

Hierarchical Agglomerative Clustering

Hierarchical Agglomerative Clustering (HAC) is a type of clustering algorithm used to group similar objects into clusters.

In HAC, each object starts as its own cluster and then these clusters are merged into larger clusters in a "bottom-up" manner until all objects belong to a single cluster or until a stopping criterion is met.

Real World Use Cases

HAC has many real world use cases, including:

Customer Segmentation: HAC can be used to segment customers based on their demographic information, purchase history, and other related data to target them with personalized marketing campaigns.

Image Segmentation: HAC can be used to segment images into different regions, for example, separating foreground from background in an image.

Document Clustering: HAC can be used to group documents into topics or categories based on their content and similarity.

Social Network Analysis: HAC can be used to analyze social networks to identify communities or groups of individuals with similar interests or relationships.

Market Basket Analysis: HAC can be used to analyze market basket data to identify items that are frequently purchased together and to make recommendations to customers.

Notebook Breakdown:

This notebook contains two analyses for which HAC was used.

The **first analysis** is intended to review core HAC concepts and apply them on artificial data. The **second analysis** is much more detailed as it brings in real-world consumer data for which HAC is used for Customer Segmentation.

First Analysis - Reviewing Core Concepts

```
In [1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
from sklearn.cluster import AgglomerativeClustering
from scipy.cluster.hierarchy import dendrogram, linkage
import matplotlib.patches as mpatches
import warnings
import seaborn as sns
warnings.filterwarnings("ignore")
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
```

```
from yellowbrick.cluster import KElbowVisualizer
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
from sklearn.metrics import silhouette_score
```

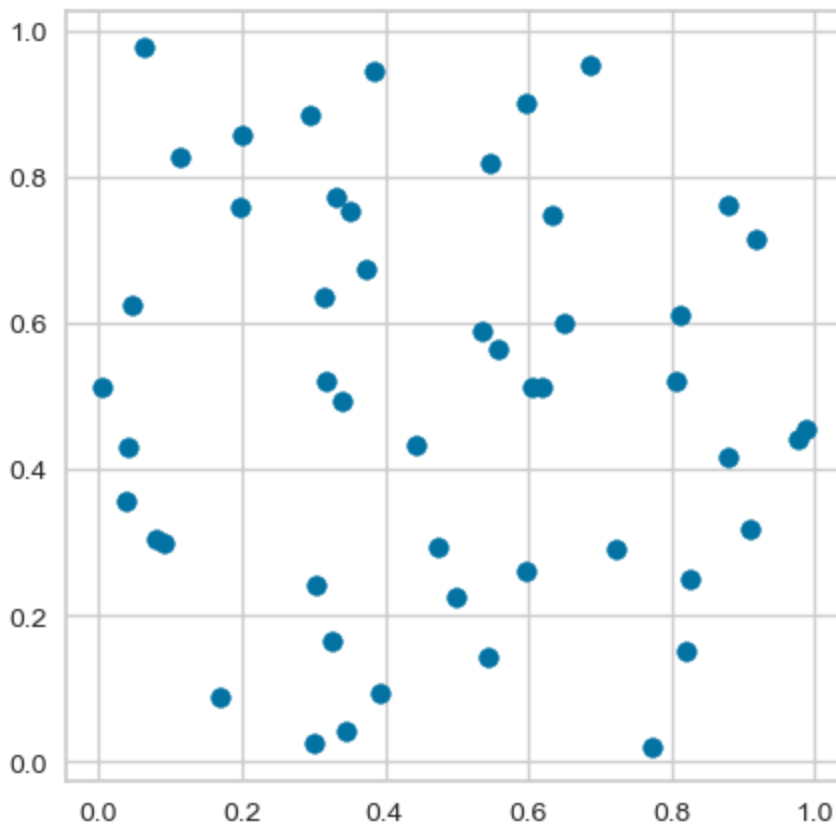
Create a random array which will be used for Hierarchical Agglomerative Clustering

```
In [2]: np.random.seed(10)
X = np.random.rand(50,2)
```

Plot the points generated in the array in order to visualize them. The goal is to cluster these using different hierarchical agglomerative clustering techniques.

```
In [3]: plt.figure(figsize=(5,5))
plt.scatter(X[:,0], X[:,1], label = 'True Position')

plt.show()
```



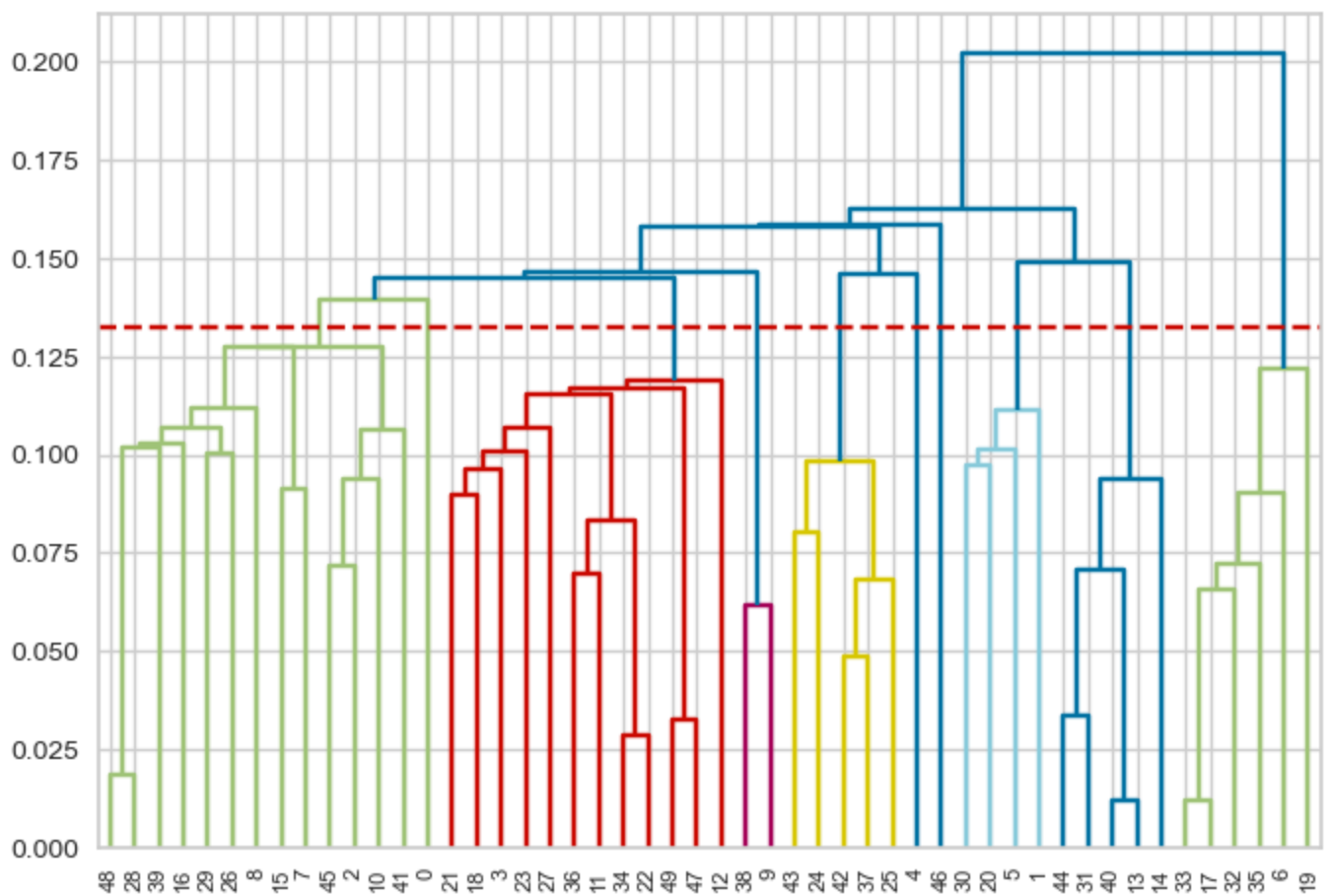
First cluster technique used, **Single Linkage**: merges two clusters if they have the closest pair of elements.

Inspecting the dendrogram helps us determine the optimal number of clusters to use. We note that the longest vertical line (largest distance) on the right-most part of the visual at roughly between 0.125 and 0.135. This spot is highlighted by the dashed red line. We note that there are *10 clusters* at this point for the Single Linkage method.

```
In [4]: linked_s = linkage(X, 'single')
labels = range(1,100)

dendrogram(linked_s, orientation = 'top', distance_sort = 'descending')
plt.axhline(y=0.1325, color='r', linestyle='--')

plt.show()
```



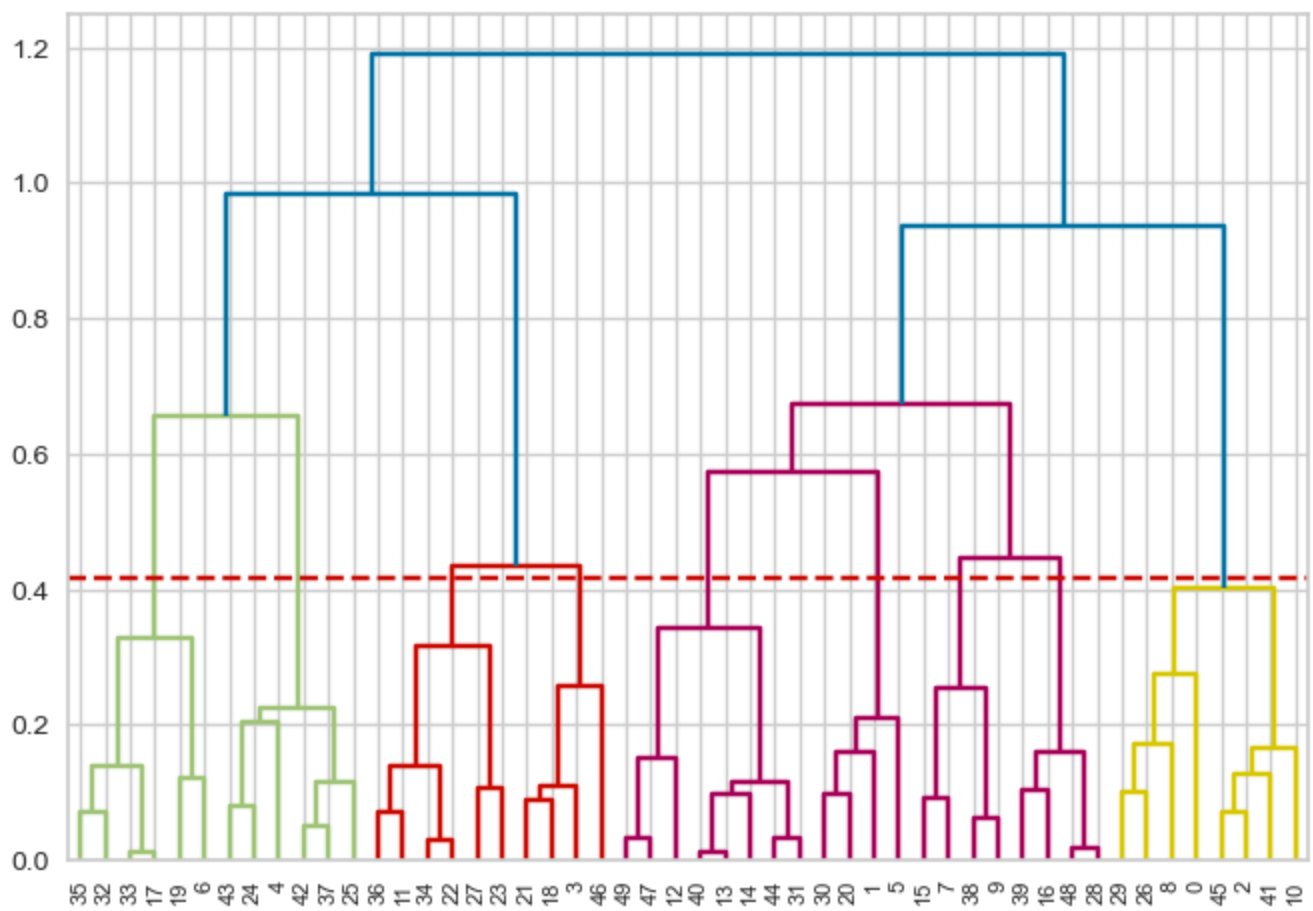
Second cluster technique used, **Complete Linkage**: merges two clusters if they have the farthest pair of elements.

Inspecting the dendrogram helps us determine the optimal number of clusters to use. We note that the longest vertical line (largest distance) on the right-most part of the visual at roughly around 0.415. This spot is highlighted by the dashed red line. We note that there are *9 clusters* at this point for the Complete Linkage method.

```
In [5]: linked_c = linkage(X, 'complete')
labels = range(1,100)

dendrogram(linked_c, orientation = 'top', distance_sort = 'descending', show_leaf_counts
plt.axhline(y=0.415, color = 'r', linestyle = '--')

plt.show()
```



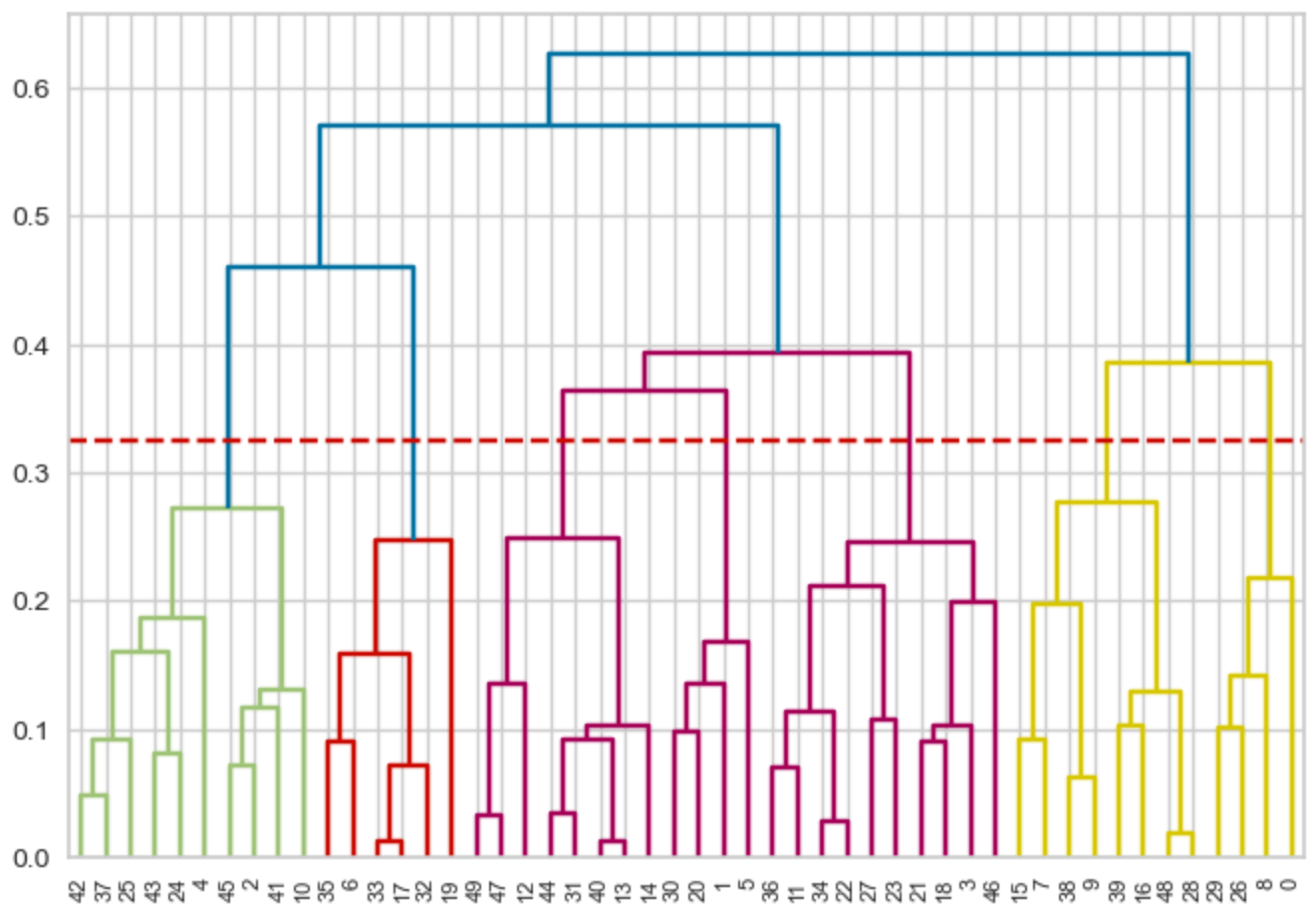
Third cluster technique used, **Average Linkage**: merges two clusters based on the average pairwise distance between elements in the two clusters.

