In [4]:

```
# Imports needed for the script
import numpy as np
import pandas as pd
import re
import xgboost as xgb
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline

import plotly.offline as py
py.init_notebook_mode(connected=True)
import plotly.graph_objs as go
import plotly.tools as tls

from sklearn import tree
from sklearn.metrics import accuracy_score
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from IPython.display import Image as PImage
from subprocess import check_call
from PIL import Image, ImageDraw, ImageFont
```

In [6]:
```
# Loading the data
train = pd.read_csv('train.csv')
test = pd.read_csv('test.csv')

# Store our test passenger IDs for easy access
PassengerId = test['PassengerId']

# Showing overview of the train dataset
train.head()
```

Out[6]:

	PassengerId	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Embarked
0	1	0	3	Braund, Mr. Owen Harris	male	22.0	1	0	A/5 21171	7.2500	NaN	S
1	2	1	1	Cumings, Mrs. John Bradley (Florence Briggs Th...	female	38.0	1	0	PC 17599	71.2833	C85	C
2	3	1	3	Heikkinen, Miss. Laina	female	26.0	0	0	STON/O2. 3101282	7.9250	NaN	S
3	4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	0	113803	53.1000	C123	S
4	5	0	3	Allen, Mr. William Henry	male	35.0	0	0	373450	8.0500	NaN	S

In [7]:
```
# Copy original dataset in case we need it later
original_train = train.copy() # Using 'copy()' allows to clone the dataset, creating a different object with the same valu

# Feature engineering steps taken from Sina and Anisotropic, with minor changes to avoid warnings
full_data = [train, test]

# Feature that tells whether a passenger had a cabin on the Titanic
train['Has_Cabin'] = train["Cabin"].apply(lambda x: 0 if type(x) == float else 1)
test['Has_Cabin'] = test["Cabin"].apply(lambda x: 0 if type(x) == float else 1)
```

In [8]:
```
# Create new feature FamilySize as a combination of SibSp and Parch
for dataset in full_data:
    dataset['FamilySize'] = dataset['SibSp'] + dataset['Parch'] + 1
# Create new feature IsAlone from FamilySize
for dataset in full_data:
    dataset['IsAlone'] = 0
    dataset.loc[dataset['FamilySize'] == 1, 'IsAlone'] = 1
```

In [9]:
```
# Remove all NULLS in the Embarked column and updating with S
for dataset in full_data:
    dataset['Embarked'] = dataset['Embarked'].fillna('S')
# Remove all NULLS in the Fare column and updating with median
for dataset in full_data:
    dataset['Fare'] = dataset['Fare'].fillna(train['Fare'].median())

# Remove all NULLS in the Age column and updating with mean and std
for dataset in full_data:
    age_avg = dataset['Age'].mean()
    age_std = dataset['Age'].std()
    age_null_count = dataset['Age'].isnull().sum()
    age_null_random_list = np.random.randint(age_avg - age_std, age_avg + age_std, size=age_null_count)
    # Next line has been improved to avoid warning
    dataset.loc[np.isnan(dataset['Age']), 'Age'] = age_null_random_list
    dataset['Age'] = dataset['Age'].astype(int)
```

In [10]:

```
# Define function to extract titles from passenger names
def get_title(name):
    title_search = re.search(' ([A-Za-z]+)\.', name)
    # If the title exists, extract and return it.
    if title_search:
        return title_search.group(1)
    return ""

for dataset in full_data:
    dataset['Title'] = dataset['Name'].apply(get_title)
# Group all non-common titles into one single grouping "Rare"
for dataset in full_data:
    dataset['Title'] = dataset['Title'].replace(['Lady', 'Countess','Capt', 'Col','Don', 'Dr', 'Major', 'Rev', 'Sir', 'Jon

    dataset['Title'] = dataset['Title'].replace('Mlle', 'Miss')
    dataset['Title'] = dataset['Title'].replace('Ms', 'Miss')
    dataset['Title'] = dataset['Title'].replace('Mme', 'Mrs')
```

In [11]:
```
for dataset in full_data:
    # Mapping Sex
    dataset['Sex'] = dataset['Sex'].map( {'female': 0, 'male': 1} ).astype(int)

    # Mapping titles
    title_mapping = {"Mr": 1, "Master": 2, "Mrs": 3, "Miss": 4, "Rare": 5}
    dataset['Title'] = dataset['Title'].map(title_mapping)
    dataset['Title'] = dataset['Title'].fillna(0)

    # Mapping Embarked
    dataset['Embarked'] = dataset['Embarked'].map( {'S': 0, 'C': 1, 'Q': 2} ).astype(int)

    # Mapping Fare
    dataset.loc[ dataset['Fare'] <= 7.91, 'Fare']                                = 0
    dataset.loc[(dataset['Fare'] > 7.91) & (dataset['Fare'] <= 14.454), 'Fare'] = 1
    dataset.loc[(dataset['Fare'] > 14.454) & (dataset['Fare'] <= 31), 'Fare']   = 2
    dataset.loc[ dataset['Fare'] > 31, 'Fare']                                   = 3
    dataset['Fare'] = dataset['Fare'].astype(int)

    # Mapping Age
    dataset.loc[ dataset['Age'] <= 16, 'Age']                            = 0
    dataset.loc[(dataset['Age'] > 16) & (dataset['Age'] <= 32), 'Age'] = 1
    dataset.loc[(dataset['Age'] > 32) & (dataset['Age'] <= 48), 'Age'] = 2
    dataset.loc[(dataset['Age'] > 48) & (dataset['Age'] <= 64), 'Age'] = 3
    dataset.loc[ dataset['Age'] > 64, 'Age'] ;
```

In [12]:
```
# Feature selection: remove variables no longer containing relevant information
drop_elements = ['PassengerId', 'Name', 'Ticket', 'Cabin', 'SibSp']
train = train.drop(drop_elements, axis = 1)
test  = test.drop(drop_elements, axis = 1)
```

