2.0-jo-data-exploration

November 23, 2020

1 Exploring and Processing Data

[1]:
```
# imports
import pandas as pd
import numpy as np
import os
```

[2]:
```
# allow plots/visuals to exist inline within this workbook
%matplotlib inline
```

1.1 Import Data

[3]:
```
# set path to raw data
raw_data_path = os.path.join(os.path.pardir, 'data', 'raw')
data_file_path = os.path.join(raw_data_path, 'APPENC05.txt')
```

[4]:
```
# read the default .txt file and print it
f = open(data_file_path, 'r')
print(f.read(500)) # print the first 500 characters
f.close()
```

```
  1     0.651    0.5599    15.959    50    0.0000    0    0.0000    6
  2     0.852    0.3716    27.660    58    0.0000    0    0.0000    7
  3     0.852    0.6005    14.732    74    0.0000    0    0.0000    7
  4     0.852    0.3012    26.576    58    0.0000    0    0.0000    6
  5     1.448    2.1170    30.877    62    0.0000    0    0.0000    6
  6     2.160    0.3499    25.280    50    0.0000    0    0.0000    6
  7     2.160    2.0959    32.137    64    1.8589    0    0.0000    6
```

[5]:
```
# create pandas dataframe with column headers
cols = [
    'Obs', 'PSALevel','CancerVol', 'Weight',
    'Age', 'BenignProstaticHyperplasia', 'SeminalVesicleInvasion',
    'CapsularPenetration', 'GleasonScore'
    ]

df = pd.read_fwf(data_file_path, names=cols, index_col='Obs')
```

1.2 Basic Structure

By instruction of the case study, I will create a new binary response variable Y, called high-grade cancer, by letting Y=1 if Gleason score equals 8, and Y=0 otherwise (i.e., if Gleason score equals 6 or 7). Let the new field be called "Y_HighGradeCancer" within the dataset. - Note: Y_HighGradeCancer and SeminalVesicleInvasion are binary indicator variables.

[6]:
```
df['Y_HighGradeCancer'] = np.where(df['GleasonScore'] == 8, 1, 0)
```

[7]:
```
# use .head() to view the first 5 rows
df.head()
```

[7]:

Obs	PSALevel	CancerVol	Weight	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion	CapsularPenetration	GleasonScore	Y_HighGradeCancer
1	0.651	0.5599	15.959	50	0.0	0	0.0	6	0
2	0.852	0.3716	27.660	58	0.0	0	0.0	7	0
3	0.852	0.6005	14.732	74	0.0	0	0.0	7	0
4	0.852	0.3012	26.576	58	0.0	0	0.0	6	0
5	1.448	2.1170	30.877	62	0.0	0	0.0	6	0

[8]:
```
# use .tail() to view the last 5 rows
df.tail()
```

[8]:

Obs	PSALevel	CancerVol	Weight	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion	CapsularPenetration	GleasonScore	Y_HighGradeCancer
93	80.640	16.9455	48.424	68	0.0000	1	1.0	7	0
94	107.770	45.6042	49.402	44	0.0000	1	1.0	7	0
95	170.716	18.3568	29.964	52	0.0000	1	1.0	7	0
96	239.847	17.8143	43.380	68	4.7588	1	1.0	7	0
97	265.072	32.1367	52.985	68	1.5527	1	1.0	7	0

```
Obs
93                          1               3.7434            8
94                          1               8.7583            8
95                          1              11.7048            8
96                          1               4.7588            8
97                          1              18.1741            8

     Y_HighGradeCancer
Obs
93                   1
94                   1
95                   1
96                   1
97                   1
```

[9]:
```
# use .info() to get basic information about the dataframe
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 97 entries, 1 to 97
Data columns (total 9 columns):
PSALevel                      97 non-null float64
CancerVol                     97 non-null float64
Weight                        97 non-null float64
Age                           97 non-null int64
BenignProstaticHyperplasia    97 non-null float64
SeminalVesicleInvasion        97 non-null int64
CapsularPenetration           97 non-null float64
GleasonScore                  97 non-null int64
Y_HighGradeCancer             97 non-null int32
dtypes: float64(5), int32(1), int64(3)
memory usage: 7.2 KB
```

[10]:
```
# filter rows based on condition
gleason_8 = len(df.loc[df.GleasonScore == 8, :])
gleason_not8 = len(df.loc[df.GleasonScore != 8, :])
print(f'Count of high-grade cancer: {gleason_8}')
print(f'Count of non high-grade cancer: {gleason_not8}')
```

```
Count of high-grade cancer: 21
Count of non high-grade cancer: 76
```

[11]:
```
# Y binary column: proportions
df.Y_HighGradeCancer.value_counts(normalize=True)
```

[11]:
```
0    0.783505
1    0.216495
Name: Y_HighGradeCancer, dtype: float64
```

1.3 Summary Statistics

[12]:
```
# use .describe() to view summary statistics for all numerical columns
df.describe()
```

[12]:

	PSALevel	CancerVol	Weight	Age	\
count	97.000000	97.000000	97.000000	97.000000	
mean	23.730134	6.998682	45.491361	63.865979	
std	40.782925	7.880869	45.705053	7.445117	
min	0.651000	0.259200	10.697000	41.000000	
25%	5.641000	1.665300	29.371000	60.000000	
50%	13.330000	4.263100	37.338000	65.000000	
75%	21.328000	8.414900	48.424000	68.000000	
max	265.072000	45.604200	450.339000	79.000000	

	BenignProstaticHyperplasia	SeminalVesicleInvasion	\
count	97.000000	97.000000	
mean	2.534725	0.216495	
std	3.031176	0.413995	
min	0.000000	0.000000	
25%	0.000000	0.000000	
50%	1.349900	0.000000	
75%	4.758800	0.000000	
max	10.277900	1.000000	

	CapsularPenetration	GleasonScore	Y_HighGradeCancer
count	97.000000	97.000000	97.000000
mean	2.245367	6.876289	0.216495
std	3.783329	0.739619	0.413995
min	0.000000	6.000000	0.000000
25%	0.000000	6.000000	0.000000
50%	0.449300	7.000000	0.000000
75%	3.254400	7.000000	0.000000
max	18.174100	8.000000	1.000000

- PSALevel, CancerVol, Weight and Age appear to have high standard deviation values. This may provoke a standardized dataset, or transformations, further in my analysis.
- Skewness will need to be investigated.

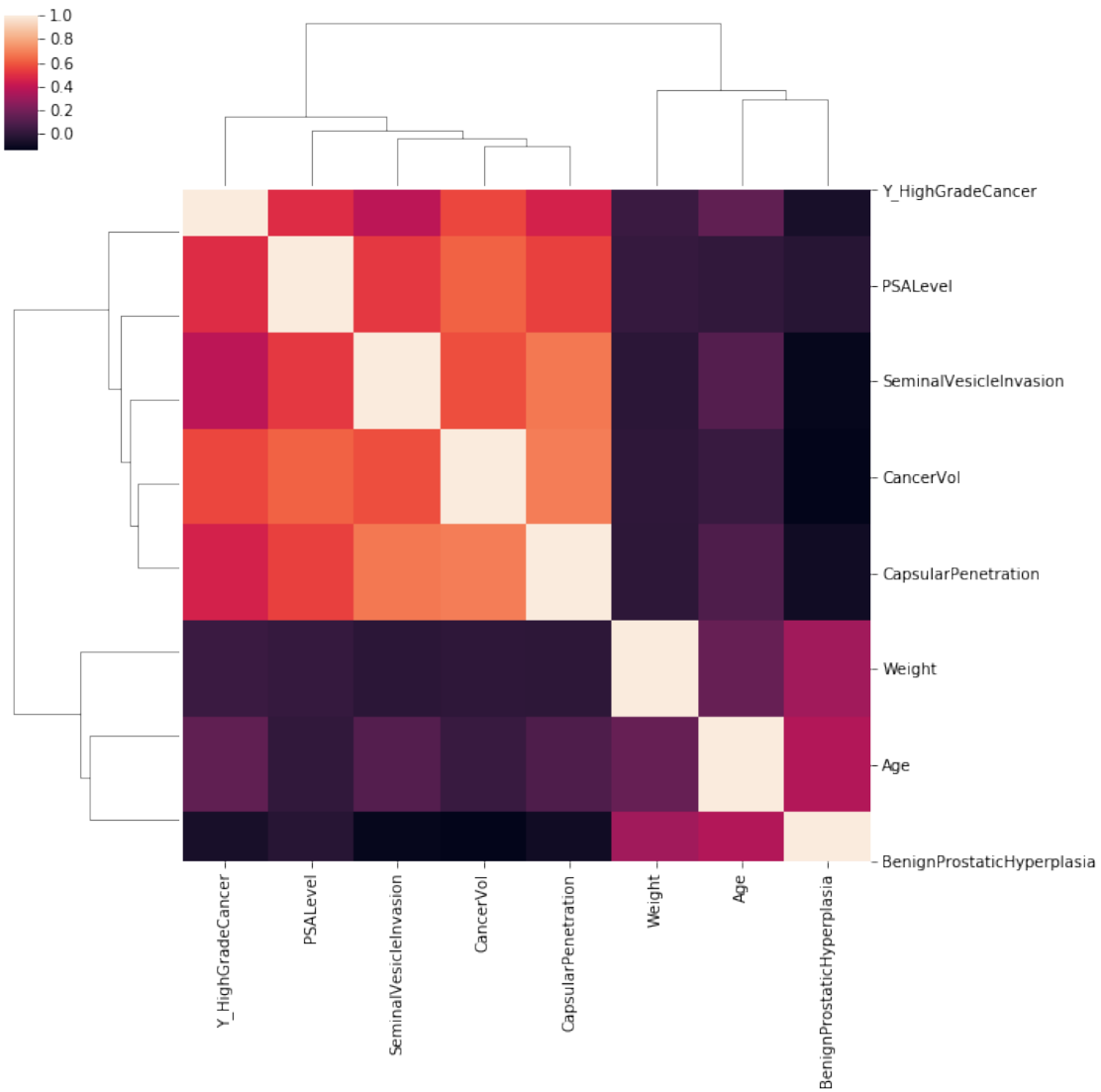
[13]:
```
# correlation matrix
# GleasonScore need not be considered
cols = [col for col in df.columns if col != 'GleasonScore']
df[cols].corr()
```

[13]:

