



(<https://databricks.com>)

Overview

This notebook will show you how to create and query a table or DataFrame that you uploaded to DBFS. DBFS (<https://docs.databricks.com/user-guide/dbfs-databricks-file-system.html>) is a Databricks File System that allows you to store data for querying inside of Databricks. This notebook assumes that you have a file already inside of DBFS that you would like to read from.

This notebook is written in **Python** so the default cell type is Python. However, you can use different languages by using the `%LANGUAGE` syntax. Python, Scala, SQL, and R are all supported.

Bringing in DATAFRAME

```
# File location and type
file_location = "/FileStore/tables/heart_disease_uci.csv"
file_type = "csv"

# CSV options
infer_schema = "true"
first_row_is_header = "true"
delimiter = ","

# The applied options are for CSV files. For other file types, these will be ignored
df = spark.read.format(file_type) \
    .option("inferSchema", infer_schema) \
    .option("header", first_row_is_header) \
    .option("sep", delimiter) \
    .load(file_location)

display(df)
```

Table



	1^2_3 id	1^2_3 age	A^B_C sex	A^B_C dataset	A^B_C cp	1^2_3 trestbps
1	1	63	Male	Cleveland	typical angina	145
2	2	67	Male	Cleveland	asymptomatic	160
3	3	67	Male	Cleveland	asymptomatic	120
4	4	37	Male	Cleveland	non-anginal	130
5	5	41	Female	Cleveland	atypical angi...	130
6	6	56	Male	Cleveland	atypical angi...	120
7	7	62	Female	Cleveland	asymptomatic	140
8	8	57	Female	Cleveland	asymptomatic	120
9	9	63	Male	Cleveland	asymptomatic	130
10	10	53	Male	Cleveland	asymptomatic	140
11	11	57	Male	Cleveland	asymptomatic	140
12	12	56	Female	Cleveland	atypical angi...	140
13	13	56	Male	Cleveland	non-anginal	130
14	14	44	Male	Cleveland	atypical angi...	120
15	15	52	Male	Cleveland	non-anginal	172

920 rows

Describe the Variables

```
# Describe the variables
variables_description = {
    'age': 'Age of the patient',
    'sex': 'Sex of the patient (1 = male, 0 = female)',
    'cp': 'Chest pain type (1 to 4)',
    'trestbps': 'Resting blood pressure (in mm Hg)',
    'chol': 'Serum cholesterol (in mg/dl)'
}
```

```
variables_description
```

```
Out[28]: {'age': 'Age of the patient',
'sex': 'Sex of the patient (1 = male, 0 = female)',
'cp': 'Chest pain type (1 to 4)',
'trestbps': 'Resting blood pressure (in mm Hg)',
'chol': 'Serum cholesterol (in mg/dl)'}
```

Converting to Pandas

```
import pandas as pd

df = df.toPandas()
print(pandas_df.head())
```

	id	age	sex	dataset	cp	trestbps	chol	fbs	\
0	1	63	Male	Cleveland	typical angina	145	233	TRUE	
1	2	67	Male	Cleveland	asymptomatic	160	286	FALSE	
2	3	67	Male	Cleveland	asymptomatic	120	229	FALSE	
3	4	37	Male	Cleveland	non-anginal	130	250	FALSE	
4	5	41	Female	Cleveland	atypical angina	130	204	FALSE	

		restecg	thalch	exang	oldpeak	slope	ca		thal	num
0	lv hypertrophy	150	FALSE	2.3	downsloping	0		fixed	defect	0
1	lv hypertrophy	108	TRUE	1.5	flat	3			normal	2
2	lv hypertrophy	129	TRUE	2.6	flat	2	reversable		defect	1
3	normal	187	FALSE	3.5	downsloping	0			normal	0
4	lv hypertrophy	172	FALSE	1.4	upsloping	0			normal	0

Selecting Certain Variables

```
variables = ['age', 'sex', 'cp', 'trestbps', 'chol']
df_selected = df[variables]

# Display the selected variables
print(df_selected.head())
```

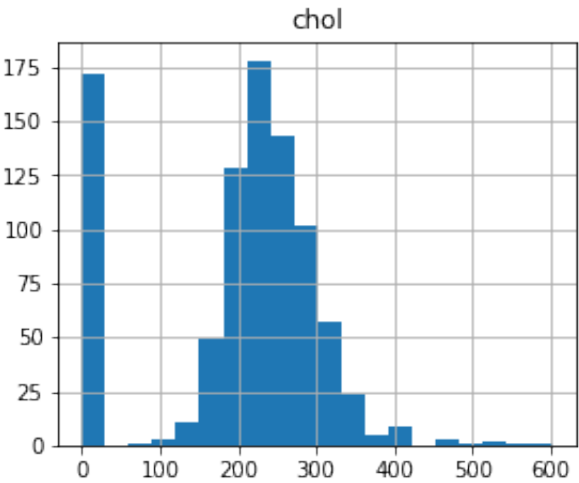
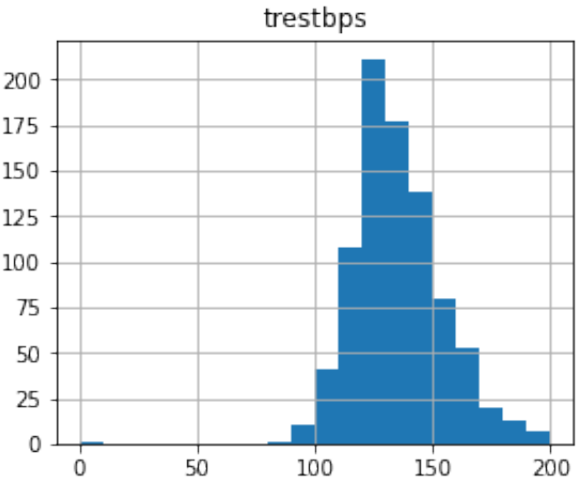
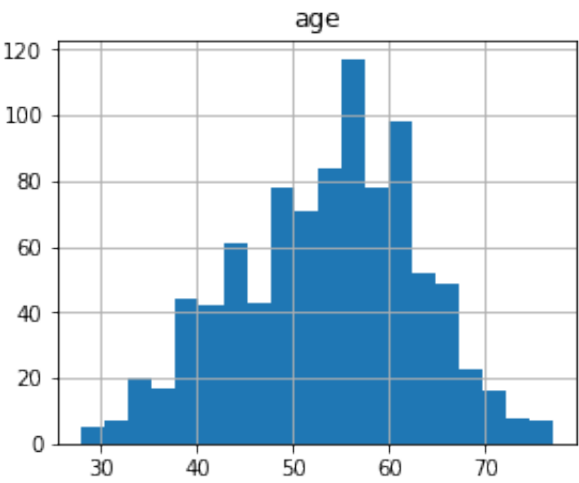
	age	sex	cp	trestbps	chol
0	63	Male	typical angina	145.0	233.0
1	67	Male	asymptomatic	160.0	286.0
2	67	Male	asymptomatic	120.0	229.0
3	37	Male	non-anginal	130.0	250.0
4	41	Female	atypical angina	130.0	204.0

Histograms and Outliers

```
import matplotlib.pyplot as plt
import matplotlib.pyplot as plt

# Plot histograms
df[['age', 'sex', 'cp', 'trestbps', 'chol']].hist(figsize=(10, 8), bins=20)
plt.show()

# Identifying outliers
df[['age', 'trestbps', 'chol']].describe()
```



	age	trestbps	chol
count	920.000000	861.000000	890.000000
mean	53.510870	132.132404	199.130337
std	9.424685	19.066070	110.780810
min	28.000000	0.000000	0.000000
25%	47.000000	120.000000	175.000000
50%	54.000000	130.000000	223.000000
75%	60.000000	140.000000	268.000000
max	77.000000	200.000000	603.000000

Descriptive Statistics

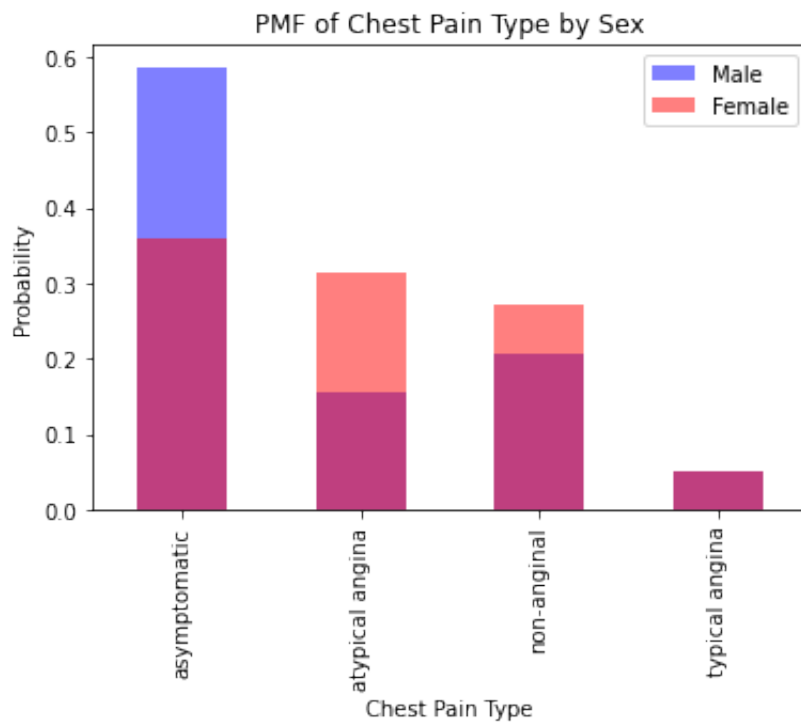
```
# Calculating and displaying descriptive statistics
descriptive_stats = df_selected.describe()
print(descriptive_stats)
```

	age	trestbps	chol
count	920.000000	861.000000	890.000000
mean	53.510870	132.132404	199.130337
std	9.424685	19.066070	110.780810
min	28.000000	0.000000	0.000000
25%	47.000000	120.000000	175.000000
50%	54.000000	130.000000	223.000000
75%	60.000000	140.000000	268.000000
max	77.000000	200.000000	603.000000

PMF Comparison

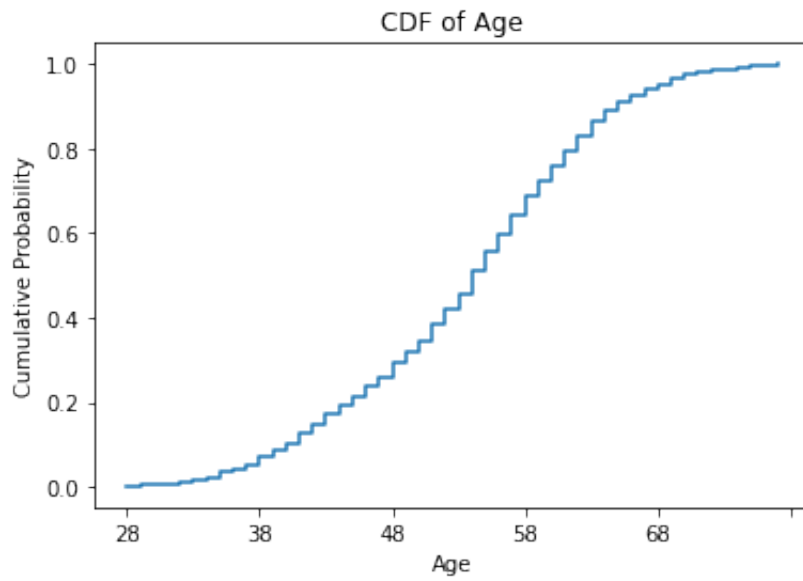
```
pmf_cp_male = df[df['sex'] == "Male"]
['cp'].value_counts(normalize=True).sort_index()
pmf_cp_female = df[df['sex'] == "Female"]
['cp'].value_counts(normalize=True).sort_index()

# Plotting the PMF comparison
pmf_cp_male.plot(kind='bar', color='blue', alpha=0.5, label='Male')
pmf_cp_female.plot(kind='bar', color='red', alpha=0.5, label='Female')
plt.title('PMF of Chest Pain Type by Sex')
plt.xlabel('Chest Pain Type')
plt.ylabel('Probability')
plt.legend()
plt.show()
```



