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```
In [1]: import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns

from imblearn.over_sampling import SMOTE

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import cross_val_score
from sklearn.metrics import accuracy_score

from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from sklearn import svm

from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import RandomizedSearchCV
```

```
In [19]: import warnings
warnings.filterwarnings('ignore')
```

```
In [2]: dataset = pd.read_csv('chronic_kidney.csv')
dataset.shape
```

```
Out[2]: (400, 14)
```

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

```
Out[3]:
```

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	Pot	Hemo	Wbcc	Rbcc	Htn	Class
0	80.0	1.020	1.0	0.0	1.0	36.0	1.2	137.53	4.63	15.4	7800.0	5.20	1.0	1
1	50.0	1.020	4.0	0.0	1.0	18.0	0.8	137.53	4.63	11.3	6000.0	4.71	0.0	1
2	80.0	1.010	2.0	3.0	1.0	53.0	1.8	137.53	4.63	9.6	7500.0	4.71	0.0	1
3	70.0	1.005	4.0	0.0	1.0	56.0	3.8	111.00	2.50	11.2	6700.0	3.90	1.0	1
4	80.0	1.010	2.0	0.0	1.0	26.0	1.4	137.53	4.63	11.6	7300.0	4.60	0.0	1

```
In [4]: dataset.tail()
```

```
Out[4]:
```

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	Pot	Hemo	Wbcc	Rbcc	Htn	Class
395	80.0	1.020	0.0	0.0	1.0	49.0	0.5	150.0	4.9	15.7	6700.0	4.9	0.0	0
396	70.0	1.025	0.0	0.0	1.0	31.0	1.2	141.0	3.5	16.5	7800.0	6.2	0.0	0
397	80.0	1.020	0.0	0.0	1.0	26.0	0.6	137.0	4.4	15.8	6600.0	5.4	0.0	0
398	60.0	1.025	0.0	0.0	1.0	50.0	1.0	135.0	4.9	14.2	7200.0	5.9	0.0	0
399	80.0	1.025	0.0	0.0	1.0	18.0	1.1	141.0	3.5	15.8	6800.0	6.1	0.0	0

```
In [5]: print('Number of Rows:',dataset.shape[0])
print('Number of Columns:',dataset.shape[1])
```

```
Number of Rows: 400
Number of Columns: 14
```

```
In [6]: dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 14 columns):
#   Column      Non-Null Count  Dtype
---  -
0   Bp           400 non-null    float64
1   Sg           400 non-null    float64
2   Al           400 non-null    float64
3   Su           400 non-null    float64
4   Rbc          400 non-null    float64
5   Bu           400 non-null    float64
6   Sc           400 non-null    float64
7   Sod          400 non-null    float64
8   Pot          400 non-null    float64
9   Hemo         400 non-null    float64
10  Wbcc         400 non-null    float64
11  Rbcc         400 non-null    float64
12  Htn          400 non-null    float64
13  Class        400 non-null    int64
dtypes: float64(13), int64(1)
memory usage: 43.9 KB
```

```
In [8]: dataset.isna().sum()
```

```
Out[8]: Bp      0
        Sg      0
        Al      0
        Su      0
        Rbc     0
        Bu      0
        Sc      0
        Sod     0
        Pot     0
        Hemo    0
        Wbcc    0
        Rbcc    0
        Htn     0
        Class   0
        dtype: int64
```

```
In [7]: dataset.isnull().sum()
```

```
Out[7]: Bp      0
        Sg      0
        Al      0
        Su      0
        Rbc     0
        Bu      0
        Sc      0
        Sod     0
        Pot     0
        Hemo    0
        Wbcc    0
        Rbcc    0
        Htn     0
        Class   0
        dtype: int64
```

```
In [9]: dataset.duplicated().sum()
```

```
Out[9]: 0
```

```
In [10]: dataset.describe()
```

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sd
count	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000
mean	76.455000	1.017712	1.015000	0.395000	0.882500	57.40550	3.07235	137.52900
std	13.476536	0.005434	1.272329	1.040038	0.322418	49.28597	5.61749	9.20420
min	50.000000	1.005000	0.000000	0.000000	0.000000	1.50000	0.40000	4.50000
25%	70.000000	1.015000	0.000000	0.000000	1.000000	27.00000	0.90000	135.00000
50%	78.000000	1.020000	1.000000	0.000000	1.000000	44.00000	1.40000	137.53000
75%	80.000000	1.020000	2.000000	0.000000	1.000000	61.75000	3.07000	141.00000
max	180.000000	1.025000	5.000000	5.000000	1.000000	391.00000	76.00000	163.00000

```
In [12]: dataset.corr()
```

Out[12]:

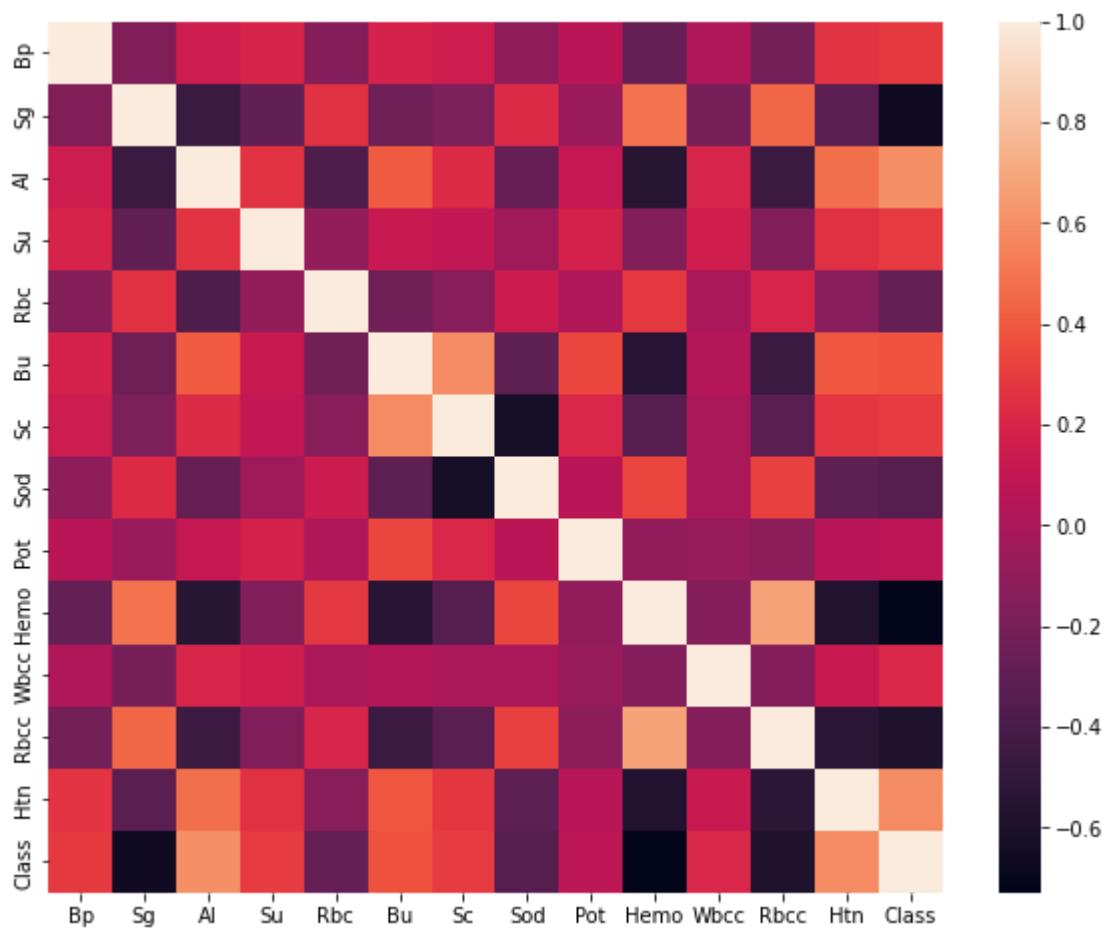
	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	P
Bp	1.000000	-0.164057	0.146060	0.190277	-0.151478	0.184173	0.144469	-0.103383	0.066791
Sg	-0.164057	1.000000	-0.460835	-0.292053	0.253894	-0.249263	-0.176141	0.217456	-0.063450
Al	0.146060	-0.460835	1.000000	0.262564	-0.374484	0.405035	0.229396	-0.270709	0.114484
Su	0.190277	-0.292053	0.262564	1.000000	-0.092940	0.126074	0.094568	-0.053448	0.180098
Rbc	-0.151478	0.253894	-0.374484	-0.092940	1.000000	-0.236270	-0.138391	0.140568	0.018164
Bu	0.184173	-0.249263	0.405035	0.126074	-0.236270	1.000000	0.581176	-0.307357	0.336954
Sc	0.144469	-0.176141	0.229396	0.094568	-0.138391	0.581176	1.000000	-0.624493	0.205361
Sod	-0.103383	0.217456	-0.270709	-0.053448	0.140568	-0.307357	-0.624493	1.000000	0.067414
Pot	0.066791	-0.063450	0.114484	0.180098	0.018164	0.336954	0.205361	0.067414	1.000000
Hemo	-0.279441	0.492103	-0.548681	-0.156875	0.280991	-0.540699	-0.342053	0.333604	-0.100679
Wbcc	0.025963	-0.206880	0.200664	0.159033	-0.002205	0.041530	-0.005420	0.006334	-0.074019
Rbcc	-0.220827	0.443437	-0.454131	-0.163825	0.202298	-0.465947	-0.323056	0.316883	-0.120479
Htn	0.268003	-0.318956	0.478309	0.253179	-0.139342	0.387503	0.273904	-0.306501	0.057003
Class	0.290145	-0.659504	0.598389	0.294555	-0.282642	0.371982	0.294076	-0.342268	0.077006

In [11]: `dataset.cov()`

Out[11]:

	Bp	Sg	Al	Su	Rbc	Bu	Sc	Sod	Pot	Hemo	Wbcc	Rbcc	Htn	Class
Bp	181.617018	-0.012014	2.504436	2.666942	-0.658183	122.328318	10.936923	-12.823866	2.538124	-10.228812	882.846165	-2.500767	1.740948	1.895363
Sg	-0.012014	0.000030	-0.003186	-0.001651	0.000445	-0.066758	-0.005377	0.010876	-0.000972	0.007263	-2.836586	0.002025	-0.000835	-0.001737
Al	2.504436	-0.003186	1.618822	0.347444	-0.153622	25.398915	1.639564	-3.170236	0.410734	-1.896169	644.204160	-0.485538	0.293343	0.369048
Su	2.666942	-0.001651	0.347444	1.081679	-0.031165	6.462484	0.552503	-0.511644	0.528170	-0.443158	417.342807	-0.143177	0.126924	0.148496
Rbc	-0.658183	0.000445	-0.153622	-0.031165	0.103954	-3.754490	-0.250651	0.417153	0.016514	0.246076	-1.793910	0.054809	-0.021656	-0.044173
Bu	122.328318	-0.066758	25.398915	6.462484	-3.754490	2429.106887	160.906503	-139.430037	46.828385	-72.382890	5164.622561	-19.297544	9.205893	8.886779
Sc	10.936923	-0.005377	1.639564	0.552503	-0.250651	160.906503	31.556195	-32.289372	3.252943	-5.219070	-76.821766	-1.524972	0.741667	0.800758
Sod	-12.823866	0.010876	-3.170236	-0.511644	0.417153	-139.430037	-32.289372	84.718606	1.749606	8.340202	147.111509	2.450909	-1.359808	-1.527006
Pot	2.538124	-0.000972	0.410734	0.528170	0.016514	46.828385	3.252943	1.749606	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000
Hemo	-10.228812	0.007263	-1.896169	-0.443158	0.246076	-72.382890	-5.219070	8.340202	0.000000	1.000000	0.000000	0.000000	0.000000	0.000000
Wbcc	882.846165	-2.836586	644.204160	417.342807	-1.793910	5164.622561	-76.821766	147.111509	0.000000	0.000000	1.000000	0.000000	0.000000	0.000000
Rbcc	-2.500767	0.002025	-0.485538	-0.143177	0.054809	-19.297544	-1.524972	2.450909	0.000000	0.000000	0.000000	1.000000	0.000000	0.000000
Htn	1.740948	-0.000835	0.293343	0.126924	-0.021656	9.205893	0.741667	-1.359808	0.000000	0.000000	0.000000	0.000000	1.000000	0.000000
Class	1.895363	-0.001737	0.369048	0.148496	-0.044173	8.886779	0.800758	-1.527006	0.000000	0.000000	0.000000	0.000000	0.000000	1.000000

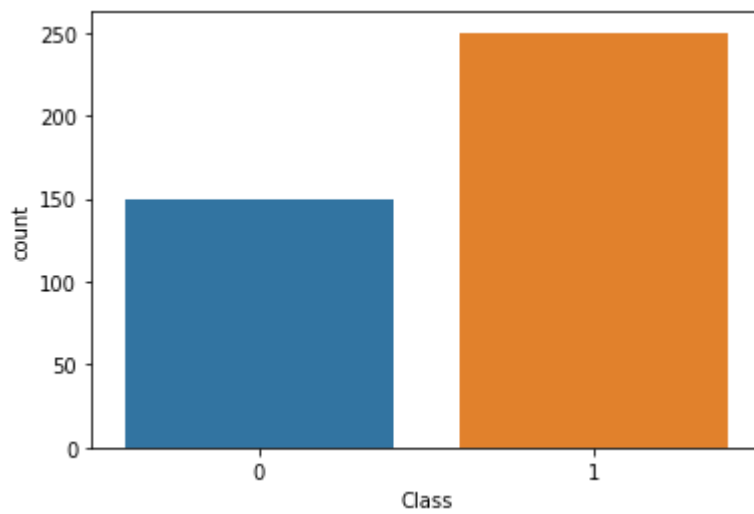
In [16]: `plt.figure(figsize=(10,8))
sns.heatmap(dataset.corr())
plt.show()`



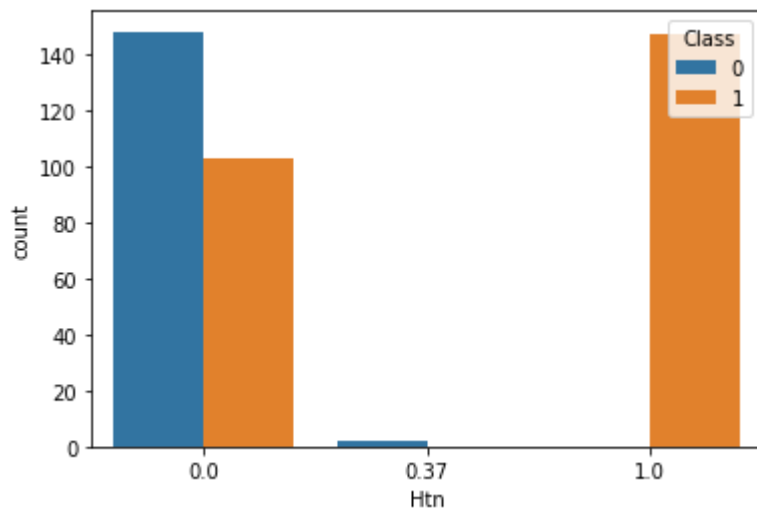
```
In [17]: dataset['Class'].value_counts()
```

```
Out[17]: 1    250
         0    150
         Name: Class, dtype: int64
```

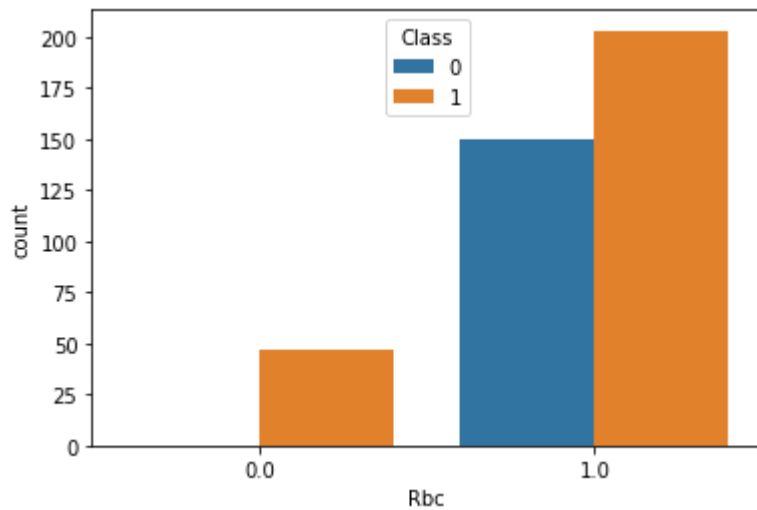
```
In [20]: sns.countplot(dataset['Class'])
         plt.show()
```



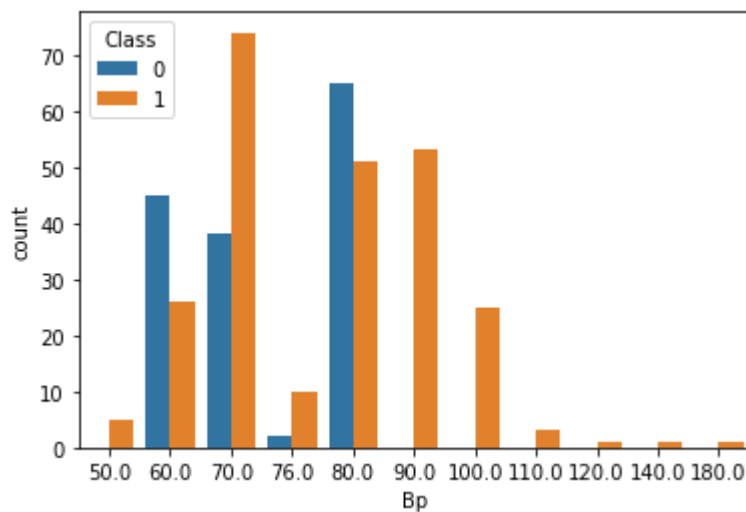
```
In [24]: sns.countplot(dataset['Htn'], hue=dataset['Class'])
         plt.show()
```



```
In [25]: sns.countplot(dataset['Rbc'],hue=dataset['Class'])
plt.show()
```

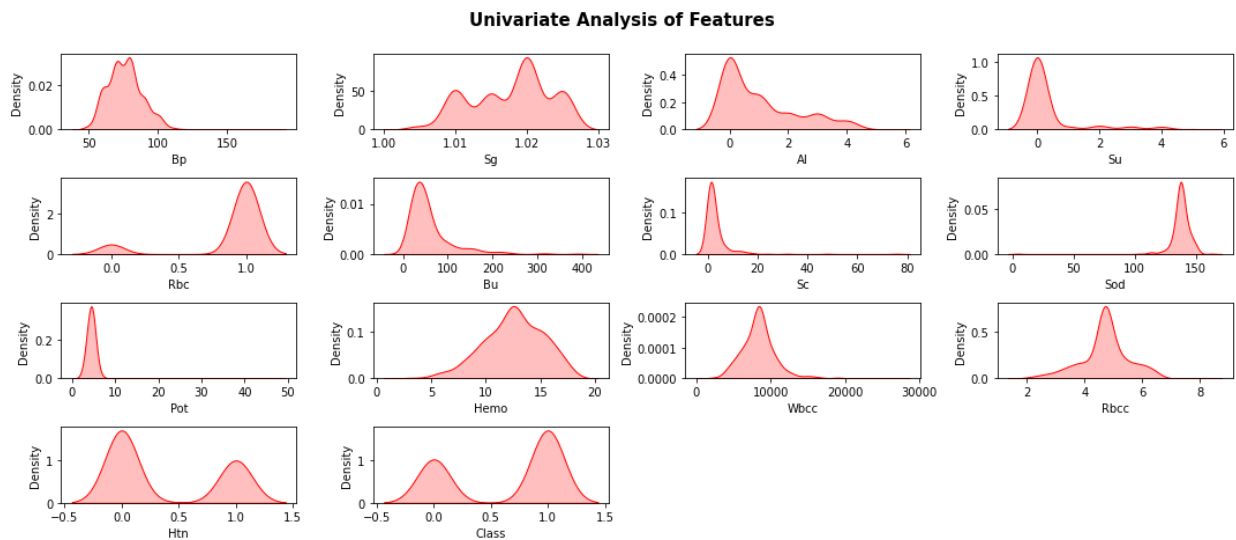


```
In [28]: sns.countplot(dataset['Bp'],hue=dataset['Class'])
plt.show()
```

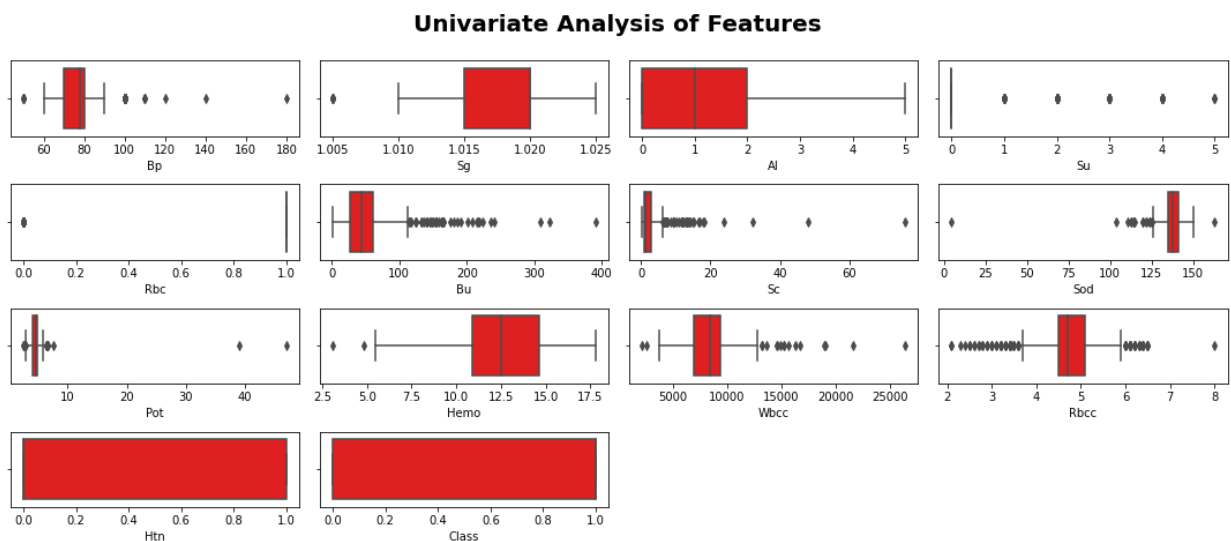


```
In [33]: num_features = [feature for feature in dataset.columns]
```

```
In [34]: plt.figure(figsize=(15,15))
plt.suptitle('Univariate Analysis of Features',fontweight='bold',fontsize=15,y=
for i in range(0,len(num_features)):
    plt.subplot(10,4,i+1)
    sns.kdeplot(x=dataset[num_features[i]],shade=True,color='red')
    plt.tight_layout()
```



```
In [35]: plt.figure(figsize = (15,15))
plt.suptitle('Univariate Analysis of Features',fontweight='bold',fontsize=20,y=
for i in range(0,len(num_features)):
    plt.subplot(10,4,i+1)
    sns.boxplot(data=dataset,x=features[i],color='red')
    plt.xlabel(num_features[i])
    plt.tight_layout()
```



```
In [36]: def remove_outliers(in_dataset, in_cols):

    first_quartile = in_dataset[in_cols].quantile(0.25)
    third_quartile = in_dataset[in_cols].quantile(0.75)
    iqr = third_quartile - first_quartile
    upper_limit = third_quartile + 1.5 * iqr
    lower_limit = first_quartile - 1.5 * iqr
```

```

in_dataset.loc[(in_dataset[in_cols] > upper_limit), in_cols] = upper_limit
in_dataset.loc[(in_dataset[in_cols] < lower_limit), in_cols] = lower_limit
return in_dataset

```

```

In [37]: for features in num_features:
        dataset = remove_outliers(dataset, features)

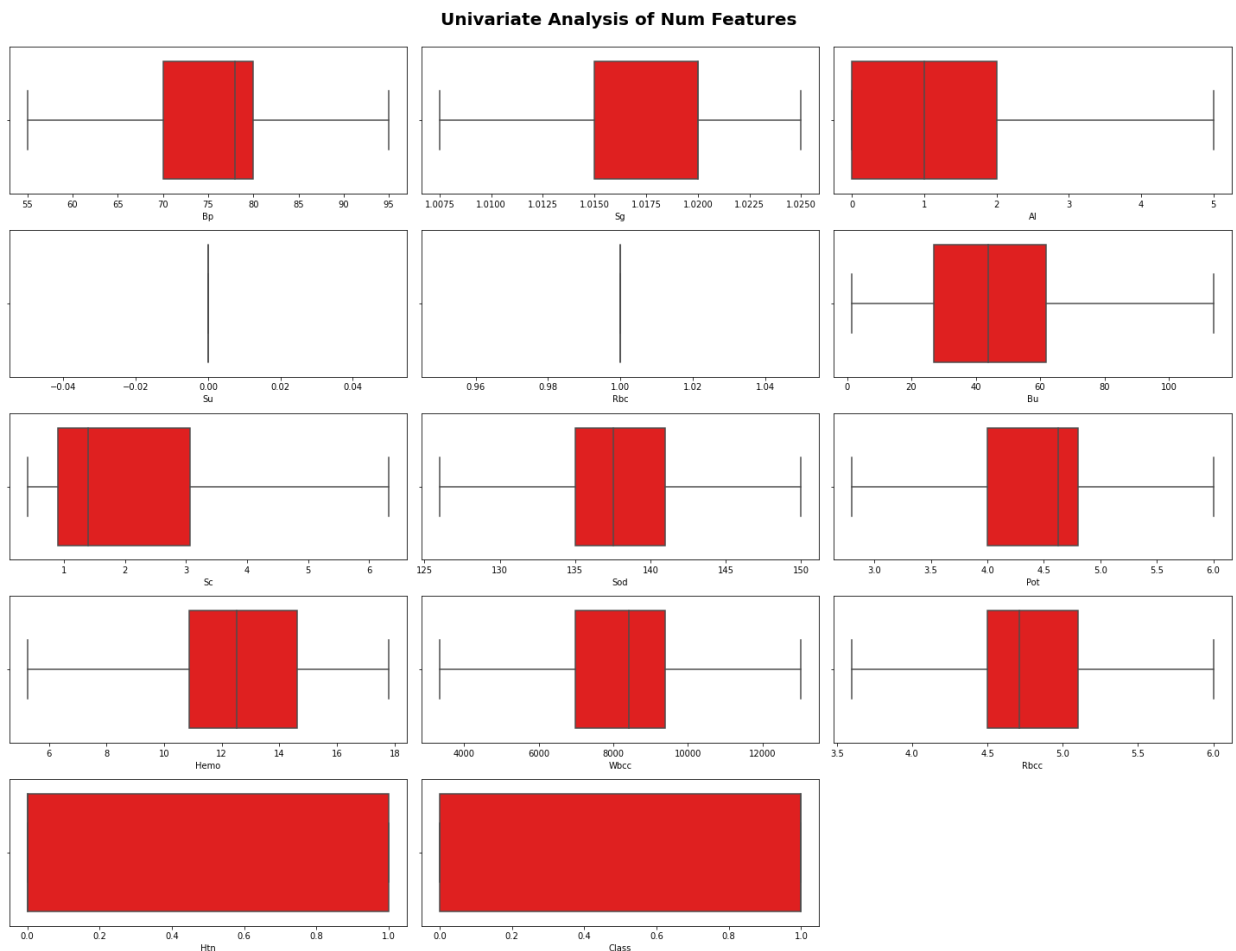
```

```

In [39]: plt.figure(figsize = (20,250))
        plt.suptitle('Univariate Analysis of Num Features',fontweight='bold',fontsize=14)

        for i in range(0,len(num_features)):
            plt.subplot(8,3,i+1)
            sns.boxplot(data=dataset,x=num_features[i],color='red')
            plt.xlabel(num_features[i])
            plt.tight_layout()

```



```

In [40]: dataset['Class'].value_counts()

```

```

Out[40]: 1.0    250
        0.0    150
        Name: Class, dtype: int64

```

```

In [43]: dataset['Class'] = dataset['Class'].astype('int64')

```

```

In [44]: dataset['Class'].value_counts()

```

```

Out[44]: 1    250
        0    150
        Name: Class, dtype: int64

```



```
In [46]: X = dataset.drop('Class',axis=1)
        y = dataset['Class']
```

```
In [47]: X_res,y_res = SMOTE().fit_resample(X,y)
```

```
In [48]: X_train,X_test,y_train,y_test = train_test_split(X_res,y_res,test_size=0.20,ra
```

```
In [49]: st = StandardScaler()
        X_train = st.fit_transform(X_train)
        X_test = st.fit_transform(X_test)
```

```
In [50]: model_df = {}

def model_val(model,X,y):
    X_train,X_test,y_train,y_test = train_test_split(X_res,y_res,test_size=0.20,ra
    model.fit(X_train,y_train)
    y_pred = model.predict(X_test)
    print(f'{model} Accuracy is {accuracy_score(y_test,y_pred)}')

    score = cross_val_score(model,X,y,cv=5,n_jobs=-1)
    print(f'{model} Average cross val score is {np.mean(score)}')
    model_df[model] = round(np.mean(score)*100,2)
```

```
In [51]: model = LogisticRegression()
        model_val(model,X,y)

LogisticRegression() Accuracy is 0.94
LogisticRegression() Average cross val score is 0.9549999999999998
```

```
In [52]: model = DecisionTreeClassifier()
        model_val(model,X,y)

DecisionTreeClassifier() Accuracy is 0.98
DecisionTreeClassifier() Average cross val score is 0.97
```

```
In [53]: model = RandomForestClassifier()
        model_val(model,X,y)

RandomForestClassifier() Accuracy is 1.0
RandomForestClassifier() Average cross val score is 0.9824999999999999
```

```
In [54]: model = GradientBoostingClassifier()
        model_val(model,X,y)

GradientBoostingClassifier() Accuracy is 0.99
GradientBoostingClassifier() Average cross val score is 0.9800000000000001
```

```
In [55]: model_df
```

```
Out[55]: {LogisticRegression(): 95.5,
         DecisionTreeClassifier(): 97.0,
         RandomForestClassifier(): 98.25,
         GradientBoostingClassifier(): 98.0}
```

```
In [67]: rf = RandomForestClassifier()
        rf.fit(X_train,y_train)
```

```
Out[67]: ▾ RandomForestClassifier
RandomForestClassifier()
```

```
In [68]: y_pred = rf.predict(X_test)
```

```
In [69]: accuracy_score(y_test,y_pred)
```

```
Out[69]: 0.99
```

```
In [56]: import pickle
import joblib
```

```
In [70]: pickle.dump(rf,open('chronic_kidney.pkl','wb'))
```

```
In [71]: model = pickle.load(open('chronic_kidney.pkl','rb'))
```

```
In [72]: new_df = pd.DataFrame({
    'Bp':80.0,
    'Sg':1.0200,
    'Al':1.0,
    'Su':0.0,
    'Rbc':1.0,
    'Bu':36.0,
    'Sc':1.2,
    'Sod':137.53,
    'Pot':4.63,
    'Hemo':15.4,
    'Wbcc':7800.0,
    'Rbcc':5.20,
    'Htn':1.0
},index=[0])
```

```
In [73]: model.predict(new_df)
```

```
Out[73]: array([1], dtype=int64)
```

```
In [74]: p = model.predict(new_df)

prob = model.predict_proba(new_df)
if p == 1:
    print('Chronic Kidney Disease!')
    print(f'You will be Chronic Kidney Disease! with Probability of {prob[0][1]}')
else:
    print('Not-Chronic Kidney Disease!')
```

```
Chronic Kidney Disease!
You will be Chronic Kidney Disease! with Probability of 0.82
```

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