

# cs109a\_MS3\_EDA

October 31, 2023

## 1 cs109a Final Project Milestone 3: EDA

```
[1]: # Import libraries
import os
import time
import numpy as np
import pandas as pd
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
from sklearn.impute import SimpleImputer, KNNImputer
from sklearn.linear_model import LinearRegression, LogisticRegression, \
    LogisticRegressionCV
from sklearn.neighbors import KNeighborsRegressor
from sklearn.model_selection import train_test_split, cross_validate
from sklearn.metrics import r2_score, confusion_matrix, classification_report, \
    roc_curve
from sklearn.metrics import roc_auc_score, precision_recall_curve, \
    average_precision_score
import warnings
warnings.filterwarnings("ignore")
plt.style.use('seaborn-notebook')
sns.set_style('darkgrid')
# pandas tricks for better display
pd.options.display.max_columns = 50
pd.options.display.max_rows = 500
pd.options.display.max_colwidth = 100
pd.options.display.precision = 3
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[2]: # helper functions

def visualize_missingness(df, figsize=(6, 7)):
    # calculate missing data percentages
    missing_data_percentage = (df.isnull().sum() / len(df)) * 100
    # sort by percentage
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    missing_data_percentage = missing_data_percentage.
↪sort_values(ascending=True)
    # visualize using horizontal barplot
    plt.figure(figsize=figsize)
    missing_data_percentage.plot(kind='barh')
    plt.title('Percentage of Missing Data by Column')
    plt.xlabel('Percentage Missing (%)')
    plt.ylabel('Columns')
    plt.show()

def visualize_class_imbalance(df, target_col, figsize=(5, 2)):
    # Visualize class imbalance
    plt.figure(figsize=figsize)
    df[target_col].value_counts().plot(kind='barh')
    plt.title('Class Distribution')
    plt.ylabel('Class Label')
    plt.xlabel('Number of Samples')
    plt.show()

def missing_values_table(df):
    # count the missing values for each column
    missing_values = df.isnull().sum()
    # calculate the percentage of missing values
    missing_percentage = (100 * df.isnull().sum() / len(df))
    # create a table with the results
    missing_values_table = pd.concat([missing_values, missing_percentage],
↪axis=1)
    # rename the columns
    missing_values_table.columns = missing_values_table.rename(
        columns = {0 : 'Missing Values', 1 : '% of Total Values'})
    # sort the table by percentage of missing in descending order
    missing_values_table.columns = missing_values_table.columns[
        missing_values_table.columns.iloc[:,1] != 0].sort_values(
        '% of Total Values', ascending=False).round(1)
    # print a summary
    print("Your selected dataframe has " + str(df.shape[1]) + " columns.\n"
          "There are " + str(missing_values_table.columns.shape[0]) +
          " columns that have missing values.")
    # return the dataframe with missing info
    return missing_values_table.columns

def handle_missing_data(df):
    # keep track of the original columns
    original_columns = df.columns.tolist()
    # create dummy columns only for columns with missing data
    for col in original_columns:
        if df[col].isna().any():

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        df[col + "_is_missing"] = df[col].isna().astype(int)
    # define imputers
    numeric_imputer = SimpleImputer(strategy='median')
    categorical_imputer = SimpleImputer(strategy='most_frequent')
    # impute median values for numeric columns and most frequent value for
    ↪non-numeric columns
    for col in original_columns:
        if df[col].dtype in [np.float64, np.int64]:
            df[col] = numeric_imputer.fit_transform(df[[col]]).flatten()
        else:
            df[col] = categorical_imputer.fit_transform(df[[col]]).flatten()
    return df

def scale_data(df, columns_to_scale):
    scaler = StandardScaler()
    df[columns_to_scale] = scaler.fit_transform(df[columns_to_scale])
    return df

```

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[3]: # load data
df = pd.read_csv('../data/diabetic_data.csv', na_values='?')