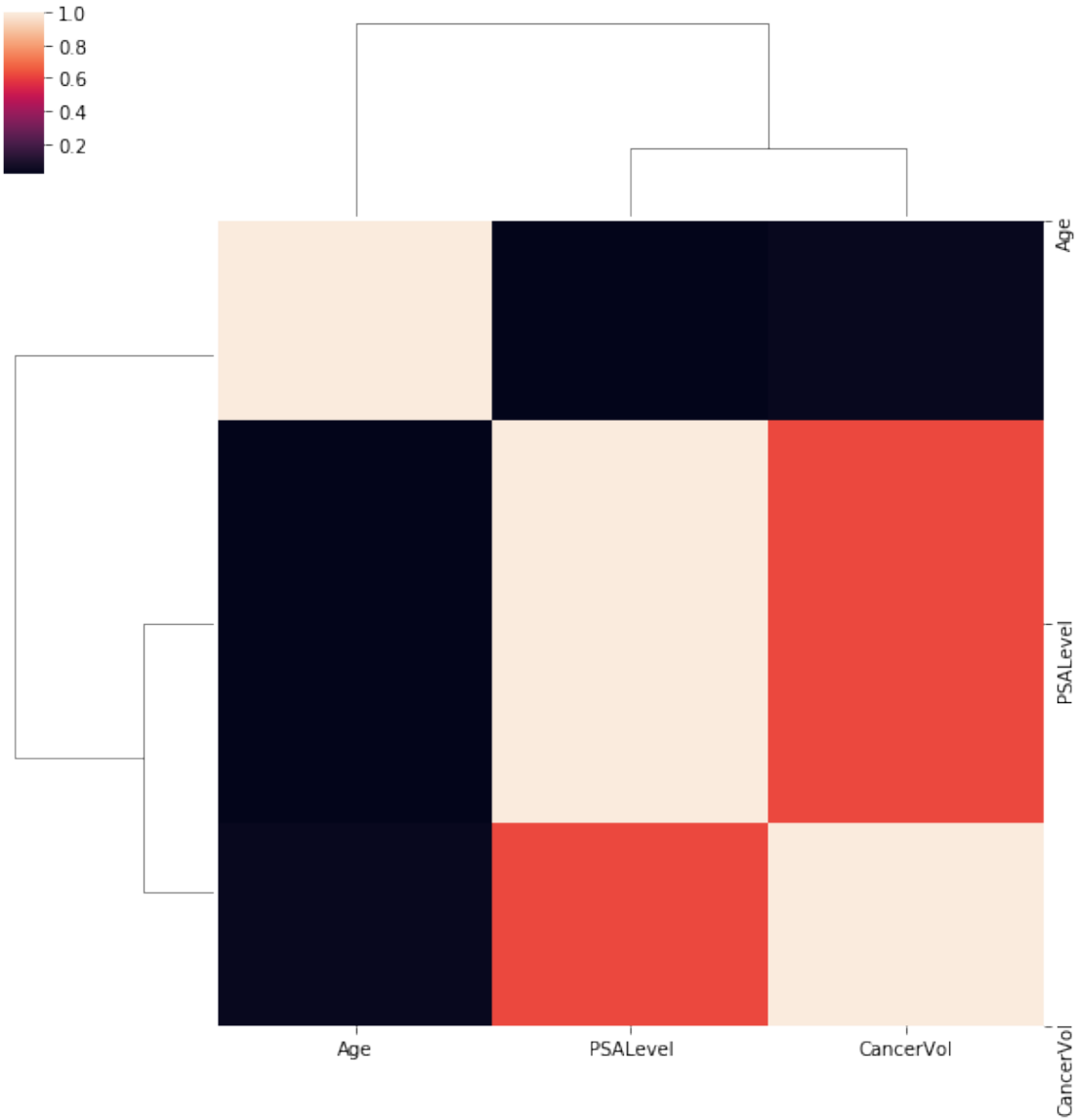
	PSALevel	CancerVol	Weight	Age	\
PSALevel	1.000000	0.624151	0.026213	0.017199	
CancerVol	0.624151	1.000000	0.005107	0.039094	
Weight	0.026213	0.005107	1.000000	0.164324	

```
Age                          0.017199   0.039094  0.164324  1.000000
BenignProstaticHyperplasia -0.016486  -0.133209  0.321849  0.366341
SeminalVesicleInvasion       0.528619   0.581742 -0.002410  0.117658
CapsularPenetration          0.550793   0.692897  0.001579  0.099555
Y_HighGradeCancer            0.497189   0.564645  0.039445  0.148074

                           BenignProstaticHyperplasia  \
PSALevel                                    -0.016486
CancerVol                                   -0.133209
Weight                                       0.321849
Age                                          0.366341
BenignProstaticHyperplasia                   1.000000
SeminalVesicleInvasion                      -0.119553
CapsularPenetration                         -0.083009
Y_HighGradeCancer                           -0.058032

                           SeminalVesicleInvasion  CapsularPenetration  \
PSALevel                                 0.528619             0.550793
CancerVol                                0.581742             0.692897
Weight                                  -0.002410             0.001579
Age                                      0.117658             0.099555
BenignProstaticHyperplasia              -0.119553            -0.083009
SeminalVesicleInvasion                   1.000000             0.680284
CapsularPenetration                      0.680284             1.000000
Y_HighGradeCancer                        0.392231             0.463134

                           Y_HighGradeCancer
PSALevel                            0.497189
CancerVol                           0.564645
Weight                              0.039445
Age                                 0.148074
BenignProstaticHyperplasia         -0.058032
SeminalVesicleInvasion              0.392231
CapsularPenetration                 0.463134
Y_HighGradeCancer                   1.000000
```

[14]:
```
# let's import searborn to help visualize the correlation matrix
import seaborn as sns

sns.clustermap(df[cols].corr());
```



[15]:
```
# view a few terms more closely
sns.clustermap(df[['PSALevel', 'CancerVol', 'Age']].corr());
```



[16]:
```
# correlation of final two predictors
df[['PSALevel', 'CancerVol']].corr()
```

[16]:

	PSALevel	CancerVol
PSALevel	1.000000	0.624151
CancerVol	0.624151	1.000000

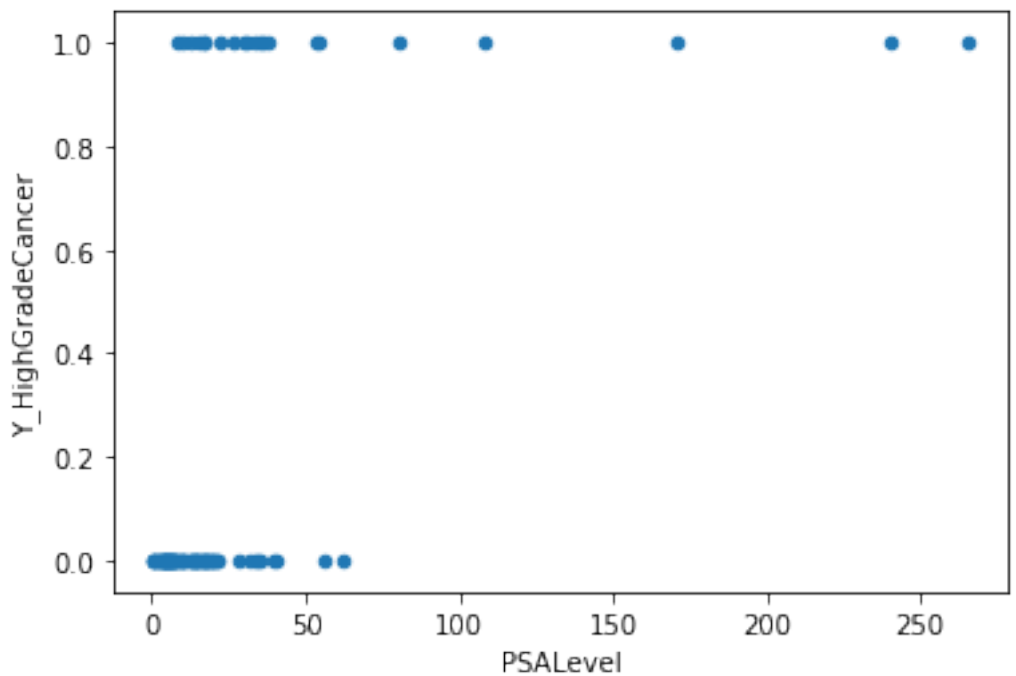
- PSALevel and CancerVol show a mild level of correlation: 0.624151

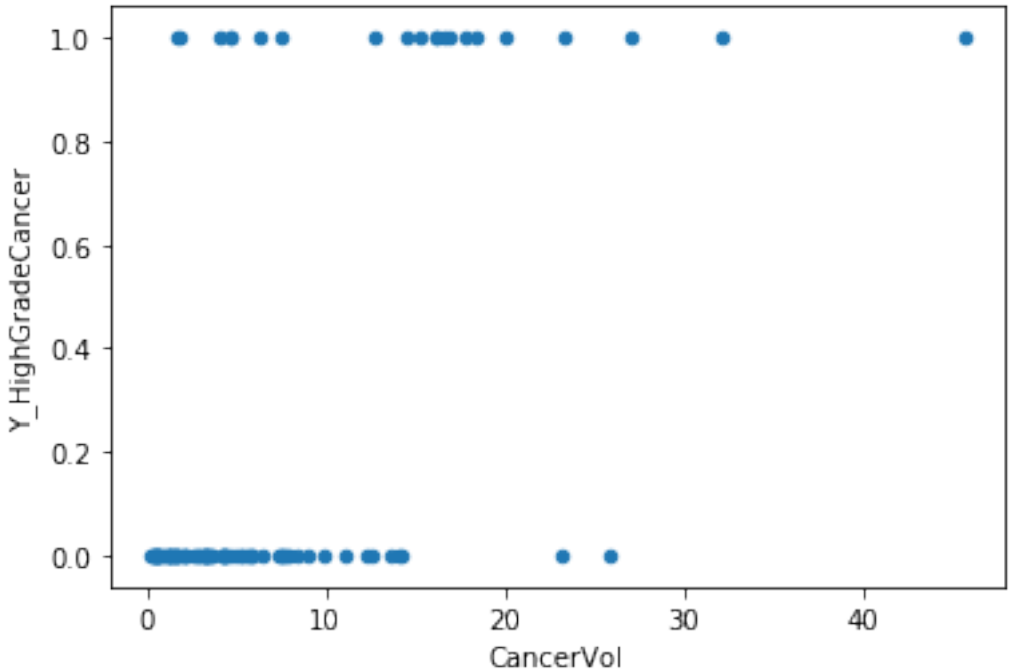
[17]:
```
# numerical features
# centrality measures
print(f'Mean Age: {round(df.Age.mean(), 2)}')
```

