

Experiment 4: GMM Clustering after PCA Dimensionality Reduction

Imports and Configuration

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%cd ..
from src.models.pca import PCA
from src.models.gmm import GMM, Covariance
from src.utils.metrics import *
from src.utils.utils import *

RANDOM_SEED = 42
np.random.seed(RANDOM_SEED)

c:\Users\ziade\OneDrive\Desktop\Term 7\ML\Lab 4\Assignment4-
Unsupervised-Clustering-Analysis
```

Data Loading and Preprocessing

```
X_scaled, y_true =
load_scale_data(data_path='./data/breast_cancer.csv')

print(f"Dataset shape: {X_scaled.shape}")
print(f"Labels shape: {y_true.shape}")

Dataset shape: (569, 30)
Labels shape: (569,)
```

Running PCA-GMM

```
dims = [2, 5, 10, 15, 20]
cov_types = [Covariance.FULL, Covariance.TIED, Covariance.DIAGONAL,
Covariance.SPHERICAL]
gmm_pca_results = []

for d in dims:
    pca = PCA(n_components=d)
    X_pca = pca.fit_transform(X_scaled)

    for cov_t in cov_types:
        # Fit GMM (k=2 for binary classification)
        gmm = GMM(k=2, covariance_type=cov_t, max_iter=100)
        gmm.fit(X_pca)
```

```

y_pred = gmm.predict(X_pca)

# Calculate external metrics
ari = compute_ari(y_true, y_pred)

gmm_pca_results.append({
    'Dimensions': d,
    'Covariance': cov_t.value,
    'Log-Likelihood': gmm.log_likelihood_[-1],
    'ARI': ari,
    'BIC': gmm.bic(X_pca)
})

gmm_df = pd.DataFrame(gmm_pca_results)
gmm_df

```

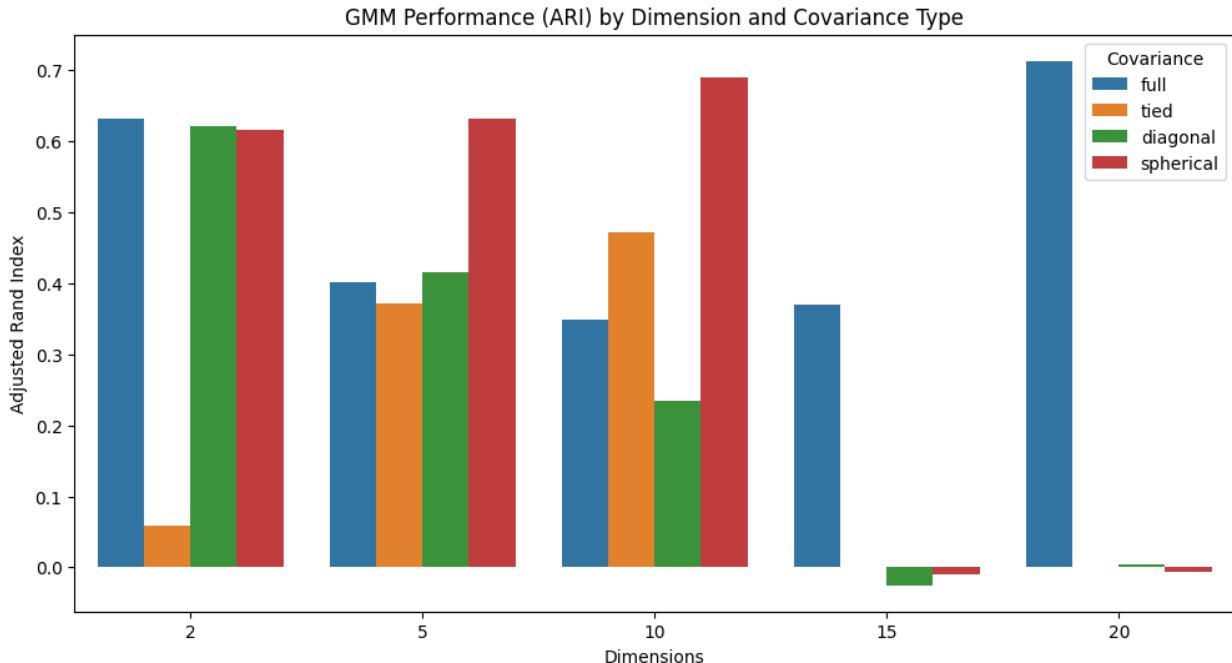
	Dimensions	Covariance	Log-Likelihood	ARI	BIC
0	2	full	-2672.468461	0.632548	5414.719606
1	2	tied	-2795.561820	0.058458	5641.874684
2	2	diagonal	-2680.089807	0.621306	5417.274538
3	2	spherical	-2681.734466	0.615591	5407.876095
4	5	full	-5471.894119	0.401536	11203.887335
5	5	tied	-5703.076638	0.372407	11571.094167
6	5	diagonal	-5622.299403	0.415050	11377.820296
7	5	spherical	-5780.693399	0.631791	11643.857244
8	10	full	-7960.009437	0.349266	16751.067212
9	10	tied	-8369.095052	0.471302	17220.325018
10	10	diagonal	-8300.205753	0.234017	16860.510603
11	10	spherical	-9361.857804	0.689312	18869.624858
12	15	full	-8520.503079	0.370575	18760.197757
13	15	tied	-13000.393561	0.000000	26958.713068
14	15	diagonal	-9369.006723	-0.025219	19124.990153
15	15	spherical	-11232.478697	-0.009584	22674.305448
16	20	full	-6651.474746	0.713256	16227.478372
17	20	tied	-13101.709179	0.000000	27795.732347
18	20	diagonal	-8484.687427	0.003724	17483.229169
19	20	spherical	-11719.757975	-0.006359	23712.302810

Visualizing Covariance Type Impact

```

plt.figure(figsize=(12, 6))
sns.barplot(data=gmm_df, x='Dimensions', y='ARI', hue='Covariance')
plt.title("GMM Performance (ARI) by Dimension and Covariance Type")
plt.ylabel("Adjusted Rand Index")
plt.show()

```



Log-Likelihood Convergence Analysis by Dimension

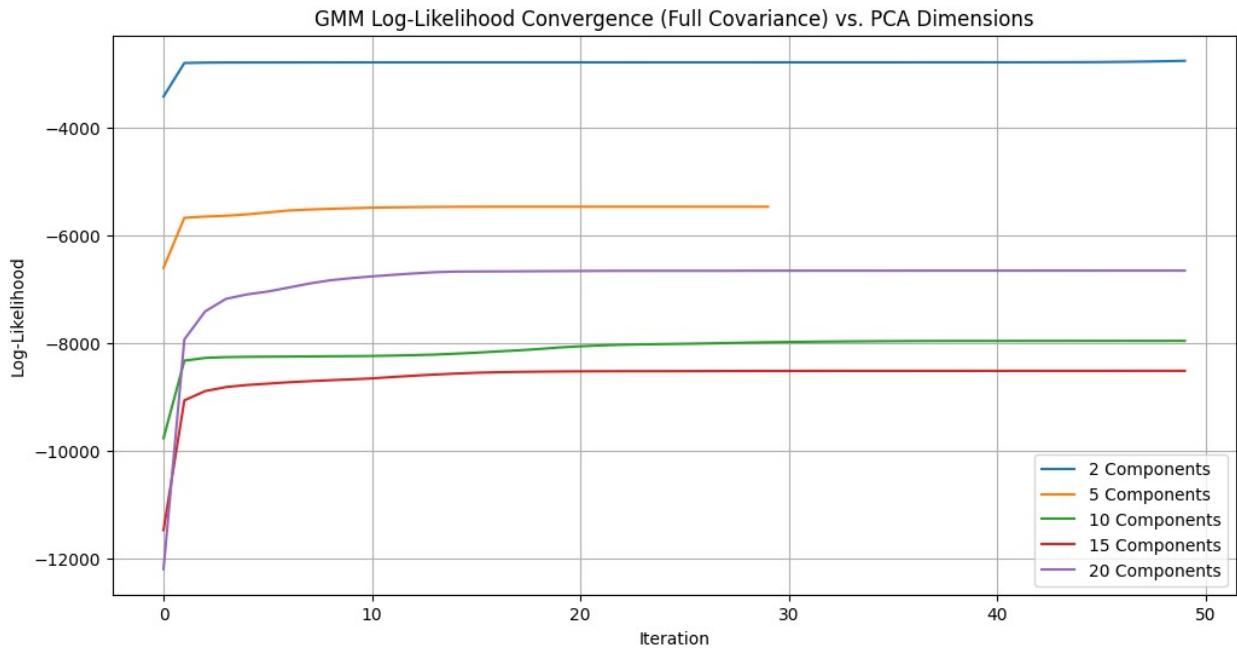
```
plt.figure(figsize=(12, 6))

for d in dims:
    pca = PCA(n_components=d)
    X_pca = pca.fit_transform(X_scaled)

    gmm = GMM(k=2, covariance_type=Covariance.FULL, max_iter=50)
    gmm.fit(X_pca)

    plt.plot(gmm.log_likelihood_, label=f'{d} Components')

plt.title("GMM Log-Likelihood Convergence (Full Covariance) vs. PCA Dimensions")
plt.xlabel("Iteration")
plt.ylabel("Log-Likelihood")
plt.legend()
plt.grid(True)
plt.show()
```



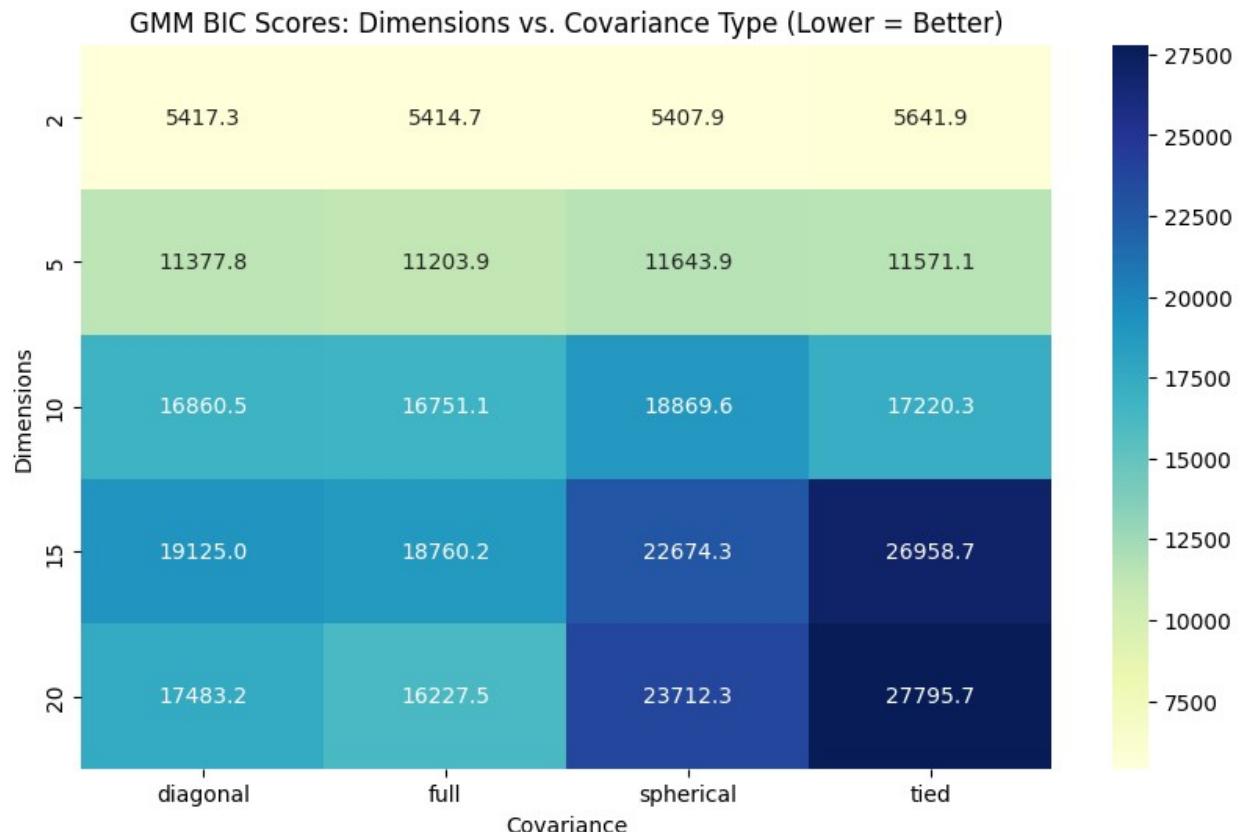
BIC/AIC Heatmap for Covariance Analysis

```

pivot_bic = gmm_df.pivot(index="Dimensions", columns="Covariance",
values="BIC")

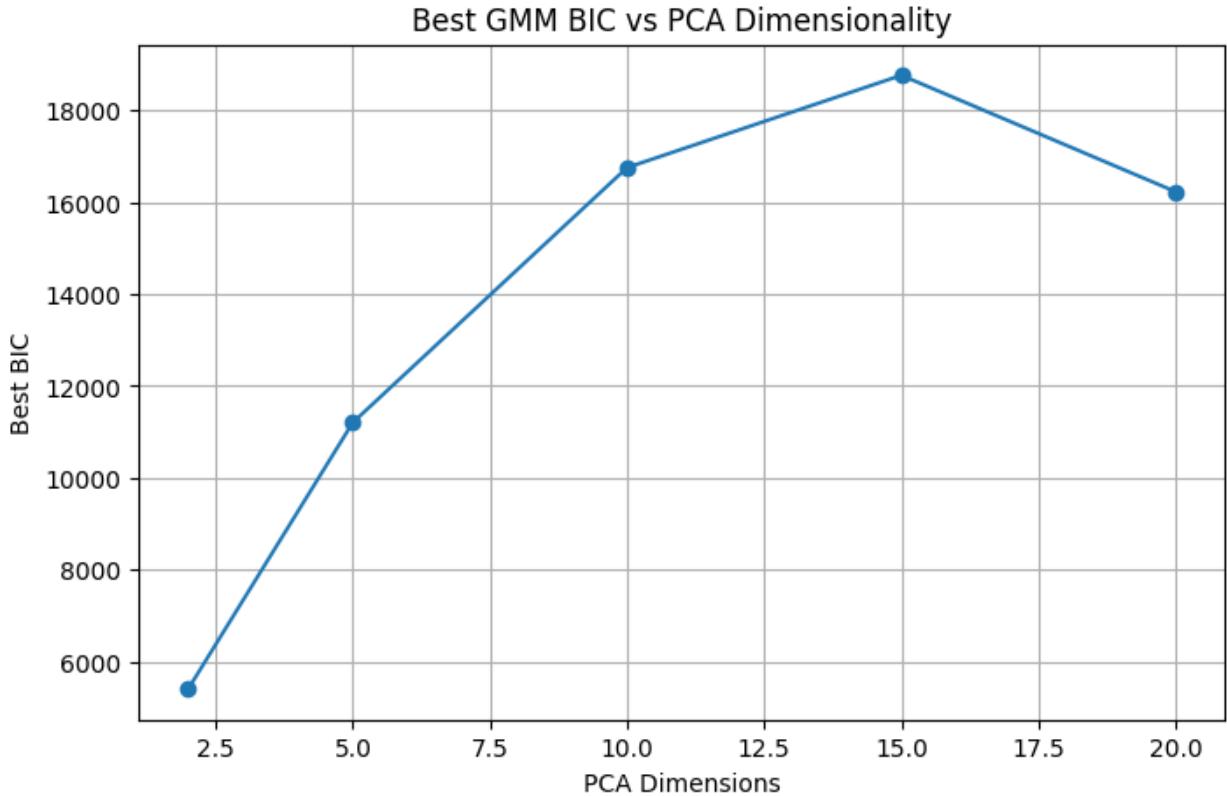
plt.figure(figsize=(10, 6))
sns.heatmap(pivot_bic, annot=True, fmt=".1f", cmap="YlGnBu")
plt.title("GMM BIC Scores: Dimensions vs. Covariance Type (Lower = Better)")
plt.show()

```



```
best_cov_per_dim = gmm_df.loc[gmm_df.groupby('Dimensions')[['BIC']].idxmin()]

plt.figure(figsize=(8, 5))
plt.plot(
    best_cov_per_dim['Dimensions'],
    best_cov_per_dim['BIC'],
    marker='o'
)
plt.xlabel("PCA Dimensions")
plt.ylabel("Best BIC")
plt.title("Best GMM BIC vs PCA Dimensionality")
plt.grid(True)
plt.show()
```



```
# 2D PCA visualization with GMM clustering (best covariance example)

pca_2d = PCA(n_components=2)
X_2d = pca_2d.fit_transform(X_scaled)

best_cov = pivot_bic.loc[2].idxmin() # best covariance for 2D PCA
gmm_2d = GMM(k=2, covariance_type=Covariance(best_cov))
gmm_2d.fit(X_2d)
y_2d_pred = gmm_2d.predict(X_2d)

plt.figure(figsize=(8, 6))
sns.scatterplot(
    x=X_2d[:, 0],
    y=X_2d[:, 1],
    hue=y_2d_pred,
    palette='viridis',
    style=y_true
)
plt.title(f"2D PCA + GMM Clusters (Covariance: {best_cov})")
plt.xlabel("PC1")
plt.ylabel("PC2")
plt.legend(title="Cluster / True Label")
plt.show()
```

2D PCA + GMM Clusters (Covariance: spherical)

