MAT 602 - Final Project: Predicting Early Hospital Readmissions

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Due 3/6/17 by 6:00 PM EST

1. State the problem/area you will focus on for your final project.

- As a means to resolve hospital readmission rates, part of the Patient Protection and Affordable Care Act penalizes hospitals with excessive readmissions at 30 days through a program called the Hospital Readmission Reduction Program.
- As such, hospitals are scrambling to target the most at-risk patients and reduce their readmission rates in the most cost effective manner.
- In this work, I studied a dataset comprising of 100,000 total patients from 5 different hosptals. My problem comprises of a binary supervised learning task where based on the features of each patient, the goal is to predict where or not the patient was readmitted to the hospital.
- In addition, a search for the 3 most important features whose results dictate whether or not the patient will be reamitted to the hospital was implemented.

2. Dataset

• Here is the dataset that was studied for this work.

In [100]: import pandas as pd import numpy as np

Loading the dataset.

df = pd.read_csv('C:\\Users\\javyr\\Documents\\GitHub\\r-server-hospital-length-of-stay\\Data\\LengthOfStay.csv')

- # Creating a binary variable 'Readmission', which is constructed from the number of readmissions
- # 'rcount' by assigning the variable a value of '-1' when the corresponding patient was not # readmitted and '1' otherwise.
- df['Readmission'] = np.where(df['rcount']=='0', -1,1)

Display the dataset.

Out[100]:

May May	df																					
No. Control 1		е	eid	vdate	rcount	gender	dialysisrenalendstage	asthma	irondef	pneum	substancedependence	psychologicaldisordermajor		bloodureanitro	creatinine	bmi	pulse	respiration	secondarydiagnosisnonicd9	discharged facio	lengthofstay	Readmission
	0	1		8/29/2012	0	F	0	0	0	0	0	0		12.0	1.390722	30.432418	96	6.5	4	9/1/2012 B	3	-1
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C	3	4	ļ	8/9/2012	0	F	0	0	0	0	0	0		12.0	0.906862	27.959007	76	6.5	1	8/10/2012 A	1	-1
	4	5	5	12/20/2012	0	F	0	0	0	1	0	1		11.5	1.242854	30.258927	67	5.6	2	12/24/2012 E	4	-1
	5	6	6	11/27/2012	3	М	0	0	0	0	0	0		11.0	0.884663	27.875940	83	6.1	1	12/3/2012 B	6	1
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1	7	8	3	6/4/2012	0	F	0	0	0	0	0	1		11.0	0.768106	32.999171	63	6.0	3	6/7/2012 E	3	-1
	8	9)	7/5/2012	0	F	0	0	0	0	1	0		12.0	1.178786	28.802682	69	6.5	1	7/8/2012 E	3	-1
	9	1	10	9/1/2012	0	F	0	0	0	0	0	0		10.0	1.585072	32.503727	65	6.5	0	9/3/2012 E	2	-1
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	14	1	15	6/15/2012	1	F	0	0	0	0	0	0		12.0	1.050820	28.577796	69	6.5	1	6/17/2012 A	2	1
	15	1	16	3/14/2012	1	F	0	0	0	0	0	0		16.0	1.239281	30.639405	68	6.5	7	3/18/2012 C	4	1
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9995 9996 1/28/2012 3 M 0	999	93 9	99994	12/6/2012	2	F	0	0	0	0	0	0		7.0	0.914914	32.952413	66	4.8	1	12/12/2012 B	6	1
9995 9996 1/28/2012 3 M 0	999	94 9	9995	1/27/2012	4	F	0	0	0	0	0	0		12.0	1.446806	33.761061	65	6.5	9	2/2/2012 A	6	1
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100000 rows × 29 columns

• Here is a list of the features involved.

In [115]: df_features = pd.read_csv('C:\\Users\\javyr\\Documents\\GitHub\\r-server-hospital-length-of-stay\\Resources\\Data_Dictionary.csv') df_features

Out[115]:

	Index	Data fields	Туре	Descriptions
0	1	eid	Integer	Unique Id of the hospital admission
1	2	vdate	String	Visit date
2	3	rcount	Integer	Number of readmissions within last 180 days
3	4	gender	String	Gender of the patient\nM or F
4	5	dialysisrenalendstage	String	Flag for renal disease during encounter
5	6	asthma	String	Flag for asthma during encounter
6	7	irondef	String	Flag for iron deficiency during encounter
7	8	pneum	String	Flag for pneumonia during encounter
8	9	substancedependence	String	Flag for substance dependence during encounter
9	10	psychologicaldisordermajor	String	Flag for major psychological disorder during e
10	11	depress	String	Flag for depression during encounter
11	12	psychother	String	Flag for other psychological disorder during e
12	13	fibrosisandother	String	Flag for fibrosis during encounter
13	14	malnutrition	String	Flag for malnutrituion during encounter
14	15	hemo	Float	Flag for blood disorder during encounter
15	16	hematocritic	Float	Average hematocritic value during encounter (g
16	17	neutrophils	Float	Average neutrophils value during encounter (c
17	18	sodium	Float	Average sodium value during encounter (mmol/L)
18	19	glucose	Float	Average sodium value during encounter (mmol/L)
19	20	bloodureanitro	Float	Average blood urea nitrogen value during encou
20	21	creatinine	Float	Average creatinine value during encounter (mg/dL)
21	22	bmi	Float	Average BMI during encounter (kg/m2)
22	23	pulse	Float	Average pulse during encounter (beats/m)
23	24	respiration	Float	Average respiration during encounter (breaths
24	25	secondarydiagnosisnonicd9	Integer	Flag for whether a non ICD 9 formatted diagnos
25	26	discharged	String	Date of discharge
26	27	facid	Integer	Facility ID at which the encounter occurred
27	28	lengthofstay	Integer	Length of stay for the encounter

- Pre-processing: Since the features 'vdate', 'gender', 'discharged' and 'facid' consisted of string values, they were excluded from the list of features for the analysis. In addition, these points don't even relate to the health of the patient. Lastly, 'rcount' was removed since it was used to create 'Readmissions'.
- Data Source: https://github.com/Microsoft/r-server-hospital-length-of-stay/tree/master/Data (https://github.com/Microsoft/r-server-hospital-length-of-stay/tree/master/Data)
- Extra Source: http://www.sciencedirect.com/science/article/pii/S1532046415000969 (http://www.sciencedirect.com/science/article/pii/S1532046415000969)

```
3. Methods
  In [101]: # Features attributes included in the analysis.
             df_feature_names = ['eid', 'dialysisrenalendstage', 'asthma',
                    'irondef', 'pneum', 'substancedependence', 'psychologicaldisordermajor',
                    'depress', 'psychother', 'fibrosisandother', 'malnutrition', 'hemo',
                    'hematocrit', 'neutrophils', 'sodium', 'glucose', 'bloodureanitro',
                    'creatinine', 'bmi', 'pulse', 'respiration',
                    'secondarydiagnosisnonicd9', 'lengthofstay']
            # Separate the data from the target attributes.
            X = df.loc[:,df_feature_names].values
            y = df['Readmission'].values
  In [102]: # Used the 'train_test_split' function and set 'test_size' = 0.3 to randomly split 'X' and 'y' into separate training
             # and test datasets, where 70 percent of the samples were assigned to 'X_train' and 'y_train', and 30 percent to
            # 'X test' and 'y test', respectively.
             from sklearn.model_selection import train_test_split
            X_train,X_test,y_train,y_test = train_test_split(X,y,test_size = 0.30,random_state=0)
            print(X_train.shape,X_test.shape,y_train.shape,y_test.shape)
            (70000, 23) (30000, 23) (70000,) (30000,)
  In [103]: from sklearn.preprocessing import StandardScaler
             # Scaling the data using the 'StandardScaler'.
            stdsc = StandardScaler()
            X_train_std = stdsc.fit_transform(X_train)
            X_test_std = stdsc.transform(X_test)
 • Since this work deals with a binary classification problem, one of the most powerful approaches to tackle a problem such as this can be a logistic regression model.
 • Logistic regression is used to obtain odds ratio in the presence of more than one explanatory variable. The procedure is quite similar to multiple linear regression, with the exception that the response variable is binomial. The result is the impact of each variable on the odds ratio of the observed event of interest.
  In [117]: #from the linear_model module of sklearn import the LogisticRegression class
             from sklearn.linear_model import LogisticRegression
             #lr is an object from the LogisticRegression class
            lr = LogisticRegression()
             #fitting the model to the labeled training set
            #X_train: input data, y_train: target attribute (labels)
            modele = lr.fit(X_train_std,y_train)
            #the coefficients and the intercept
            print(modele.coef_,modele.intercept_)
            [[ 0.00192766 -0.15009026 -0.17327901 -0.25836592 -0.15103778 -0.25245198
               -0.61422537 -0.11266596 -0.19269591 -0.11242514 -0.12602399 -0.39091032
               -0.04083838 -0.11294494 -0.01100164 -0.01393363 -0.14508847 0.00313519
               0.00690782  0.00480912  0.00488537  0.01195433  2.57816064]] [-0.07136727]
  In [111]: #prediction on the test sample
            y_pred = modele.predict(X_test_std)
             #metrics - quantifying the quality of the prediction
             from sklearn import metrics
             #confusion matrix : comparing observed target values and predictions
            cm = metrics.confusion_matrix(y_test,y_pred)
            print("Confusion Matrix")
            print(cm)
             #accuracy rate
            acc = metrics.accuracy_score(y_test,y_pred)
            print("Accuracy Rate")
            print(acc) # 0.819 = (14488 + 10100)/ (14488 + 1889 + 3523 + 10100)
             #error rate
            err = 1.0 - acc
            print("Error Rate")
            print(err) # 0.180 = 1.0 - 0.819
            Confusion Matrix
             [[14488 1889]
              [ 3523 10100]]
```