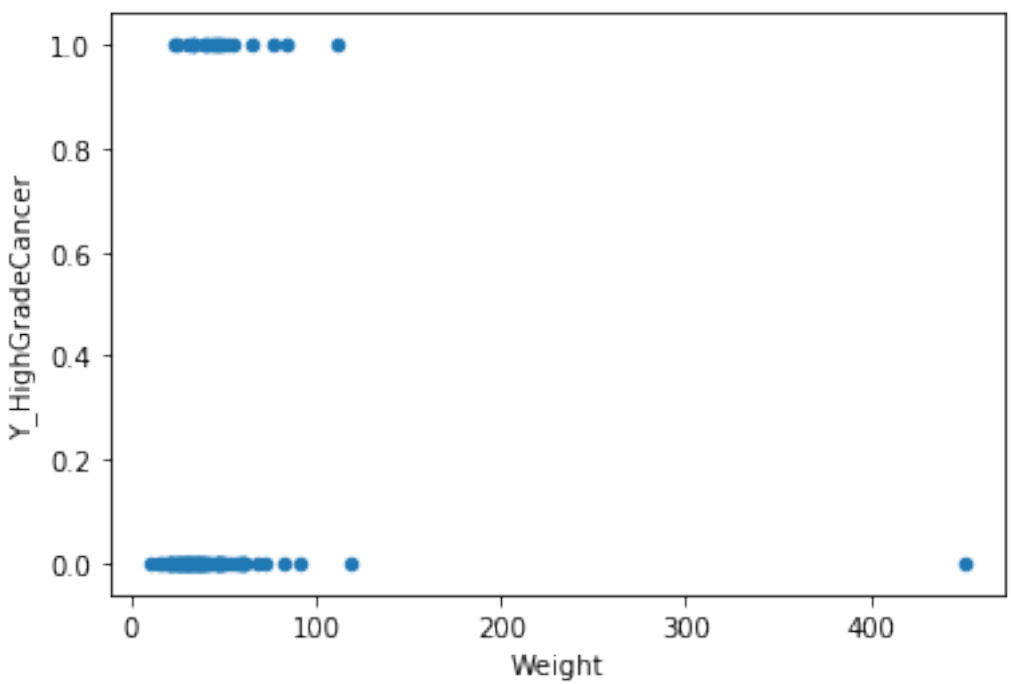
```
print(f'Median Age: {df.Age.median()}')
```

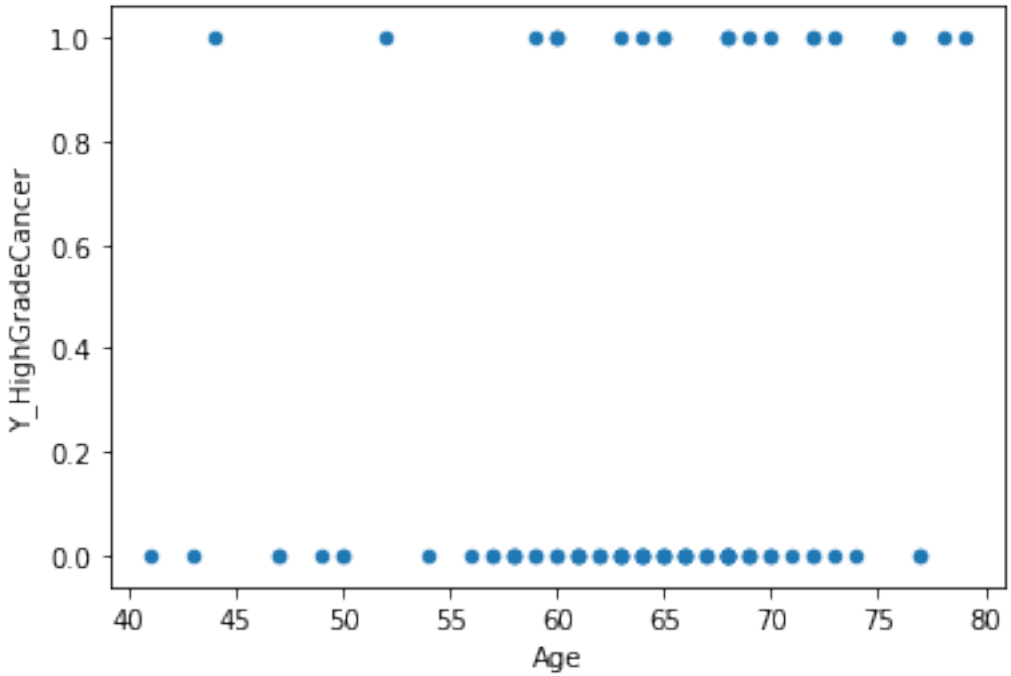
```
Mean Age: 63.87
Median Age: 65.0
```

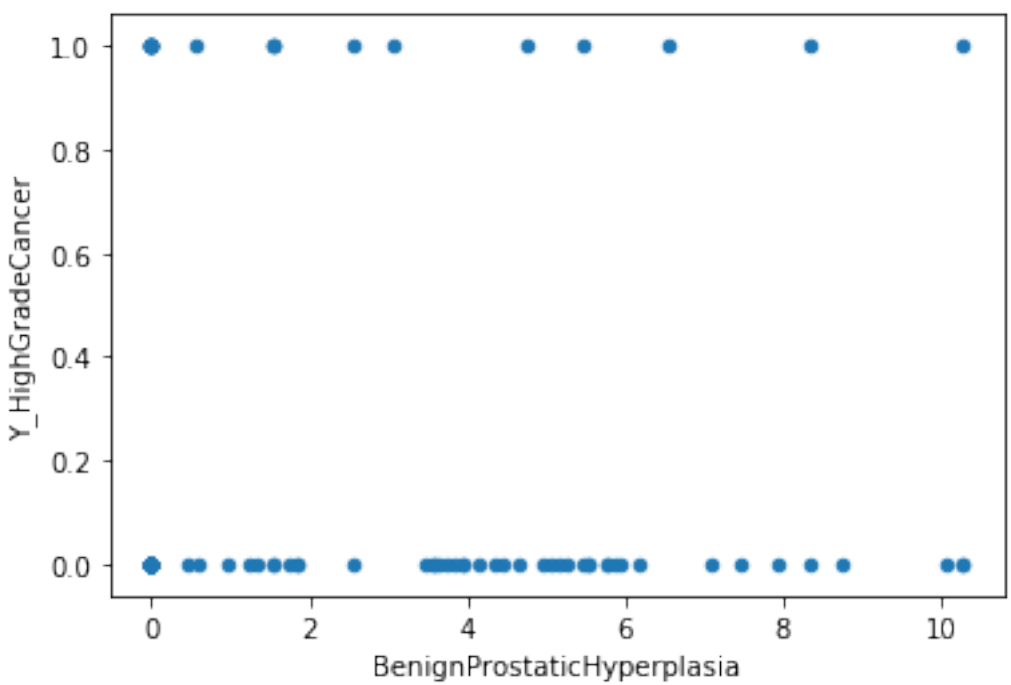
[18]:
```
# print all relevant scatter plots
# examine visuals for outliers
for col in cols:
    df[['Y_HighGradeCancer', col]].plot.scatter(x=col, y='Y_HighGradeCancer');
```

