knn-regression

November 11, 2018

1 Breast Cancer Survival Time after Diagnosis

k Nearest Neighbors Data source: U.S. Department of Health and Human Services, National Institutes of Health, National Cancer Institute
Surveillance, Epidemiology, and End Results (SEER) Program - Incidences of Breast Cancer
https://seer.cancer.gov/

```
In [1]: #Standard modules
        import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt

        #Statistical modules
        import scipy.stats as stats

        #Modules
        from sklearn.neighbors import KNeighborsRegressor
        from sklearn.model_selection import train_test_split
```

Data set The data set has been formatted and cleaned, then read into a csv file. Many of the independent variables are categorical, dummy variables were constructed to ease analysis. The data set contains patient by patient data, covering survival times, some basic patient and neoplasm characteristics. The variables are:
srv_time_mon - Main dependent variable. Number of months the patient survives after a diagnosis.
p_srv - Constructed from the depenedent variable, the probability of survival after a diagnosis.
c_srv - Constructed from the dependent variable, the count of patients surviving to the time point.
log_odds - An alternate dependent variable and constructed from the dependent variable, the log odds of the patient survival after a diagnosis.
REG - Independent variable, the US region where the diagnosis occurred.
MAR_STAT - Independent variable, marital status of the patient.
RACE1V - Independent variable, ethnicity of the patient.
NHIADE - Independent variable, for hispanic ethnicities, further classifications.
SEX - Independent variable, gender of the patient.
AGE_DX - Independent variable, age of the patient at diagnosis.
SEQ_NUM - Independent variable, number of previous diagnoses.
LATERAL - Independent variable, side of body of the diagnosis.

HISTO3V - Independent variable, histologic characteristics of the diagnosis.
BEHO3V - Independent variable, behvior characterization of the neoplasm.
GRADE - Independent variable, a classification of the severity of the neoplasm.
HST_STGA - Independent variable, histologic stage of the neoplasm.
MALIGCOUNT - Independent variable, the number of malignant neoplasms at diagnosis.
BENBORDCOUNT - Independent variable, the number of benign neoplasms at diagnosis.
PRIMSITE_coded - Independent variable, the primary site of the diagnosis.

```
In [2]: #Bring in data set
        cancer_sruviv = pd.read_csv('./data/dummied.csv')


        cancer_sruviv = cancer_sruviv.drop('Unnamed: 0', axis=1)
```

```
In [3]: #Split data set
        train, test = train_test_split(cancer_sruviv)
```

Analysis k nearest neighbors shows considerable overfitting. No solution was identified.

```
In [4]: #knn regression
        x = train.drop(['srv_time_mon', 'p_srv', 'c_srv', 'log_odds'], axis=1)
        y = train.srv_time_mon

        model = KNeighborsRegressor().fit(x, y)
```

```
In [5]: print(f'Coefficient of determination of the model: {np.round(model.score(x, y),2)}')
```

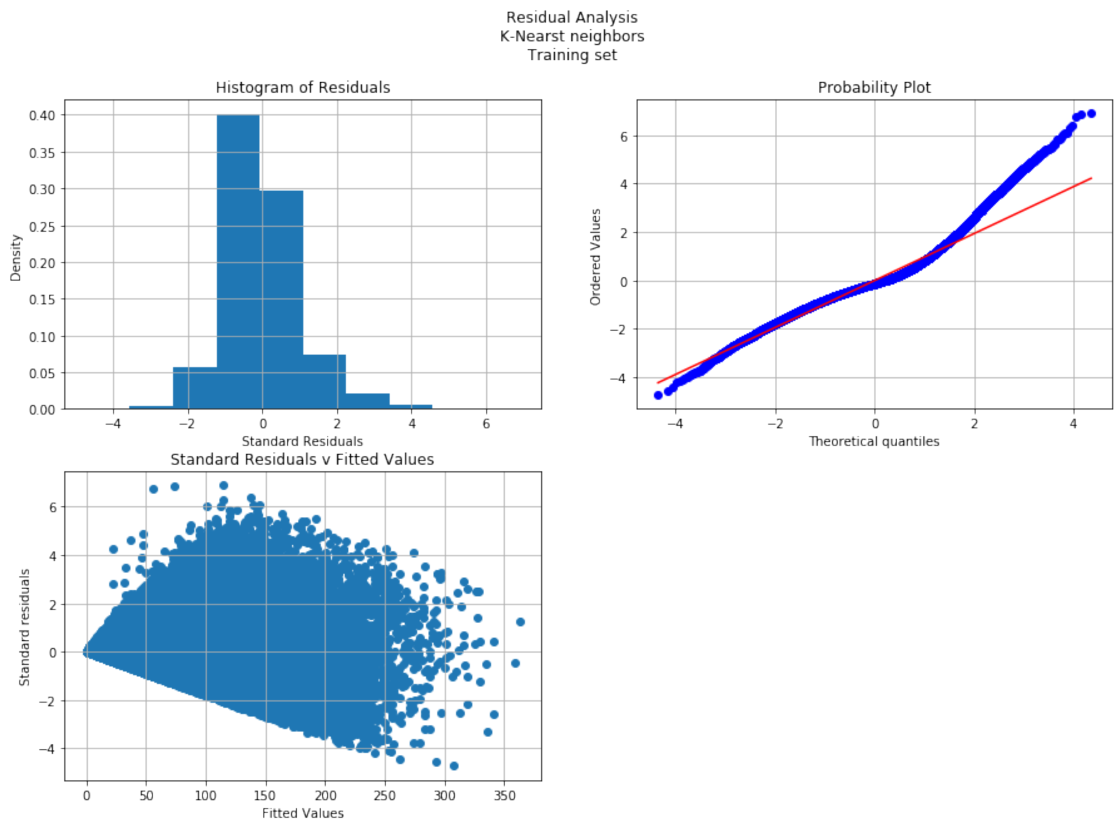
```
Coefficient of determination of the model: 0.41
```

