```
In [1]: # Jessica Gallo, Kevin Fremgan & Omar Guzman
        # Created: 9/18/2020
        # Last modified: 9/28/2020
        # Neural Networks & Deep Learning
        # HW#1 Descriptive Statistics, Classification and Analysis Using
        # Python & Python Libraries
        # Part 2
```

```
In [2]: # ----------------
        # Setting up GPU |
        # ---------------

        # anaconda prompt: activate tensorflow

        from tensorflow.python.client import device_lib

        # Checks to see available devices (CPU and GPU)
        def get_available_devices():
            local_device_protos = device_lib.list_local_devices()
            return [x.name for x in local_device_protos]

        print(get_available_devices())
```

```
        ['/device:CPU:0', '/device:GPU:0']
```

```
In [3]: from __future__ import absolute_import, division, print_function, unicode_literals
        import tensorflow as tf

        # Configures GPU Usage
        print("Num GPUs Available: ",
              len(tf.config.experimental.list_physical_devices('GPU')))
```

```
        Num GPUs Available:  1
```

```
In [4]: # Imports
        # Data Preprocessing
        from pandas import concat
        import numpy as np
        from sklearn.impute import SimpleImputer
        from sklearn.preprocessing import OneHotEncoder, LabelEncoder
        from sklearn import preprocessing
        # listing 6
        from pandas import read_csv
        from pandas import set_option  # Pairwise Pearson Corr
        from matplotlib import pyplot  # Histograms/Density/Box & Whisker/Correlation Matrix
        import numpy  # Correlation Matrix
        # listing 7
        from numpy import set_printoptions  # Rescaling/Standardize/Normalize/Binarize
        from sklearn.preprocessing import MinMaxScaler, Binarizer  # Rescaling
        from sklearn.preprocessing import StandardScaler  # Standardize
        from sklearn.preprocessing import Normalizer  # Normalize
        import pandas as pd
```

In [5]:
```
# ----------------------
# Wine Quality DATASET |
# ---------------------

filename = "./Downloads/winequalityN.csv"  # csv/text file
# names = ['type', 'fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar', 'c
#           'total sulfur dioxide', 'density', 'pH', 'sulphates', 'alcohol', 'quality']  # c
# data = read_csv(filename, names=names)  # reads the info on csv/txt file
dataSetCsv = pd.read_csv(filename, ',', error_bad_lines=False) #, names=names)
dataset = pd.DataFrame(dataSetCsv)

print('Original Dataset:\n'
     '-----------------')
dataset.head(10)
```

```
Original Dataset:
-----------------
```

Out[5]:

	type	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	qualit
0	white	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	(
1	white	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	(
2	white	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	(
3	white	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	(
4	white	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	(
5	white	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	(
6	white	6.2	0.32	0.16	7.0	0.045	30.0	136.0	0.9949	3.18	0.47	9.6	(
7	white	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	(
8	white	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	(
9	white	8.1	0.22	0.43	1.5	0.044	28.0	129.0	0.9938	3.22	0.45	11.0	(

In [6]:
```
# ===========================================================================
# Data Preprocessing
# ===========================================================================
```

In [7]:
```
types = dataset.select_dtypes(include=[object])
# takes out object type columns

print('Type Column:\n'
     '------------')
print(types.head(3), '\n')
print(types.tail(3))
```

```
Type Column:
------------
    type
0  white
1  white
2  white

     type
6494  red
6495  red
6496  red
```

In [8]:
```
print(types.shape)
# displays types column shape
print(types.columns)
# shows types column is still an object datatype
```

```
(6497, 1)
Index(['type'], dtype='object')
```

In [9]:
```
le = preprocessing.LabelEncoder()
types_num = types.apply(le.fit_transform)
# use label encorder to change white -> 1 and red-> 0

print(types_num.head(3),'\n') # shows the first 3 rows that have type=white
print(types_num.tail(3)) # shows the last 3 rows that have type=red
```

```
   type
0     1
1     1
2     1

      type
6494     0
6495     0
6496     0
```

In [10]:
```python
df = concat([types_num, dataset], axis=1)
# shows concatonated datasets with both label encoded type column and object type column

print('Concatinated Dataset with both type columns:\n'
     '--------------------------------------------')
df.head(3)
```

```
Concatinated Dataset with both type columns:
--------------------------------------------
```

Out[10]:

	type	type	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
0	1	white	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8
1	1	white	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5
2	1	white	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1

In [11]:
```python
df.columns = ['type', 'char_type', 'fixed acidity', 'volatile acidity',
              'citric acid', 'residual sugar', 'chlorides',
              'free sulfur dioxide', 'total sulfur dioxide', 'density',
              'pH', 'sulphates', 'alcohol', 'quality']
# changed name of object type column

print('Dataset with new column name:\n'
     '-----------------------------')
df.head(3)
```

```
Dataset with new column name:
-----------------------------
```

Out[11]:

	type	char_type	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alco
0	1	white	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	
1	1	white	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	
2	1	white	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	1

In [12]:
```
df.drop(['char_type'], axis=1, inplace=True)
# drops the char_type or object type column
# all columns are numeric now
# inplace=True permanantely takes out the column

print('All numeric dataset:\n'
     '--------------------')
df.head(3)
```

```
All numeric dataset:
--------------------
```

Out[12]:

	type	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	qu
0	1	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	
1	1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	
2	1	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	

In [13]:
```
df.isnull().sum().sum()
# shows there are missing values labeled NaN
```

Out[13]:
```
38
```

In [14]:
```
df.fillna(0, inplace=True)
# replaces Nan values with 0
df.isnull().sum().sum()
# no more Nan values
```

Out[14]:
```
0
```

In [15]:
```
df.shape
```

Out[15]:
```
(6497, 13)
```

In [16]:
```
# ============================================================================
# Listing 6
# ============================================================================
```

In [17]:
```
# ------------------------------
# Pairwise Pearson Correlation |
# -----------------------------

set_option('display.width', 100)  # width of the display in characters
set_option('precision', 3)  # sets number of digits
correlations = df.corr(method='pearson')  # corr() function to calculate correlation matri
print("Pairwise Pearson Correlction of Wine Quality Dataset:")
print(correlations)
```

```
Pairwise Pearson Correlction of Wine Quality Dataset:
                       type  fixed acidity  volatile acidity  citric acid  residual sugar  
\
type                  1.000         -0.477            -0.652        0.187           0.349
fixed acidity        -0.477          1.000             0.213        0.321          -0.111
volatile acidity     -0.652          0.213             1.000       -0.378          -0.195
citric acid           0.187          0.321            -0.378        1.000           0.142
residual sugar        0.349         -0.111            -0.195        0.142           1.000
chlorides            -0.513          0.293             0.376        0.039          -0.129
free sulfur dioxide   0.472         -0.275            -0.352        0.133           0.403
total sulfur dioxide  0.700         -0.322            -0.415        0.195           0.495
density              -0.391          0.449             0.271        0.096           0.552
pH                   -0.265         -0.169             0.211       -0.266          -0.212
sulphates            -0.483          0.294             0.222        0.059          -0.184
alcohol               0.033         -0.093            -0.037       -0.010          -0.359
quality               0.119         -0.074            -0.266        0.086          -0.037

                      chlorides  free sulfur dioxide  total sulfur dioxide  density     p
H  \
type                     -0.513                0.472                 0.700   -0.391 -0.26
5
fixed acidity             0.293               -0.275                -0.322    0.449 -0.16
9
volatile acidity          0.376               -0.352                -0.415    0.271  0.21
1
citric acid               0.039                0.133                 0.195    0.096 -0.26
6
residual sugar           -0.129                0.403                 0.495    0.552 -0.21
2
chlorides                 1.000               -0.195                -0.280    0.363  0.03
7
free sulfur dioxide      -0.195                1.000                 0.721    0.026 -0.11
5
total sulfur dioxide     -0.280                0.721                 1.000    0.032 -0.18
7
density                   0.363                0.026                 0.032    1.000  0.01
1
pH                        0.037               -0.115                -0.187    0.011  1.00
0
sulphates                 0.393               -0.188                -0.273    0.258  0.14
8
alcohol                  -0.257               -0.180                -0.266   -0.687  0.10
0
quality                  -0.200                0.055                -0.041   -0.306  0.01
4

                      sulphates  alcohol  quality
type                     -0.483    0.033    0.119
fixed acidity             0.294   -0.093   -0.074
```

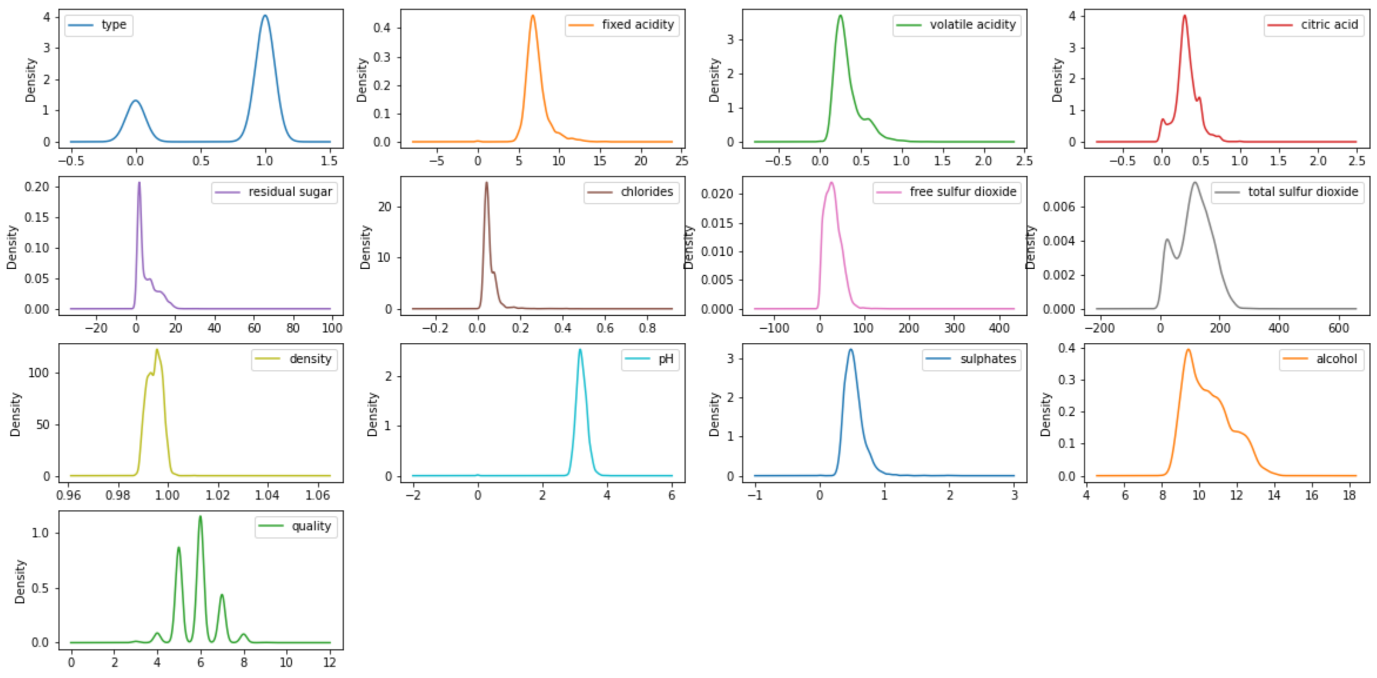
```
volatile acidity          0.222   -0.037   -0.266
citric acid               0.059   -0.010    0.086
residual sugar           -0.184   -0.359   -0.037
chlorides                 0.393   -0.257   -0.200
free sulfur dioxide      -0.188   -0.180    0.055
total sulfur dioxide     -0.273   -0.266   -0.041
density                   0.258   -0.687   -0.306
pH                        0.148    0.100    0.014
sulphates                 1.000   -0.003    0.040
alcohol                  -0.003    1.000    0.444
quality                   0.040    0.444    1.000
```

In [18]:
```python
# -------------------------
# Skew for each Attribute |
# ------------------------

skew = df.skew()  # calculates skew of dataset
print("\nSkewness for Each Attribute of Wine Quality Dataset:")
print(skew)
```

```
Skewness for Each Attribute of Wine Quality Dataset:
type                   -1.179
fixed acidity           1.385
volatile acidity        1.482
citric acid             0.470
residual sugar          1.435
chlorides               5.395
free sulfur dioxide     1.220
total sulfur dioxide   -0.001
density                 0.504
pH                     -5.480
sulphates               1.757
alcohol                 0.566
quality                 0.190
dtype: float64
```

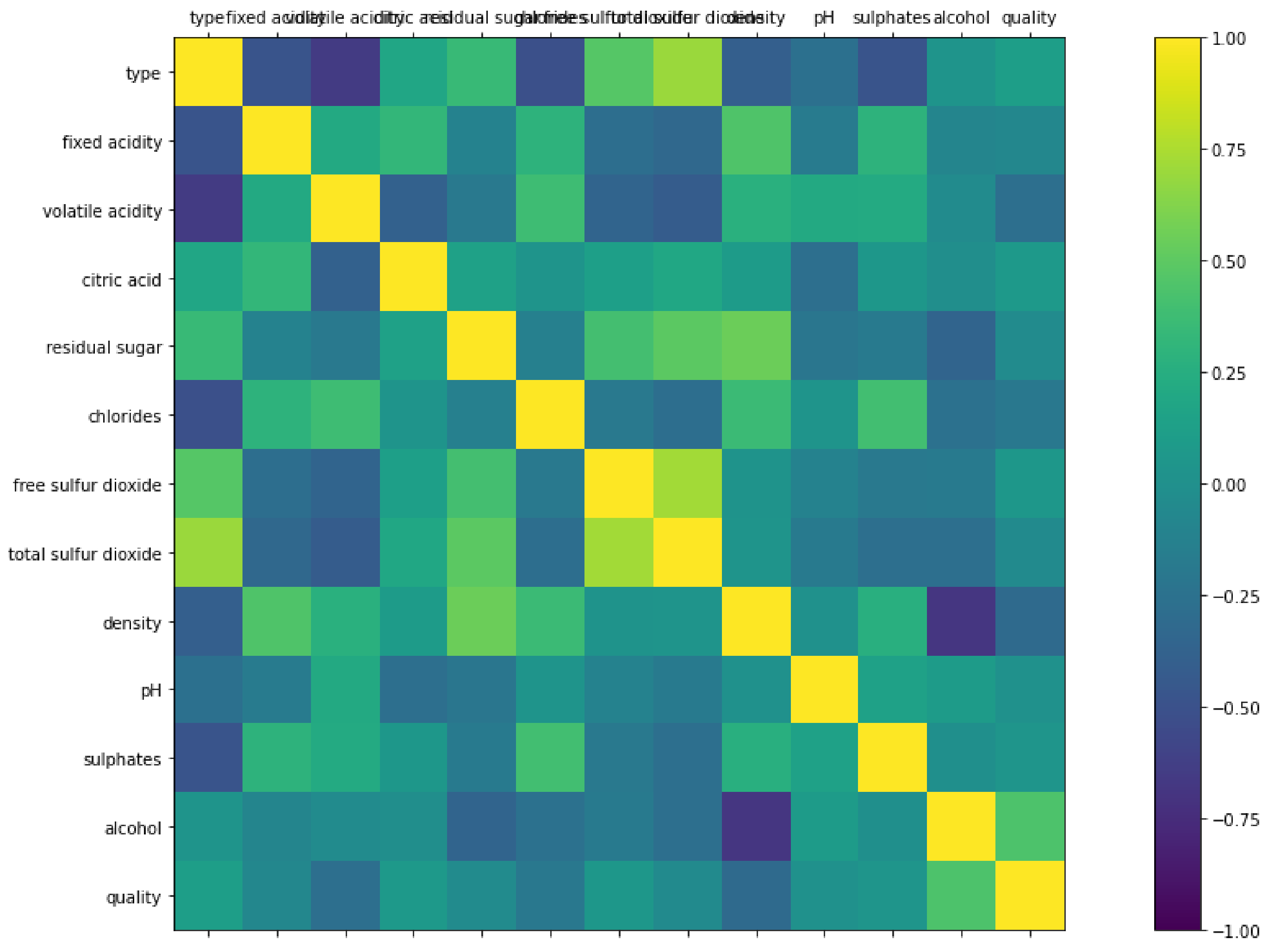
In [19]:
```
# ------------------------
# Univariate Denisty Plot |
# -----------------------

df.plot(kind='density', subplots=True, layout=(4,4), sharex=False, figsize=(20, 10))
# subplots True: make separate subplot for each column
# sharex False: an ax is passed in
print("\nUnivariable Density Plot of Wine Quality Dataset:")
pyplot.show()  # displays the plot
```

```
Univariable Density Plot of Wine Quality Dataset:
```



```
In [20]: # -------------------------
         # Correlation Matrix Plot |
         # -------------------------

         names = ['type', 'fixed acidity', 'volatile acidity',
                  'citric acid', 'residual sugar', 'chlorides',
                  'free sulfur dioxide', 'total sulfur dioxide', 'density',
                  'pH', 'sulphates', 'alcohol', 'quality']

         fig = pyplot.figure(figsize=(20, 10))
         ax = fig.add_subplot(111)  # subplot grid parameters 1x1 grid, 1st subplot
         cax = ax.matshow(correlations, vmin=-1, vmax=1)
         fig.colorbar(cax)  # creates colorbar on axes
         ticks = numpy.arange(0,13,1)  # returns evenly spaced values within a given interval
         ax.set_xticks(ticks)
         ax.set_yticks(ticks)
         ax.set_xticklabels(names)
         ax.set_yticklabels(names)
         print("\nCorrelation Matrix Plot for Wine Quality Dataset:")
         pyplot.show()  # displays plot
```

```
Correlation Matrix Plot for Wine Quality Dataset:
```



```
In [ ]: '''
Listing 6 Analysis:

The Pairwise Pearson Correlation which is a plot showing the strength of
relationship or correlation between the columns, the closer to 1.00 the number
is, the closer the relationship is. A column or variable being 1.00 means it have
a very strong relationship. -1.00 shows that it has less of a relationship. For
example, volatile acidity is -0.652 on type so it shows that volatile acidity has
very little relation to type. Also, total sulfur dioxide is 0.700 on type, which
means it which means that total sulfur dioxide has a close relationship to type.

For skewness of attributes, which is a measure of asymmetry of a distribution,
it shows that type and pH are highly skewed since skewness is greater than -1;
fixed acidity, volatile acidity, residual sugar, chlorides, free sulfur dioxide,
citric acid and sulphates are also highly skewed because skewness is greater
than +1; total sulfur dioxide and quality are approximately symmetric in
distribution since skewness is between -1/2 and +1/2; and density and alcohol are
moderately skewed since skewness is between +1/2 and +1.

For the univariate density plot, which is the distribution of a variable in a
dataset plotted on a continuous interval, it shows that there is more white wine
than red wine, fixed acidity is greatest at about 6 and ends at 10, volatile
acidity is greatest around 0.3 and drops and ends at 1.0, citric acid is greatest
at 0.3 but starts increasing at around 0.0 and drops at 0.8, residual sugar is
greatest at 0 and ends at 20, chlorides is greatest at 0.0 and drops and ends at
0.1, free sulfur dioxide is greatest at 0 and drops at about 80, total sulfur
dioxide starts at 0 and is greatest at about 150 and drops at around 230, density
starts at 0.99 and is greatest at 0.999 and drops at 1.00, pH is greatest at 3,
sulphates is greatest at 0.5, alcohol is greatest at 9.5 and drop and ends at 14
with a little fluctuation, quality fluctuates a lot from 4 to 8 and is greatest
at 6.

For the correlation matrix plot, which is a plot showing the strength of relationship
or correlation between the columns, the closer to yellow (or 1.00) the color is, the
closer the relationship is. The diagonal yellow boxes are represent each column being
obviously fully related to each other. The darker or bluer (-1.00) the color, the less
it has in relationship. For example, volatile acidity is dark blue on type so it shows
that volatile acidity has no relation to type. Also, total sulfur dioxide is a very
light green on type, which means it is closer to yellow or 1.00, which means that total
sulfur dioxide has a close relationship to type.
'''
```

```
In [ ]:
# ===========================================================================
# Listing 7
# ===========================================================================
```

```
In [21]:
# Listing 7 data
array = df.values
# separate array into input and output components
X = array[:,0:-1]
Y = array[:,12]
```

```
In [22]:
# ----------------
# Rescaling Data |
# ---------------

min_max = MinMaxScaler(feature_range=(0,1))  # desired range of transformed data
rescaledX = min_max.fit_transform(X)  # fit to data, then transform it
set_printoptions(precision=3)  # sets number of digits
print("\nRescaling Data between 0 and 1 from Wine Quality Dataset:\n")
print(rescaledX)
```

```

Rescaling Data between 0 and 1 from Wine Quality Dataset:

[[1.    0.44  0.171 ... 0.748 0.225 0.116]
 [1.    0.396 0.19  ... 0.823 0.245 0.217]
 [1.    0.509 0.177 ... 0.813 0.22  0.304]
 ...
 [0.    0.396 0.323 ... 0.853 0.375 0.435]
 [0.    0.371 0.408 ... 0.89  0.355 0.319]
 [0.    0.377 0.196 ... 0.845 0.33  0.435]]
```

```
In [23]:
# ------------------
# Standardize Data |
# ------------------

standardize = StandardScaler().fit(X)  # standardize features by removing the mean and scal
rescaledX = standardize.transform(X)
set_printoptions(precision=3)  # sets number of digits
print("\nStandardize Data from Wine Quality Dataset:\n")
print(rescaledX)
```

```

Standardize Data from Wine Quality Dataset:

[[ 0.571 -0.155 -0.42  ... -1.068 -0.542 -1.419]
 [ 0.571 -0.683 -0.238 ...  0.43  -0.274 -0.832]
 [ 0.571  0.675 -0.359 ...  0.23  -0.609 -0.329]
 ...
 [-1.75  -0.683  1.035 ...  1.029  1.467  0.426]
 [-1.75  -0.984  1.853 ...  1.777  1.199 -0.245]
 [-1.75  -0.909 -0.177 ...  0.879  0.865  0.426]]
```