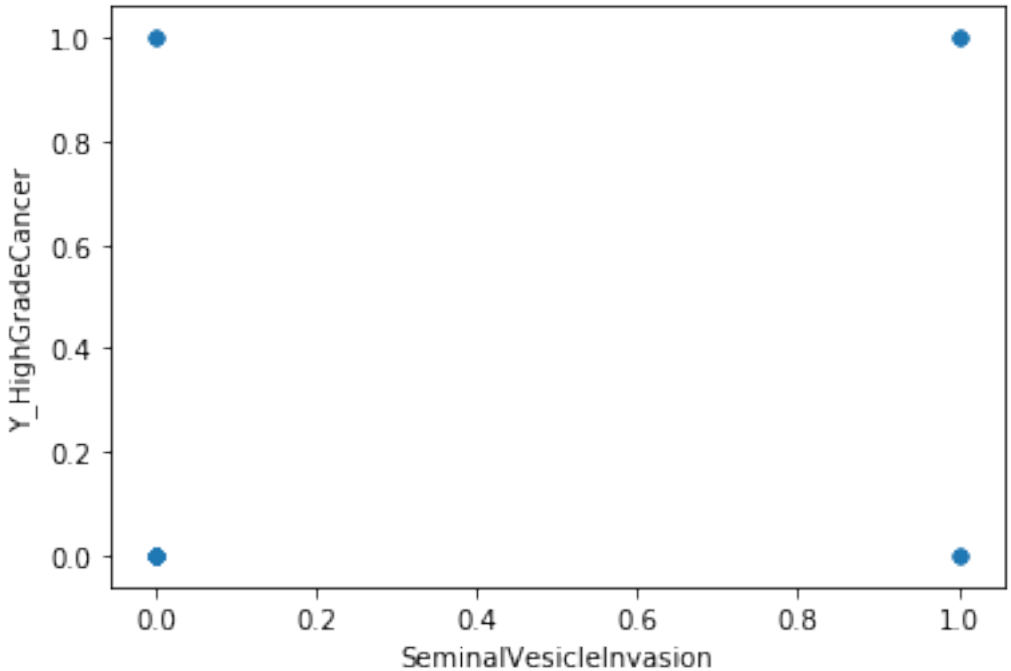


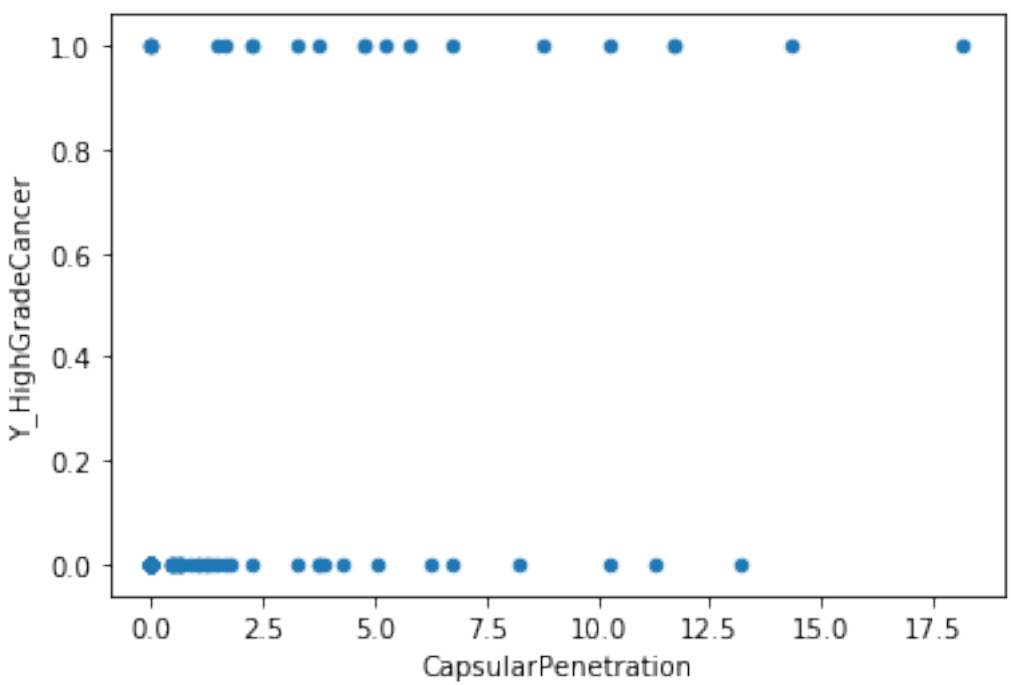

1.0
0.8
0.6
0.4
0.2
0.0
Y_HighGradeCancer
0
10
20
30
40
CancerVol

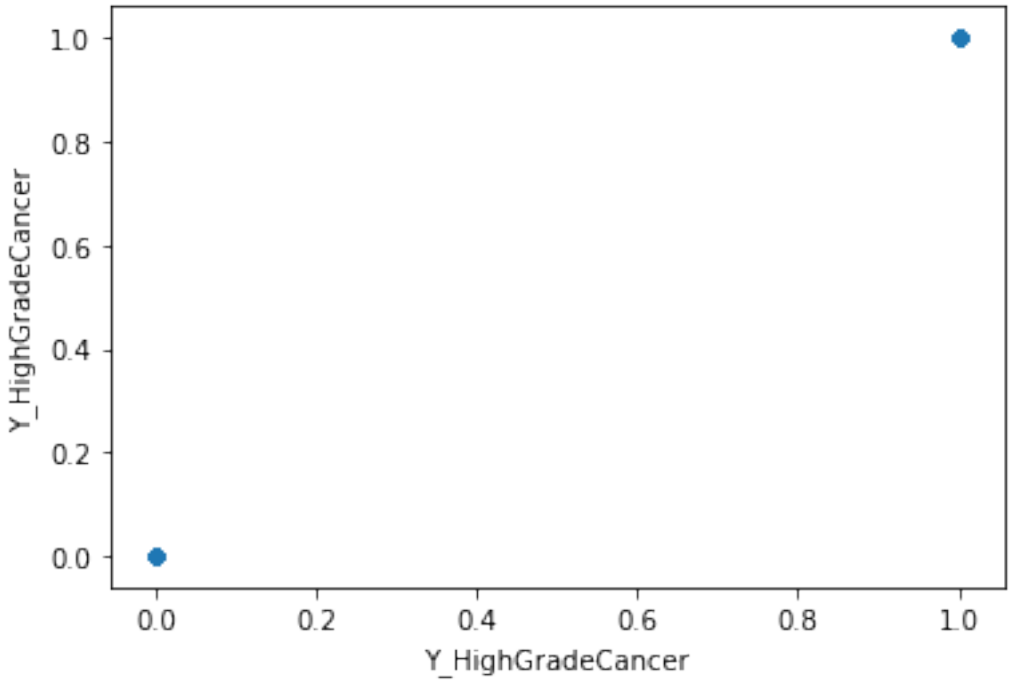

1.0
0.8
0.6
0.4
0.2
0.0
Y_HighGradeCancer
0
100
200
300
400
Weight


Y_HighGradeCancer
1.0
0.8
0.6
0.4
0.2
0.0
40
45
50
55
60
65
70
75
80
Age


Y_HighGradeCancer
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
BenignProstaticHyperplasia


Y_HighGradeCancer
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
SeminalVesicleInvasion


Y_HighGradeCancer
1.0
0.8
0.6
0.4
0.2
0.0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
CapsularPenetration

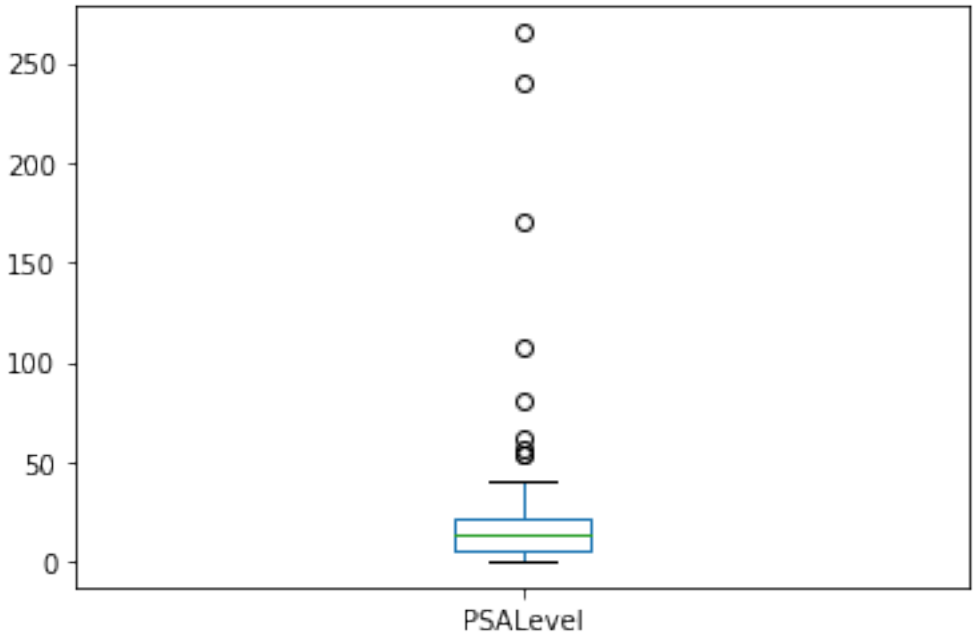


- PSALevel and CancerVol may be good predictors for Y_HighGradeCancer in a Logistic Regression model.
- Weight appears to contain an extreme outlier.
- CancerVol may present two outliers, when Y_HighGradeCancer = 0.
- Via a priori knowledge, Age may be a valuable predictor of Prostate Cancer, so I will retain it in my onging analysis.

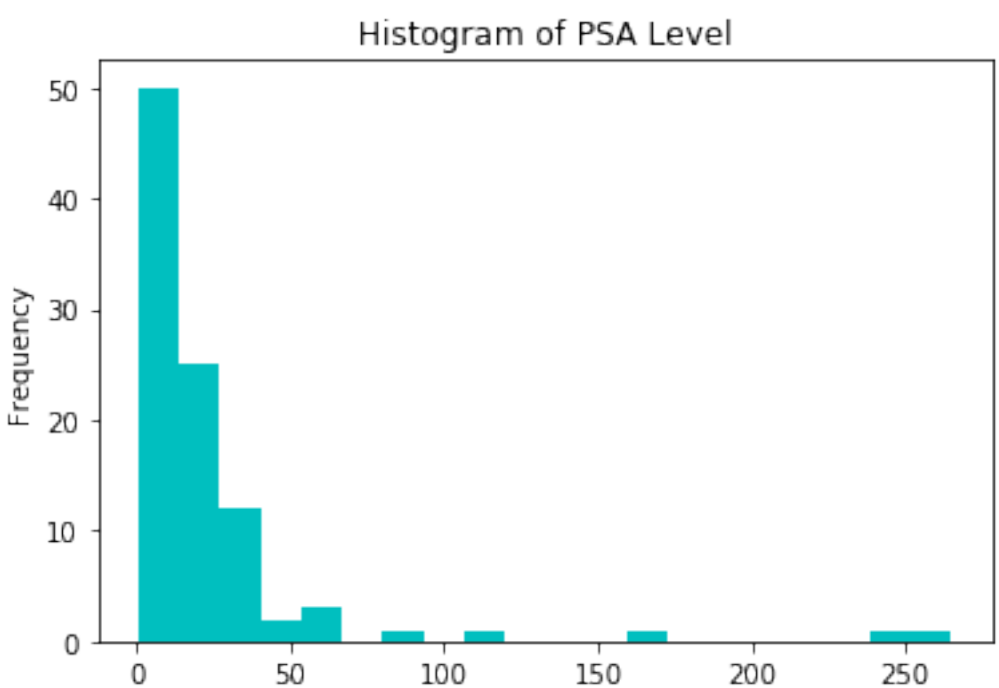
1.4 Distributions

1.4.1 PSALevel

[19]:
```
# box-whisker plot
df.PSALevel.plot(kind='box');
```



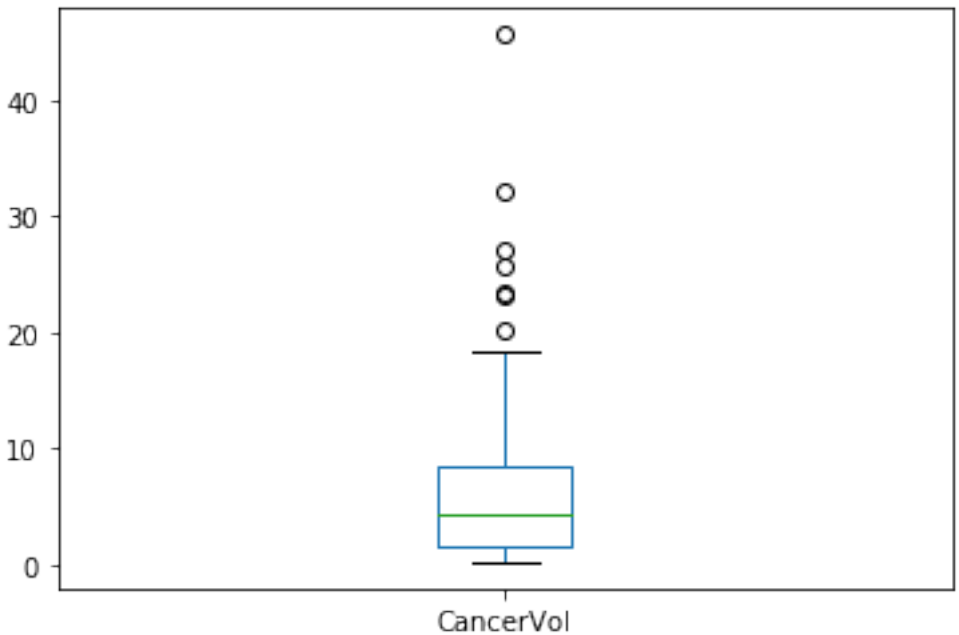
[20]:
```
# use hist to create histogram
df.PSALevel.plot(kind='hist', title='Histogram of PSA Level', color='c',␣
↪bins=20);
```



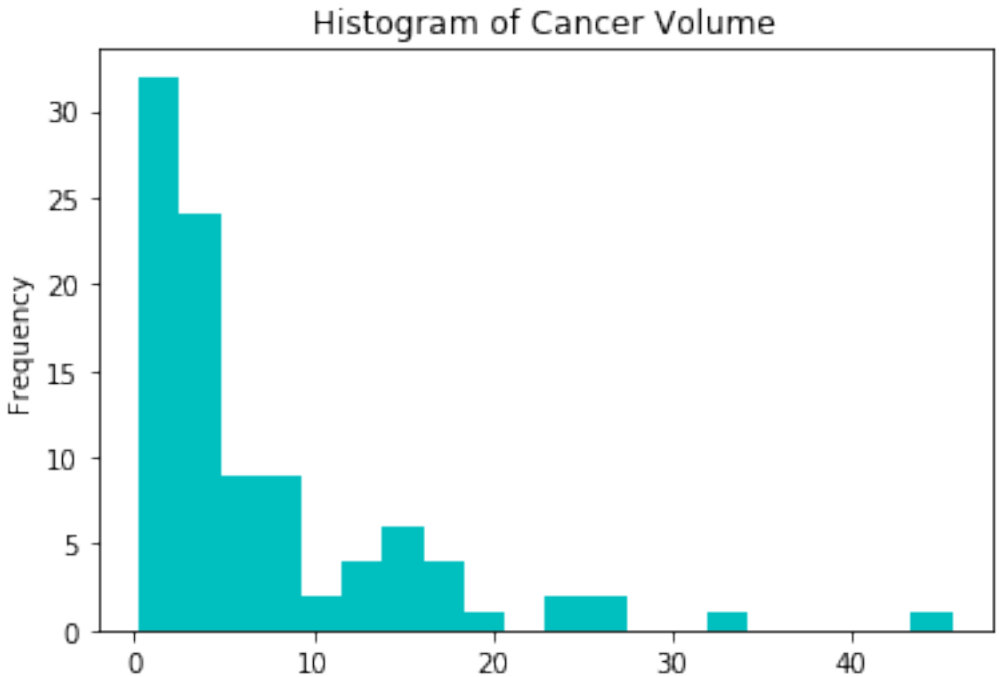
- PSALevel shows high positive skewness.

