

Use the Heart Disease database:

• Apply Singular Value Decomposition (SVD) to analyze the decomposed features.

• Apply data visualization to the outcomes of SVD

```
import pandas as pd
```

```
import numpy as np
```

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

```
import seaborn as sns
```

```
from sklearn.preprocessing import StandardScaler
```

```
from sklearn.decomposition import TruncatedSVD
```

```
from mpl_toolkits.mplot3d import Axes3D
```

```
from sklearn.model_selection import train_test_split
```

```
from sklearn.linear_model import LogisticRegression
```

```
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score
```

```
data=pd.read_csv("C:/Users/HP/OneDrive/Desktop/ml 7th sem codes/datasets/heart.csv")
```

```
data.head()
```

```
data.info()
```

```
features = data.drop(columns=['target'])
```

```
target = data['target']
```

```
scaler = StandardScaler()
```

```
scaled_features = scaler.fit_transform(features)
```

```
svd = TruncatedSVD(n_components=5, random_state=42)
```

```
svd_features = svd.fit_transform(scaled_features)
```

```
explained_variance = svd.explained_variance_ratio_
```

```
svd_features_df = pd.DataFrame(svd_features, columns=[f'SVD_Component_{i+1}' for i in
range(svd_features.shape[1])])
explained_variance, svd_features_df.head()
```

```
svd = TruncatedSVD(n_components=5)
```

```
svd.fit(features)
```

```
singular_values = svd.singular_values_
```

```
plt.figure(figsize=(12, 5))
```

```
plt.figure(figsize=(12, 5))
```

```
plt.subplot(1, 2, 1)
```

```
sns.barplot(x=np.arange(1, len(singular_values) + 1), y=singular_values)
```

```
plt.xlabel('Component')
```

```
plt.ylabel('Singular Value')
```

```
plt.title('Singular Values of Components')
```

```
plt.subplot(1, 2, 2)
```

```
sns.barplot(x=np.arange(1, len(explained_variance) + 1), y=explained_variance)
```

```
plt.xlabel('Component')
```

```
plt.ylabel('Explained Variance Ratio')
```

```
plt.title('Explained Variance Ratio of Components')
```

```
cumulative_explained_ratios = np.cumsum(explained_variance)

plt.figure(figsize=(6, 4))

sns.lineplot(x=np.arange(1, len(cumulative_explained_ratios) + 1),
             y=cumulative_explained_ratios, marker='o')

plt.xlabel('Number of Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Cumulative Explained Variance by Components')
plt.grid(True)

plt.tight_layout()
plt.show()
```

```
correlations = pd.DataFrame(np.dot(scaled_features.T, svd_features) / (len(scaled_features) - 1),
                           index=features.columns,
                           columns=[f'SVD_Component_{i+1}' for i in range(svd_features.shape[1])])
```

```
correlations
```

```
plt.figure(figsize=(10, 8))

sns.scatterplot(x=svd_features[:, 0], y=svd_features[:, 1], hue=target, palette="viridis", edgecolor='k')

plt.xlabel('SVD Component 1')
plt.ylabel('SVD Component 2')

plt.title('Data Visualization in SVD Component Space (Colored by Heart Disease Target)')

plt.legend(title="Heart Disease Target", labels=['No Disease', 'Disease'])

plt.show()
```

```
explained_variance = svd.explained_variance_ratio_  
plt.figure(figsize=(8,6))  
sns.barplot(x=[f'Component {i+1}' for i in range(len(explained_variance))],  
            y=explained_variance * 100)  
plt.ylabel('Explained Variance (%)')  
plt.xlabel('SVD Components')  
plt.title('Scree Plot')  
plt.show()
```

```
svd_plot_df = svd_features_df.copy()  
svd_plot_df['target'] = target  
plt.figure(figsize=(10,8))  
sns.scatterplot(data=svd_plot_df,  
                x='SVD_Component_1',  
                y='SVD_Component_2',  
                hue='target',  
                palette=['blue', 'red'],  
                alpha=0.6)  
plt.title('SVD Components 1 vs 2 Colored by Heart Disease Diagnosis')  
plt.xlabel('SVD Component 1')  
plt.ylabel('SVD Component 2')  
plt.legend(title='Heart Disease', labels=['No Disease', 'Disease'])  
plt.show()
```

```
fig = plt.figure(figsize=(12,10))  
ax = fig.add_subplot(111, projection='3d')
```

```
colors = svd_plot_df['target'].map({0: 'blue', 1: 'red'})
```

```
ax.scatter(svd_plot_df['SVD_Component_1'],  
          svd_plot_df['SVD_Component_2'],  
          svd_plot_df['SVD_Component_3'],  
          c=colors, alpha=0.6)
```

```
ax.set_title('3D Scatter Plot of SVD Components Colored by Heart Disease Diagnosis')  
ax.set_xlabel('SVD Component 1')  
ax.set_ylabel('SVD Component 2')  
ax.set_zlabel('SVD Component 3')
```

```
from matplotlib.lines import Line2D
```

```
legend_elements = [Line2D([0], [0], marker='o', color='w', label='No Disease',  
                           markerfacecolor='blue', markersize=10),  
                   Line2D([0], [0], marker='o', color='w', label='Disease',  
                           markerfacecolor='red', markersize=10)]  
ax.legend(handles=legend_elements, title='Heart Disease')
```

```
plt.show()
```

```
melted_df = svd_plot_df.melt(id_vars='target',  
                             value_vars=[f'SVD_Component_{i+1}' for i in range(svd.n_components)], # Use  
                             svd.n_components  
                             var_name='SVD_Component',  
                             value_name='Value')  
plt.figure(figsize=(14,10))  
sns.boxplot(x='SVD_Component', y='Value', hue='target', data=melted_df, palette='Set2')
```

```
plt.title('Distribution of SVD Components by Heart Disease Diagnosis')
plt.xlabel('SVD Components')
plt.ylabel('Component Values')
plt.legend(title='Heart Disease', labels=['No Disease', 'Disease'])
plt.show()
```

```
X_train, X_test, y_train, y_test = train_test_split(svd_features_df, target,
                                                    test_size=0.2,
                                                    random_state=42,
                                                    stratify=target)
```

```
# Initialize and train the model
```

```
model = LogisticRegression(max_iter=1000, random_state=42)
model.fit(X_train, y_train)
```

```
# Predictions
```

```
y_pred = model.predict(X_test)
```

```
# Confusion matrix
```

```
cm = confusion_matrix(y_test, y_pred)
```

```
# Plot confusion matrix as heatmap
```

```
plt.figure(figsize=(8,6))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False,
            xticklabels=["No Disease", "Disease"],
            yticklabels=["No Disease", "Disease"])
plt.xlabel("Predicted Labels")
plt.ylabel("True Labels")
plt.title("Confusion Matrix of Heart Disease Classification")
```

```
plt.show()
```

```
report = classification_report(y_test, y_pred, target_names=["No Disease", "Disease"],  
output_dict=True)
```

```
report_df = pd.DataFrame(report).transpose()
```

```
report_df = report_df.round(2)
```

```
report_df = report_df.rename(columns={  
    "precision": "Precision",  
    "recall": "Recall",  
    "f1-score": "F1-Score",  
    "support": "Support"  
})
```

```
print("Classification Report:")
```

```
print(report_df)
```

```
print(f"\nOverall Accuracy:{accuracy_score(y_test, y_pred):.2f}")
```