

# Số hóa và quản trị thông tin số

## Lab4

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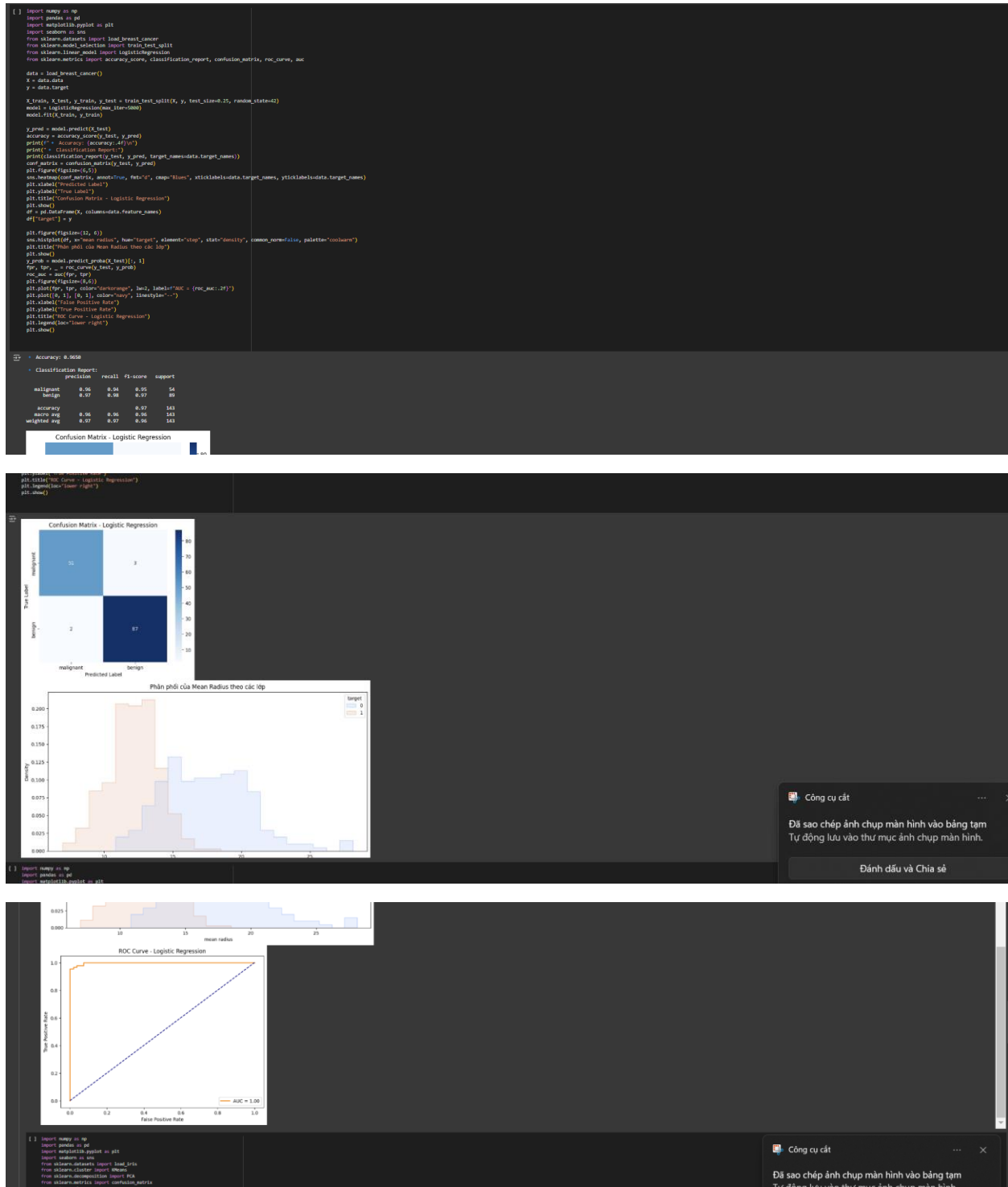
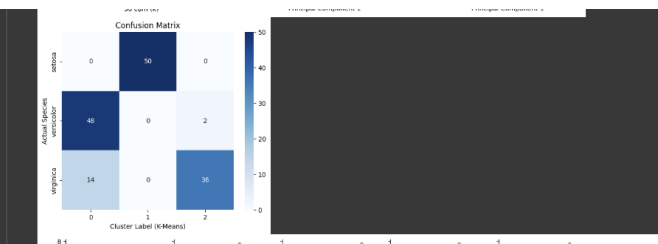
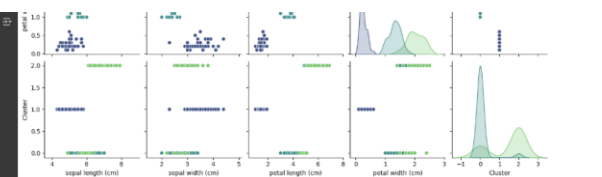


Figure 1 consists of three plots. The left plot, titled 'Elbow Method', shows the Sum of Squared Errors (SSE) on the y-axis (ranging from 0 to 700) against the number of clusters (K) on the x-axis (ranging from 1 to 9). The SSE decreases sharply from K=1 to K=3 and then levels off. The middle plot, titled 'Actual Clusters (Iris Species)', shows the principal components (PC1 and PC2) for three species: setosa (purple), versicolour (green), and virginica (yellow). The right plot, titled 'K-Means Clustering', shows the principal components (PC1 and PC2) for the same three species, with each species assigned to a different cluster (1, 2, or 3) based on the K-Means algorithm.



```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from google.colab import files
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
```



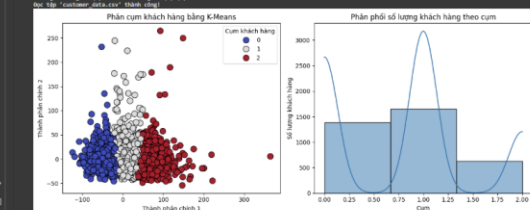
- Mẫu thực tế:  
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0]
- Mẫu phân cực K-Pearson:  
[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1]

```
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from sklearn.decomposition import PCA
```

```
plt.subplots(1, 2)
ax = AxesGrid(fig, 111, axes_labels=axes_labels)
plt.title("Mô phỏng về lượng chất hàng theo km")
plt.xlabel("km")
plt.ylabel("Số lượng chất hàng")

plt.tight_layout()
plt.show()

print("Số liệu bình ổn đã được phân tích bằng quy luật Gauss, và số liệu khác nhau đã được phân tích bằng t-Mann.")
```

[illegible]

Thành phần chính 1