1.4.2 CancerVol

[21]:
```
df.CancerVol.plot(kind='box');
```



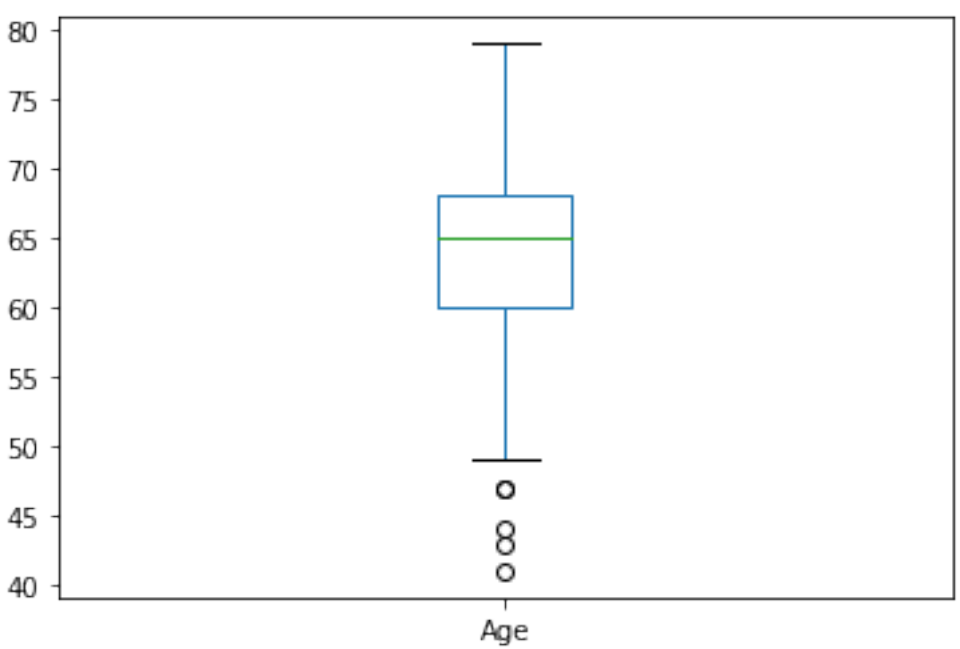
[22]:
```
df.CancerVol.plot(kind='hist', title='Histogram of Cancer Volume', color='c',␣
↪bins=20);
```



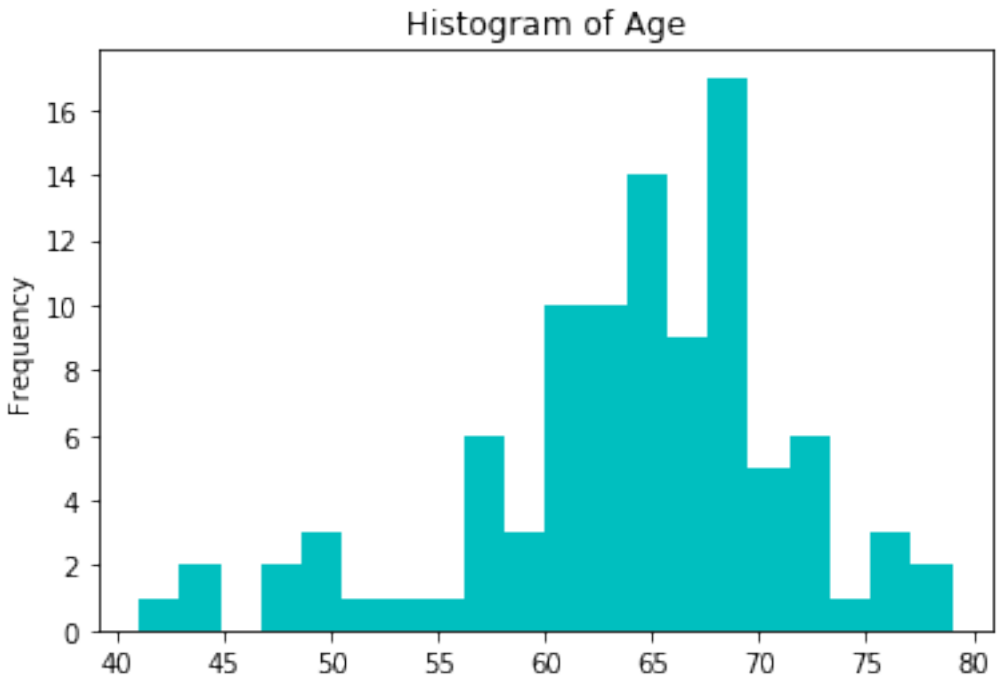
- CancerVol shows high positive skewness.

1.4.3 Age

[23]:
```
df.Age.plot(kind='box');
```

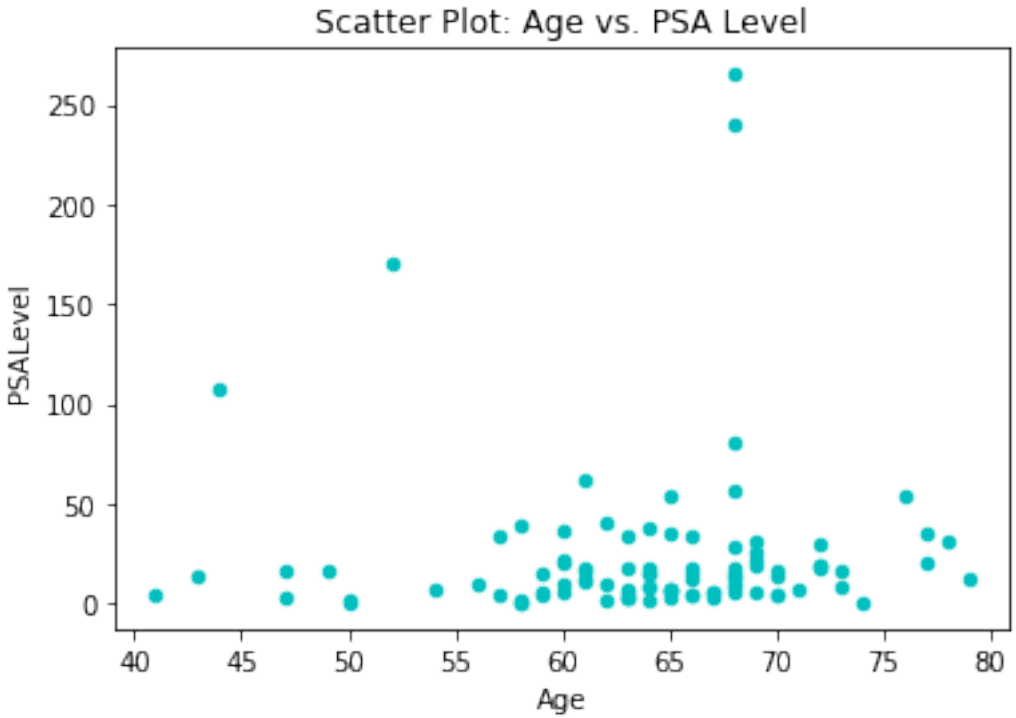


[24]:
```
df.Age.plot(kind='hist', title='Histogram of Age', color='c', bins=20);
```

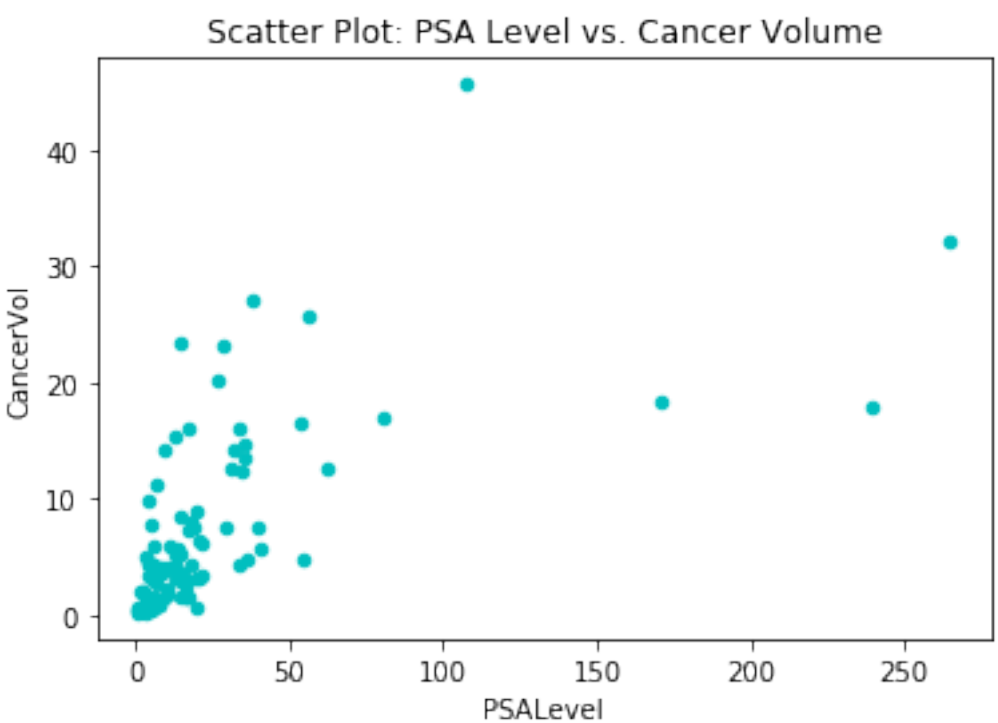


1.4.4 Bi-variate Interactions

[25]:
```
# use scatter plot for bi-variate distribution
df.plot.scatter(x='Age', y='PSALevel', color='c', title='Scatter Plot: Age vs.␣
↪PSA Level');
```