Residuals The distribution of residuals show deviation from normal and possible heteroskedasticity (against fitted values). The training set and testing set look similar. Check for correct model specification.

```
In [6]: #Resdiual analysis
        y_pred = model.predict(x)
        resid = y_pred - y
        resid_stand = (resid.mean() - resid) / resid.std()

        ks = stats.kstest(resid_stand, 'norm')[1]
        rsd = np.round(np.sqrt(np.sum(resid**2) / (len(resid) - len(x.columns))) ,2)
        rrse = np.round(np.sqrt(np.sum(resid**2) / np.sum((y.mean() - y)**2)), 2)
        print(f'Residual sd: {rsd}\n'
              f'Relative root residual error:  {rrse}\n'
              f'KS test for normal residual distribution: '
              f'{ks}')
```

```
Residual sd: 55.1
Relative root residual error:  0.77
KS test for normal residual distribution: 0.0
```

```
In [7]: #Plot residuals
        plt.figure(figsize=(15,10))
        plt.suptitle('Residual Analysis\nK-Nearst neighbors\nTraining set')

        ax1 = plt.subplot(221)
        plt.hist(resid_stand, density=True)
        plt.title('Histogram of Residuals')
        plt.xlabel('Standard Residuals')
        plt.ylabel('Density')
        plt.grid()

        ax2 = plt.subplot(222)
        plot = stats.probplot(resid_stand, plot=plt)
        plt.grid()

        ax3= plt.subplot(223)
        plt.scatter(y_pred, resid_stand)
        plt.title('Standard Residuals v Fitted Values')
        plt.xlabel('Fitted Values')
        plt.ylabel('Standard residuals')

        plt.grid()


        # plt.savefig('./images/fig_1_knn.png', transparent=True)

        plt.show()
```



```
In [8]: x_test = test.drop(['srv_time_mon', 'p_srv', 'c_srv', 'log_odds'], axis=1)
        y_test = test.srv_time_mon
        print(f'Coefficient of determination: {np.round(model.score(x_test, y_test), 2)}')
```

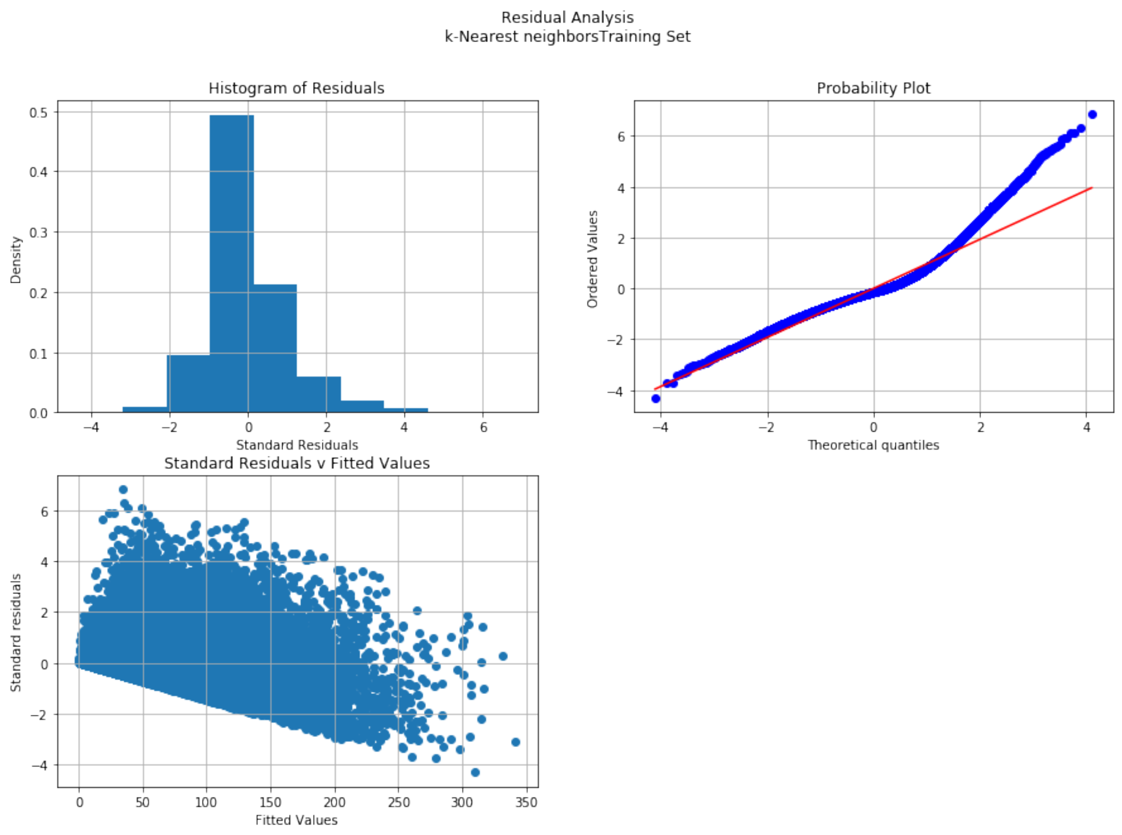
```
Coefficient of determination: 0.13
```

```
In [9]: #Residual analysis of the test set

        test_fit = model.predict(x_test)
        test_resid = test_fit - y_test
        test_resid_stand = (test_resid.mean() - test_resid) / test_resid.std()

        ks_test = stats.kstest(test_resid_stand, 'norm')[1]
        rsd_test = np.round(np.sqrt(np.sum(test_resid**2) / (len(test_resid) - len(x_test.colu
        rrse_test = np.round(np.sqrt(np.sum(test_resid**2) / np.sum((y_test.mean() - y_test)**
        print(f'Residual sd: {rsd_test}\n'
              f'Relative root residual error:  {rrse_test}\n'
              f'KS test for normal residual distribution: '
              f'{ks_test}')
```

```
Residual sd: 67.84
Relative root residual error:  0.93
```

```
KS test for normal residual distribution: 0.0
```

```
In [10]: #Graphical analysis of training set
         plt.figure(figsize=(15,10))
         plt.suptitle('Residual Analysis\nk-Nearest neighbors'
                      'Training Set')

         ax1 = plt.subplot(221)
         plt.hist(test_resid_stand, density=True)
         plt.title('Histogram of Residuals')
         plt.xlabel('Standard Residuals')
         plt.ylabel('Density')
         plt.grid()

         ax2 = plt.subplot(222)
         plot = stats.probplot(test_resid_stand, plot=plt)
         plt.grid()

         ax3 = plt.subplot(223)
         plt.scatter(test_fit, test_resid_stand)
         plt.title('Standard Residuals v Fitted Values')
         plt.xlabel('Fitted Values')
         plt.ylabel('Standard residuals')

         plt.grid()

         # plt.savefig('./images/fig_2_knn.png', transparent=True)
         plt.show()
```



```
In [11]: # a = list()
         # for i in range(5,80, 5):
         #     model_2 = KNeighborsRegressor(n_neighbors  = i,).fit(x,y)
         #     train_score = model_2.score(x, y)
         #     test_score = model_2.score(x_test, y_test)
         #     b = [i, train_score, test_score]
         #     a.append(b)
         #     print(i,train_score)
         #     print(i,test_score)

In [ ]:
```