```
import pandas as pd
```

```
path = "/content/mcdonalds.csv"
import pandas as pd
from sklearn.decomposition import PCA
import numpy as np
from sklearn import preprocessing
from bioinfokit.visuz import cluster
import matplotlib.pyplot as plt
from sklearn.cluster import KMeans
from sklearn.utils import resample
from sklearn.metrics import adjusted_rand_score
```

```
pip install bioinfokit
```

```
Requirement already satisfied: bioinfokit in /usr/local/lib/python3.10/dist-packages (2.1.4)
Requirement already satisfied: pandas in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (2.0.3)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (1.25.2)
Requirement already satisfied: matplotlib in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (3.7.1)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (1.11.4)
Requirement already satisfied: scikit-learn in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (1.2.2)
Requirement already satisfied: seaborn in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (0.13.1)
Requirement already satisfied: matplotlib-venn in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (0.11.10)
Requirement already satisfied: tabulate in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (0.9.0)
Requirement already satisfied: statsmodels in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (0.14.2)
Requirement already satisfied: textwrap3 in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (0.9.2)
Requirement already satisfied: adjustText in /usr/local/lib/python3.10/dist-packages (from bioinfokit) (1.2.0)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (1.2.1)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (4.53.1)
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (1.4.5)
Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (24.1)
Requirement already satisfied: pillow>=6.2.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (9.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (3.1.2)
Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib->bioinfokit) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas->bioinfokit) (2023.4)
Requirement already satisfied: tzdata>=2022.1 in /usr/local/lib/python3.10/dist-packages (from pandas->bioinfokit) (2024.1)
Requirement already satisfied: joblib>=1.1.1 in /usr/local/lib/python3.10/dist-packages (from scikit-learn->bioinfokit) (1.4.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in /usr/local/lib/python3.10/dist-packages (from scikit-learn->bioinfokit) (3.5.0)
Requirement already satisfied: patsy>=0.5.6 in /usr/local/lib/python3.10/dist-packages (from statsmodels->bioinfokit) (0.5.6)
Requirement already satisfied: six in /usr/local/lib/python3.10/dist-packages (from patsy>=0.5.6->statsmodels->bioinfokit) (1.16.0)
```

```
data=pd.read_csv("mcdonalds.csv")
data1=pd.read_csv("mcdonalds.csv")
data.columns.values.tolist()
```

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

```
data.shape
```

```
(1453, 15)
```

```
data.head(6)
```

	yummy	convenient	spicy	fattening	greasy	fast	cheap	tasty	expensive	healthy	disgusting	Like	Age	VisitFrequency	Gender
0	No	Yes	No	Yes	No	Yes	Yes	No	Yes	No	No	-3	61	Every three months	Female
1	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	No	No	+2	51	Every three months	Female
2	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No	+1	62	Every three months	Female
3	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	No	No	Yes	+4	69	Once a week	Female

```
MD=data.iloc[:,0:11].replace("Yes",1).replace("No",0)
mean=round(MD.mean(),2)
mean
```

```
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
```

```
pca = PCA()
MD_pca=pca.fit_transform(MD)
MD_p=pca.fit(MD)

SD=np.sqrt(pca.explained_variance_)
PV=pca.explained_variance_ratio_
index=[]
for i in range(len(SD)):
    i=i+1
    index.append("PC{}".format(i))

sum=pd.DataFrame({
    "Standard deviation":SD,"Proportion of Variance":PV,"Cumulative Proportion":PV.cumsum()
},index=index)
sum
```

	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

```
print("Standard Deviation:\n",SD.round(1))

load = (pca.components_)
i=0
rot_matrix = MD_p.components_.T

rot_df = pd.DataFrame(rot_matrix, index=MD.columns.values, columns=index)
rot_df=round(-rot_df,2)
rot_df
```

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

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
yummy	0.48	-0.36	0.30	-0.06	0.31	-0.17	0.28	-0.01	-0.57	0.11	-0.05
convenient	0.16	-0.02	0.06	0.14	-0.28	0.35	0.06	0.11	0.02	0.67	0.54
spicy	0.01	-0.02	0.04	-0.20	-0.07	0.36	-0.71	-0.38	-0.40	0.08	-0.14
fattening	-0.12	0.03	0.32	0.35	0.07	0.41	0.39	-0.59	0.16	0.01	-0.25
greasy	-0.30	0.06	0.80	-0.25	-0.36	-0.21	-0.04	0.14	0.00	-0.01	-0.00
fast	0.11	0.09	0.06	0.10	-0.11	0.59	0.09	0.63	-0.17	-0.24	-0.34
cheap	0.34	0.61	0.15	-0.12	0.13	0.10	0.04	-0.14	-0.08	-0.43	0.49
tasty	0.47	-0.31	0.29	0.00	0.21	0.08	-0.36	0.07	0.64	-0.08	-0.02
expensive	-0.33	-0.60	-0.02	-0.07	0.00	0.26	0.07	-0.03	-0.07	-0.45	0.49
healthy	0.21	-0.08	-0.19	-0.76	-0.29	0.18	0.35	-0.18	0.19	0.04	-0.16
disgusting	-0.37	0.14	0.09	-0.37	0.73	0.21	0.03	0.17	0.07	0.29	0.04

```
rot_df
```

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
yummy	0.48	-0.36	0.30	-0.06	0.31	-0.17	0.28	-0.01	-0.57	0.11	-0.05
convenient	0.16	-0.02	0.06	0.14	-0.28	0.35	0.06	0.11	0.02	0.67	0.54
spicy	0.01	-0.02	0.04	-0.20	-0.07	0.36	-0.71	-0.38	-0.40	0.08	-0.14
fattening	-0.12	0.03	0.32	0.35	0.07	0.41	0.39	-0.59	0.16	0.01	-0.25
greasy	-0.30	0.06	0.80	-0.25	-0.36	-0.21	-0.04	0.14	0.00	-0.01	-0.00
fast	0.11	0.09	0.06	0.10	-0.11	0.59	0.09	0.63	-0.17	-0.24	-0.34
cheap	0.34	0.61	0.15	-0.12	0.13	0.10	0.04	-0.14	-0.08	-0.43	0.49
tasty	0.47	-0.31	0.29	0.00	0.21	0.08	-0.36	0.07	0.64	-0.08	-0.02
expensive	-0.33	-0.60	-0.02	-0.07	0.00	0.26	0.07	-0.03	-0.07	-0.45	0.49
healthy	0.21	-0.08	-0.19	-0.76	-0.29	0.18	0.35	-0.18	0.19	0.04	-0.16
disgusting	-0.37	0.14	0.09	-0.37	0.73	0.21	0.03	0.17	0.07	0.29	0.04

```
from bioinfokit.visuz import cluster


cluster.biplot(cscore=MD_pca, loadings=-load, labels=data.columns.values,var1=0,var2=0, show=True, dim=(10, 10))
```

```
WARNING:matplotlib.font_manager:findfont: Font family 'Arial' not found.
WARNING:matplotlib.font_manager:findfont: Font family 'Arial' not found.
WARNING:matplotlib.font_manager:findfont: Font family 'Arial' not found.
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WARNING:matplotlib.font_manager:findfont: Font family 'Arial' not found.
```
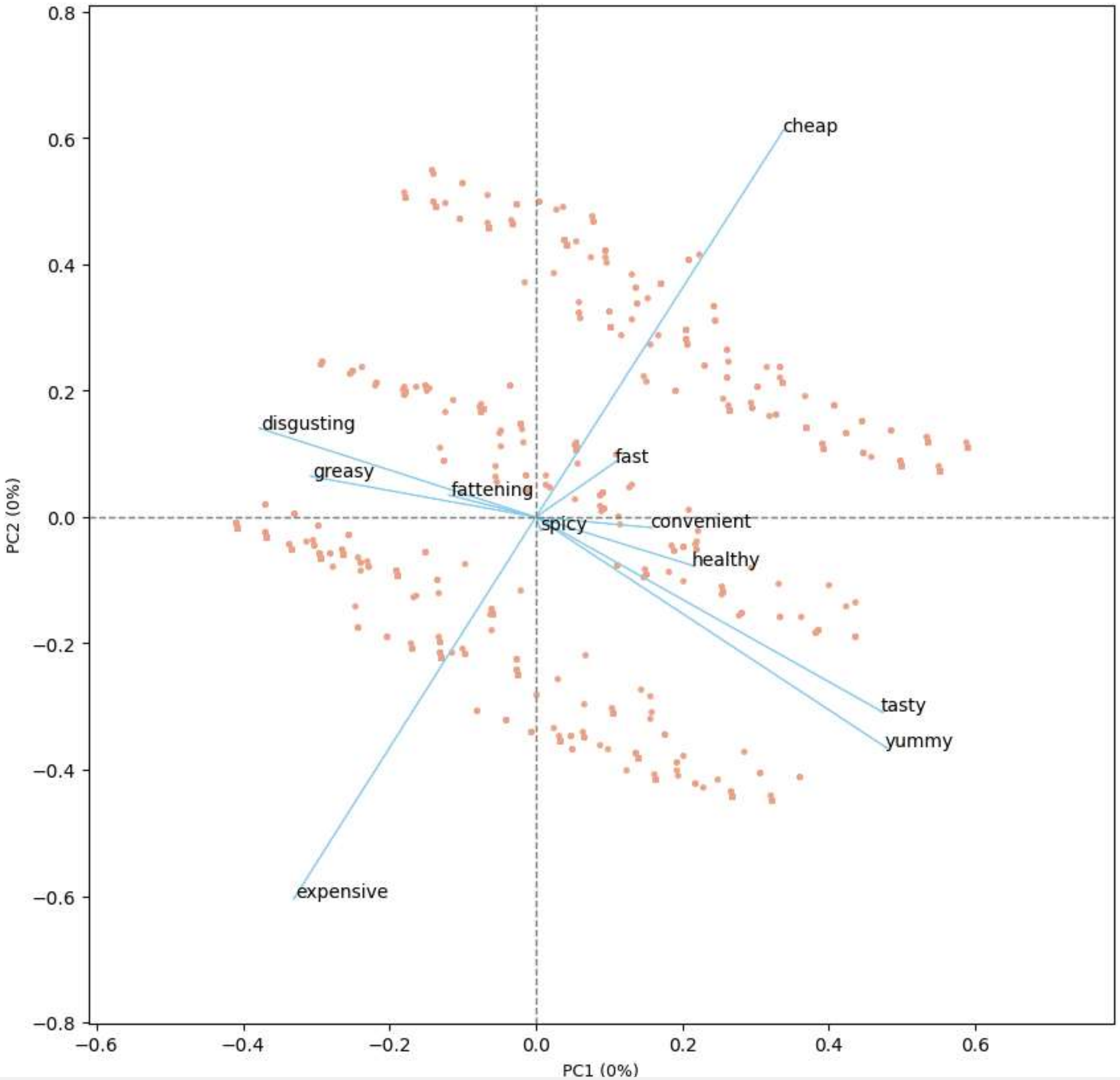
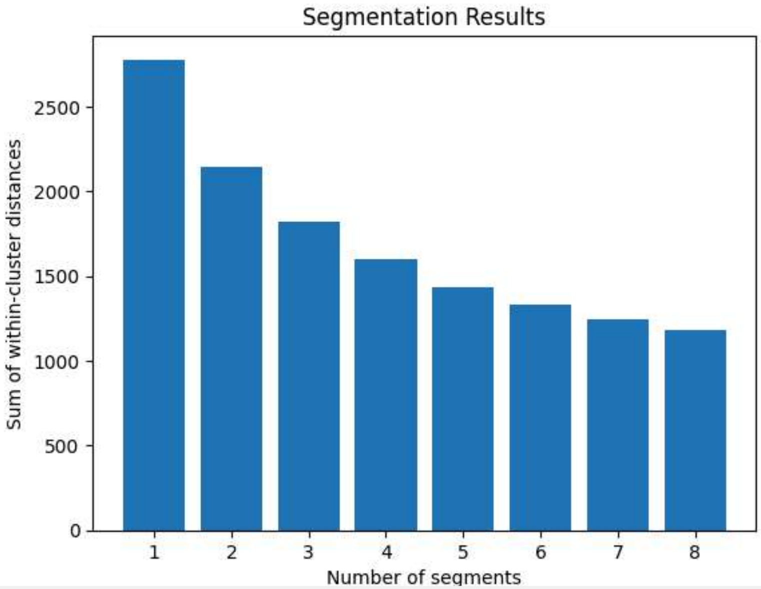
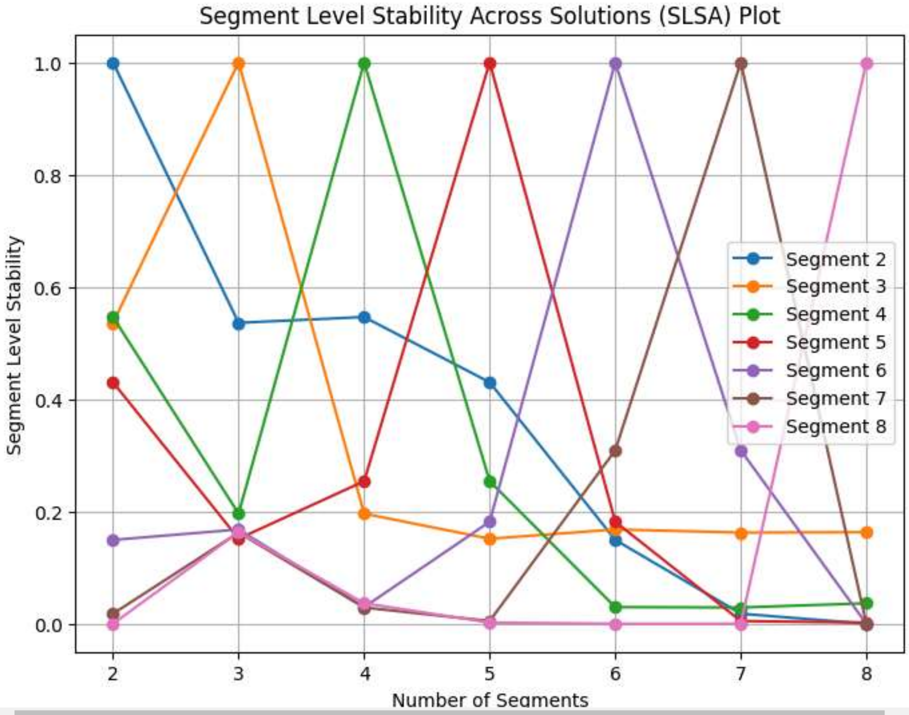



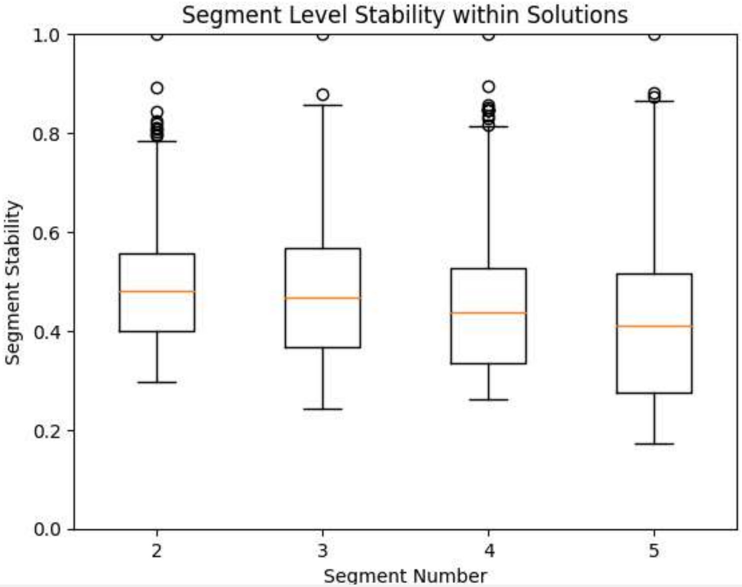
```
np.random.seed(1234)

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()
```



```
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 in segment_stability], marker='o', label=f'Segment {segment}'

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()
```



```
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()
```



```
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, icl))
MD_m28 = pd.DataFrame(MD_m28, columns=['iter', 'converged', 'k', 'k0', 'logLik', 'AIC', 'BIC', 'ICL'])

print(MD_m28)
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
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/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
   iter  converged  k  k0       logLik          AIC          BIC          ICL
0     6       True  2   2 -2145.503727  4295.007454  4305.570225  4304.904547
1     6       True  3   3 -1818.717659  3643.435318  3659.279475  3658.209672
2     9       True  4   4 -1604.107292  3216.214583  3237.340126  3235.989403
3    11       True  5   5 -1434.610417  2879.220835  2905.627763  2904.035975
4     8       True  6   6 -1331.652440  2675.304880  2706.993194  2705.228430
5     6       True  7   7 -1248.417887  2510.835774  2547.805474  2545.884829
6     9       True  8   8 -1182.100019  2380.200037  2422.451123  2420.433939
```
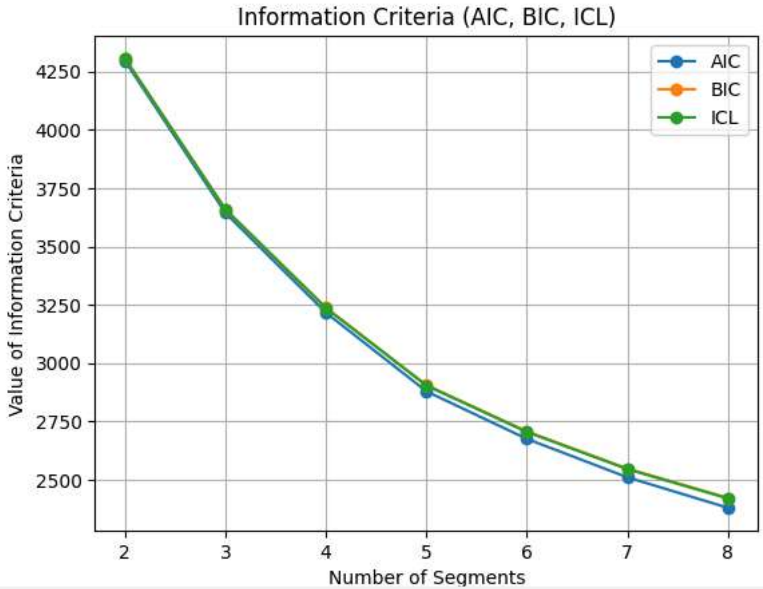

```
num_segments = MD_m28["k"]
AIC_values = MD_m28["AIC"]
BIC_values = MD_m28["BIC"]
ICL_values = MD_m28["ICL"]

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()
```



```
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']))
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
mixture   0    1   2    3
kmeans
0        20  302   0  191
1         2  116  59  189
2        90   30  14  108
3        17  150   1  164
kmeans   0   1   2   3
kmeans
0       76  52  73  32
1       40  39  51  27
2       27  30  31  11
3       43  35  51  34
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
```

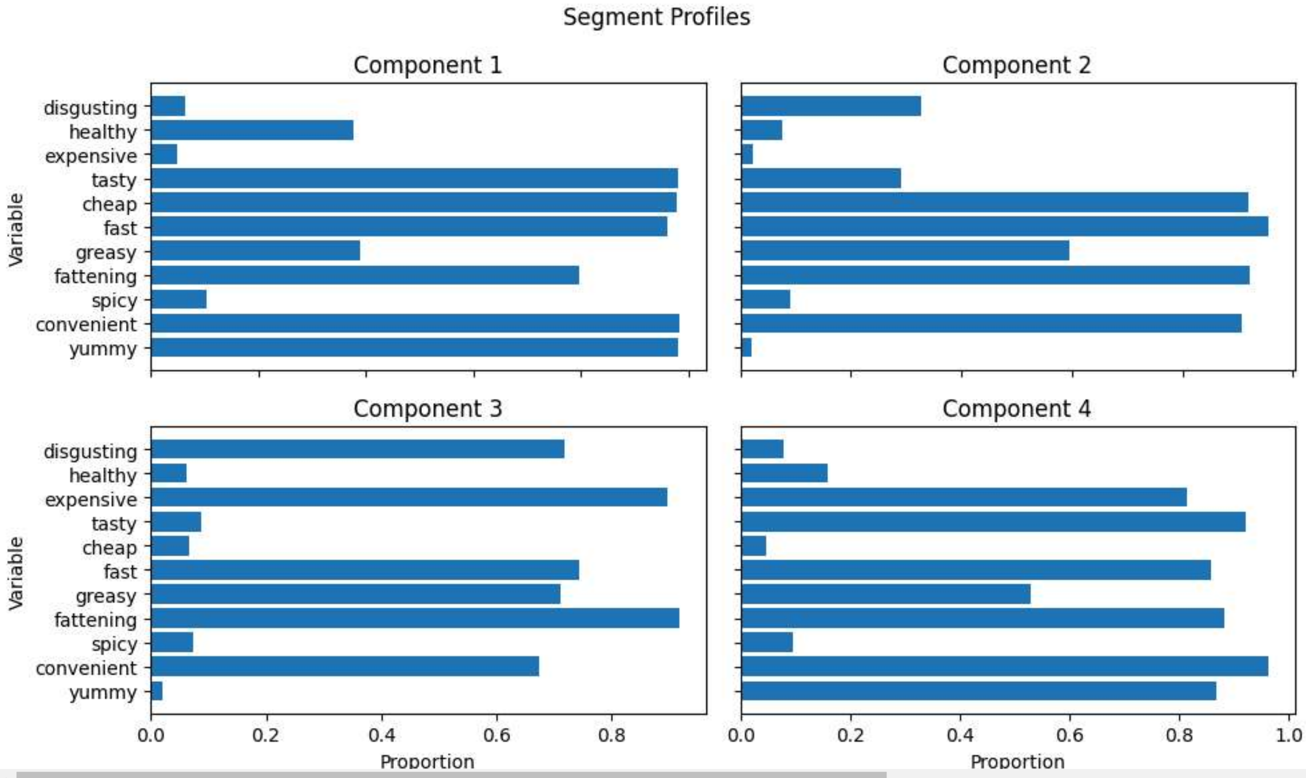
```
like_mapping = {
    'I HATE IT!-5': -5,
    '-4': -4,
    '-3': -3,
    '-2': -2,
    '-1': -1,
    '0': 0,
    '1': 1,
    '2': 2,
    '3': 3,
    '4': 4,
    'I LOVE IT!+5': 5
}

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
```

```
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)
```

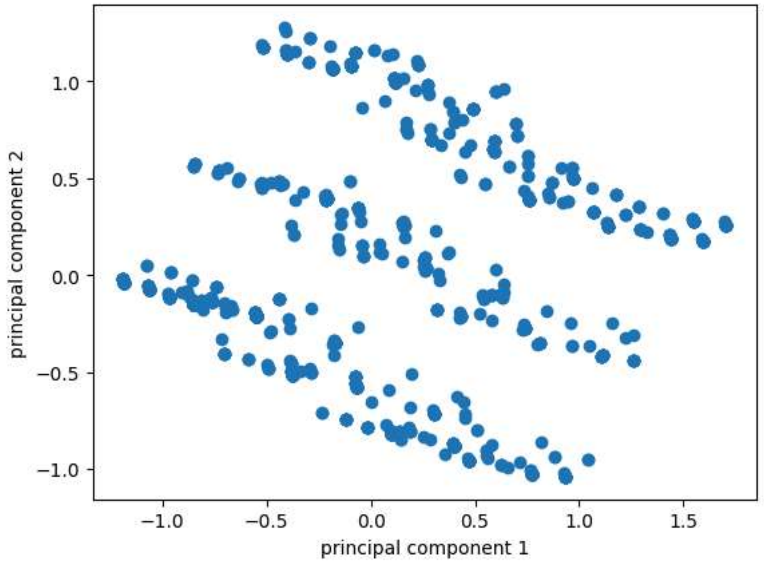
```
[[1. 0. 1. ... 1. 0. 0.]
 [1. 1. 1. ... 1. 0. 0.]
 [1. 0. 1. ... 1. 1. 0.]
 ...
 [1. 1. 1. ... 1. 0. 0.]
 [1. 1. 1. ... 0. 1. 0.]
 [1. 0. 1. ... 1. 0. 1.]]
```

```
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()
```



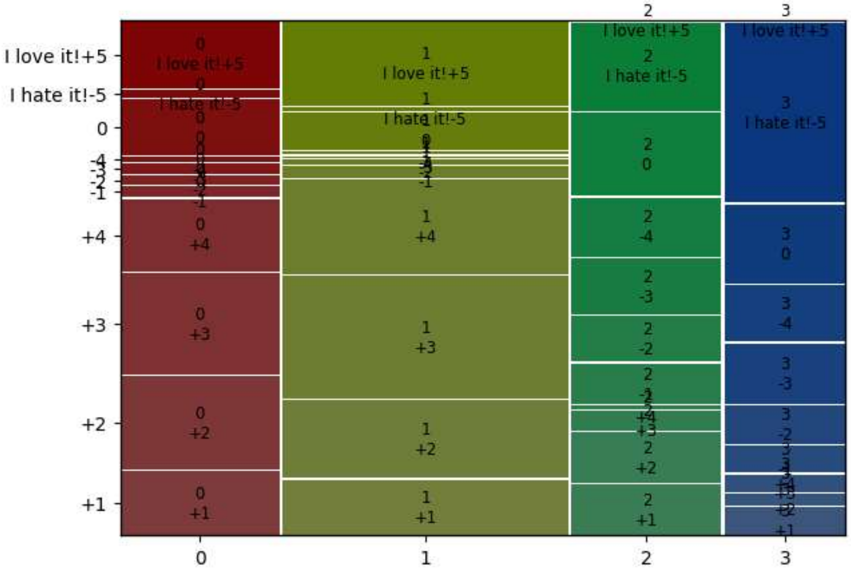
```
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt

kmeans = KMeans(n_clusters=4)
kmeans.fit(MD)

pca = PCA(n_components=2)
MD_pca = pca.fit_transform(MD)

fig, ax = plt.subplots()

ax.scatter(MD_pca[:, 0], MD_pca[:, 1])
ax.set_xlabel('principal component 1')
ax.set_ylabel('principal component 2')
plt.show()
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 1
  warnings.warn(
```

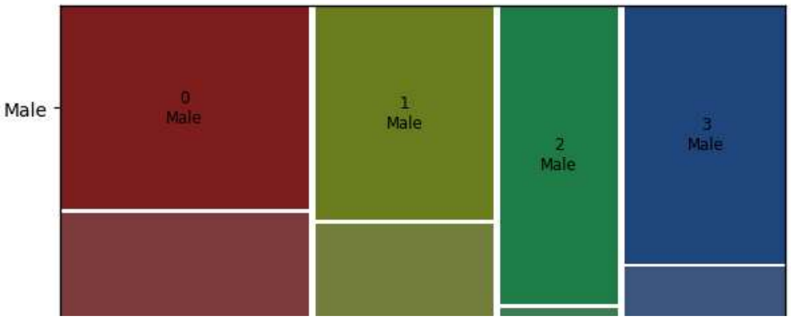


```
from statsmodels.graphics.mosaicplot import mosaic
from itertools import product
#Label encoding for categorical - Converting 11 cols with yes/no

from sklearn.preprocessing import LabelEncoder
def labelling(x):
    data1[x] = LabelEncoder().fit_transform(data1[x])
    return data1

cat = ['yummy', 'convenient', 'spicy', 'fattening', 'greasy', 'fast', 'cheap',
       'tasty', 'expensive', 'healthy', 'disgusting']

for i in cat:
    labelling(i)
data1
df_eleven = data1.loc[:,cat]
df_eleven
kmeans = KMeans(n_clusters=4, init='k-means++', random_state=0).fit(df_eleven)
data1['cluster_num'] = kmeans.labels_
crosstab =pd.crosstab(data1['cluster_num'],data1['Like'])
#Reordering cols
data1
# crosstab = crosstab[['I hate it!-5','-4','-3','-2','-1','0','1','2','3','4','I love it!+5']]
crosstab
plt.rcParams['figure.figsize'] = (7,5)
mosaic(crosstab.stack())
plt.show()
```

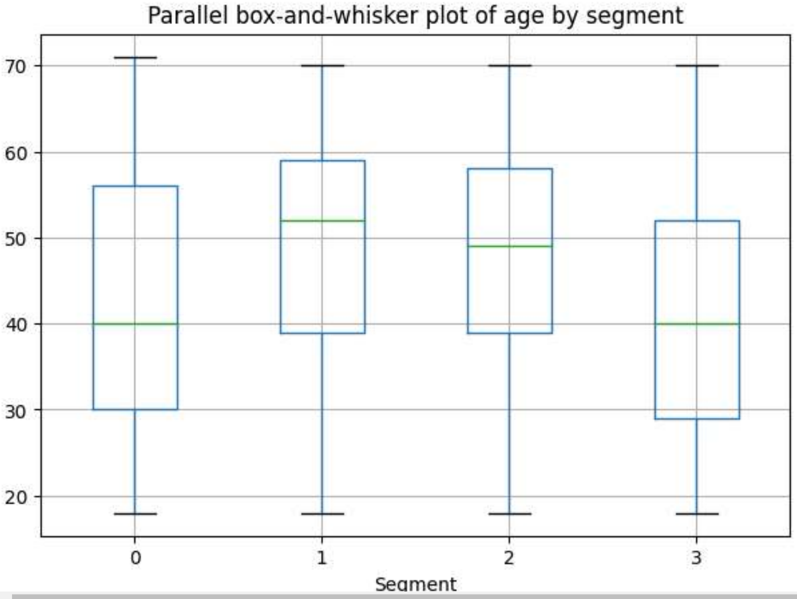
```
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10
  warnings.warn(
```



```
from statsmodels.graphics.mosaicplot import mosaic

MD_k4=MD_km28['4']
k4 = MD_k4.labels_

ct = pd.crosstab(k4, data['Gender'])
ct
mosaic(ct.stack(),gap=0.01)

plt.show()
```



```
df = pd.DataFrame({'Segment': k4, 'Age': data['Age']})

df.boxplot(by='Segment', column='Age')
plt.title('Parallel box-and-whisker plot of age by segment')
plt.suptitle('')
plt.show()
```



```
data1['VisitFrequency'] = LabelEncoder().fit_transform(data1['VisitFrequency'])
visit = data1.groupby('cluster_num')['VisitFrequency'].mean()
visit = visit.to_frame().reset_index()
visit
```

```
   cluster_num  VisitFrequency
0            0        2.547988
1            1        2.584483
2            2        2.822368
3            3        2.654472
```

```
#Like
data1['Like'] = LabelEncoder().fit_transform(data1['Like'])
Like = data1.groupby('cluster_num')['Like'].mean()
```