Inspecting the dendrogram helps us determine the optimal number of clusters to use. We note that the longest vertical line (largest distance) is in the middle of the visual around 0.325. This spot is highlighted by the dashed red line. We note that there are *7 clusters* at this point for the Average Linkage method.

```
In [6]: linked_a = linkage(X, 'average')
labels = range(1,100)

dendrogram(linked_a, orientation = 'top', distance_sort = 'descending', show_leaf_counts
plt.axhline(y=0.325, color='r', linestyle='--')

plt.show()
```



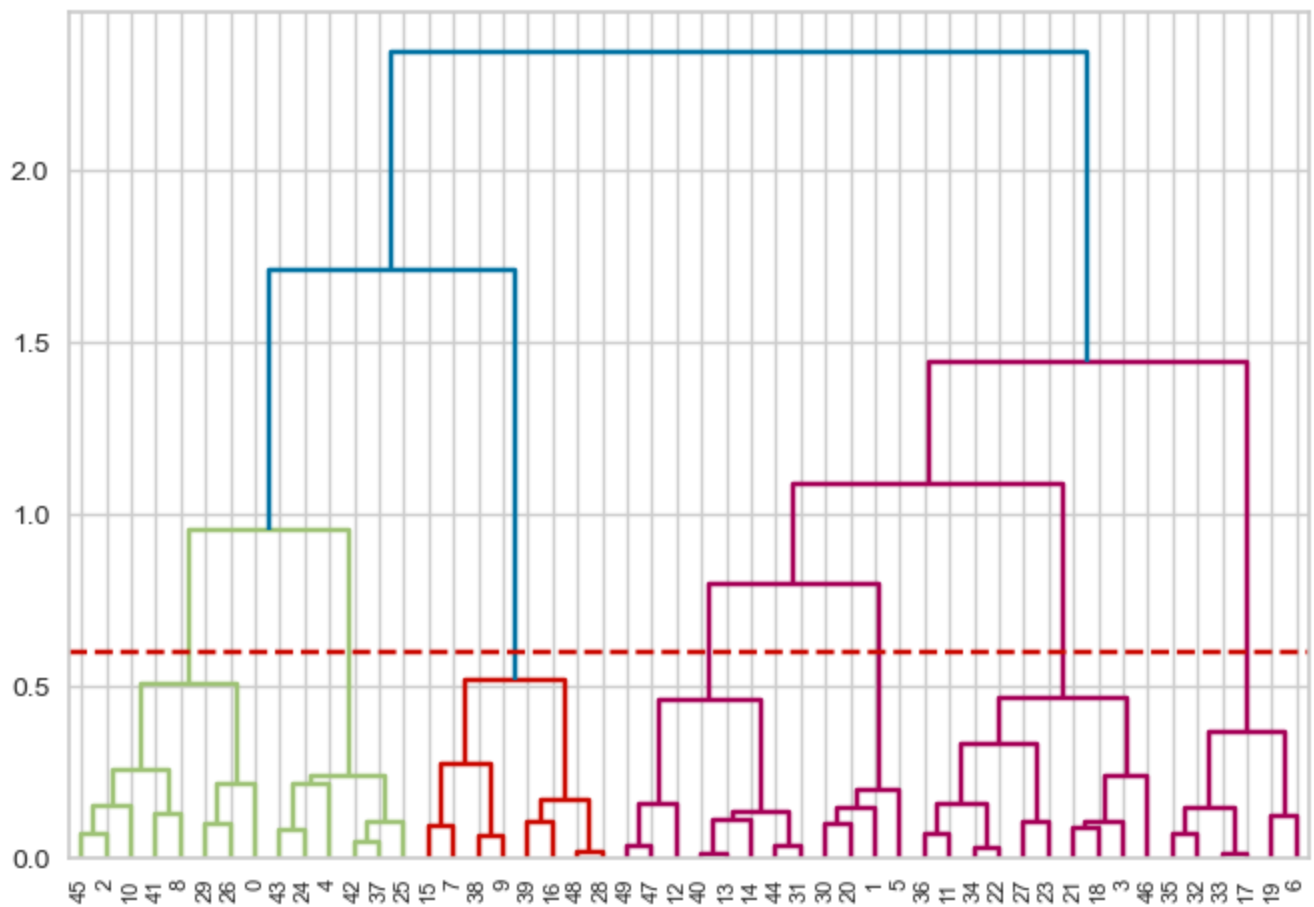
Fourth cluster technique used, **Ward Linkage**: minimizes the variance of the distances between the merged cluster and all other points.

Inspecting the dendrogram helps us determine the optimal number of clusters to use. We note that the longest vertical line (largest distance) is in the middle of the visual around 0.6. This spot is highlighted by the dashed red line. We note that there are 7 clusters at this point for the Ward Linkage method.

```
In [7]: linked_w = linkage(X, 'ward')
labels = range(1,100)

dendrogram(linked_w, orientation = 'top', distance_sort = 'descending', show_leaf_counts
plt.axhline(y=0.6, color = 'r', linestyle='--')

plt.show()
```



Grouping the clusters using the cluster sizes calculated above.

```
In [8]: cluster_s = AgglomerativeClustering(n_clusters=10, affinity='euclidean', linkage='single')
print('Single Cluster:', cluster_s.fit_predict(X), '\n')

cluster_c = AgglomerativeClustering(n_clusters=9, affinity='euclidean', linkage='complete')
print('Complete Cluster:', cluster_c.fit_predict(X), '\n')

cluster_a = AgglomerativeClustering(n_clusters=7, affinity='euclidean', linkage='average')
print('Average Cluster:', cluster_a.fit_predict(X), '\n')

cluster_w = AgglomerativeClustering(n_clusters=7, affinity='euclidean', linkage='ward')
print('Ward Cluster:', cluster_w.fit_predict(X))
```

Single Cluster: [9 4 0 3 5 4 1 0 0 6 0 3 3 2 2 0 0 1 3 1 4 3 3 3 8 8 0 3 0 0 4 2 1 1 3 1
3
8 6 0 2 0 8 8 2 0 7 3 0 3]

Complete Cluster: [0 6 0 8 5 6 4 2 0 2 0 3 1 1 1 2 7 4 8 4 6 8 3 3 5 5 0 3 7 0 6 1 4 4 3
4 3
5 2 7 1 0 5 5 1 0 8 1 7 1]

Average Cluster: [5 6 2 4 2 6 3 0 5 0 2 4 1 1 1 0 0 3 4 3 6 4 4 4 2 2 5 4 0 5 6 1 3 3 4
3 4
2 0 0 1 2 2 2 1 2 4 1 0 1]

Ward Cluster: [1 6 1 4 5 6 3 0 1 0 1 4 2 2 2 0 0 3 4 3 6 4 4 4 5 5 1 4 0 1 6 2 3 3 4 3 4
5 0 0 2 1 5 5 2 1 4 2 0 2]

Plotting the clusters using color-coded points to highlight each cluster.

```
In [9]: plt.figure(figsize=(2,2))
plt.scatter(X[:,0], X[:,1], c = cluster_s.labels_, cmap='rainbow')

##Below is code to show the cluster names in the plot legend if desired.
```

```

##Given these clusters correspond to a created array and are not from real-world data,
##the legend is currently hidden as there is no additional benefit to showing cluster na

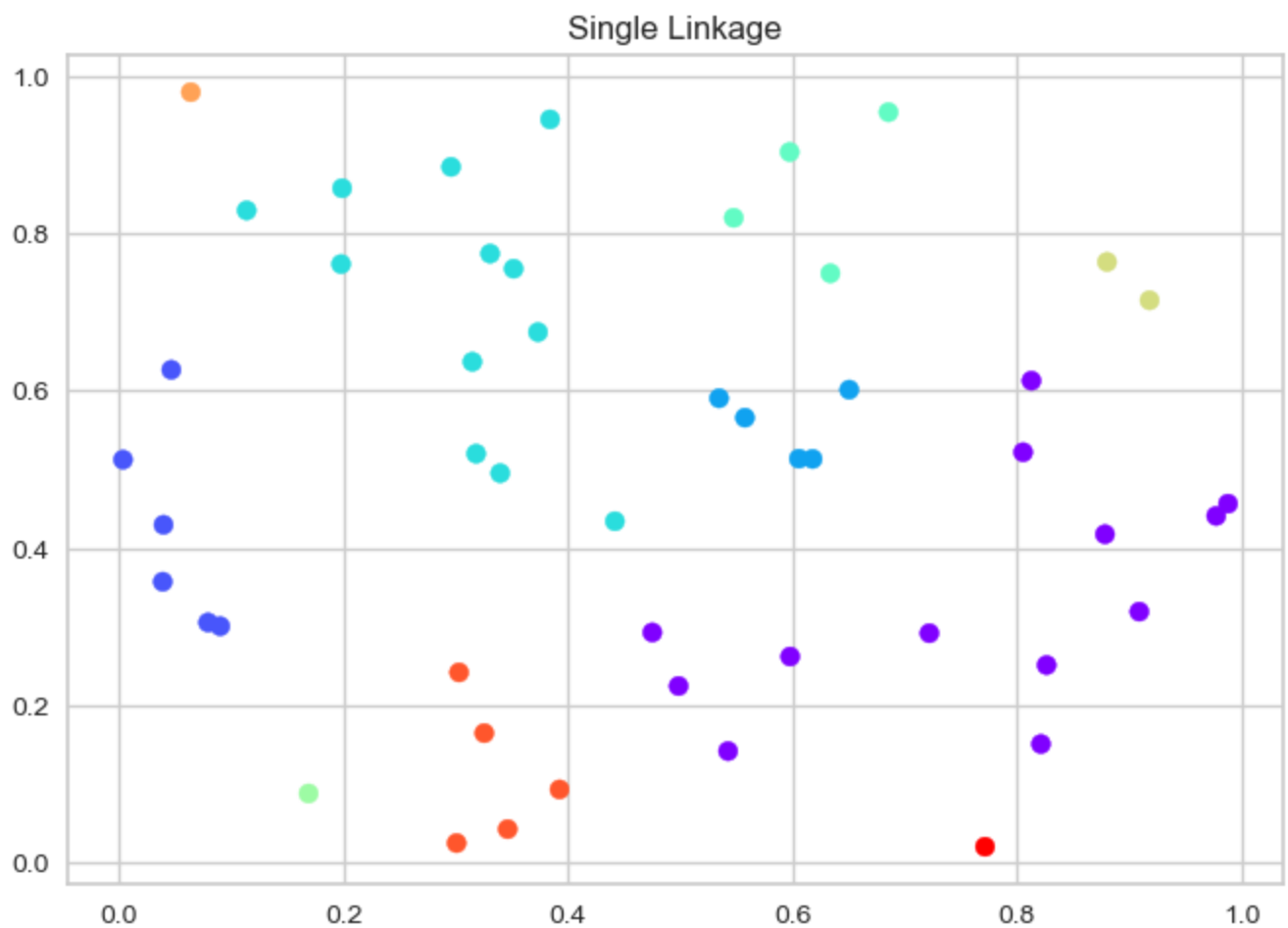
# clusters_s = set(cluster_s.labels_)
# colors = [plt.cm.rainbow(i) for i in np.linspace(0, 1, len(clusters_s))]
# legend_handles = [mpatches.Patch(color=colors[i], label=f"Cluster {cluster}") for i, c
# plt.legend(handles=legend_handles, loc="upper right")
plt.title('Single Linkage')
plt.show()

plt.scatter(X[:,0], X[:,1], c = cluster_c.labels_, cmap='rainbow')
plt.title('Complete Linkage')
plt.show()

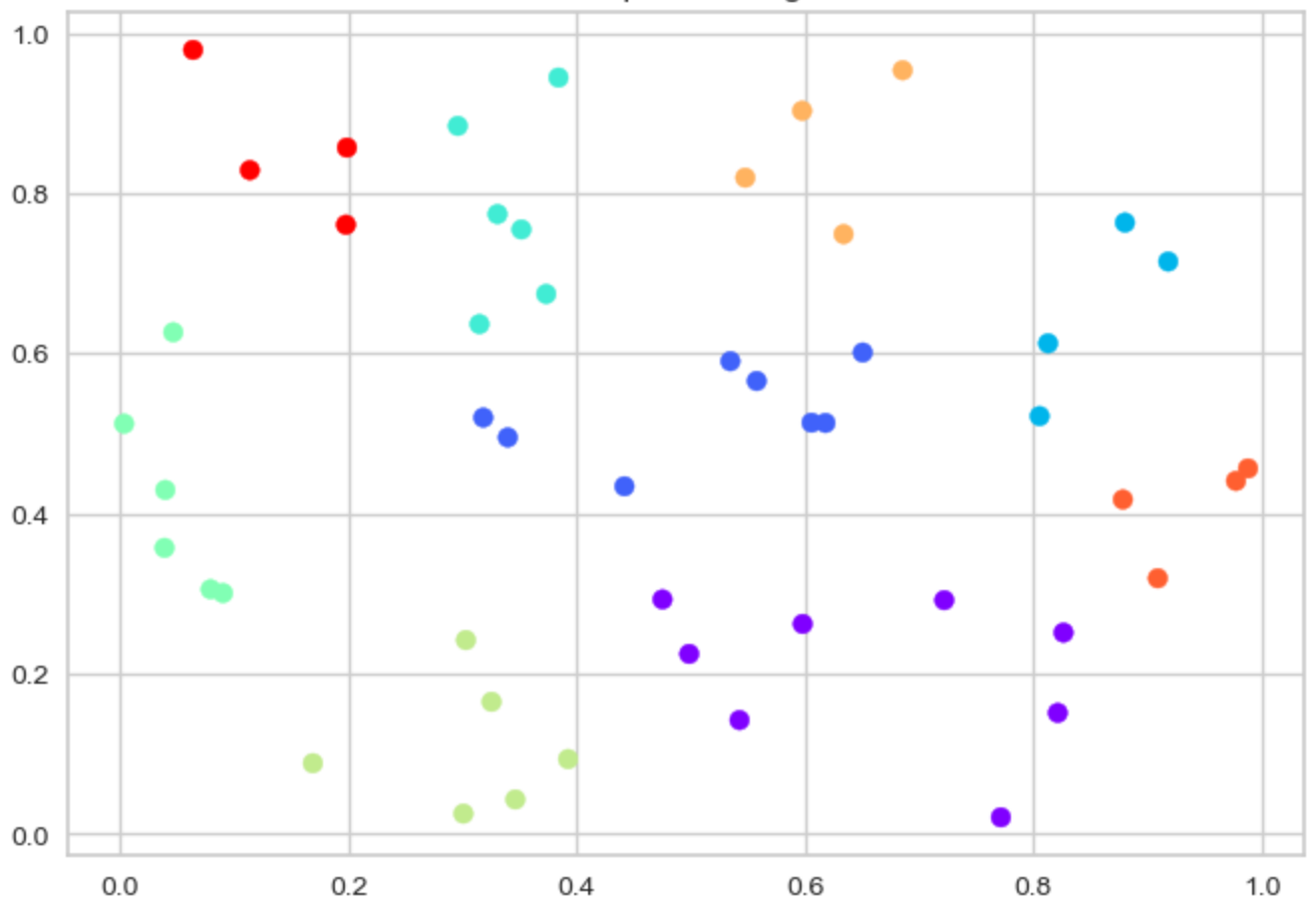
plt.scatter(X[:,0], X[:,1], c = cluster_a.labels_, cmap='rainbow')
plt.title('Average Linkage')
plt.show()

plt.scatter(X[:,0], X[:,1], c = cluster_w.labels_, cmap='rainbow')
plt.title('Ward Linkage')
plt.show()

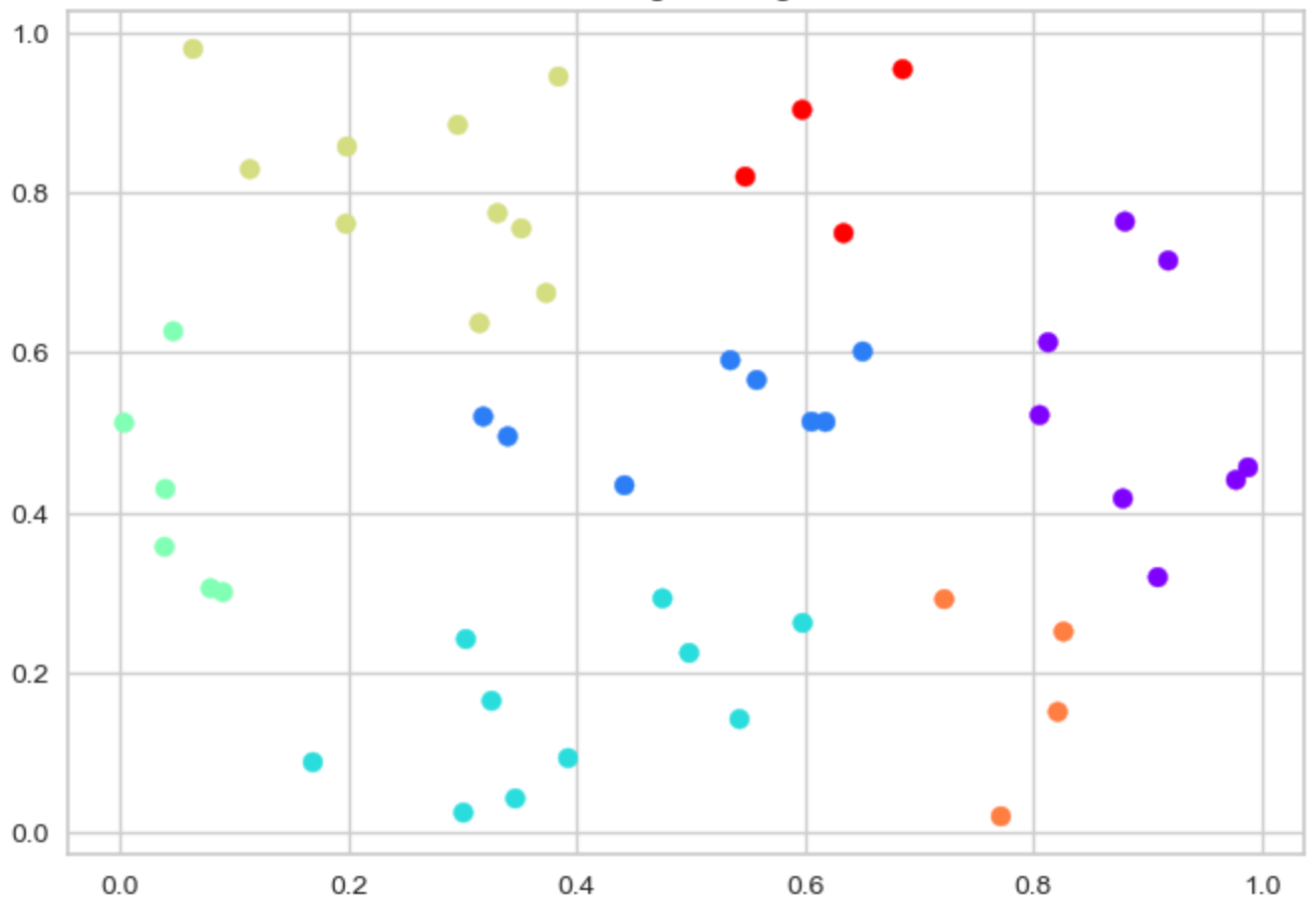
```

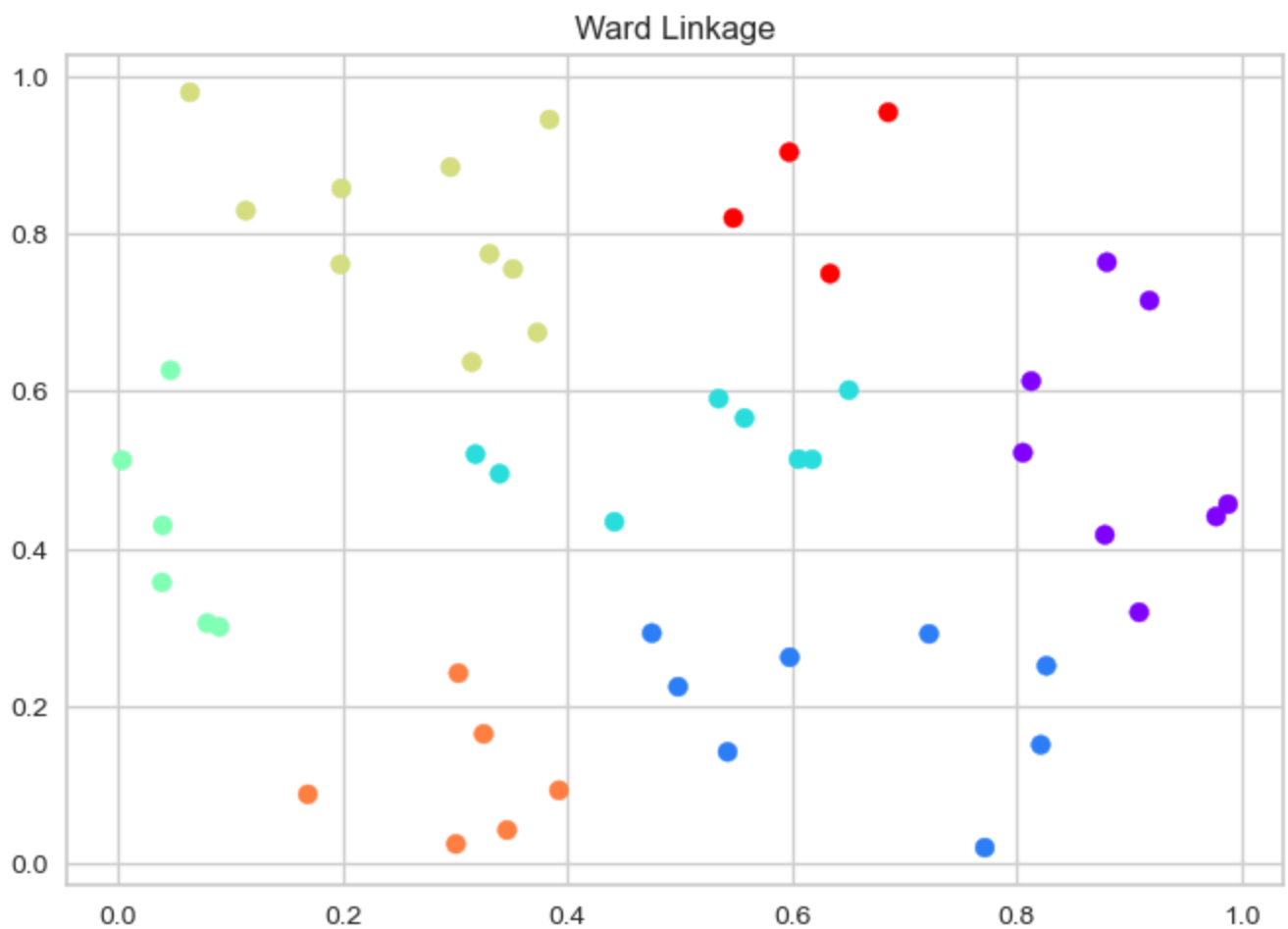


Complete Linkage



Average Linkage





Second Analysis: Customer Segmentation via HAC

Below is an analysis completed on real-world consumer data which was used to segment customers based on various characteristics.

```
In [10]: data = pd.read_csv("marketing_campaign.csv", sep='\t')
```

```
In [11]: data.head()
```

```
Out[11]:
```

	ID	Year_Birth	Education	Marital_Status	Income	Kidhome	Teenhome	Dt_Customer	Recency	MntWines
0	5524	1957	Graduation	Single	58138.0	0	0	04-09-2012	58	635
1	2174	1954	Graduation	Single	46344.0	1	1	08-03-2014	38	11
2	4141	1965	Graduation	Together	71613.0	0	0	21-08-2013	26	426
3	6182	1984	Graduation	Together	26646.0	1	0	10-02-2014	26	11
4	5324	1981	PhD	Married	58293.0	1	0	19-01-2014	94	173

5 rows × 29 columns

A few interesting things to note upon inspecting the information below: 1) There are a few object type variables that will be needed to be converted into numeric form 2) There is a date (Dt_Customer) that is currently in object form 3) There are Missing values for Income

```
In [12]: print(data.info())
```

```
<class 'pandas.core.frame.DataFrame'>
```

RangeIndex: 2240 entries, 0 to 2239

Data columns (total 29 columns):

#	Column	Non-Null Count	Dtype
0	ID	2240 non-null	int64
1	Year_Birth	2240 non-null	int64
2	Education	2240 non-null	object
3	Marital_Status	2240 non-null	object
4	Income	2216 non-null	float64
5	Kidhome	2240 non-null	int64
6	Teenhome	2240 non-null	int64
7	Dt_Customer	2240 non-null	object
8	Recency	2240 non-null	int64
9	MntWines	2240 non-null	int64
10	MntFruits	2240 non-null	int64
11	MntMeatProducts	2240 non-null	int64
12	MntFishProducts	2240 non-null	int64
13	MntSweetProducts	2240 non-null	int64
14	MntGoldProds	2240 non-null	int64
15	NumDealsPurchases	2240 non-null	int64
16	NumWebPurchases	2240 non-null	int64
17	NumCatalogPurchases	2240 non-null	int64
18	NumStorePurchases	2240 non-null	int64
19	NumWebVisitsMonth	2240 non-null	int64
20	AcceptedCmp3	2240 non-null	int64
21	AcceptedCmp4	2240 non-null	int64
22	AcceptedCmp5	2240 non-null	int64
23	AcceptedCmp1	2240 non-null	int64
24	AcceptedCmp2	2240 non-null	int64
25	Complain	2240 non-null	int64
26	Z_CostContact	2240 non-null	int64
27	Z_Revenue	2240 non-null	int64
28	Response	2240 non-null	int64

dtypes: float64(1), int64(25), object(3)

memory usage: 507.6+ KB

None

Cleaning the data for analysis

```
In [13]: #Removing NA values - this should result in 2216 rows with complete data
data = data.dropna()
print(data.count())
```

ID	2216
Year_Birth	2216
Education	2216
Marital_Status	2216
Income	2216
Kidhome	2216
Teenhome	2216
Dt_Customer	2216
Recency	2216
MntWines	2216
MntFruits	2216
MntMeatProducts	2216
MntFishProducts	2216
MntSweetProducts	2216
MntGoldProds	2216
NumDealsPurchases	2216
NumWebPurchases	2216
NumCatalogPurchases	2216
NumStorePurchases	2216
NumWebVisitsMonth	2216
AcceptedCmp3	2216
AcceptedCmp4	2216

```

AcceptedCmp5          2216
AcceptedCmp1          2216
AcceptedCmp2          2216
Complain              2216
Z_CostContact         2216
Z_Revenue             2216
Response              2216
dtype: int64

```

```

In [14]: #Updating the Dt_Customer column to date format
data['Dt_Customer'] = pd.to_datetime(data['Dt_Customer'])
print('Dt_Customer updated datatype:', data['Dt_Customer'].dtype)

```

```
Dt_Customer updated datatype: datetime64[ns]
```

With the date type updated, we can now use this new variable to calculate the number of days a customer has been in the system.

```

In [15]: #Create a new list to pull date from datetime data type.
dates = []
for i in data['Dt_Customer']:
    i = i.date()
    dates.append(i)

#Calculate the number of days a customer is in the system, with
#the latest date as newest (day 0).
days = []
d1 = max(dates)
for i in dates:
    delta = d1 - i
    days.append(delta)
data['Customer_For'] = days
data['Customer_For'] = pd.to_numeric(data['Customer_For'], errors = 'coerce')

```

Next, we can turn our attention to the categorical variables to better understand how to convert them into numeric values.

We can start by understanding the category counts for each variable.

```

In [16]: print('Marital Status:\n', data['Marital_Status'].value_counts())
print('\nEducation:\n', data['Education'].value_counts())

```

```

Marital Status:
Married      857
Together     573
Single       471
Divorced     232
Widow        76
Alone         3
Absurd        2
YOLO          2
Name: Marital_Status, dtype: int64

```

```

Education:
Graduation   1116
PhD           481
Master       365
2n Cycle     200
Basic         54
Name: Education, dtype: int64

```

Now using the gathered information on the above categories + other variable information at hand, we can create a few new, more useful, variables.

```
In [17]: #Use the marital status variable to create a new
#variable to understand if one is living alone or with a partner

data['Living_With_Adults'] = data['Marital_Status'].replace({'Married':'Partner', 'Toget
data['Adults'] = data['Living_With_Adults'].replace({'Alone':1, 'Partner':2})

#Calculating the number of children at home
data['Children'] = data['Kidhome'] + data['Teenhome']

#Merging the above 2 pieces of info (partner + children) to calculate the
#total family size
data["Family_Size"] = data['Adults'] + data["Children"]

#Create a new variable indicating whether one is a parent or not
data['Is_Parent'] = np.where(data.Children > 0, 1, 0)

#Create a new variable to identify the age of the customer
data['Age'] = 2023 - data['Year_Birth']

#Calculate the total amount the customer spends on various items
data['Spent'] = data["MntWines"] + data["MntFruits"] + data["MntMeatProducts"] + data["M

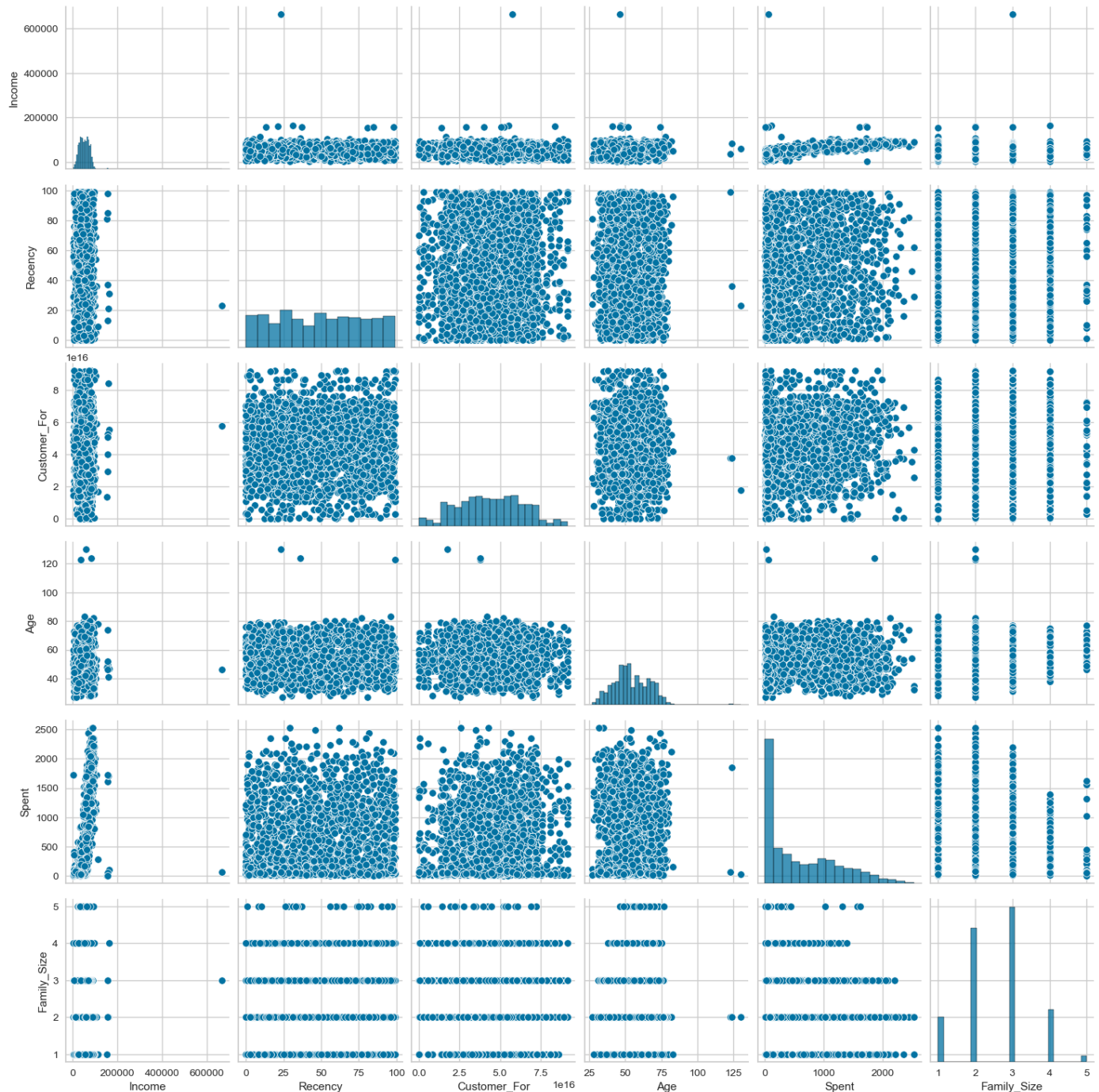
#Simplify education segment such that it's only in 3 groups
data['Education'] = data['Education'].replace({'Graduation':'Graduate', 'PhD':'Postgrad'

#Drop the unnecessary columns
data.drop(columns=['Living_With_Adults', 'Adults', 'Children', 'Marital_Status', 'Dt_Cus
```

Visualizing the data to better understand it

```
In [18]: Plot = ['Income', 'Recency', 'Customer_For', 'Age', 'Spent', 'Family_Size']
plt.figure()
sns.pairplot(data[Plot])
plt.show()
```

<Figure size 800x550 with 0 Axes>



Reviewing the visuals shows us there are **clear outliers** in age and income which should be addressed.

```
In [19]: data = data[(data['Age'] < 90)]
data = data[(data['Income'] < 600000)]

print('Remaining customers:', len(data))
```

Remaining customers: 2212

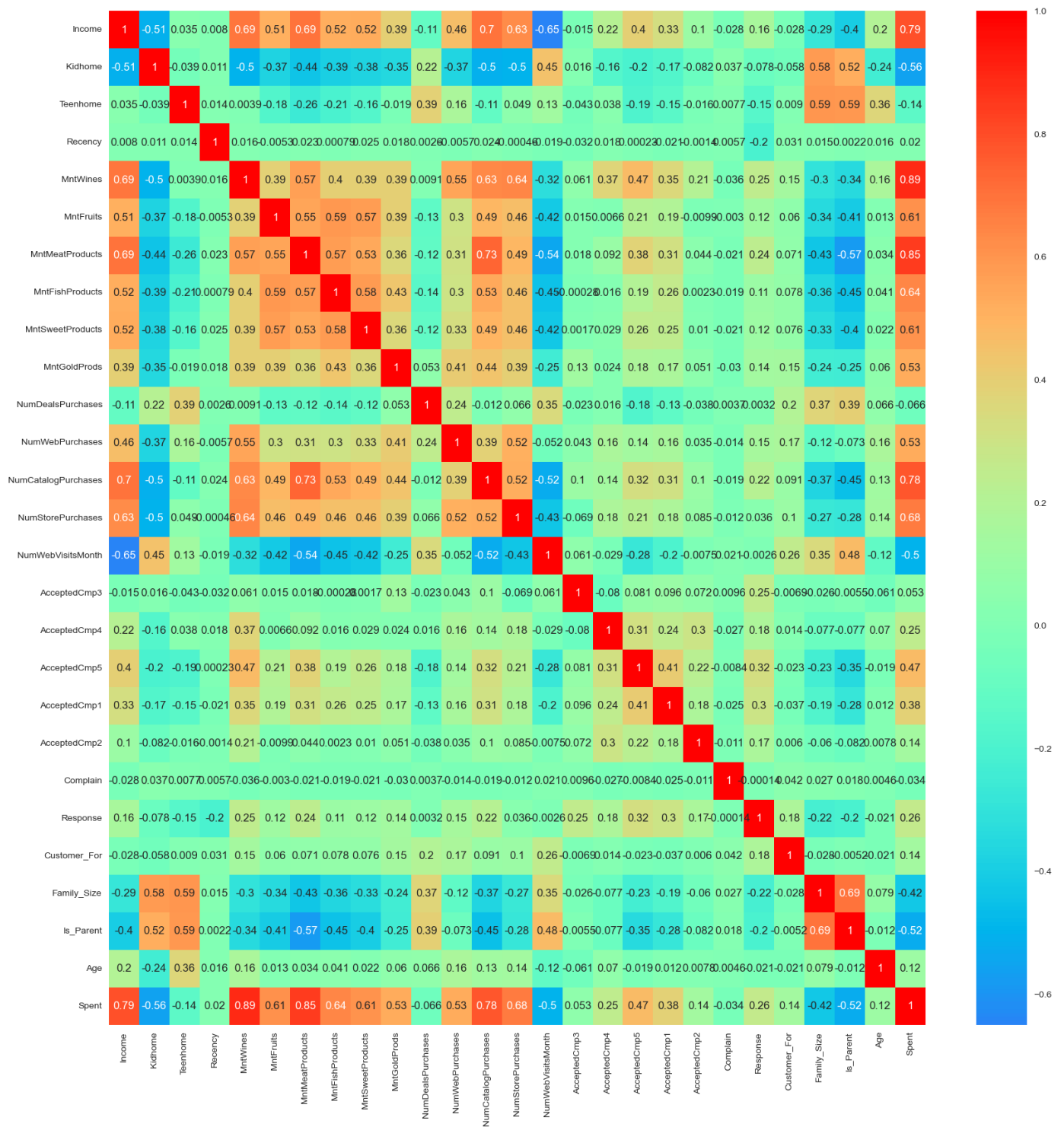
Having cleaned up the data and added a few new useful variables, we can now **create a correlation matrix** to view the correlation between the variables.

The correlation heatmap below shows us what is expected. For example, variables that directly contributed to "Spent" are strongly correlated with "Spent" whereas "Is_Parent" is strongly correlated with family size.

```
In [20]: corrmatrix = data.corr()
plt.figure(figsize = (20,20))
sns.heatmap(corrmatrix, annot=True, cmap='rainbow', center=0)
```

<AxesSubplot:>

Out[20]:



Having reviewed the numeric variables, let us now shift our attention to the categorical variables. We need to **convert them to numeric variables** in order to use them for our statistical model.

```
In [21]: #Identifying a list of categorical variables
cat = (data.dtypes == 'object')
object_columns = list(cat[cat].index)

print('Categorical variables:', object_columns)

#We can use LabelEncoder() from SK Learn to encode categorical variables
#as numerical values.
encoder = LabelEncoder()
for i in object_columns:
    data[i]=data[[i]].apply(encoder.fit_transform)
```

Categorical variables: ['Education']

Next up is **scaling our variables**. This is important as it helps ensure that no variable in the model has a disproportionate effect on the final results due to its scale. It also helps with addressing issues such as skewed distributions, unequal variances, and large outlier impact (which we have already addressed for Income and Age).

There are various methods to scaling variables including normalization, standardization, and Min-Max scaling. We will use standardization for our scaling.

```
In [22]: #Start by creating a copy of our data frame
datacopy = data.copy()

#Delete columns that don't need to be scaled
datacopy.drop(['AcceptedCmp3', 'AcceptedCmp4', 'AcceptedCmp5', 'AcceptedCmp1', 'AcceptedCmp2'], axis=1)

#Scale the remaining variables

scaler = StandardScaler()
scaler.fit(datacopy)
scaled_data = pd.DataFrame(scaler.transform(datacopy), columns=datacopy.columns)

scaled_data.head()
```

```
Out[22]:
```

	Education	Income	Kidhome	Teenhome	Recency	MntWines	MntFruits	MntMeatProducts	MntFishProducts
0	-0.893586	0.287105	-0.822754	-0.929699	0.310353	0.977660	1.552041	1.690293	2.4534
1	-0.893586	-0.260882	1.040021	0.908097	-0.380813	-0.872618	-0.637461	-0.718230	-0.6510
2	-0.893586	0.913196	-0.822754	-0.929699	-0.795514	0.357935	0.570540	-0.178542	1.3395
3	-0.893586	-1.176114	1.040021	-0.929699	-0.795514	-0.872618	-0.561961	-0.655787	-0.5049
4	0.571657	0.294307	1.040021	-0.929699	1.554453	-0.392257	0.419540	-0.218684	0.1525

5 rows × 28 columns

Now we are ready to use our dataframe for modeling!

Dimensionality Reduction:

Dimensionality reduction is the process of reducing the number of features or variables in a dataset while preserving as much of the information content as possible. This is often done in statistical modeling to remove irrelevant or redundant features, reduce noise in the data, improve the interpretability of the model, or to speed up the training time of machine learning algorithms.

There are a few different methods that can be used such as principal component analysis (PCA), linear discriminant analysis (LDA), and t-distribution stochastic neighbor embedding (t-SNE).

We will use PCA here: technique used to transform a set of correlated variables into a set of linearly uncorrelated variables called principal components.

```
In [23]: #Apply PCA to reduce components to 3
pca = PCA(n_components = 3)

#Fitting the PCA model on the scaled data. The model is trained on the
#scaled data to find the eigenvectors and eigenvalues of the covariane matrix (used
#to calculate the principal components)
pca.fit(scaled_data)
```

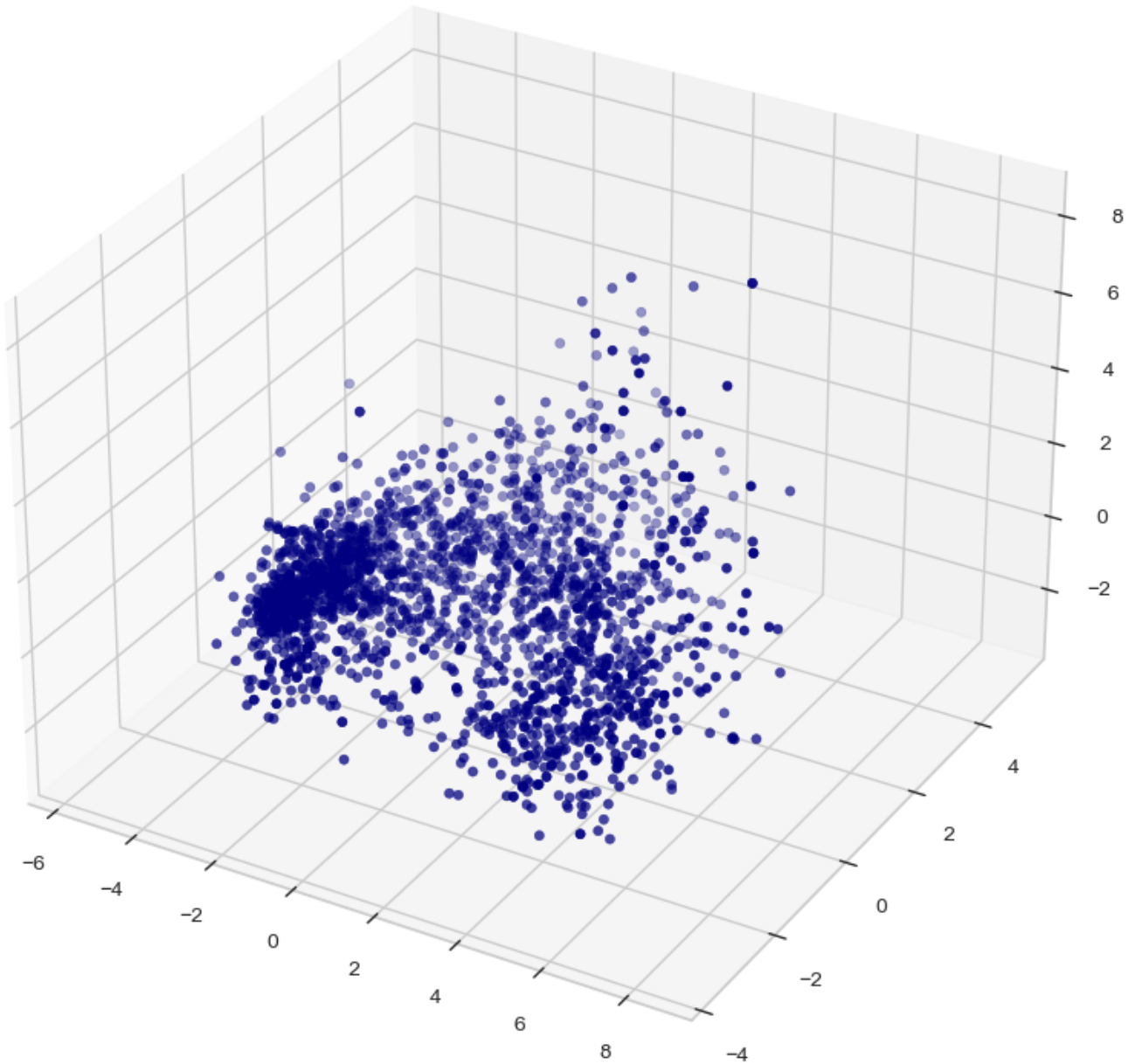
```
#Transforming the scaled data into a set of principal components and stores  
#into a dataframe.  
PCA_data = pd.DataFrame(pca.transform(scaled_data), columns=['var1', 'var2', 'var3'])  
  
PCA_data.head()
```

```
Out[23]:
```

	var1	var2	var3
0	4.719534	-0.053942	0.058071
1	-2.711823	-0.126269	-0.552979
2	2.111964	-0.594447	-1.147715
3	-2.826951	-1.535894	-0.054185
4	-0.761030	0.088784	-0.644106

We can visualize the new dataframe we have created. Our goal is to cluster these data points.

```
In [24]: x = PCA_data['var1']  
y = PCA_data['var2']  
z = PCA_data['var3']  
  
fig = plt.figure(figsize = (10,10))  
ax = fig.add_subplot(111, projection="3d")  
ax.scatter(x,y,z, c='navy', marker="o" )  
plt.show()
```

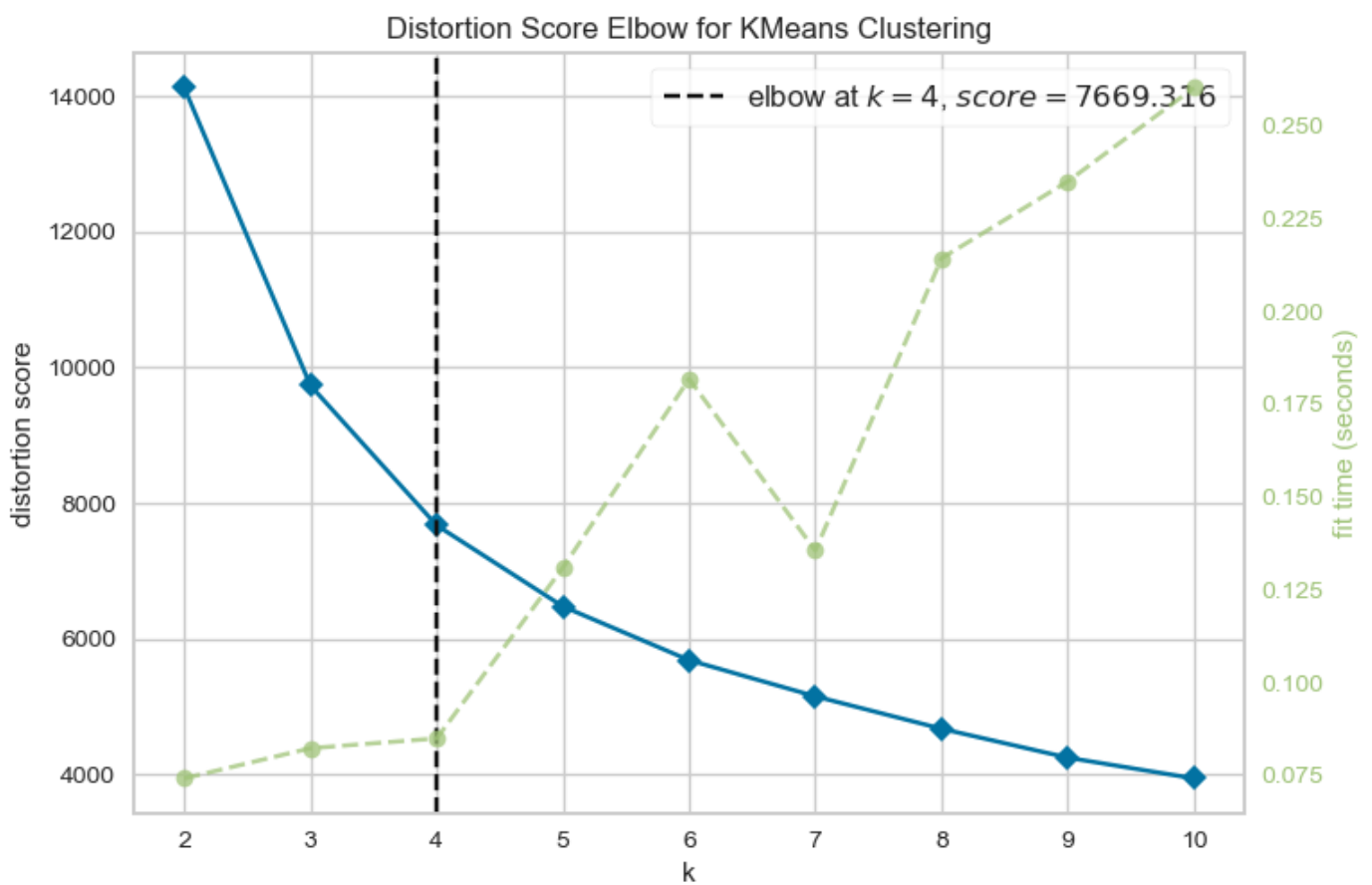



Great! Now we can finally move onto the fun step: **Clustering**.

The first question we need to answer is: how many clusters should be formed? There are several ways to determine this.

We will use the **Elbow Method**: plot the explained variance against the number of clusters and select the number of clusters where the change in explained variance slows down. This point is interpreted as the best trade-off between having a small number of clusters with low explained variance and a high number of clusters with low explained variance.

```
In [25]: #Using the elbow method:  
Elbow = KElbowVisualizer(KMeans(), k=10)  
Elbow.fit(PCA_data)  
Elbow.show()
```



Out[25]: <AxesSubplot:title={'center':'Distortion Score Elbow for KMeans Clustering'}, xlabel='k', ylabel='distortion score'>

The above graph suggests that 4 is the optimal number of clusters for our data.

With the number of clusters determined, now we can move on to **Hierarchical Agglomerative Cluster (HAC)** to get our final clusters.

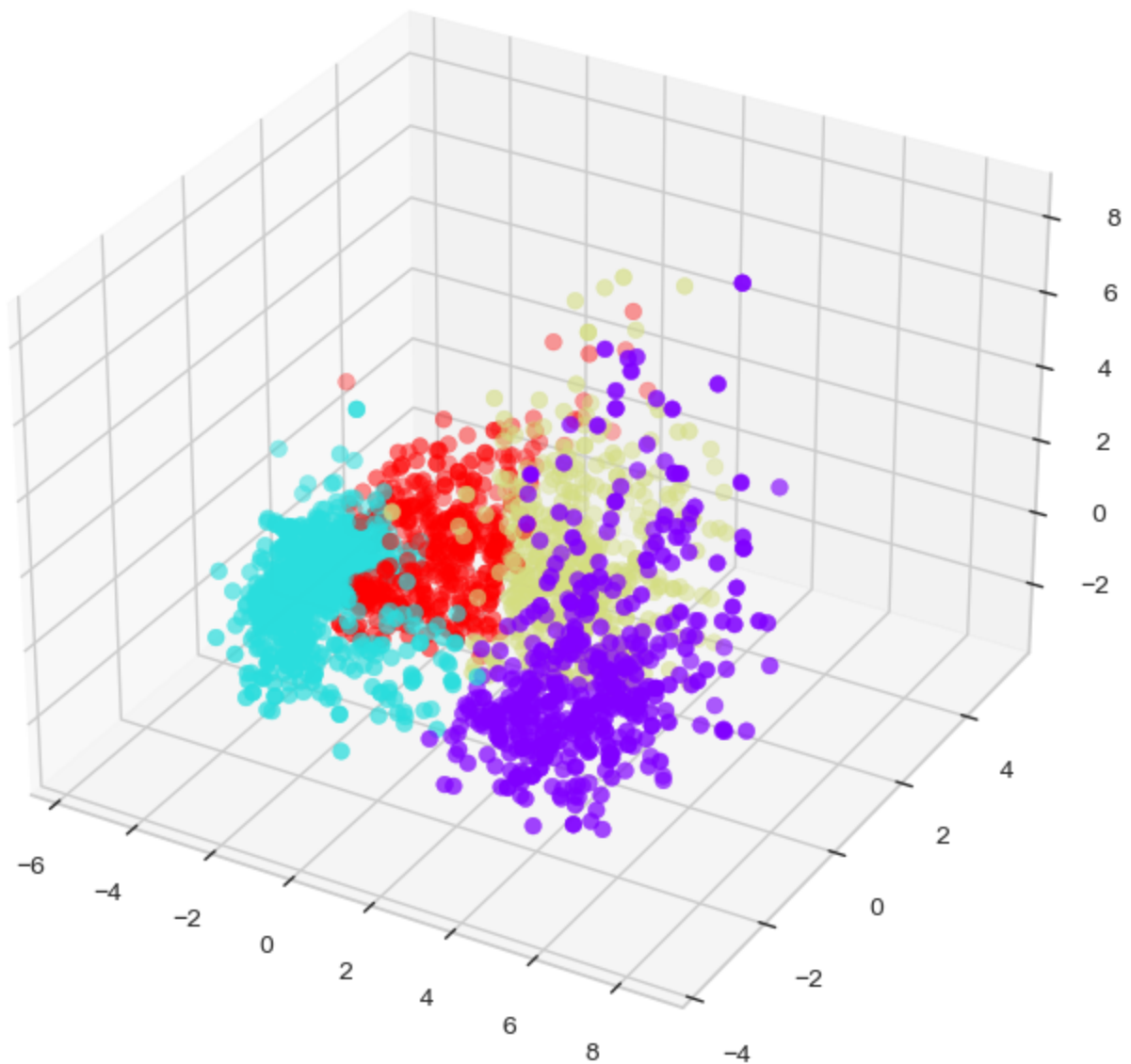
```
In [50]: cluster = AgglomerativeClustering(n_clusters=4, affinity='euclidean', linkage='ward')

prediction = cluster.fit_predict(PCA_data)
PCA_data['Clusters'] = prediction
```

Having created our clusters, let's now re-plot the 3D scatter plot to visualize what our clusters look like.

```
In [51]: fig = plt.figure(figsize = (10,8))
ax = plt.subplot(111, projection='3d', label='bla')
ax.scatter(x, y, z, s=40, c=PCA_data['Clusters'], marker="o", cmap='rainbow')
plt.title('HAC Applied on Marketing Data - 4 Clusters')
plt.show()
```

HAC Applied on Marketing Data - 4 Clusters



Amazing! Now we can add these clusters back to the original dataset to assess our model and derive cool business insights.

```
In [52]: data['Clusters'] = prediction
         data.head()
```

```
Out[52]:
```

	Education	Income	Kidhome	Teenhome	Recency	MntWines	MntFruits	MntMeatProducts	MntFishProducts
0	0	58138.0	0	0	58	635	88	546	172
1	0	46344.0	1	1	38	11	1	6	2
2	0	71613.0	0	0	26	426	49	127	111
3	0	26646.0	1	0	26	11	4	20	10
4	1	58293.0	1	0	94	173	43	118	46

5 rows × 30 columns

Model Evaluation

Having created the clusters and plotted them, it is now important to evaluate our model to see how it is.

There are several ways to do this including: 1) Silhouette Score: The silhouette score measures the similarity of an instance to its own cluster compared to other clusters. A score close to 1 indicates a well-formed cluster.

2) Calinski-Harabasz Index: This index measures the ratio of the between-cluster variance to the within-cluster variance. A high score indicates that the clusters are well separated.

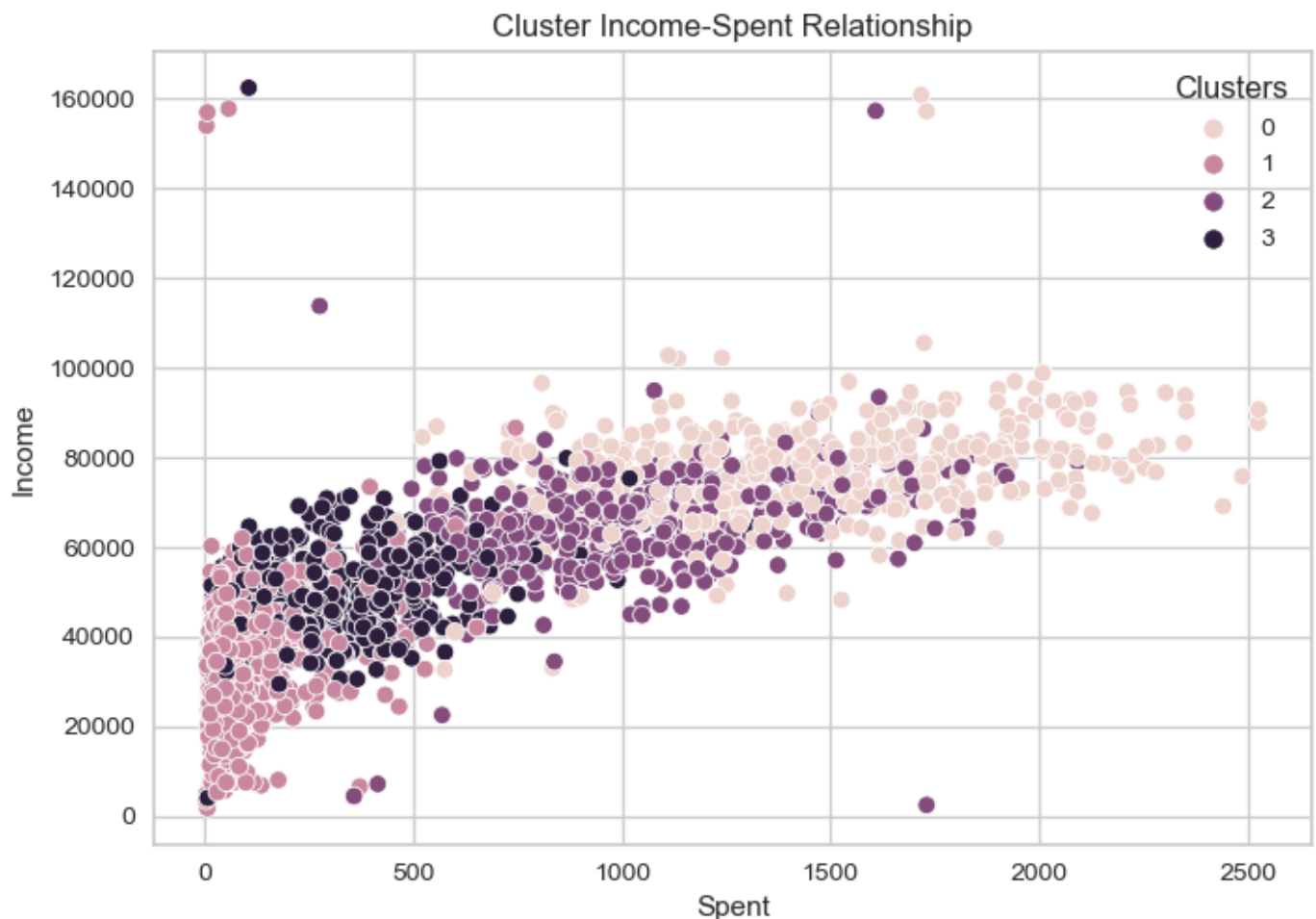
3) Davies-Bouldin Index: The Davies-Bouldin Index calculates the average similarity between each cluster and its most similar cluster. Lower values indicate a better cluster structure.

4) Confusion Matrix: A confusion matrix can be used to evaluate the accuracy of the clustering model by comparing the actual class labels of instances with the predicted class labels.

5) Visualization: The cluster structure can also be visually inspected through plotting the instances and coloring them according to their cluster assignments.

We will start off with **Visualization** and then use the **Silhouette Score**.

```
In [53]: #Let's visualize the Income-Spent relationship for the clusters.  
pl = sns.scatterplot(data=data, x=data['Spent'], y=data['Income'], hue=data['Clusters'])  
pl.set_title('Cluster Income-Spent Relationship')  
plt.show()
```

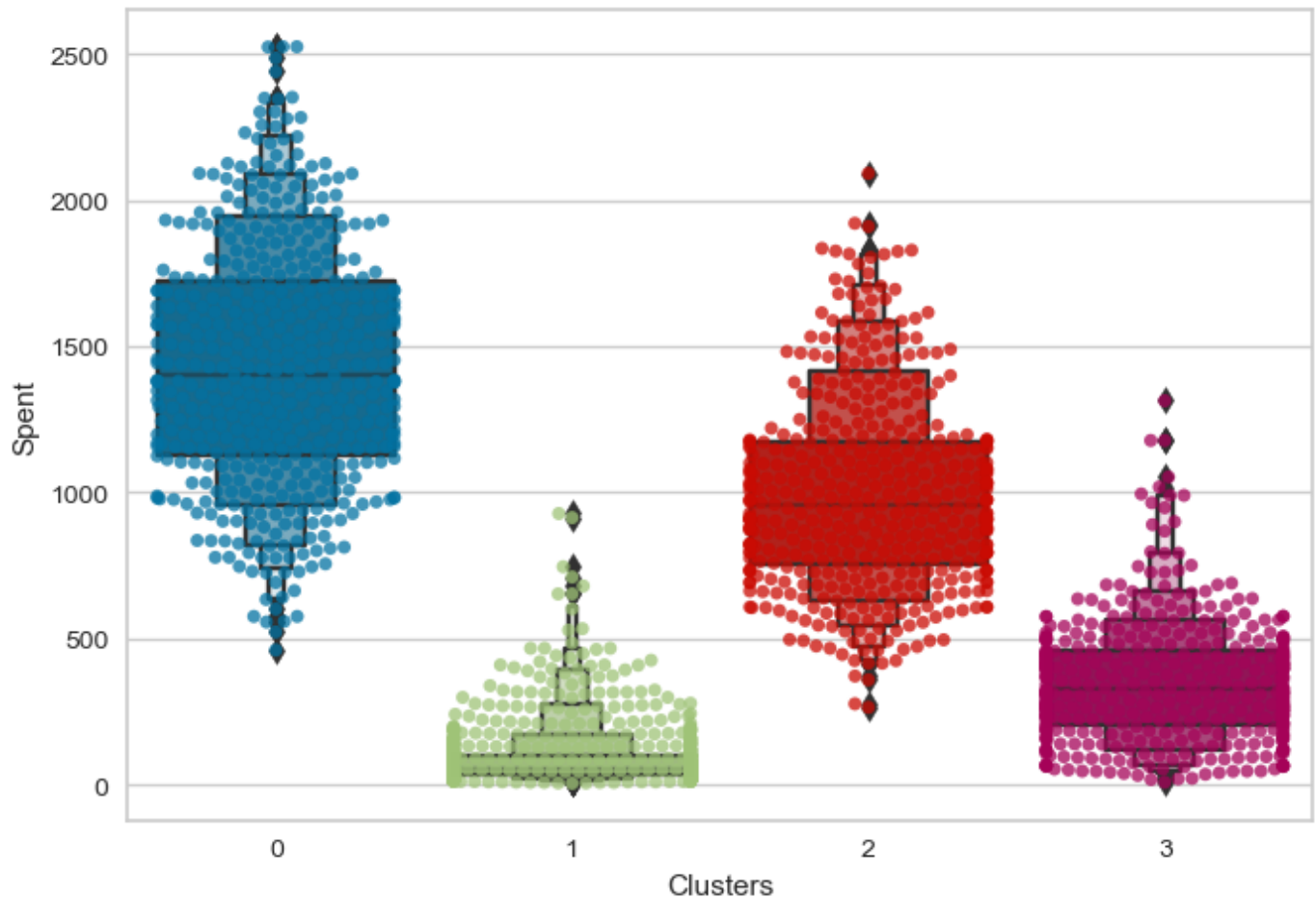


The above graph is quite useful in providing informatino on the clusters. We note the following: 1) Cluster 0 customers are in the higher income-spent bracket. 2) Cluster 1 customers are in the low income-spent

bracket. 3) Cluster 2 customers are in the medium income-spent bracket. 4) Cluster 3 customers are in the low-medium income-spent bracket.

Next, we can observe the distribution of spend amount per cluster.

```
In [54]: plt.figure()
pl=sns.swarmplot(x=data['Clusters'], y=data['Spent'], alpha=0.75)
pl=sns.boxenplot(x=data['Clusters'], y=data['Spent'])
```

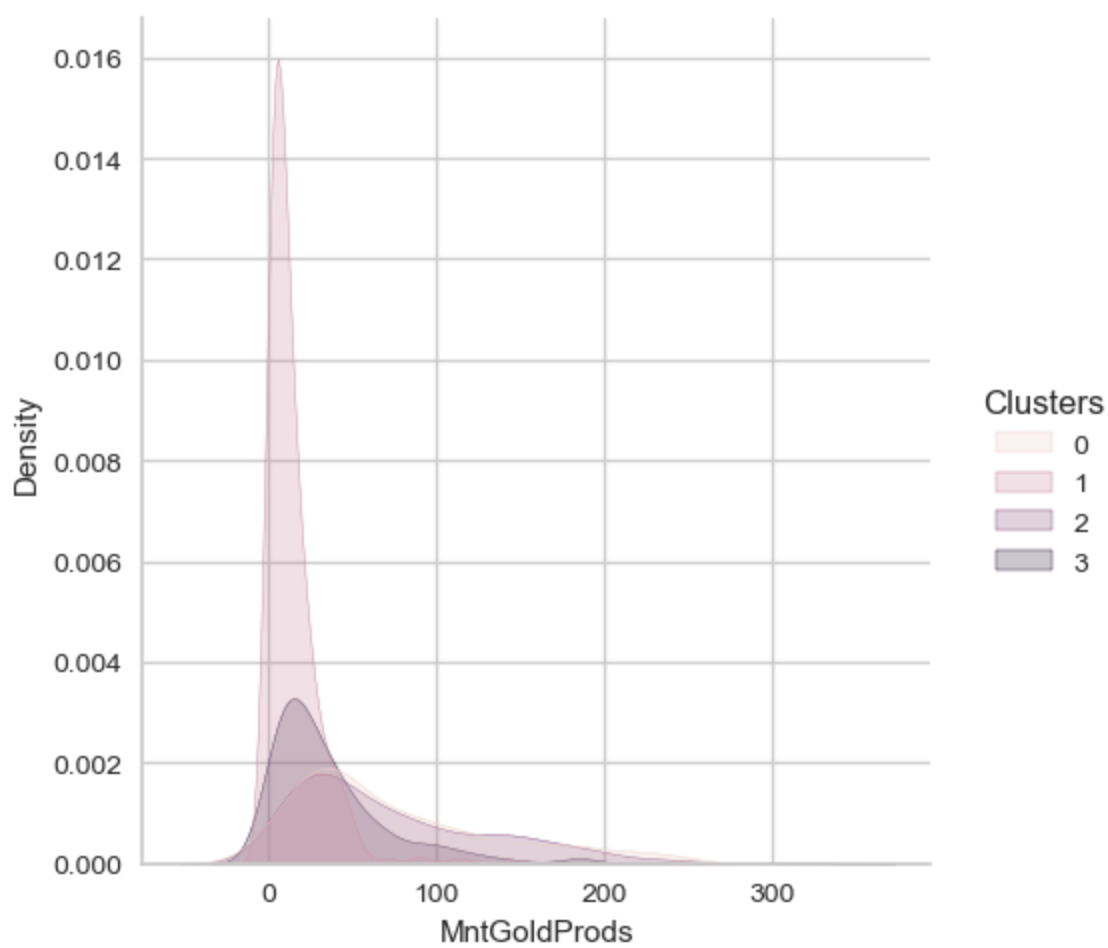


We can see that cluster 0 has the largest spend distribution, followed by cluster 2. This information is valuable as now we can further analyze clusters 0 and 2 to assess their highest areas of spend to identify targeted marketing strategies.

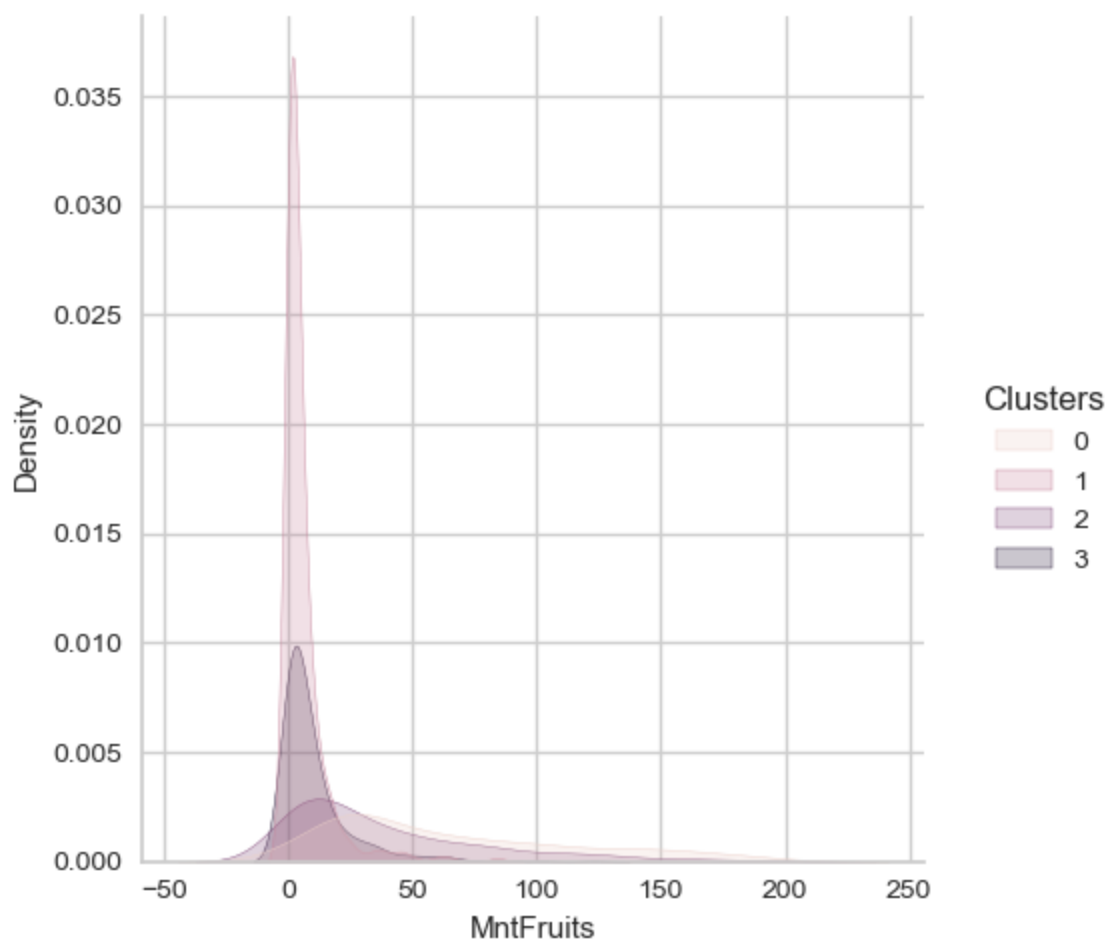
```
In [55]: SpentPlot = ['MntGoldProds', 'MntFruits', 'MntWines', 'MntMeatProducts', 'MntFishProducts']

for i in SpentPlot:
    plt.figure(figsize = (5,5))
    sns.displot(data, x=i, hue='Clusters', kind="kde", fill=True)
    plt.show()
```

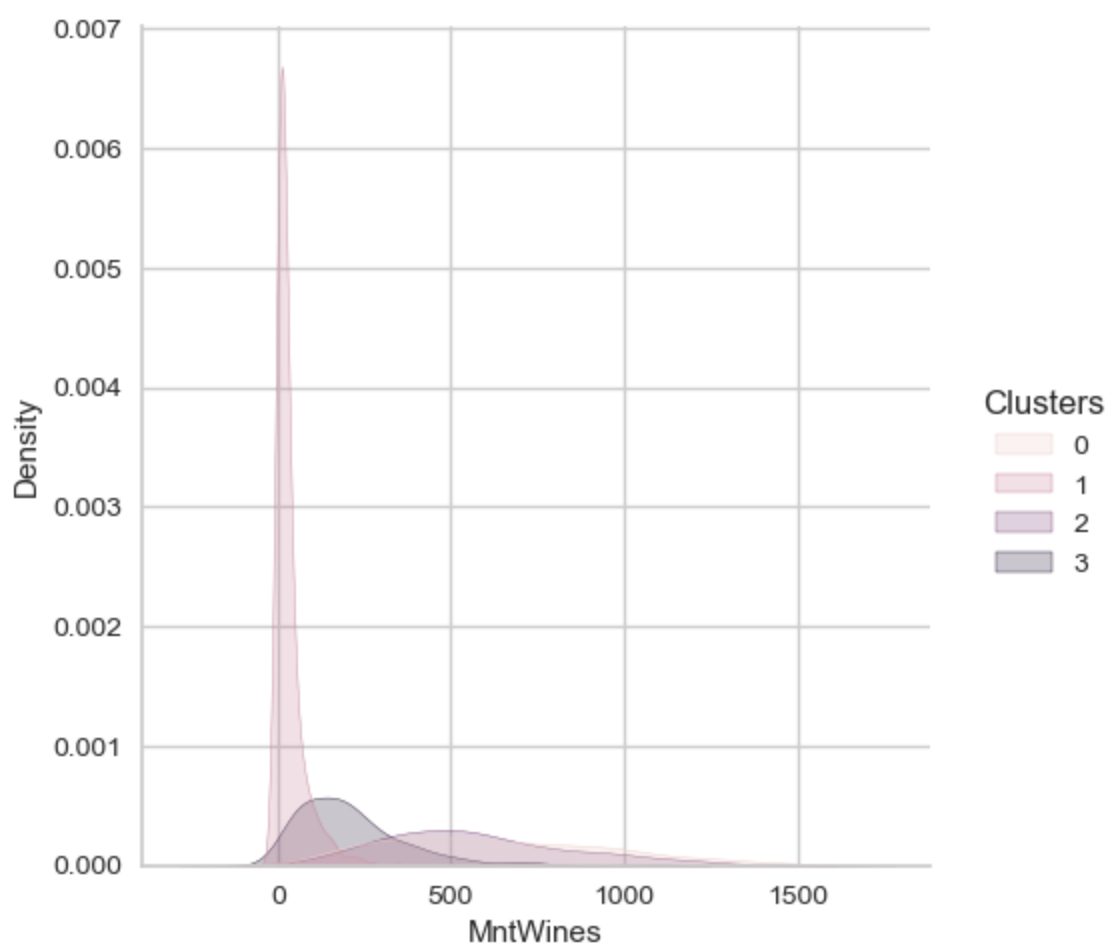
<Figure size 500x500 with 0 Axes>



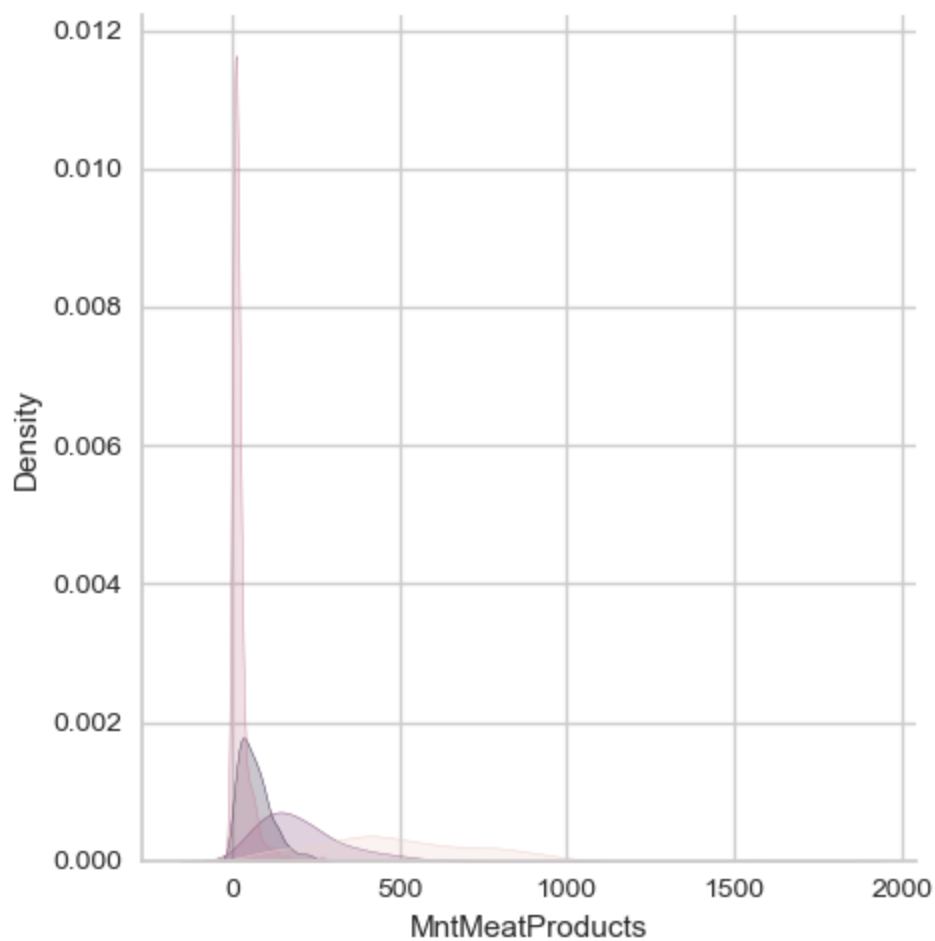
<Figure size 500x500 with 0 Axes>



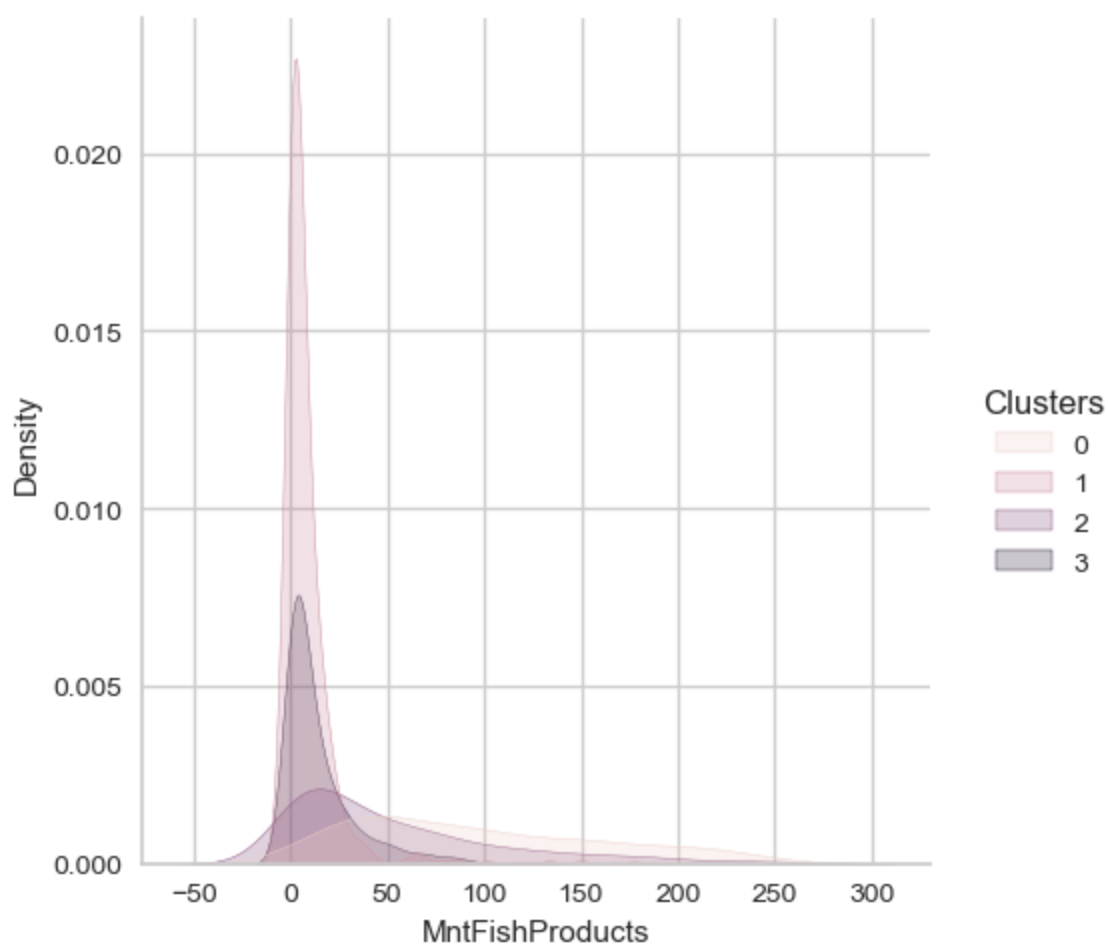
<Figure size 500x500 with 0 Axes>



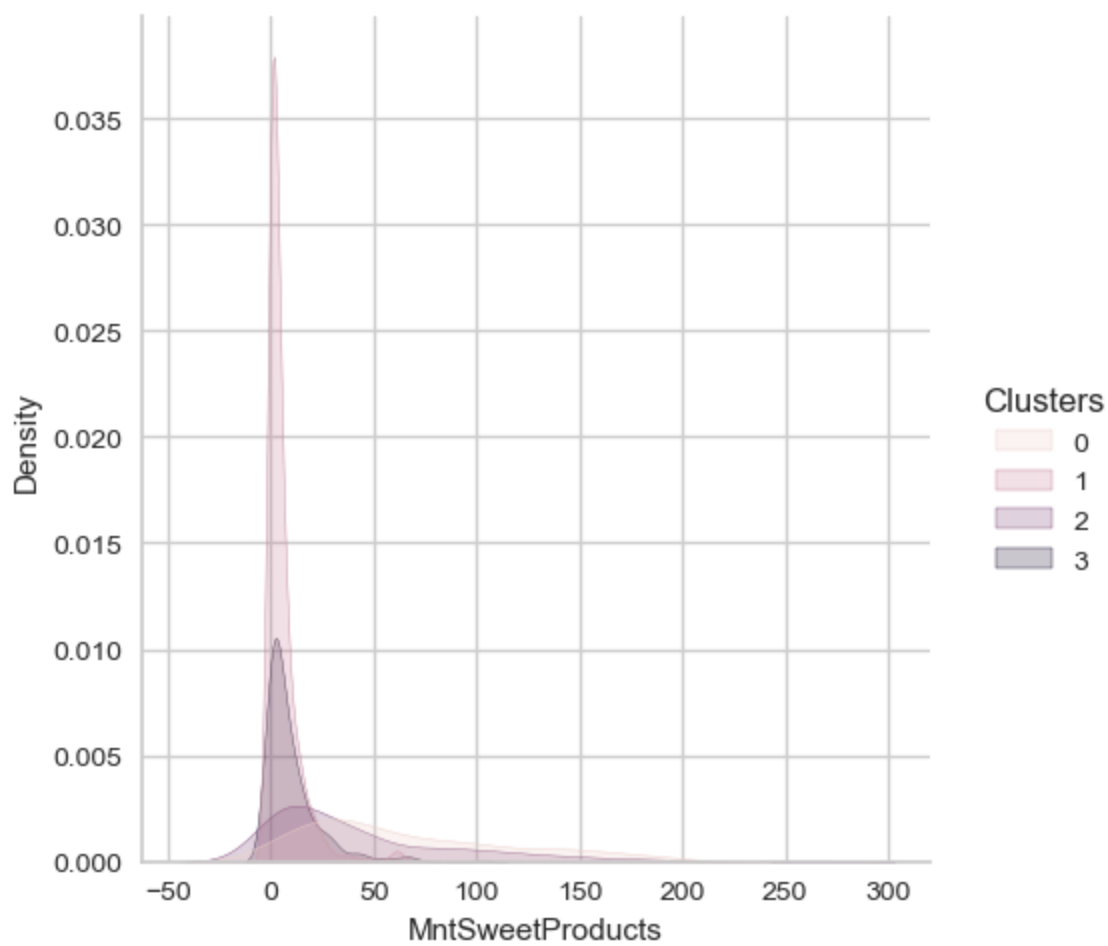
<Figure size 500x500 with 0 Axes>



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<Figure size 500x500 with 0 Axes>

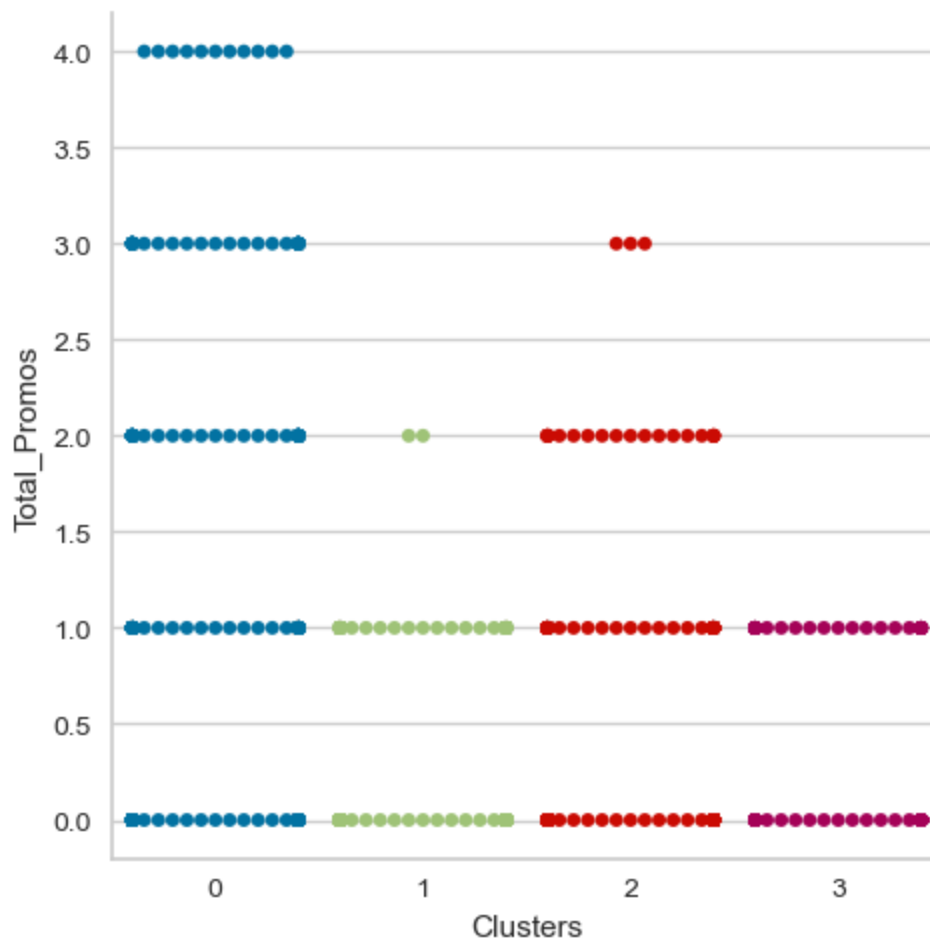


```
In [56]: data['Total_Promos'] = data["AcceptedCmp1"] + data["AcceptedCmp2"] + data["AcceptedCmp3"]
plt.figure()
```



```
sns.catplot(data=data, x='Clusters', y='Total_Promos', kind='swarm')  
plt.show()
```

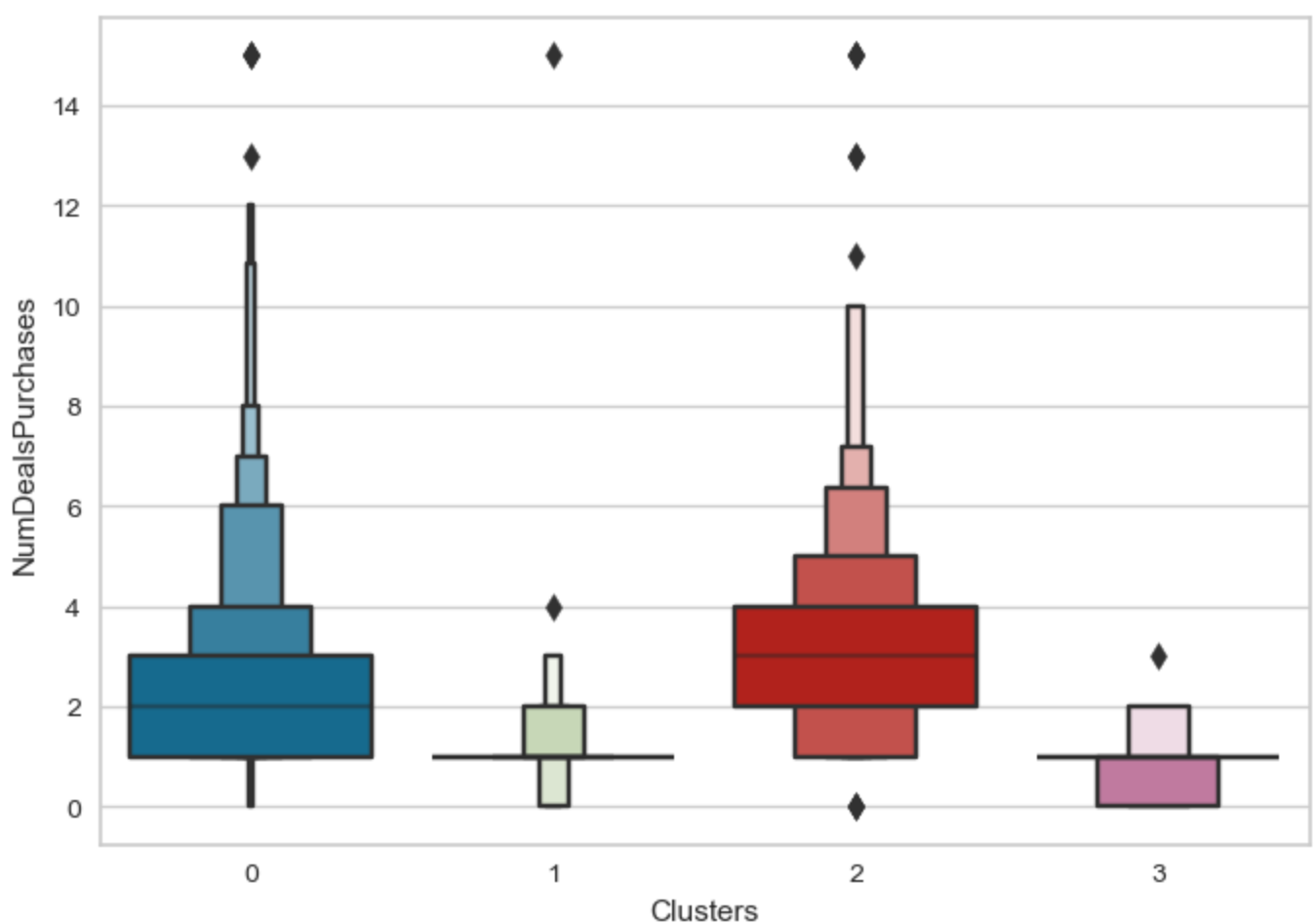
<Figure size 800x550 with 0 Axes>



We see that clusters 0 and 2 are most prone to accepting promotions. This is in line with the earlier graph that showed clusters 0 and 2 as the highest spenders.

Now let's review the responses to the deals offered.

```
In [33]: #Plotting the distribution of deal purchases by cluster  
plt.figure()  
pl=sns.boxenplot(y=data['NumDealsPurchases'], x=data['Clusters'])  
plt.show()
```



Similar to amount spent and promotions acceptance, deal purchases are also higher for clusters 0 and 2.

Now, let's evaluate our HAC model by calculating its **Silhouette Score**.

```
In [58]: score = silhouette_score(PCA_data, prediction)
print("Silhouette score:", score)
```

Silhouette score: 0.39666132655597747

Interpreting the **Silhouette Score**: this score is a value between -1 and 1 where a higher score indicates a better cluster.

A score close to 1 means that the clusters are well separated from each other whereas a score close to 0 means the clusters are near each other with poorly defined boundaries. Finally, a score of -1 means that the instances in a cluster are far away from other instances within that cluster and much closer to instances in another cluster, indicating poor assignment.

Given our data are dense and highly clustered, a score of 0.40 still indicates a good clustering solution. However, we should note that there is likely some overlap between the clusters.

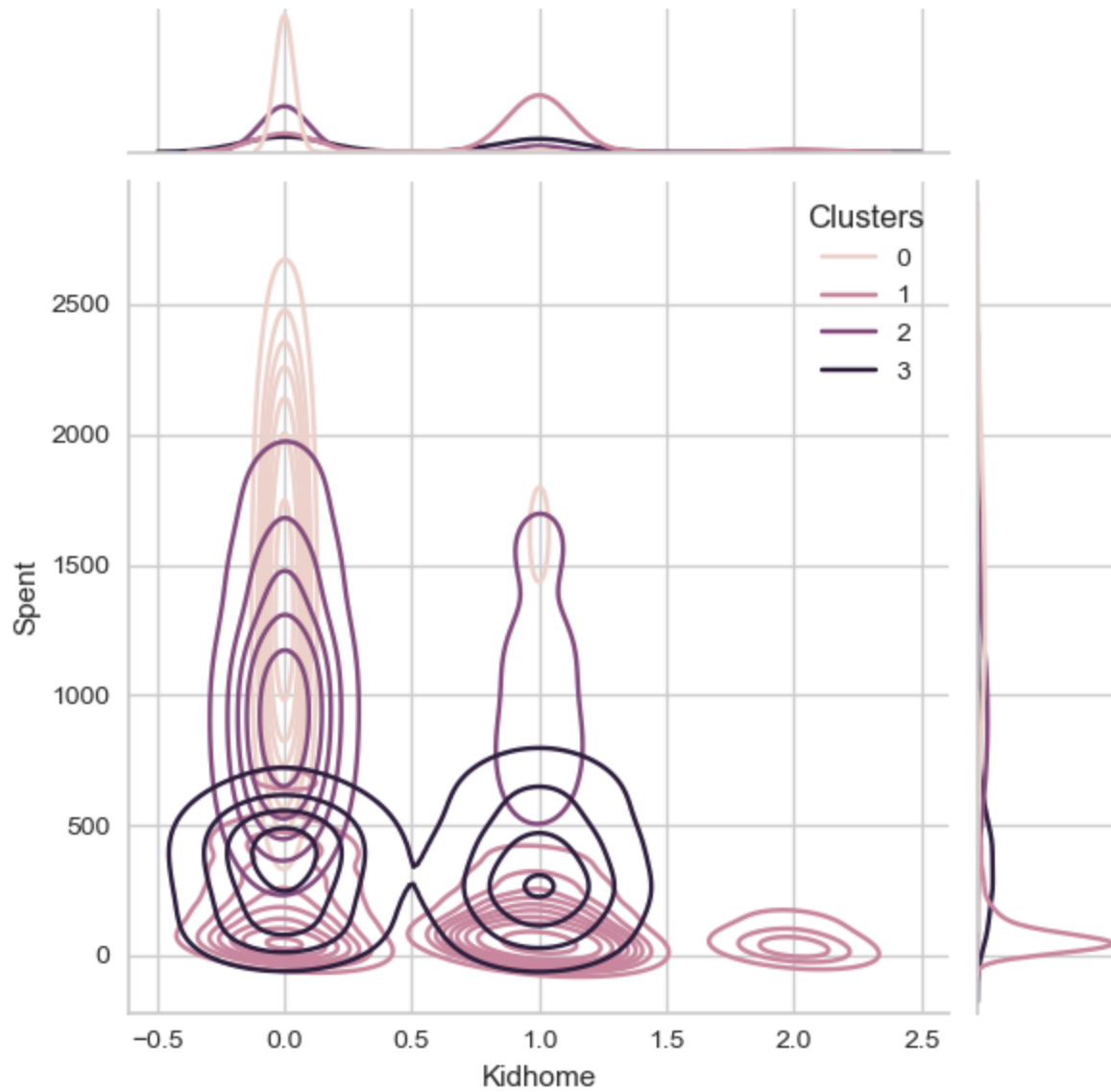
Now that we have evaluated our model and understand some characteristics of our clusters, let's dive deeper into understanding which consumer type comprises each cluster. We can use Seaborn's **Joint Plot** here.

Joint plots can be very useful in visualizing the relationship between two variables alongside their distributions.

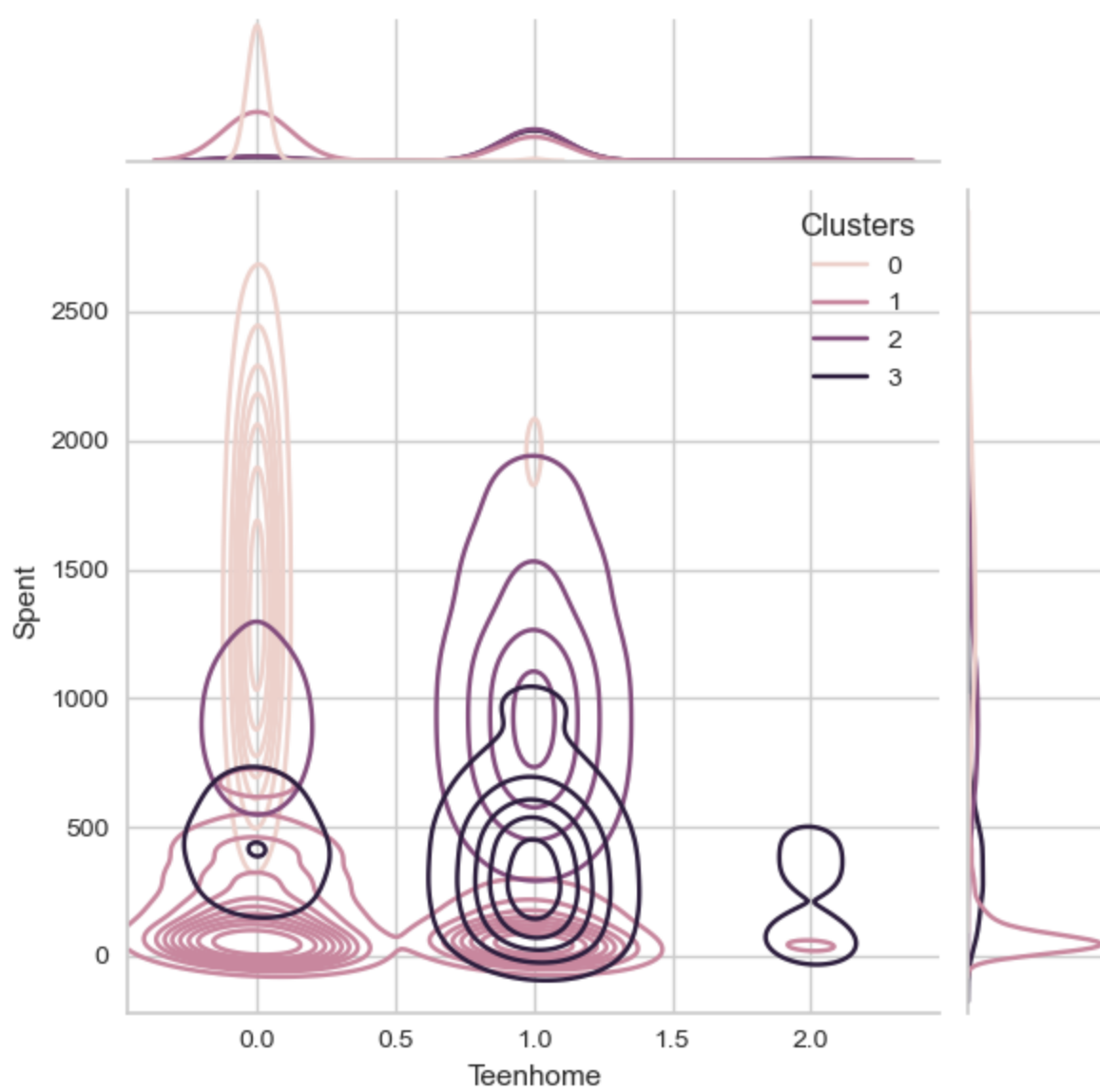
```
In [60]: PersonalInfo = [ "Kidhome", "Teenhome", "Customer_For", "Age", "Family_Size", "Is_Parent",
```

```
for i in PersonalInfo:
    plt.figure()
    sns.jointplot(x=data[i], y=data['Spent'], hue=data['Clusters'], kind='kde')
    plt.show()
```

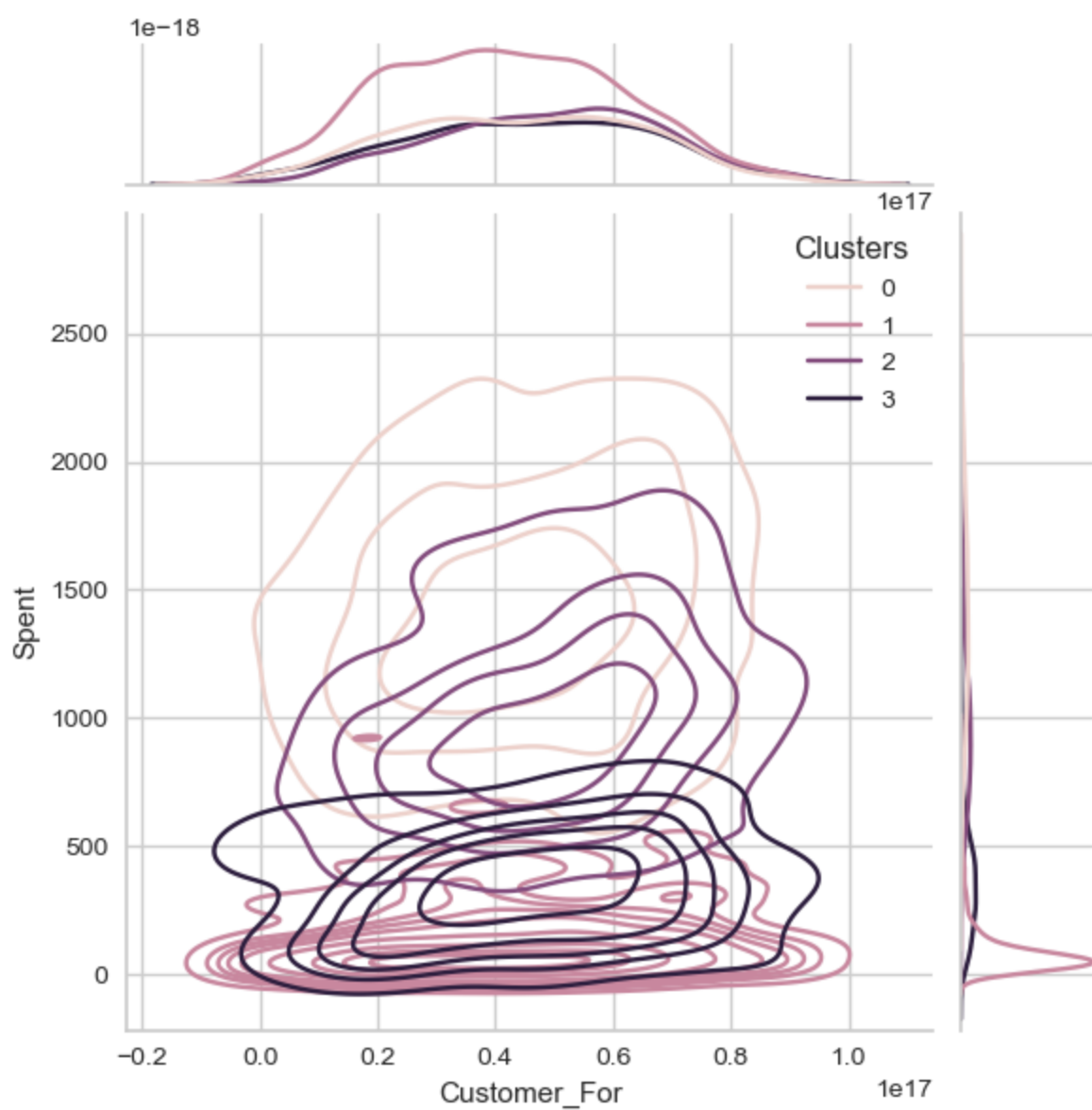
<Figure size 800x550 with 0 Axes>



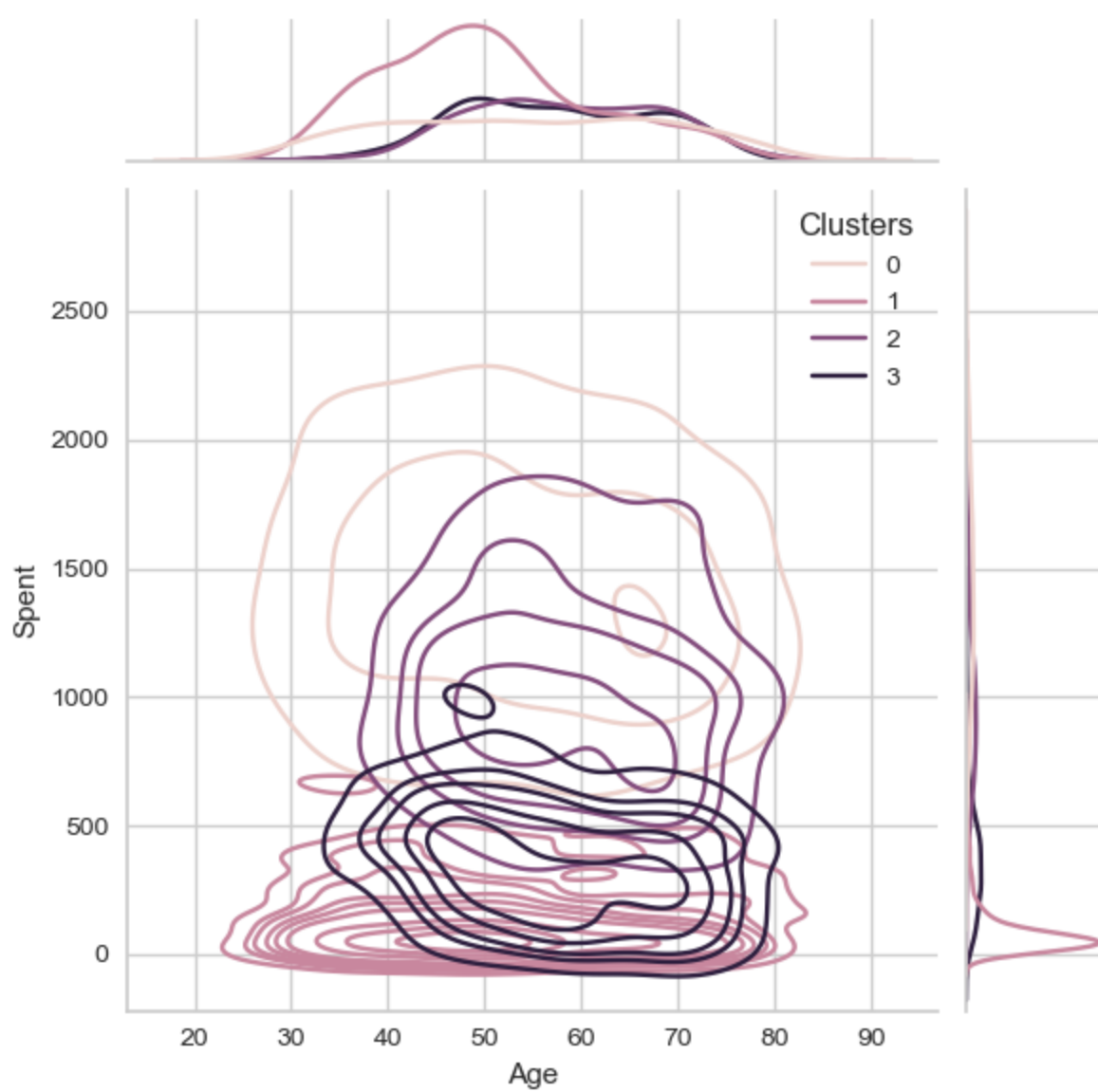
<Figure size 800x550 with 0 Axes>



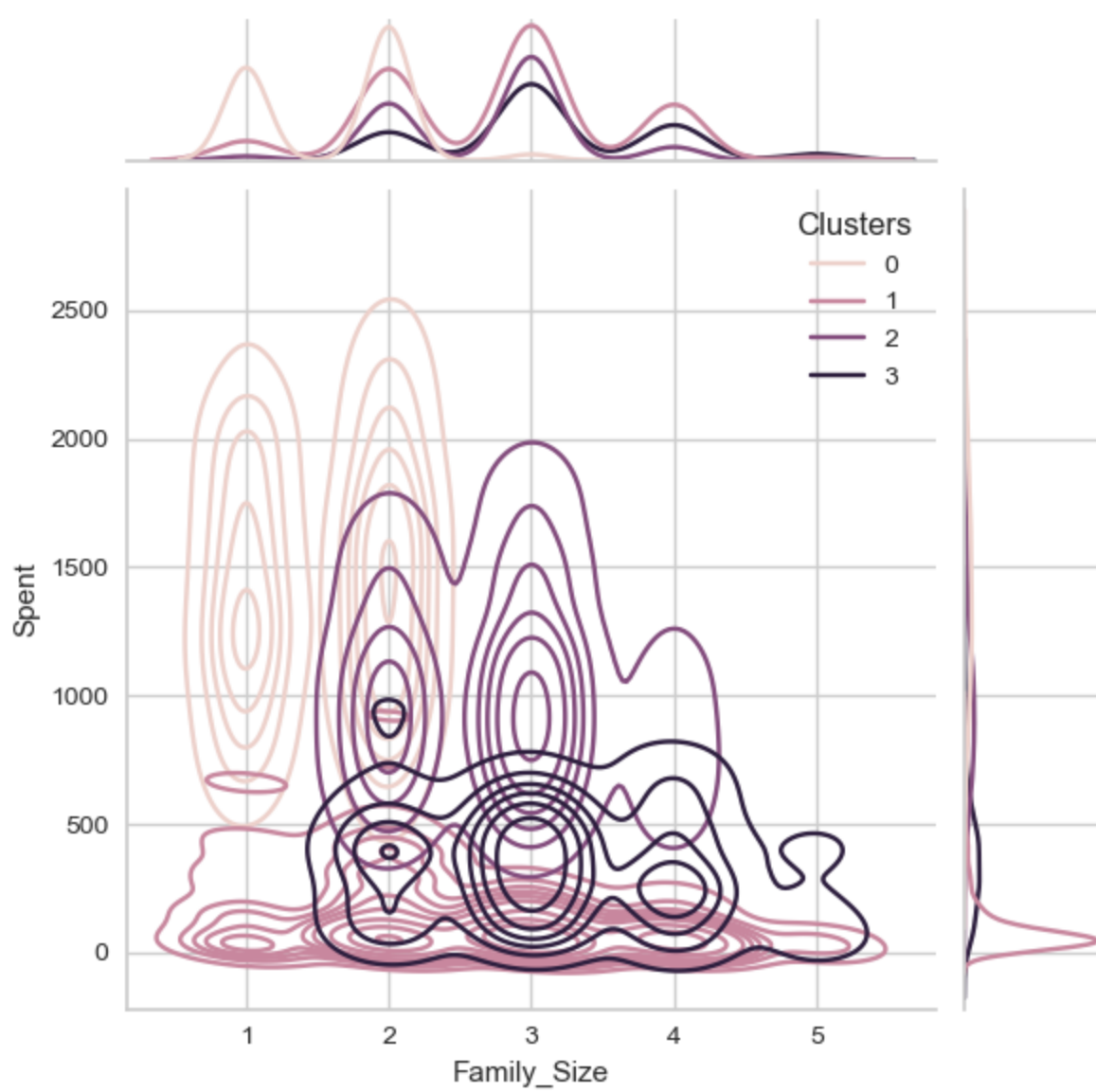
<Figure size 800x550 with 0 Axes>



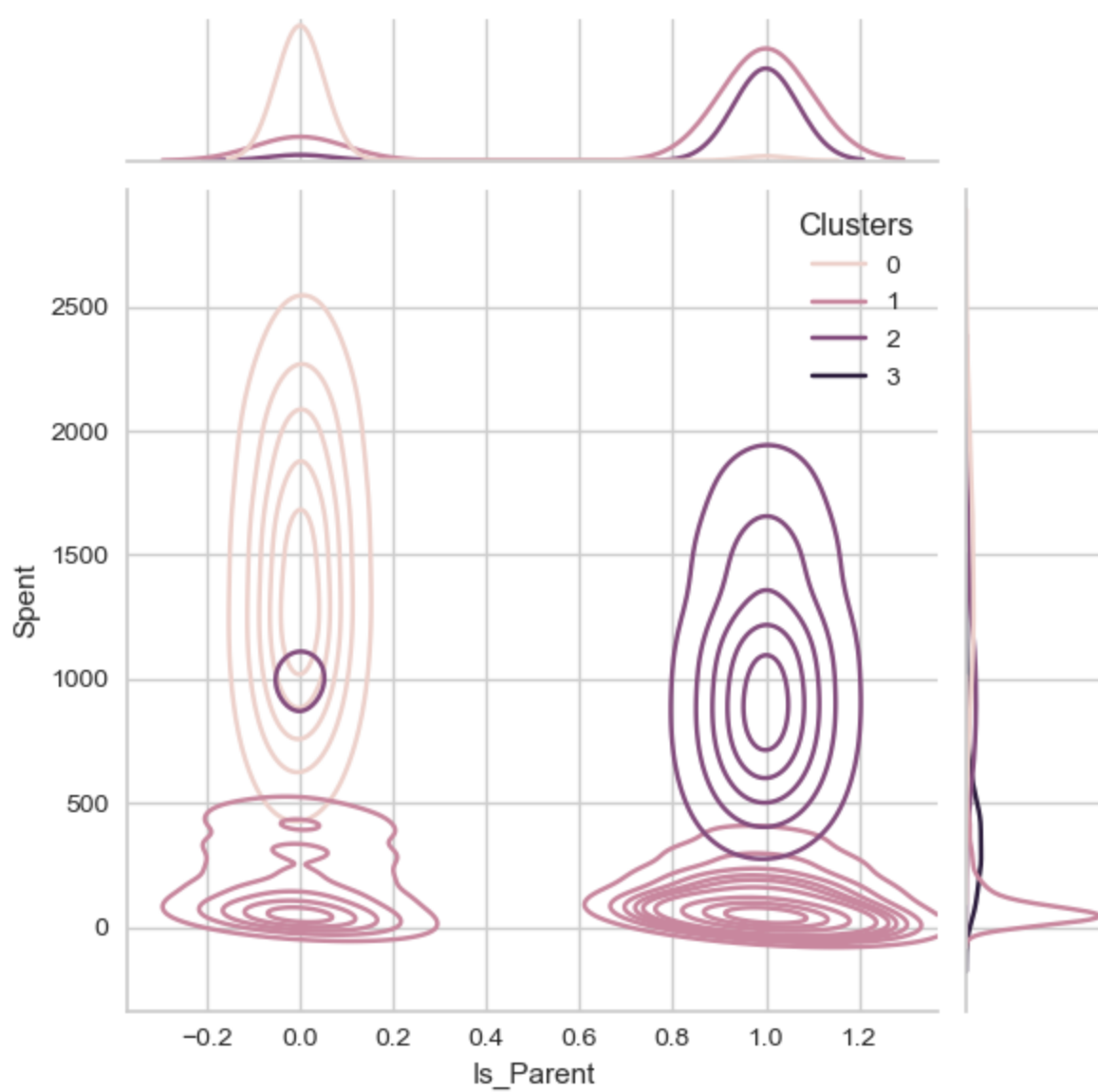
<Figure size 800x550 with 0 Axes>



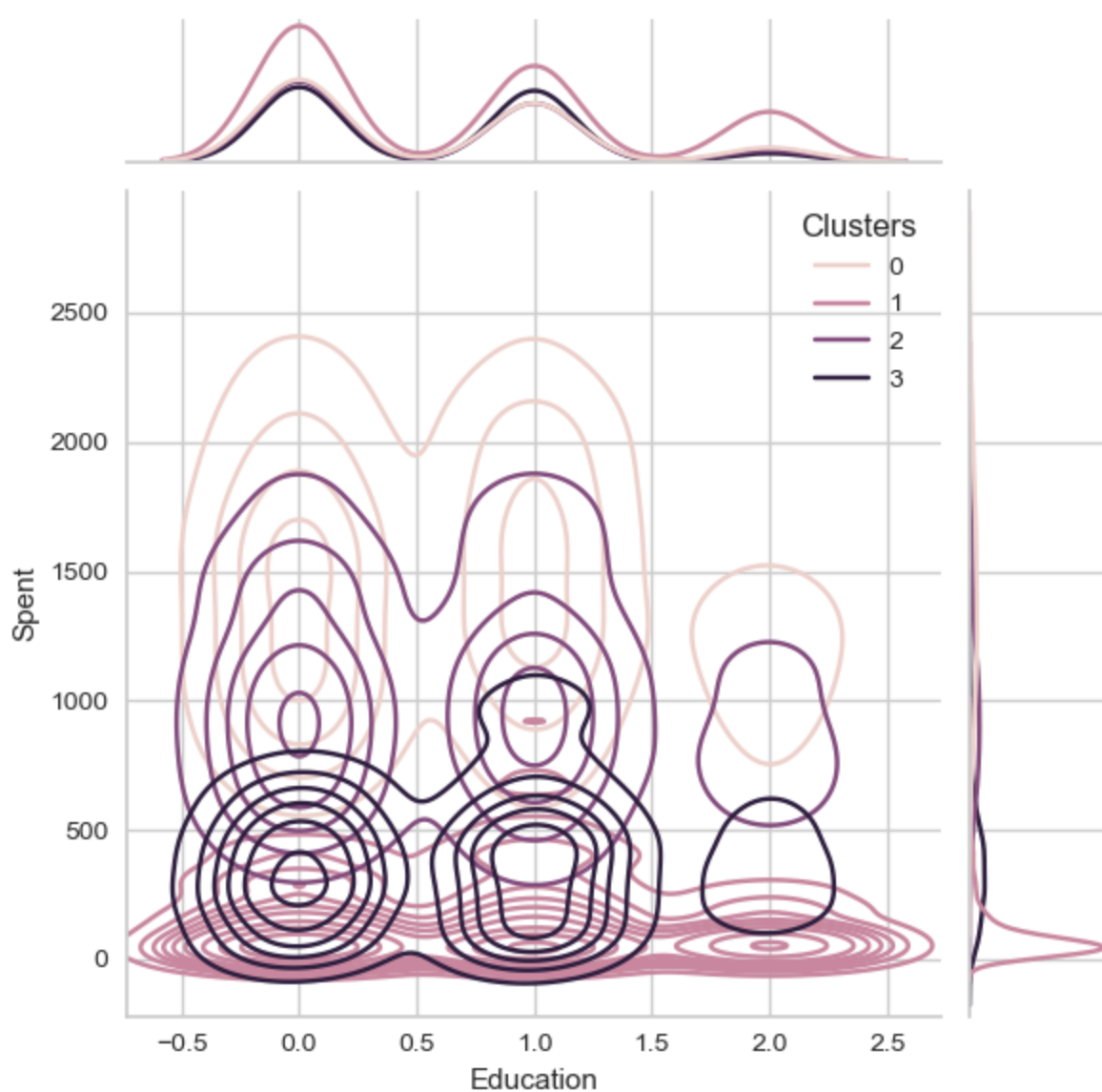
<Figure size 800x550 with 0 Axes>



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Through the graphs above, we are able to observe the following general information for our clusters: 1) Cluster 0: high spenders, no kids, small family size, middle aged. 2) Cluster 1: low spenders, between 0-2 kids, varying family size with potential for large. 3) Cluster 2: medium spenders, up to 1 kid, medium family size. 4) Cluster 3: low-medium spenders, up to 1 kid, medium family size.

Conclusion

In this notebook, we first generally reviewed Hierarchical Agglomerative Clustering (HAC) and applied its various methods to artificial data.

Next, we brought in a real-world consumer data to apply HAC on in order to derive insights into potential customer types. Like all real data, we first had to clean and prepare it for analysis which was then followed by clustering consumers into 4 distinct groups. These clusters can now be used for a variety of business needs such as targeted marketing.