In [1]:
```
# Importing necessary libraries
import pandas as pd  # For data manipulation and analysis
from sklearn.decomposition import PCA  # For Principal Component Analysis (PCA)
import numpy as np  # For numerical operations
from sklearn import preprocessing  # For scaling and normalization of data
from bioinfokit.visuz import cluster  # For data visualization, specifically clu
import matplotlib.pyplot as plt  # For plotting graphs
from sklearn.cluster import KMeans  # For K-Means clustering algorithm
from sklearn.utils import resample  # For resampling methods like bootstrapping
from sklearn.metrics import adjusted_rand_score  # For evaluating clustering res
```

In [2]:
```
!pip install bioinfokit
```

```
Requirement already satisfied: bioinfokit in c:\users\akhil\anaconda3\lib\site-pa
ckages (2.1.4)
Requirement already satisfied: pandas in c:\users\akhil\anaconda3\lib\site-packag
es (from bioinfokit) (2.2.2)
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ackages (from bioinfokit) (0.14.2)
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packages (from matplotlib->bioinfokit) (0.11.0)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\akhil\anaconda3\lib
\site-packages (from matplotlib->bioinfokit) (4.51.0)
Requirement already satisfied: kiwisolver>=1.3.1 in c:\users\akhil\anaconda3\lib
\site-packages (from matplotlib->bioinfokit) (1.4.4)
Requirement already satisfied: packaging>=20.0 in c:\users\akhil\anaconda3\lib\si
te-packages (from matplotlib->bioinfokit) (24.1)
Requirement already satisfied: pillow>=8 in c:\users\akhil\anaconda3\lib\site-pac
kages (from matplotlib->bioinfokit) (10.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in c:\users\akhil\anaconda3\lib\s
ite-packages (from matplotlib->bioinfokit) (3.1.2)
Requirement already satisfied: python-dateutil>=2.7 in c:\users\akhil\anaconda3\l
ib\site-packages (from matplotlib->bioinfokit) (2.9.0.post0)
Requirement already satisfied: pytz>=2020.1 in c:\users\akhil\anaconda3\lib\site-
packages (from pandas->bioinfokit) (2024.1)
Requirement already satisfied: tzdata>=2022.7 in c:\users\akhil\anaconda3\lib\sit
e-packages (from pandas->bioinfokit) (2023.3)
Requirement already satisfied: joblib>=1.2.0 in c:\users\akhil\anaconda3\lib\site
-packages (from scikit-learn->bioinfokit) (1.4.2)
Requirement already satisfied: threadpoolctl>=3.1.0 in c:\users\akhil\anaconda3\l
ib\site-packages (from scikit-learn->bioinfokit) (3.5.0)
Requirement already satisfied: patsy>=0.5.6 in c:\users\akhil\anaconda3\lib\site-
packages (from statsmodels->bioinfokit) (0.5.6)
Requirement already satisfied: six in c:\users\akhil\anaconda3\lib\site-packages
(from patsy>=0.5.6->statsmodels->bioinfokit) (1.16.0)
```

In [3]:

```
# Reading the McDonald's dataset from the CSV file into a DataFrame
data = pd.read_csv("mcdonalds.csv")  # Load the dataset into 'data' DataFrame

# Reading the same dataset into a second DataFrame
data1 = pd.read_csv("mcdonalds.csv")  # Load the dataset again into 'data1' Data
```

```
# Displaying the list of column names in the dataset
data.columns.values.tolist()  # Get the column names of the dataset as a list
```

Out[3]:

```
['yummy',
 'convenient',
 'spicy',
 'fattening',
 'greasy',
 'fast',
 'cheap',
 'tasty',
 'expensive',
 'healthy',
 'disgusting',
 'Like',
 'Age',
 'VisitFrequency',
 'Gender']
```

In [4]:

```
# Getting the shape of the dataset, which returns the number of rows and columns
data.shape
```

Out[4]:

```
(1453, 15)
```

In [5]:

```
# Displaying the first 3 rows of the dataset to inspect the data
data.head(3)
```

Out[5]:

	yummy	convenient	spicy	fattening	greasy	fast	cheap	tasty	expensive	healthy
0	No	Yes	No	Yes	No	Yes	Yes	No	Yes	No
1	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	No
2	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes

In [6]:

```
# Selecting the first 11 columns of the dataset and replacing 'Yes' with 1 and '
MD=data.iloc[:,0:11].replace("Yes",1).replace("No",0)
# Calculating the mean of each column in the transformed DataFrame, rounded to 2
mean=round(MD.mean(),2)
mean   # Output the mean values
```

```
C:\Users\akhil\AppData\Local\Temp\ipykernel_11232\4102938980.py:2: FutureWarning:
Downcasting behavior in `replace` is deprecated and will be removed in a future v
ersion. To retain the old behavior, explicitly call `result.infer_objects(copy=Fa
lse)`. To opt-in to the future behavior, set `pd.set_option('future.no_silent_dow
ncasting', True)`
  MD=data.iloc[:,0:11].replace("Yes",1).replace("No",0)
```

Out[6]:
```
yummy         0.55
convenient    0.91
spicy         0.09
fattening     0.87
greasy        0.53
fast          0.90
cheap         0.60
tasty         0.64
expensive     0.36
healthy       0.20
disgusting    0.24
dtype: float64
```

In [7]:
```
# Initializing PCA (Principal Component Analysis) object
pca = PCA()
# Applying PCA on the MD data and transforming it to a new space with fewer dime
MD_pca=pca.fit_transform(MD)
# Fitting PCA on the MD data to learn the principal components (without transfor
MD_p=pca.fit(MD)

# Calculating the standard deviation for each principal component
SD=np.sqrt(pca.explained_variance_)
# Calculating the proportion of variance explained by each principal component
PV=pca.explained_variance_ratio_
# Creating a list of principal component names (e.g., 'PC1', 'PC2', etc.)
index=[]
for i in range(len(SD)):
    i=i+1
    index.append("PC{}".format(i))

# Creating a DataFrame to summarize standard deviations, proportion of variance,
sum=pd.DataFrame({
    "Standard deviation":SD,"Proportion of Variance":PV,"Cumulative Proportion":
},index=index)
sum   #Display the summary DataFrame
```

Out[7]:

	Standard deviation	Proportion of Variance	Cumulative Proportion
PC1	0.757050	0.299447	0.299447
PC2	0.607456	0.192797	0.492244
PC3	0.504619	0.133045	0.625290
PC4	0.398799	0.083096	0.708386
PC5	0.337405	0.059481	0.767866
PC6	0.310275	0.050300	0.818166
PC7	0.289697	0.043849	0.862015
PC8	0.275122	0.039548	0.901563
PC9	0.265251	0.036761	0.938323
PC10	0.248842	0.032353	0.970677
PC11	0.236903	0.029323	1.000000

In [8]:
```
# Printing the standard deviation of each principal component, rounded to 1 deci
print("Standard Deviation:\n",SD.round(1))

# Getting the loadings (principal component coefficients)
load = (pca.components_)
# Extracting the rotation matrix (principal components in the original space)
i=0
rot_matrix = MD_p.components_.T

# Creating a DataFrame to display the rotation matrix, with column names as prin
rot_df = pd.DataFrame(rot_matrix, index=MD.columns.values, columns=index)
# Rounding the rotation matrix values to 3 decimal places and flipping the signs
rot_df=round(-rot_df,3)
rot_df   # Display the rotated matrix DataFrame
```

```
Standard Deviation:
 [0.8 0.6 0.5 0.4 0.3 0.3 0.3 0.3 0.3 0.2 0.2]
```

Out[8]:

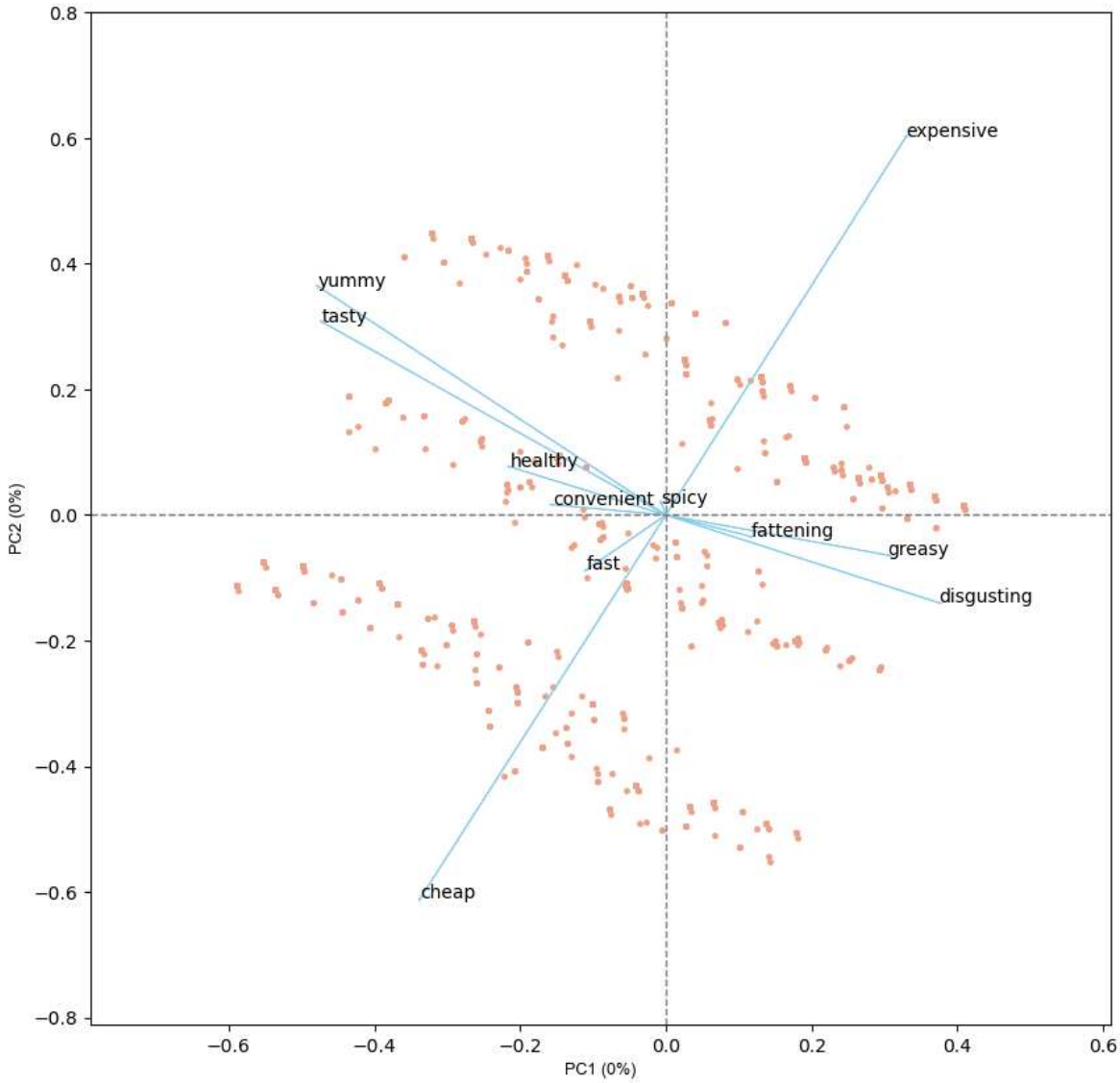
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
yummy	-0.477	0.364	-0.304	-0.055	-0.308	0.171	0.281	0.013	0.572	-0.110
convenient	-0.155	0.016	-0.063	0.142	0.278	-0.348	0.060	-0.113	-0.018	-0.666
spicy	-0.006	0.019	-0.037	-0.198	0.071	-0.355	-0.708	0.376	0.400	-0.076
fattening	0.116	-0.034	-0.322	0.354	-0.073	-0.407	0.386	0.590	-0.161	-0.005
greasy	0.304	-0.064	-0.802	-0.254	0.361	0.209	-0.036	-0.138	-0.003	0.009
fast	-0.108	-0.087	-0.065	0.097	0.108	-0.595	0.087	-0.628	0.166	0.240
cheap	-0.337	-0.611	-0.149	-0.119	-0.129	-0.103	0.040	0.140	0.076	0.428
tasty	-0.472	0.307	-0.287	0.003	-0.211	-0.077	-0.360	-0.073	-0.639	0.079
expensive	0.329	0.601	0.024	-0.068	-0.003	-0.261	0.068	0.030	0.067	0.454
healthy	-0.214	0.077	0.192	-0.763	0.288	-0.178	0.350	0.176	-0.186	-0.038
disgusting	0.375	-0.140	-0.089	-0.370	-0.729	-0.211	0.027	-0.167	-0.072	-0.290

In [9]:
```
# Displaying the rotation matrix (loadings of original features for each princip
rot_df
```

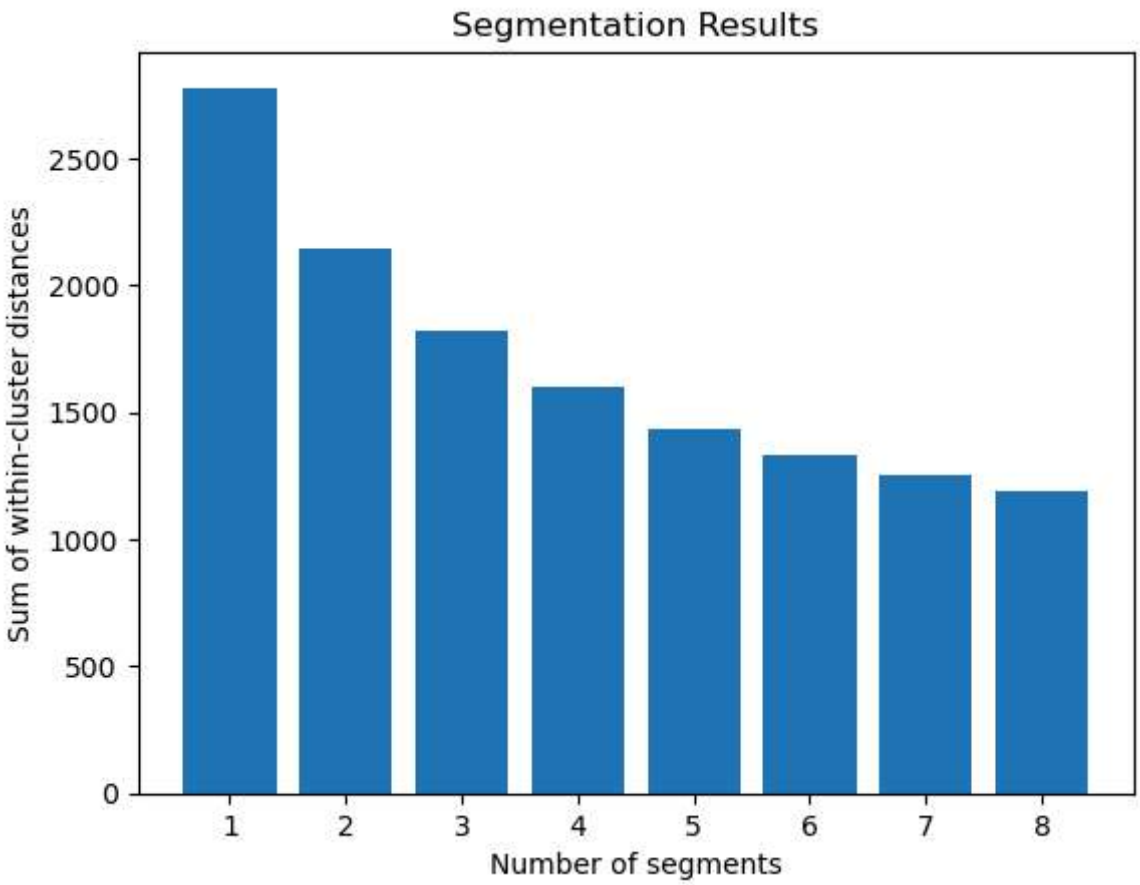
Out[9]:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
yummy	-0.477	0.364	-0.304	-0.055	-0.308	0.171	0.281	0.013	0.572	-0.110
convenient	-0.155	0.016	-0.063	0.142	0.278	-0.348	0.060	-0.113	-0.018	-0.666
spicy	-0.006	0.019	-0.037	-0.198	0.071	-0.355	-0.708	0.376	0.400	-0.076
fattening	0.116	-0.034	-0.322	0.354	-0.073	-0.407	0.386	0.590	-0.161	-0.005
greasy	0.304	-0.064	-0.802	-0.254	0.361	0.209	-0.036	-0.138	-0.003	0.009
fast	-0.108	-0.087	-0.065	0.097	0.108	-0.595	0.087	-0.628	0.166	0.240
cheap	-0.337	-0.611	-0.149	-0.119	-0.129	-0.103	0.040	0.140	0.076	0.428
tasty	-0.472	0.307	-0.287	0.003	-0.211	-0.077	-0.360	-0.073	-0.639	0.079
expensive	0.329	0.601	0.024	-0.068	-0.003	-0.261	0.068	0.030	0.067	0.454
healthy	-0.214	0.077	0.192	-0.763	0.288	-0.178	0.350	0.176	-0.186	-0.038
disgusting	0.375	-0.140	-0.089	-0.370	-0.729	-0.211	0.027	-0.167	-0.072	-0.290

In [10]:
```
cluster.biplot(cscore=MD_pca, loadings=-load, labels=data.columns.values,var1=0,
```



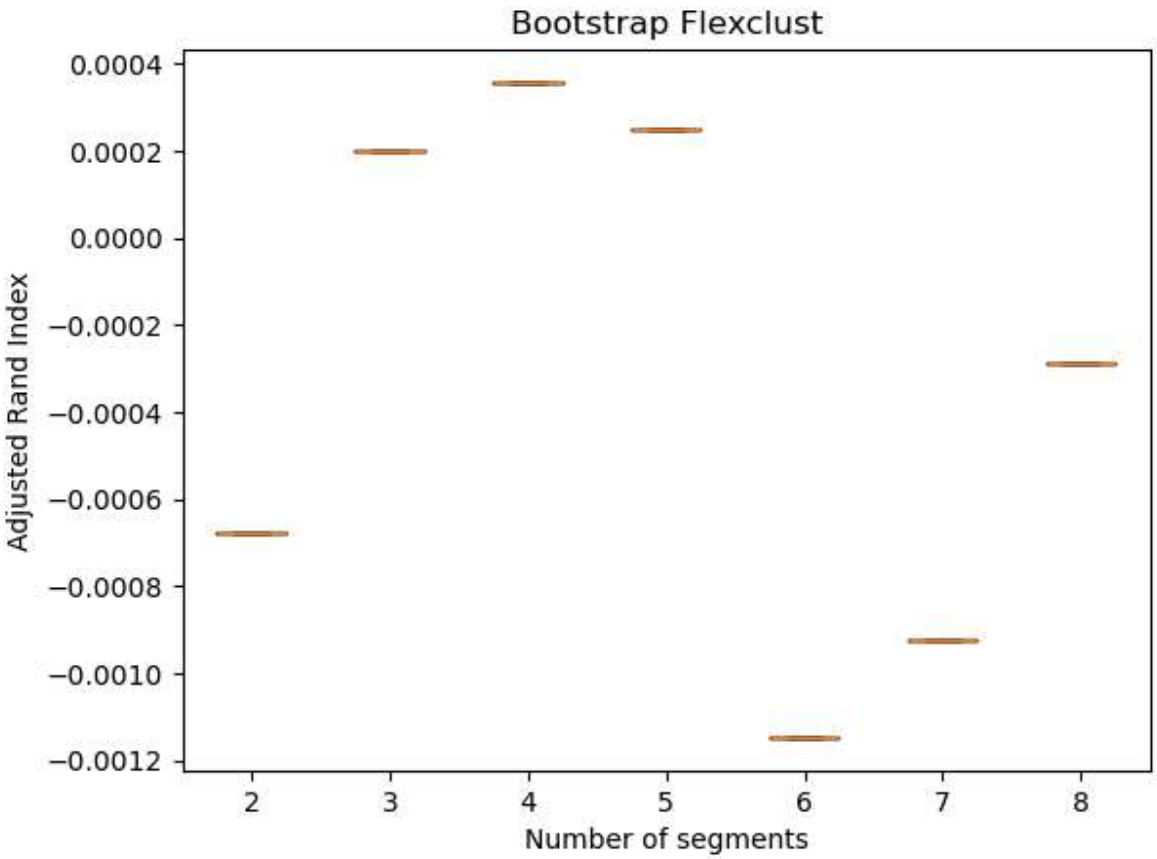
In [11]:
```
np.random.seed(1234)

nrep = 10

num_segments = range(1, 9)
within_cluster_distances = []
MD_km28 = {}

for k in num_segments:
    kmeans = KMeans(n_clusters=k, n_init=nrep, random_state=1234)
    kmeans.fit(MD)
    within_cluster_distances.append((kmeans.inertia_))
    MD_km28[str(k)] = kmeans

plt.bar(num_segments, within_cluster_distances)
plt.xlabel("Number of segments")
plt.ylabel("Sum of within-cluster distances")
plt.title("Segmentation Results")
plt.show()
```



In [12]:
```
np.random.seed(1234)
nboot = 100
nrep = 10

bootstrap_samples = []
for _ in range(nboot):
    bootstrap_sample = resample(MD.values, random_state=1234)
    bootstrap_samples.append(bootstrap_sample)

adjusted_rand_index = []
num_segments = range(2, 9)
for k in num_segments:
```

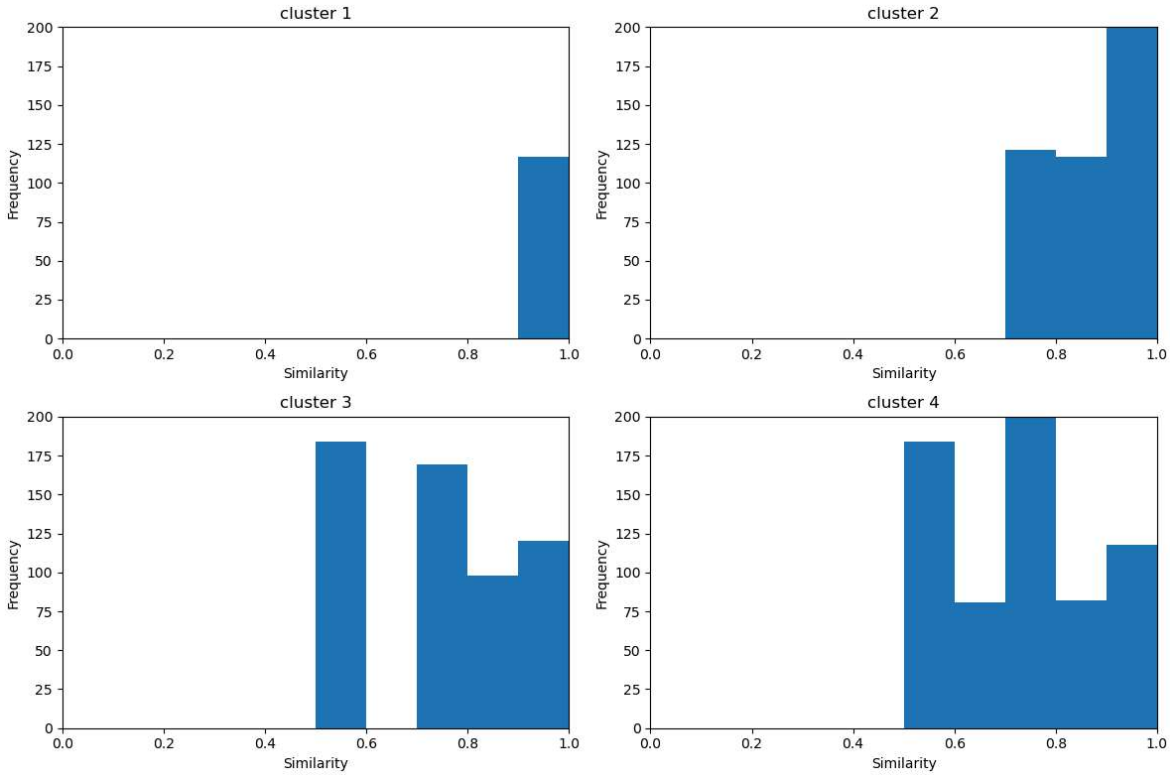
```
    stability_scores = []
    for bootstrap_sample in bootstrap_samples:
        kmeans = KMeans(n_clusters=k, n_init=nrep, random_state=1234)
        kmeans.fit(bootstrap_sample)
        cluster_labels = kmeans.predict(bootstrap_sample)
        true_labels = kmeans.predict(MD.values)
        stability_score = adjusted_rand_score(true_labels, cluster_labels)
        stability_scores.append(stability_score)
    adjusted_rand_index.append(stability_scores)

# Transpose the adjusted_rand_index list
adjusted_rand_index = np.array(adjusted_rand_index).T

# Create boxplot of adjusted Rand index
plt.boxplot(adjusted_rand_index, labels=num_segments, whis=10)
plt.xlabel("Number of segments")
plt.ylabel("Adjusted Rand Index")
plt.title("Bootstrap Flexclust")
plt.show()
```

```
C:\Users\akhil\AppData\Local\Temp\ipykernel_11232\3897380082.py:27: MatplotlibDep
recationWarning: The 'labels' parameter of boxplot() has been renamed 'tick_label
s' since Matplotlib 3.9; support for the old name will be dropped in 3.11.
  plt.boxplot(adjusted_rand_index, labels=num_segments, whis=10)
```



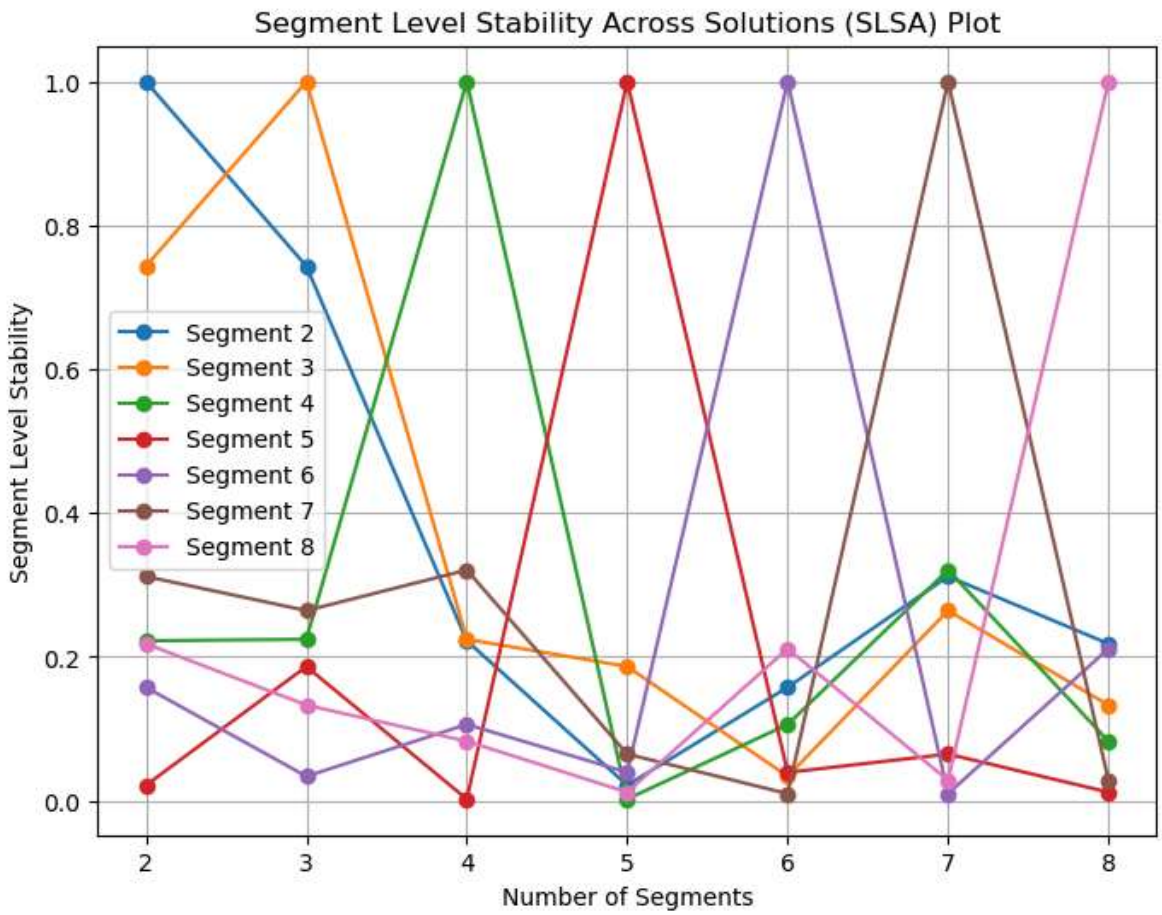
In [13]:
```
range_values = (0, 1)
num_bins = 10
max_frequency = 200


fig, axs = plt.subplots(2, 2, figsize=(12, 8))


for i in range(1, 5):
```

```
    labels = MD_km28[str(i)].predict(MD)
    similarities = MD_km28[str(i)].transform(MD).min(axis=1)
    row = (i - 1) // 2
    col = (i - 1) % 2

    axs[row, col].hist(similarities, bins=num_bins, range=range_values)
    axs[row, col].set_xlabel('Similarity')
    axs[row, col].set_ylabel('Frequency')
    axs[row, col].set_title('cluster {}'.format(i))

    axs[row, col].set_xlim(range_values)
    axs[row, col].set_ylim(0, max_frequency)


    axs[row, col].set_xticks([0, 0.2, 0.4, 0.6, 0.8, 1.0])

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

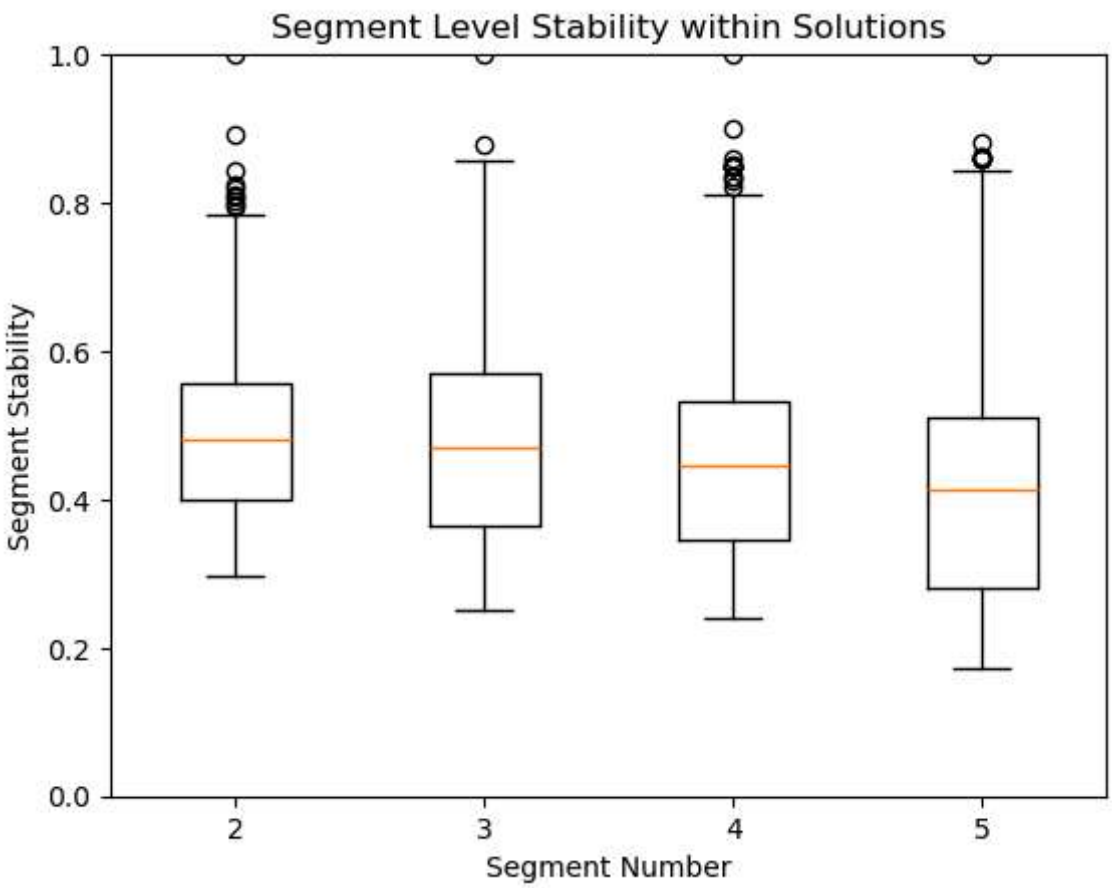


In [14]:
```
num_segments = range(2, 9)

segment_stability = []
for segment in range(2, 9):
    labels_segment = MD_km28[str(segment)].predict(MD)
    segment_stability.append(labels_segment)

plt.figure(figsize=(8, 6))
for i, segment in enumerate(range(2, 9)):
    plt.plot(num_segments, [np.mean(segment_stability[i] == labels) for labels i

plt.xlabel('Number of Segments')
plt.ylabel('Segment Level Stability')
plt.title('Segment Level Stability Across Solutions (SLSA) Plot')
plt.xticks(num_segments)
plt.legend()
plt.grid(True)
```

```
plt.show()
```



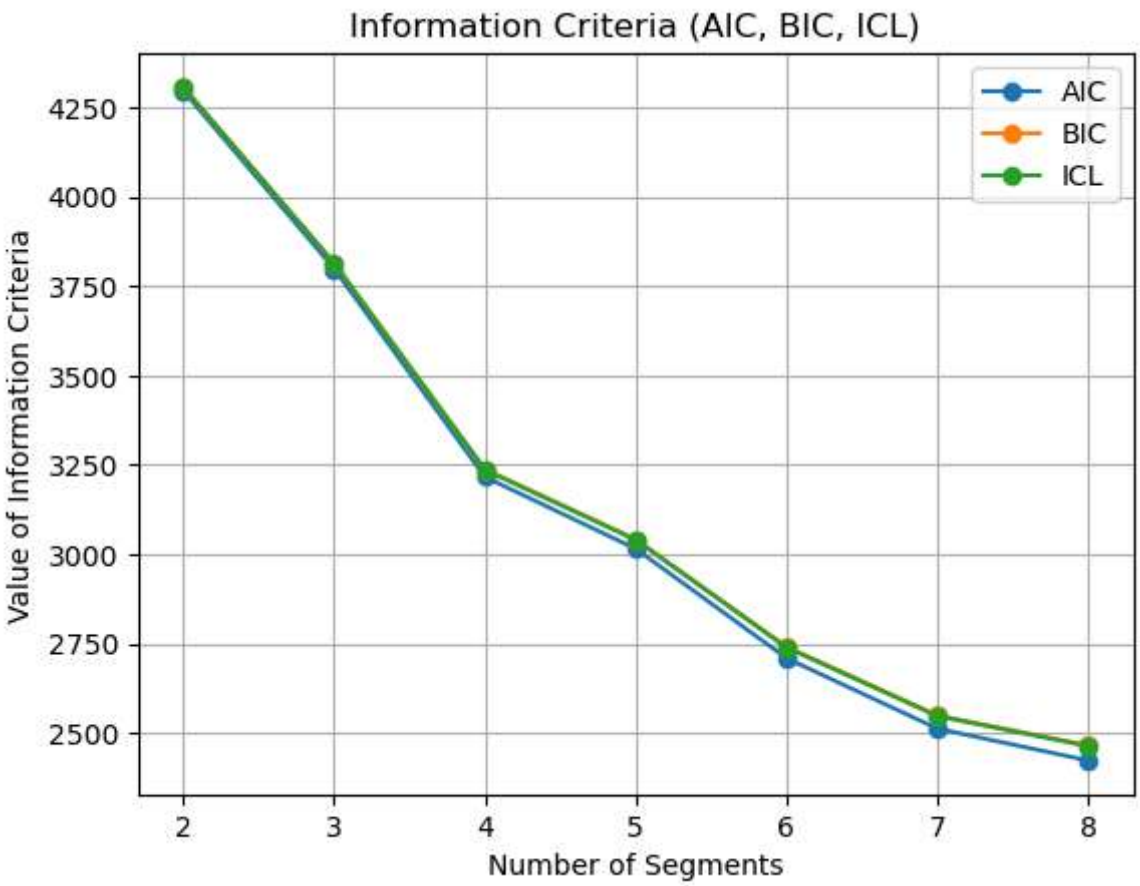
In [15]:
```
segment_solutions = ["2", "3", "4", "5"]
segment_labels = {}
segment_similarities = {}

for segment in segment_solutions:
    segment_labels[segment] = MD_km28[segment].predict(MD)
    segment_similarities[segment] = MD_km28[segment].transform(MD).min(axis=1)

segment_stability_values = []
for segment in segment_solutions:
    similarities = segment_similarities[segment]
    normalized_similarities = similarities / np.max(similarities)
    segment_stability_values.append(normalized_similarities)

plt.boxplot(segment_stability_values, whis=1.5)
plt.xlabel("Segment Number")
plt.ylabel("Segment Stability")
plt.xticks(range(1, len(segment_solutions) + 1), segment_solutions)
plt.ylim(0, 1)
plt.title("Segment Level Stability within Solutions")

plt.show()
```



In [16]:
```
from scipy.stats import entropy

np.random.seed(1234)
k_values = range(2, 9)
MD_m28 = []

for k in k_values:
    model = KMeans(n_clusters=k, random_state=1234)
    model.fit(MD.values)
    iter_val = model.n_iter_
    converged = True
    k_val = k
    k0_val = k
    log_likelihood = -model.inertia_
    n_samples, _ = MD.shape
    aic = -2 * log_likelihood + 2 * k
    bic = -2 * log_likelihood + np.log(n_samples) * k
    labels = model.labels_
    counts = np.bincount(labels)
    probs = counts / float(counts.sum())
    class_entropy = entropy(probs)
    icl = bic - class_entropy

    MD_m28.append((iter_val, converged, k_val, k0_val, log_likelihood, aic, bic,
MD_m28 = pd.DataFrame(MD_m28, columns=['iter', 'converged', 'k', 'k0', 'logLik',

print(MD_m28)
```

	iter	converged	k	k0	logLik	AIC	BIC	ICL
0	13	True	2	2	-2146.062044	4296.124088	4306.686859	4306.015908
1	5	True	3	3	-1896.330266	3798.660532	3814.504689	3813.529671
2	8	True	4	4	-1604.234391	3216.468783	3237.594326	3236.258023
3	9	True	5	5	-1502.697153	3015.394306	3041.801234	3040.267284
4	7	True	6	6	-1348.665399	2709.330799	2741.019113	2739.277954
5	10	True	7	7	-1249.233890	2512.467780	2549.437480	2547.530062
6	9	True	8	8	-1203.646165	2423.292330	2465.543415	2463.533662

In [17]:
```
num_segments = MD_m28["k"]
AIC_values = MD_m28["AIC"]
BIC_values = MD_m28["BIC"]
ICL_values = MD_m28["ICL"]

plt.plot(num_segments, AIC_values, marker='o', label='AIC')
plt.plot(num_segments, BIC_values, marker='o', label='BIC')
plt.plot(num_segments, ICL_values, marker='o', label='ICL')

plt.xlabel('Number of Segments')
plt.ylabel('Value of Information Criteria')
plt.title('Information Criteria (AIC, BIC, ICL)')
plt.legend()
plt.grid(True)

plt.show()
```



In [18]:
```
from sklearn.mixture import GaussianMixture
k = 4
kmeans = KMeans(n_clusters=k, random_state=1234)
kmeans.fit(MD)
kmeans_clusters = kmeans.predict(MD)

gmm = GaussianMixture(n_components=k, random_state=1234)
```

```
gmm.fit(MD)
gmm_clusters = gmm.predict(MD)

results = pd.DataFrame({'kmeans': kmeans_clusters, 'mixture': gmm_clusters})

MD_m4 = MD[results['mixture'] == 3]

k4_m4 = KMeans(n_clusters=k, random_state=1234)
k4_m4.fit(MD_m4)
k4_m4_clusters = k4_m4.predict(MD_m4)

results_m4 = pd.DataFrame({'kmeans': k4_m4_clusters, 'mixture': 3})

print(pd.crosstab(results['kmeans'], results['mixture']))
print(pd.crosstab(results['kmeans'], results_m4['kmeans']))
```

```
mixture    0    1    2    3
kmeans
0        508    0    4   39
1          0  215   11    4
2         44    3  267    8
3          0   36   15  299
kmeans   0   1   2   3
kmeans
0       22  29  14  73
1        9  10   7  26
2       15  14   5  42
3        9  20  13  42
```

```
c:\Users\akhil\anaconda3\Lib\site-packages\sklearn\cluster\_kmeans.py:1429: UserW
arning: KMeans is known to have a memory leak on Windows with MKL, when there are
less chunks than available threads. You can avoid it by setting the environment v
ariable OMP_NUM_THREADS=2.
  warnings.warn(
```

In [19]:

```
from sklearn.mixture import GaussianMixture
import numpy as np

gmm_m4a = GaussianMixture(n_components=4)
gmm_m4a.fit(MD)

log_likelihood_m4a = gmm_m4a.score(MD)

gmm_m4 = GaussianMixture(n_components=4)
gmm_m4.fit(MD)

log_likelihood_m4 = gmm_m4.score(MD)

print("Log-likelihood for MD.m4a:", log_likelihood_m4a)
print("Log-likelihood for MD.m4:", log_likelihood_m4)
```

```
Log-likelihood for MD.m4a: 11.068744792060572
Log-likelihood for MD.m4: 3.6427464011765824
```

In [20]:

```
like_counts = pd.value_counts(data['Like'])
reversed_counts = like_counts.iloc[::-1]

print(reversed_counts)
```

```
Like
-1                 58
-2                 59
-4                 71
-3                 73
I love it!+5      143
I hate it!-5      152
+1                152
+4                160
0                 169
+2                187
+3                229
Name: count, dtype: int64
```

```
C:\Users\akhil\AppData\Local\Temp\ipykernel_11232\1008934694.py:1: FutureWarning:
pandas.value_counts is deprecated and will be removed in a future version. Use p
d.Series(obj).value_counts() instead.
  like_counts = pd.value_counts(data['Like'])
```

In [21]:

```python
# Define a mapping of string values to numeric codes
like_mapping = {
    'I HATE IT!-5': -5,
    '-4': -4,
    '-3': -3,
    '-2': -2,
    '-1': -1,
    '0': 0,
    '1': 1,
    '2': 2,
    '3': 3,
    '4': 4,
    'I LOVE IT!+5': 5
}

data['Like.n'] = data['Like'].map(like_mapping)


like_n_counts = data['Like.n'].value_counts()


print(like_n_counts)
```

```
Like.n
 0.0    169
-3.0     73
-4.0     71
-2.0     59
-1.0     58
Name: count, dtype: int64
```

In [22]:

```python
from patsy import dmatrices

independent_vars = data.columns[0:11]

formula_str = ' + '.join(independent_vars)

formula_str = 'Like ~ ' + formula_str


f = dmatrices(formula_str, data=data)[1]
```

```
print(f)
```

```
[[1. 0. 1. ... 1. 0. 0.]
 [1. 1. 1. ... 1. 0. 0.]
 [1. 0. 1. ... 1. 1. 0.]
 ...
 [1. 1. 1. ... 1. 0. 0.]
 [1. 1. 1. ... 0. 1. 0.]
 [1. 0. 1. ... 1. 0. 1.]]
```

In [23]:

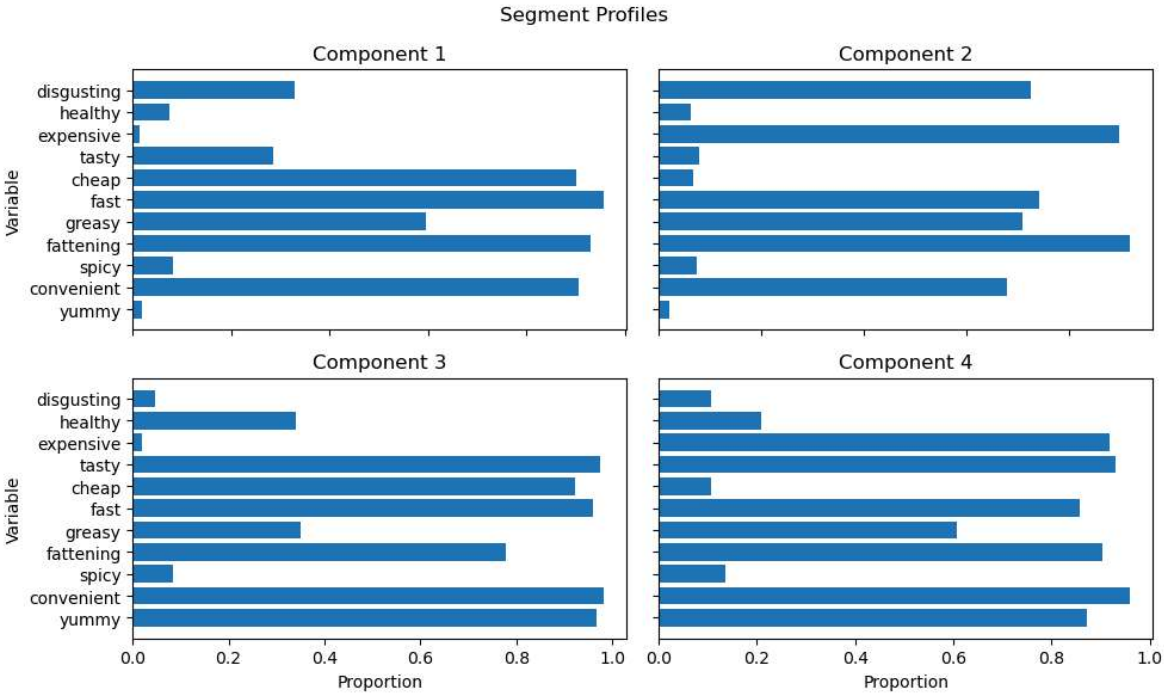
```
from sklearn.mixture import GaussianMixture
from patsy import dmatrix
np.random.seed(1234)

X = dmatrix(f.design_info, data=data)
y = dmatrix('Like', data=data)

n_components = 2
n_init = 10
verbose = False
n_rep=10

model = GaussianMixture(n_components=n_components, n_init=n_init, verbose=verbos
MD_reg2 = model.fit(X, y)

print(MD_reg2)
cluster_sizes = np.bincount(model.predict(X))

print("Cluster sizes:")
for i, size in enumerate(cluster_sizes):
    print(f"{i+1}: {size}")
```

```
GaussianMixture(n_components=2, n_init=10, verbose=False)
Cluster sizes:
1: 985
2: 468
```

In [24]:

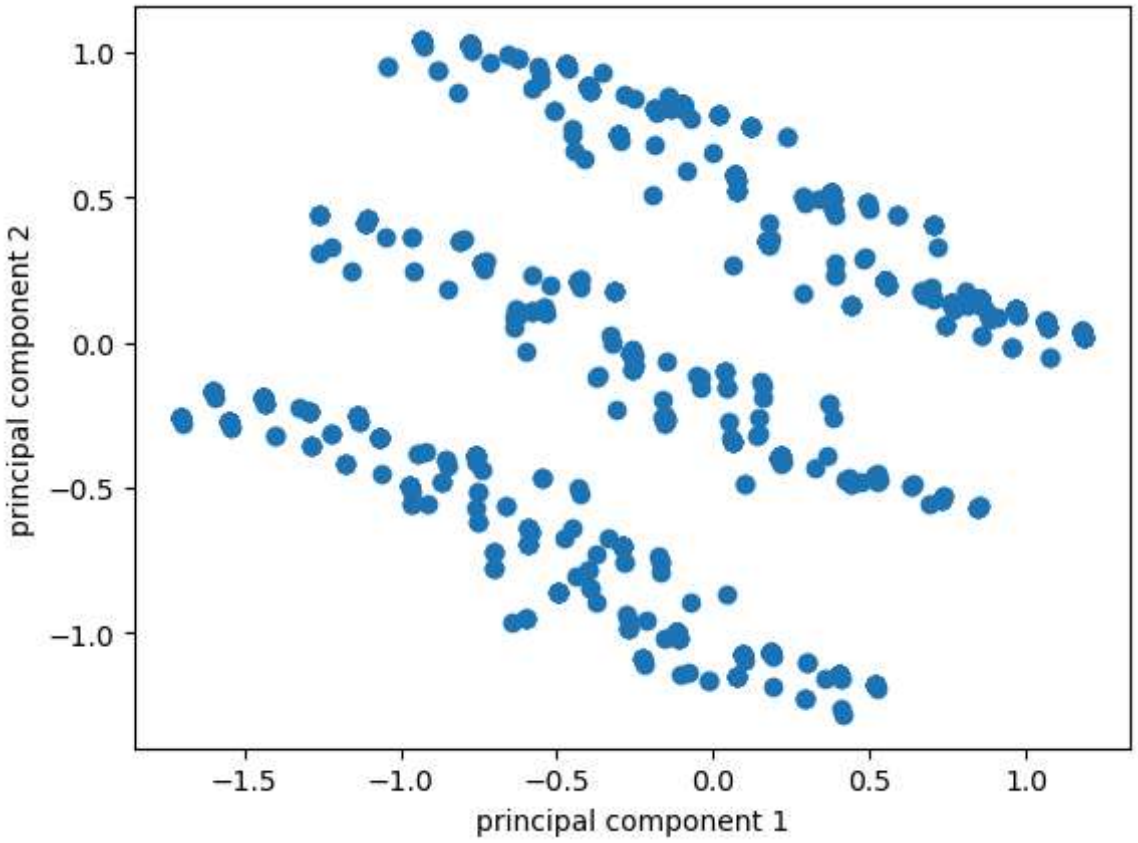
```
import pandas as pd
# Importing pandas for data manipulation

import matplotlib.pyplot as plt
# Importing matplotlib for plotting
kmeans = MD_km28['4']

import pandas as pd
import matplotlib.pyplot as plt

kmeans = MD_km28['4']

labels = kmeans.labels_

MD_mean = MD.groupby(labels).mean()

fig, axs = plt.subplots(2, 2, figsize=(10, 6))
axs[0, 0].barh(range(MD_mean.shape[1]), MD_mean.iloc[0])
axs[0, 0].set_title('Component 1')
axs[0, 1].barh(range(MD_mean.shape[1]), MD_mean.iloc[1])
axs[0, 1].set_title('Component 2')
axs[1, 0].barh(range(MD_mean.shape[1]), MD_mean.iloc[2])
axs[1, 0].set_title('Component 3')
```

```
axs[1, 1].barh(range(MD_mean.shape[1]), MD_mean.iloc[3])
axs[1, 1].set_title('Component 4')

for ax in axs.flat:
    ax.set(ylabel='Variable', xlabel='Proportion')
    ax.set_yticks(range(MD_mean.shape[1]))
    ax.set_yticklabels(MD.columns)

for ax in axs.flat:
    ax.label_outer()

fig.suptitle('Segment Profiles')

fig.tight_layout()

plt.show()
```



In [25]:

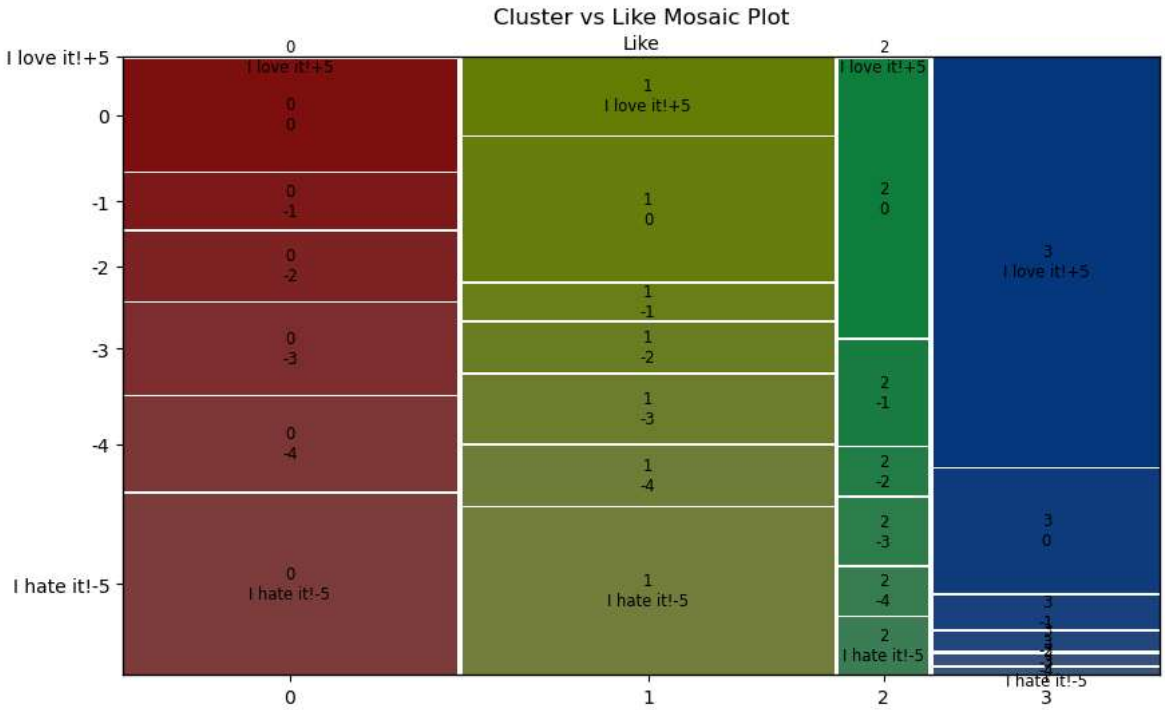
```
from sklearn.cluster import KMeans # Importing KMeans clustering algorithm from

from sklearn.decomposition import PCA # Importing PCA (Principal Component Analy
import matplotlib.pyplot as plt # Importing matplotlib for plotting
kmeans = KMeans(n_clusters=4) # Creating a KMeans model with 4 clusters
kmeans.fit(MD) # Fitting the KMeans model on the dataset 'MD'
pca = PCA(n_components=2) # Initializing PCA to reduce data to 2 principal compo
MD_pca = pca.fit_transform(MD) # Applying PCA on 'MD' to transform it into 2D da
fig, ax = plt.subplots() # Creating a new matplotlib figure and axis
ax.scatter(MD_pca[:, 0], MD_pca[:, 1]) # Creating a scatter plot using the two p
ax.set_xlabel('principal component 1') # Labeling the x-axis as the first princi
ax.set_ylabel('principal component 2') # Labeling the y-axis as the second princ
plt.show() # Displaying the scatter plot
```



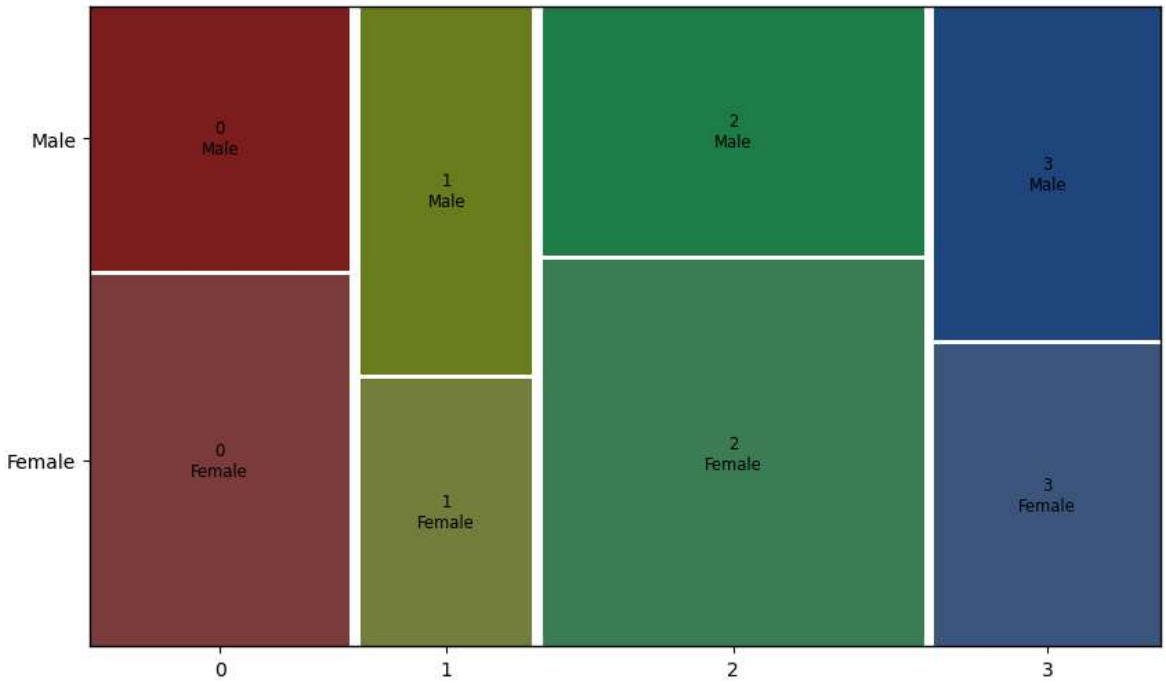
In [27]:

```
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from sklearn.preprocessing import LabelEncoder
from statsmodels.graphics.mosaicplot import mosaic

# Sample: assuming you already have `data1` DataFrame loaded
# If not, load it here like: data1 = pd.read_csv('your_file.csv')

# Define a function to apply label encoding
def labelling(x):
    data1[x] = LabelEncoder().fit_transform(data1[x])
    return data1

# List of 11 categorical columns (yes/no features)
cat = ['yummy', 'convenient', 'spicy', 'fattening', 'greasy', 'fast',
       'cheap', 'tasty', 'expensive', 'healthy', 'disgusting']

# Apply label encoding to each categorical column
for i in cat:
    labelling(i)

# Extract only the 11 encoded columns into a new DataFrame
df_eleven = data1.loc[:, cat]

# Apply KMeans clustering
kmeans = KMeans(n_clusters=4, init='k-means++', random_state=0)
data1['cluster_num'] = kmeans.fit_predict(df_eleven)

# Create a crosstab of clusters vs. 'Like' column
crosstab = pd.crosstab(data1['cluster_num'], data1['Like'])

# Check actual column types in crosstab
```

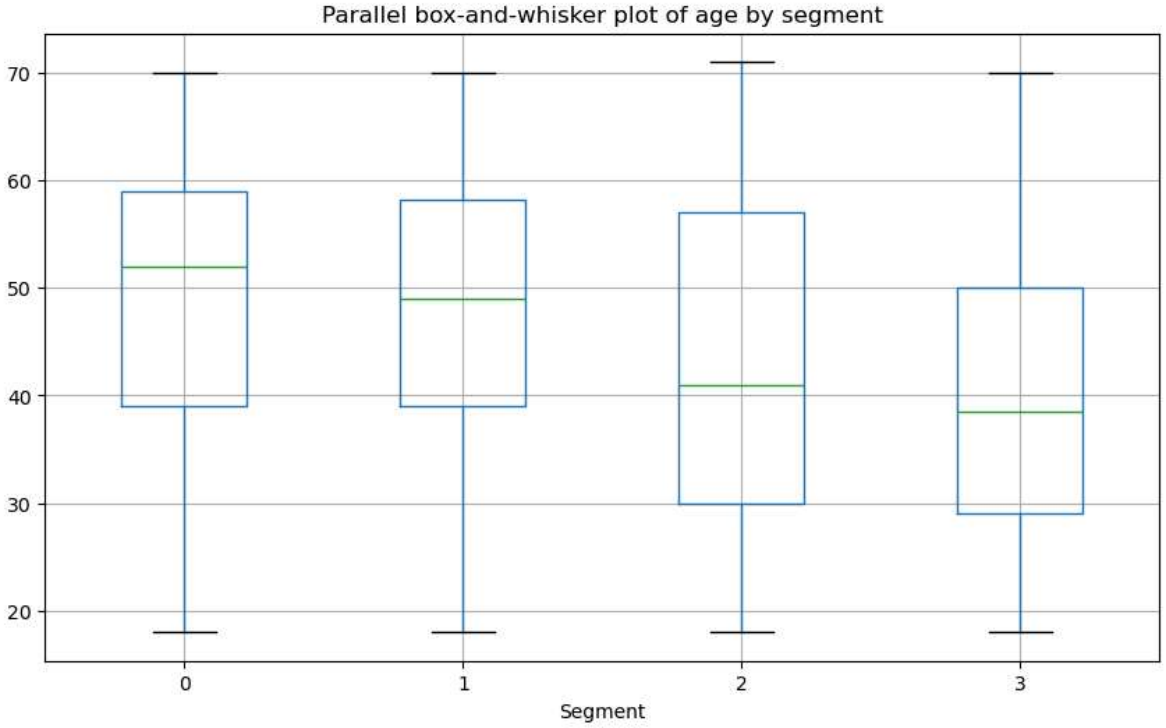
```
# Convert column names to string for consistent plotting
crosstab.columns = crosstab.columns.astype(str)

# Define the desired order of Like responses (only include those that exist)
ordered_columns = ['I hate it!-5', '-4', '-3', '-2', '-1', '0', '1', '2', '3', '
ordered_columns = [col for col in ordered_columns if col in crosstab.columns]

# Reorder crosstab columns
crosstab = crosstab[ordered_columns]

# Set plot size and display mosaic plot
plt.rcParams['figure.figsize'] = (10, 6)
mosaic(crosstab.stack(), title='Cluster vs Like Mosaic Plot')
plt.xlabel("Like")
plt.ylabel("Cluster")
plt.show()
```



In [28]:
```
from statsmodels.graphics.mosaicplot import mosaic # Importing the mosaic plot f
MD_k4=MD_km28['4'] # Extracting the clustering model for 4 clusters from the dic
k4 = MD_k4.labels_ # Getting the cluster labels assigned by the k-means model fo
ct = pd.crosstab(k4, data['Gender']) # Creating a cross-tabulation table of clus
ct # Displaying the cross-tabulation table
mosaic(ct.stack(),gap=0.01) # Plotting a mosaic plot to visually compare gender
plt.show() # Displaying the mosaic plot
```



In [29]:
```
df = pd.DataFrame({'Segment': k4, 'Age': data['Age']}) # Creating a new DataFram
df.boxplot(by='Segment', column='Age') # Creating a box-and-whisker plot of 'Age
plt.title('Parallel box-and-whisker plot of age by segment') # Setting the title
plt.suptitle('') # Removing the default subplot title to keep the plot clean
plt.show() # Displaying the box plot
```



In [30]:
```
data1['VisitFrequency'] = LabelEncoder().fit_transform(data1['VisitFrequency'])
# Encoding the 'VisitFrequency' column into numeric values using LabelEncoder
visit = data1.groupby('cluster_num')['VisitFrequency'].mean()
# Calculating the average visit frequency for each cluster
visit = visit.to_frame().reset_index()
# Converting the result to a DataFrame and resetting the index
visit
# Displaying the DataFrame showing average visit frequency per cluster
```

Out[30]:

	cluster_num	VisitFrequency
0	0	2.787162
1	1	2.596195
2	2	2.618321
3	3	2.598553

In [31]:

```
#Like
data1['Like'] = LabelEncoder().fit_transform(data1['Like']) # Encoding the 'Like
Like = data1.groupby('cluster_num')['Like'].mean()# Calculating the average 'Lik
Like = Like.to_frame().reset_index() # Converting the result into a DataFrame an
Like # Displaying the DataFrame with average 'Like' scores per cluster
```

Out[31]:

	cluster_num	Like
0	0	5.888514
1	1	4.957717
2	2	3.694656
3	3	3.915009

In [32]:

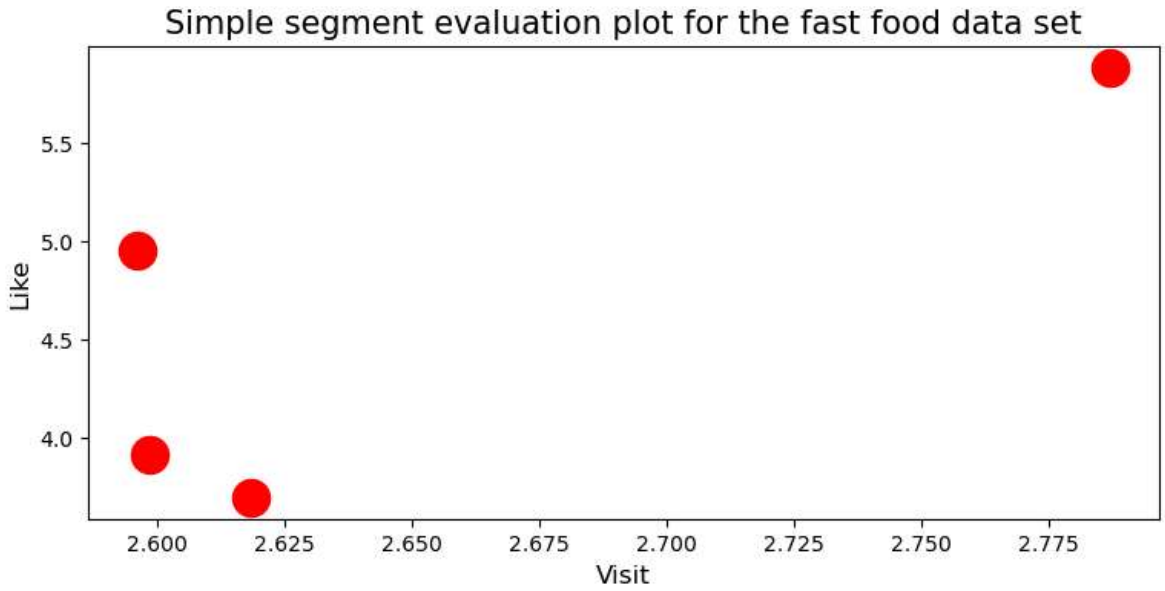
```
data1['Gender'] = LabelEncoder().fit_transform(data1['Gender']) # Encoding the '
Gender = data1.groupby('cluster_num')['Gender'].mean()# Calculating the mean gen
Gender = Gender.to_frame().reset_index()# Converting the Series to a DataFrame a
Gender # Displaying the final DataFrame showing average gender per cluster
```

Out[32]:

	cluster_num	Gender
0	0	0.432432
1	1	0.547569
2	2	0.427481
3	3	0.401447

In [33]:

```
import seaborn as sns # Importing the seaborn library for statistical data visua
segment = Gender.merge(Like, on='cluster_num', how='left').merge(visit, on='clus

segment# Displaying the merged DataFrame
plt.figure(figsize = (9,4))# Creating a new figure with a specific size of 9 inc
sns.scatterplot(x = "VisitFrequency", y = "Like",data=segment,s=400, color="r")
plt.title("Simple segment evaluation plot for the fast food data set",fontsize =
plt.xlabel("Visit", fontsize = 12)# Labeling the x-axis as "Visit" with font siz
plt.ylabel("Like", fontsize = 12)# Labeling the y-axis as "Like" with font size
plt.show()# Displaying the final plot
```


Simple segment evaluation plot for the fast food data set
Like
5.5
5.0
4.5
4.0
2.600
2.625
2.650
2.675
2.700
2.725
2.750
2.775
Visit

```
In [ ]:
```