# examine first 5 rows of dataframe
print(f'Shape of diabetic data: {df.shape}')
display(df.head())

```

Shape of diabetic data: (101766, 50)

	encounter_id	patient_nbr	race	gender	age	weight	\
0	2278392	8222157	Caucasian	Female	[0-10)	NaN	
1	149190	55629189	Caucasian	Female	[10-20)	NaN	
2	64410	86047875	AfricanAmerican	Female	[20-30)	NaN	
3	500364	82442376	Caucasian	Male	[30-40)	NaN	
4	16680	42519267	Caucasian	Male	[40-50)	NaN	

	admission_type_id	discharge_disposition_id	admission_source_id	\
0	6	25	1	
1	1	1	7	
2	1	1	7	
3	1	1	7	
4	1	1	7	

	time_in_hospital	payer_code	medical_specialty	num_lab_procedures	\
0	1	NaN	Pediatrics-Endocrinology	41	
1	3	NaN	NaN	59	
2	2	NaN	NaN	11	
3	2	NaN	NaN	44	
4	1	NaN	NaN	51	

	num_procedures	num_medications	number_outpatient	number_emergency	\
0	0	1	0	0	
1	0	18	0	0	
2	5	13	2	0	
3	1	16	0	0	
4	0	8	0	0	

	number_inpatient	diag_1	diag_2	diag_3	number_diagnoses	max_glu_serum	\
0	0	250.83	NaN	NaN	1	NaN	
1	0	276	250.01	255	9	NaN	
2	1	648	250	V27	6	NaN	
