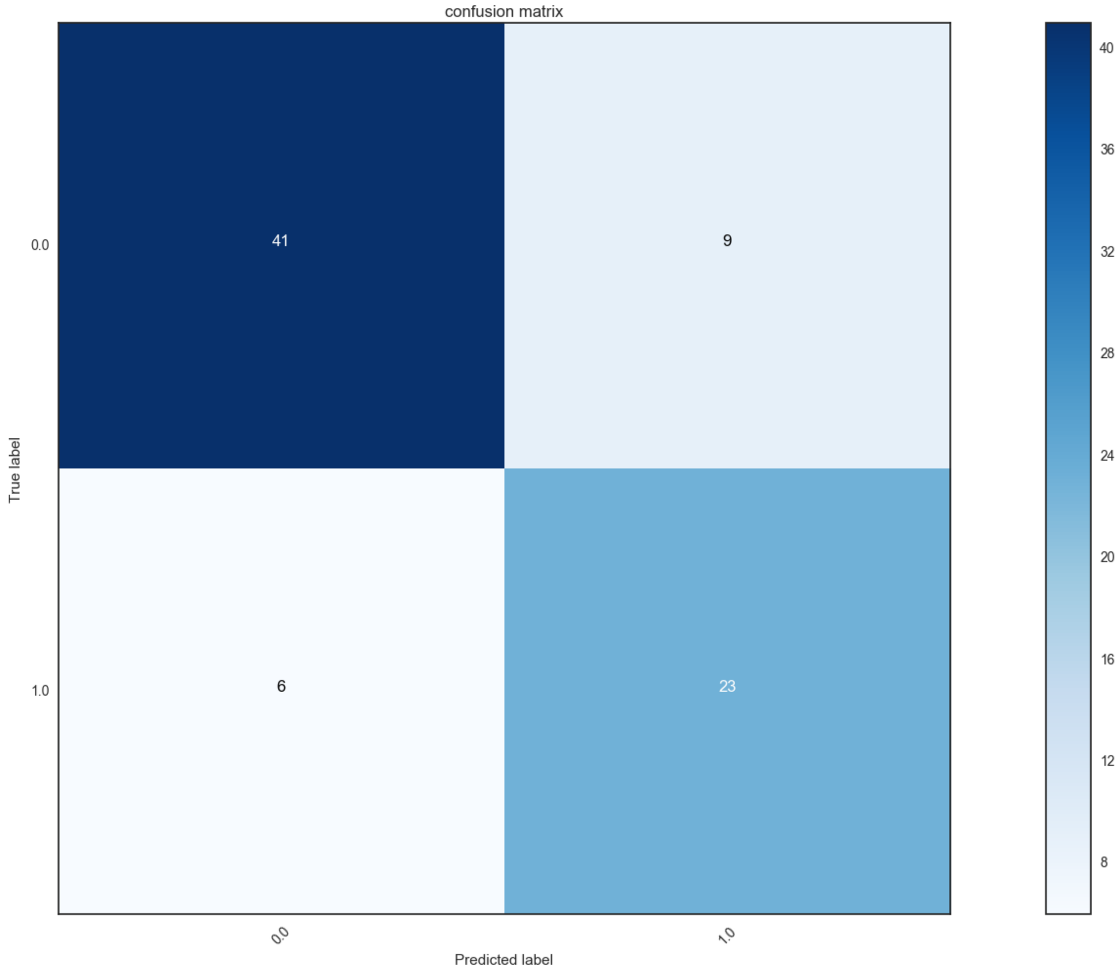

Receiver Operating Characteristic for LDA
True Positive Rate
False Positive Rate
AUC = 0.87
0.0
0.2
0.4
0.6
0.8
1.0

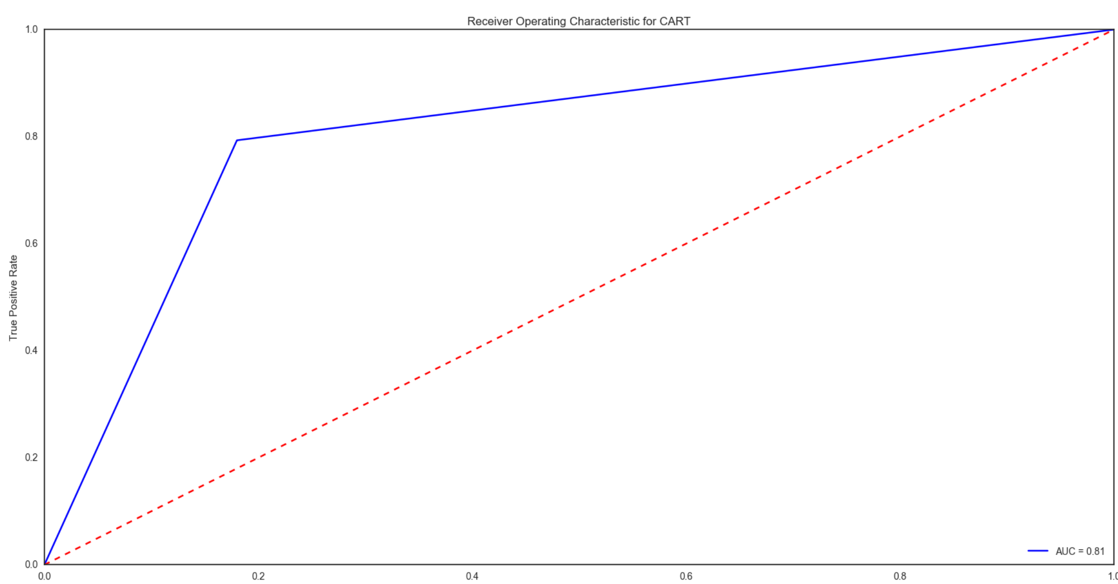
```
Validation based on KNN
0.79746835443
[[38 12]
 [ 4 25]]
[[38 12]
 [ 4 25]]
             precision    recall  f1-score   support

        0.0       0.90      0.76      0.83        50
        1.0       0.68      0.86      0.76        29

avg / total       0.82      0.80      0.80        79
```



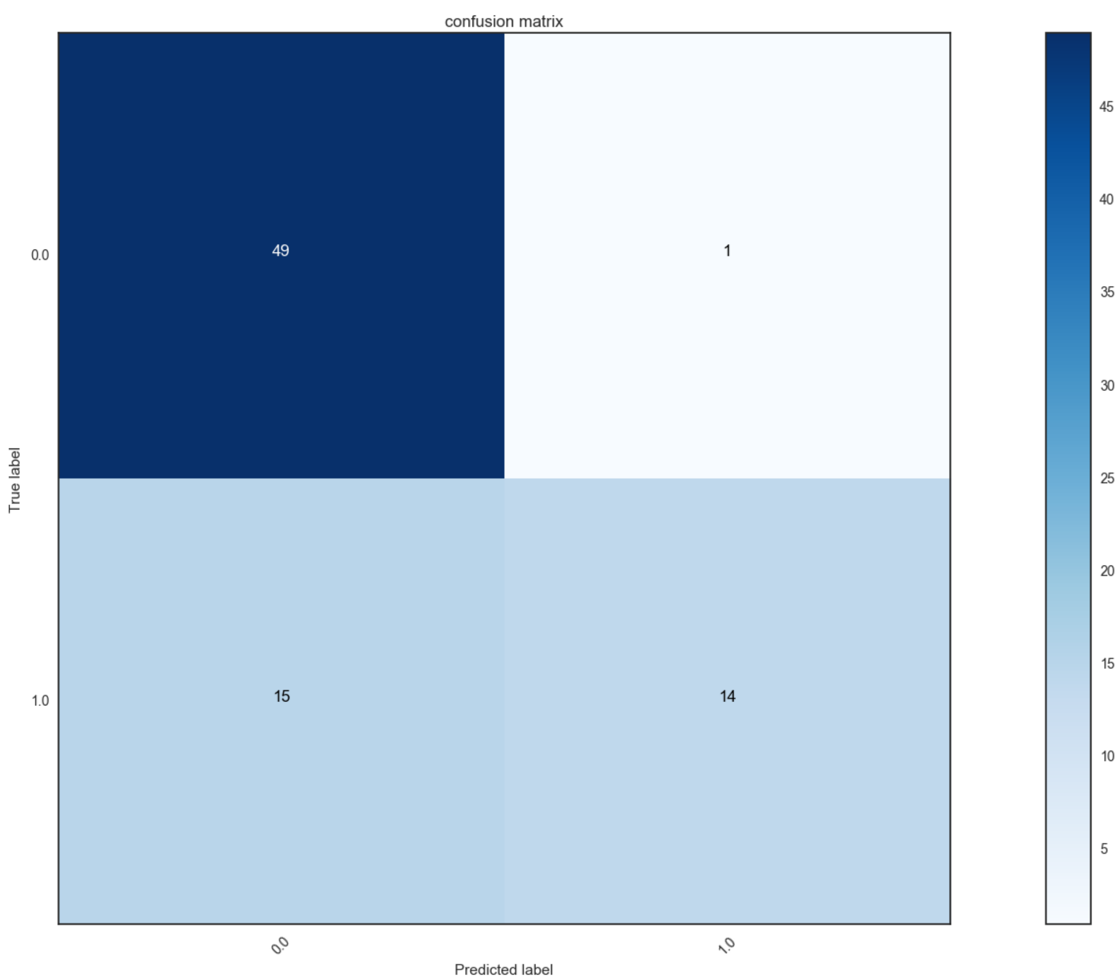


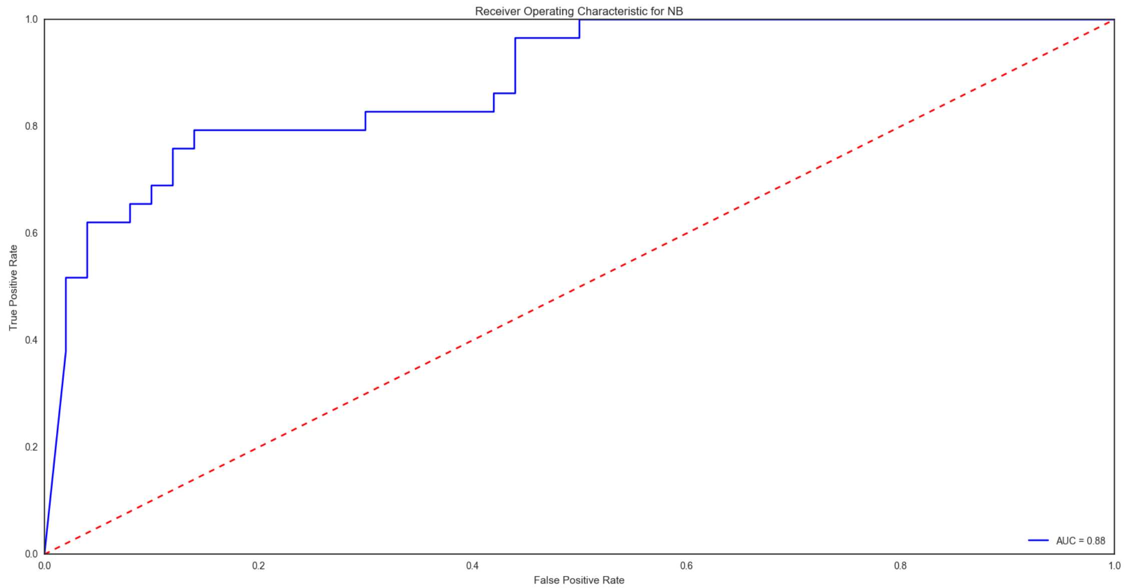

```
Validation based on CART
0.810126582278
[[41  9]
 [ 6 23]]
[[41  9]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.82      0.85        50
        1.0       0.72      0.79      0.75        29

avg / total       0.82      0.81      0.81        79
```


confusion matrix
41
9
6
23
0.0
1.0
True label
Predicted label
40
36
32
28
24
20
16
12
8

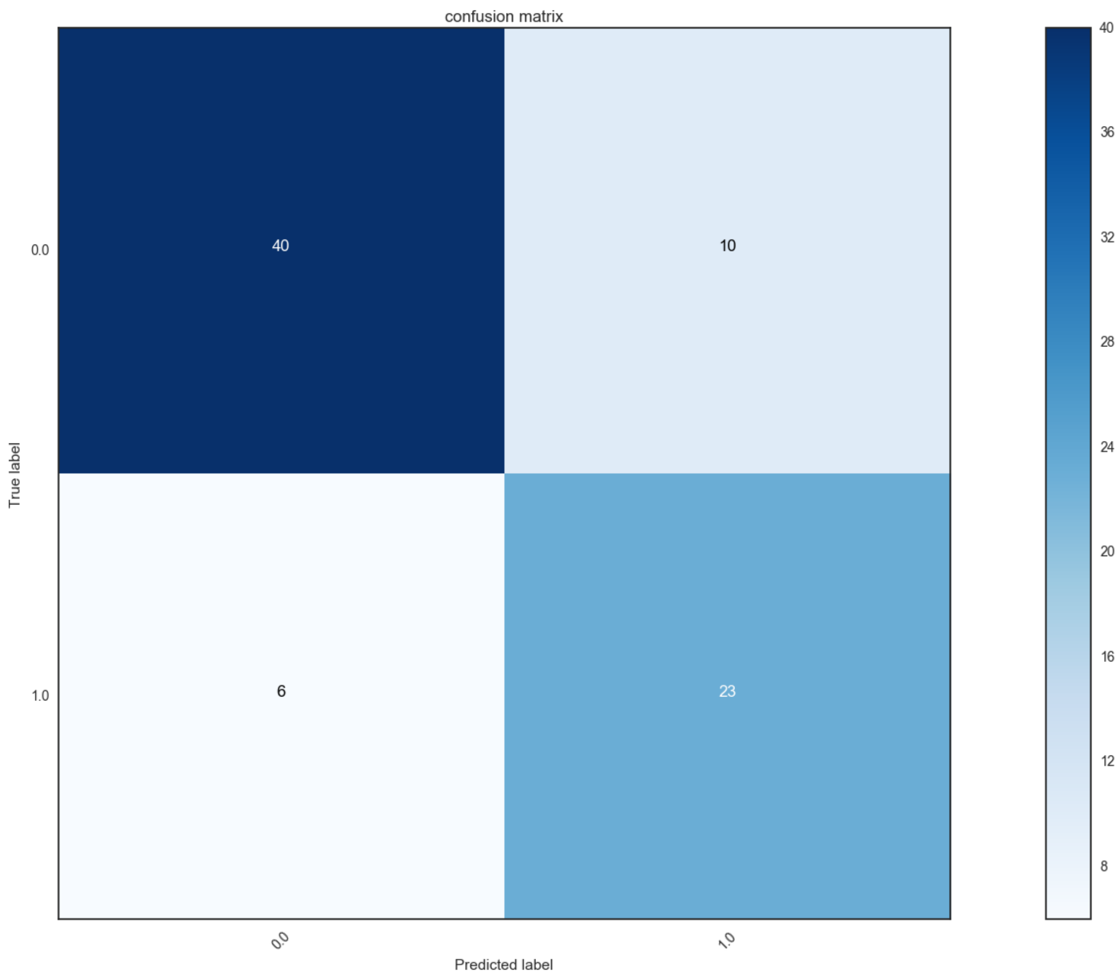

Receiver Operating Characteristic for CART
True Positive Rate
False Positive Rate
AUC = 0.81
0.0
0.2
0.4
0.6
0.8
1.0

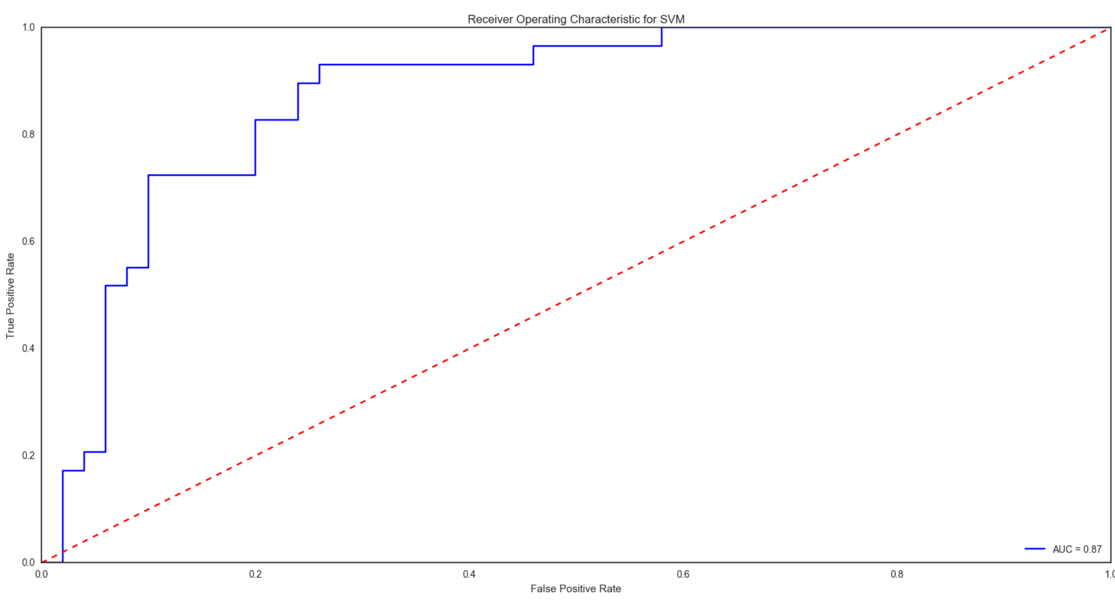
```
Validation based on NB
0.79746835443
[[49  1]
 [15 14]]
[[49  1]
 [15 14]]
             precision    recall  f1-score   support

        0.0       0.77      0.98      0.86        50
        1.0       0.93      0.48      0.64        29

avg / total       0.83      0.80      0.78        79
```