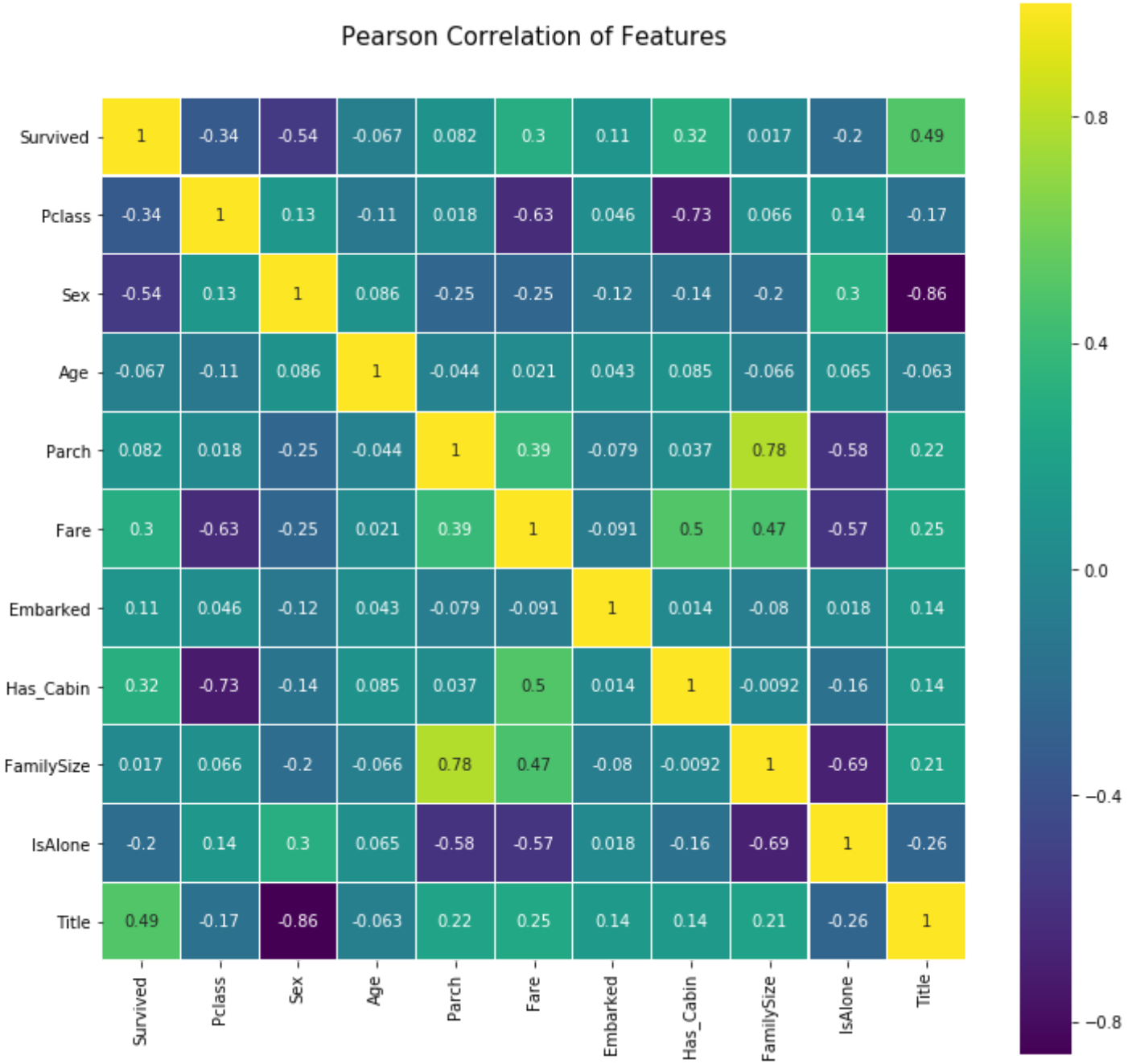
In [13]:
```
train.head()
```

Out[13]:

	Survived	Pclass	Sex	Age	Parch	Fare	Embarked	Has_Cabin	FamilySize	IsAlone	Title
0	0	3	1	1	0	0	0	0	2	0	1
1	1	1	0	2	0	3	1	1	2	0	3
2	1	3	0	1	0	1	0	0	1	1	4
3	1	1	0	2	0	3	0	1	2	0	3
4	0	3	1	2	0	1	0	0	1	1	1

In [14]:
```
"""
Our dataset is now much cleaner than before, with only numerical values and potentially meaningful features.
Let's now explore the relationship between our variables by plotting the Pearson Correlation [1] between all the attribute
"""
colormap = plt.cm.viridis
plt.figure(figsize=(12,12))
plt.title('Pearson Correlation of Features', y=1.05, size=15)
sns.heatmap(train.astype(float).corr(),linewidths=0.1,vmax=1.0, square=True, cmap=colormap, linecolor='white', annot=True)
```

Out[14]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x229dec65e10>
```


Pearson Correlation of Features
Survived 1 -0.34 -0.54 -0.067 0.082 0.3 0.11 0.32 0.017 -0.2 0.49
Pclass -0.34 1 0.13 -0.11 0.018 -0.63 0.046 -0.73 0.066 0.14 -0.17
Sex -0.54 0.13 1 0.086 -0.25 -0.25 -0.12 -0.14 -0.2 0.3 -0.86
Age -0.067 -0.11 0.086 1 -0.044 0.021 0.043 0.085 -0.066 0.065 -0.063
Parch 0.082 0.018 -0.25 -0.044 1 0.39 -0.079 0.037 0.78 -0.58 0.22
Fare 0.3 -0.63 -0.25 0.021 0.39 1 -0.091 0.5 0.47 -0.57 0.25
Embarked 0.11 0.046 -0.12 0.043 -0.079 -0.091 1 0.014 -0.08 0.018 0.14
Has_Cabin 0.32 -0.73 -0.14 0.085 0.037 0.5 0.014 1 -0.0092 -0.16 0.14
FamilySize 0.017 0.066 -0.2 -0.066 0.78 0.47 -0.08 -0.0092 1 -0.69 0.21
IsAlone -0.2 0.14 0.3 0.065 -0.58 -0.57 0.018 -0.16 -0.69 1 -0.26
Title 0.49 -0.17 -0.86 -0.063 0.22 0.25 0.14 0.14 0.21 -0.26 1
Survived
Pclass
Sex
Age
Parch
Fare
Embarked
Has_Cabin
FamilySize
IsAlone
Title
0.8
0.4
0.0
−0.4
−0.8

In [15]:
```
# Define function to calculate Gini Impurity
def get_gini_impurity(survived_count, total_count):
    survival_prob = survived_count/total_count
    not_survival_prob = (1 - survival_prob)
    random_observation_survived_prob = survival_prob
    random_observation_not_survived_prob = (1 - random_observation_survived_prob)
    mislabelling_survided_prob = not_survival_prob * random_observation_survived_prob
    mislabelling_not_survided_prob = survival_prob * random_observation_not_survived_prob
    gini_impurity = mislabelling_survided_prob + mislabelling_not_survided_prob
    return gini_impurity
```

In [16]:
```
# Gini Impurity of starting node
gini_impurity_starting_node = get_gini_impurity(342, 891)
gini_impurity_starting_node
```

Out[16]:
```
0.47301295786144265
```

In [17]:
```
# Gini Impurity decrease of node for 'male' observations
gini_impurity_men = get_gini_impurity(109, 577)
gini_impurity_men
```

Out[17]:
```
0.3064437162277843
```

In [18]:
```
# Gini Impurity decrease if node splited for 'female' observations
gini_impurity_women = get_gini_impurity(233, 314)
gini_impurity_women
```

Out[18]:
```
0.3828350034484158
```

In [19]:
```
# Gini Impurity decrease if node splited by Sex
men_weight = 577/891
women_weight = 314/891
weighted_gini_impurity_sex_split = (gini_impurity_men * men_weight) + (gini_impurity_women * women_weight)

sex_gini_decrease = weighted_gini_impurity_sex_split - gini_impurity_starting_node
sex_gini_decrease
```

Out[19]:
```
-0.13964795747285214
```

In [20]:
```
"""
If we split by Title == 1 (== Mr), we'll have the two following nodes:

Node with only Mr: 517 observations with only 81 survived
Node with other titles: 374 observations with 261 survived
"""
# Gini Impurity decrease of node for observations with Title == 1 == Mr
gini_impurity_title_1 = get_gini_impurity(81, 517)
gini_impurity_title_1
```

Out[20]:
```
0.26425329886377663
```

In [21]:
```
# Gini Impurity decrease if node splited for observations with Title != 1 != Mr
gini_impurity_title_others = get_gini_impurity(261, 374)
gini_impurity_title_others
```

Out[21]:
```
0.42170207898424317
```

In [22]:

```
cv = KFold(n_splits=10)            # Desired number of Cross Validation folds
accuracies = list()
max_attributes = len(list(test))
depth_range = range(1, max_attributes + 1)

# Testing max_depths from 1 to max attributes
# Uncomment prints for details about each Cross Validation pass
for depth in depth_range:
    fold_accuracy = []
    tree_model = tree.DecisionTreeClassifier(max_depth = depth)
    # print("Current max depth: ", depth, "\n")
    for train_fold, valid_fold in cv.split(train):
        f_train = train.loc[train_fold] # Extract train data with cv indices
        f_valid = train.loc[valid_fold] # Extract valid data with cv indices

        model = tree_model.fit(X = f_train.drop(['Survived'], axis=1),
                               y = f_train["Survived"]) # We fit the model with the fold train data
        valid_acc = model.score(X = f_valid.drop(['Survived'], axis=1),
                                y = f_valid["Survived"])# We calculate accuracy with the fold validation data
        fold_accuracy.append(valid_acc)

    avg = sum(fold_accuracy)/len(fold_accuracy)
    accuracies.append(avg)
    # print("Accuracy per fold: ", fold_accuracy, "\n")
    # print("Average accuracy: ", avg)
    # print("\n")

# Just to show results conveniently
df = pd.DataFrame({"Max Depth": depth_range, "Average Accuracy": accuracies})
df = df[["Max Depth", "Average Accuracy"]]
print(df.to_string(index=False))
```

```
 Max Depth  Average Accuracy
         1          0.782285
         2          0.799189
         3          0.828277
         4          0.819288
         5          0.819326
         6          0.807029
         7          0.813720
```

```
8          0.806991
9          0.818240
10         0.813745
```

In [23]:
```
# Create Numpy arrays of train, test and target (Survived) dataframes to feed into our models
y_train = train['Survived']
x_train = train.drop(['Survived'], axis=1).values
x_test = test.values

