3.0-jo-building-predictive-model

December 3, 2020

1 Building Predictive Models

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

1.1 Import Data

Train and test data were randomly split within R, using 0.80 ratio. The two dataframes were written to independent csv files, and will be brought into the Python notebook now.

```
[2]: # set path to processed train/test data
     processed_data_path = os.path.join(os.path.pardir, 'data', 'processed')
     train_file_path = os.path.join(processed_data_path, 'train.txt')
     test_file_path = os.path.join(processed_data_path, 'test.txt')
```

```
[3]: df_train = pd.read_csv(train_file_path, index_col='Obs')
     df_test = pd.read_csv(test_file_path, index_col='Obs')
```

```
[4]: print('Train data:')
     df_train.info()
     print('\n')
     print('Test data:')
     df_test.info()
```

```
Train data:
<class 'pandas.core.frame.DataFrame'>
Int64Index: 76 entries, 1 to 97
Data columns (total 9 columns):
Unnamed: 0                  76 non-null int64
Y_HighGradeCancer           76 non-null int64
PSALevel                    76 non-null float64
CancerVol                   76 non-null float64
Weight                      76 non-null float64
Age                         76 non-null float64
BenignProstaticHyperplasia  76 non-null float64
SeminalVesicleInvasion      76 non-null int64
```

```
CapsularPenetration           76 non-null float64
dtypes: float64(6), int64(3)
memory usage: 5.9 KB


Test data:
<class 'pandas.core.frame.DataFrame'>
Int64Index: 21 entries, 5 to 95
Data columns (total 9 columns):
Unnamed: 0                    21 non-null int64
Y_HighGradeCancer             21 non-null int64
PSALevel                      21 non-null float64
CancerVol                     21 non-null float64
Weight                        21 non-null float64
Age                           21 non-null float64
BenignProstaticHyperplasia    21 non-null float64
SeminalVesicleInvasion        21 non-null int64
CapsularPenetration           21 non-null float64
dtypes: float64(6), int64(3)
memory usage: 1.6 KB
```

[5]: `df_train.columns`

[5]: Index(['Unnamed: 0', 'Y_HighGradeCancer', 'PSALevel', 'CancerVol', 'Weight',
           'Age', 'BenignProstaticHyperplasia', 'SeminalVesicleInvasion',
           'CapsularPenetration'],
          dtype='object')

It looks like R appended an additional "Unnamed: 0" column, most likely related to indexing. I will remove that now.

[6]:
```python
# drop the redudent columns (R auto-created an index column of its own); can be␣
 ↪seen in info() cell above
df_train = df_train.drop(columns='Unnamed: 0')
df_test = df_test.drop(columns='Unnamed: 0')
```

[7]:
```python
# examine train set
df_train
```

[7]:
```
     Y_HighGradeCancer  PSALevel  CancerVol    Weight       Age  \
Obs
1                    0 -2.533700  -1.645747 -1.785921 -1.872101
2                    0 -2.299250  -1.995368 -0.673281 -0.791989
3                    0 -2.299250  -1.586043 -1.947772  1.368234
4                    0 -2.299250  -2.174506 -0.754163 -0.791989
6                    0 -1.488689  -2.046685 -0.855308 -1.872101

..                 ...       ...        ...       ...       ...
92                   0  1.438825   1.006641  0.055045 -0.386947
```

```
93                      1  1.665361  1.262501  0.459679  0.558151
94                      1  1.918045  2.106830  0.500132 -2.682185
96                      1  2.615096  1.305144  0.237142  0.558151
97                      1  2.702227  1.808328  0.641786  0.558151

       BenignProstaticHyperplasia  SeminalVesicleInvasion  CapsularPenetration
Obs
1                       -0.840562                       0            -0.596573
2                       -0.840562                       0            -0.596573
3                       -0.840562                       0            -0.596573
4                       -0.840562                       0            -0.596573
6                       -0.840562                       0            -0.596573
..                            ...                     ...                  ...
92                       0.438624                       1            -0.596573
93                      -0.840562                       1             0.398013
94                      -0.840562                       1             1.730425
96                       0.737545                       1             0.667795
97                      -0.325658                       1             4.232114

[76 rows x 8 columns]
```

```
[8]: # examine test set
     df_test.head()
```

```
[8]:      Y_HighGradeCancer  PSALevel  CancerVol    Weight       Age  \
     Obs
     5                    0 -1.837148  -0.511447 -0.450690 -0.251933
     8                    0 -1.418947  -0.562625 -0.228166 -0.791989
     14                   0 -0.983519   0.111131 -1.320605  0.423137
     17                   0 -0.878912  -1.509353 -0.268658  0.828178
     23                   0 -0.678455  -1.611706 -0.551853 -0.656975

          BenignProstaticHyperplasia  SeminalVesicleInvasion  CapsularPenetration
     Obs
     5                     -0.840562                       0            -0.596573
     8                      0.706307                       0            -0.596573
     14                    -0.840562                       0            -0.596573
     17                     0.305380                       0            -0.450762
     23                    -0.691566                       0            -0.596573
```
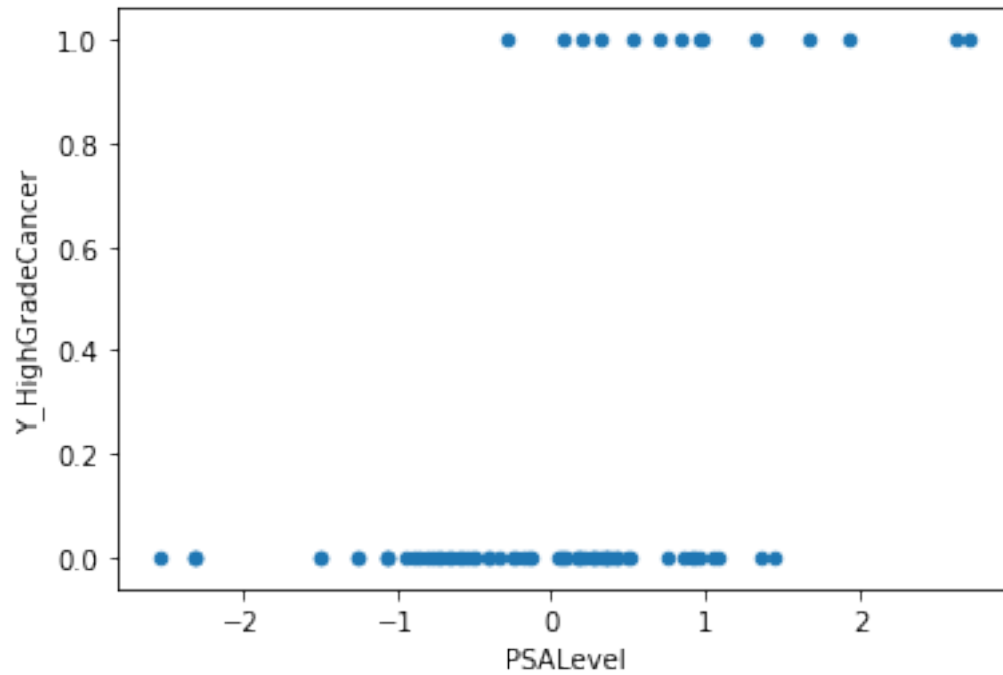
```
[9]: # create a list which captures fields to ommit from model
     skip = ['Y_HighGradeCancer'
           , 'Age'
           , 'Weight'
           , 'BenignProstaticHyperplasia'
           , 'SeminalVesicleInvasion'
           , 'CapsularPenetration'
```

```
        ]
cols_model = [col for col in df_train.columns if col not in skip]
cols_model
```
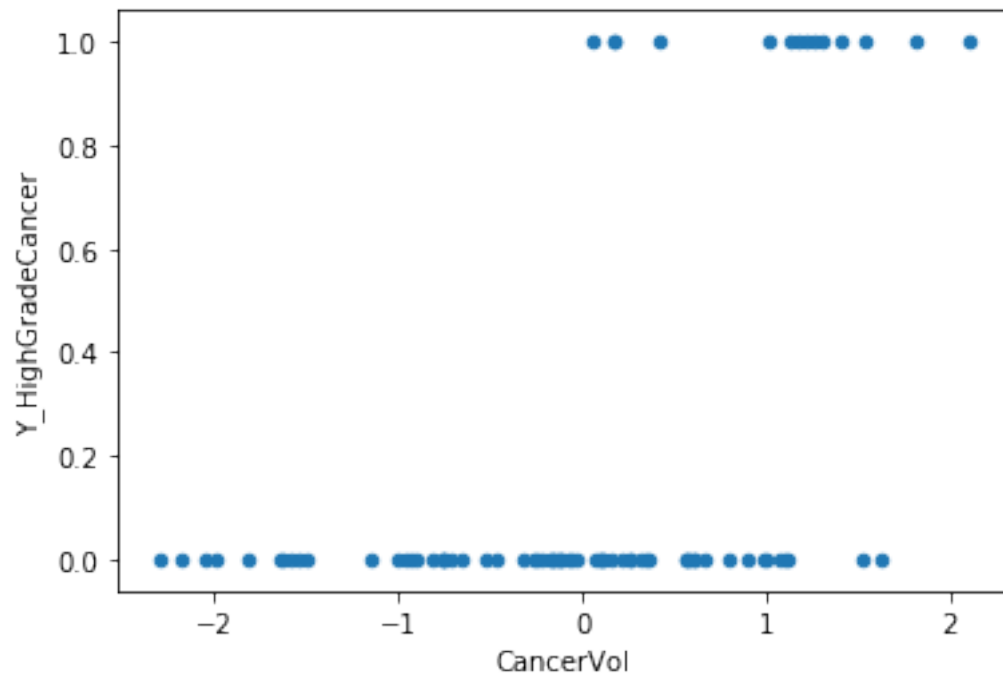
[9]: ['PSALevel', 'CancerVol']

1.2 Visuals

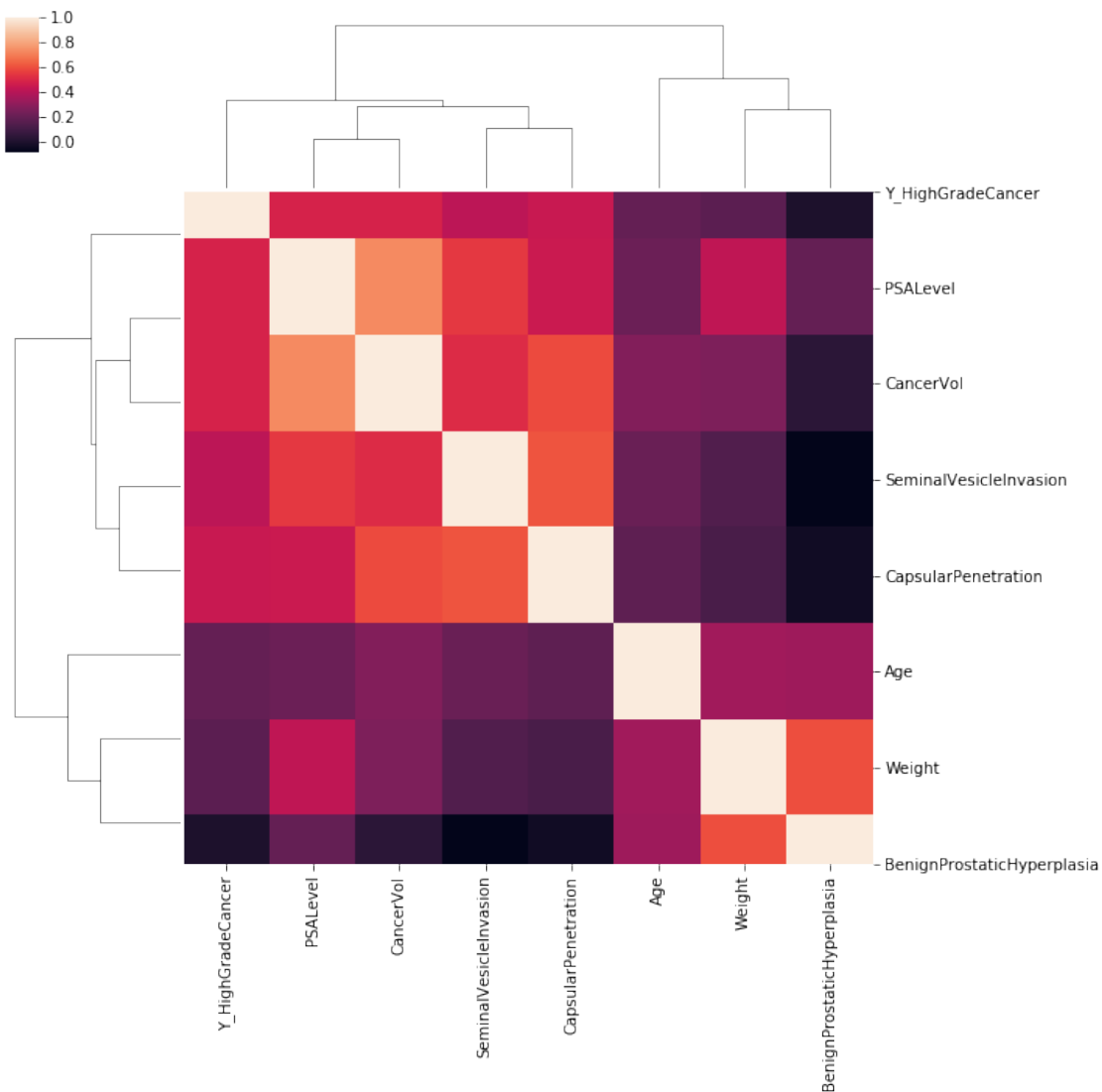[11]: `df_train.plot.scatter(x='PSALevel', y='Y_HighGradeCancer');`

[12]: `df_train.plot.scatter(x='CancerVol', y='Y_HighGradeCancer');`

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

       sns.clustermap(df_train.corr());
```

```
[14]: df_train.corr()
```

```
[14]:                          Y_HighGradeCancer  PSALevel  CancerVol    Weight  \
      Y_HighGradeCancer                1.000000  0.488609   0.492580  0.173835
      PSALevel                         0.488609  1.000000   0.737585  0.427753
      CancerVol                        0.492580  0.737585   1.000000  0.264202
      Weight                           0.173835  0.427753   0.264202  1.000000
      Age                              0.196961  0.217748   0.274467  0.350116
      BenignProstaticHyperplasia       0.000539  0.199778   0.044290  0.599560
      SeminalVesicleInvasion           0.420664  0.550701   0.515015  0.148291
      CapsularPenetration              0.452185  0.457590   0.593430  0.128845

                               Age  BenignProstaticHyperplasia  \
```

```
Y_HighGradeCancer           0.196961                    0.000539
PSALevel                    0.217748                    0.199778
CancerVol                   0.274467                    0.044290
Weight                      0.350116                    0.599560
Age                         1.000000                    0.344029
BenignProstaticHyperplasia  0.344029                    1.000000
SeminalVesicleInvasion      0.209401                   -0.082420
CapsularPenetration         0.183055                   -0.035408

                            SeminalVesicleInvasion  CapsularPenetration
Y_HighGradeCancer                         0.420664             0.452185
PSALevel                                  0.550701             0.457590
CancerVol                                 0.515015             0.593430
Weight                                    0.148291             0.128845
Age                                       0.209401             0.183055
BenignProstaticHyperplasia               -0.082420            -0.035408
SeminalVesicleInvasion                    1.000000             0.611239
CapsularPenetration                       0.611239             1.000000
```

[15]:
```python
# correlation of final two predictors
df_train[['PSALevel', 'CancerVol']].corr()
```

[15]:
```
          PSALevel  CancerVol
PSALevel  1.000000   0.737585
CancerVol 0.737585   1.000000
```

1.3 Data Preperation

Because R has already prepared the training and test sets, I will manually assign the split data to appropriate variables now.

[16]:
```python
# train-test split
X_train = df_train.loc[:, cols_model]
y_train = df_train['Y_HighGradeCancer']
X_test = df_test.loc[:, cols_model]
y_test = df_test['Y_HighGradeCancer']
```

[17]:
```python
print(X_train.shape, y_train.shape)
print(X_test.shape, y_test.shape)
```

```
(76, 2) (76,)
(21, 2) (21,)
```

[18]:
```python
# average survival in train and test sets
print(f'Mean y in train set: {round(np.mean(y_train), 3)}')
print(f'Mean y in test set: {round(np.mean(y_test), 3)}')
```

```
Mean y in train set: 0.184
Mean y in test set: 0.333
```

1.4 Baseline Model

Developing a basline model: - Here, I will feed the dummy model training data, and sklearn will determine the most frequent classification within the Y_HighGradeCancer field (via prior analysis we know this to value to be 0). Because Y_HighGradeCancer = 0 most freqently, the model will be designed to predict 0 on every single observation. - After the design of the baseline model, I will implement it on both the training and testing data, and calculate accuracy scores and confusion matrixes for good measure. - Subsequent model fittings can therefore be compared to the baseline model.

```python
[19]: # import function
      from sklearn.dummy import DummyClassifier
```

```python
[20]: # create model
      # because mean y in train = 0.184 (shown above), this "most frequent" model
       →will predict y=0 for all test observations
      model_dummy = DummyClassifier(strategy='most_frequent', random_state=0)
```

```python
[21]: # train model
      model_dummy.fit(X_train, y_train)
```

```
[21]: DummyClassifier(constant=None, random_state=0, strategy='most_frequent')
```

```python
[22]: # run dummy_model with training data
      print(f'Score for baseline model (TRAINING): {round(model_dummy.score(X_train,
       →y_train), 2)}')

      # run dummy_model with testing data
      print(f'Score for baseline model (TESTING): {round(model_dummy.score(X_test,
       →y_test), 2)}')
```

```
Score for baseline model (TRAINING): 0.82
Score for baseline model (TESTING): 0.67
```

```python
[23]: # performance metrics
      from sklearn.metrics import accuracy_score, confusion_matrix, precision_score,
       →recall_score
```

```python
[24]: # training confusion matrix
      print(f'Confusion matrix for baseline model (TRAINING): \n
       →{confusion_matrix(y_train, model_dummy.predict(X_train))} \n')

      # testing confusion matrix
      print(f'Confusion matrix for baseline model (TESTING): \n
       →{confusion_matrix(y_test, model_dummy.predict(X_test))}')
```

```
Confusion matrix for baseline model (TRAINING):
 [[62  0]
 [14  0]]
```

```
Confusion matrix for baseline model (TESTING):
 [[14  0]
 [ 7  0]]
```

1.5 Statsmodels Library

1.5.1 Full Logistics Model

```
[25]: import statsmodels.api as sm
```

```
[26]: X_model = sm.add_constant(X_train)
      model = sm.Logit(y_train, X_model)
```

```
C:\Users\jaosi\Anaconda3\envs\datSci\lib\site-
packages\numpy\core\fromnumeric.py:2389: FutureWarning: Method .ptp is
deprecated and will be removed in a future version. Use numpy.ptp instead.
  return ptp(axis=axis, out=out, **kwargs)
```

```
[27]: results = model.fit()
```

```
Optimization terminated successfully.
        Current function value: 0.293604
        Iterations 8
```

```
[28]: ### full model statistical output
      print(results.summary2(alpha=0.05))
```

```
                          Results: Logit
=================================================================
Model:              Logit             Pseudo R-squared: 0.385
Dependent Variable: Y_HighGradeCancer AIC:              50.6278
Date:               2020-12-03 15:26  BIC:              57.6200
No. Observations:   76                Log-Likelihood:   -22.314
Df Model:           2                 LL-Null:          -36.307
Df Residuals:       73                LLR p-value:      8.3761e-07
Converged:          1.0000            Scale:            1.0000
No. Iterations:     8.0000
-----------------------------------------------------------------
            Coef.    Std.Err.    z      P>|z|    [0.025   0.975]
-----------------------------------------------------------------
const      -2.6867   0.6186   -4.3429  0.0000  -3.8992  -1.4742
PSALevel    1.0577   0.6198    1.7067  0.0879  -0.1570   2.2725
CancerVol   1.5502   0.6859    2.2599  0.0238   0.2058   2.8945
=================================================================
```

```
[29]: PSALevel_list = X_train['PSALevel'].tolist()
      CancerVol_list = X_train['CancerVol'].tolist()
```

```
Y_HighGradeCancer_list = y_train.tolist()
```

[30]:
```
type(np.arange(1, 2, 0.5))
```

[30]: `numpy.ndarray`

1.6 Advanced Visualizations Using Matplotlib

[31]:
```
import math
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
import numpy as np
```

1.6.1 Logistic Regression Plot

[32]:
```
%matplotlib inline

# bring in and store the coefficients of the fitted model
const_coeff, x1_coeff, x2_coeff = results.params

# define a sigmoid function of 2 variables
def sigmoid(x1, x2):
    func = 1.0 / (1.0 + math.exp(-(const_coeff + x1_coeff*x1 + x2_coeff*x2)))
    return func

# design plot
fig = plt.figure()
ax = fig.add_subplot(111, projection='3d')
plt.tight_layout()
x = y = np.arange(-3.0, 4.0, 0.05)
X, Y = np.meshgrid(x, y)
zs = np.array([sigmoid(x,y) for x,y in zip(np.ravel(X), np.ravel(Y))])
Z = zs.reshape(X.shape)

# draw plots
ax.plot_surface(X, Y, Z, alpha=0.5)
ax.scatter(PSALevel_list, CancerVol_list, Y_HighGradeCancer_list, c='red',
 ↪marker='o')

# modify axes and labels
ax.set_xticklabels([])
ax.set_yticklabels([])
ax.set_zticklabels([0, 0, '', '', '', '', 1])
ax.set_xlabel('PSALevel')
ax.set_ylabel('CancerVol')
ax.set_zlabel('Y_HighGradeCancer')
ax.set_title('Prostate Cancer: Logistic Regression')
```

[32]: Text(0.5, 0.92, 'Prostate Cancer: Logistic Regression')

Prostate Cancer: Logistic Regression