In [24]:
```
# ----------------
# Normalize Data |
# ---------------

normalize = Normalizer().fit(X)  # normalize samples individually to unit norm
normalizedX = normalize.transform(X)
set_printoptions(precision=3)  # sets number of digits
print("\nNormalized Data from Wine Quality Dataset:\n")
print(normalizedX)
```

```

Normalized Data from Wine Quality Dataset:

[[0.006 0.039 0.002 ... 0.017 0.003 0.05 ]
 [0.008 0.047 0.002 ... 0.025 0.004 0.071]
 [0.01  0.079 0.003 ... 0.032 0.004 0.098]
 ...
 [0.    0.123 0.01  ... 0.067 0.015 0.215]
 [0.    0.106 0.012 ... 0.064 0.013 0.183]
 [0.    0.126 0.007 ... 0.071 0.014 0.231]]
```

In [25]:
```
# ---------------
# Binarize Data |
# --------------

binarizer = Binarizer(threshold=0.0).fit(X)  # binarize data according to threshold
# threshold: feature values below or equal to this are replaced by 0, above it by 1
# fit is there to implement the usual API
binaryX = binarizer.transform(X)
set_printoptions(precision=3)  # sets number of digits
print("\nBinarized Data from Wine Quality Dataset:")
print(binaryX)
```

```

Binarized Data from Wine Quality Dataset:
[[1. 1. 1. ... 1. 1. 1.]
 [1. 1. 1. ... 1. 1. 1.]
 [1. 1. 1. ... 1. 1. 1.]
 ...
 [0. 1. 1. ... 1. 1. 1.]
 [0. 1. 1. ... 1. 1. 1.]
 [0. 1. 1. ... 1. 1. 1.]]
```

```
In [ ]: '''
Listing 7 Analysis:

The Min-Max Scaler scales or normalizes the input features/variables. The
features are transformed into the range [0,1], or the minimum and maximum
value of a feature if going to be 0 and 1 respectively. Normalization scales
each input variable separately, also in the range of 0-1. Standardization
scales each input variable separately by subtracting the mean and dividing
by the standard deviation to shift the distribution to have a mean of zero
and a standard deviation of one. Binarizing the data converts the data to 0
or 1 depending the threshold. Values below the threshold are converted to 0
and above the threshold are converted to 1.
'''
```

/