Import Modules

Import libraries required for ETL and Feature Selection

In [1]:
```
# Set the seed value for the notebook so the results are reproducible
from numpy.random import seed
seed(42)

import numpy as np
import pandas as pd

import warnings
warnings.simplefilter('ignore', FutureWarning)

%matplotlib inline
import matplotlib.pyplot as plt

from sklearn.model_selection import train_test_split
from tensorflow.keras.utils import to_categorical
from sklearn.preprocessing import LabelEncoder, StandardScaler, MinMaxScaler,
RobustScaler, minmax_scale, MaxAbsScaler, Normalizer, QuantileTransformer, Pow
erTransformer
```

Method Definitions

Plot Histogram Method

In [2]:
```
# Code referenced from RealPython example:  https://realpython.com/python-hist
ograms/
def plotHistogram(xValues, lbl):
    n, bins, patches = plt.hist(x=xValues, bins='auto', color='#0504aa', alpha
=0.7, rwidth=0.85)
    plt.grid(axis='y', alpha=0.75)
    plt.xlabel(lbl)
    plt.ylabel('Frequency')
    plt.title(lbl + ' Histogram')
    maxfreq = n.max()

    # Set a clean upper y-axis limit.
    plt.ylim(ymax=np.ceil(maxfreq / 10) * 10 if maxfreq % 10 else maxfreq + 10
)
```

In [3]:
```python
# Code to prep X and y
def prepData(data, scaler):

    # drop the dependent column from the independent columns
    X = data.drop(dependent, axis=1)

    # set the dependent column to y
    y = data[dependent]

    # Make a copy of the independent field matrix
    copyData = X.copy()

    # call pandas get dummies to convert to 1's and 0's in separate columns
    X = pd.get_dummies(copyData)

    # Split the data into test and train groups
    X_train, X_test, y_train, y_test = train_test_split(X, y, random_state=42,
stratify=y)

    # Save data out for use in other Jupyter Notebooks
    X_train_csv = X_train.to_csv ('X_train.csv', index = None, header=True)
    X_test_csv = X_test.to_csv ('X_test.csv', index = None, header=True)
    y_train_csv = y_train.to_csv ('y_train.csv', index = None, header=True)
    y_test_csv = y_test.to_csv ('y_test.csv', index = None, header=True)


    # Apply a scalar, first train then scale test and train data
    # TO DO:  Insert function to select scalar
    X_scaler = scaler.fit(X_train)
    X_train_scaled = X_scaler.transform(X_train)
    X_test_scaled = X_scaler.transform(X_test)

    # Label encode the dependent variable, then Hot encode it
    label_encoder = LabelEncoder()
    label_encoder.fit(y_train)
    y_train_categorical = to_categorical(label_encoder.transform(y_train))
    y_test_categorical = to_categorical(label_encoder.transform(y_test))

    return X, y, X_train_scaled, X_test_scaled, y_train_categorical, y_test_ca
tegorical
```

Arythmia - Cleveland Data Set

Create standard csv with header

In [4]:
```
######## Dependent variable (column) in our dataset ###########
# Arythmia data set:  We will use the binary sick/healthy column buff as our o
utput and remove the 'healthy' column
dependent = 'buff'
remove = 'healthy'

# Set the original file and new file names
originalFile = 'cleve.csv'
csvFile = 'cleveland.csv'
clean_csv = 'cleveland_clean.csv'

scalers = {"Robust": RobustScaler(),
           "Standard": StandardScaler(),
           "MinMax": MinMaxScaler(),
           "MaxAbs": MaxAbsScaler(),
           "Normalizer": Normalizer(),
           "Quantile": QuantileTransformer(),
           "Power": PowerTransformer()}
```

In [5]:
```
# Open the Cleveland original file, add a header and convert to csv
with open(originalFile) as fin, open(csvFile,'w') as fout:
    fout.write("age,sex,chestPain,trestBps,cholesterol,bloodSugar,ecg,maxHeart
Rate,exerciseInducedAngina,oldPeak,slope,vesselsColored,thal,buff,healthy\n")
    for line in fin:
        fout.write( ",".join(line.split()) + "\n" )
```