# Create Decision Tree with max_depth = 3
decision_tree = tree.DecisionTreeClassifier(max_depth = 3)
decision_tree.fit(x_train, y_train)
```

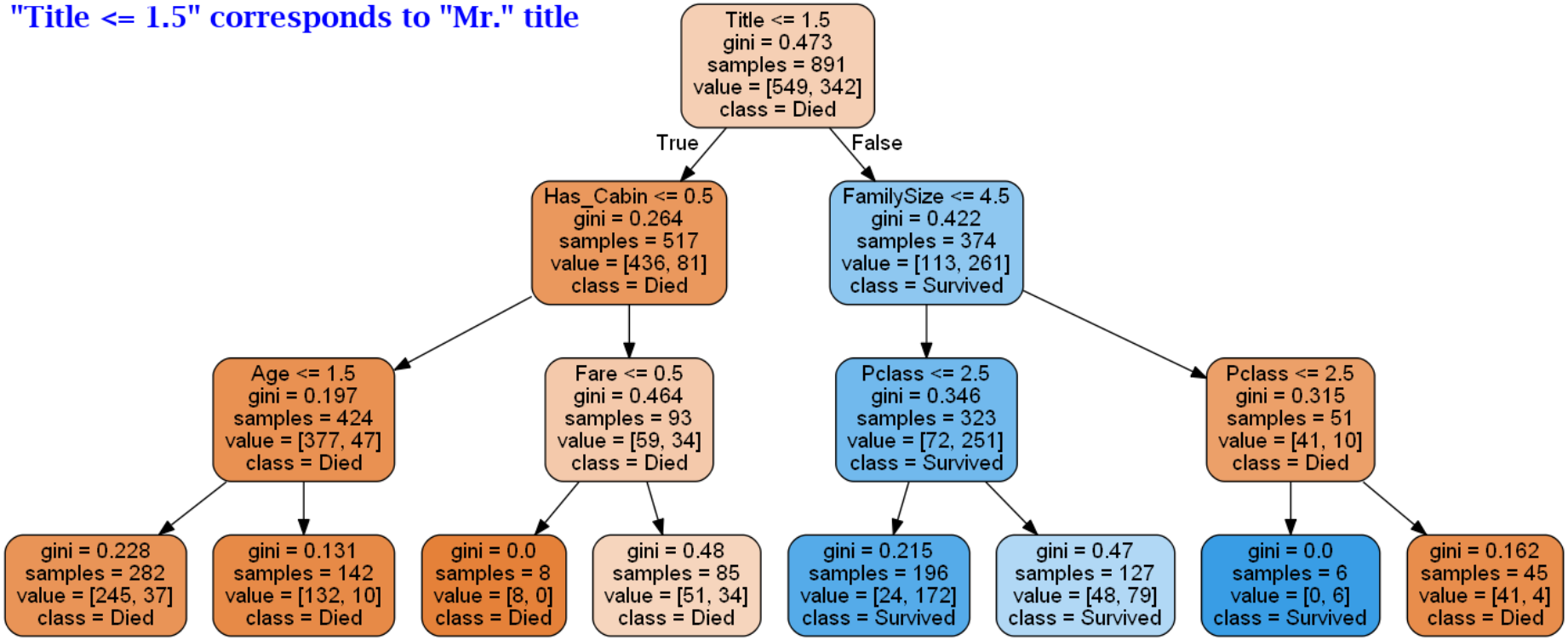
Out[23]:
```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=3,
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best')
```

In [24]:
```
# Predicting results for test dataset
y_pred = decision_tree.predict(x_test)
submission = pd.DataFrame({
        "PassengerId": PassengerId,
        "Survived": y_pred
    })
submission.to_csv('dt-submission1.csv', index=False)
```

In [26]:
```
# Export our trained model as a .dot file
with open("tree1.dot", 'w') as f:
     f = tree.export_graphviz(decision_tree,
                              out_file=f,
                              max_depth = 3,
                              impurity = True,
                              feature_names = list(train.drop(['Survived'], axis=1)),
                              class_names = ['Died', 'Survived'],
                              rounded = True,
                              filled= True )

#Convert .dot to .png to allow display in web notebook
check_call(['dot','-Tpng','tree1.dot','-o','tree1.png'])

# Annotating chart with PIL
img = Image.open("tree1.png")
draw = ImageDraw.Draw(img)
font = ImageFont.truetype('C://WINDOWS//FONTS/LBRITED.ttf', 26)
draw.text((10, 0), # Drawing offset (position)
          '"Title <= 1.5" corresponds to "Mr." title', # Text to draw
          (0,0,255), # RGB desired color
          font=font) # ImageFont object with desired font
img.save('sample-out.png')
PImage("sample-out.png")

# Code to check available fonts and respective paths
# import matplotlib.font_manager
# matplotlib.font_manager.findSystemFonts(fontpaths=None, fontext='ttf')
```

Out[26]:

"Title <= 1.5" corresponds to "Mr." title



In [27]:
```
acc_decision_tree = round(decision_tree.score(x_train, y_train) * 100, 2)
acc_decision_tree
```

Out[27]: 82.38

In [ ]: