Drug Classification Dataset

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The porpuse of the following notebook is get started and familiar with the Drug Classification Dataset

DataSet Access

```
# Install dependencies as needed:
# pip install kagglehub[pandas-datasets]
import kagglehub
from kagglehub import KaggleDatasetAdapter
# Set the path to the file you'd like to load
file_path = "drug200.csv"
# Load the latest version
df = kagglehub.load_dataset(
 KaggleDatasetAdapter.PANDAS,
  "prathamtripathi/drug-classification",
 file_path,
 # Provide any additional arguments like
 # sql_query or pandas_kwargs. See the
 # documenation for more information:
  {\tt\#\ https://github.com/Kaggle/kagglehub/blob/main/README.md\#kaggledatasetadapterpandas}
🛨 /tmp/ipython-input-3788353275.py:10: DeprecationWarning: load_dataset is deprecated and will be removed in a future version.
       df = kagglehub.load_dataset(
```

Kwnowing the Dataset

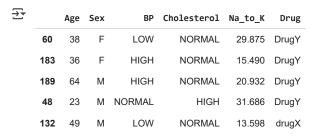
The first 5 entries are showed

df.head()

_		Age	Sex	ВР	Cholesterol	Na_to_K	Drug
	0	23	F	HIGH	HIGH	25.355	DrugY
	1	47	М	LOW	HIGH	13.093	drugC
	2	47	М	LOW	HIGH	10.114	drugC
	3	28	F	NORMAL	HIGH	7.798	drugX
	4	61	F	LOW	HIGH	18.043	DrugY

df.tail()

_ *		Age	Sex	ВР	Cholesterol	Na_to_K	Drug
	195	56	F	LOW	HIGH	11.567	drugC
	196	16	М	LOW	HIGH	12.006	drugC
	197	52	М	NORMAL	HIGH	9.894	drugX
	198	23	М	NORMAL	NORMAL	14.020	drugX
	199	40	F	LOW	NORMAL	11.349	drugX



Column Description

Target Column

Drug Type

Drug applied to the Patient

→ Features Columns

Age

Age of the Patient (Numeric)

Sex

Sex of the Patient (F: Femenine, M: Masculine)

BP (Bload Pressure Levels)

Bload Pressure Level of the Patient (LOW, NORMAL, HIGH)

Cholesterol

Cholesterol Level of the Patient (LOW, NORMAL, HIGH)

Na_to_K (Na to Potassium Ration)

Amount of sodium (Na) to potassium (K) in the Patient bload

Basic Overview of the Dataset

df.info()

```
<<class 'pandas.core.frame.DataFrame'>
    RangeIndex: 200 entries, 0 to 199
    Data columns (total 6 columns):
     # Column
                     Non-Null Count Dtype
     0 Age
                     200 non-null
                     200 non-null
                                    object
     1 Sex
                     200 non-null
                                    object
        Cholesterol 200 non-null
                                    object
                     200 non-null
                                    float64
        Na_to_K
     5 Drug
                     200 non-null
                                    object
    dtypes: float64(1), int64(1), object(4)
    memory usage: 9.5+ KB
```

Data statistics

df.describe(include='all')

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-	→	4

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
count	200.000000	200	200	200	200.000000	200
unique	NaN	2	3	2	NaN	5
top	NaN	М	HIGH	HIGH	NaN	DrugY
freq	NaN	104	77	103	NaN	91
mean	44.315000	NaN	NaN	NaN	16.084485	NaN
std	16.544315	NaN	NaN	NaN	7.223956	NaN
min	15.000000	NaN	NaN	NaN	6.269000	NaN
25%	31.000000	NaN	NaN	NaN	10.445500	NaN
50%	45.000000	NaN	NaN	NaN	13.936500	NaN
75%	58.000000	NaN	NaN	NaN	19.380000	NaN
max	74.000000	NaN	NaN	NaN	38.247000	NaN

print("\nMissing value:\n", df.isna().sum())



```
Missing value:
Age 0
Sex 0
BP 0
Cholesterol 0
Na_to_K 0
Drug 0
dtype: int64
```

df.duplicated().sum()

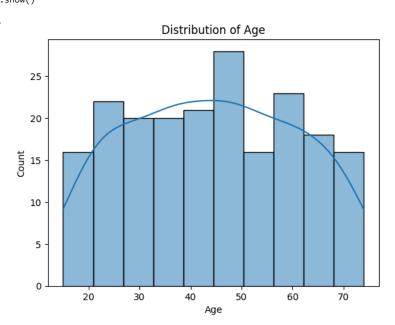
→ np.int64(0)

Age Distribution

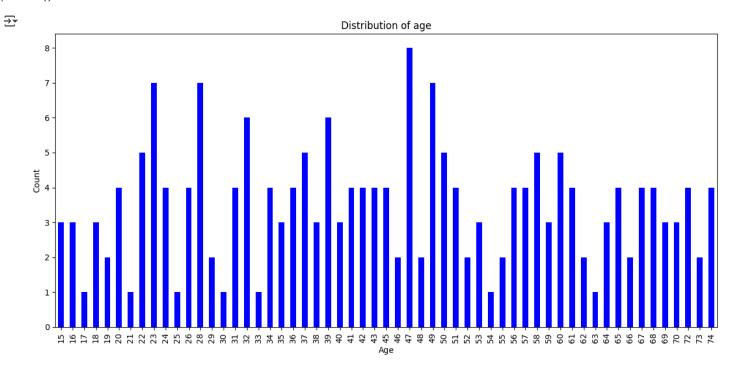
```
import matplotlib.pyplot as plt
import seaborn as sns

targetCol = "Age"
sns.histplot(df[targetCol], kde=True, bins=10)
plt.title(f'Distribution of {targetCol}')
plt.show()
```

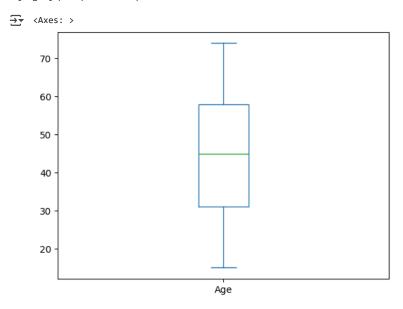




```
df['Age'].value_counts().sort_index().plot(kind = "bar", color = "blue")
plt.xlabel("Age")
plt.ylabel("Count")
plt.title("Distribution of age")
plt.tight_layout()
plt.show()
```



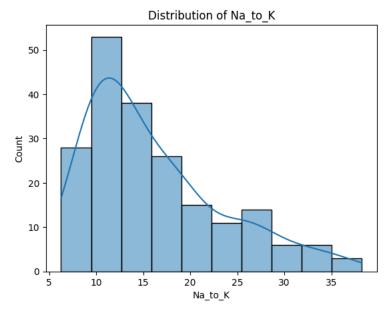




→ Na to Potassium Ratio Distribution

```
targetCol = "Na_to_K"
sns.histplot(df[targetCol], kde=True, bins=10)
plt.title(f'Distribution of {targetCol}')
plt.show()
```





✓ Sex Distribution

```
targetCol = 'Sex'
gender_counts = df[targetCol].value_counts()
gender_counts
gender_counts.plot(kind='pie', autopct='%1.1f%%', colors=['#66b3ff', '#ff99cc'], startangle=90, legend=False)
plt.title(f'{targetCol} Distribution')
plt.ylabel('')
plt.show()
```

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Sex Distribution

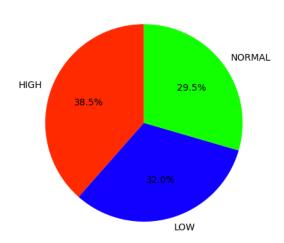


→ Bload Pressure Levels Distribution

```
targetCol = 'BP'
gender_counts = df[targetCol].value_counts()
gender_counts
gender_counts.plot(kind='pie', autopct='%1.1f%%', colors=['#FF2A00','#1100FF','#11FF00',], startangle=90, legend=False)
plt.title(f'{targetCol} Distribution')
plt.ylabel('')
plt.show()
```



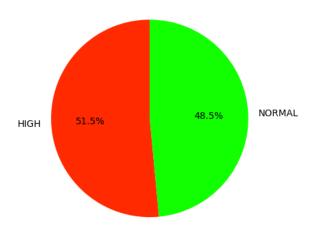
BP Distribution




```
targetCol = 'Cholesterol'
gender_counts = df[targetCol].value_counts()
gender_counts
gender_counts.plot(kind='pie', autopct='%1.1f%%', colors=['#FF2A00','#11FF00',], startangle=90, legend=False)
plt.title(f'{targetCol} Distribution')
plt.ylabel('')
plt.show()
```

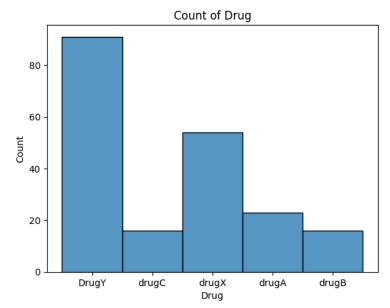


Cholesterol Distribution



→ Drug Distribution

```
targetCol = 'Drug'
sns.histplot(df[targetCol], bins=10)
plt.title(f'Count of {targetCol}')
plt.show()
```



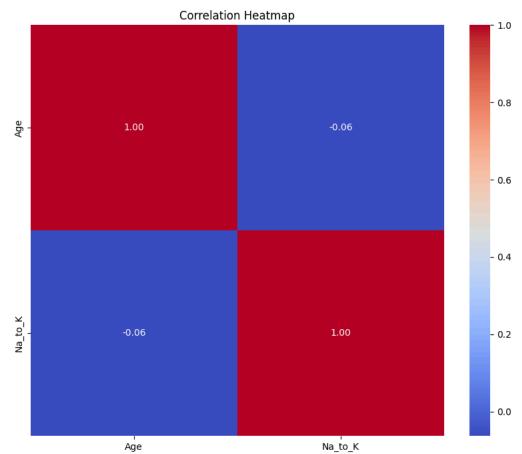
→ Data Correlation

The following plots are used to show possible correlations between the columns on the dataset

```
# Suppose df is your drugs dataset
numeric_df = df.select_dtypes(include='number') # only numeric columns

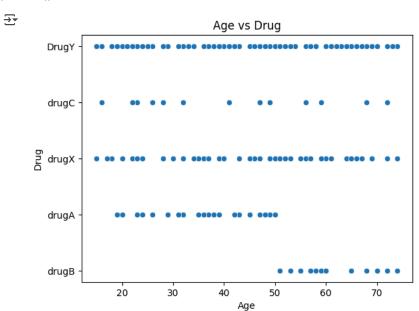
corr_matrix = numeric_df.corr()

plt.figure(figsize=(10,8))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', fmt=".2f")
plt.title("Correlation Heatmap")
plt.show()
```

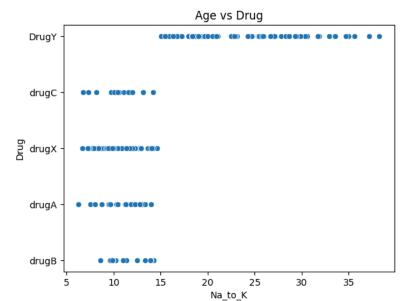


This means age and the sodium-to-potassium ratio are almost independent

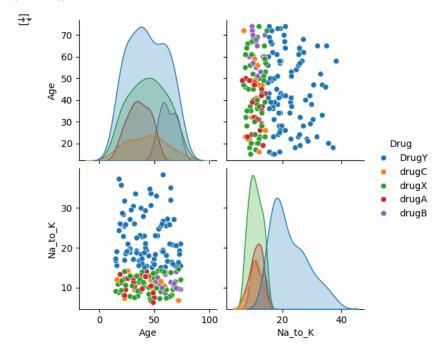
```
sns.scatterplot(data=df, x="Age", y="Drug")
plt.title("Age vs Drug")
plt.show()
```



```
sns.scatterplot(data=df, x="Na_to_K", y="Drug")
plt.title("Age vs Drug")
plt.show()
```



 $sns.pairplot(df, \ hue="Drug", \ vars=numeric_df.columns) \\ plt.show()$



import matplotlib.pyplot as plt
import seaborn as sns

sns.scatterplot(data=df,x="Age",y='Na_to_K',hue=df['Drug'],s=100)
plt.title("Age vs Na/K")
plt.show()