Describe the data and look for unique values, remove bad data and any columns not needed

In [6]:
```
# Describe the continuous data and look for any anomalies
data = pd.read_csv(csvFile)
data.describe()
```

Out[6]:

	age	trestBps	cholesterol	maxHeartRate	oldPeak
count	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	131.623762	246.264026	149.646865	1.039604
std	9.082101	17.538143	51.830751	22.905161	1.161075
min	29.000000	94.000000	126.000000	71.000000	0.000000
25%	47.500000	120.000000	211.000000	133.500000	0.000000
50%	55.000000	130.000000	240.000000	153.000000	0.800000
75%	61.000000	140.000000	274.500000	166.000000	1.600000
max	77.000000	200.000000	564.000000	202.000000	6.200000

In [7]:
```
# determine column names to be able to look at all unique values for classific
ation columns
data.columns
```
Out[7]:
```
Index(['age', 'sex', 'chestPain', 'trestBps', 'cholesterol', 'bloodSugar',
       'ecg', 'maxHeartRate', 'exerciseInducedAngina', 'oldPeak', 'slope',
       'vesselsColored', 'thal', 'buff', 'healthy'],
      dtype='object')
```
In [8]:
```
data['sex'].value_counts()
```
Out[8]:
```
male    207
fem      96
Name: sex, dtype: int64
```
In [9]:
```
data['chestPain'].value_counts()
```
Out[9]:
```
asympt    143
notang     87
abnang     50
angina     23
Name: chestPain, dtype: int64
```
In [10]:
```
data['bloodSugar'].value_counts()
```
Out[10]:
```
fal     258
true     45
Name: bloodSugar, dtype: int64
```
In [11]:
```
data['ecg'].value_counts()
```
Out[11]:
```
norm    152
hyp     147
abn       4
Name: ecg, dtype: int64
```
In [12]:
```
data['exerciseInducedAngina'].value_counts()
```
Out[12]:
```
fal     204
true     99
Name: exerciseInducedAngina, dtype: int64
```
In [13]:
```
data['slope'].value_counts()
```
Out[13]:
```
up      142
flat    140
down     21
Name: slope, dtype: int64
```

In [14]:
```
data['vesselsColored'].value_counts()
```

Out[14]:
```
0.0    175
1.0     65
2.0     38
3.0     20
?        5
Name: vesselsColored, dtype: int64
```

In [15]:
```
# drop the data with rows where ? appear
data.drop(data[data.vesselsColored == '?'].index, inplace=True)
```

In [16]:
```
data['thal'].value_counts()
```

Out[16]:
```
norm    163
rev     115
fix      18
?         2
Name: thal, dtype: int64
```

In [17]:
```
# drop the data with rows where ? appear
data.drop(data[data.thal == '?'].index, inplace=True)
```

In [18]:
```
data['buff'].value_counts()
```

Out[18]:
```
buff    160
sick    136
Name: buff, dtype: int64
```

In [19]:
```
data['healthy'].value_counts()
```

Out[19]:
```
H     160
S1     53
S2     35
S3     35
S4     13
Name: healthy, dtype: int64
```

In [20]:
```
# We determined we were discarding this column and using the binary column 'bu
ff' instead to indicate healthy vs sick
# so delete this column
data = data.drop(remove, axis=1)
```

In [21]:
```python
#display the data without ? rows
data
```

Out[21]:

	age	sex	chestPain	trestBps	cholesterol	bloodSugar	ecg	maxHeartRate	exerciseIndu
0	63.0	male	angina	145.0	233.0	true	hyp	150.0	
1	67.0	male	asympt	160.0	286.0	fal	hyp	108.0	
2	67.0	male	asympt	120.0	229.0	fal	hyp	129.0	
3	37.0	male	notang	130.0	250.0	fal	norm	187.0	
4	41.0	fem	abnang	130.0	204.0	fal	hyp	172.0	
...	...	...	...	...	...	...	...	...	
298	48.0	male	notang	124.0	255.0	true	norm	175.0	
299	57.0	male	asympt	132.0	207.0	fal	norm	168.0	
300	49.0	male	notang	118.0	149.0	fal	hyp	126.0	
301	74.0	fem	abnang	120.0	269.0	fal	hyp	121.0	
302	54.0	fem	notang	160.0	201.0	fal	norm	163.0	

296 rows × 14 columns

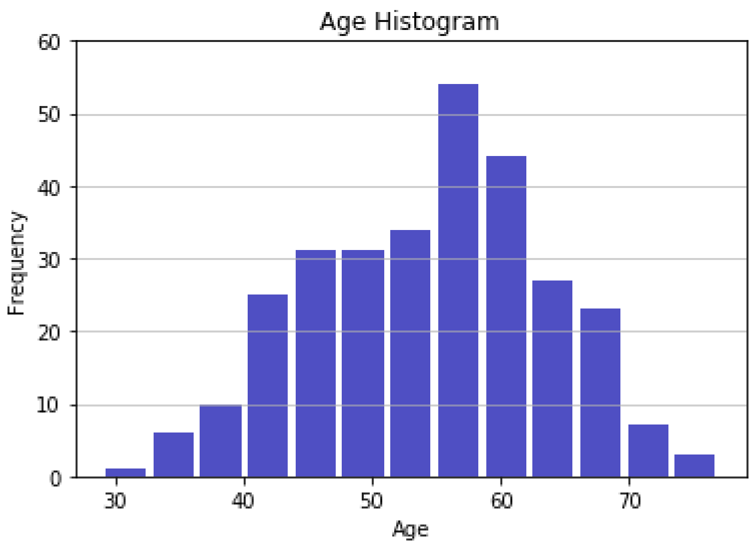
Save our cleaned data set

In [22]:
```python
# overwrite the csv so we have a clean copy
export_csv = data.to_csv (clean_csv, index = None, header=True)
```

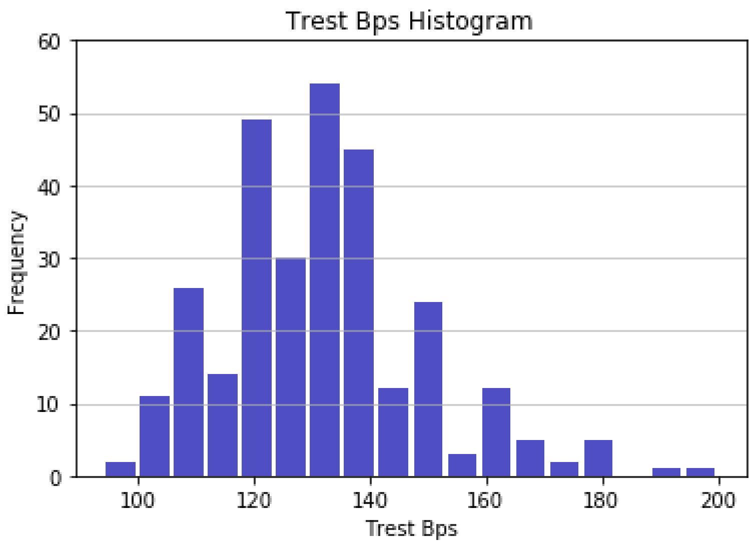
Now plot each continuous column in a histogram to examine the distribution

These can be referenced when selecting machine learning options

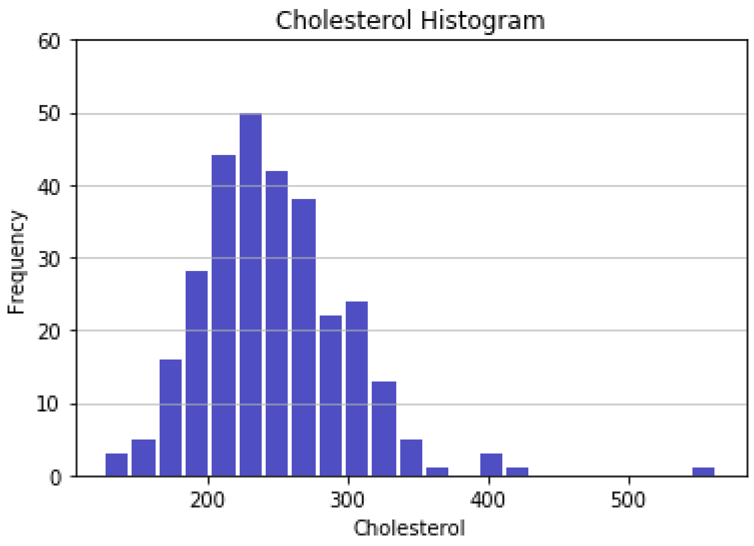
```
In [23]: plotHistogram(data['age'], 'Age')
```