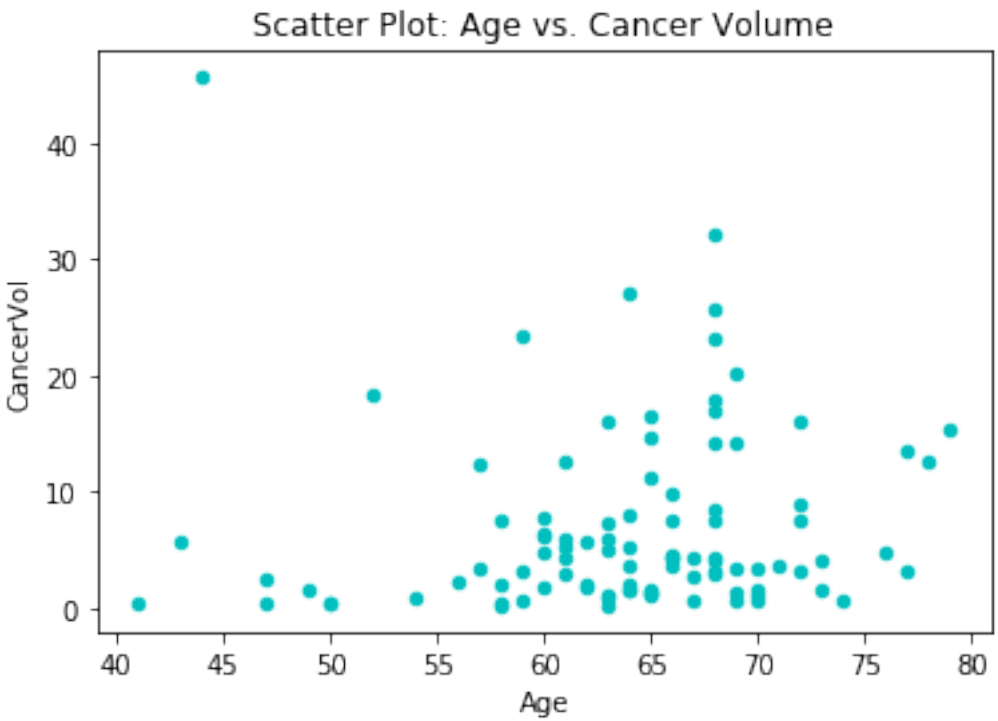


[26]:
```
df.plot.scatter(x='PSALevel', y='CancerVol', color='c', title='Scatter Plot:␣
↪PSA Level vs. Cancer Volume');
```

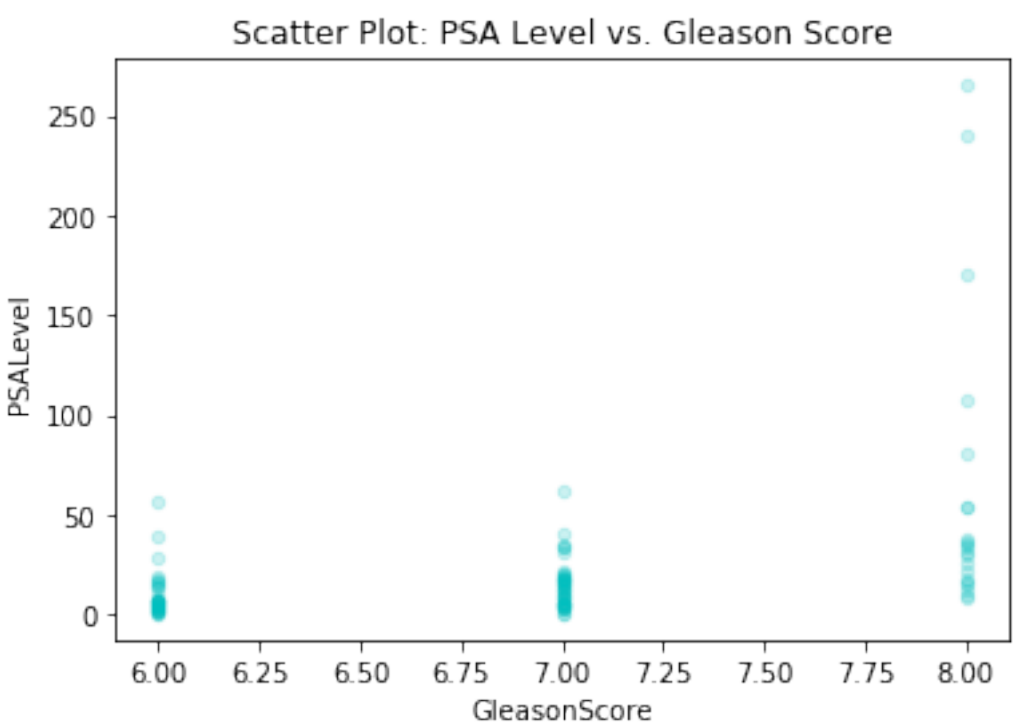


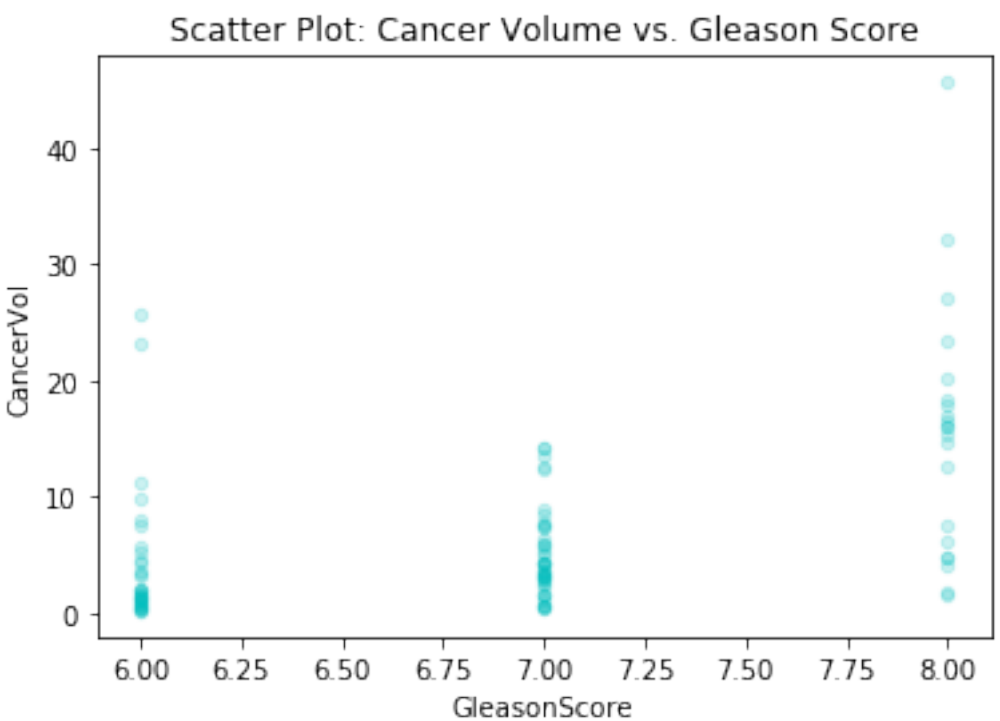
- PSA Level & Cancer Volume display a mild level of correlation

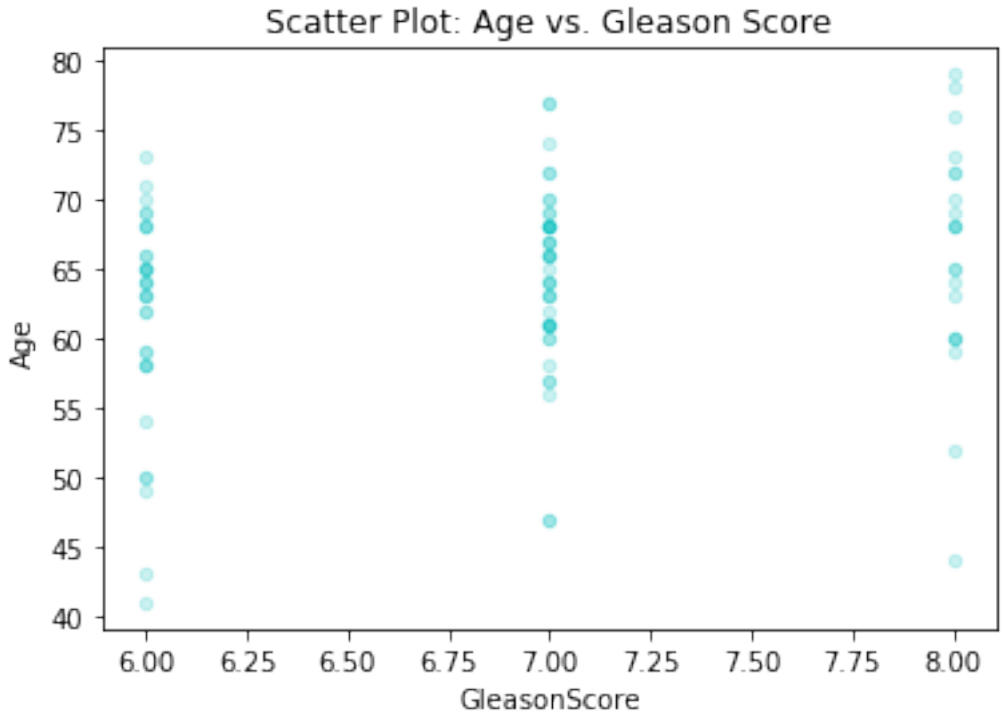
[27]:
```
df.plot.scatter(x='Age', y='CancerVol', color='c', title='Scatter Plot: Age vs.␣
↪Cancer Volume');
```



[28]:
```
# plot PSALevel, CancerVol, and Age against GleasonScore
df.plot.scatter(x='GleasonScore', y='PSALevel', color='c', alpha=0.2,␣
↪title='Scatter Plot: PSA Level vs. Gleason Score');
df.plot.scatter(x='GleasonScore', y='CancerVol', color='c', alpha=0.2,␣
↪title='Scatter Plot: Cancer Volume vs. Gleason Score');
df.plot.scatter(x='GleasonScore', y='Age', color='c', alpha=0.2, title='Scatter␣
↪Plot: Age vs. Gleason Score');
```


Scatter Plot: PSA Level vs. Gleason Score
PSALevel
0
50
100
150
200
250
6.00
6.25
6.50
6.75
7.00
7.25
7.50
7.75
8.00
GleasonScore


Scatter Plot: Cancer Volume vs. Gleason Score
CancerVol
0
10
20
30
40
6.00
6.25
6.50
6.75
7.00
7.25
7.50
7.75
8.00
GleasonScore



- High levels of PSALevel and/or CancerVol may suggest GleasonScore = 8.

[29]:
```
# calculate skewness for all columns in dataframe
for label, content in df.items():
    print(f'The skewness of {label} is: {round(content.skew(), 2)}')
```

```
The skewness of PSALevel is: 4.39
The skewness of CancerVol is: 2.18
The skewness of Weight is: 7.46
The skewness of Age is: -0.83
The skewness of BenignProstaticHyperplasia is: 0.98
The skewness of SeminalVesicleInvasion is: 1.4
The skewness of CapsularPenetration is: 2.13
The skewness of GleasonScore is: 0.2
The skewness of Y_HighGradeCancer is: 1.4
```

- PSALevel, CancerVol, and Weight are showing high skew values, and may require transformations in my analysis.

1.5 Working With Outliers

1.5.1 PSA Level

[30]:
```
# calculate IQR and find upper outlier fence

PSALevel_Q1 = np.percentile(df.PSALevel, 25)
PSALevel_Q2 = np.percentile(df.PSALevel, 50)
PSALevel_Q3 = np.percentile(df.PSALevel, 75)
PSALevel_IQR = PSALevel_Q3 - PSALevel_Q1  # inner quartile range
PSALevel_upper_fence = PSALevel_Q3 + 1.5 * PSALevel_IQR
print(f'The upper boundry for outliers in PSALevel is:␣
 ↪{round(PSALevel_upper_fence, 2)}')

# show relevant outlier data
df.loc[df.PSALevel >= PSALevel_upper_fence, :]
```

```
The upper boundry for outliers in PSALevel is: 44.86
```

[30]:

Obs	PSALevel	CancerVol	Weight	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion	CapsularPenetration	GleasonScore	Y_HighGradeCancer
89	53.517	16.6099	112.168	65	0.0000	1	11.7048	8	1
90	54.055	4.7588	40.447	76	2.5600	1	2.2479	8	1
91	56.261	25.7903	60.340	68	0.0000	0	0.0000	6	0
92	62.178	12.5535	39.646	61	3.8574	1	0.0000	7	1
93	80.640	16.9455	48.424	68	0.0000	1	3.7434	8	1
94	107.770	45.6042	49.402	44	0.0000	1	8.7583	8	1
95	170.716	18.3568	29.964	52	0.0000	1	11.7048	8	1
96	239.847	17.8143	43.380	68	4.7588	1	4.7588	8	1
97	265.072	32.1367	52.985	68	1.5527	1	18.1741	8	1

```
92                    0
93                    1
94                    1
95                    1
96                    1
97                    1
```

1.5.2 Cancer Volume

[31]:
```
# calculate IQR and find upper outlier fences (mild and extreme)
# consider only where Y_HighGradeCancer == 0

CancerVol_Q1 = np.percentile(df.loc[df.Y_HighGradeCancer == 0, :]['CancerVol'],␣
↪25)
CancerVol_Q2 = np.percentile(df.loc[df.Y_HighGradeCancer == 0, :]['CancerVol'],␣
↪50)
CancerVol_Q3 = np.percentile(df.loc[df.Y_HighGradeCancer == 0, :]['CancerVol'],␣
↪75)
CancerVol_IQR = CancerVol_Q3 - CancerVol_Q1  # inner quartile range
CancerVol_mild_upper_fence = CancerVol_Q3 + 1.5 * CancerVol_IQR
CancerVol_extreme_upper_fence = CancerVol_Q3 + 2.0 * CancerVol_IQR
print(f'The upper boundry for MILD OUTLIERS in CancerVol is:␣
↪{round(CancerVol_mild_upper_fence, 2)}')
print(f'The upper boundry for EXTREME OUTLIERS in CancerVol is:␣
↪{round(CancerVol_extreme_upper_fence, 2)}')

df.loc[(df.CancerVol > CancerVol_extreme_upper_fence) & (df.Y_HighGradeCancer␣
↪== 0) ]
```

```
The upper boundry for MILD OUTLIERS in CancerVol is: 12.55
The upper boundry for EXTREME OUTLIERS in CancerVol is: 14.77
```

[31]:
```
     PSALevel  CancerVol  Weight  Age  BenignProstaticHyperplasia  \
Obs
76     28.219    23.1039   26.05   68                      0.9512
91     56.261    25.7903   60.34   68                      0.0000

     SeminalVesicleInvasion  CapsularPenetration  GleasonScore  \
Obs
76                        1              11.2459             6
91                        0               0.0000             6

     Y_HighGradeCancer
Obs
76                   0
91                   0
```

1.5.3 Age

[32]:
```
# calculate IQR and find lower outlier fence

Age_Q1 = np.percentile(df.Age, 25)
Age_Q2 = np.percentile(df.Age, 50)
Age_Q3 = np.percentile(df.Age, 75)
Age_IQR = Age_Q3 - Age_Q1 # inner quartile range
Age_lower_fence = Age_Q1 -  1.5 * Age_IQR
print(f'The lower boundry for outliers in Age is: {Age_lower_fence}')

df.loc[df.Age < Age_lower_fence]
```

```
The lower boundry for outliers in Age is: 48.0
```

[32]:

Obs	PSALevel	CancerVol	Weight	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion	CapsularPenetration	GleasonScore	Y_HighGradeCancer
9	2.858	0.4584	34.467	47	0.0	0	0.0000	7	0
19	4.759	0.5712	26.311	41	0.0	0	0.0000	6	0
49	13.330	5.7546	33.115	43	0.0	0	0.0000	6	0
57	16.281	2.6379	17.637	47	0.0	0	1.6487	7	0
94	107.770	45.6042	49.402	44	0.0	1	8.7583	8	1

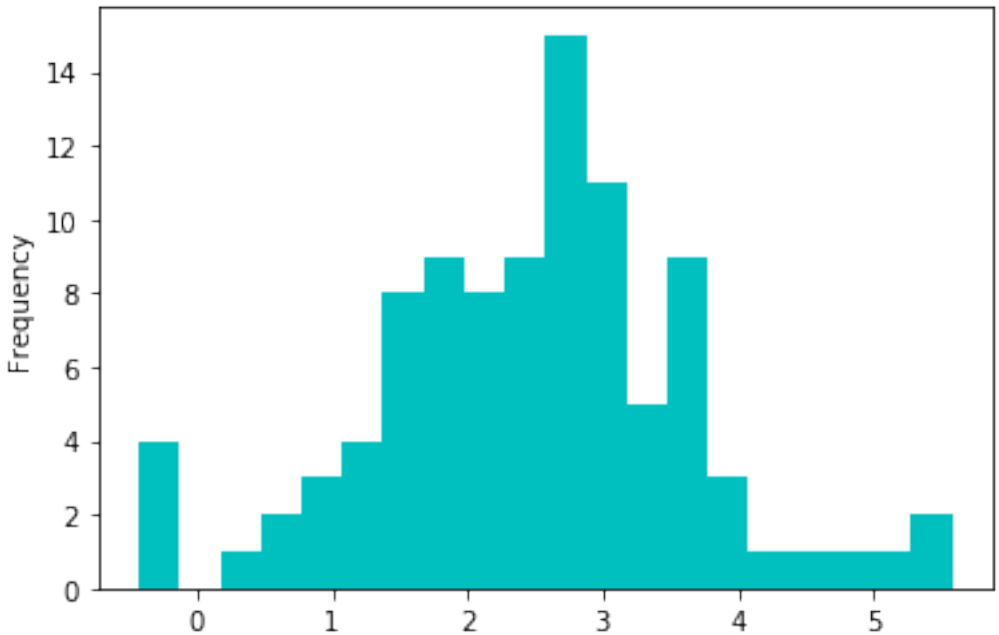
1.6 Transformations

- This section is for investigation/analysis purposes only. I may or may not include transformations in the finalized processed dataset.
- Considering only PSALevel, CancerVol, and Weight at this time.

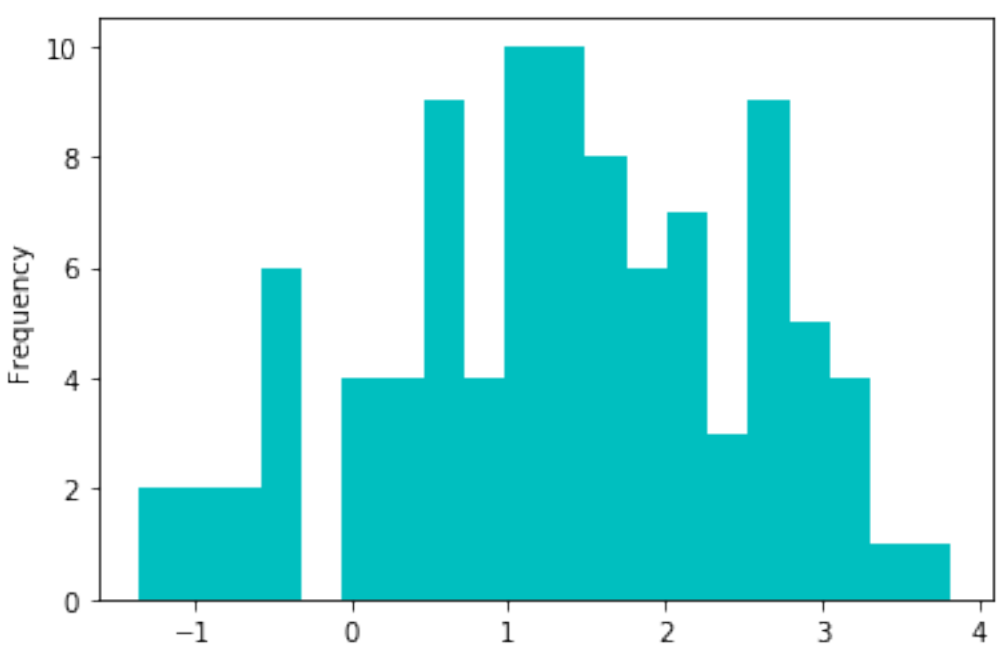
[33]:
```
# try log transformations to reduce skewness
log_PSALevel = np.log(df.PSALevel)
log_CancerVol = np.log(df.CancerVol)
```

```
log_Weight = np.log(df.Weight)
```

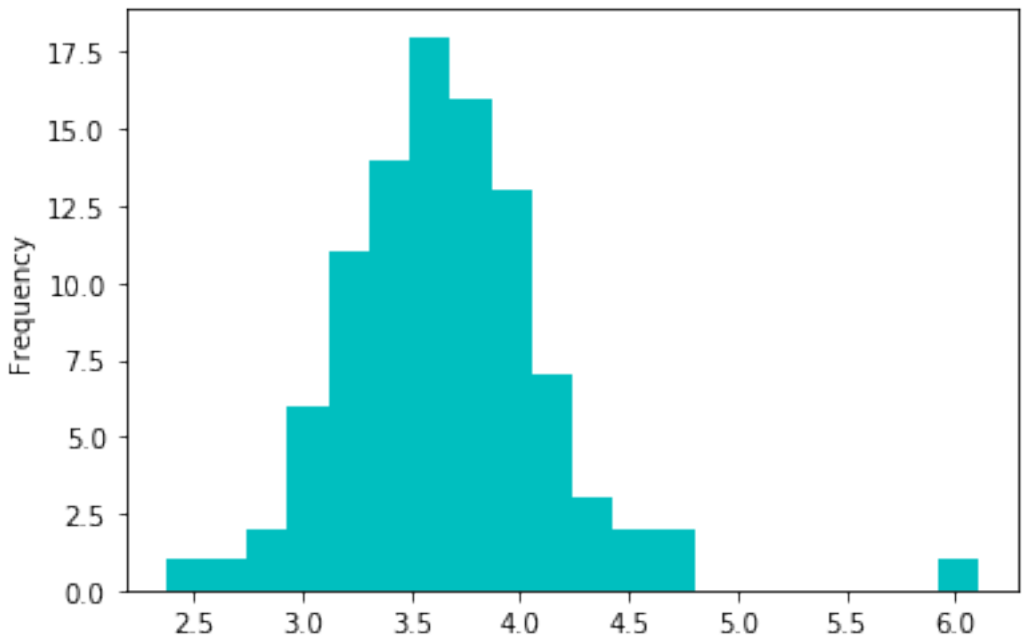
[34]:
```
# histogram of log PSALevel
log_PSALevel.plot(kind='hist', color='c', bins=20);
```



[35]:
```
# histogram of log CancerVol
log_CancerVol.plot(kind='hist', color='c', bins=20);
```



[36]:
```
# histogram of log Weight
log_Weight.plot(kind='hist', color='c', bins=20);
```



[37]:
```
# print original skew values
print(f'Original PSALevel skewness: {round(df.PSALevel.skew(), 2)}')
print(f'Original CancerVol skewness: {round(df.CancerVol.skew(), 2)}')
print(f'Original Weight skewness: {round(df.Weight.skew(), 2)}')

# print transformed skew values
print(f'Log Transformed PSALevel skewness: {round(log_PSALevel.skew(), 2)}')
print(f'Log Transformed CancerVol skewness: {round(log_CancerVol.skew(), 2)}')
print(f'Log Transformwed Weight skewness: {round(log_Weight.skew(), 2)}')
```

```
Original PSALevel skewness: 4.39
Original CancerVol skewness: 2.18
Original Weight skewness: 7.46
Log Transformed PSALevel skewness: 0.0
Log Transformed CancerVol skewness: -0.25
Log Transformwed Weight skewness: 1.21
```

- Log transformations have dramatically improved PSALevel and CancerVol skewness.
- I will include the transformed fields within final processed dataset.

1.7 Drop, Modify, and Reorder Columns

GleasonScore can now be removed from the dataset, as it will not be considered as a predictor of Y_HighGradeCancer. Let's also move the response variable to the 1st column, for ease of use durring model building.

[38]:
```
# remove GleasonScore from dataset and assign to new "df_trimmed" dataframe
df_trimmed = df.drop(columns=['GleasonScore'], axis=1)
```

[39]:
```
# reorder columns
cols = [col for col in df_trimmed.columns if col != 'Y_HighGradeCancer']
cols = ['Y_HighGradeCancer'] + cols
df_trimmed = df_trimmed[cols]
df_trimmed.head()
```

[39]:

Obs	Y_HighGradeCancer	PSALevel	CancerVol	Weight	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion	CapsularPenetration
1	0	0.651	0.5599	15.959	50	0.0	0	0.0
2	0	0.852	0.3716	27.660	58	0.0	0	0.0
3	0	0.852	0.6005	14.732	74	0.0	0	0.0
4	0	0.852	0.3012	26.576	58	0.0	0	0.0
5	0	1.448	2.1170	30.877	62	0.0	0	0.0

[40]:
```
df_trimmed.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 97 entries, 1 to 97
Data columns (total 8 columns):
Y_HighGradeCancer             97 non-null int32
PSALevel                      97 non-null float64
CancerVol                     97 non-null float64
Weight                        97 non-null float64
Age                           97 non-null int64
BenignProstaticHyperplasia    97 non-null float64
SeminalVesicleInvasion        97 non-null int64
CapsularPenetration           97 non-null float64
dtypes: float64(5), int32(1), int64(2)
memory usage: 6.4 KB
```

1.8 Standardize DataFrame

- Variable transformation and standardization is an important technique used to create robust models using logistic regression.

[41]:
```
# import and create instance of standardization class from sklearn module
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
```

[42]:
```
# select columns which need to be standardized
# do not inclue Y_HighGradeCancer or SeminalVesicleInvasion (categorical␣
 ↪variables)
cols = [col for col in df_trimmed.columns if col not in ['Y_HighGradeCancer',␣
 ↪'SeminalVesicleInvasion']]
```

[43]:
```
# make a copy of trimmed dataframe
df_stand = df_trimmed.copy()
```

[44]:
```
# apply log transformations to both PSALevel and CancerVol
df_stand['PSALevel'] = np.log(df_stand.PSALevel)
df_stand['CancerVol'] = np.log(df_stand.CancerVol)
df_stand['Weight'] = np.log(df_stand.Weight)
```

[45]:
```
# standardize the dataframe
df_stand[cols] = scaler.fit_transform(df_stand[cols])
```

[46]:
```
# the standardized features should now have mean=0 and sd=1
df_stand.describe()
```

[46]:

	Y_HighGradeCancer	PSALevel	CancerVol	Weight
count	97.000000	9.700000e+01	9.700000e+01	9.700000e+01
mean	0.216495	7.783007e-17	-2.403576e-16	-5.013172e-16
std	0.413995	1.005195e+00	1.005195e+00	1.005195e+00
min	0.000000	-2.533700e+00	-2.302583e+00	-2.595287e+00
25%	0.000000	-6.522705e-01	-7.161288e-01	-5.518528e-01
50%	0.000000	9.701907e-02	8.555117e-02	-6.629801e-02
75%	0.000000	5.065387e-01	6.655015e-01	4.596790e-01
max	1.000000	2.702227e+00	2.106830e+00	4.971231e+00

	Age	BenignProstaticHyperplasia	SeminalVesicleInvasion
count	9.700000e+01	9.700000e+01	97.000000
mean	3.433679e-16	6.409535e-17	0.216495
std	1.005195e+00	1.005195e+00	0.413995
min	-3.087227e+00	-8.405624e-01	0.000000
25%	-5.219612e-01	-8.405624e-01	0.000000
50%	1.531086e-01	-3.929102e-01	0.000000
75%	5.581506e-01	7.375452e-01	0.000000
max	2.043304e+00	2.567782e+00	1.000000

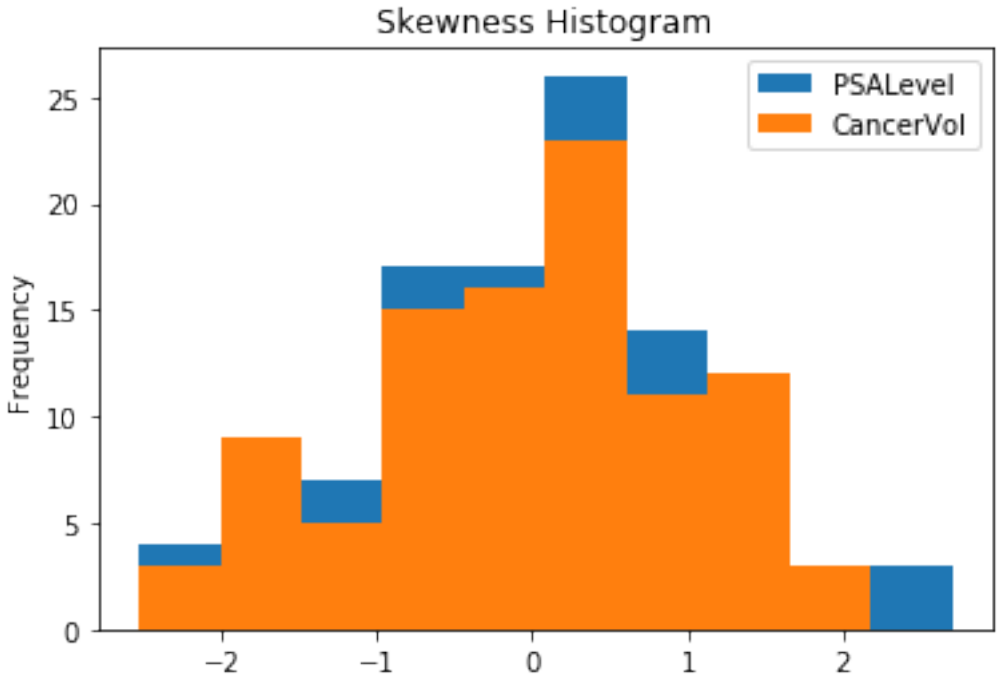
```
       CapsularPenetration
count         9.700000e+01
mean          1.281907e-16
std           1.005195e+00
min          -5.965729e-01
25%          -5.965729e-01
50%          -4.771981e-01
75%           2.680906e-01
max           4.232114e+00
```

Sanity check… As a final measure, let's examine skew values of the final trimmed and transformed dataset:

[47]:
```
# print skewness for all columns in trimmed and transformed dataset
for label, content in df_stand.items():
    if label != 'Y_HighGradeCancer':
        print(f'The skewness of {label} is: {round(content.skew(), 2)}')
```

```
The skewness of PSALevel is: 0.0
The skewness of CancerVol is: -0.25
The skewness of Weight is: 1.21
The skewness of Age is: -0.83
The skewness of BenignProstaticHyperplasia is: 0.98
The skewness of SeminalVesicleInvasion is: 1.4
The skewness of CapsularPenetration is: 2.13
```

[48]:
```
# visualize skewness of a few impactful feautures
df_stand[['PSALevel', 'CancerVol']].plot(kind='hist', title='Skewness␣
 ↪Histogram');
```



1.9 Save Processed Data

[49]:
```
# define paths
processed_data_path = os.path.join(os.path.pardir, 'data', 'processed')
write_data_path = os.path.join(processed_data_path, 'APPENC05.txt')
```

[50]:
```
# save data
df_stand.to_csv(write_data_path)
```