3	0	8	250.43	403	7	NaN	
4	0	197	157	250	5	NaN	

	A1Cresult	metformin	repaglinide	nateglinide	chlorpropamide	glimepiride	\
0	NaN	No	No	No	No	No	
1	NaN	No	No	No	No	No	
2	NaN	No	No	No	No	No	
3	NaN	No	No	No	No	No	
4	NaN	No	No	No	No	No	

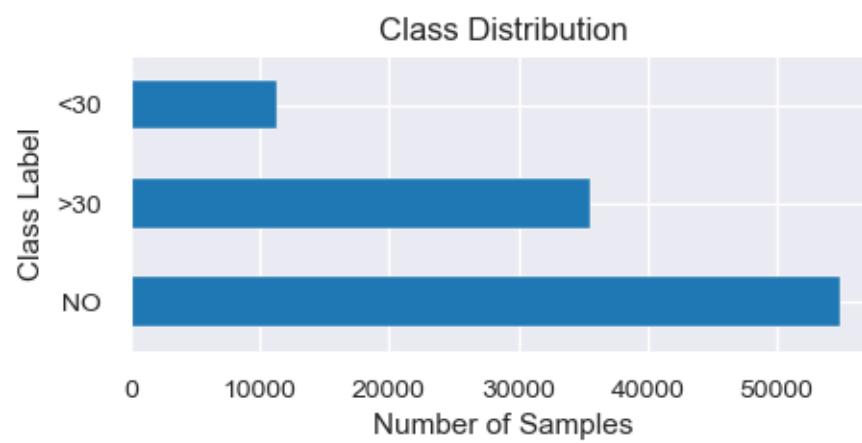
	acetohexamide	glipizide	glyburide	tolbutamide	pioglitazone	rosiglitazone	\
0	No	No	No	No	No	No	
1	No	No	No	No	No	No	
2	No	Steady	No	No	No	No	
3	No	No	No	No	No	No	
4	No	Steady	No	No	No	No	

	acarbose	miglitol	troglitazone	tolazamide	examide	citoglipton	insulin	\
0	No	No	No	No	No	No	No	
1	No	No	No	No	No	No	Up	
2	No	No	No	No	No	No	No	
3	No	No	No	No	No	No	Up	
4	No	No	No	No	No	No	Steady	

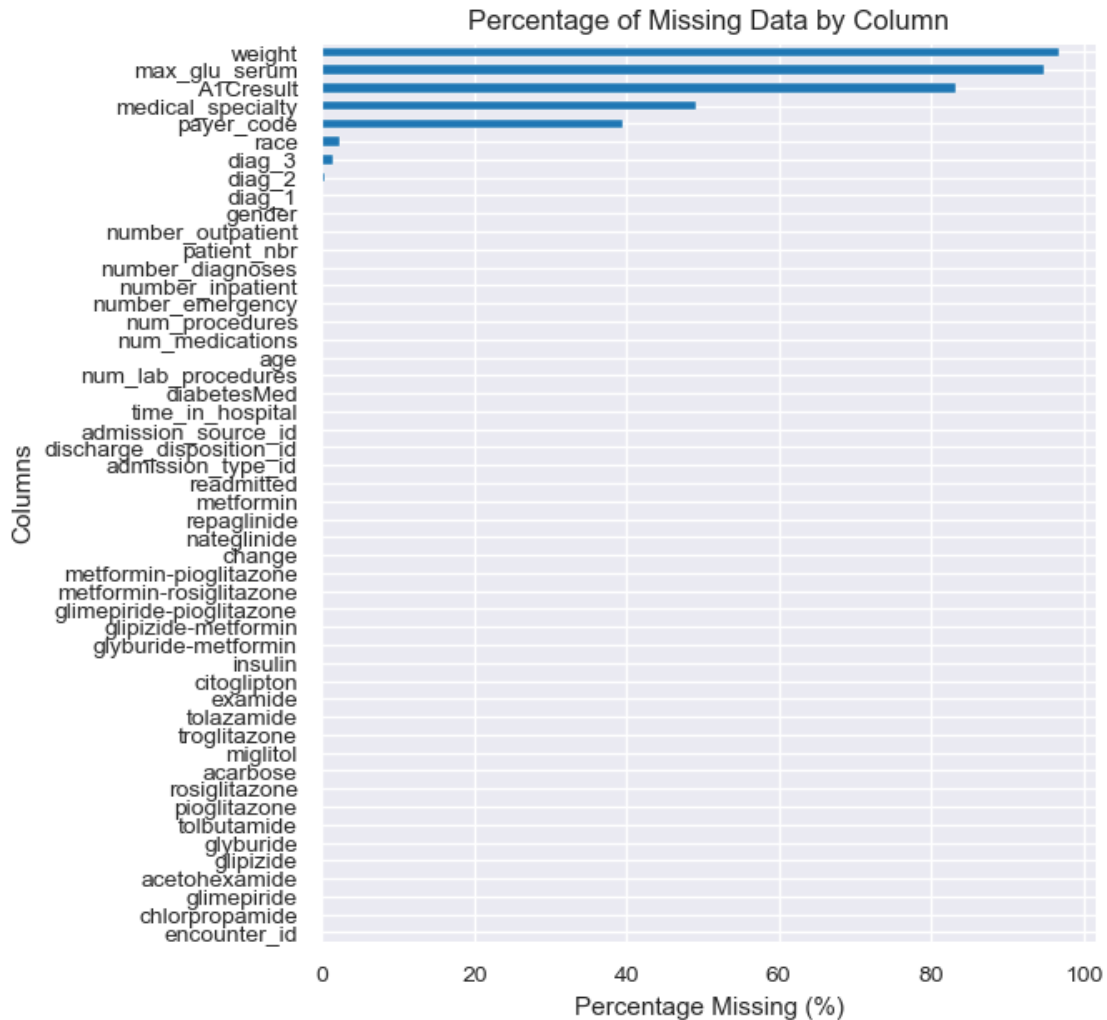
	glyburide-metformin	glipizide-metformin	glimepiride-pioglitazone	\
0	No	No	No	
1	No	No	No	
2	No	No	No	
3	No	No	No	
4	No	No	No	

	metformin-rosiglitazone	metformin-pioglitazone	change	diabetesMed	readmitted
0	No	No	No	No	NO
1	No	No	Ch	Yes	>30
2	No	No	No	Yes	NO
3	No	No	Ch	Yes	NO
4	No	No	Ch	Yes	NO