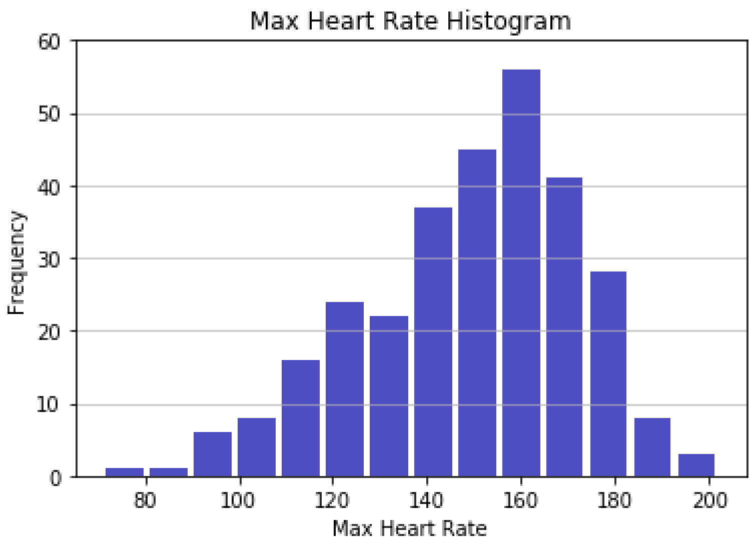
```
In [24]: plotHistogram(data['trestBps'], 'Trest Bps')
```



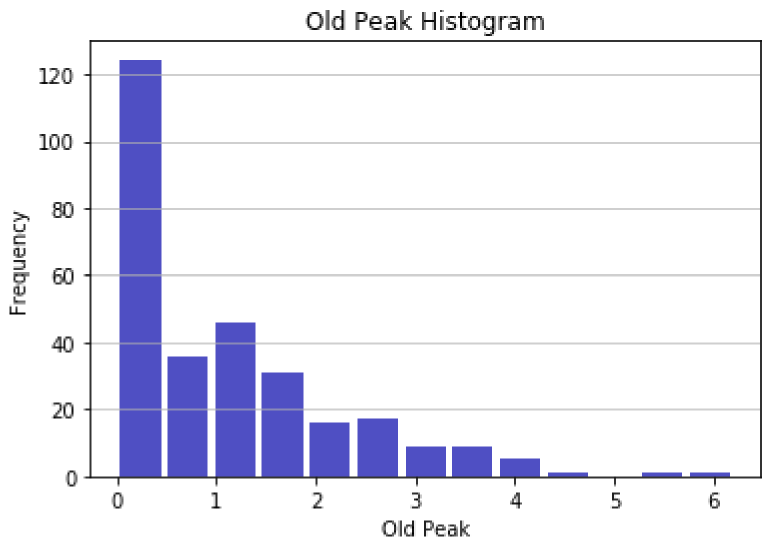
```
In [25]: plotHistogram(data['cholesterol'], 'Cholesterol')
```



```
In [26]: plotHistogram(data['maxHeartRate'], 'Max Heart Rate')
```



In [27]:
```
plotHistogram(data['oldPeak'], 'Old Peak')
```



Let's Try Some Feature Selection Techniques

This is an attempt to limit the number of features used in the models to simplify and remove noise

NOTE: These three methods and code were obtained from the following website:

https://towardsdatascience.com/feature-selection-techniques-in-machine-learning-with-python-f24e7da3f36e (https://towardsdatascience.com/feature-selection-techniques-in-machine-learning-with-python-f24e7da3f36e)

First we need to create our X and y

```
In [28]: # X, y, X_train_scaled, X_test_scaled, y_train_categorical, y_test_categorical
         = prepData(data, scalers['MinMax'])
         X, y, X_train_scaled, X_test_scaled, y_train_categorical, y_test_categorical =
         prepData(data, scalers['MinMax'])
         X
```

Out[28]:

	age	trestBps	cholesterol	maxHeartRate	oldPeak	sex_fem	sex_male	chestPain_abnang
0	63.0	145.0	233.0	150.0	2.3	0	1	0
1	67.0	160.0	286.0	108.0	1.5	0	1	0
2	67.0	120.0	229.0	129.0	2.6	0	1	0
3	37.0	130.0	250.0	187.0	3.5	0	1	0
4	41.0	130.0	204.0	172.0	1.4	1	0	1
...	...	...	...	...	...	...	...	...
298	48.0	124.0	255.0	175.0	0.0	0	1	0
299	57.0	132.0	207.0	168.0	0.0	0	1	0
300	49.0	118.0	149.0	126.0	0.8	0	1	0
301	74.0	120.0	269.0	121.0	0.2	1	0	1
302	54.0	160.0	201.0	163.0	0.0	1	0	0

296 rows × 28 columns

Univariate Selection using ChiSquare

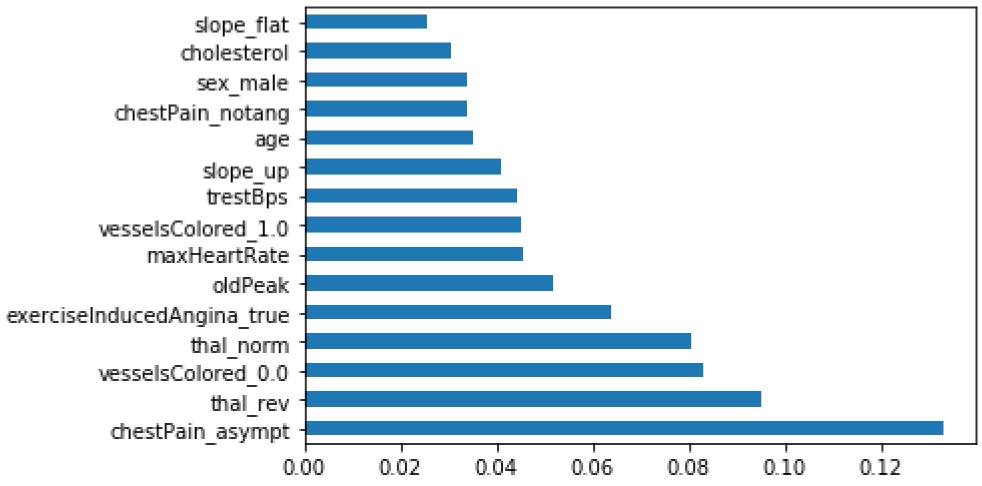
In [29]:
```python
# REference:  https://towardsdatascience.com/feature-selection-techniques-in-machine-learning-with-python-f24e7da3f36e
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2

#apply SelectKBest class to extract best features
bestfeatures = SelectKBest(score_func=chi2, k=10)
fit = bestfeatures.fit(X_train_scaled,y_train_categorical)
dfscores = pd.DataFrame(fit.scores_)
dfcolumns = pd.DataFrame(X.columns)

#concat two dataframes for better visualization
featureScores = pd.concat([dfcolumns,dfscores],axis=1)
featureScores.columns = ['Specs','Score']  #naming the dataframe columns
print(featureScores.nlargest(27,'Score'))  #print best features reverse order
```

```
                          Specs      Score
27                     thal_rev  34.200294
17   exerciseInducedAngina_true  33.418728
9                chestPain_asympt  32.604218
26                    thal_norm  28.482451
21             vesselsColored_0.0  21.540903
20                     slope_up  18.872001
19                   slope_flat  15.823077
16    exerciseInducedAngina_fal  14.756322
7                chestPain_abnang  14.126050
10               chestPain_notang  13.687783
23             vesselsColored_2.0  12.695136
5                       sex_fem  12.124316
22             vesselsColored_1.0  11.352036
4                       oldPeak  10.745139
24             vesselsColored_3.0   7.004118
6                      sex_male   5.700838
13                      ecg_abn   3.529412
8                chestPain_angina   2.826471
15                     ecg_norm   2.605742
3                  maxHeartRate   1.955725
14                      ecg_hyp   1.548633
0                           age   0.975826
25                     thal_fix   0.741422
18                   slope_down   0.684007
1                      trestBps   0.355538
2                   cholesterol   0.136939
12               bloodSugar_true   0.022368
```

Feature Importance

In [30]:
```
from sklearn.ensemble import ExtraTreesClassifier
import matplotlib.pyplot as plt
model = ExtraTreesClassifier()
model.fit(X_train_scaled,y_train_categorical)
print(model.feature_importances_) #use inbuilt class feature_importances of tr
ee based classifiers
#plot graph of feature importances for better visualization
feat_importances = pd.Series(model.feature_importances_, index=X.columns)
feat_importances.nlargest(15).plot(kind='barh')
plt.show()
```

```
[0.03502496 0.04442578 0.03073113 0.04561243 0.0516222  0.01905353
 0.03392827 0.00337018 0.0093416  0.13287963 0.03397756 0.0074519
 0.01069452 0.00024183 0.02261995 0.02012887 0.01899636 0.06371845
 0.01080309 0.02556698 0.04095077 0.08324723 0.04526443 0.0121062
 0.01591545 0.00653634 0.08058911 0.09520124]
```



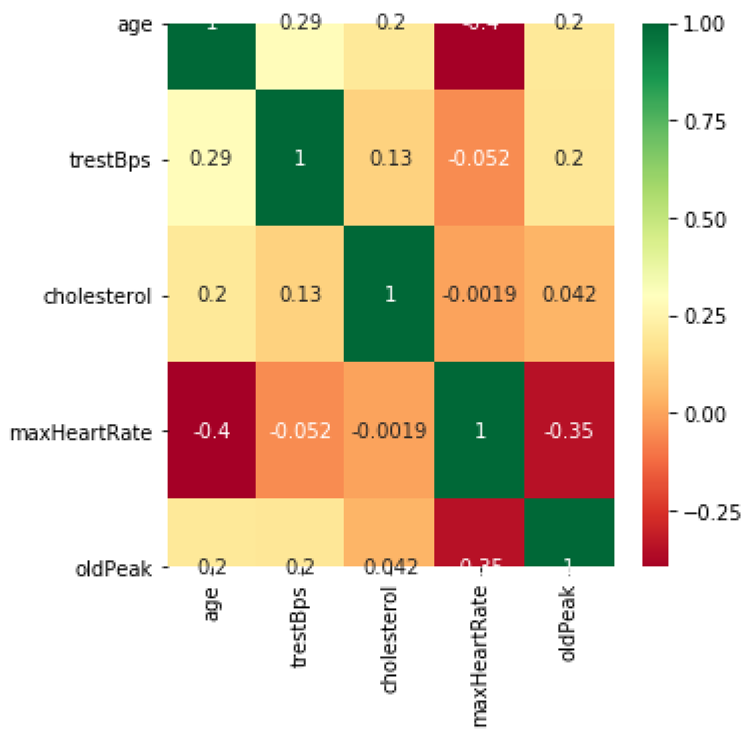
Correlation Matrix with Heatmap

Notice that only continuous variables are plotted and there are no variables with a high correlation in our dataset

In [31]:
```
import seaborn as sns

#get correlations of each features in dataset
corrmat = data.corr()
top_corr_features = corrmat.index
plt.figure(figsize=(5,5))

#plot heat map
g=sns.heatmap(data[top_corr_features].corr(),annot=True,cmap="RdYlGn")
corrmat
```

Out[31]:

	age	trestBps	cholesterol	maxHeartRate	oldPeak
age	1.000000	0.288701	0.200920	-0.395989	0.199373
trestBps	0.288701	1.000000	0.126705	-0.051817	0.196793
cholesterol	0.200920	0.126705	1.000000	-0.001947	0.042144
maxHeartRate	-0.395989	-0.051817	-0.001947	1.000000	-0.346742
oldPeak	0.199373	0.196793	0.042144	-0.346742	1.000000



In [ ]: