Healthcare Data Cleaning for Disease Prediction Accuracy

Title:
Healthcare Data Cleaning: Improving Disease Prediction Accuracy by Handling Missing, Inconsistent, and Noisy Patient Data

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2. Introduction

In healthcare, accurate disease prediction is crucial for improving patient care and outcomes. However, the data used to

predict diseases often contains missing, inconsistent, or noisy values. Such issues can adversely affect the performance of prediction models. The purpose of this project is to improve disease prediction accuracy by effectively handling missing, inconsistent, and noisy data in a healthcare dataset.

Data cleaning is a crucial preprocessing step in machine learning workflows. By applying data cleaning techniques such as imputation of missing values, correcting inconsistent data, and reducing noise, we can ensure that the dataset is accurate, consistent, and ready for modeling. This report outlines the methodology for cleaning the dataset and presents the outcomes of the data cleaning process.

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3. Methodology

The methodology followed in this project involves the following steps:

Step 1: Data Collection

A dummy healthcare dataset was created to simulate real-world healthcare data. This dataset includes patient information such as age, blood pressure, cholesterol levels, presence of symptoms, and disease outcomes (whether the patient has a disease or not).

Step 2: Data Cleaning

The dataset was cleaned by performing the following tasks:

1. Handling Missing Data:
    - Numerical columns (age, blood pressure, cholesterol) with missing values were imputed using the median value.

- Categorical columns (symptom) with missing values were imputed using the most frequent value.

2. Data Encoding:
   - The categorical column 'symptom' was encoded using LabelEncoder, converting values such as 'Y' and 'N' to numerical values (1 and 0).

Step 3: Data Analysis and Visualization

After cleaning the data, several visualizations were created to gain insights into the distribution of the data and potential patterns:

- Histograms for numerical columns (e.g., age, blood pressure, cholesterol).
- Bar plot to show the distribution of disease outcomes.
- Box plots to observe the spread and outliers of numerical data.

- Pair plots to analyze relationships between different variables in the dataset.

Step 4: Implementation

The data cleaning process was implemented using Python, specifically with the following libraries:

- Pandas for data manipulation.
- NumPy for handling missing values (np.nan).
- Scikit-learn for imputation (SimpleImputer) and encoding (LabelEncoder).
- Matplotlib and Seaborn for data visualization.

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4. Code Typed

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

```
import seaborn as sns
from sklearn.impute import
SimpleImputer # Importing
SimpleImputer

# Create a dummy dataset
data = {
    'age': [25, 30, 35, 40, 45, 50, np.nan,
60, 65, 70],
    'blood_pressure': [120, 130, 140, 150,
np.nan, 160, 170, 180, 190, 200],
    'cholesterol': [200, 220, 240, 250, 260,
270, 280, 290, np.nan, 310],
    'symptom': ['Y', 'N', 'Y', 'Y', 'N', 'Y', 'Y', 'N',
np.nan, 'Y'],
    'disease_outcome': [0, 1, 0, 1, 0, 1, 1, 0,
1, 0]  # 0 = No disease, 1 = Disease
}

# Create a DataFrame
```

```
df = pd.DataFrame(data)

# Save the dummy data to a CSV file
df.to_csv('healthcare_data.csv',
index=False)

# Preview the dataset
print(df)

# Data Cleaning: Handling missing values
(as shown in the previous code)
# Impute numerical columns with the
median value
numerical_cols =
df.select_dtypes(include=[np.number]).co
lumns
imputer_num =
SimpleImputer(strategy='median') # Use
SimpleImputer to handle missing data
```

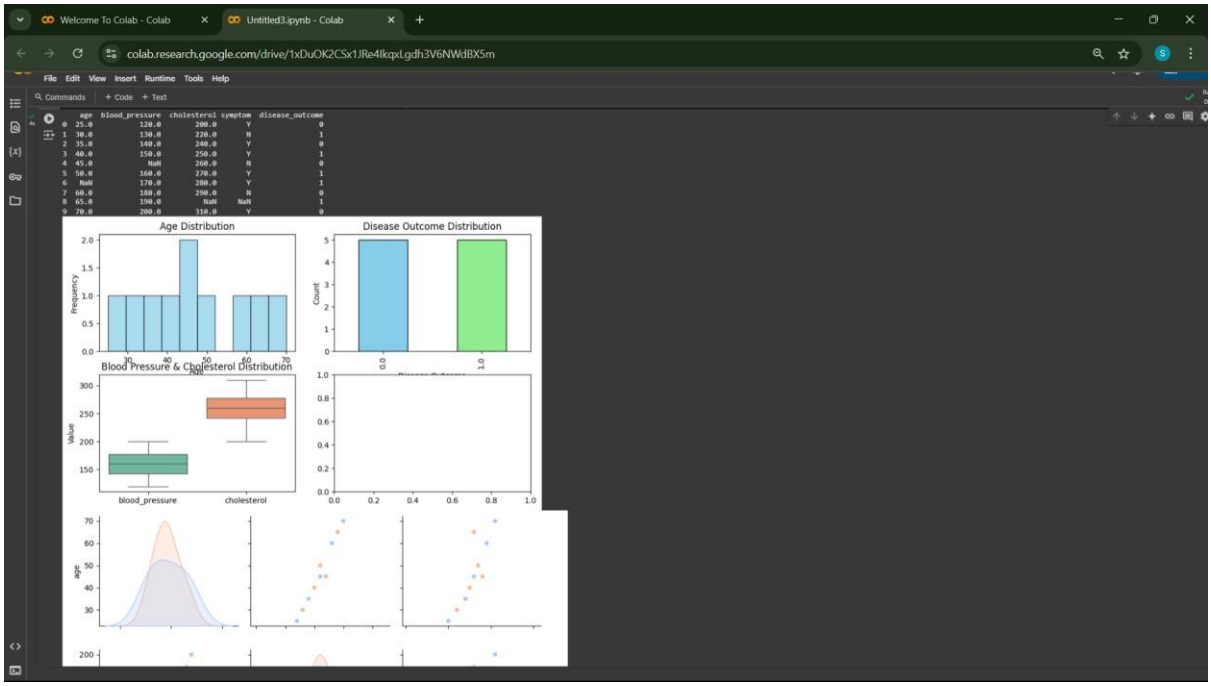
```
df[numerical_cols] =
imputer_num.fit_transform(df[numerical
_cols])

# Impute categorical columns with the
most frequent value (mode)
categorical_cols =
df.select_dtypes(include=[object]).colum
ns
imputer_cat =
SimpleImputer(strategy='most_frequent')
df[categorical_cols] =
imputer_cat.fit_transform(df[categorical_
cols])

# Encoding Categorical Data
from sklearn.preprocessing import
LabelEncoder # Importing LabelEncoder
for encoding categorical data
```

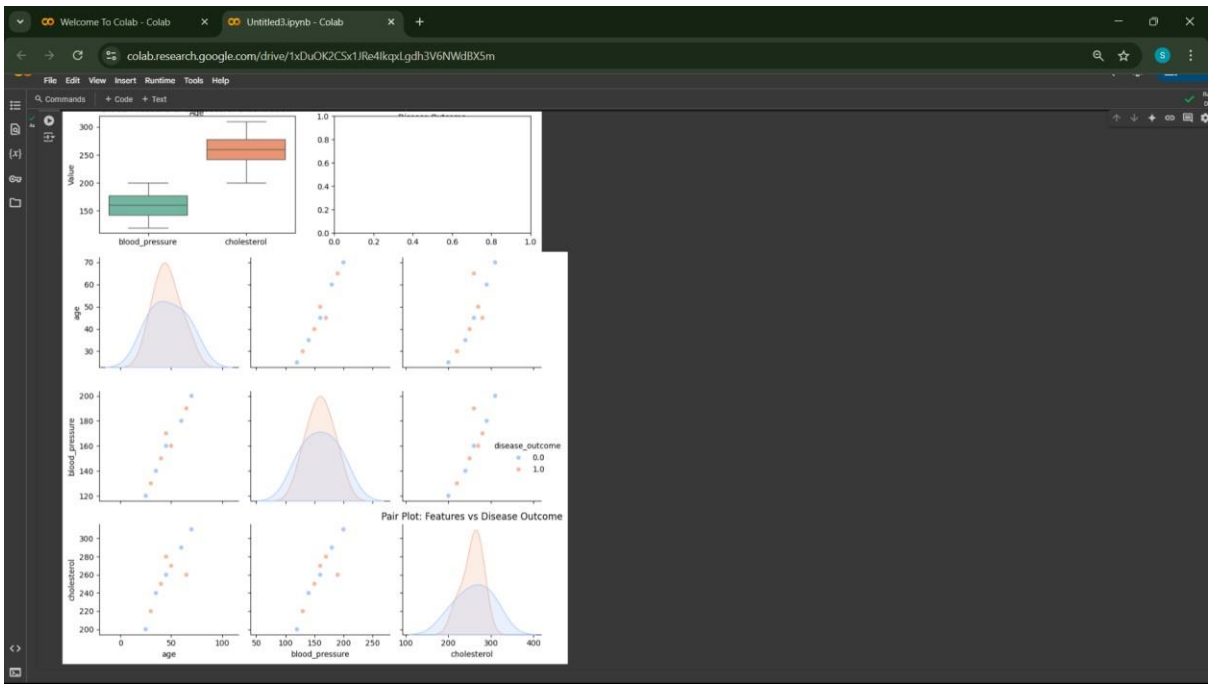
```
encoder = LabelEncoder()
for col in categorical_cols:
    df[col] = encoder.fit_transform(df[col])

# Now we can create figures to visualize
the cleaned dataset.

# Set up the plotting environment
plt.figure(figsize=(10, 6))

# 1. Histogram of numerical columns
plt.subplot(2, 2, 1) # 2 rows, 2 columns,
1st plot
df['age'].plot(kind='hist', bins=10,
color='skyblue', edgecolor='black',
alpha=0.7)
plt.title('Age Distribution')
plt.xlabel('Age')
plt.ylabel('Frequency')
```

```
# 2. Bar plot of disease_outcome distribution
plt.subplot(2, 2, 2) # 2 rows, 2 columns, 2nd plot
df['disease_outcome'].value_counts().plot(kind='bar', color=['skyblue', 'lightgreen'], edgecolor='black')
plt.title('Disease Outcome Distribution')
plt.xlabel('Disease Outcome')
plt.ylabel('Count')

# 3. Box plot of blood_pressure and cholesterol
plt.subplot(2, 2, 3) # 2 rows, 2 columns, 3rd plot
sns.boxplot(data=df[['blood_pressure', 'cholesterol']], palette='Set2')
plt.title('Blood Pressure & Cholesterol Distribution')
plt.ylabel('Value')
```

```
# 4. Pair plot to visualize relationships between variables
plt.subplot(2, 2, 4) # 2 rows, 2 columns, 4th plot
sns.pairplot(df[['age', 'blood_pressure', 'cholesterol', 'disease_outcome']], hue='disease_outcome', palette='coolwarm')
plt.title('Pair Plot: Features vs Disease Outcome')

# Adjust layout for better spacing
plt.tight_layout()

# Show all the plots
plt.show()
```

5. Screenshots / Output Photos


Welcome To Colab - Colab
Untitled3.ipynb - Colab
colab.research.google.com/drive/1xDuOK2CSx1JRe4lkqxLgdh3V6NWdBX5m
File Edit View Insert Runtime Tools Help
Commands + Code + Text
age blood_pressure cholesterol symptom disease_outcome
0 25.0 120.0 200.0 Y 0
1 30.0 130.0 220.0 N 1
2 35.0 140.0 240.0 Y 0
3 40.0 150.0 250.0 Y 1
4 45.0 NaN 260.0 N 0
5 50.0 160.0 270.0 Y 1
6 NaN 170.0 280.0 Y 1
7 60.0 180.0 290.0 N 0
8 65.0 190.0 NaN NaN 1
9 70.0 200.0 310.0 Y 0
Age Distribution
Frequency
Disease Outcome Distribution
Count
Blood Pressure & Cholesterol Distribution
Value
blood_pressure
cholesterol
age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Value
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0.0
1.0
Pair Plot: Features vs Disease Outcome
age
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cholesterol