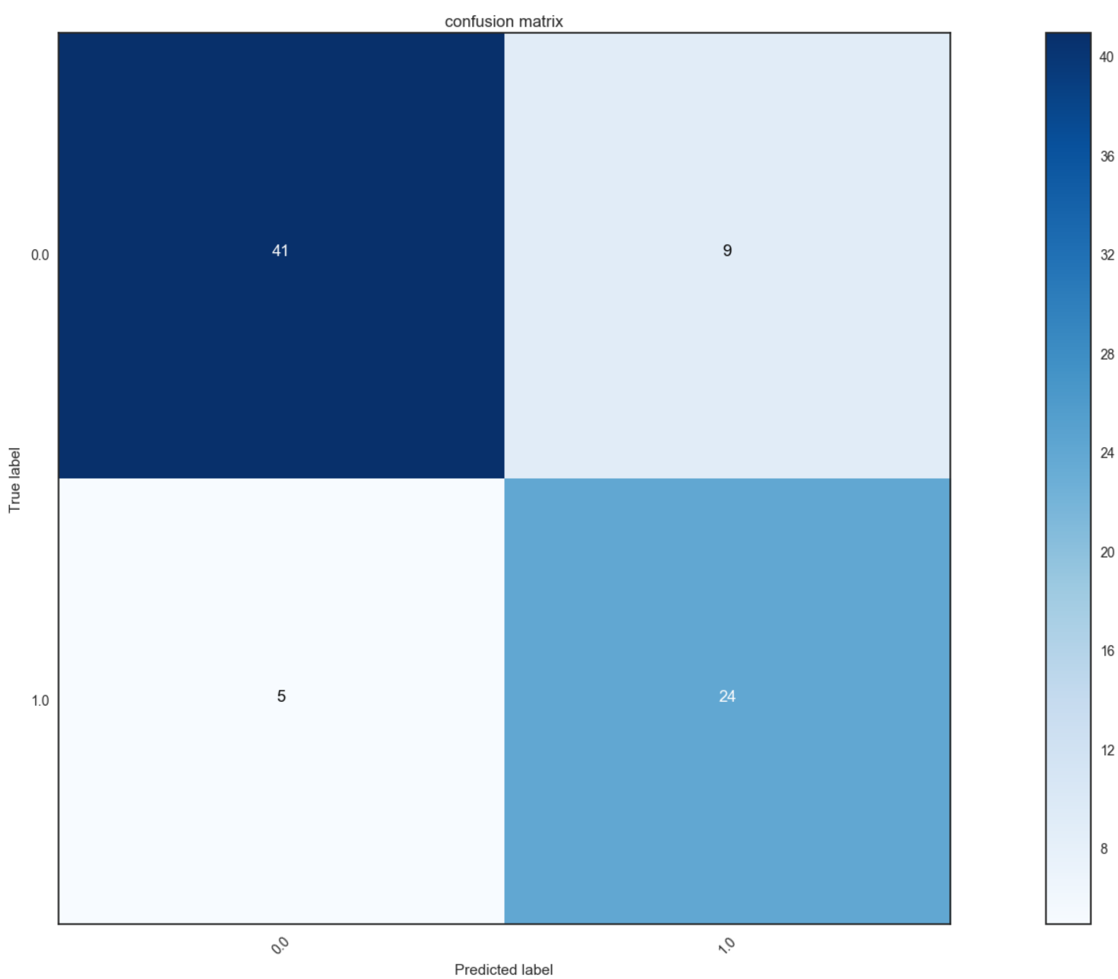


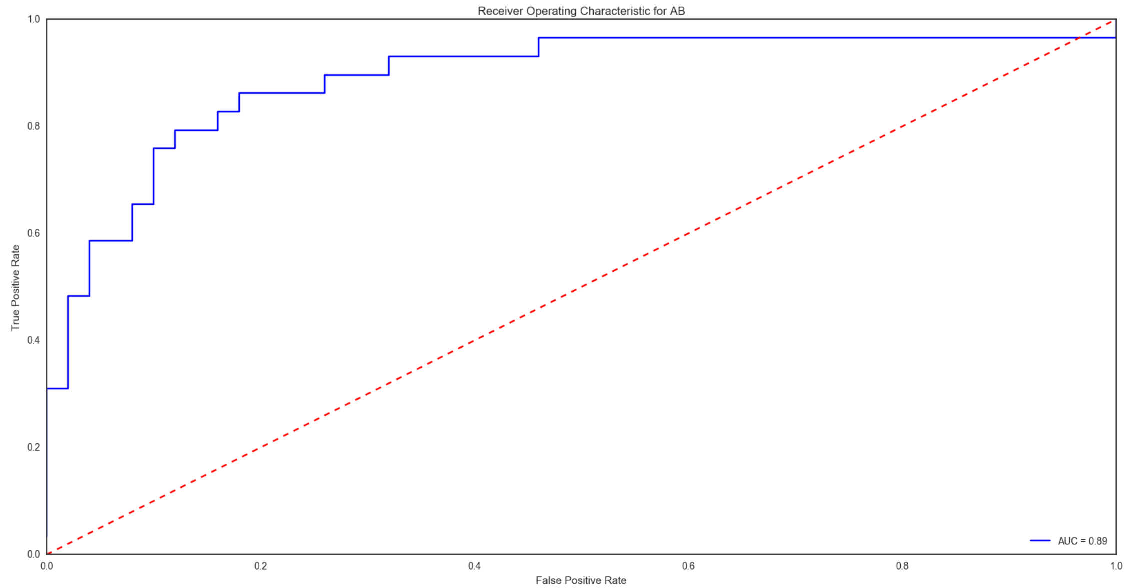

```
Validation based on SVM
0.79746835443
[[40 10]
 [ 6 23]]
[[40 10]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.80      0.83        50
        1.0       0.70      0.79      0.74        29

avg / total       0.81      0.80      0.80        79
```


confusion matrix
40
10
6
23
0.0
1.0
True label
0.0
1.0
Predicted label
40
36
32
28
24
20
16
12
8

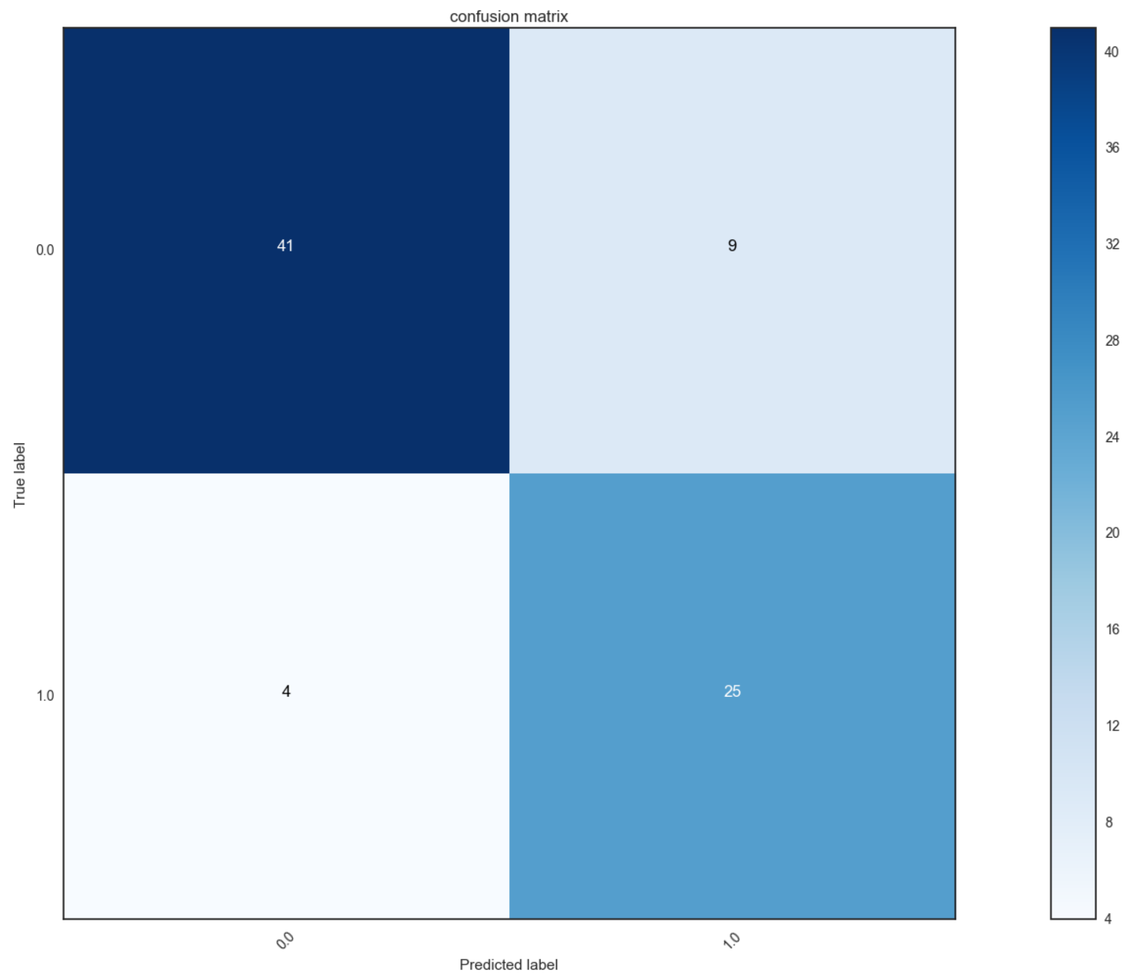

Receiver Operating Characteristic for SVM
True Positive Rate
False Positive Rate
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.87

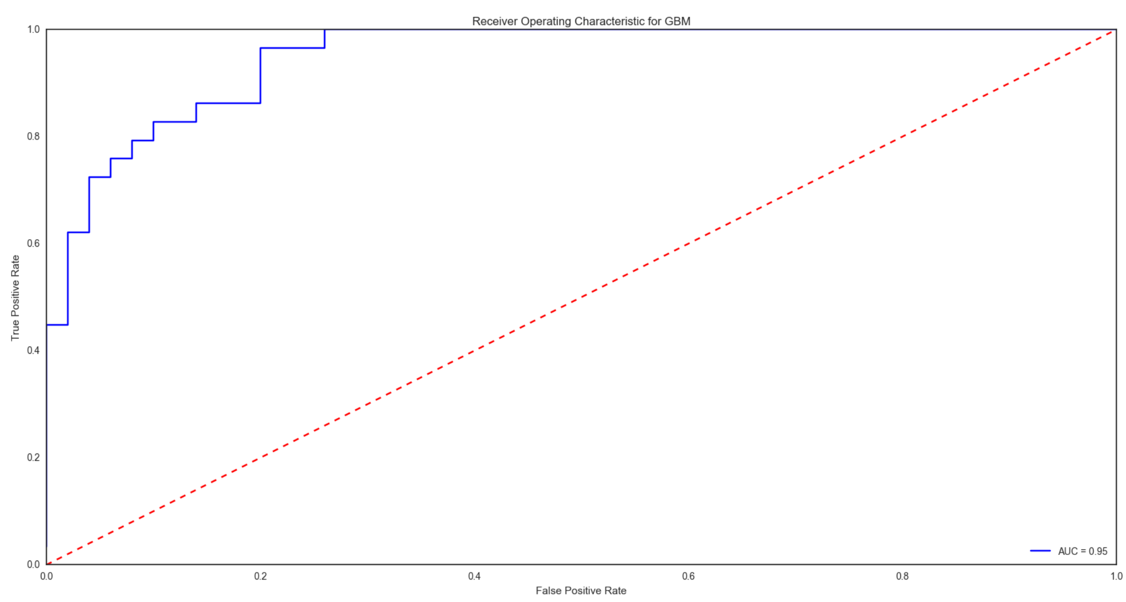
```
Validation based on AB
0.822784810127
[[41  9]
 [ 5 24]]
[[41  9]
 [ 5 24]]
             precision    recall  f1-score   support

        0.0       0.89      0.82      0.85        50
        1.0       0.73      0.83      0.77        29

avg / total       0.83      0.82      0.82        79
```



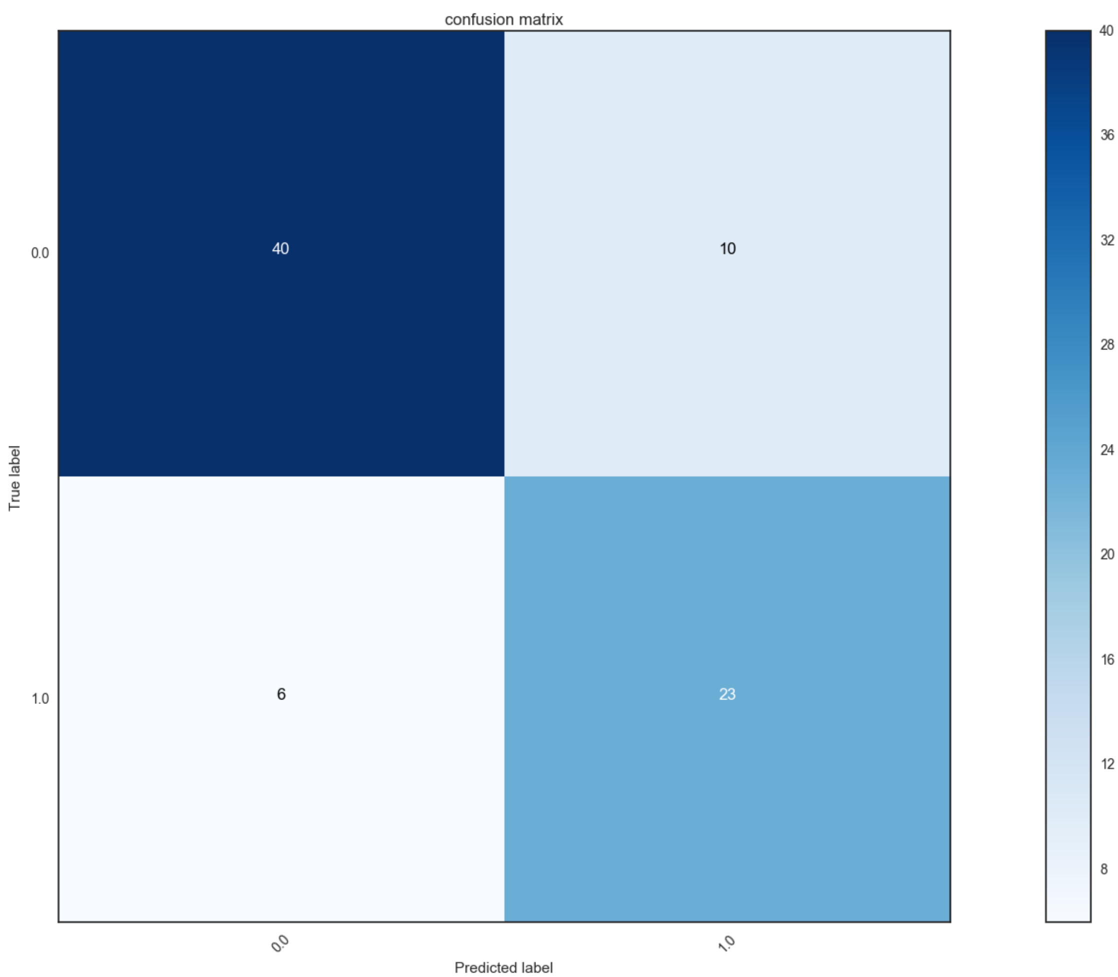


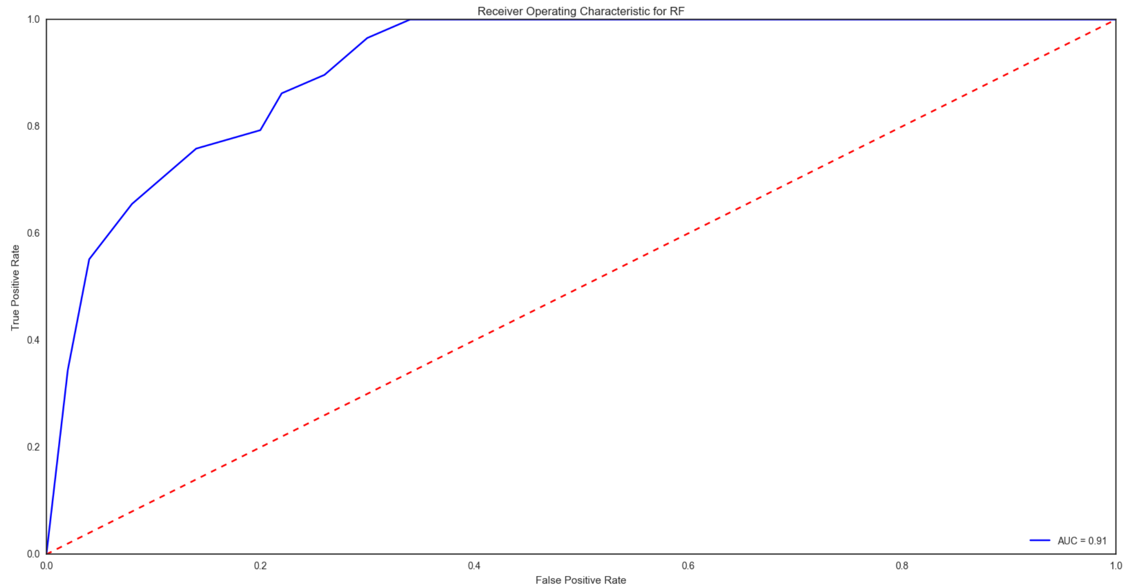

```
Validation based on GBM
0.835443037975
[[41  9]
 [ 4 25]]
[[41  9]
 [ 4 25]]
             precision    recall  f1-score   support

        0.0       0.91      0.82      0.86        50
        1.0       0.74      0.86      0.79        29

avg / total       0.85      0.84      0.84        79
```


confusion matrix
41
9
4
25
0.0
1.0
True label
0.0
1.0
Predicted label
40
36
32
28
24
20
16
12
8
4

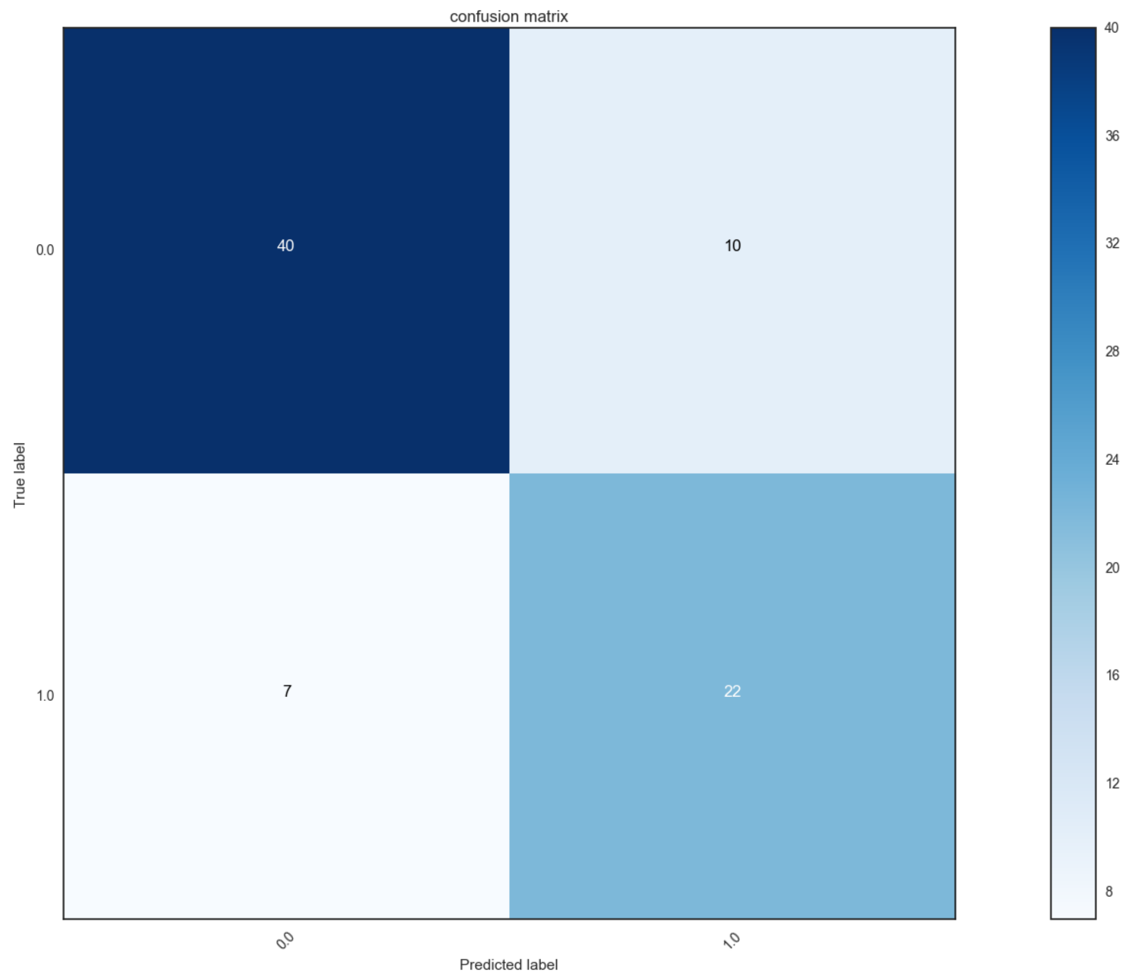

Receiver Operating Characteristic for GBM
True Positive Rate
False Positive Rate
AUC = 0.95
0.0
0.2
0.4
0.6
0.8
1.0

