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**Roll no - 50**

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| Experiment No.1   |
| Collect, Clean, Integrate and Transform Healthcare Data based on specific disease |
| Date of Performance: 4/8/2023   |
| Date of Submission: 11/8/2023   |

**Aim:** Collect, Clean, Integrate and Transform Healthcare Data based on specific disease

**Objective:** The objective of this experiment is to perform basic pre processing on healthcare data set using python libraries

**Theory:**

Data Collection- Data collection is the process of gathering and measuring information from countless different sources. In order to use the data we collect to develop practical artificial intelligence (AI) and machine learning solutions, it must be collected and stored in a way that makes sense for the business problem at hand.

Data Cleaning: Cleaning data refers to the way of deleting wrong, corrupted, wrongly formatted, duplicate information, or incomplete information from a dataset. The possibility of duplicating or mislabelling data increases when two or more data sources are combined.

Data Integration: Data integration is the practice of consolidating data from disparate sources into a single dataset with the ultimate goal of providing users with consistent access and delivery of data across the spectrum of subjects and structure types, and to meet the information needs of all applications and business processes.

Data transformation: Data transformation is the process of converting, cleansing, and structuring data into a usable format that can be analyzed to support decision making processes, and to propel the growth of an organization. Data transformation is used when data needs to be converted to match that of the destination system.



Code: -

```
[9] # import the pandas library
import pandas as pd
import numpy as np
from sklearn.preprocessing import OneHotEncoder

[10] # read csv
df = pd.read_csv("diabetes_prediction_dataset.csv")

[11]
# To print no. of samples and attributes
print(df.shape)

(100000, 9)

[12] # getting the columns of the dataset
columns = list(df.columns)
print(columns)

['gender', 'age', 'hypertension', 'heart_disease', 'smoking_history', 'bmi', 'HbA1c_level', 'blood_glucose_level', 'diabetes']

[13] # To print first five samples
print(df.head())
```

|   | gender | age  | hypertension | heart_disease | smoking_history | bmi   | \ |
|---|--------|------|--------------|---------------|-----------------|-------|---|
| 0 | Female | 80.0 | 0            | 1             | never           | 25.19 |   |
| 1 | Female | 54.0 | 0            | 0             | No Info         | 27.32 |   |
| 2 | Male   | 28.0 | 0            | 0             | never           | 27.32 |   |
| 3 | Female | 36.0 | 0            | 0             | current         | 23.45 |   |
| 4 | Male   | 76.0 | 1            | 1             | current         | 20.14 |   |

  

|   | HbA1c_level | blood_glucose_level | diabetes |
|---|-------------|---------------------|----------|
| 0 | 6.6         | 140                 | 0        |
| 1 | 6.6         | 80                  | 0        |
| 2 | 5.7         | 158                 | 0        |
| 3 | 5.0         | 155                 | 0        |
| 4 | 4.8         | 155                 | 0        |



```
✓ 0s ▶ #New dataframe
new_df = df
#new_df.isnull()
#Checking for null values
print(new_df.isnull().sum())
print("Missing values distribution: ")
print(new_df.isnull().mean())
#print(new_df.shape)
#new_df.duplicated()
```

  

```
↳ gender          0
age              0
hypertension     0
heart_disease    0
smoking_history  0
bmi             0
HbA1c_level      0
blood_glucose_level 0
diabetes         0
dtype: int64
Missing values distribution:
gender          0.0
age            0.0
hypertension    0.0
heart_disease   0.0
smoking_history 0.0
bmi            0.0
HbA1c_level     0.0
blood_glucose_level 0.0
diabetes        0.0
dtype: float64
```



```
0s ✓ #Checking for duplicates
print(new_df.duplicated().any())
print(new_df.duplicated())
print(new_df.shape)

[ ] True
0      False
1      False
2      False
3      False
4      False
...
99995   True
99996   False
99997   False
99998   False
99999   False
Length: 100000, dtype: bool
(100000, 9)

0s ✓ [16] df['gender'].value_counts()
      df['heart_disease'].value_counts()

0      96058
1       3942
Name: heart_disease, dtype: int64
```

```
0s ✓ [19] print(df['gender'].unique())
      print(df['heart_disease'].unique())

['Female' 'Male' 'Other']
[1 0]

0s ✓ [20] print(df['heart_disease'].unique())

[1 0]
```



```
one_hot_encoded_data = pd.get_dummies(df, columns = ['gender', 'heart_disease'])
print(one_hot_encoded_data)
```

|       | age  | hypertension | smoking_history | bmi   | HbA1c_level | \   |
|-------|------|--------------|-----------------|-------|-------------|-----|
| 0     | 80.0 | 0            | never           | 25.19 | 6.6         |     |
| 1     | 54.0 | 0            | No Info         | 27.32 | 6.6         |     |
| 2     | 28.0 | 0            | never           | 27.32 | 5.7         |     |
| 3     | 36.0 | 0            | current         | 23.45 | 5.0         |     |
| 4     | 76.0 | 1            | current         | 20.14 | 4.8         |     |
| ...   | ...  | ...          | ...             | ...   | ...         | ... |
| 99995 | 80.0 | 0            | No Info         | 27.32 | 6.2         |     |
| 99996 | 2.0  | 0            | No Info         | 17.37 | 6.5         |     |
| 99997 | 66.0 | 0            | former          | 27.83 | 5.7         |     |
| 99998 | 24.0 | 0            | never           | 35.42 | 4.0         |     |
| 99999 | 57.0 | 0            | current         | 22.43 | 6.6         |     |

  

|       | blood_glucose_level | diabetes | gender_Female | gender_Male | \   |
|-------|---------------------|----------|---------------|-------------|-----|
| 0     | 140                 | 0        | 1             | 0           |     |
| 1     | 80                  | 0        | 1             | 0           |     |
| 2     | 158                 | 0        | 0             | 1           |     |
| 3     | 155                 | 0        | 1             | 0           |     |
| 4     | 155                 | 0        | 0             | 1           |     |
| ...   | ...                 | ...      | ...           | ...         | ... |
| 99995 | 90                  | 0        | 1             | 0           |     |
| 99996 | 100                 | 0        | 1             | 0           |     |
| 99997 | 155                 | 0        | 0             | 1           |     |
| 99998 | 100                 | 0        | 1             | 0           |     |
| 99999 | 90                  | 0        | 1             | 0           |     |

  

|       | gender_Other | heart_disease_0 | heart_disease_1 |
|-------|--------------|-----------------|-----------------|
| 0     | 0            | 0               | 1               |
| 1     | 0            | 1               | 0               |
| 2     | 0            | 1               | 0               |
| 3     | 0            | 1               | 0               |
| 4     | 0            | 0               | 1               |
| ...   | ...          | ...             | ...             |
| 99995 | 0            | 1               | 0               |
| 99996 | 0            | 1               | 0               |
| 99997 | 0            | 1               | 0               |
| 99998 | 0            | 1               | 0               |
| 99999 | 0            | 1               | 0               |

[100000 rows x 12 columns]

Google Collaboratory Link: -

AIMLE1.ipynb

**Conclusion:** - Thus, we have successfully Collected, Cleaned, Integrated and Transformed our healthcare data.