CDF

```
age_cdf = df['age'].value_counts().sort_index().cumsum() / len(df)
age_cdf.plot(drawstyle='steps-post')
plt.title('CDF of Age')
plt.xlabel('Age')
plt.ylabel('Cumulative Probability')
plt.show()
```



Analytical Distribution


```
import numpy as np
import scipy.stats as stats
import matplotlib.pyplot as plt

# Ensure the 'age' column is numeric
df_selected['age'] = pd.to_numeric(df_selected['age'], errors='coerce')

# Drop any rows with NaN values in the 'age' column
df_selected = df_selected.dropna(subset=['age'])

# Fit a normal distribution to the 'age' data
mu, std = stats.norm.fit(df_selected['age'])

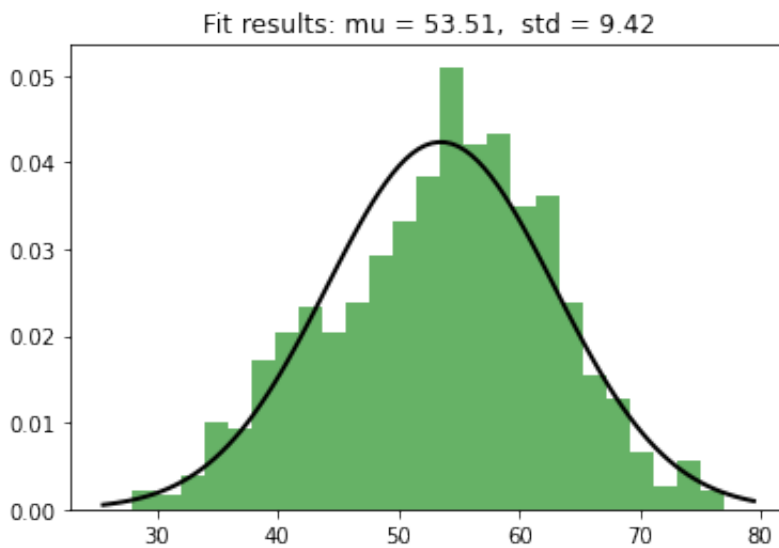
# Plot the histogram and the fitted distribution
plt.hist(df_selected['age'], bins=25, density=True, alpha=0.6, color='g')

# Plot the probability density function (PDF)
xmin, xmax = plt.xlim()
x = np.linspace(xmin, xmax, 100)
p = stats.norm.pdf(x, mu, std)
plt.plot(x, p, 'k', linewidth=2)
plt.title(f"Fit results: mu = {mu:.2f}, std = {std:.2f}")
plt.show()
```

```
<command-4255733837626512>:6: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead
```

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)

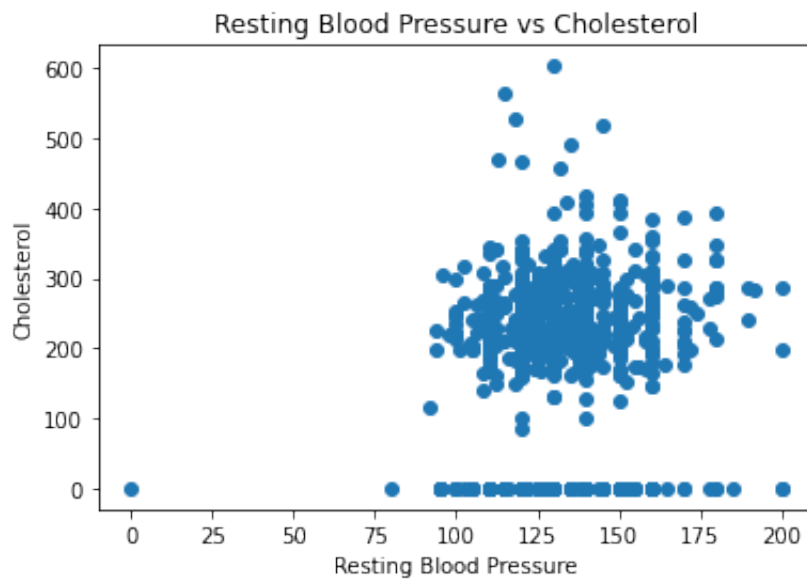
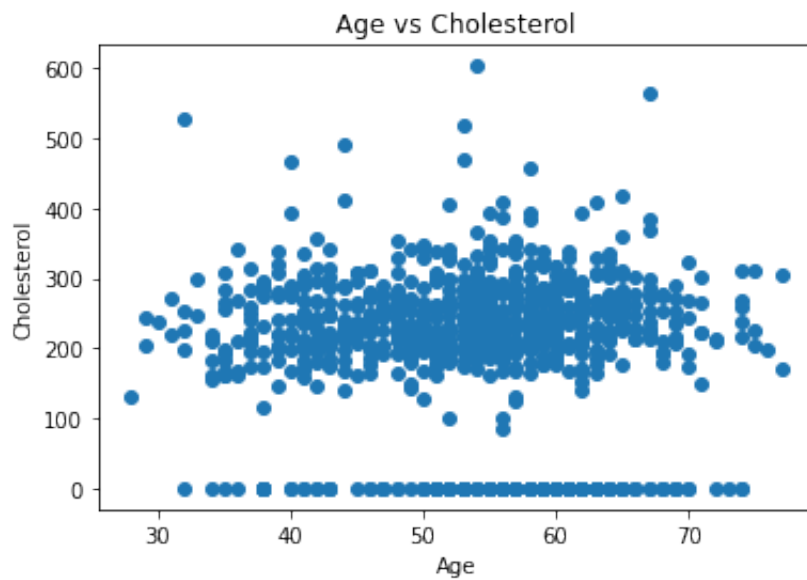
```
df_selected['age'] = pd.to_numeric(df_selected['age'], errors='coerce')
```



Scatter Plots

```
plt.scatter(df['age'], df['chol'])
plt.title('Age vs Cholesterol')
plt.xlabel('Age')
plt.ylabel('Cholesterol')
plt.show()

# Scatter plot for resting blood pressure vs cholesterol
plt.scatter(df['trestbps'], df['chol'])
plt.title('Resting Blood Pressure vs Cholesterol')
plt.xlabel('Resting Blood Pressure')
plt.ylabel('Cholesterol')
plt.show()
```



Hypothesis Testing

```

from scipy.stats import ttest_ind

# Check for NaN values and drop them
chol_male = df[df['sex'] == "Male"]['chol'].dropna()
chol_female = df[df['sex'] == "Female"]['chol'].dropna()

# Check that the groups have valid data
if len(chol_male) == 0 or len(chol_female) == 0:
    print("One of the groups has no data. Hypothesis test cannot be performed.")
elif chol_male.mean() == chol_female.mean():
    print("The two groups have identical means. Hypothesis test results will be NaN.")
else:
    # Perform the hypothesis test
    t_stat, p_value = ttest_ind(chol_male, chol_female)
    print(f"T-statistic: {t_stat}, P-value: {p_value}")

```

T-statistic: -5.9967029323480725, P-value: 2.927317272597984e-09

Regression Analysis

Df Residuals:	830	BIC:	2436.
Df Model:	3		
Covariance Type:	nonrobust		

	coef	std err	t	P> t	[0.025	0.975]
const	-1.0224	0.294	-3.474	0.001	-1.600	-0.445
age	0.0354	0.004	8.929	0.000	0.028	0.043
trestbps	0.0045	0.002	2.291	0.022	0.001	0.008
chol	-0.0024	0.000	-7.257	0.000	-0.003	-0.002

Omnibus:	86.106	Durbin-Watson:	1.728
Prob(Omnibus):	0.000	Jarque-Bera (JB):	110.970
Skew:	0.875	Prob(JB):	8.00e-25
Kurtosis:	3.363	Cond. No.	2.17e+03

Notes:

- [1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
- [2] The condition number is large, $2.17e+03$. This might indicate that there are