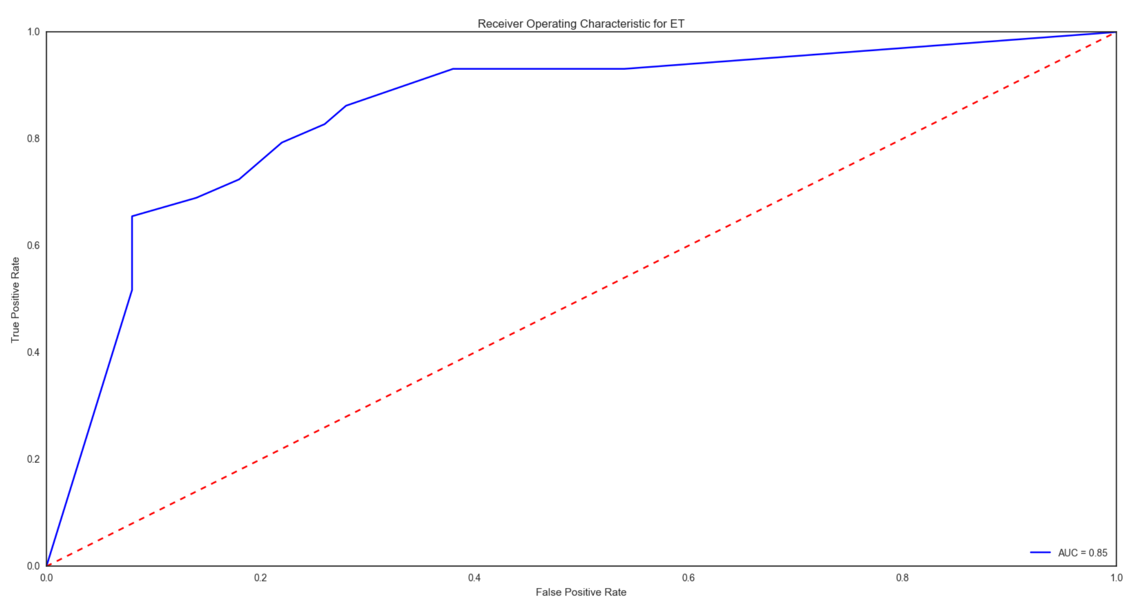
```
Validation based on RF
0.79746835443
[[40 10]
 [ 6 23]]
[[40 10]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.80      0.83        50
        1.0       0.70      0.79      0.74        29

avg / total       0.81      0.80      0.80        79
```



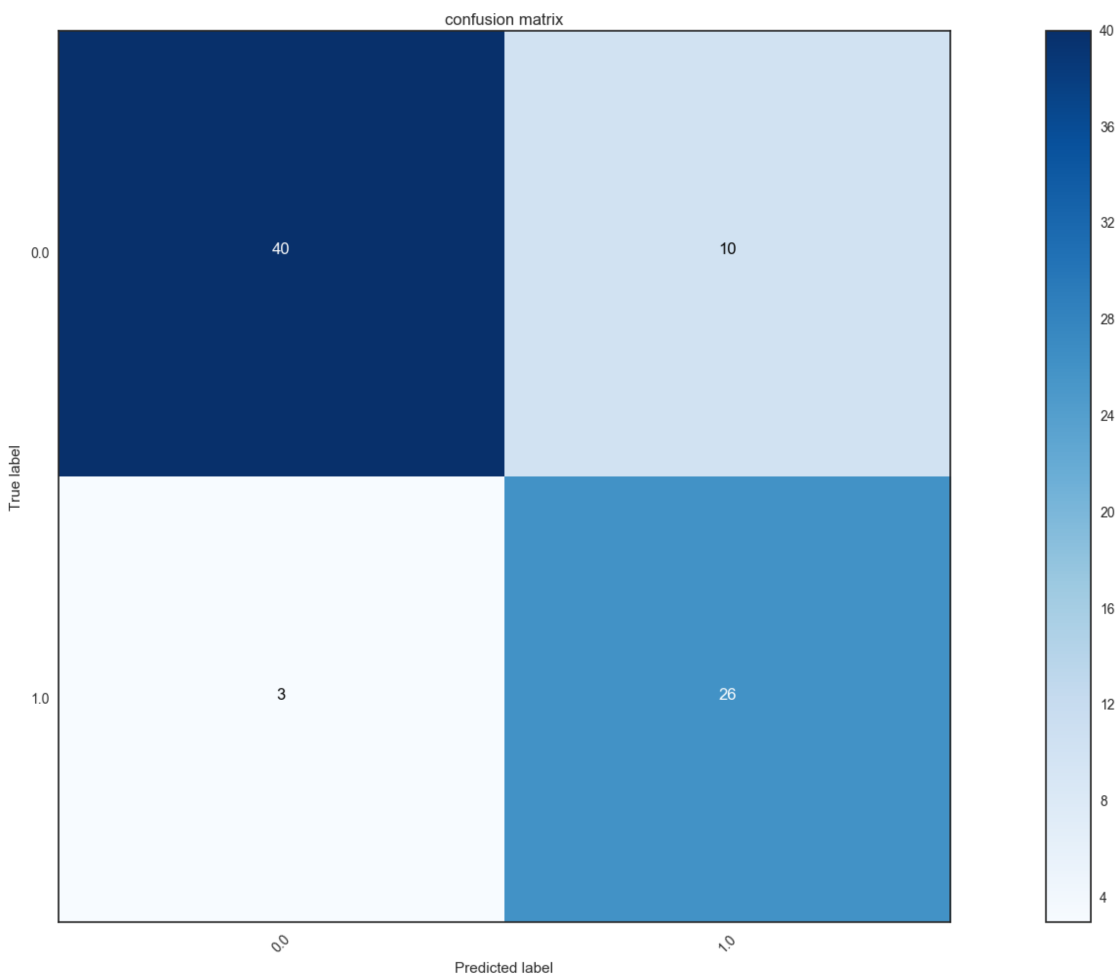


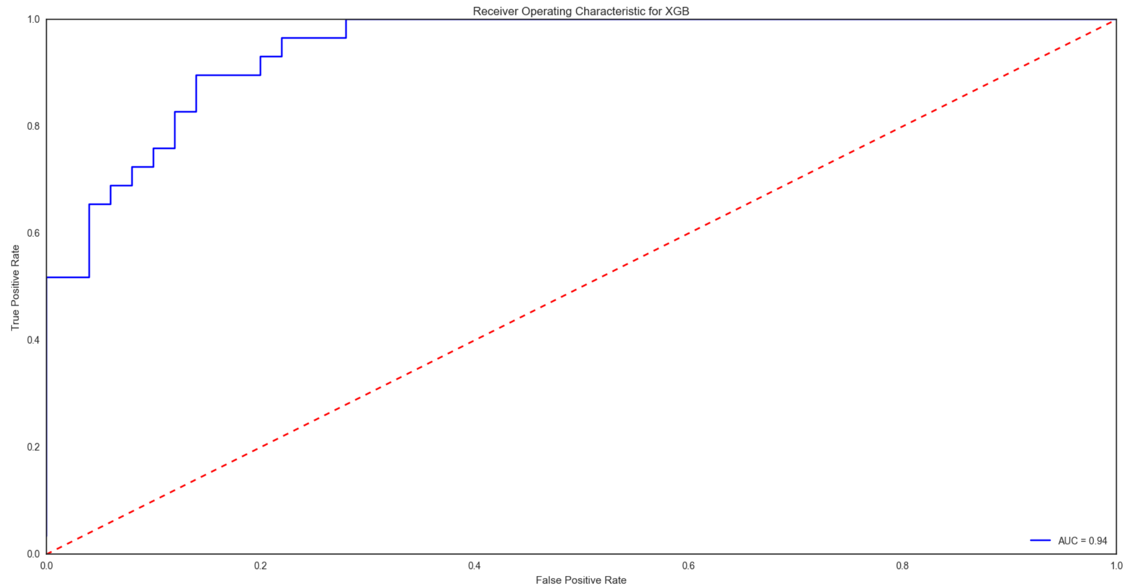

```
Validation based on ET
0.784810126582
[[40 10]
 [ 7 22]]
[[40 10]
 [ 7 22]]
             precision    recall  f1-score   support

        0.0       0.85      0.80      0.82        50
        1.0       0.69      0.76      0.72        29

avg / total       0.79      0.78      0.79        79
```


confusion matrix
True label
0.0
1.0
40
10
7
22
0.0
1.0
Predicted label
40
36
32
28
24
20
16
12
8


Receiver Operating Characteristic for ET
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.85

```
Validation based on XGB
0.835443037975
[[40 10]
 [ 3 26]]
[[40 10]
 [ 3 26]]
             precision    recall  f1-score   support

        0.0       0.93      0.80      0.86        50
        1.0       0.72      0.90      0.80        29

avg / total       0.85      0.84      0.84        79
```





3.5 Predicting outcome WITH feature selection

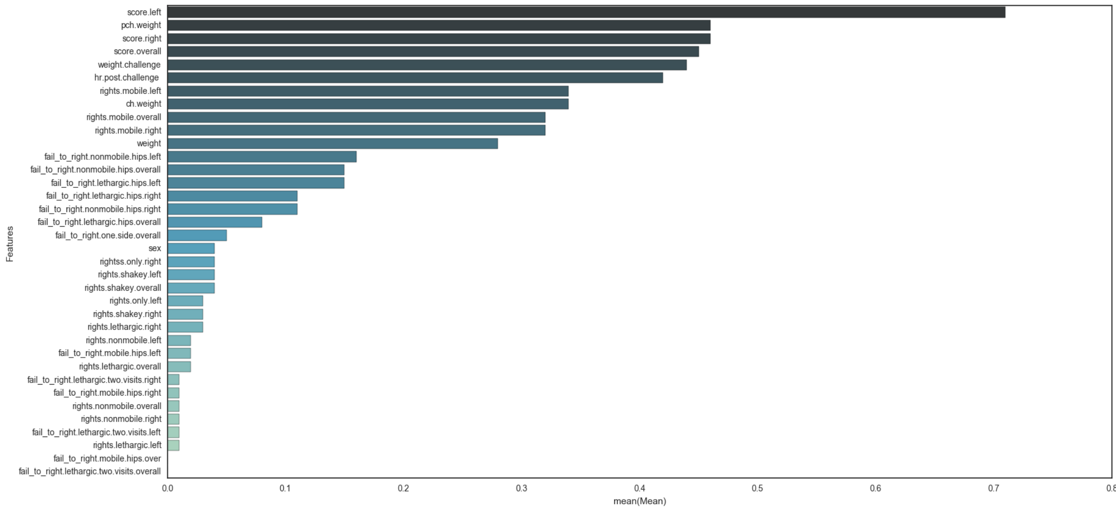
In [40]:
```
X = df_scaled_df
Y = df_clean_2["outcome"]
names = df_scaled_df.columns

names = X.columns
X = X.values
Y = Y.values

ranks = {}

def rank_to_dict(ranks, names, order=1):
    minmax = MinMaxScaler()
    ranks = minmax.fit_transform(order*np.array([ranks]).T).T[0]
    ranks = map(lambda x: round(x, 2), ranks)
    return dict(zip(names, ranks ))

lr = LinearRegression(normalize=True)
lr.fit(X, Y)
ranks["Linear reg"] = rank_to_dict(np.abs(lr.coef_), names)

ridge = Ridge(alpha=7)
ridge.fit(X, Y)
ranks["Ridge"] = rank_to_dict(np.abs(ridge.coef_), names)

rlasso = RandomizedLasso(alpha=0.04)
rlasso.fit(X, Y)
```

```python
ranks["Stability"] = rank_to_dict(np.abs(rlasso.scores_), names)

rfe = RFE(lr, n_features_to_select=5)
rfe.fit(X,Y)
ranks["RFE"] = rank_to_dict(map(float, rfe.ranking_), names, order=-1)

rf = RandomForestRegressor()
rf.fit(X,Y)
ranks["RF"] = rank_to_dict(rf.feature_importances_, names)

xgb = xgboost.XGBRegressor()
xgb.fit(X,Y)
ranks["XGB"] = rank_to_dict(xgb.feature_importances_, names)

f, pval  = f_regression(X, Y, center=True)
ranks["Corr."] = rank_to_dict(f, names)

mine = MINE()
mic_scores = []
for i in range(X.shape[1]):
    mine.compute_score(X[:,i], Y)
    m = mine.mic()
    mic_scores.append(m)

ranks["MIC"] = rank_to_dict(mic_scores, names)

r = {}
for name in names:
    r[name] = round(np.median([ranks[method][name]
                             for method in ranks.keys()]), 2)

methods = sorted(ranks.keys())
ranks["Mean"] = r
methods.append("Mean")

print "\t%s" % "\t".join(methods)
for name in names:
    print "%s\t%s" % (name, "\t".join(map(str,
                         [ranks[method][name] for method in methods])))


results_FS = pd.DataFrame(columns=methods)
for name in names:
    results_FS.loc[name] = map(float, [ranks[method][name] for method in methods])

results_FS['Features'] = results_FS.index
results_FS.reset_index(level=0, inplace=True)
results_FS.sort(['Ridge'], ascending=False).head()
```

```
results_FS = results_FS.drop(['index'], axis=1)
ax = sns.barplot(y="Features", x="Mean", data=results_FS.sort(['Mean'], ascending=False
```

```
        Corr.        Linear reg        MIC        RF        RFE        Ridge        Stability
sex        0.0        0.15        0.0        0.04        0.55        0.25        0.0        0.03
weight.challenge        0.0        0.57        1.0        0.26        0.81        0.32        0.
weight        0.02        0.52        0.3        0.23        0.77        0.26        0.0
ch.weight        0.13        0.85        0.35        0.24        1.0        0.39        0.0
pch.weight        0.15        1.0        0.44        0.49        1.0        0.87        0.0
hr.post.challenge        0.2        0.19        0.56        0.71        0.68        0.32
score.overall        0.98        0.18        0.73        1.0        0.9        0.13        0.0
score.left        1.0        0.67        0.75        0.61        1.0        1.0        0.0
score.right        0.89        0.61        0.69        0.21        0.32        0.68        0.0
rights.mobile.overall        0.31        0.54        0.32        0.0        0.74        0.35
rights.shakey.overall        0.04        0.23        0.05        0.0        0.16        0.11
rights.lethargic.overall        0.02        0.61        0.02        0.01        1.0        0.51
rights.nonmobile.overall        0.0        0.59        0.0        0.0        0.84        0.65
fail_to_right.one.side.overall        0.07        0.03        0.07        0.0        0.1
fail_to_right.mobile.hips.over        0.0        0.01        0.0        0.0        0.06        0
fail_to_right.lethargic.hips.overall        0.1        0.16        0.11        0.0        0.61
fail_to_right.lethargic.two.visits.overall        0.03        0.0        0.03        0.0
fail_to_right.nonmobile.hips.overall        0.14        0.19        0.16        0.0        0.29
rights.mobile.left        0.33        0.68        0.34        0.0        1.0        0.8        0
rights.shakey.left        0.04        0.57        0.05        0.01        0.97        0.6
rights.lethargic.left        0.01        0.4        0.01        0.01        0.35        0.24
rights.nonmobile.left        0.02        0.7        0.02        0.0        0.71        0.78
rights.only.left        0.03        0.21        0.03        0.0        0.39        0.25        0
fail_to_right.mobile.hips.left        0.01        0.28        0.01        0.02        0.94
fail_to_right.lethargic.hips.left        0.15        0.25        0.15        0.01        0.23
fail_to_right.lethargic.two.visits.left        0.03        0.0        0.03        0.0        0.1
fail_to_right.nonmobile.hips.left        0.14        0.29        0.17        0.0        0.26
rights.mobile.right        0.32        0.49        0.34        0.02        0.87        0.31
rights.shakey.right        0.03        0.03        0.03        0.01        0.45        0.07
rights.lethargic.right        0.0        0.33        0.01        0.02        0.52        0.37
rights.nonmobile.right        0.01        0.23        0.01        0.01        0.48        0.25
rightss.only.right        0.04        0.32        0.04        0.0        0.42        0.47
fail_to_right.mobile.hips.right        0.01        0.17        0.01        0.01        0.58
fail_to_right.lethargic.hips.right        0.11        0.36        0.11        0.01        0.65
fail_to_right.lethargic.two.visits.right        0.03        0.0        0.03        0.0        0.
fail_to_right.nonmobile.hips.right        0.14        0.11        0.17        0.0        0.19
```

```
/Users/Rad/anaconda2/lib/python2.7/site-packages/ipykernel/__main__.py:74: FutureWarning: sort(c
/Users/Rad/anaconda2/lib/python2.7/site-packages/ipykernel/__main__.py:76: FutureWarning: sort(c
```



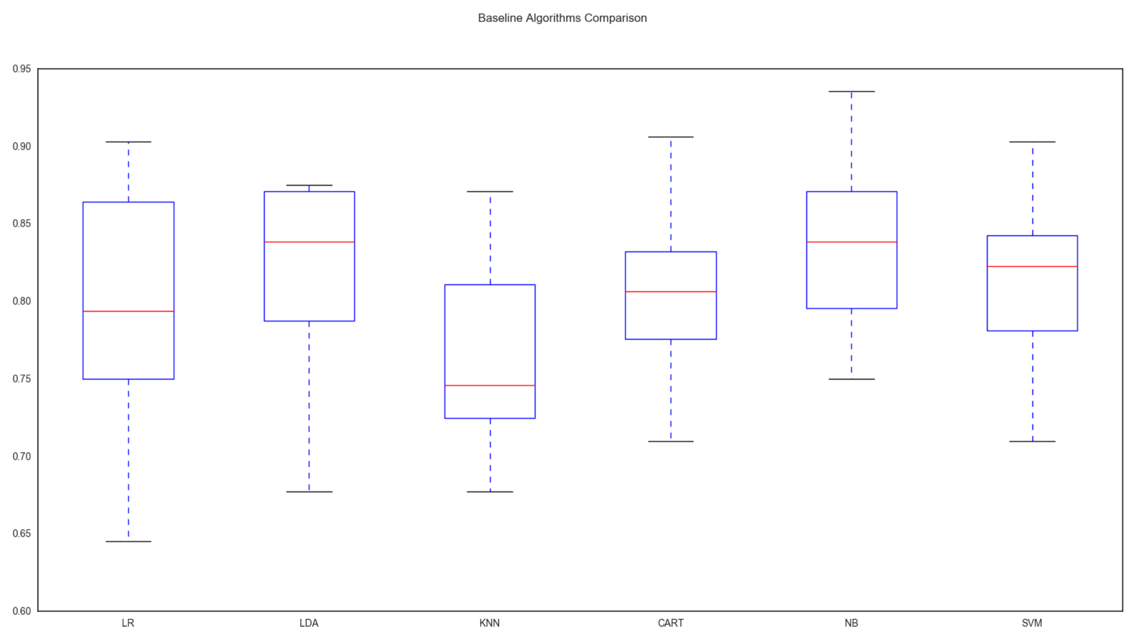

```
In [41]: X = df_scaled_df
         Y = df_clean_2["outcome"]
         names = df_scaled_df.columns

         X = X[["weight.challenge", "pch.weight", "score.left", "score.right", "score.overall",

         # Validation dataset

         validation_size = 0.20
         seed = 7
         X_train, X_validation, Y_train, Y_validation = cross_validation.train_test_split(X, Y,t
```

3.5.1 Base line Models

```
In [42]: def base_line_models(training_set, outcome):
             # Test options and evaluation metric
             num_folds = 10
             num_instances = len(training_set)
             seed = 7
             scoring = 'accuracy'

             # Spot-Check Algorithms
             models = []
             models.append(('LR', LogisticRegression()))
             models.append(('LDA', LinearDiscriminantAnalysis()))
             models.append(('KNN', KNeighborsClassifier()))
             models.append(('CART', DecisionTreeClassifier()))
             models.append(('NB', GaussianNB()))
             models.append(('SVM', SVC()))
             results = []
```

```
        names = []
        for name, model in models:
            kfold = cross_validation.KFold(n=num_instances, n_folds=num_folds, random_state
            cv_results = cross_validation.cross_val_score(model, training_set, outcome, cv=
            results.append(cv_results)
            names.append(name)
            msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
            print(msg)
        # Compare Algorithms
        fig = plt.figure()
        fig.suptitle('Baseline Algorithms Comparison')
        ax = fig.add_subplot(111)
        plt.boxplot(results)
        ax.set_xticklabels(names)
        plt.show()

    base_line_models(X_train, Y_train)
```