```
[4]: # class imbalance
visualize_class_imbalance(df, target_col='readmitted')
```



```
[5]: # visualize missingness
visualize_missingness(df)
```



```
[6]: # missing values table
missing_values_table(df)
```

Your selected dataframe has 50 columns.  
There are 9 columns that have missing values.

```
[6]:
```

	Missing Values	% of Total Values
weight	98569	96.9
max_glu_serum	96420	94.7
A1Cresult	84748	83.3
medical_specialty	49949	49.1
payer_code	40256	39.6
race	2273	2.2
diag_3	1423	1.4
diag_2	358	0.4

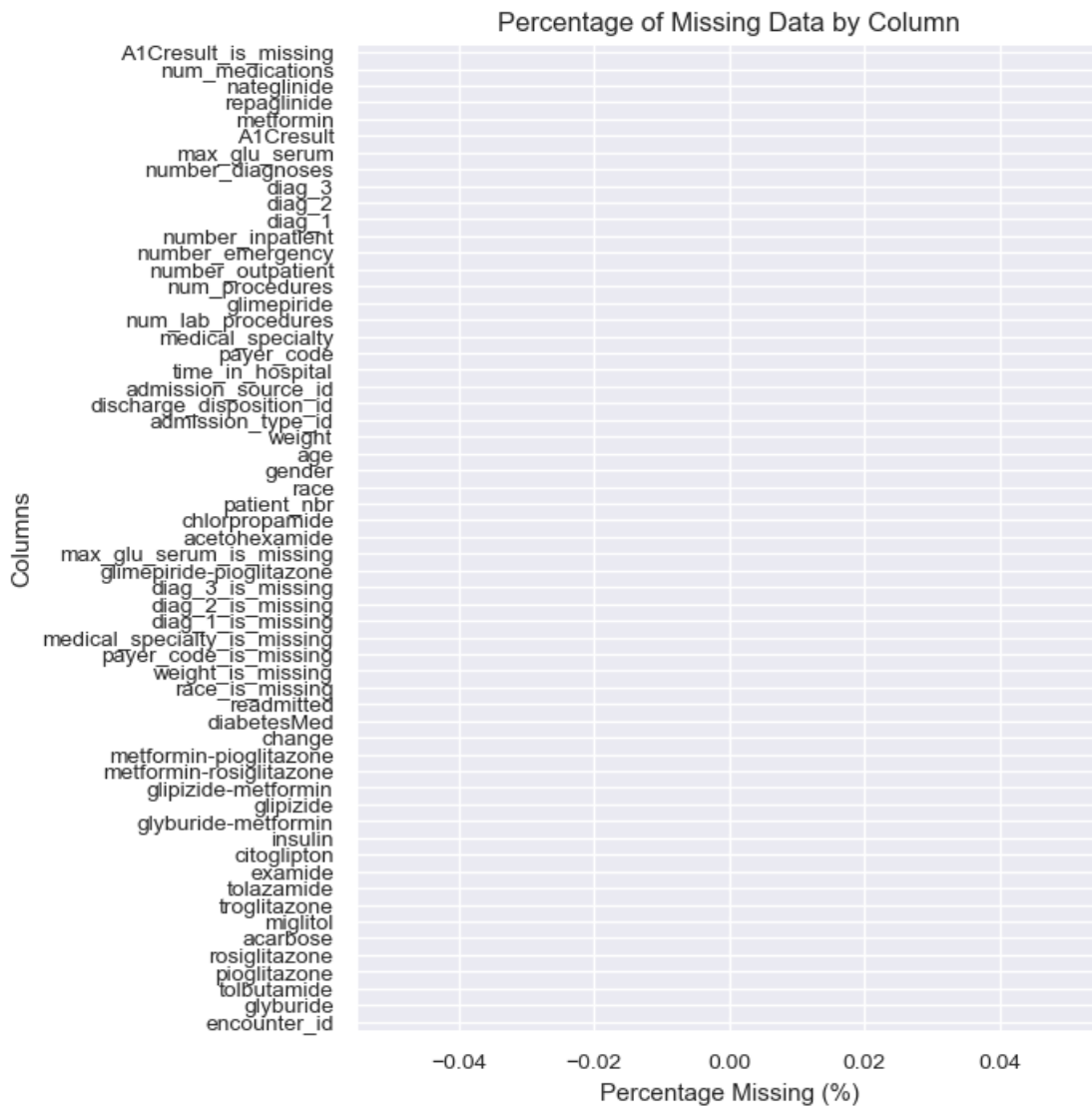
diag\_1

21

0.0

