Project Overview

The notebook conducts a comparative analysis of three major clustering algorithms: K-Means, Agglomerative Hierarchical Clustering, and DBSCAN.

- Dataset: Pima Indians Diabetes Dataset.
- Goal: Cluster patients based on diagnostic measurements (Glucose, BMI, Insulin, etc.) after removing the known `Outcome` label.
- Best Model: Based on the Silhouette Score, DBSCAN achieved the best separation (0.37).

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

from sklearn.preprocessing import MinMaxScaler

from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score

import numpy as np
from sklearn.neighbors import NearestNeighbors
from sklearn.cluster import DBSCAN

from sklearn.cluster import AgglomerativeClustering
from scipy.cluster.hierarchy import linkage, dendrogram
```

Data Loading and Preprocessing

```
data = pd.read_csv('/Users/hrishinandanmacbook/Developer/Brocamp/M24/pima-diabetes.csv')
df = data.copy()
```

```
df.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

```
df.drop('Outcome', axis=1, inplace=True)
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 8 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
dtypes: float64(2), int64(6)
memory usage: 48.1 KB
```

```
df.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000

```
df.isna().sum().sum()
```

```
np.int64(0)
```

```
df.duplicated().sum()
```

```
np.int64(0)
```

Feature Scaling

```
scaler = MinMaxScaler()
df = pd.DataFrame(scaler.fit_transform(df), columns=df.columns)
```

Clustering Algorithms Analysis

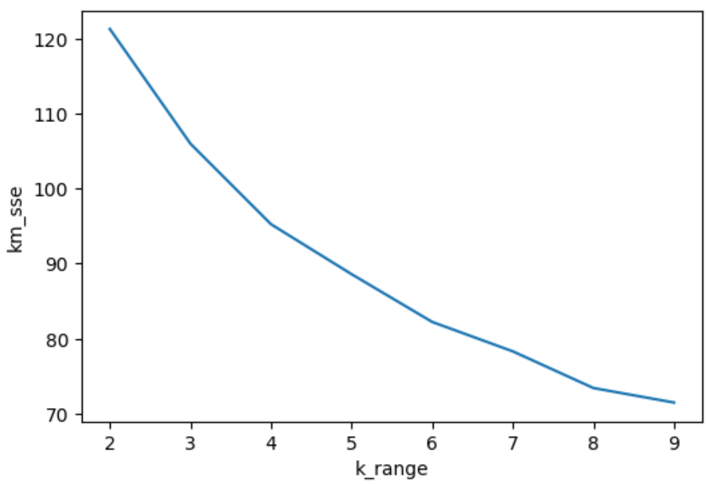
K-Means Clustering

```
k_range = range(2, 10)
km_sse = []
km_score = []

for k in k_range:
    km = KMeans(n_clusters=k, random_state=42)
    km.fit(df)

    km_sse.append(km.inertia_)
```

```
plt.figure(figsize=(6, 4))
plt.plot(k_range, km_sse)
plt.xlabel('k_range')
plt.ylabel('km_sse')
plt.show()
```

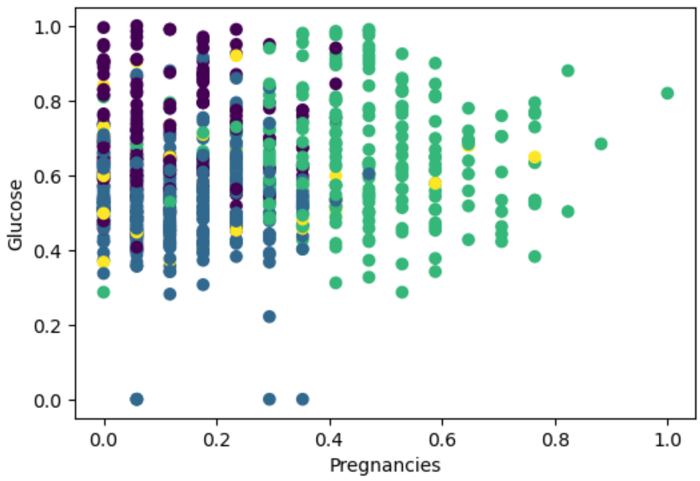



```
km = KMeans(n_clusters=4, random_state=42)
km_label = km.fit_predict(df)
print('KMeans silhouette score: ', silhouette_score(df, km_label))
```

```
KMeans silhouette score:  0.2048057549090295
```

Agglomerative (Hierarchical) Clustering

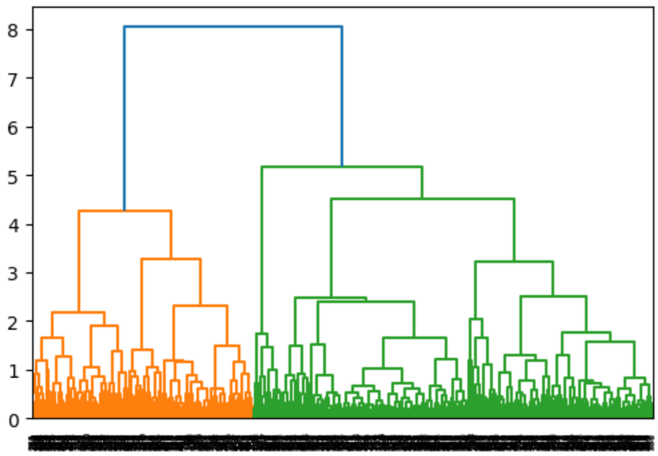
```
plt.figure(figsize=(6, 4))
plt.scatter(df.iloc[:, 0], df.iloc[:, 1], c=km_label)
plt.xlabel('Pregnancies')
plt.ylabel('Glucose')
plt.show()
```




```
hier = AgglomerativeClustering(n_clusters=4, linkage='ward')
hier_label = hier.fit_predict(df)
print('Agglomerative silhouette score:', silhouette_score(df, hier_label))
```

```
Agglomerative silhouette score: 0.1383402410426239
```

```
dfL = linkage(df, method='ward')
plt.figure(figsize=(6,4))
dendrogram(dfL)
plt.show()
```



DBSCAN (Density-Based Spatial Clustering)

```
nn = NearestNeighbors(n_neighbors=3)
nn.fit(df)

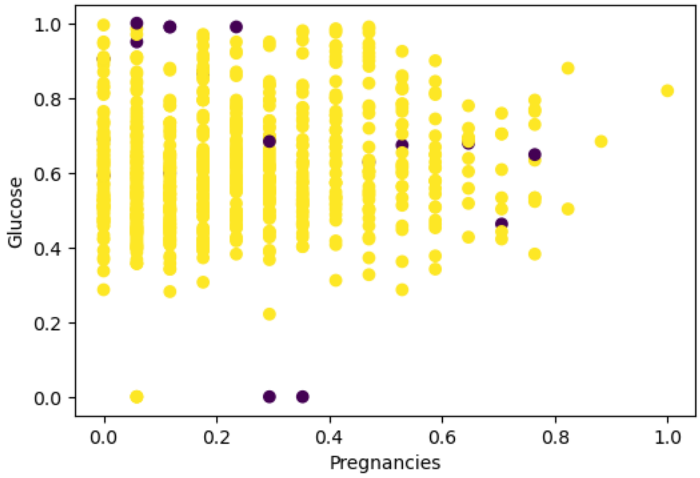
distance, _ = nn.kneighbors(df)
k_dist = np.sort(distance[:, 2])

plt.figure(figsize=(6, 4))
plt.plot(k_dist)
plt.xlabel('data_points')
plt.ylabel('distance')
plt.show()
```


```
db = DBSCAN(eps=0.35, min_samples=5)
db_label = db.fit_predict(df)
print('DBSCAN silhouette score:', silhouette_score(df, db_label))
```

```
DBSCAN silhouette score: 0.37142087446145067
```

```
plt.figure(figsize=(6, 4))
plt.scatter(df.iloc[:, 0], df.iloc[:, 1], c=db_label)
plt.xlabel('Pregnancies')
plt.ylabel('Glucose')
plt.show()
```



Summary of Results based on Silhouette score

Algorithm	Configuration	Silhouette Score
K-Means	k = 4	0.2048
Agglomerative	k = 4, linkage = 'ward'	0.1383
DBSCAN	ε = 0.35, min_samples = 5	0.3714

- **Conclusion:** DBSCAN provided the highest quality clustering for this specific feature set and preprocessing method.

```
Start coding or generate with AI.
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Start coding or generate with AI.
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