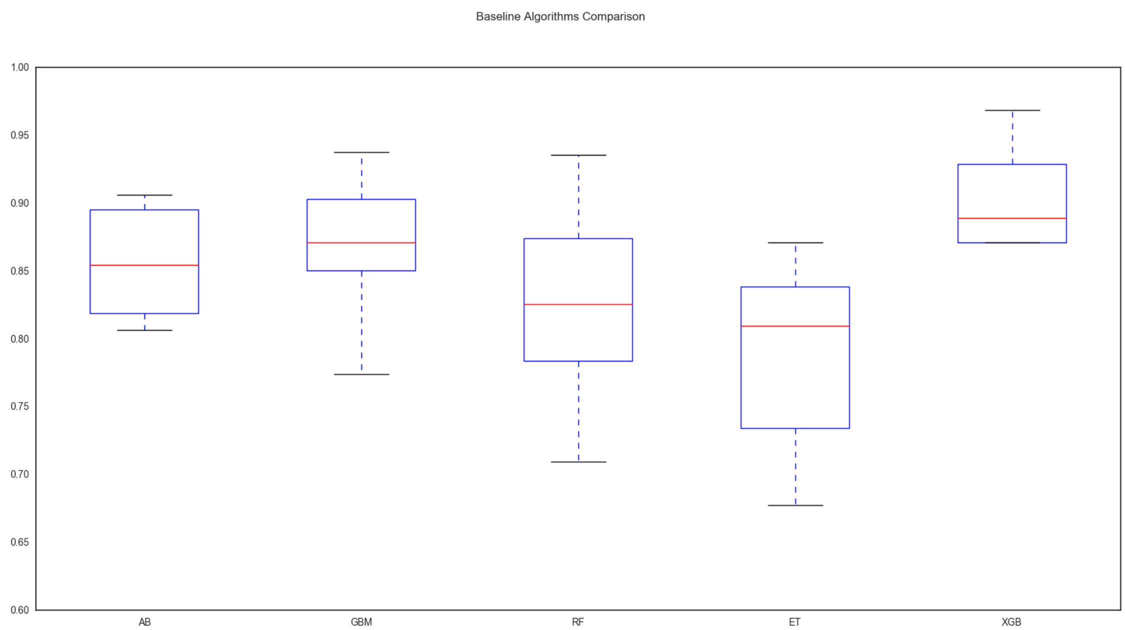
```
LR: 0.795665 (0.075804)
LDA: 0.818044 (0.061963)
KNN: 0.763609 (0.062758)
CART: 0.804839 (0.049125)
NB: 0.824496 (0.077055)
SVM: 0.801915 (0.073106)
```



3.5.2 Ensemble Methods

```
In [43]: def ensemble_models(training_set, outcome):
             # Test options and evaluation metric
             num_folds = 10
             num_instances = len(training_set)
             seed = 7
             scoring = 'accuracy'

             # ensembles
             ensembles = []
             ensembles.append(('AB', AdaBoostClassifier()))
             ensembles.append(('GBM', GradientBoostingClassifier()))
             ensembles.append(('RF', RandomForestClassifier()))
             ensembles.append(('ET', ExtraTreesClassifier()))
             ensembles.append(('XGB', xgboost.XGBClassifier()))
             results = []
             names = []
             for name, model in ensembles:
                 kfold = cross_validation.KFold(n=num_instances, n_folds=num_folds, random_state
                 cv_results = cross_validation.cross_val_score(model, training_set, outcome, cv=
                 results.append(cv_results)
                 names.append(name)
                 msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
                 print(msg)
             # Compare Algorithms
             fig = plt.figure()
             fig.suptitle('Baseline Algorithms Comparison')
             ax = fig.add_subplot(111)
             plt.boxplot(results)
             ax.set_xticklabels(names)
             plt.show()

         ensemble_models(X_train, Y_train)
```

```
AB: 0.856048 (0.038896)
GBM: 0.868750 (0.046874)
RF: 0.817742 (0.084342)
ET: 0.792540 (0.065459)
XGB: 0.891028 (0.061705)
```



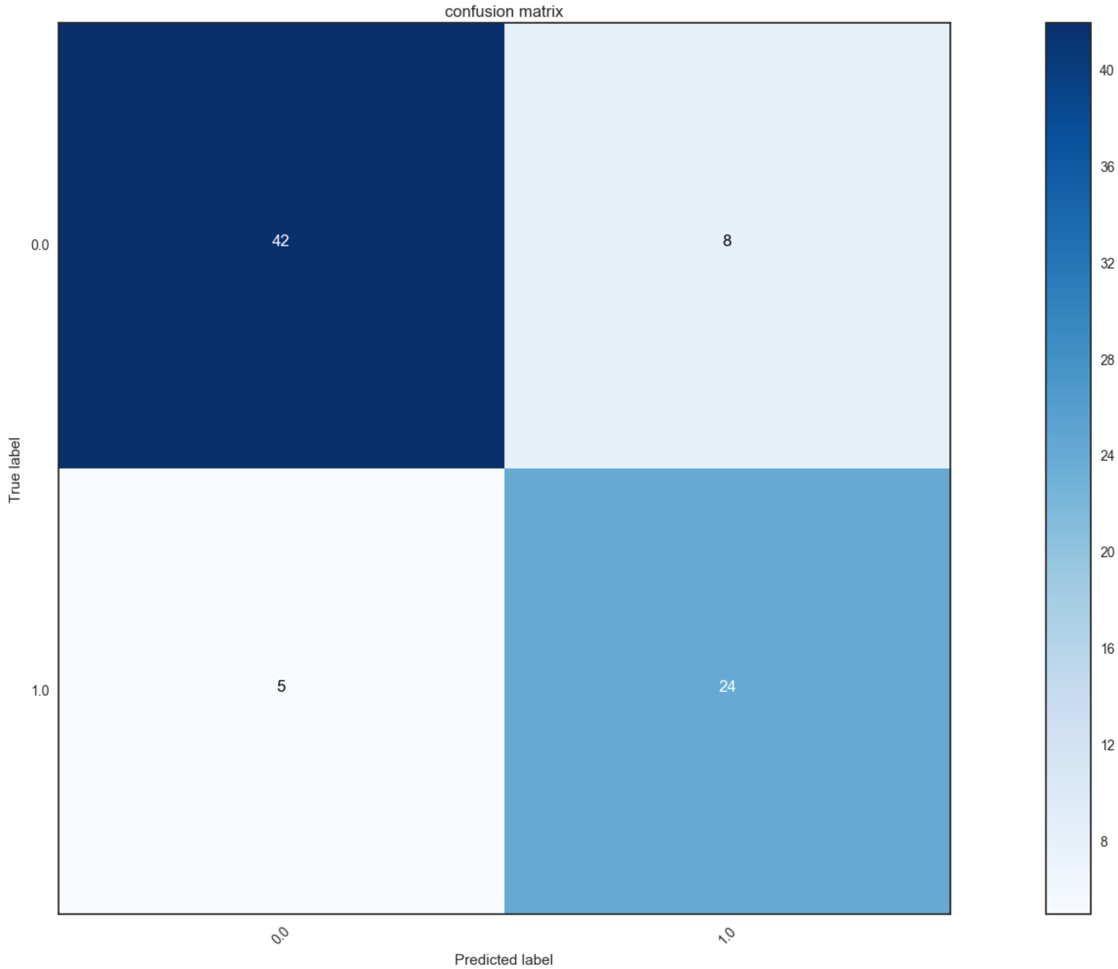
3.5.3 Model Validation

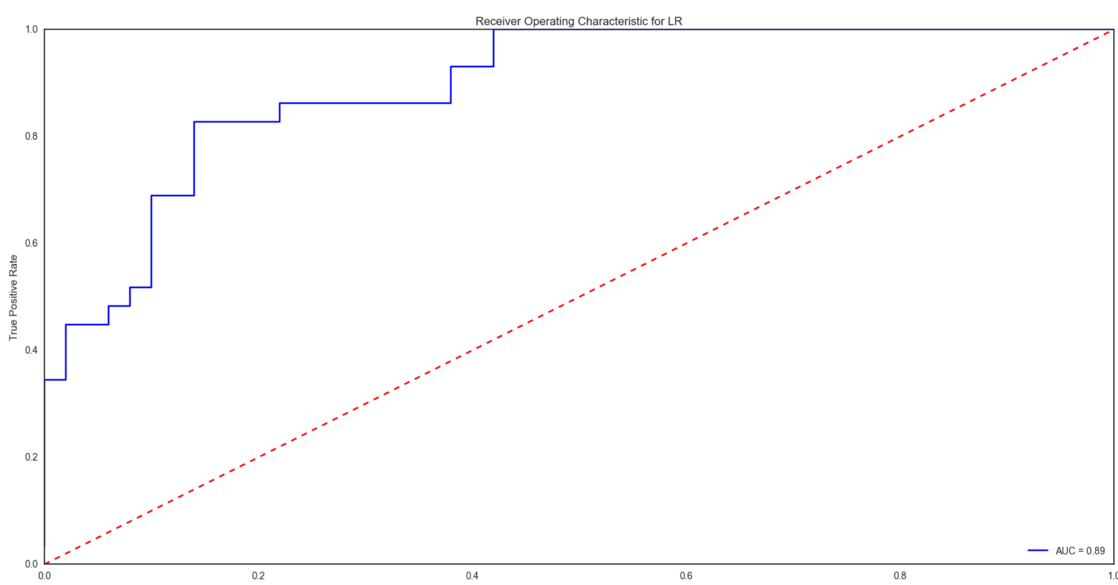
```
In [44]: import itertools
         import matplotlib.pyplot as plt


         def plot_confusion_matrix(cm, classes,
                                   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`.
             """
             plt.figure(1)
             plt.imshow(cm, interpolation='nearest', cmap=cmap)
             plt.title(title)
             plt.colorbar()
             tick_marks = np.arange(len(classes))
             plt.xticks(tick_marks, classes, rotation=45)
             plt.yticks(tick_marks, classes)

             #if normalize:
             #    cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
             #    print("Normalized confusion matrix")
             #else:
             #    print('Confusion matrix, without normalization')
```

```python
    print(cm)

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

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


def validate_models(training_set, outcome, validation_data, validation_outcome):

    models = []

    #baselines

    models.append(('LR', LogisticRegression()))
    models.append(('LDA', LinearDiscriminantAnalysis()))
    models.append(('KNN', KNeighborsClassifier()))
    models.append(('CART', DecisionTreeClassifier()))
    models.append(('NB', GaussianNB()))
    models.append(('SVM', SVC(probability=True)))

    #ensemble

    models.append(('AB', AdaBoostClassifier()))
    models.append(('GBM', GradientBoostingClassifier()))
    models.append(('RF', RandomForestClassifier()))
    models.append(('ET', ExtraTreesClassifier()))
    models.append(('XGB', xgboost.XGBClassifier()))


    for name, model in models:
        mod = model
        mod.fit(training_set, outcome)
        # estimate accuracy on validation dataset
        predictions = mod.predict(validation_data)
        print "Validation based on " + name
        print(accuracy_score(validation_outcome, predictions))
        print(confusion_matrix(validation_outcome, predictions))
        cfmat = confusion_matrix(validation_outcome, predictions)
        plot_confusion_matrix(cfmat, classes=[0.0, 1.0] , title='confusion matrix')

        print(classification_report(validation_outcome, predictions))
```

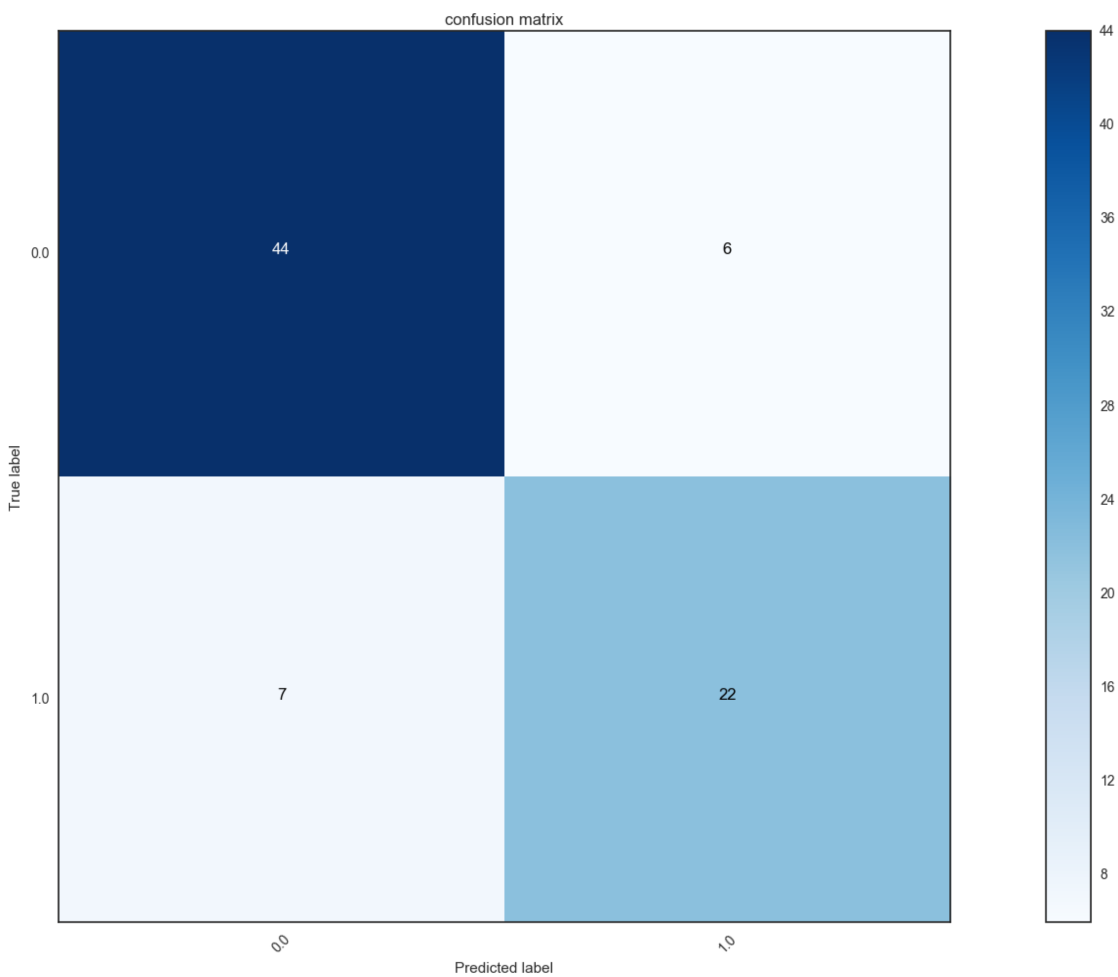
```
                # calculate the fpr and tpr for all thresholds of the classification
                probs = mod.predict_proba(validation_data)
                preds = probs[:,1]
                fpr, tpr, threshold = roc_curve(validation_outcome, preds)
                roc_auc = auc(fpr, tpr)

                # method I: plt
                plt.figure(2)
                plt.title('Receiver Operating Characteristic for ' + name)
                plt.plot(fpr, tpr, 'b', label = 'AUC = %0.2f' % roc_auc)
                plt.legend(loc = 'lower right')
                plt.plot([0, 1], [0, 1],'r--')
                plt.xlim([0, 1])
                plt.ylim([0, 1])
                plt.ylabel('True Positive Rate')
                plt.xlabel('False Positive Rate')
                plt.show()

        validate_models(X_train, Y_train, X_validation, Y_validation)
```

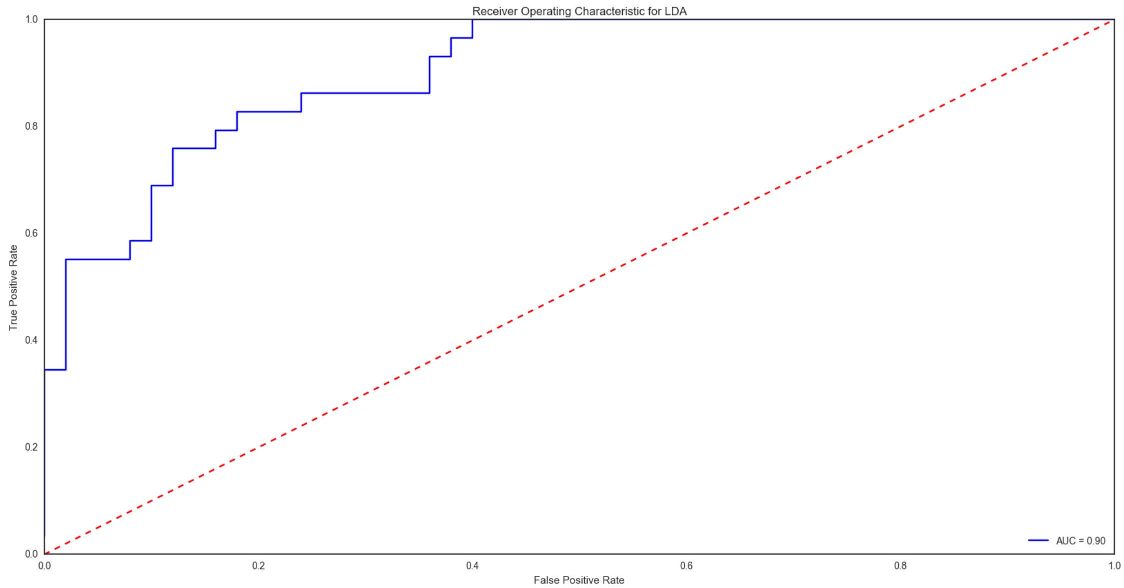
```
Validation based on LR
0.835443037975
[[42  8]
 [ 5 24]]
[[42  8]
 [ 5 24]]
             precision    recall  f1-score   support

        0.0       0.89      0.84      0.87        50
        1.0       0.75      0.83      0.79        29

avg / total       0.84      0.84      0.84        79
```


confusion matrix
42
8
5
24
0.0
1.0
True label
Predicted label
40
36
32
28
24
20
16
12
8

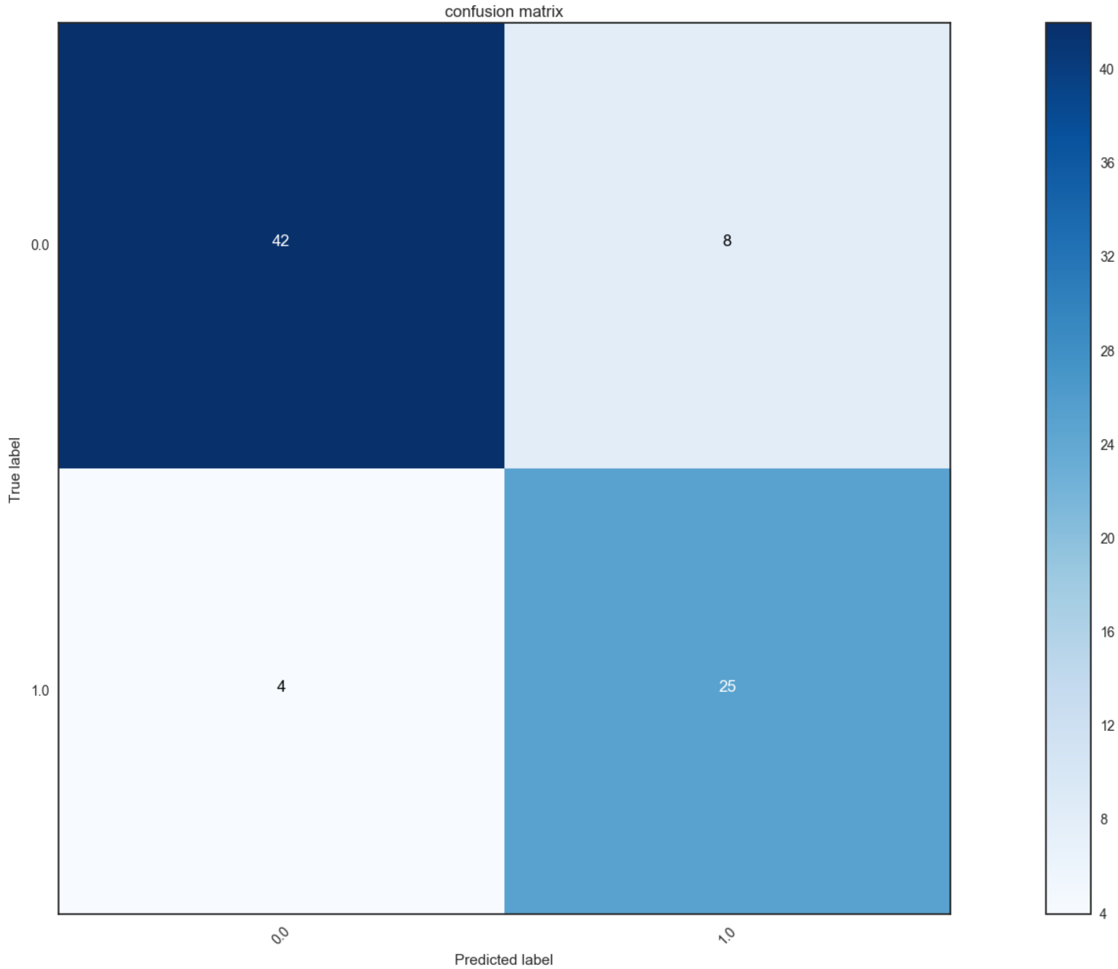

Receiver Operating Characteristic for LR
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.89

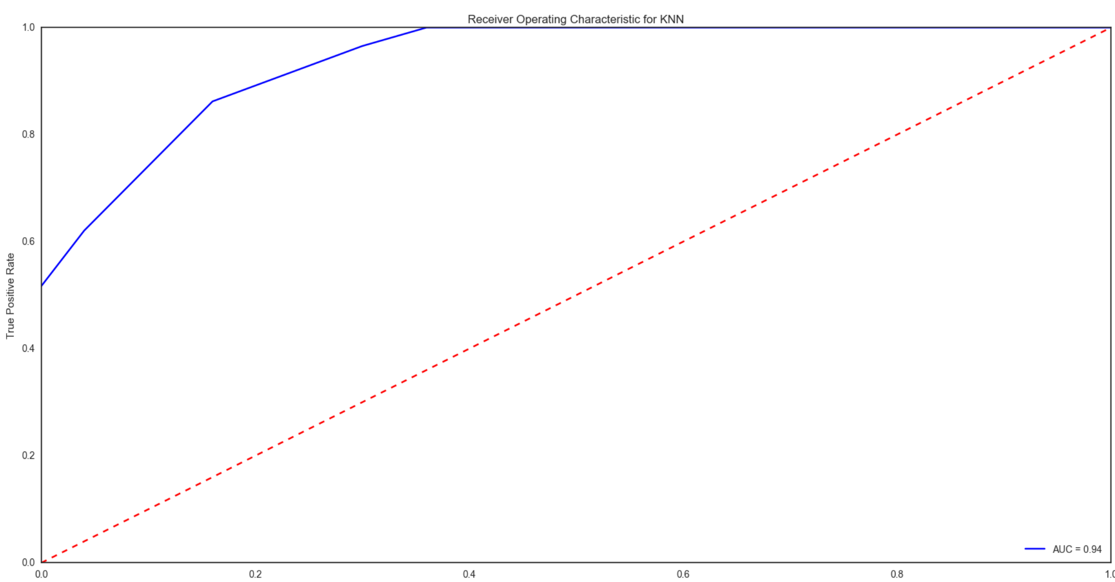
```
Validation based on LDA
0.835443037975
[[44  6]
 [ 7 22]]
[[44  6]
 [ 7 22]]
             precision    recall  f1-score   support

        0.0       0.86      0.88      0.87        50
        1.0       0.79      0.76      0.77        29

avg / total       0.83      0.84      0.83        79
```



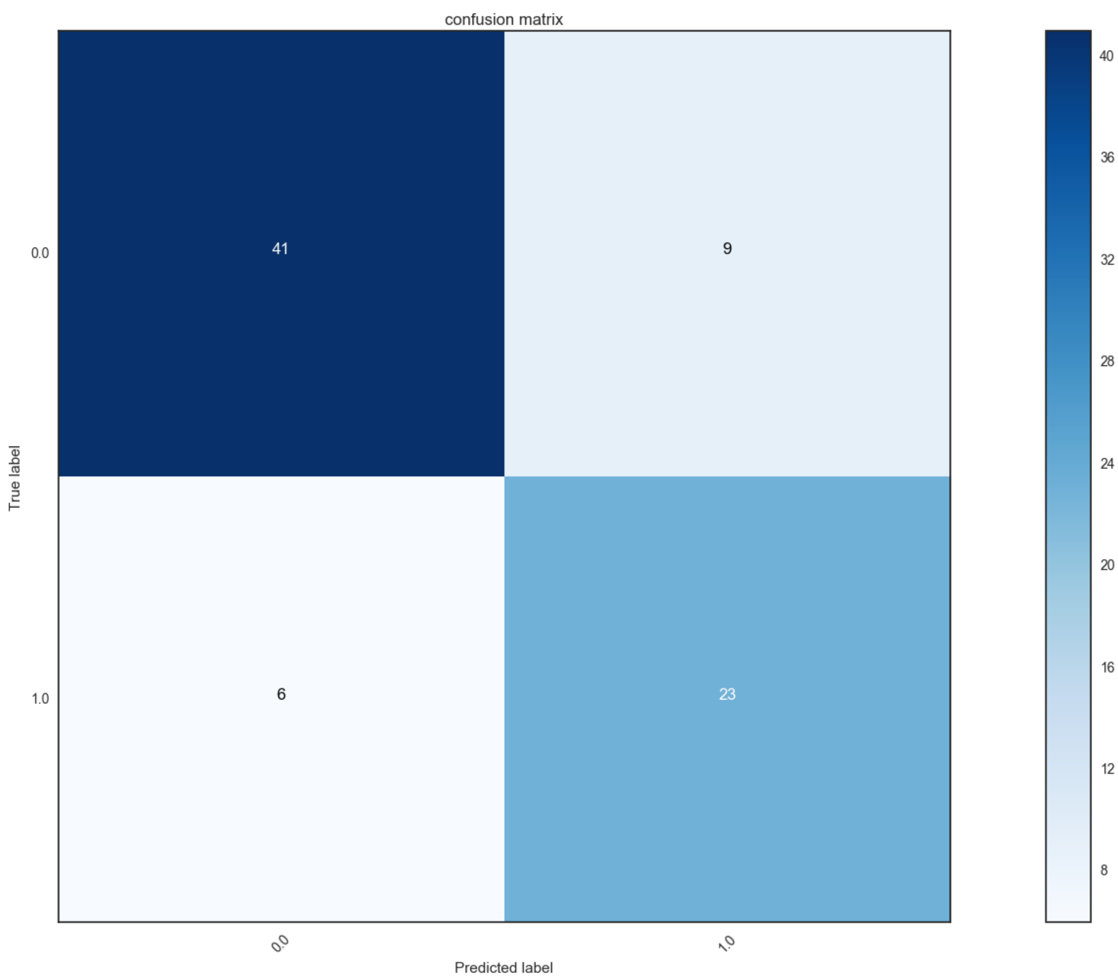


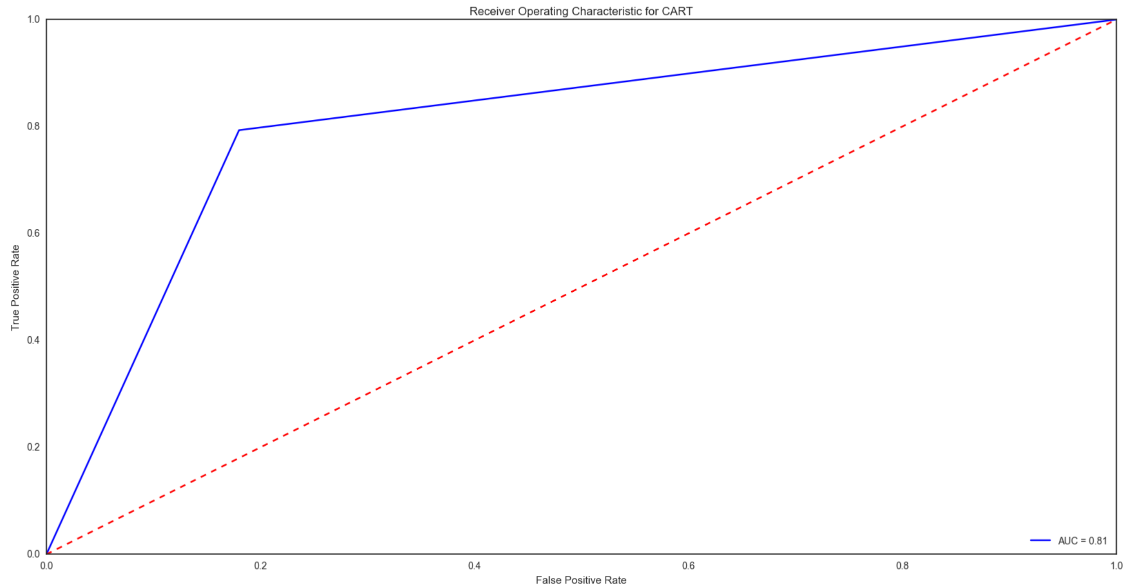

```
Validation based on KNN
0.848101265823
[[42  8]
 [ 4 25]]
[[42  8]
 [ 4 25]]
             precision    recall  f1-score   support

        0.0       0.91      0.84      0.87        50
        1.0       0.76      0.86      0.81        29

avg / total       0.86      0.85      0.85        79
```


confusion matrix
True label
0.0
1.0
42
8
4
25
Predicted label
0.0
1.0
40
36
32
28
24
20
16
12
8
4

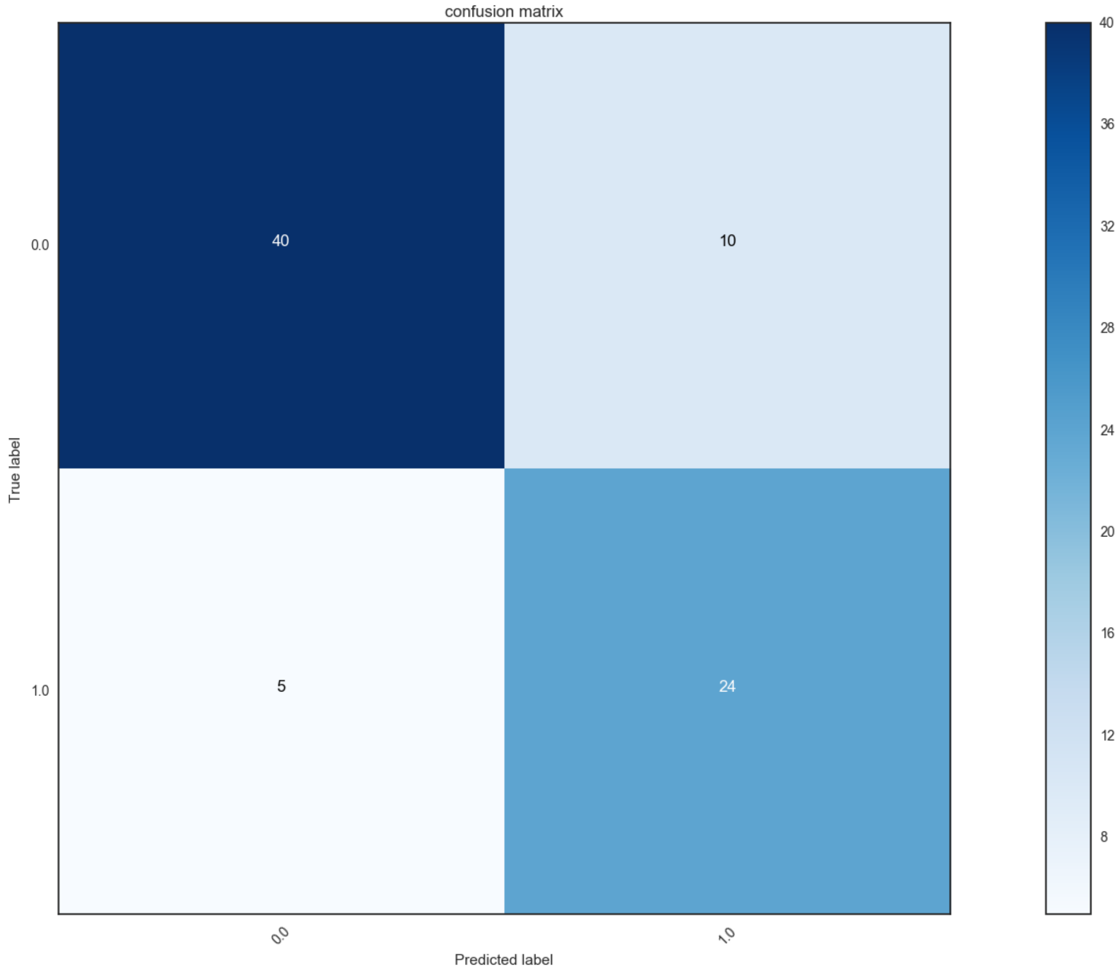

Receiver Operating Characteristic for KNN
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.94

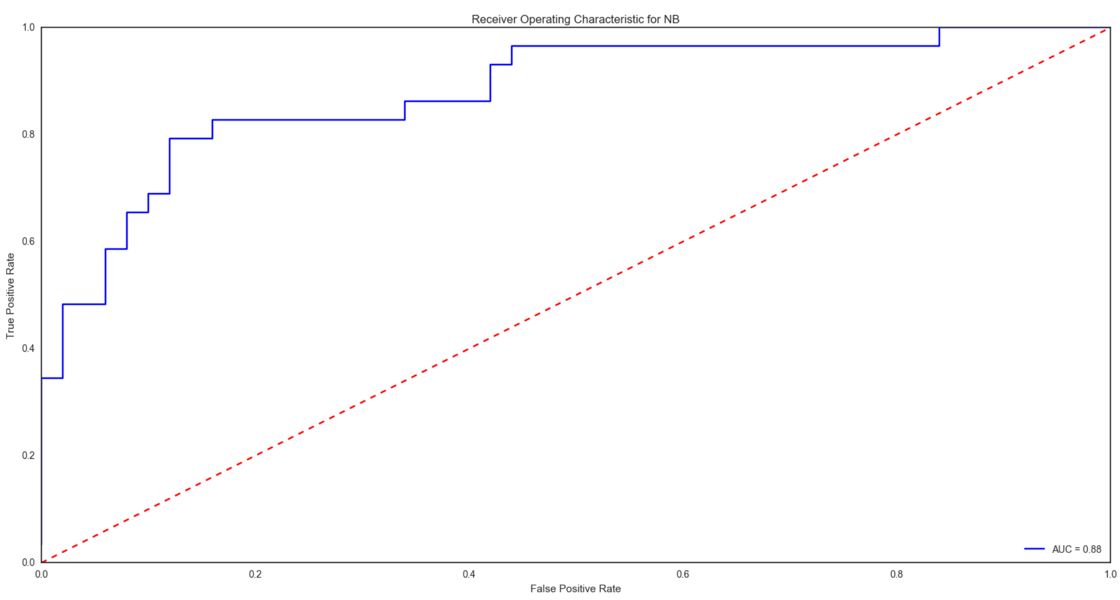
```
Validation based on CART
0.810126582278
[[41  9]
 [ 6 23]]
[[41  9]
 [ 6 23]]
             precision    recall  f1-score   support

        0.0       0.87      0.82      0.85        50
        1.0       0.72      0.79      0.75        29

avg / total       0.82      0.81      0.81        79
```



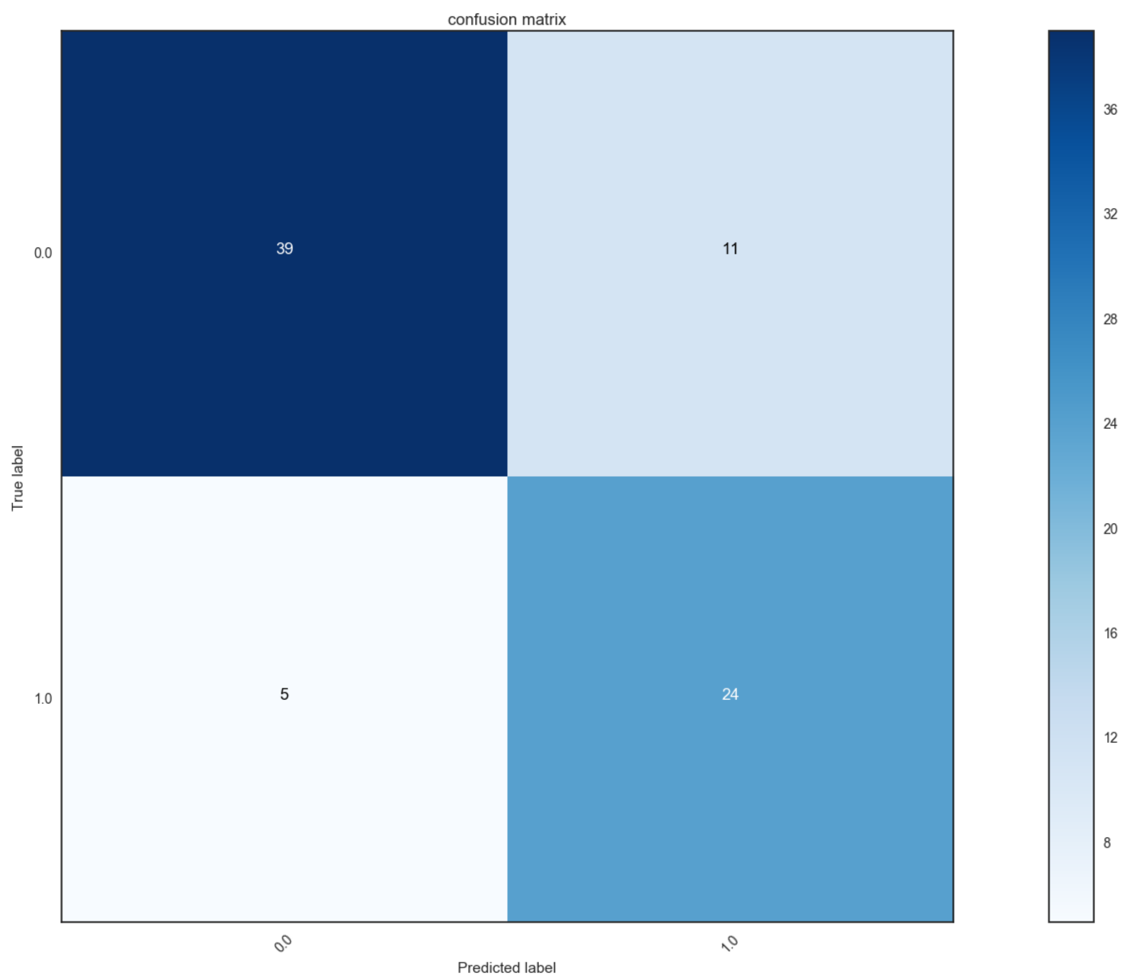


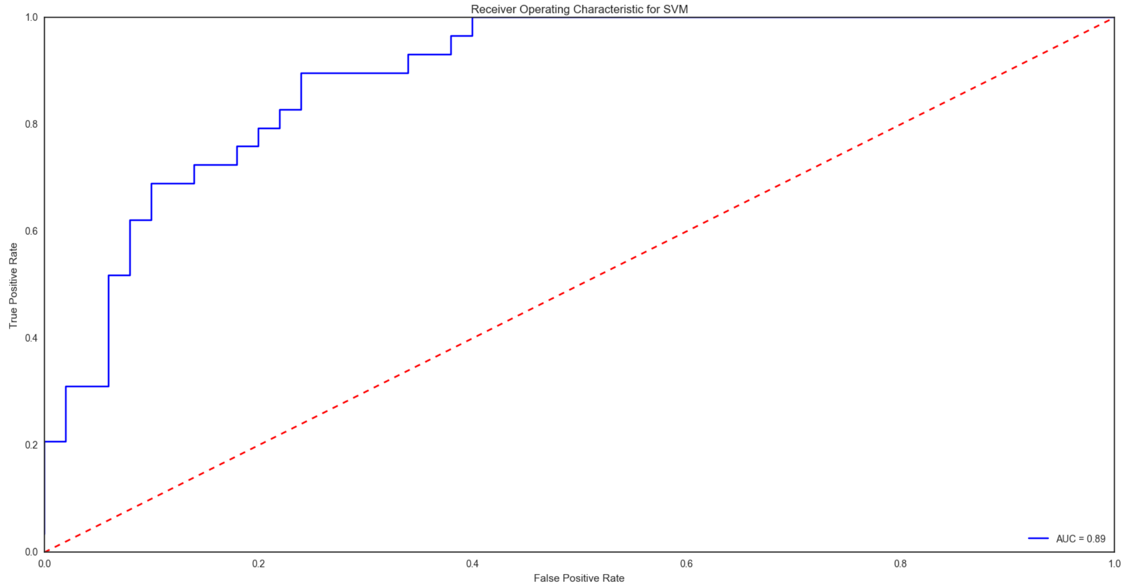

```
Validation based on NB
0.810126582278
[[40 10]
 [ 5 24]]
[[40 10]
 [ 5 24]]
             precision    recall  f1-score   support

        0.0       0.89      0.80      0.84        50
        1.0       0.71      0.83      0.76        29

avg / total       0.82      0.81      0.81        79
```


confusion matrix
True label
0.0
1.0
40
10
5
24
0.0
1.0
Predicted label
40
36
32
28
24
20
16
12
8

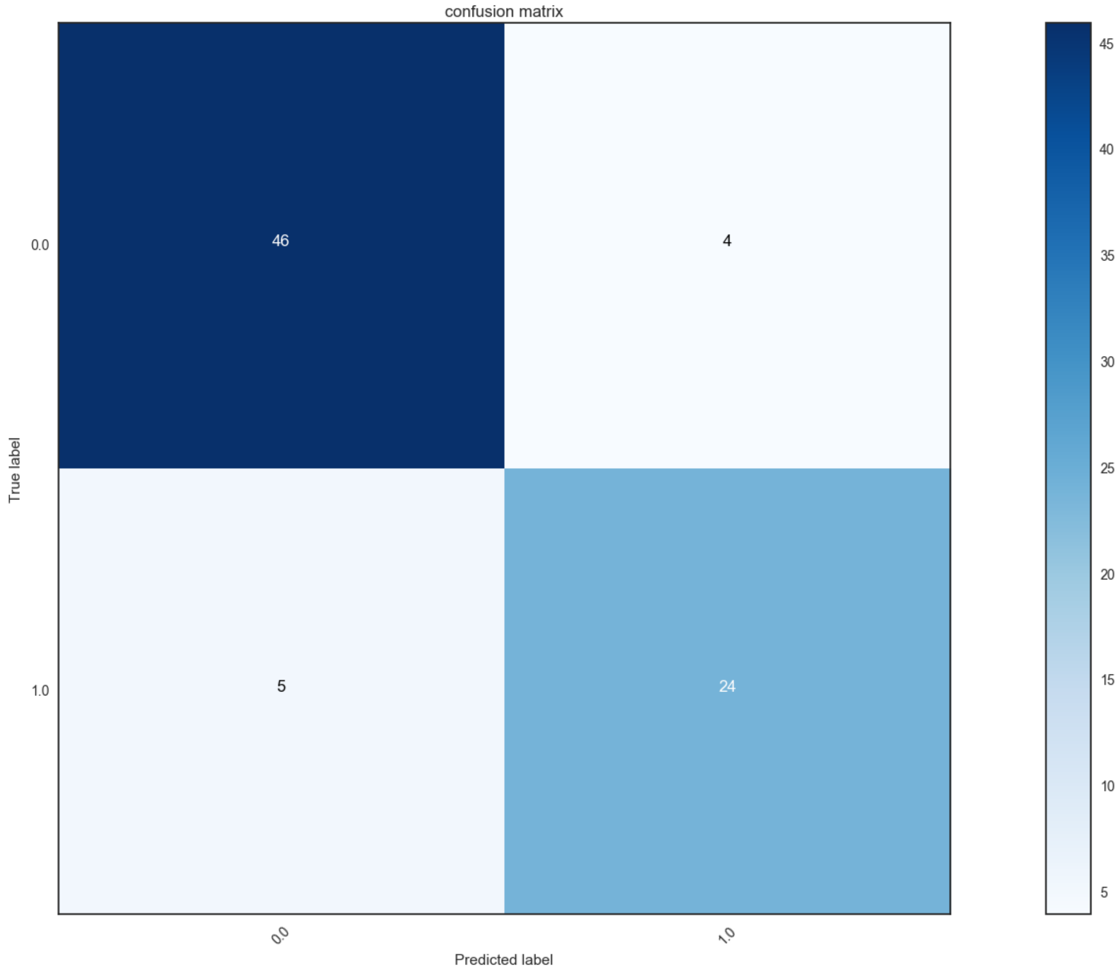

Receiver Operating Characteristic for NB
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.88

```
Validation based on SVM
0.79746835443
[[39 11]
 [ 5 24]]
[[39 11]
 [ 5 24]]
             precision    recall  f1-score   support

        0.0       0.89      0.78      0.83        50
        1.0       0.69      0.83      0.75        29

avg / total       0.81      0.80      0.80        79
```

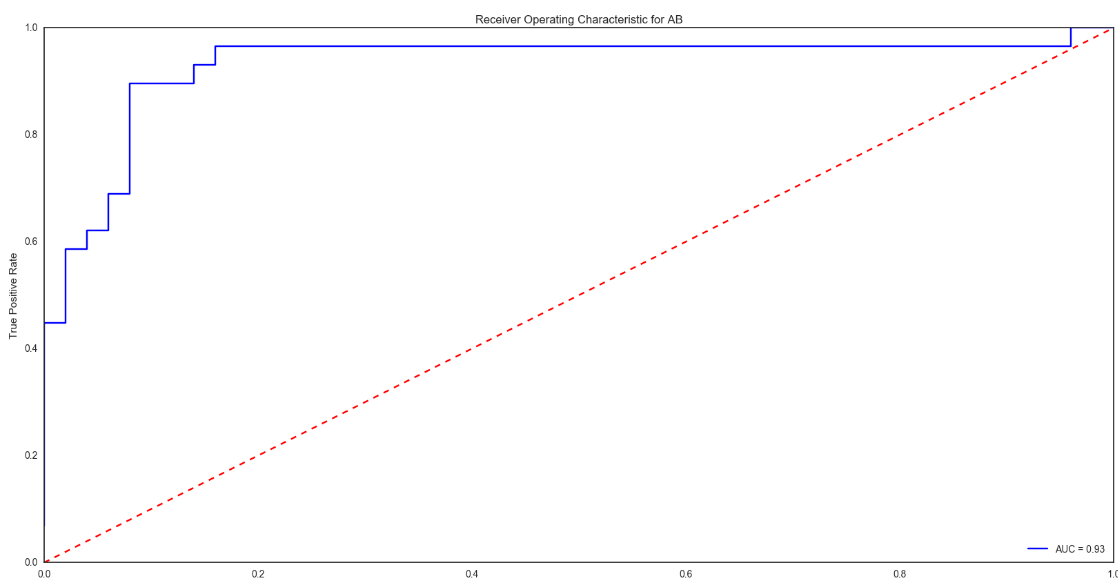





```
Validation based on AB
0.886075949367
[[46  4]
 [ 5 24]]
[[46  4]
 [ 5 24]]
             precision    recall  f1-score   support

        0.0       0.90      0.92      0.91        50
        1.0       0.86      0.83      0.84        29

avg / total       0.89      0.89      0.89        79
```

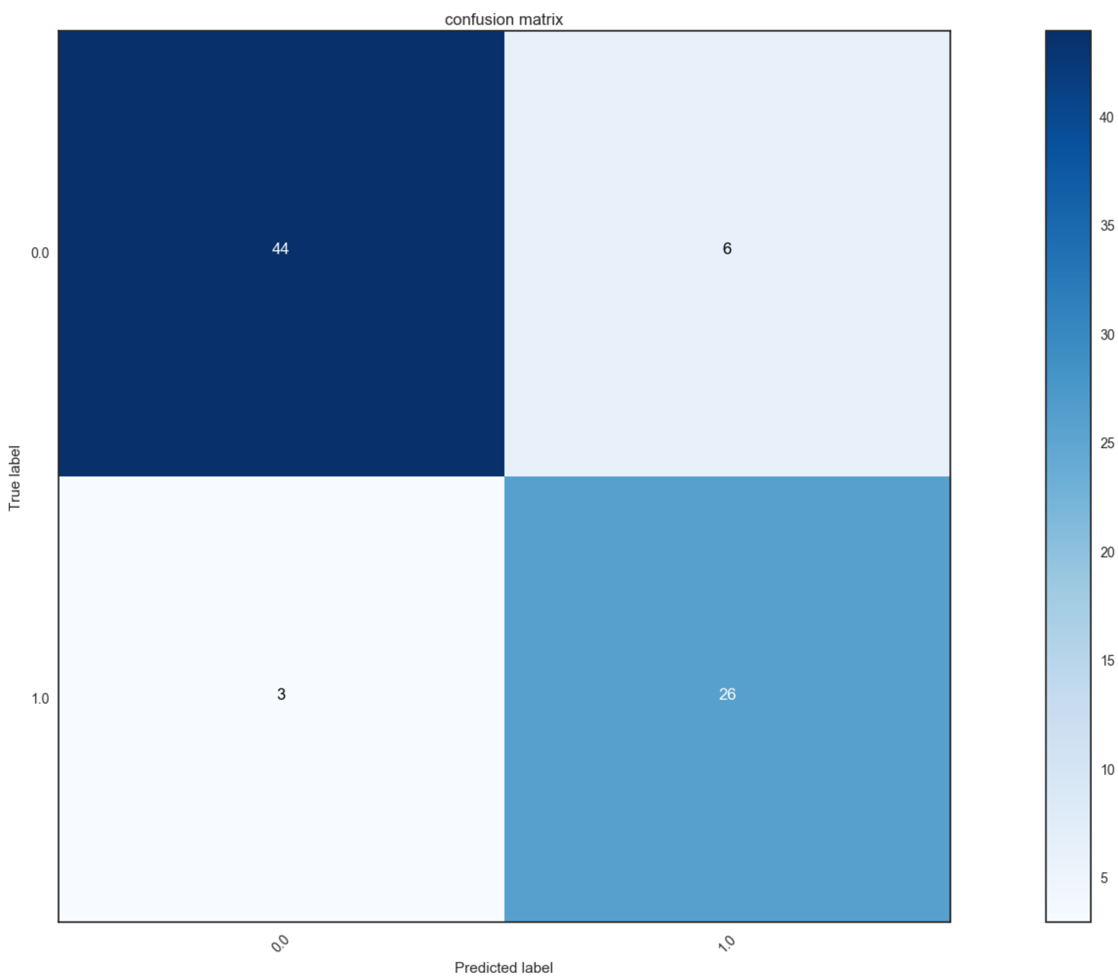


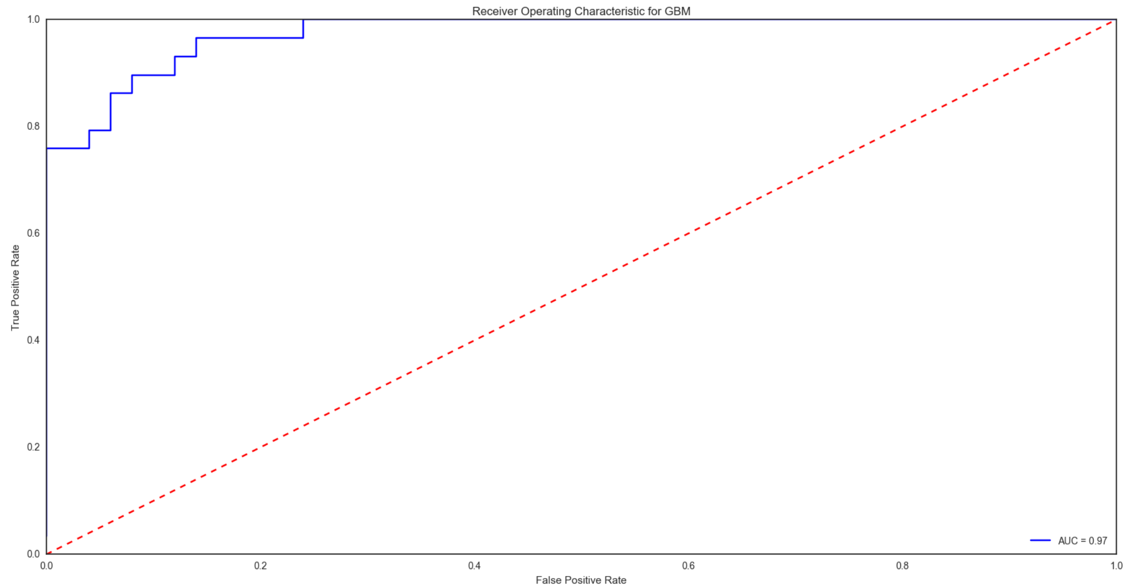
confusion matrix
46
4
5
24
0.0
1.0
True label
Predicted label
45
40
35
30
25
20
15
10
5



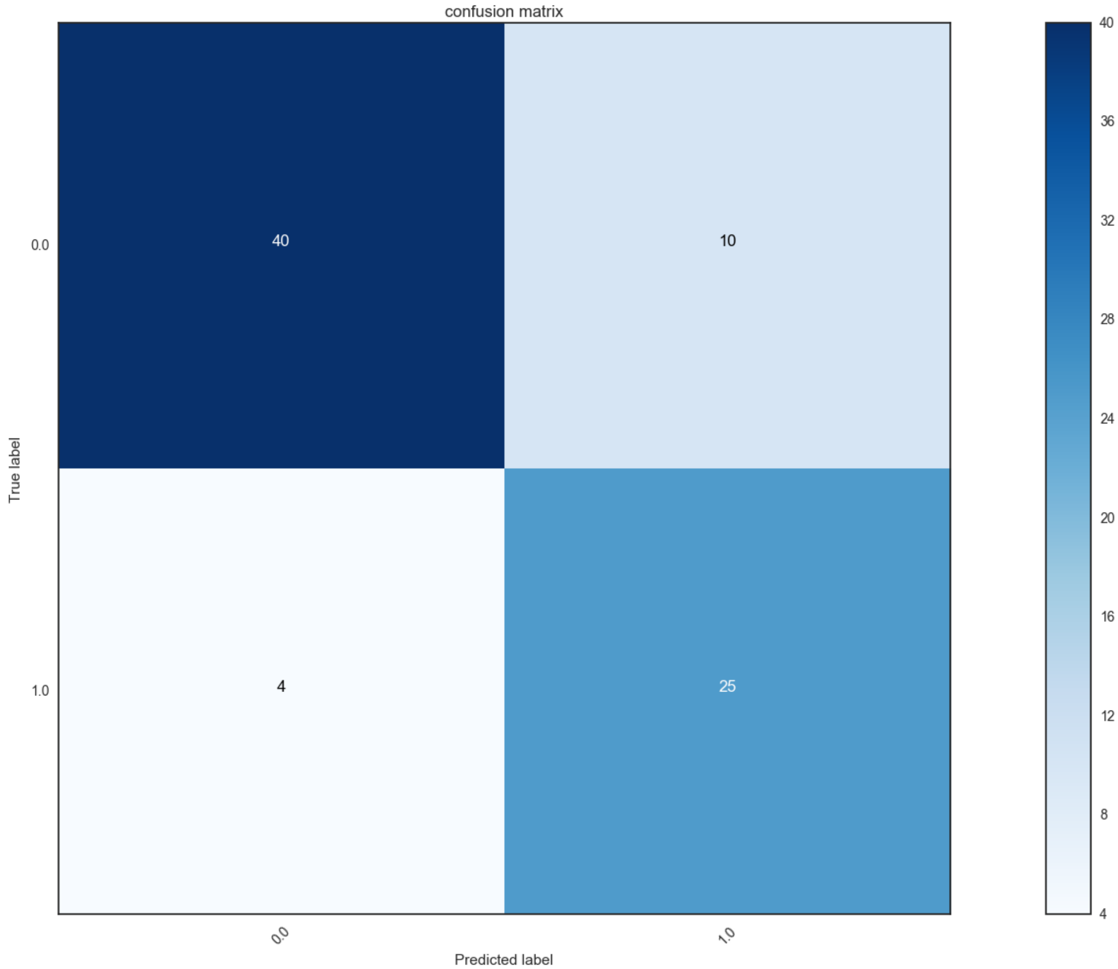
Receiver Operating Characteristic for AB
True Positive Rate
False Positive Rate
AUC = 0.93
0.0
0.2
0.4
0.6
0.8
1.0

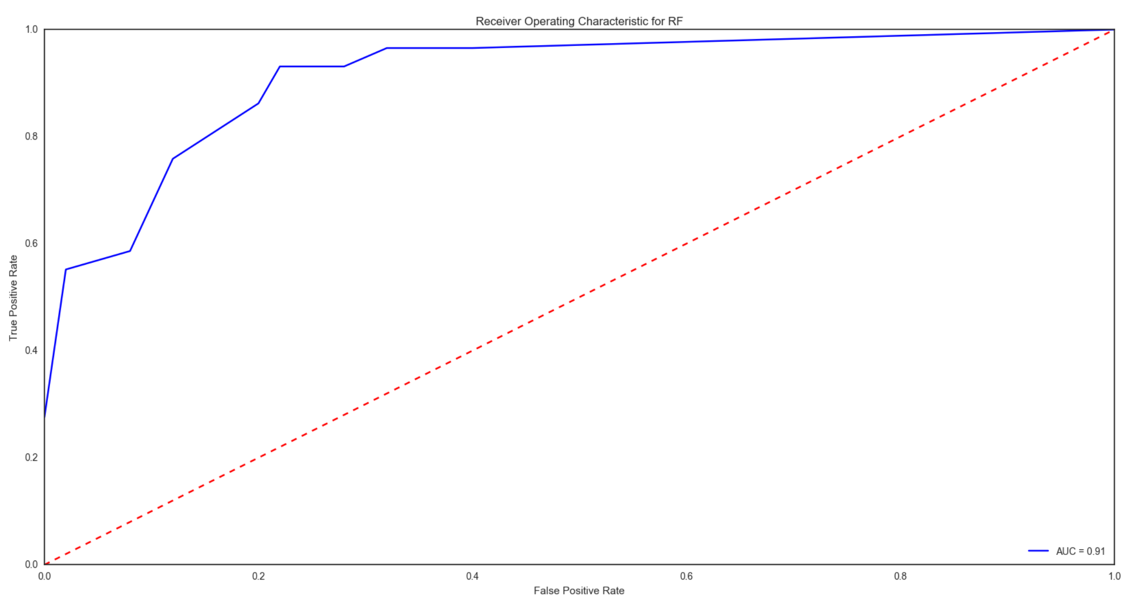
```
Validation based on GBM
0.886075949367
[[44  6]
 [ 3 26]]
[[44  6]
 [ 3 26]]
             precision    recall  f1-score   support

        0.0       0.94      0.88      0.91        50
        1.0       0.81      0.90      0.85        29

avg / total       0.89      0.89      0.89        79
```