```
[7]: # deal with missing data
df_imp = handle_missing_data(df)
```

```
[8]: # look at imputed data
visualize_missingness(df_imp, figsize=(6, 8))
```



```
[9]: # standardize data
df_std = scale_data(df_imp, ['time_in_hospital'])
df_std.head()
```

```

[9]:  encounter_id  patient_nbr          race  gender    age    weight \
0      2.278e+06   8.222e+06      Caucasian  Female  [0-10)  [75-100)
1      1.492e+05   5.563e+07      Caucasian  Female  [10-20)  [75-100)
2      6.441e+04   8.605e+07 AfricanAmerican  Female  [20-30)  [75-100)
3      5.004e+05   8.244e+07      Caucasian   Male  [30-40)  [75-100)
4      1.668e+04   4.252e+07      Caucasian   Male  [40-50)  [75-100)

      admission_type_id  discharge_disposition_id  admission_source_id \
0                6.0                25.0                1.0
1                1.0                1.0                7.0
2                1.0                1.0                7.0
3                1.0                1.0                7.0
4                1.0                1.0                7.0

      time_in_hospital  payer_code          medical_specialty  num_lab_procedures \
0          -1.138         MC  Pediatrics-Endocrinology          41.0
1          -0.468         MC          InternalMedicine          59.0
2          -0.803         MC          InternalMedicine          11.0
3          -0.803         MC          InternalMedicine          44.0
4          -1.138         MC          InternalMedicine          51.0

      num_procedures  num_medications  number_outpatient  number_emergency \
0                0.0                1.0                0.0                0.0
1                0.0               18.0                0.0                0.0
2                5.0               13.0                2.0                0.0
3                1.0               16.0                0.0                0.0
4                0.0                8.0                0.0                0.0

      number_inpatient  diag_1  diag_2  diag_3  number_diagnoses  max_glu_serum \
0                0.0  250.83    276    250                1.0      Norm
1                0.0    276  250.01    255                9.0      Norm
2                1.0   648    250   V27                6.0      Norm
3                0.0     8  250.43   403                7.0      Norm
4                0.0   197   157    250                5.0      Norm

      A1Cresult  metformin  ...  rosiglitazone  acarbose  miglitol  troglitazone \
0          >8        No  ...          No        No        No        No
1          >8        No  ...          No        No        No        No
2          >8        No  ...          No        No        No        No
3          >8        No  ...          No        No        No        No
4          >8        No  ...          No        No        No        No

      tolazamide  examide  citoglipton  insulin  glyburide-metformin \
0          No        No        No        No        No
1          No        No        No        Up        No
2          No        No        No        No        No
3          No        No        No        Up        No

```



4	No	No	No	Steady	No
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	glipizide-metformin	glimepiride-pioglitazone	metformin-rosiglitazone	\
0	No	No	No	
1	No	No	No	
2	No	No	No	
3	No	No	No	
4	No	No	No	

	metformin-pioglitazone	change	diabetesMed	readmitted	race_is_missing	\
0	No	No	No	NO	0	
1	No	Ch	Yes	>30	0	
2	No	No	Yes	NO	0	
3	No	Ch	Yes	NO	0	
4	No	Ch	Yes	NO	0	

	weight_is_missing	payer_code_is_missing	medical_specialty_is_missing	\
0	1	1	0	
1	1	1	1	
2	1	1	1	
3	1	1	1	
4	1	1	1	

	diag_1_is_missing	diag_2_is_missing	diag_3_is_missing	\
0	0	1	1	
1	0	0	0	
2	0	0	0	
3	0	0	0	
4	0	0	0	

	max_glu_serum_is_missing	A1Cresult_is_missing
0	1	1
1	1	1
2	1	1
3	1	1
4	1	1

[5 rows x 59 columns]

[ ]: