Final Project - Echo

April 23, 2024

[1]:
```python
import re
import os
import platform
import sys

# flag if notebook is running on Gradescope
if re.search(r'amzn', platform.uname().release):
    GS = True
else:
    GS = False

# flag if notebook is running on Colaboratory
try:
  import google.colab
  COLAB = True
except:
  COLAB = False

# flag if running on Linux lab machines.
cname = platform.uname().node
if re.search(r'(guardian|colossus|c28)', cname):
    LLM = True
else:
    LLM = False

print("System: GS - %s, COLAB - %s, LLM - %s" % (GS, COLAB, LLM))

# Import standard DS packages
import pandas as pd
import numpy as np
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

```
System: GS - False, COLAB - False, LLM - True
```

1 1. Load the Liver Study Dataset

[2]:
```
# Connect to Google Drive
# Comment out in linux Environment
# from google.colab import drive
# drive.mount('/content/drive')
```

[3]:
```
liverDF = pd.read_csv(filepath_or_buffer='Indian Liver Patient Dataset (ILPD).
 ↪csv',
                     header=0)

print(liverDF.head())
```

```
   Age  Gender    TB   DB  Alkphos  Sgpt  Sgot   TP  ALB  A/G Ratio  Selector
0   65  Female   0.7  0.1      187    16    18  6.8  3.3       0.90         1
1   62    Male  10.9  5.5      699    64   100  7.5  3.2       0.74         1
2   62    Male   7.3  4.1      490    60    68  7.0  3.3       0.89         1
3   58    Male   1.0  0.4      182    14    20  6.8  3.4       1.00         1
4   72    Male   3.9  2.0      195    27    59  7.3  2.4       0.40         1
```

2 2. Conduct Exploratory Analysis

[4]:
```
# number of rows, number of columns
liverDF.shape
```

[4]:
```
(583, 11)
```

[5]:
```
# the data type of each attribute (column)
liverDF.dtypes
```

[5]:
```
Age            int64
Gender        object
TB           float64
DB           float64
Alkphos        int64
Sgpt           int64
Sgot           int64
TP           float64
ALB          float64
A/G Ratio    float64
Selector       int64
dtype: object
```

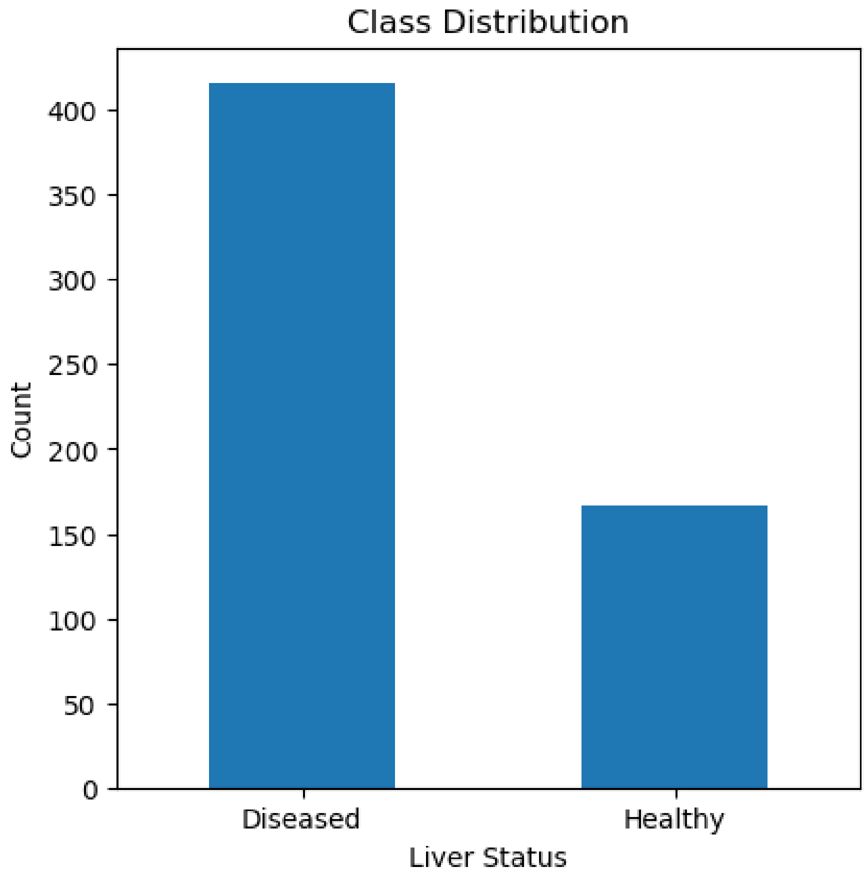
[6]:
```
# Initial Summary Statistics
liverDF.describe()
```

[6]:

```
              Age          TB          DB      Alkphos         Sgpt  \
count  583.000000  583.000000  583.000000   583.000000   583.000000
mean    44.746141    3.298799    1.486106   290.576329    80.713551
std     16.189833    6.209522    2.808498   242.937989   182.620356
min      4.000000    0.400000    0.100000    63.000000    10.000000
25%     33.000000    0.800000    0.200000   175.500000    23.000000
50%     45.000000    1.000000    0.300000   208.000000    35.000000
75%     58.000000    2.600000    1.300000   298.000000    60.500000
max     90.000000   75.000000   19.700000  2110.000000  2000.000000

              Sgot          TP         ALB   A/G Ratio    Selector
count   583.000000  583.000000  583.000000  579.000000  583.000000
mean    109.910806    6.483190    3.141852    0.947064    1.286449
std     288.918529    1.085451    0.795519    0.319592    0.452490
min      10.000000    2.700000    0.900000    0.300000    1.000000
25%      25.000000    5.800000    2.600000    0.700000    1.000000
50%      42.000000    6.600000    3.100000    0.930000    1.000000
75%      87.000000    7.200000    3.800000    1.100000    2.000000
max    4929.000000    9.600000    5.500000    2.800000    2.000000
```

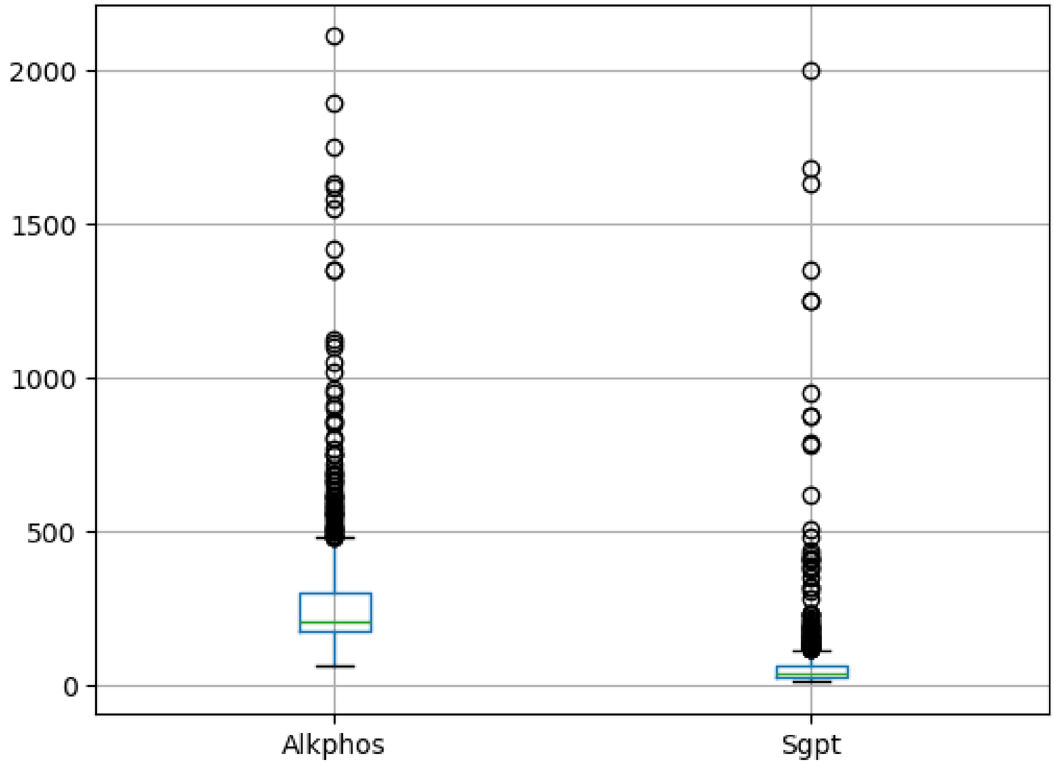
[7]:

```python
# Observe a potential imbalance between possible selectors
plt.figure(figsize=(5, 5))
ax = liverDF['Selector'].value_counts().plot(kind='bar',
                                              figsize=(5, 5),
                                              title="Class Distribution")

plt.xticks((0, 1), ('Diseased','Healthy'), rotation='horizontal')
ax.set_xlabel('Liver Status')
ax.set_ylabel('Count')

plt.show()
```



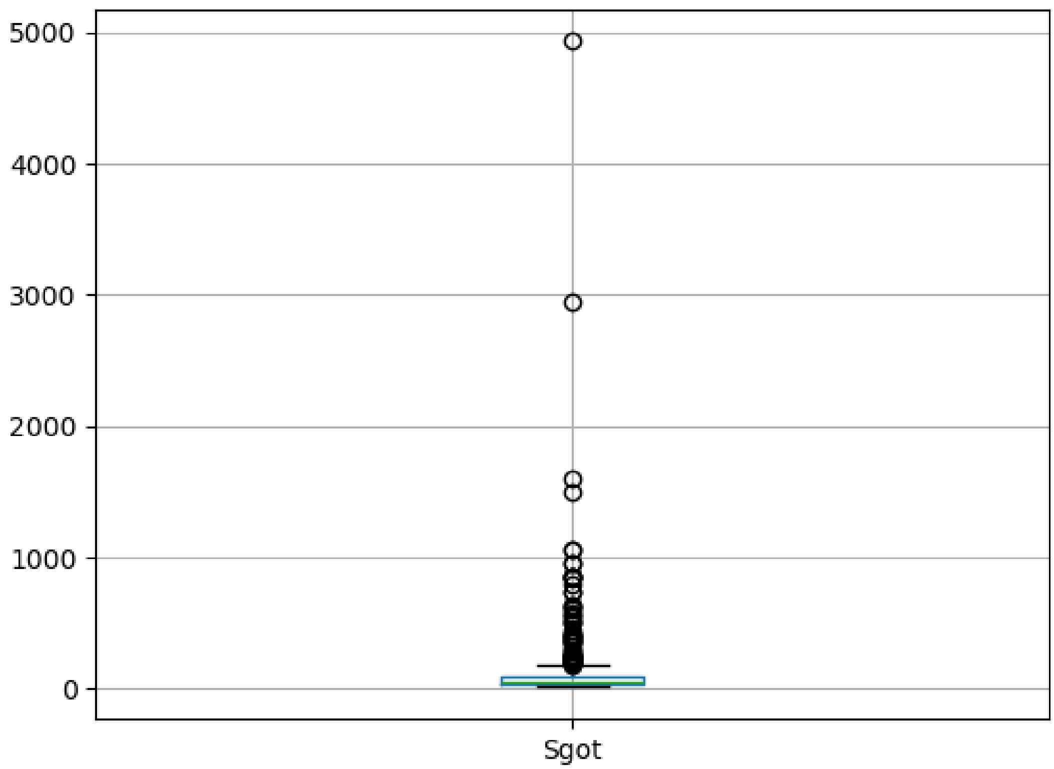
[8]:
```
# Visualize the range and spread of the data fields using box plots
liverDF.boxplot(column=['Alkphos','Sgpt'])
```

[8]: <Axes: >



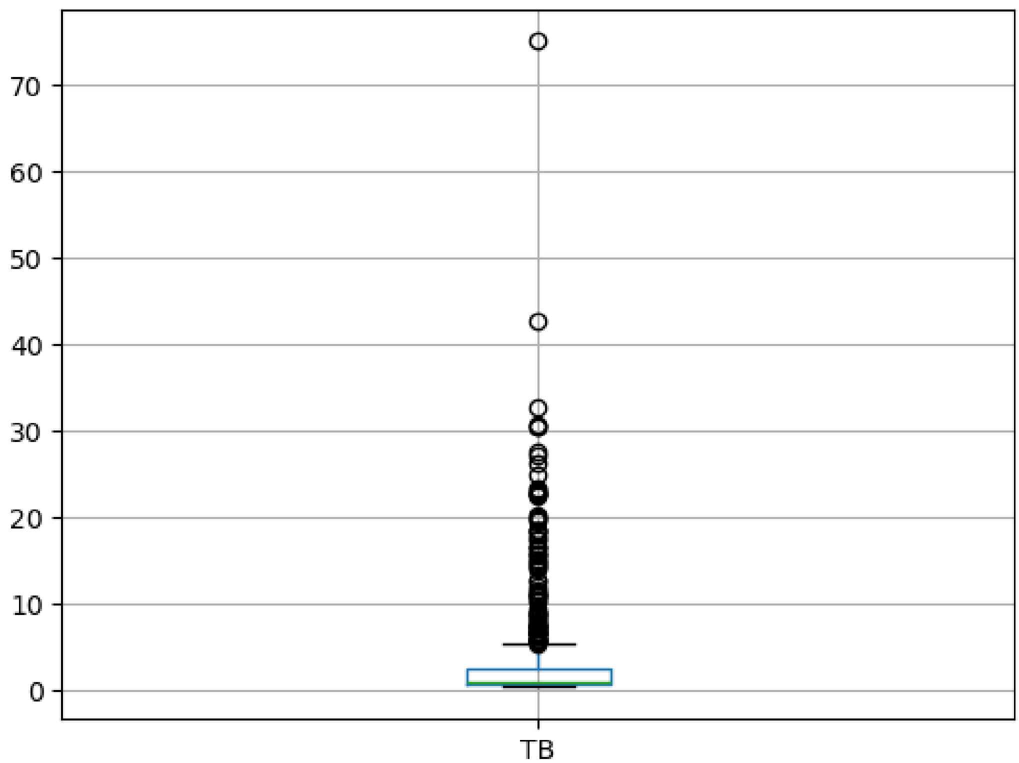
[9]:
```
liverDF.boxplot(column=['Sgot'])
```

[9]: <Axes: >



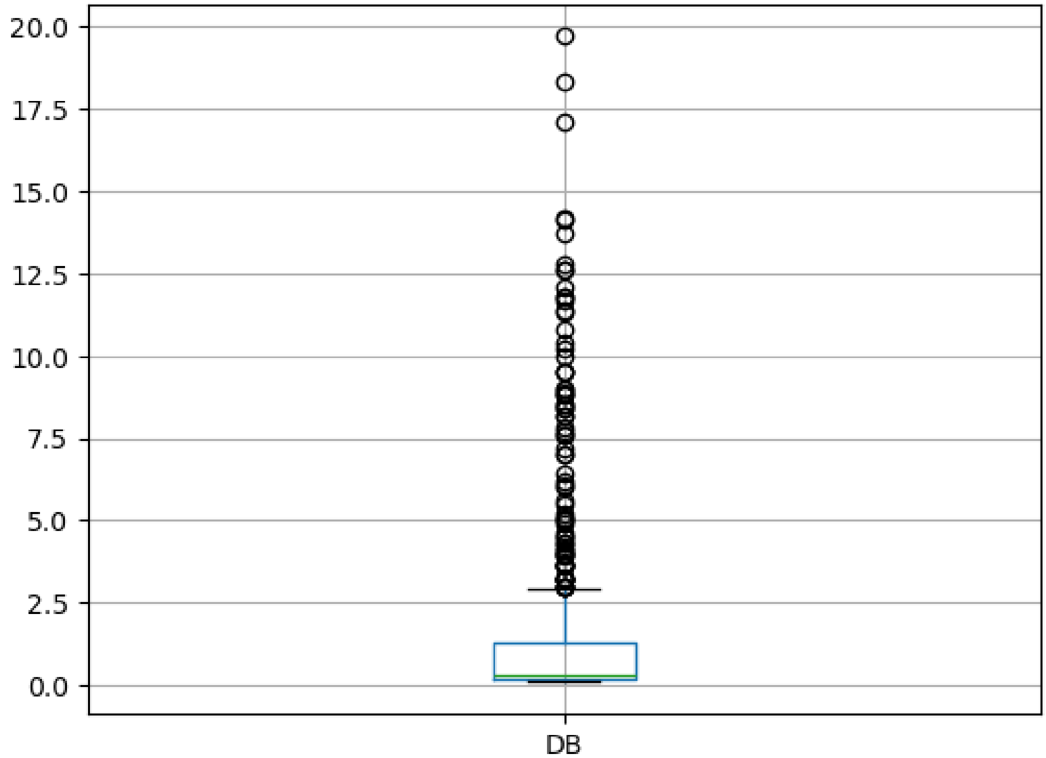

```
[10]: liverDF.boxplot(column=['TB'])
```

[10]: <Axes: >



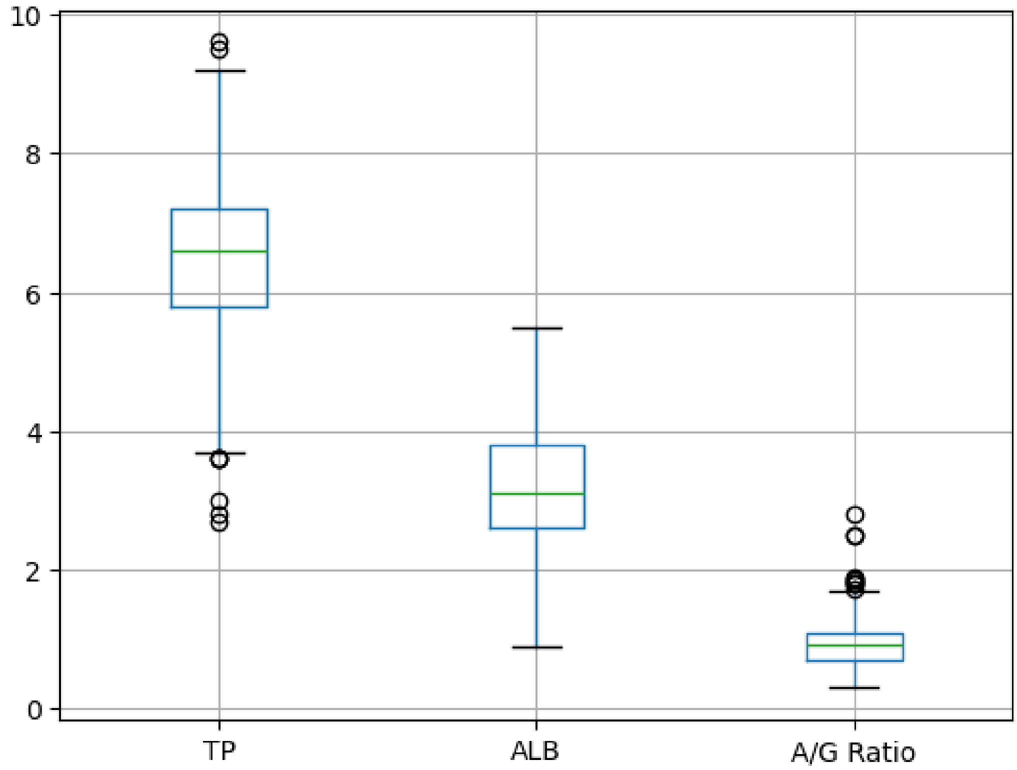
[11]:
```
liverDF.boxplot(column=['DB'])
```

[11]: <Axes: >



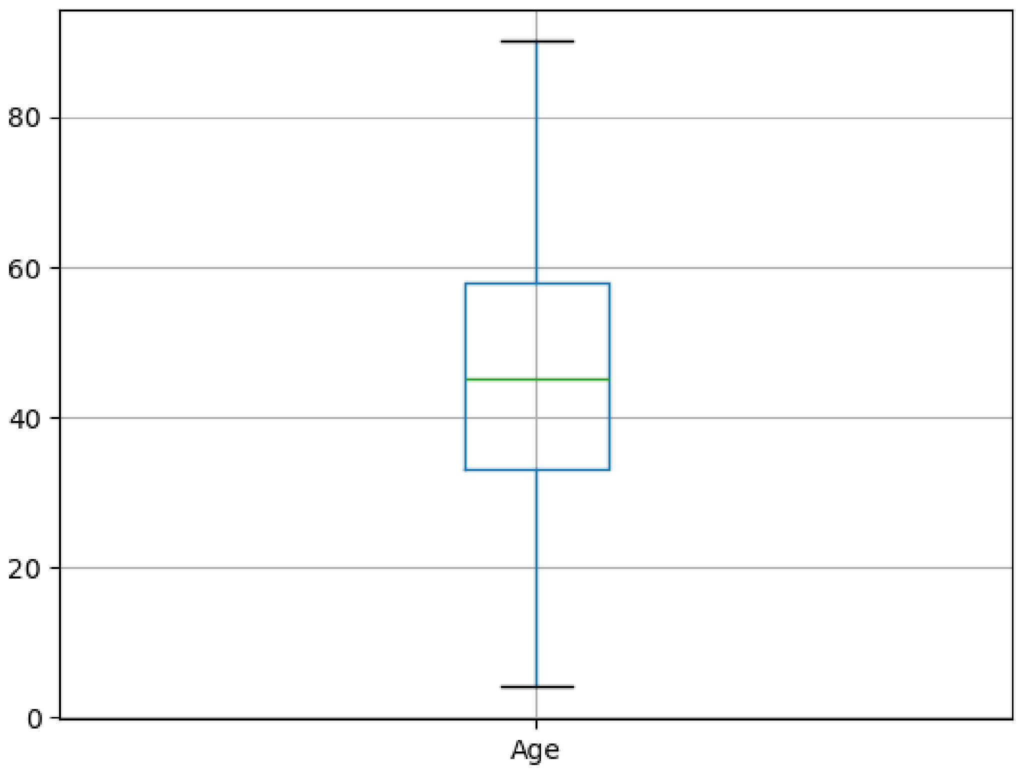
[12]:
```
liverDF.boxplot(column=['TP','ALB','A/G Ratio'])
```

[12]: <Axes: >



[13]:
```
liverDF.boxplot(column=['Age'])
```

[13]: <Axes: >



[14]:
```
from scipy.stats.mstats import winsorize

print(liverDF[(liverDF['Sgpt']>=2000) | (liverDF['Sgot']>=2000) |␣
↪(liverDF['Alkphos']>=1000)])
print(liverDF.isna().sum())

# Save all rows for further testing
liverDFAll = liverDF

# Preprocessing technique #1, Drop rows with extreme outliers
# liverDF.drop(liverDF[(liverDF['Sgpt']>=2000) | (liverDF['Sgot']>=2000) |␣
↪(liverDF['Alkphos']>=1000)].index, inplace=True)
# Winsorize to move the outliers closer to the 1-3 IQR
winsorize(liverDF['Alkphos'], limits=(0, 0.075), inplace = True)
winsorize(liverDF['Sgpt'], limits=(0, 0.075), inplace = True)
winsorize(liverDF['Sgot'], limits=(0, 0.075), inplace = True)
winsorize(liverDF['TB'], limits=(0, 0.075), inplace = True)
winsorize(liverDF['DB'], limits=(0, 0.075), inplace = True)

# Preprocessing technique #2, Drop NaN
#liverDF.dropna(subset=['A/G Ratio'], inplace=True)
```

```
# or use an imputation to fill with median values based on like values by␣
↪Selector
# liverDF['A/G Ratio'].fillna(liverDF.groupby('Selector')['A/G Ratio'].
↪transform('median'), inplace=True)
liverDF['A/G Ratio'].fillna(liverDF.groupby('Selector')['A/G Ratio'].
↪transform('mean'), inplace=True)

# Fill NaN Values with median because of strong outliers
# Commented out section, current data does not have NaN values in these fields
'''liverDFScaled = liverDFScaled.fillna(liverDFScaled['TB'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['DB'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['Alkphos'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['Sgpt'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['TP'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['ALB'].median())
liverDFScaled = liverDFScaled.fillna(liverDFScaled['A/G Ratio'].median())'''

# number of rows, number of columns
print(liverDF.shape)
# Updated Summary Statistics
liverDF.describe()
```

```
     Age  Gender    TB    DB  Alkphos  Sgpt  Sgot   TP  ALB  A/G Ratio  \
77    68  Female   0.6   0.1     1620    95   127  4.6  2.1       0.80
115   50    Male   7.3   3.6     1580    88    64  5.6  2.3       0.60
116   48    Male   0.7   0.1     1630    74   149  5.3  2.0       0.60
117   32    Male  12.7   6.2      194  2000  2946  5.7  3.3       1.30
128   58  Female   1.7   0.8     1896    61    83  8.0  3.9       0.95
135   66    Male  11.3   5.6     1110  1250  4929  7.0  2.4       0.50
161   60    Male  11.5   5.0     1050    99   187  6.2  2.8       0.80
177   75    Male  14.8   9.0     1020    71    42  5.3  2.2       0.70
195   60    Male   2.4   1.0     1124    30    54  5.2  1.9       0.50
199    7  Female  27.2  11.8     1420   790  1050  6.1  2.0       0.40
233   33    Male   2.0   1.4     2110    48    89  6.2  3.0       0.90
419   55  Female   8.2   3.9     1350    52    65  6.7  2.9       0.70
420   55  Female  10.9   5.1     1350    48    57  6.4  2.3       0.50
429   73    Male   1.9   0.7     1750   102   141  5.5  2.0       0.50
447   45  Female  23.3  12.8     1550   425   511  7.7  3.5       0.80
452   58    Male   0.9   0.2     1100    25    36  7.1  3.5       0.90

     Selector
77          1
115         2
116         1
117         1
128         1
135         1
```

```
161          1
177          1
195          1
199          1
233          1
419          1
420          1
429          1
447          1
452          1
Age           0
Gender        0
TB            0
DB            0
Alkphos       0
Sgpt          0
Sgot          0
TP            0
ALB           0
A/G Ratio     4
Selector      0
dtype: int64
(583, 11)
```

[14]:

	Age	TB	DB	Alkphos	Sgpt	Sgot \
count	583.000000	583.000000	583.000000	583.000000	583.000000	583.000000
mean	44.746141	2.536707	1.173242	261.531732	53.777015	71.236707
std	16.189833	3.133067	1.709827	132.971467	47.049419	68.765643
min	4.000000	0.400000	0.100000	63.000000	10.000000	10.000000
25%	33.000000	0.800000	0.200000	175.500000	23.000000	25.000000
50%	45.000000	1.000000	0.300000	208.000000	35.000000	42.000000
75%	58.000000	2.600000	1.300000	298.000000	60.500000	87.000000
max	90.000000	11.300000	6.000000	592.000000	178.000000	248.000000

	TP	ALB	A/G Ratio	Selector
count	583.000000	583.000000	583.000000	583.000000
mean	6.483190	3.141852	0.947234	1.286449
std	1.085451	0.795519	0.318534	0.452490
min	2.700000	0.900000	0.300000	1.000000
25%	5.800000	2.600000	0.700000	1.000000
50%	6.600000	3.100000	0.930000	1.000000
75%	7.200000	3.800000	1.100000	2.000000
max	9.600000	5.500000	2.800000	2.000000

2.1 2.1 Due to extreme variability across fields, scale the numerical attributes.

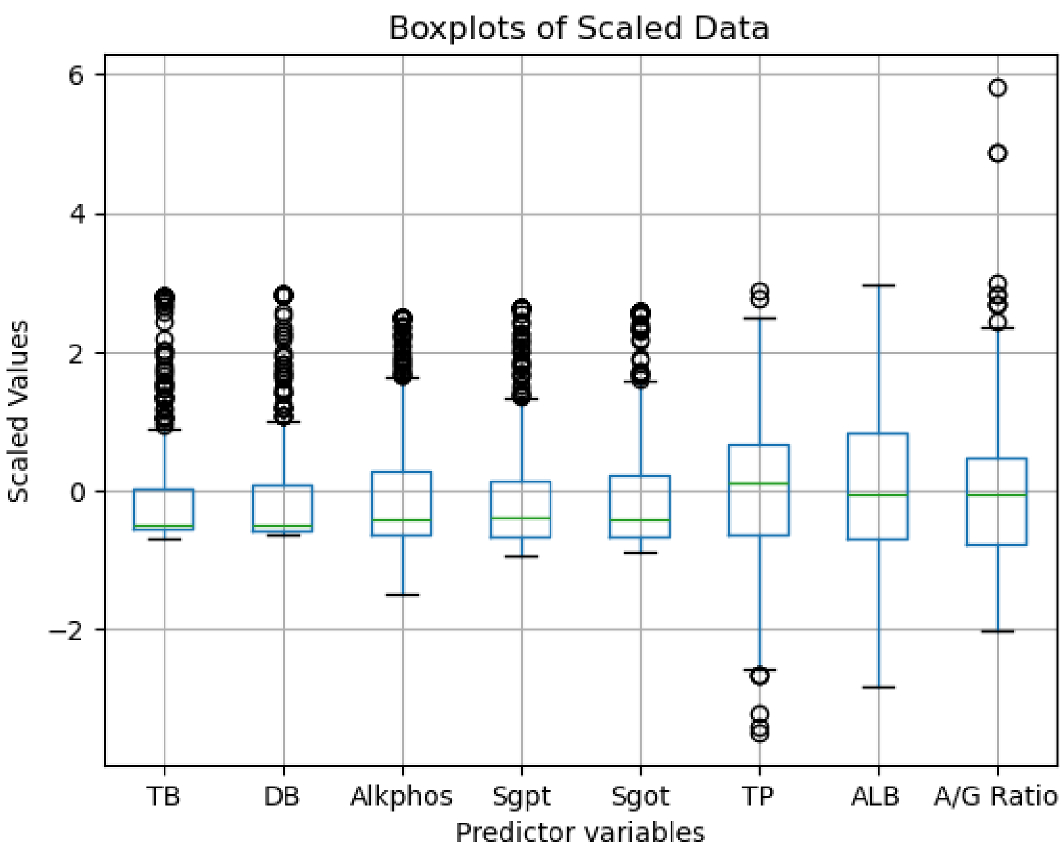
[15]:
```
# Preprocessing technique #3, Scale the data
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler

scaler = StandardScaler()
#scaler = MinMaxScaler()

liverDFScaled = liverDF

scaledColumns = ['TB','DB','Alkphos','Sgpt','Sgot','TP','ALB','A/G Ratio']
liverDFScaled[scaledColumns] = scaler.
 ↪fit_transform(liverDFScaled[scaledColumns])

liverDFScaled.head()
```

[15]:
```
   Age  Gender        TB        DB   Alkphos      Sgpt      Sgot        TP  \
0   65  Female -0.586736 -0.628229 -0.560991 -0.803612 -0.774841  0.292120
1   62    Male  2.671656  2.532696  2.487391  0.217468  0.418639  0.937566
2   62    Male  1.521635  1.713197  1.719651  0.132378 -0.047109  0.476533
3   58    Male -0.490901 -0.452622 -0.598625 -0.846157 -0.745731  0.292120
4   72    Male  0.435504  0.483948 -0.500776 -0.569614 -0.178101  0.753153

        ALB  A/G Ratio  Selector
0  0.198969  -0.148413         1
1  0.073157  -0.651145         1
2  0.198969  -0.179834         1
3  0.324781   0.165794         1
4 -0.933340  -1.719450         1
```

2.1.1 2.2.1 Replot the data and distributions.

[16]:
```
# Note that with the data fields scaled it's easier to make observations from a␣
 ↪single chart
# More exploration is required for TB, DB, Alkphos, Sgpt, and Sgot due to␣
 ↪extreme skewness
#plt.figure(figsize=(8, 6))
ax = liverDFScaled.boxplot(scaledColumns)
ax.set_title('Boxplots of Scaled Data')
ax.set_xlabel('Predictor variables')
ax.set_ylabel('Scaled Values')
#ax.grid(False)

plt.show()
```

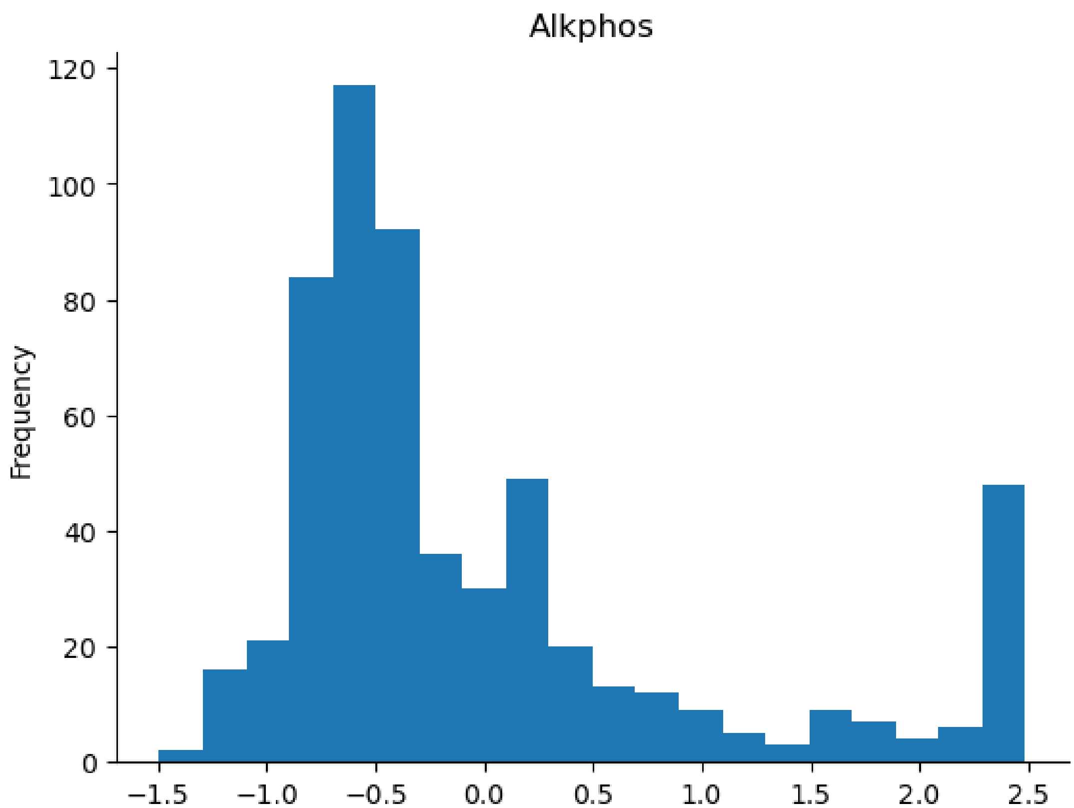
```
# Testing to rescale fields of greater importance according to medical␣
↪documentation
# Provided little impact to training and testing - commented out for exploration
# in future work.
'''weighted_scaler = 10
# Increase range for heavily weighted features
liverDFScaled['ALB'] = liverDFScaled['ALB'] * weighted_scaler
liverDFScaled['A/G Ratio'] = liverDFScaled['A/G Ratio'] * weighted_scaler

# Reduce range for lesser weighted features
liverDFScaled['Alkphos'] = liverDFScaled['Alkphos'] / weighted_scaler
liverDFScaled['Sgpt'] = liverDFScaled['Sgpt'] / weighted_scaler
liverDFScaled['Sgot'] = liverDFScaled['Sgot'] / weighted_scaler'''
```



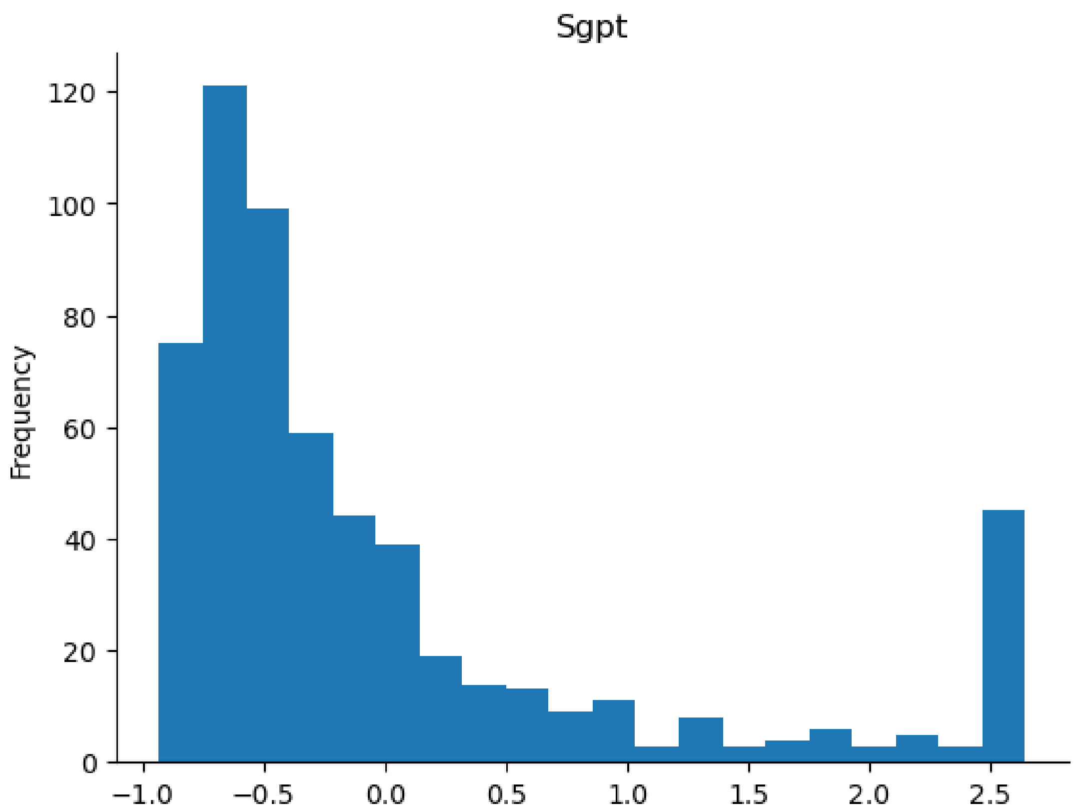

```
[16]: "weighted_scaler = 10\n# Increase range for heavily weighted
features\nliverDFScaled['ALB'] = liverDFScaled['ALB'] *
weighted_scaler\nliverDFScaled['A/G Ratio'] = liverDFScaled['A/G Ratio'] *
weighted_scaler\n\n# Reduce range for lesser weighted
features\nliverDFScaled['Alkphos'] = liverDFScaled['Alkphos'] /
```

```
weighted_scaler\nliverDFScaled['Sgpt'] = liverDFScaled['Sgpt'] /
weighted_scaler\nliverDFScaled['Sgot'] = liverDFScaled['Sgot'] /
weighted_scaler"
```

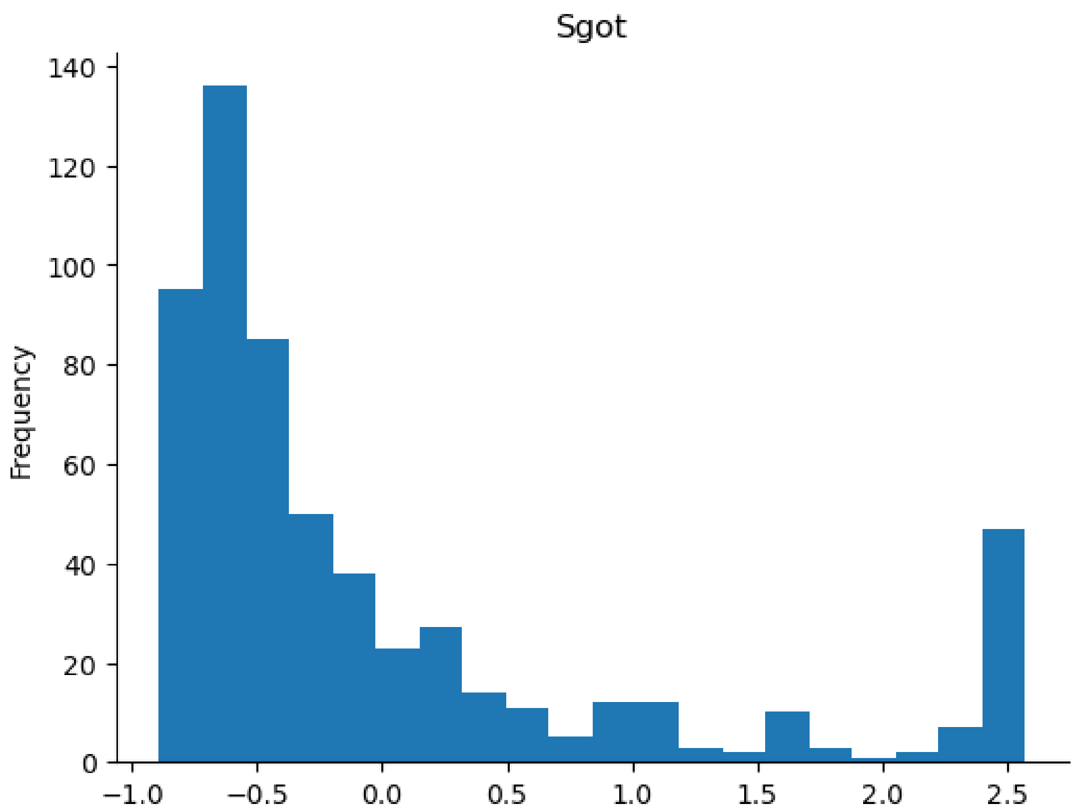
[17]:
```
# Observe the distribution of fields with a large range and outliers
liverDFScaled['Alkphos'].plot(kind='hist', bins=20, title='Alkphos')
plt.gca().spines[['top', 'right',]].set_visible(False)
```



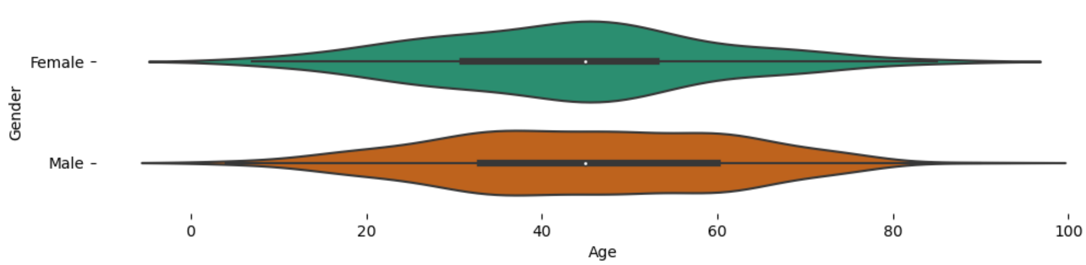
[18]:
```
# Observe the distribution of fields with a large range and outliers
liverDFScaled['Sgpt'].plot(kind='hist', bins=20, title='Sgpt')
plt.gca().spines[['top', 'right',]].set_visible(False)
```



[19]:
```
# Observe the distribution of fields with a large range and outliers
liverDFScaled['Sgot'].plot(kind='hist', bins=20, title='Sgot')
plt.gca().spines[['top', 'right',]].set_visible(False)
```

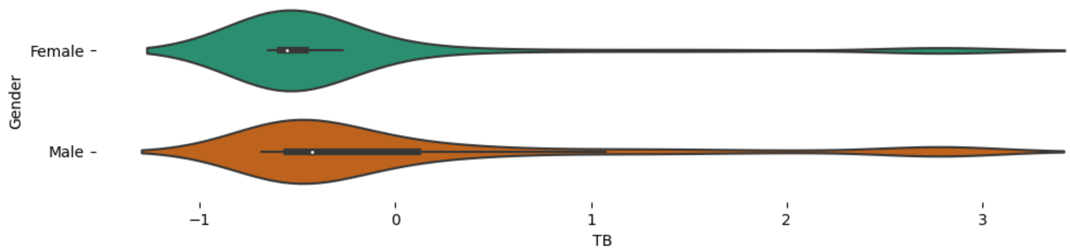


[20]:
```
# Observe the relationships between various fields: Gender vs Age
figsize = (12, 1.2 * len(liverDFScaled['Gender'].unique()))
plt.figure(figsize=figsize)
sns.violinplot(liverDFScaled, x='Age', y='Gender', inner='box', palette='Dark2')
sns.despine(top=True, right=True, bottom=True, left=True)
```

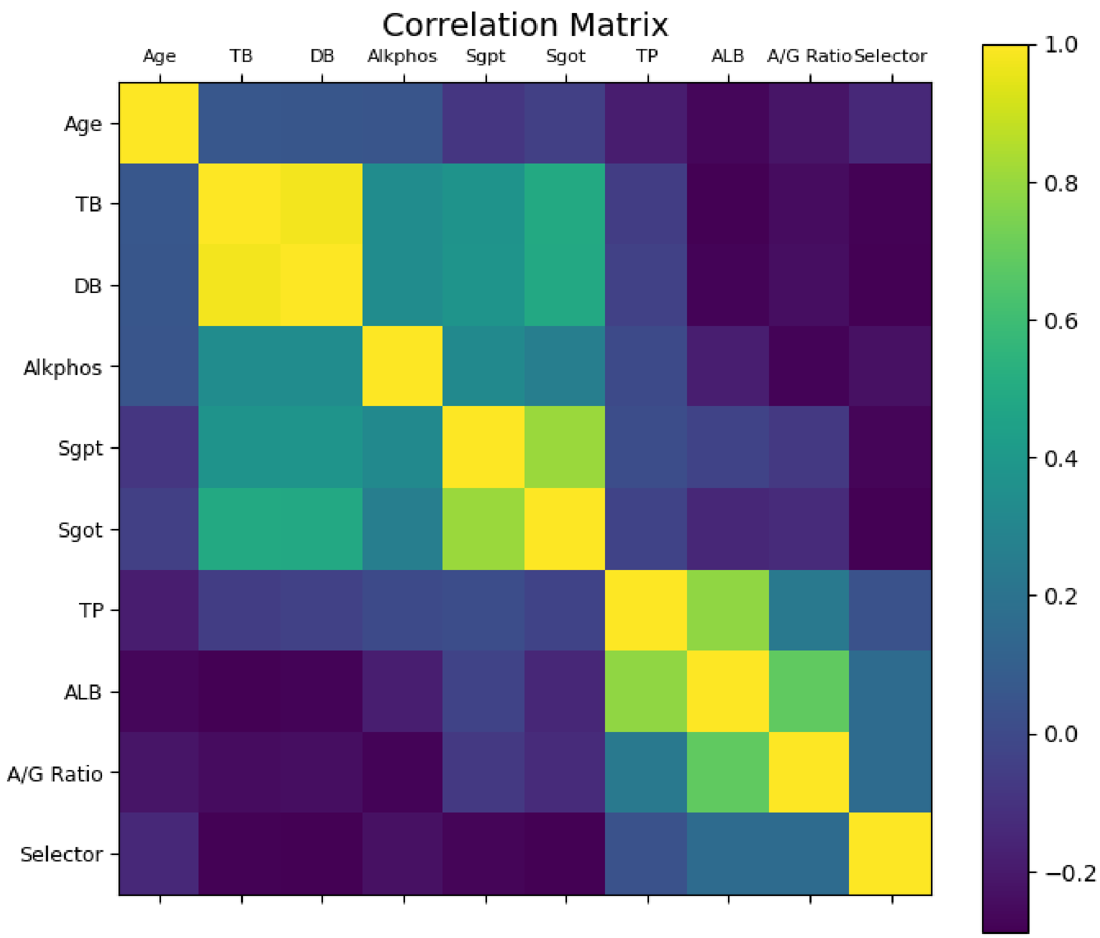


[21]:
```
# Gender vs TB
figsize = (12, 1.2 * len(liverDFScaled['Gender'].unique()))
plt.figure(figsize=figsize)
sns.violinplot(liverDFScaled, x='TB', y='Gender', inner='box', palette='Dark2')
```

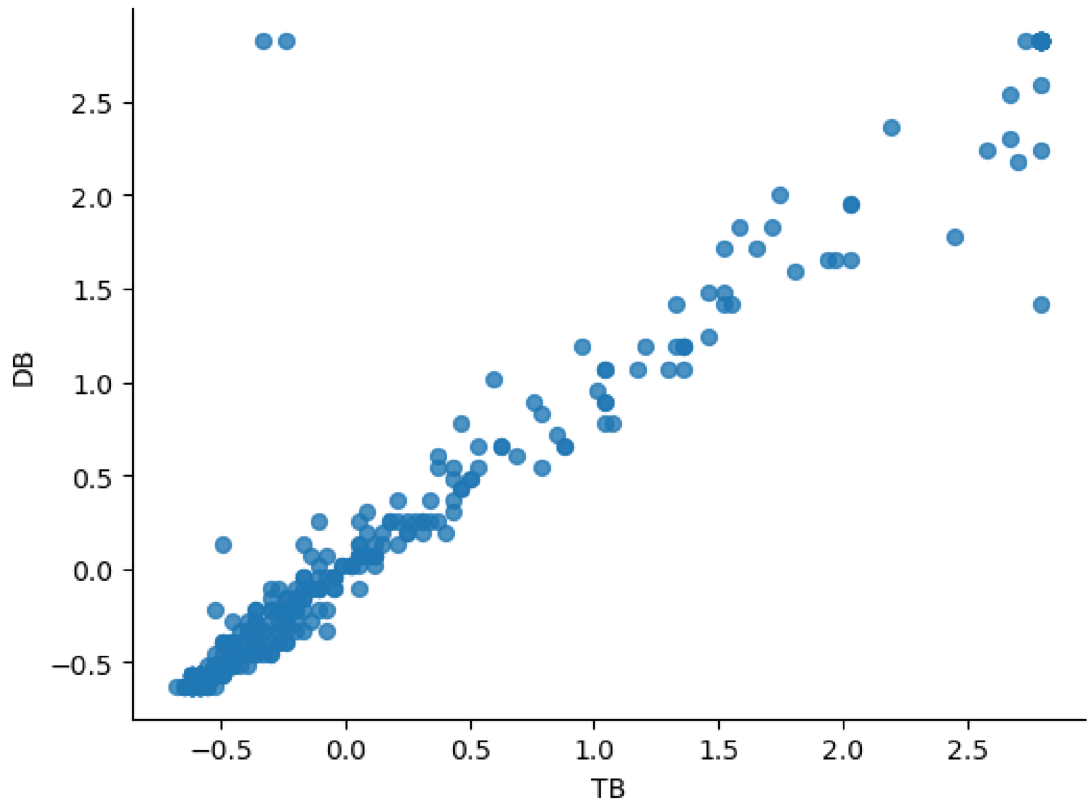
```
sns.despine(top=True, right=True, bottom=True, left=True)
```




```
[22]: # Plot correlation matrix to observe potential correlation between numeric␣
      ↪fields
      Columns = ['Age','TB','DB','Alkphos','Sgpt','Sgot','TP','ALB','A/G␣
      ↪Ratio','Selector']
      f = plt.figure(figsize=(8, 7))
      plt.matshow(liverDFScaled[Columns].corr(), fignum=f.number)
      plt.xticks(range(len(Columns)), Columns, fontsize=8)
      plt.yticks(range(len(Columns)), Columns, fontsize=9)
      cb = plt.colorbar()
      cb.ax.tick_params(labelsize=10)
      plt.title('Correlation Matrix', fontsize=14);
```



[23]:
```
# Observing potential correlation between specific fields: TB vs DB
liverDFScaled.plot(kind='scatter', x='TB', y='DB', s=32, alpha=.8)
plt.gca().spines[['top', 'right',]].set_visible(False)
```



2.1.2 2.2.2 Final Pre-processing, mapping Gender and Selector to binary values, 0 and 1.

[24]:
```
import matplotlib.pyplot as plt
from sklearn import neighbors
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, precision_score, recall_score,␣
↪confusion_matrix, ConfusionMatrixDisplay
from sklearn.linear_model import LogisticRegression

# Final Pre-Processing Steps prior to testing the models
# Convert Gender to binary values
liverDFScaled['Gender'].replace('Male', 0, inplace = True)
liverDFScaled['Gender'].replace('Female', 1, inplace = True)

# Re-map Selector: Unhealthy = 1; Healthy = 2, convert to 0 and 1 respectively
liverDFScaled['Selector'] = liverDFScaled['Selector'].map({1:0,2:1})
```

```
# Column List ['Age', 'Gender', 'TB','DB','Alkphos','Sgpt','Sgot','TP','ALB','A/
↪G Ratio']
# Ingore the following fields: Age, Gender, TB, and A/G Ratio
# Future runs will incorporate testing only male or female records to check bias
X_Columns = ['TB','Alkphos','Sgpt','Sgot','TP','ALB']
```

3 3. Generate the Model

3.0.1 3.1.1 Training the Model.

[25]:

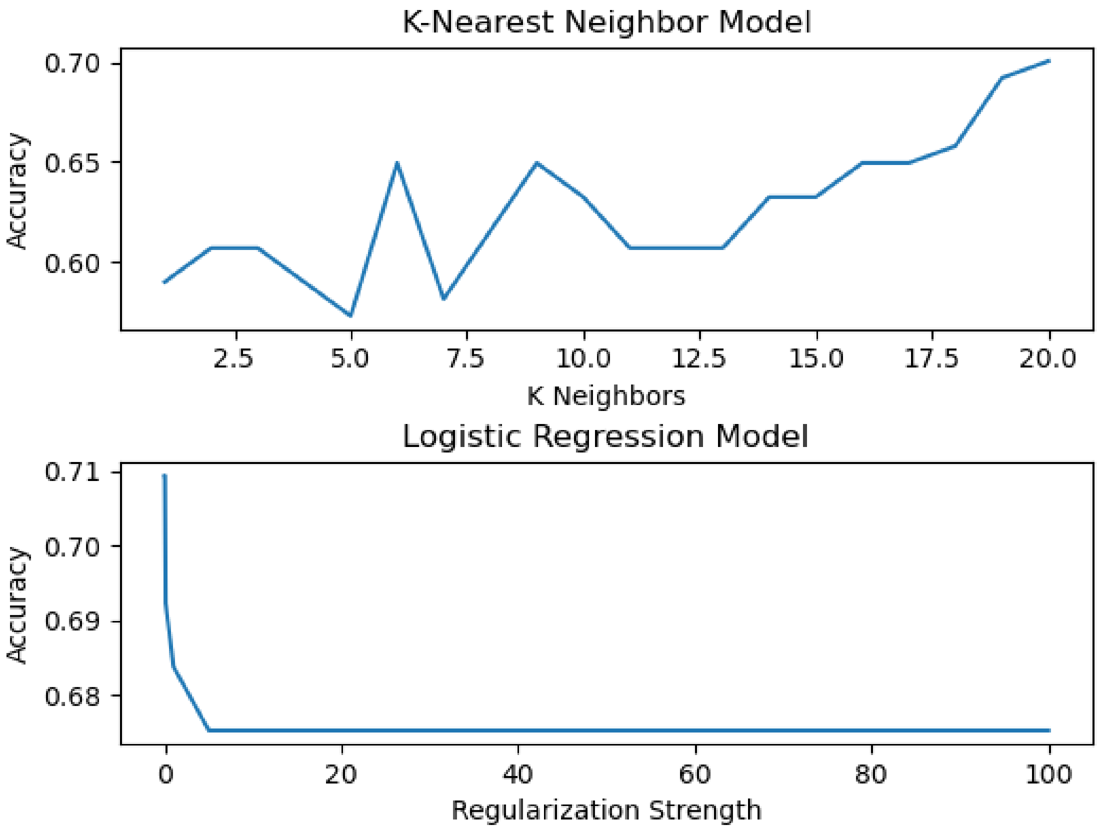
```
# Split Features and Targets
liverDFScaled_X = liverDFScaled[X_Columns]
liverDFScaled_y = liverDFScaled['Selector']

# Split Data
train_X, test_X, train_y, test_y = train_test_split(liverDFScaled_X,
      liverDFScaled_y, test_size = .2, shuffle = True,
      stratify = liverDFScaled_y, random_state = 42)

# Create Graph for Accuracy
fig, (ax1, ax2) = plt.subplots(2, 1)
fig.tight_layout(pad = 3)

# K-Nearest Neighbor
k_range = range(1, 21)
acc = []
maxKnnAcc = 0
bestKnn = 0

for k in k_range:
  knn = KNeighborsClassifier(n_neighbors = k)
  knn.fit(train_X, train_y)
  yhat = knn.predict(test_X)
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related nearest neighbor value
  if accuracy > maxKnnAcc :
    maxKnnAcc = accuracy
    bestKnn = k
  acc.append(accuracy)

# Put KNN Accuracy in Axes
ax1.plot(k_range, acc)
ax1.set(xlabel = 'K Neighbors', ylabel = 'Accuracy')
ax1.set_title('K-Nearest Neighbor Model')
```

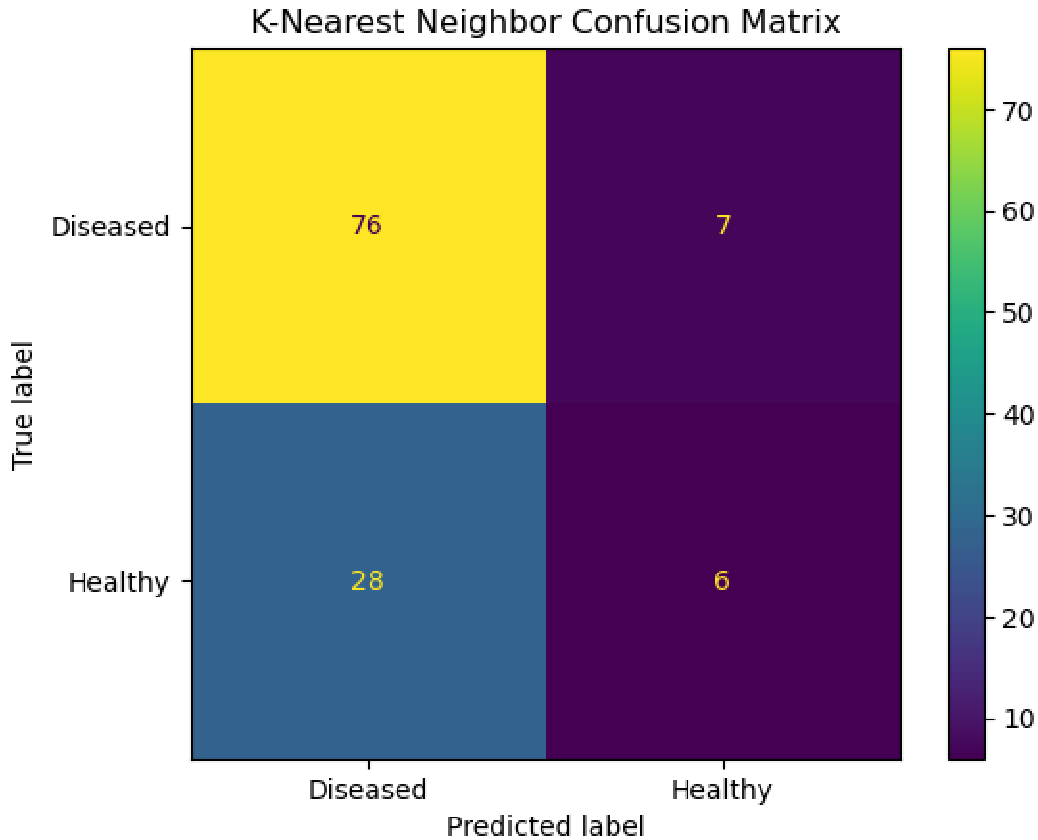
```
# KNN Confusion Matrix
knn_con = KNeighborsClassifier(n_neighbors = bestKnn)
knn_con.fit(train_X, train_y)
yhat = knn_con.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_knn_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
↪'Healthy'])
conf_knn_disp.plot()
conf_knn_disp.ax_.set_title('K-Nearest Neighbor Confusion Matrix')

# Print Primary Scores of Consideration
print('KNN Model Results, K=',bestKnn)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Logistic Regression
c_range = [.0001, .001, .01, .1, 1, 5, 10, 20, 50, 100]
acc = []
maxLogAcc = 0
bestC = 0

for c in c_range:
  lg = LogisticRegression(C = c)
  lg.fit(train_X, train_y)
  yhat = lg.predict(test_X)
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related C value
  if accuracy > maxLogAcc :
    maxLogAcc = accuracy
    bestC = c
  acc.append(accuracy)

# Put LG Accuracy in Axes
ax2.plot(c_range, acc)
ax2.set(xlabel = 'Regularization Strength', ylabel = 'Accuracy')
ax2.set_title('Logistic Regression Model')

# Log. Regression Confusion Matrix
lg = LogisticRegression(C = bestC)
lg.fit(train_X, train_y)
yhat = lg.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_lg_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
↪'Healthy'])
conf_lg_disp.plot()
```

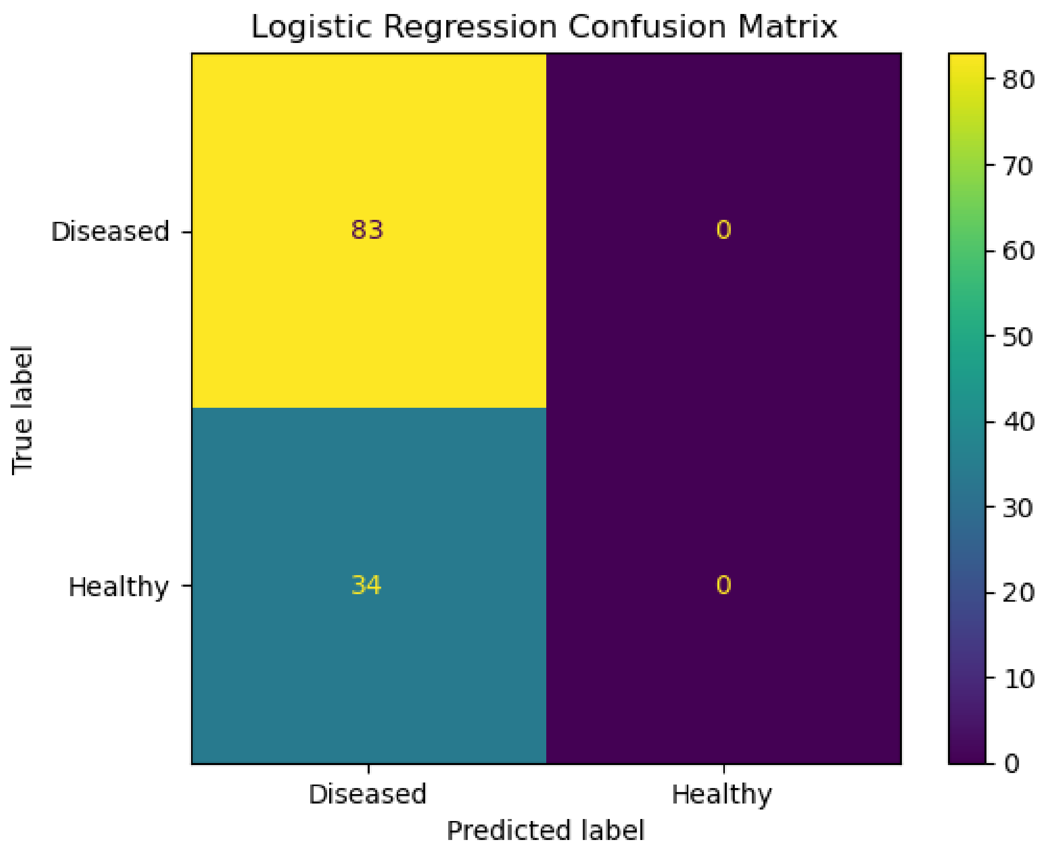
```python
conf_lg_disp.ax_.set_title('Logistic Regression Confusion Matrix')

# Print Primary Scores of Consideration
print('Logistic Regression Model Results, C=', bestC)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Plot Model Results
plt.show()
```

```
KNN Model Results, K= 20
Accuracy = 0.7008547008547008
Recall = 0.17647058823529413
Precision = 0.46153846153846156

Logistic Regression Model Results, C= 0.0001
Accuracy = 0.7094017094017094
Recall = 0.0
Precision = 0.0
```

```
/home/campus05/psweiss/.conda/envs/cs5831/lib/python3.10/site-
packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 due to no predicted samples. Use
`zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```


K-Nearest Neighbor Model
Accuracy
0.70
0.65
0.60
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
K Neighbors
Logistic Regression Model
Accuracy
0.71
0.70
0.69
0.68
0
20
40
60
80
100
Regularization Strength


K-Nearest Neighbor Confusion Matrix
Diseased
Healthy
True label
76
7
28
6
Diseased
Healthy
Predicted label
70
60
50
40
30
20
10



4 4. Test for Gender Bias

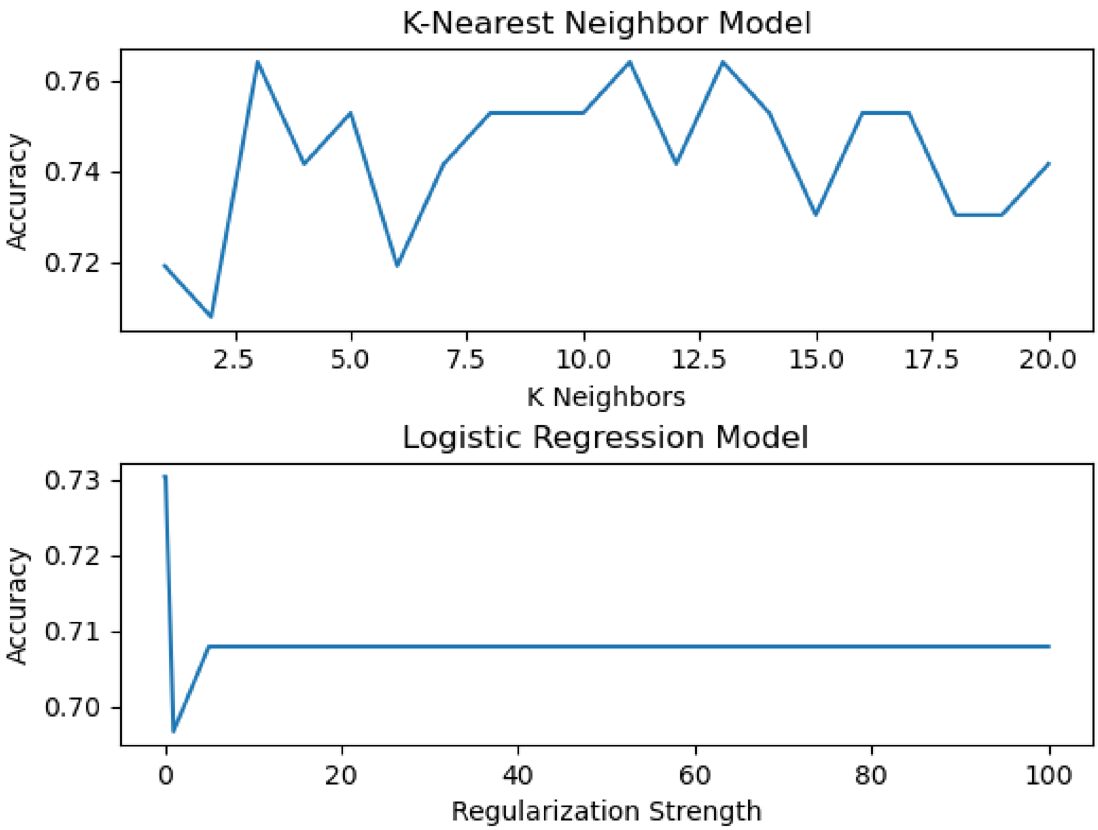
[26]:
```
# Split Features and Targets
# Column List ['Age', 'Gender', 'TB','DB','Alkphos','Sgpt','Sgot','TP','ALB','A/
↪G Ratio']
# Ingore the following fields: Age, Gender, TB, and A/G Ratio
# Future runs will incorporate testing only male or female records to check bias
liverDFScaledMale_X = liverDFScaled[X_Columns].loc[liverDFScaled['Gender'] == 0]
liverDFScaledMale_y = liverDFScaled['Selector'].loc[liverDFScaled['Gender'] ==␣
↪0]

# Split Data
train_X, test_X, train_y, test_y = train_test_split(liverDFScaledMale_X,
      liverDFScaledMale_y, test_size = .2, shuffle = True,
      stratify = liverDFScaledMale_y, random_state = 42)

# Create Graph for Accuracy
fig, (ax1, ax2) = plt.subplots(2, 1)
```

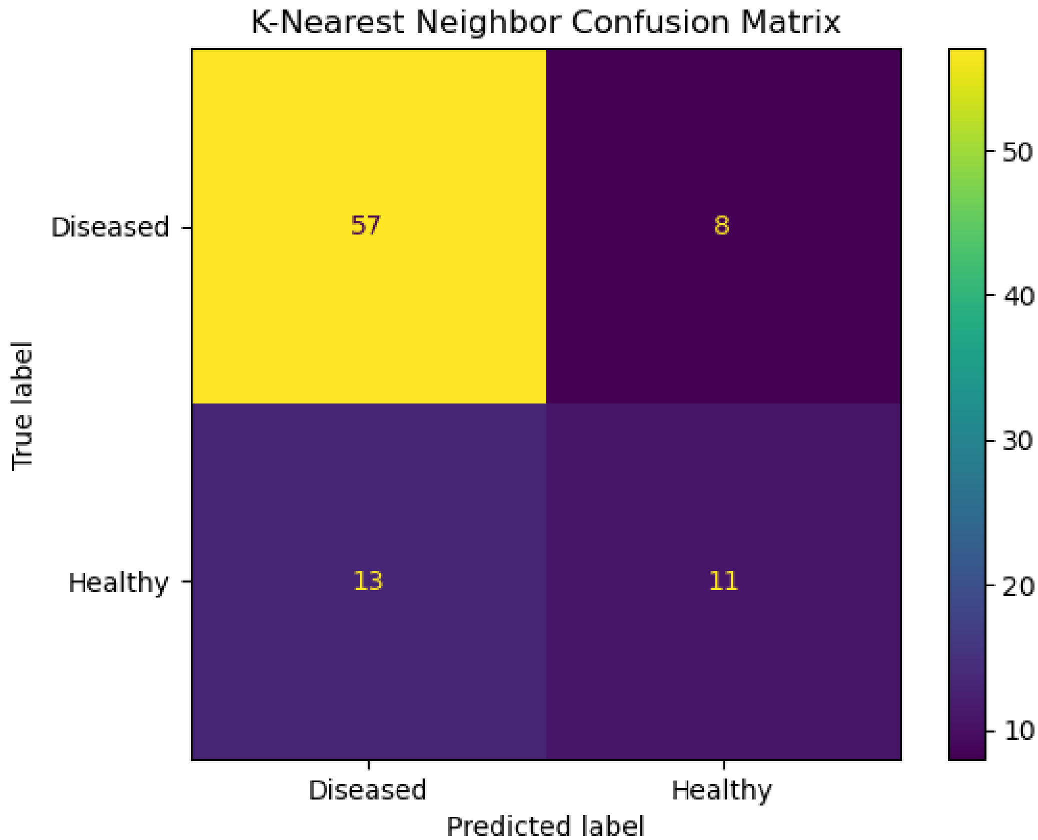
```python
fig.tight_layout(pad = 3)

# K-Nearest Neighbor
k_range = range(1, 21)
acc = []
maxKnnAcc = 0
bestKnn = 0

for k in k_range:
  knn = KNeighborsClassifier(n_neighbors = k)
  knn.fit(train_X, train_y)
  yhat = knn.predict(test_X)
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related nearest neighbor value
  if accuracy > maxKnnAcc :
    maxKnnAcc = accuracy
    bestKnn = k
  acc.append(accuracy)

# Put KNN Accuracy in Axes
ax1.plot(k_range, acc)
ax1.set(xlabel = 'K Neighbors', ylabel = 'Accuracy')
ax1.set_title('K-Nearest Neighbor Model')

# KNN Confusion Matrix
knn_con = KNeighborsClassifier(n_neighbors = bestKnn)
knn_con.fit(train_X, train_y)
yhat = knn_con.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_knn_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
 ↪'Healthy'])
conf_knn_disp.plot()
conf_knn_disp.ax_.set_title('K-Nearest Neighbor Confusion Matrix')

# Print Primary Scores of Consideration
print('KNN Model Results, K=',bestKnn)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Logistic Regression
c_range = [.0001, .001, .01, .1, 1, 5, 10, 20, 50, 100]
acc = []
maxLogAcc = 0
bestC = 0
```

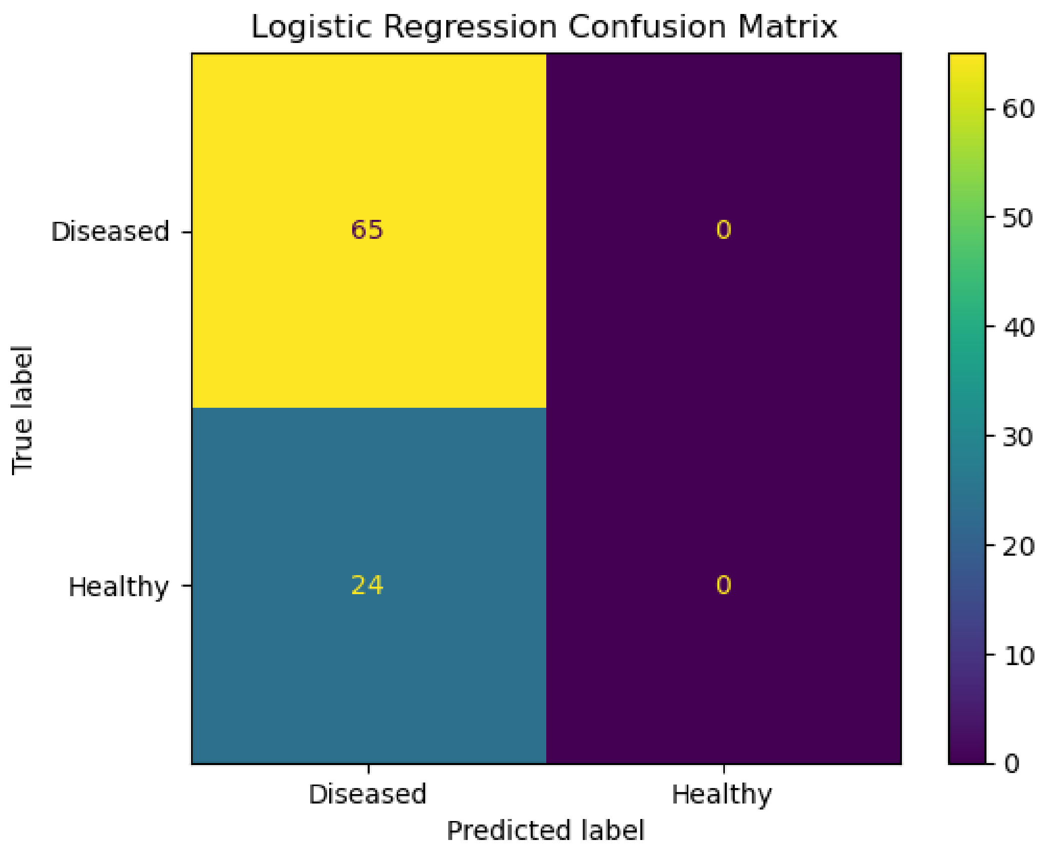
```python
for c in c_range:
  lg = LogisticRegression(C = c)
  lg.fit(train_X, train_y)
  yhat = lg.predict(test_X)
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related C value
  if accuracy > maxLogAcc :
    maxLogAcc = accuracy
    bestC = c
  acc.append(accuracy)

# Put LG Accuracy in Axes
ax2.plot(c_range, acc)
ax2.set(xlabel = 'Regularization Strength', ylabel = 'Accuracy')
ax2.set_title('Logistic Regression Model')

# Log. Regression Confusion Matrix
lg = LogisticRegression(C = bestC)
lg.fit(train_X, train_y)
yhat = lg.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_lg_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
↪'Healthy'])
conf_lg_disp.plot()
conf_lg_disp.ax_.set_title('Logistic Regression Confusion Matrix')

# Print Primary Scores of Consideration
print('Logistic Regression Model Results, C=', bestC)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Plot Model Results
plt.show()
```

```
KNN Model Results, K= 3
Accuracy = 0.7640449438202247
Recall = 0.4583333333333333
Precision = 0.5789473684210527

Logistic Regression Model Results, C= 0.0001
Accuracy = 0.7303370786516854
Recall = 0.0
Precision = 0.0


/home/campus05/psweiss/.conda/envs/cs5831/lib/python3.10/site-
```

```
packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 due to no predicted samples. Use
`zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```




K-Nearest Neighbor Confusion Matrix
True label
Diseased
Healthy
57
8
13
11
Predicted label
Diseased
Healthy
50
40
30
20
10

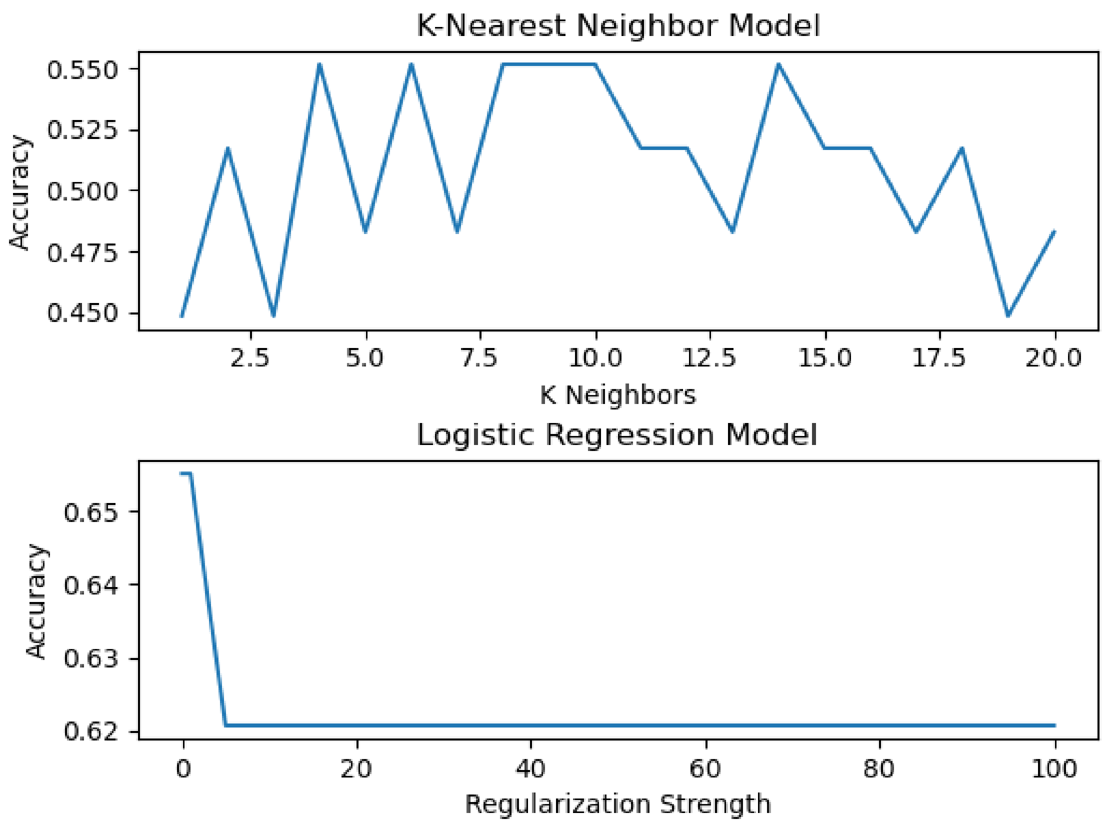


[27]:
```
# Split Features and Targets
# Column List ['Age', 'Gender', 'TB','DB','Alkphos','Sgpt','Sgot','TP','ALB','A/
↪G Ratio']
# Ingore the following fields: Age, Gender, TB, and A/G Ratio
# Future runs will incorporate testing only male or female records to check bias
liverDFScaledMale_X = liverDFScaled[X_Columns].loc[liverDFScaled['Gender'] == 1]
liverDFScaledMale_y = liverDFScaled['Selector'].loc[liverDFScaled['Gender'] ==␣
↪1]

# Split Data
train_X, test_X, train_y, test_y = train_test_split(liverDFScaledMale_X,
      liverDFScaledMale_y, test_size = .2, shuffle = True,
      stratify = liverDFScaledMale_y, random_state = 42)

# Create Graph for Accuracy
fig, (ax1, ax2) = plt.subplots(2, 1)
fig.tight_layout(pad = 3)

# K-Nearest Neighbor
k_range = range(1, 21)
```

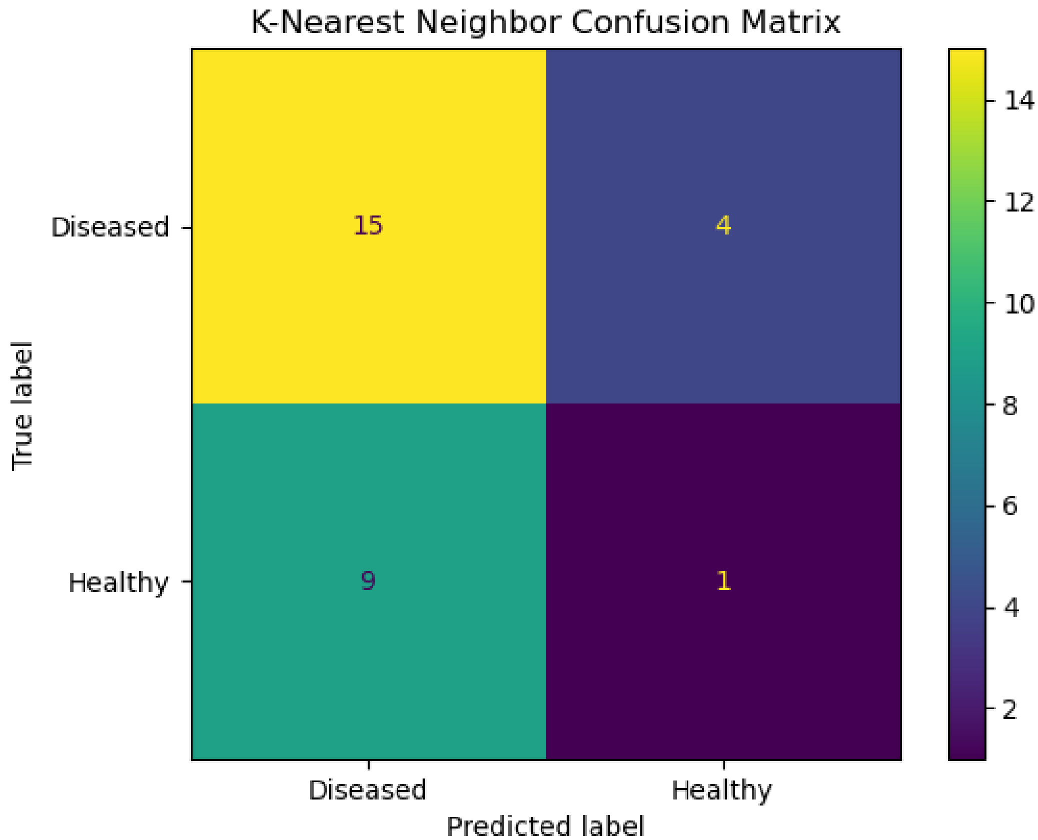
```python
acc = []
maxKnnAcc = 0
bestKnn = 0

for k in k_range:
  knn = KNeighborsClassifier(n_neighbors = k)
  knn.fit(train_X, train_y)
  yhat = knn.predict(test_X)
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related nearest neighbor value
  if accuracy > maxKnnAcc :
    maxKnnAcc = accuracy
    bestKnn = k
  acc.append(accuracy)

# Put KNN Accuracy in Axes
ax1.plot(k_range, acc)
ax1.set(xlabel = 'K Neighbors', ylabel = 'Accuracy')
ax1.set_title('K-Nearest Neighbor Model')

# KNN Confusion Matrix
knn_con = KNeighborsClassifier(n_neighbors = bestKnn)
knn_con.fit(train_X, train_y)
yhat = knn_con.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_knn_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
 ↪'Healthy'])
conf_knn_disp.plot()
conf_knn_disp.ax_.set_title('K-Nearest Neighbor Confusion Matrix')

# Print Primary Scores of Consideration
print('KNN Model Results, K=',bestKnn)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Logistic Regression
c_range = [.0001, .001, .01, .1, 1, 5, 10, 20, 50, 100]
acc = []
maxLogAcc = 0
bestC = 0

for c in c_range:
  lg = LogisticRegression(C = c)
  lg.fit(train_X, train_y)
  yhat = lg.predict(test_X)
```

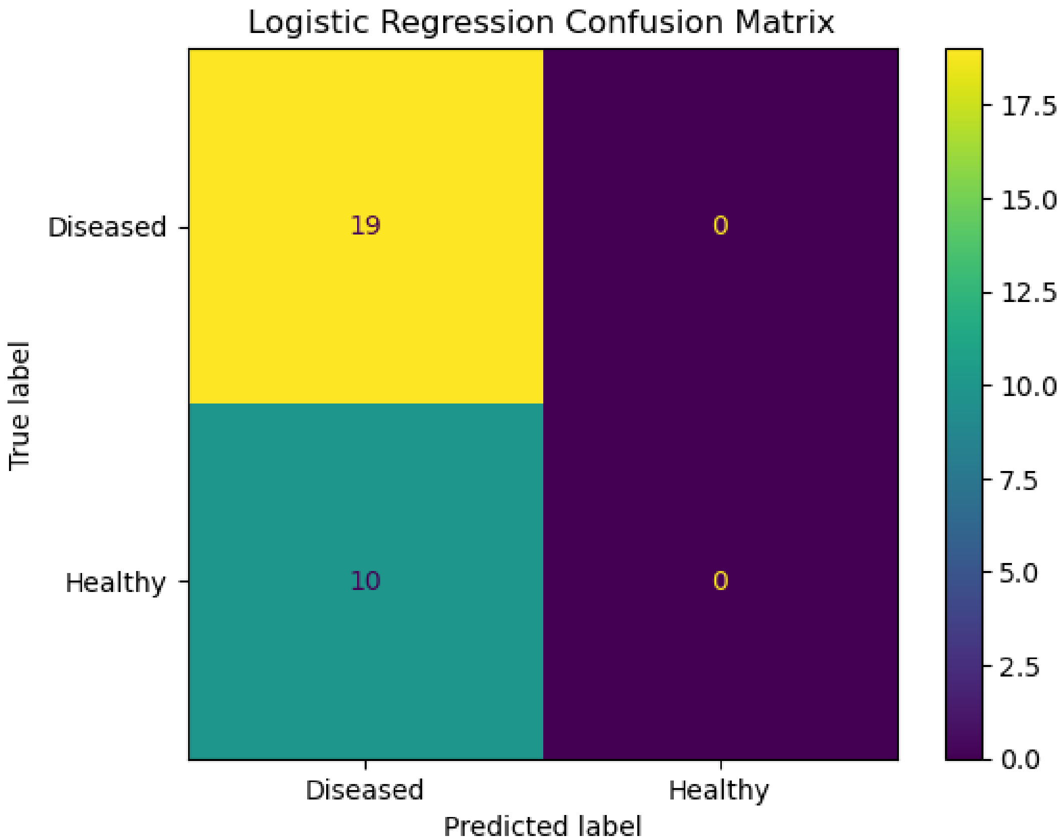
```python
  accuracy = accuracy_score(test_y, yhat)
  # Retain the best found accuracy and related C value
  if accuracy > maxLogAcc :
    maxLogAcc = accuracy
    bestC = c
  acc.append(accuracy)

# Put LG Accuracy in Axes
ax2.plot(c_range, acc)
ax2.set(xlabel = 'Regularization Strength', ylabel = 'Accuracy')
ax2.set_title('Logistic Regression Model')

# Log. Regression Confusion Matrix
lg = LogisticRegression(C = bestC)
lg.fit(train_X, train_y)
yhat = lg.predict(test_X)
conf_mat = confusion_matrix(test_y, yhat)
conf_lg_disp = ConfusionMatrixDisplay(conf_mat, display_labels = ['Diseased',␣
 ↪'Healthy'])
conf_lg_disp.plot()
conf_lg_disp.ax_.set_title('Logistic Regression Confusion Matrix')

# Print Primary Scores of Consideration
print('Logistic Regression Model Results, C=', bestC)
print(f"Accuracy = {accuracy_score(test_y, yhat)}")
print(f"Recall = {recall_score(test_y, yhat)}")
print(f"Precision = {precision_score(test_y, yhat)}")
print('')

# Plot Model Results
plt.show()
```

```
KNN Model Results, K= 4
Accuracy = 0.5517241379310345
Recall = 0.1
Precision = 0.2

Logistic Regression Model Results, C= 0.0001
Accuracy = 0.6551724137931034
Recall = 0.0
Precision = 0.0


/home/campus05/psweiss/.conda/envs/cs5831/lib/python3.10/site-
packages/sklearn/metrics/_classification.py:1469: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 due to no predicted samples. Use
`zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```



K-Nearest Neighbor Model
Accuracy
0.550
0.525
0.500
0.475
0.450
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
K Neighbors
Logistic Regression Model
Accuracy
0.65
0.64
0.63
0.62
0
20
40
60
80
100
Regularization Strength


K-Nearest Neighbor Confusion Matrix
True label
Diseased
Healthy
15
4
9
1
Diseased
Healthy
Predicted label
14
12
10
8
6
4
2


Logistic Regression Confusion Matrix
True label
Predicted label
Diseased
Healthy
Diseased
Healthy
19
0
10
0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0

```
[ ]:
```