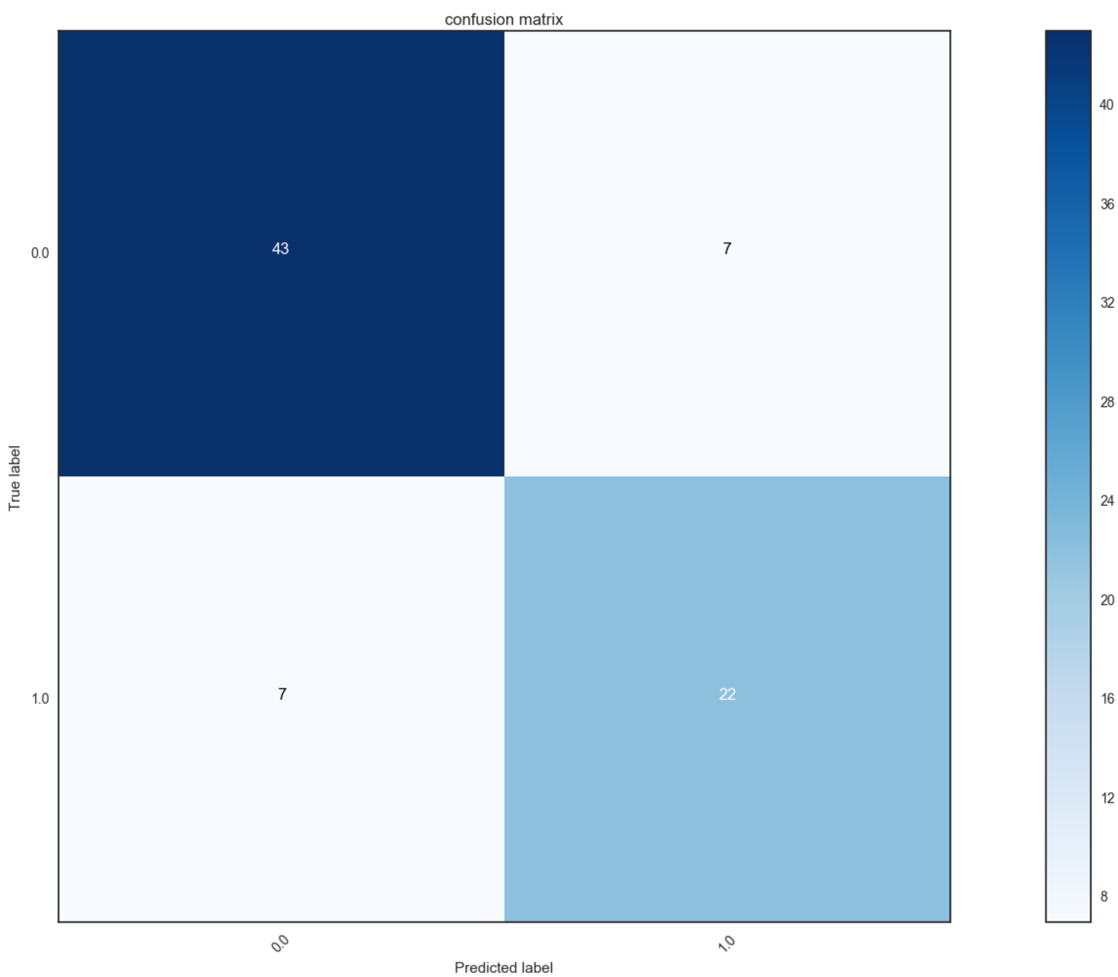


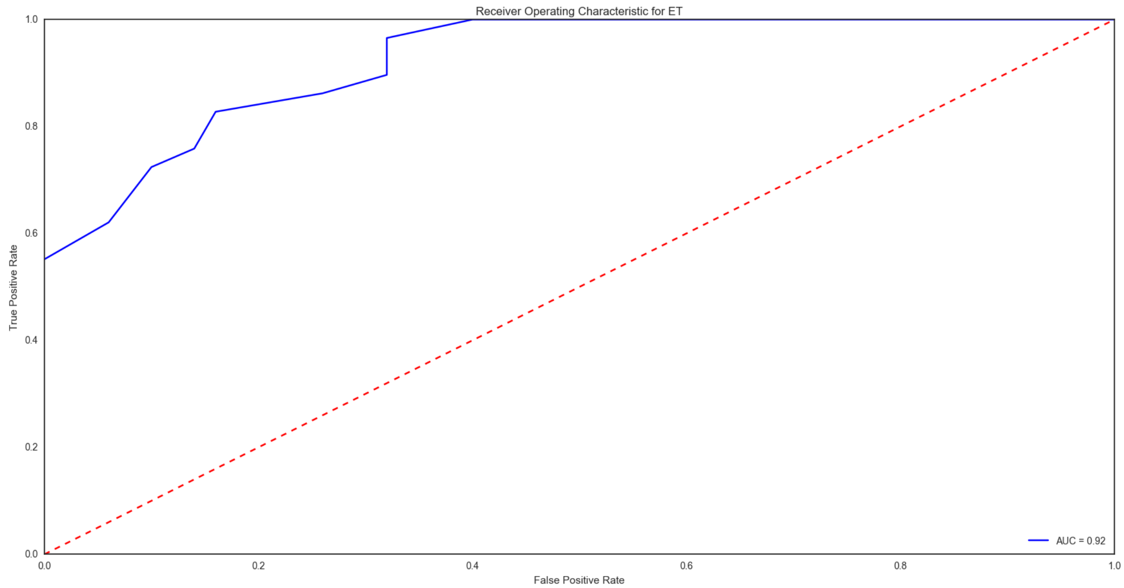

```
Validation based on RF
0.822784810127
[[40 10]
 [ 4 25]]
[[40 10]
 [ 4 25]]
             precision    recall  f1-score   support

        0.0       0.91      0.80      0.85        50
        1.0       0.71      0.86      0.78        29

avg / total       0.84      0.82      0.83        79
```


confusion matrix
40
10
4
25
0.0
1.0
True label
0.0
1.0
Predicted label
40
36
32
28
24
20
16
12
8
4

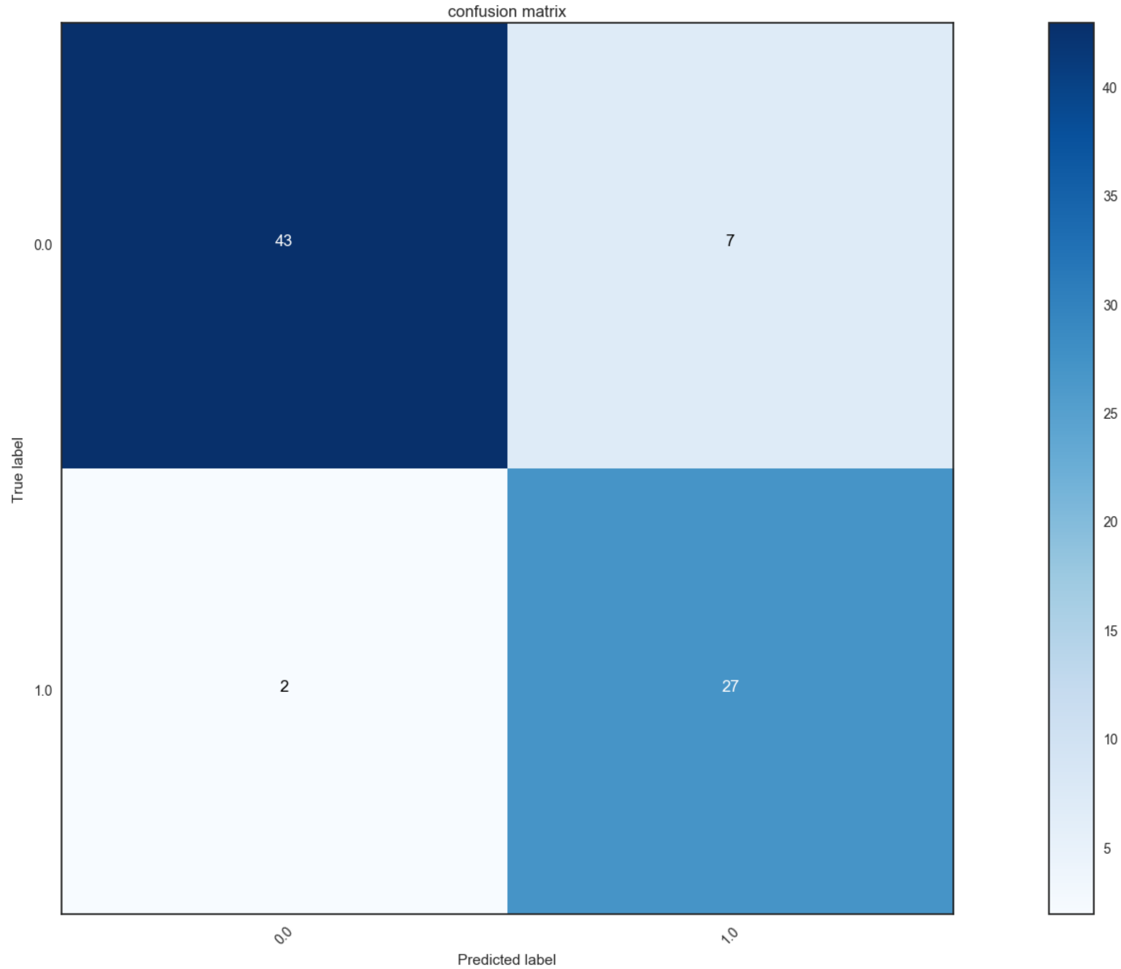

Receiver Operating Characteristic for RF
True Positive Rate
False Positive Rate
AUC = 0.91
0.0
0.2
0.4
0.6
0.8
1.0

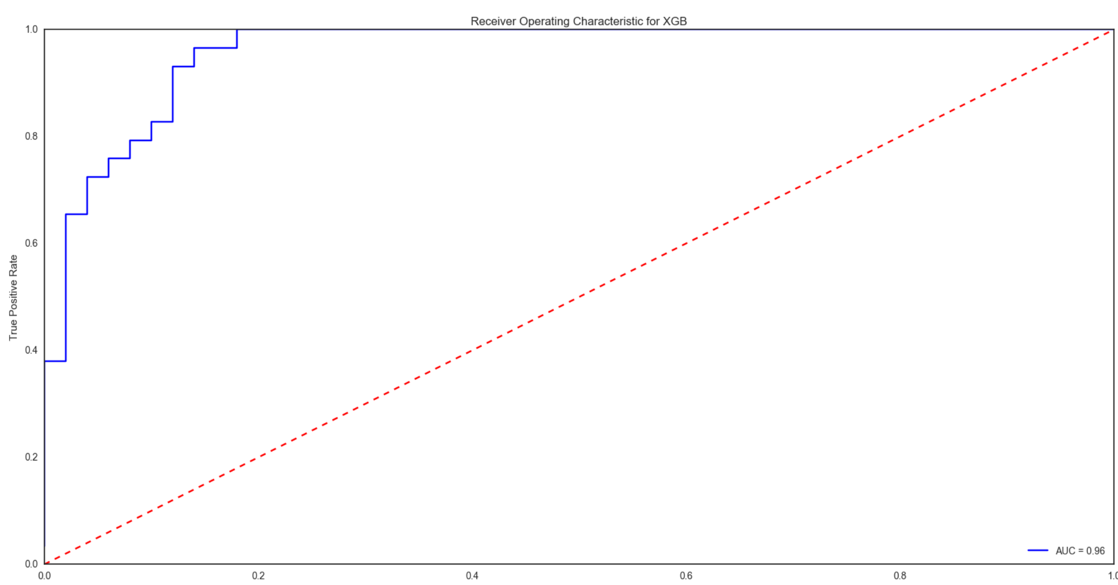
```
Validation based on ET
0.822784810127
[[43  7]
 [ 7 22]]
[[43  7]
 [ 7 22]]
             precision    recall  f1-score   support

        0.0       0.86      0.86      0.86        50
        1.0       0.76      0.76      0.76        29

avg / total       0.82      0.82      0.82        79
```






```
Validation based on XGB
0.886075949367
[[43  7]
 [ 2 27]]
[[43  7]
 [ 2 27]]
             precision    recall  f1-score   support

        0.0       0.96      0.86      0.91        50
        1.0       0.79      0.93      0.86        29

avg / total       0.90      0.89      0.89        79
```

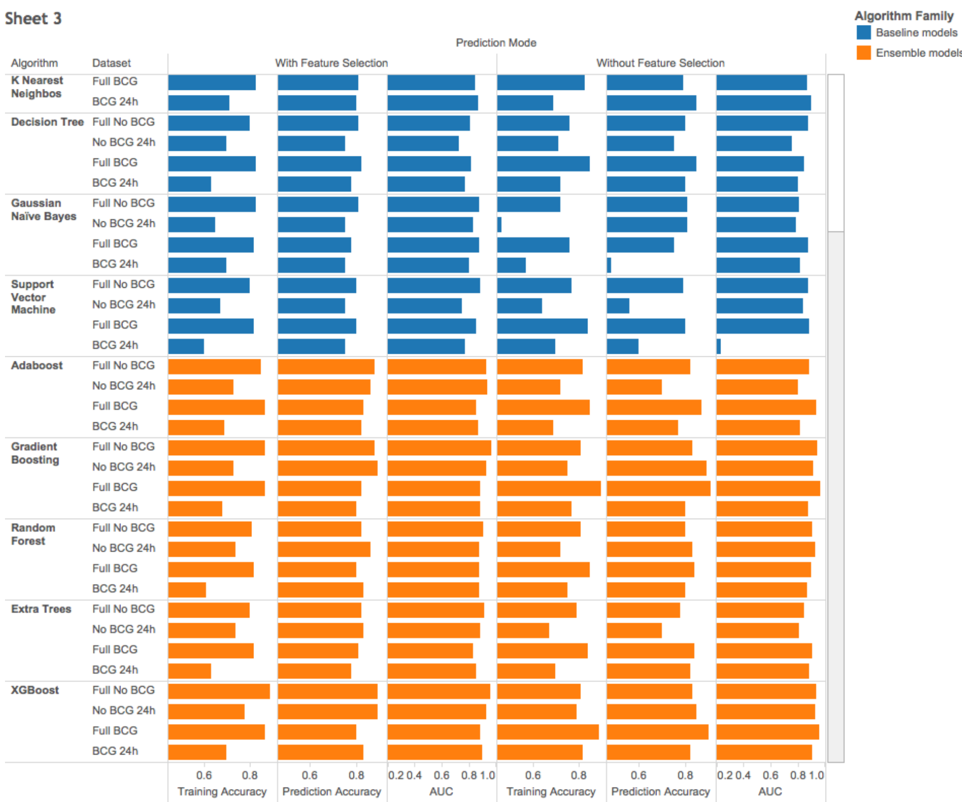

confusion matrix
True label
0.0
1.0
43
7
2
27
0.0
1.0
Predicted label
40
35
30
25
20
15
10
5


Receiver Operating Characteristic for XGB
True Positive Rate
False Positive Rate
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
AUC = 0.96

3.6 Classification across all datasets

Now that we discovered how the dataset is analyzed for classification we can reproduce the same approach to the other datasets and visualize all classification for all datasets in a single plot.

In these two views we're reporting 3 measures that we discovered earlier, the prediction accuracy, the training accuracy as well as the AUC for each round of training



We have some important points to notice here from this plot :

- Across all datasets, ensemble methods seem to work much better than the baseline algorithms for both training and prediction accuracy, the models trained with boosting algorithms perform better
- xgboost outperforms most of the algorithms almost in all datasets
- We see a slight improvement in accuracy **after feature selection** which proves two important things, the feature selection approach we had is efficient (trying several feature selection algorithms and use the overall average of feature importance) and the features selected are enough to predict the right classes, other features bringing noise are thus discarded and the prediction is more accurate
- There is a sort of pattern in the prediciton accuracies with focus only on the 12-24h time frame, a slight decrease in accuracy related to the reduction of the dataset mainly is obsereved.

- xgboost looks not sensitive to the dataset reduction, and accuracy is almost the same wether it is a full dataset or a sampled one.

4 Phase 2 : Visualizing thresholds

In This section we will pick **xgboost** as our winner algorithm and try to visualize the selected features and how they impact the final outcome. To do that we will rollback to the original data instead of the transformed ones, just to see if there is any trend so far

```
In [45]: df_clean_2 = df_clean_2.reset_index(drop=True)
         df_final = df_final.reset_index(drop=True)
```

```
In [46]: X = df_final
         Y = df_clean_2["outcome"]
         X = X[["weight.challenge", "pch.weight", "score.left", "score.right", "score.overall",
         names = df_scaled_df.columns


         X_final = pd.DataFrame(X, index=X_validation.index)
         Y_final = pd.DataFrame(Y, index=X_validation.index)
```

```
In [47]: table = pd.concat([X_final, Y_final], axis=1)
         table.head()
```

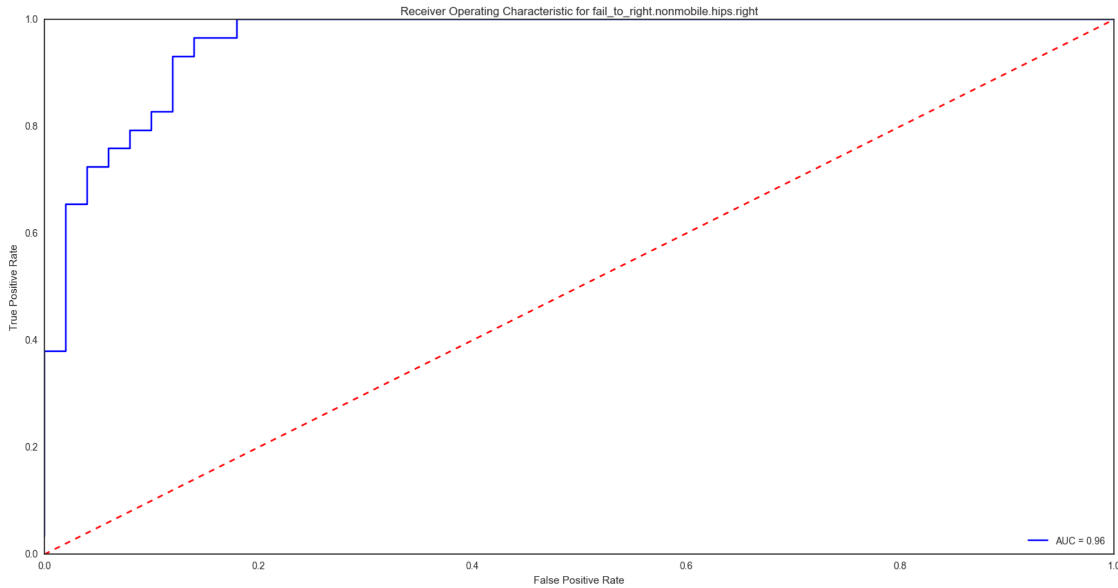
```
Out[47]:      weight.challenge  pch.weight  score.left  score.right  score.overall  \
         238              3.83       2.350         8.0          8.0            8.0
         270              3.38      -4.438         5.0          3.0            4.0
         213              3.93       5.344         8.0          8.0            8.0
         357              3.23       8.050         8.0          8.0            8.0
         57               4.99      -7.214         6.0          6.0            6.0

              hr.post.challenge  outcome
         238             41.333      0.0
         270             13.250      0.0
         213             41.583      0.0
         357             47.420      0.0
         57              35.433      0.0
```

Let's use XGBOOST to classify our data

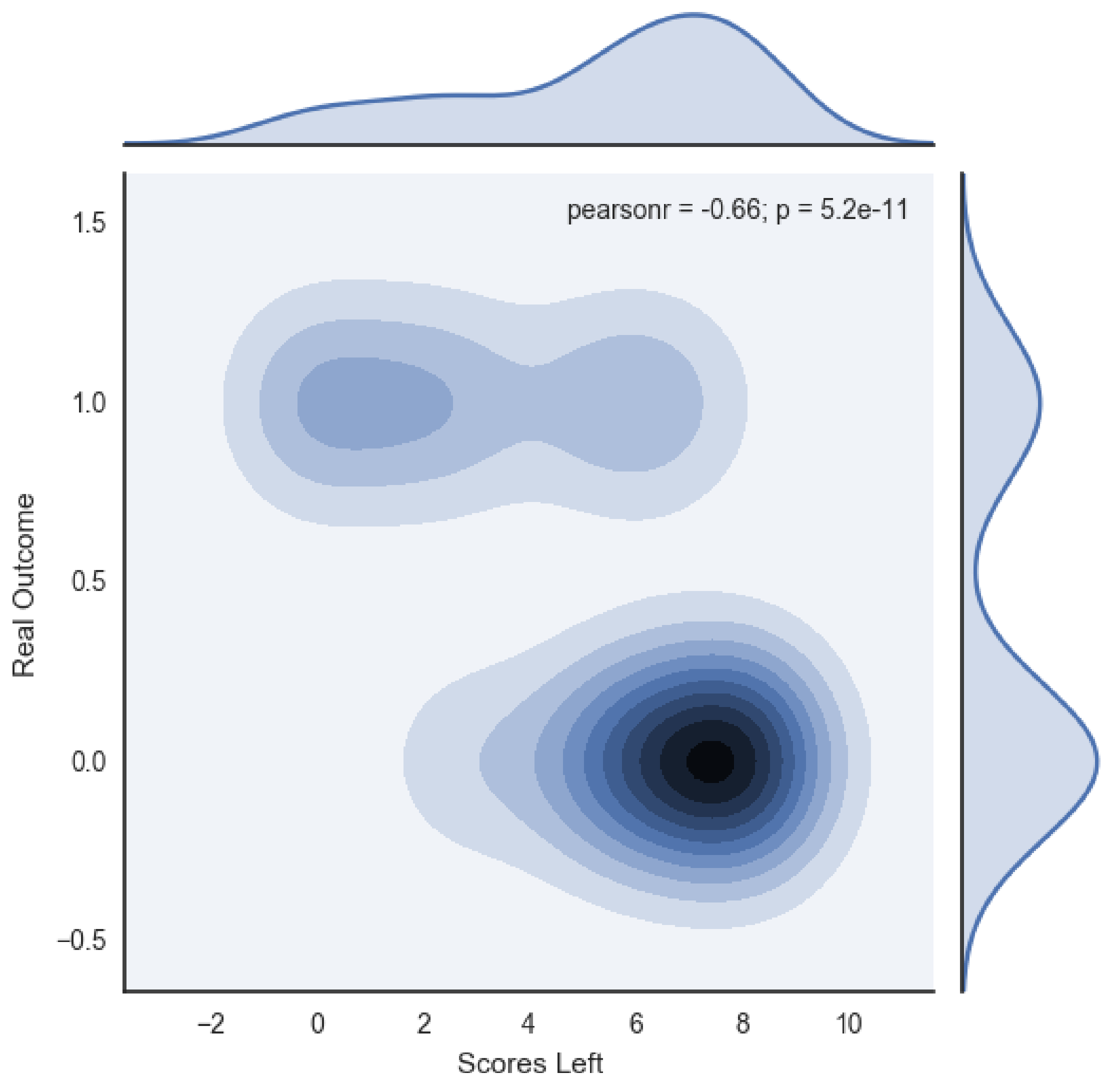
```
In [48]: training_set = X_train
         outcome = Y_train
         validation_data = X_validation
         validation_outcome = Y_validation

         mod = xgboost.XGBClassifier()
         mod.fit(training_set, outcome)
         # estimate accuracy on validation dataset
```

```python
        predictions = mod.predict(validation_data)
        print "Validation based "
        print(accuracy_score(validation_outcome, predictions))
        print(confusion_matrix(validation_outcome, predictions))
        cfmat = confusion_matrix(validation_outcome, predictions)
        #plot_confusion_matrix(cfmat, classes=[0.0, 1.0] , title='confusion matrix')
        print(classification_report(validation_outcome, predictions))
        # calculate the fpr and tpr for all thresholds of the classification
        probs = mod.predict_proba(validation_data)
        preds = probs[:,1]
        fpr, tpr, threshold = roc_curve(validation_outcome, preds)
        roc_auc = auc(fpr, tpr)

        # method I: plt
        plt.figure()
        plt.title('Receiver Operating Characteristic for ' + name)
        plt.plot(fpr, tpr, 'b', label = 'AUC = %0.2f' % roc_auc)
        plt.legend(loc = 'lower right')
        plt.plot([0, 1], [0, 1],'r--')
        plt.xlim([0, 1])
        plt.ylim([0, 1])
        plt.ylabel('True Positive Rate')
        plt.xlabel('False Positive Rate')
        plt.show()
```

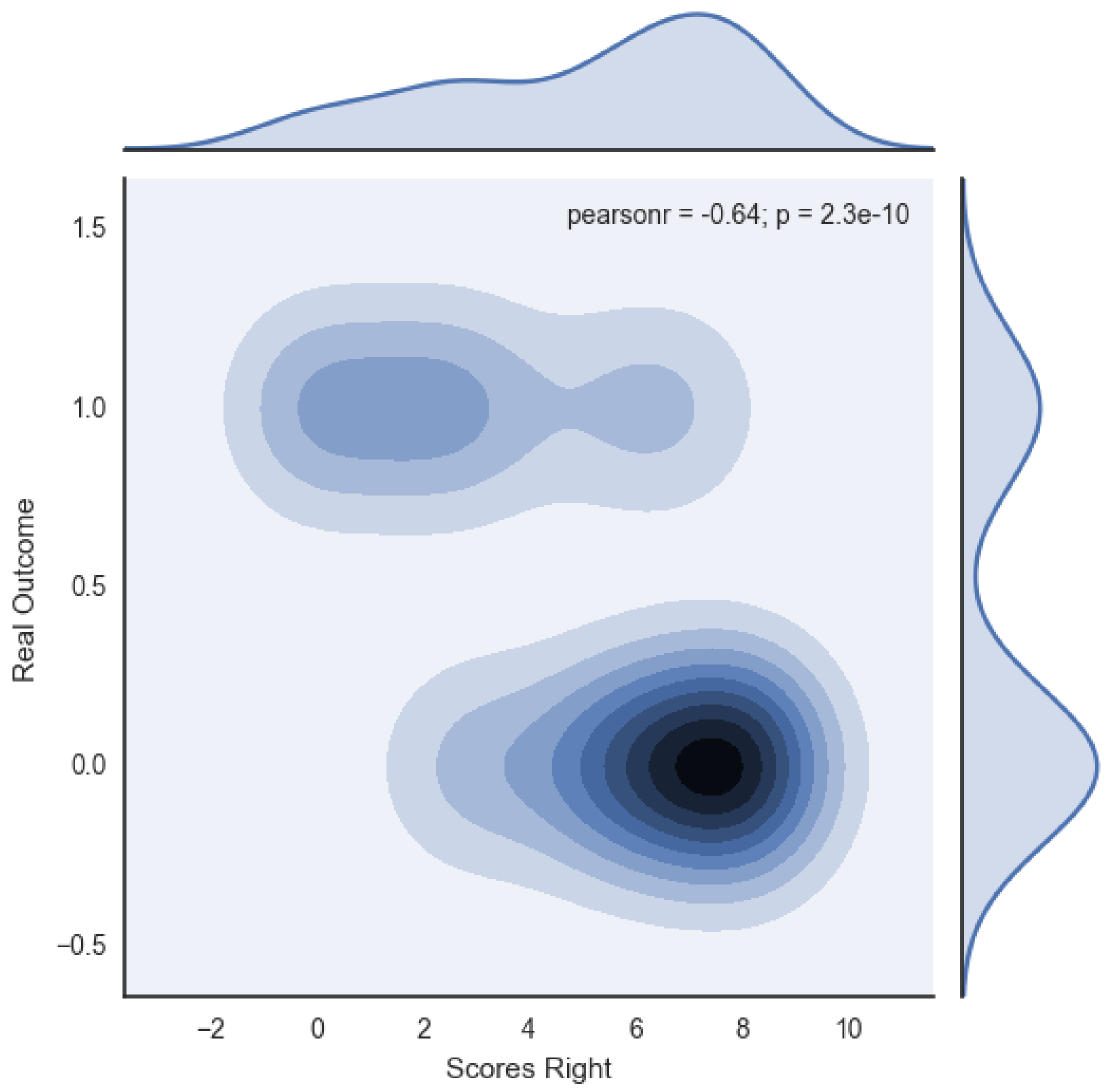
```
Validation based
0.886075949367
[[43  7]
 [ 2 27]]
             precision    recall  f1-score   support

        0.0       0.96      0.86      0.91        50
        1.0       0.79      0.93      0.86        29

avg / total       0.90      0.89      0.89        79
```



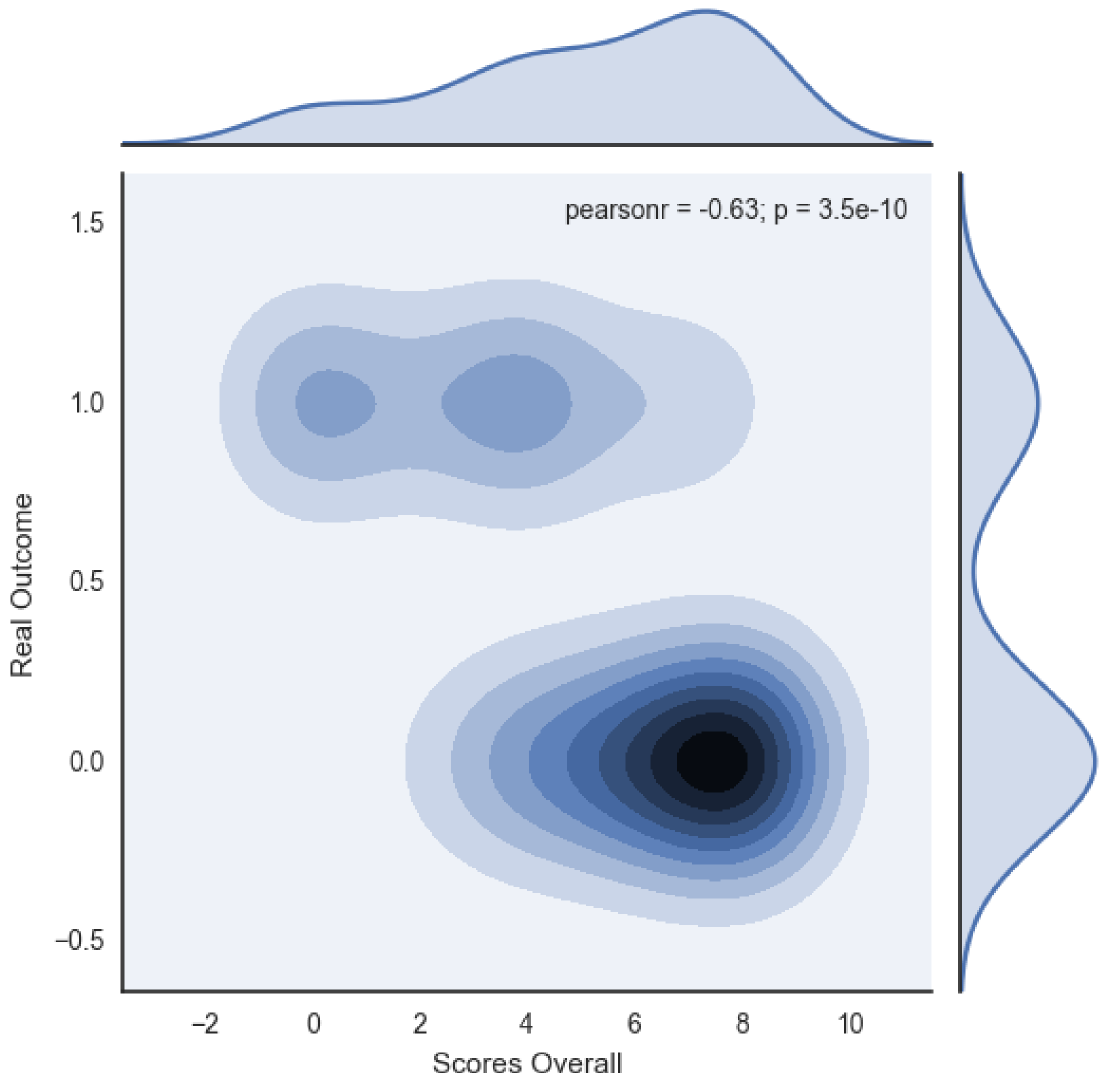

```
In [49]: x1 = pd.Series(table["score.left"].values, name="Scores Left")
         x2 = pd.Series(Y_validation.values, name="Real Outcome")
         g = sns.jointplot(x1, x2, kind="kde")
```




```
In [50]: x1 = pd.Series(table["score.right"].values, name="Scores Right")
         x2 = pd.Series(Y_validation.values, name="Real Outcome")
         g = sns.jointplot(x1, x2, kind="kde")
```

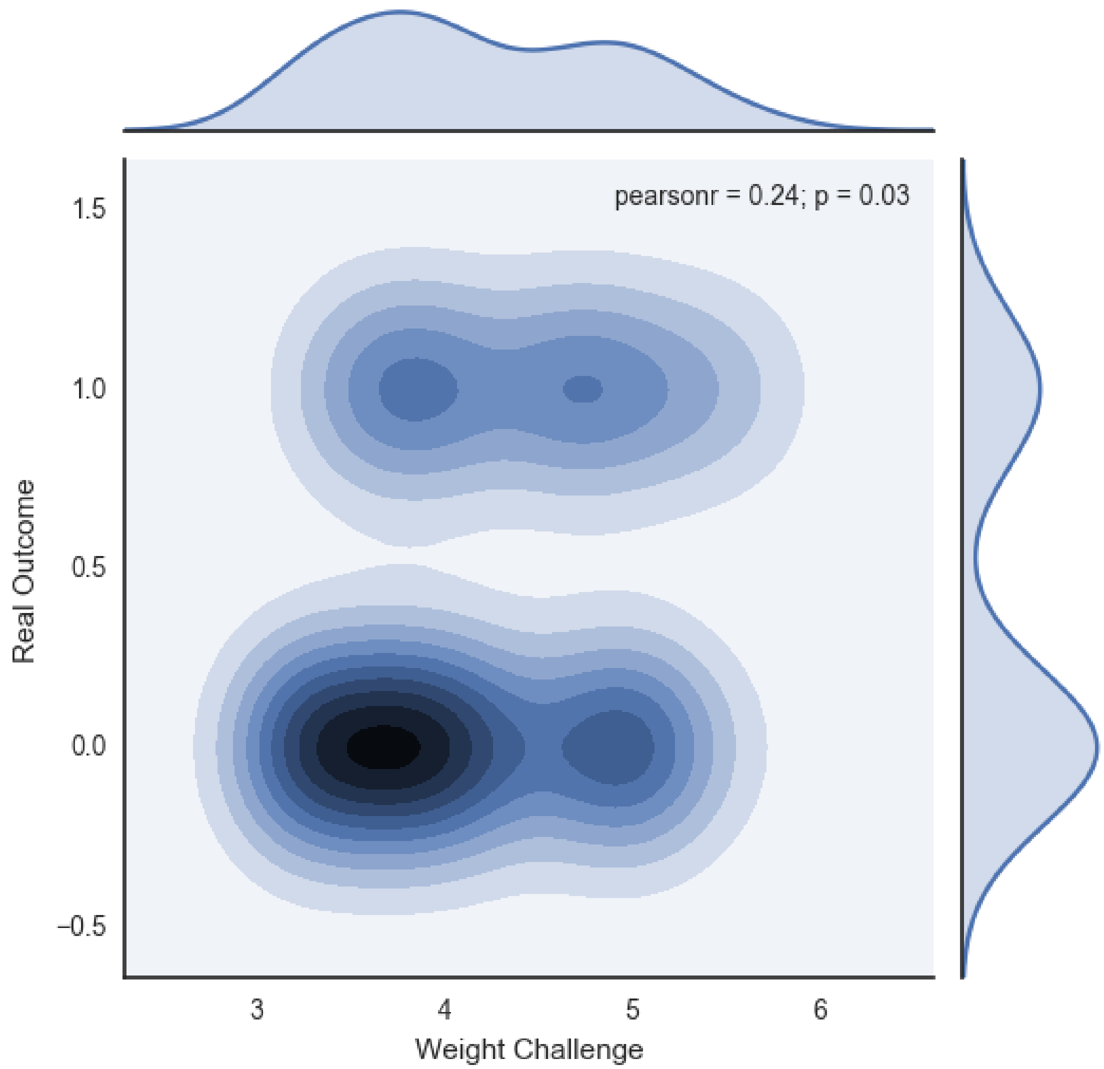



```
In [51]: x1 = pd.Series(table["score.overall"].values, name="Scores Overall")
         x2 = pd.Series(Y_validation.values, name="Real Outcome")
         g = sns.jointplot(x1, x2, kind="kde")
```

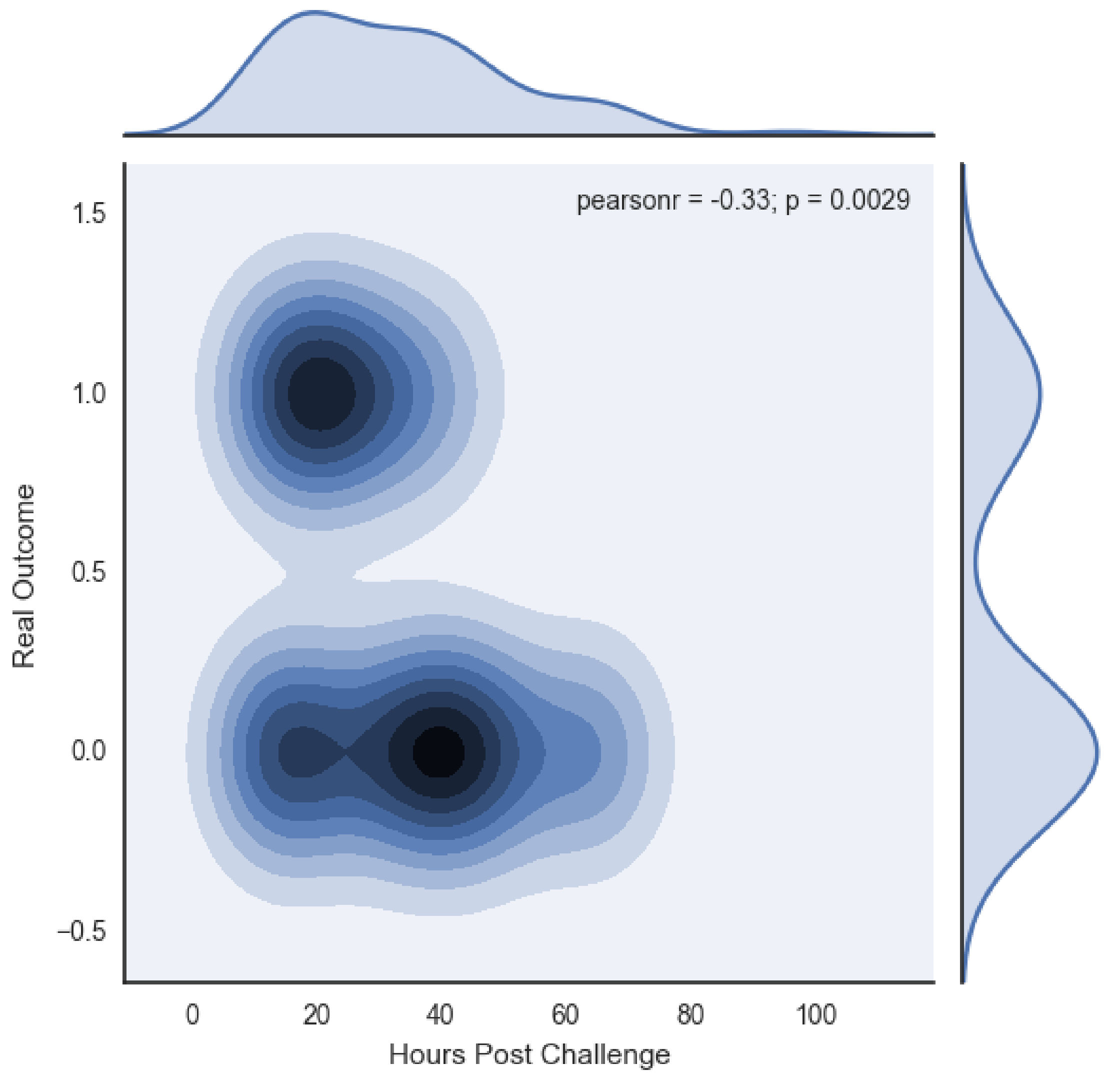


We see a trend here that is confirmed by the data, higher scores seem to be enough to split the data into the class `live` or `die`, there is a strong signal suggesting that scores 7 and up are enough to predict the `live` outcome, **whereas the `die` class seems to be hard to predict with the score features alone**

```
In [52]: x1 = pd.Series(table["weight.challenge"].values, name="Weight Challenge")
         x2 = pd.Series(Y_validation.values, name="Real Outcome")
         g = sns.jointplot(x1, x2, kind="kde")
```




```
In [55]: x1 = pd.Series(table["hr.post.challenge "].values, name="Hours Post Challenge")
         x2 = pd.Series(Y_validation.values, name="Real Outcome")
         g = sns.jointplot(x1, x2, kind="kde")
```


pearsonr = -0.33; p = 0.0029
1.5
1.0
0.5
0.0
−0.5
Real Outcome
0
20
40
60
80
100
Hours Post Challenge

```
In [ ]:
```