- The goal of recursive feature elimination (RFE) is to select features by recursively considering smaller and smaller sets of features. • First, the estimator is trained on the initial set of features and weights are assigned to each one of them.
- Then, features whose absolute weights are the smallest are pruned from the current set features.

Accuracy Rate

0.8196 Error Rate 0.1804

• That procedure is recursively repeated on the pruned set until the desired number of features to select is eventually reached.

```
In [112]: from sklearn.feature_selection import RFE
          rfe = RFE(1r, 3)
          fit = rfe.fit(X_train_std,y_train)
          print ("Features sorted by their rank:")
          print (sorted(zip(map(lambda x: round(x, 4), fit.ranking_), df_feature_names)))
          Features sorted by their rank:
```

[(1, 'hemo'), (1, 'lengthofstay'), (1, 'psychologicaldisordermajor'), (2, 'irondef'), (3, 'psychother'), (4, 'substancedependence'), (6, 'asthma'), (7, 'pneum'), (8, 'dialysisrenalendstage'), (9, 'malnutrition'), (10, 'neutrophils'), (11, 'psychother'), (12, 'irondef'), (13, 'psychother'), (14, 'substancedependence'), (15, 'bloodureanitro'), (15, 'bloodureanitro'), (15, 'bloodureanitro'), (15, 'pneum'), (16, 'asthma'), (17, 'pneum'), (18, 'dialysisrenalendstage'), (19, 'malnutrition'), (19, 'neutrophils'), (19, 'malnutrition'), (19, 'malnutriti 'depress'), (12, 'fibrosisandother'), (13, 'hematocrit'), (14, 'glucose'), (15, 'secondarydiagnosisnonicd9'), (16, 'sodium'), (17, 'bmi'), (18, 'respiration'), (19, 'pulse'), (20, 'creatinine'), (21, 'eid')]

• From the results of RFE, the 3 most important features are: 1) hemo - blood disorder 2) lengthofstay - length of stay for the encounter 3) psychological disorder major psychological disorder

```
In [113]: #prediction on the test sample
y_pred = fit.predict(X_test_std)

metrics - quantifying the quality of the prediction
from sklearm import metrics

#confusion metrix - comporing observed target values and predictions
cm = metrics.confusion_metrix(Y_test,y_pred)
print("confusion Matrix")
print(can)
#accuracy rate
acc = metrics.acuracy_score(y_test,y_pred)
print("Accuracy Nate")
print("Accuracy Nate")
print("Error Rate")
print("Error Ra
```

• Based on the results, we can conclude that the logistic regression model can be a good model candidate to implement in problems such as this one in order to obtain high accuracy, which leads to a low error rate.

Error Rate 0.192433333333