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0.0.1 Data Mining

Lab 5 Matric: 17201091/1
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1 1. Preparing data for clustering

[1]:
```
# import libraries
import pandas as pd
import numpy as np
import seaborn as sns, numpy as np
import matplotlib.pyplot as plt
```

[2]:
```
#read file
df = pd.read_csv('lab3.csv')
df.head()
```

[2]:

	ID	LocX	LocY	RegDens	RegPop	MedHHInc	MeanHHSz
0	00601	-66.749472	18.180103	70.0	19143	9888	3.24
1	00602	-67.180247	18.363285	83.0	42042	11384	3.10
2	00603	-67.134224	18.448619	86.0	55592	10748	2.84
3	00604	-67.136995	18.498987	83.0	3844	31199	3.00
4	00606	-66.958807	18.182151	65.0	6449	9243	3.20

[3]:
```
#describe RegPop
df.describe()
```

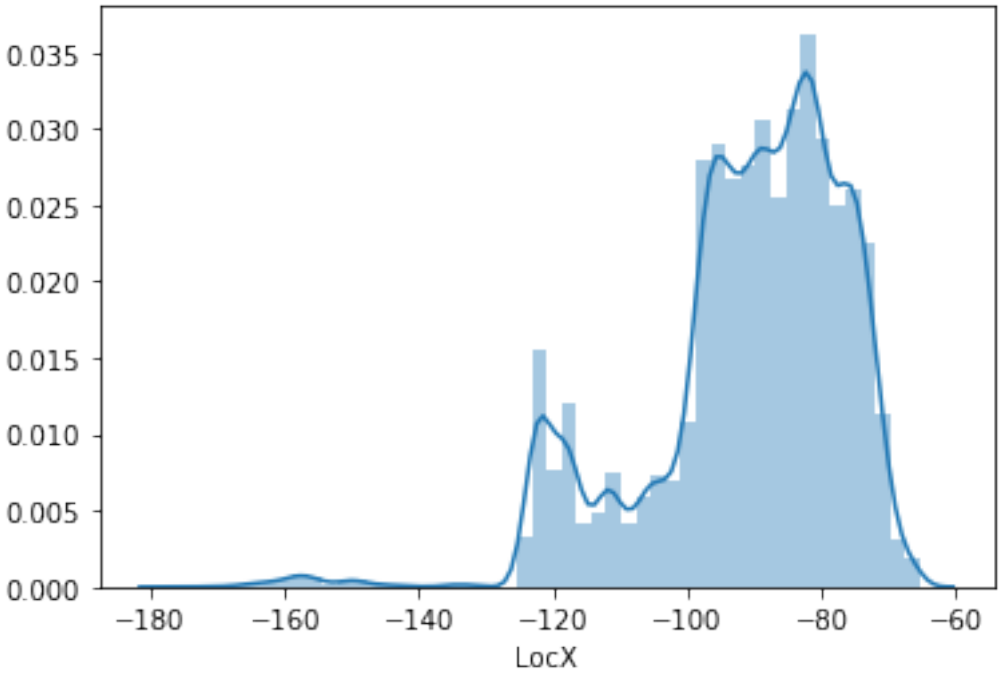
[3]:

	LocX	LocY	RegDens	RegPop	MedHHInc	MeanHHSz
count	33178.000000	33178.000000	32165.000000	33178.000000	33178.000000	33178.000000
mean	-91.084343	38.830389	50.500016	8596.977395	38248.093857	
std	15.070689	5.359397	28.865519	12978.758221	17469.135891	
min	-176.636755	17.962234	1.000000	0.000000	0.000000	
25%	-97.219483	35.383955	26.000000	656.000000	28903.750000	
50%	-88.308757	39.460478	51.000000	2515.000000	35762.000000	
75%	-80.380665	42.105602	75.000000	11167.500000	45229.250000	
max	-65.292575	71.299525	100.000000	144024.000000	200001.000000	

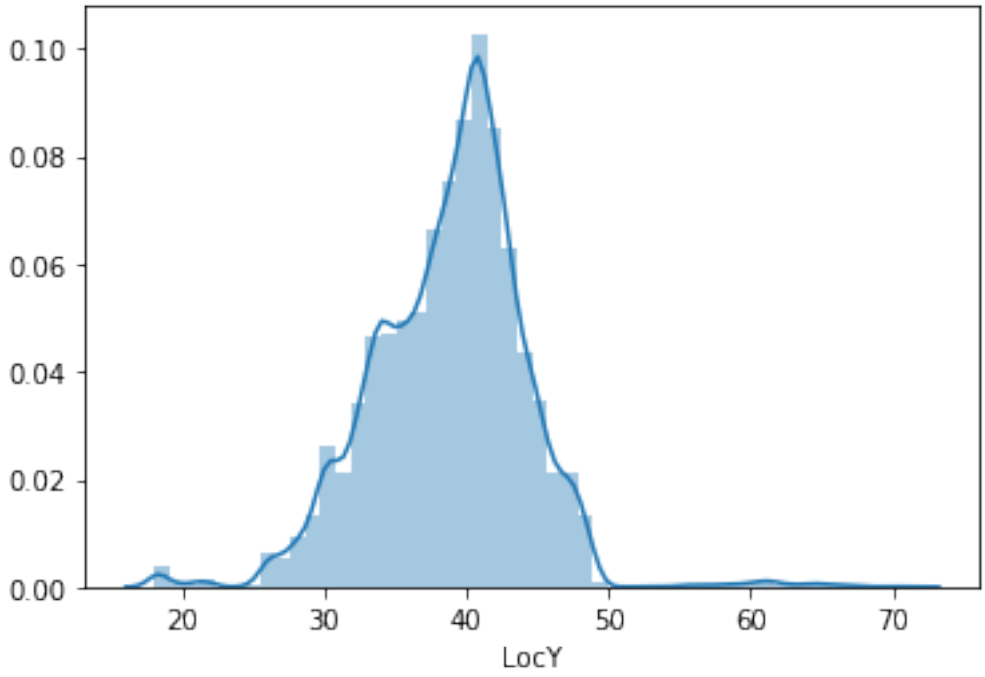
```
mean        2.500710
std         0.595747
min         0.000000
25%         2.360000
50%         2.550000
75%         2.740000
max         8.490000
```

[4]:
```
# fill nan  and typecast it into the correct float
df['RegDens'] = df['RegDens'].fillna(np.nan).astype(float)
```

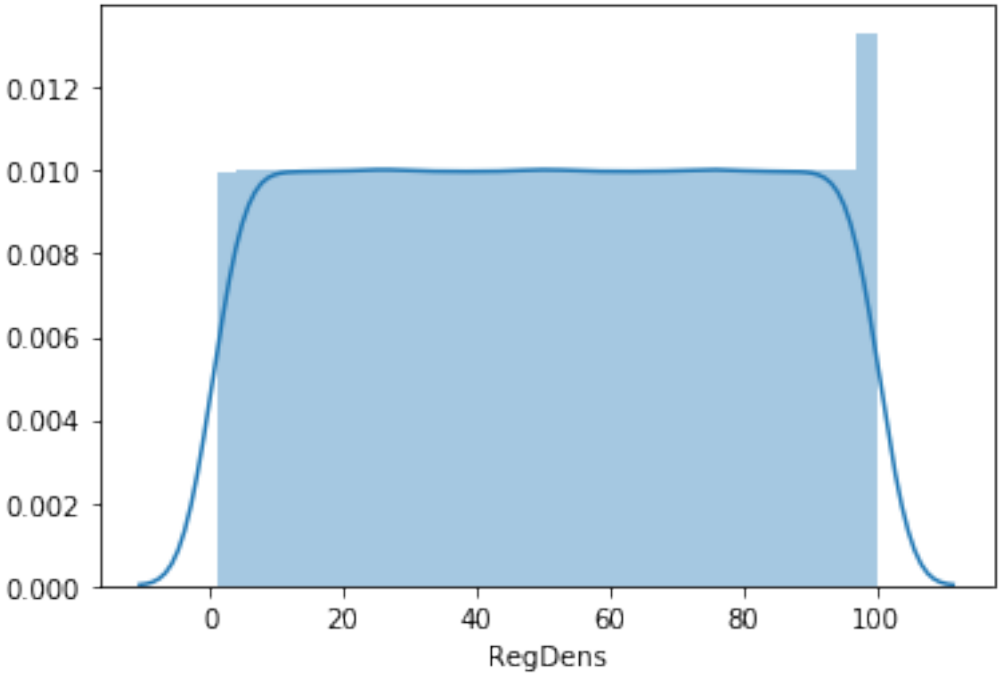
[5]:
```
# Plot the distribution
locx = sns.distplot(df['LocX'])
```



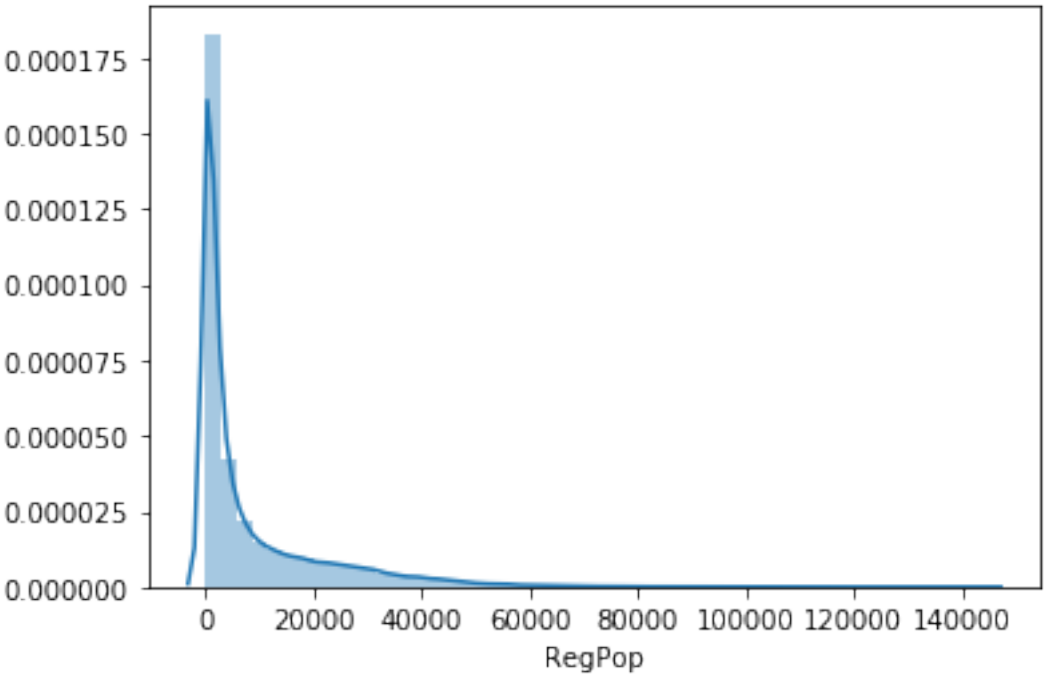
[6]:
```
locy = sns.distplot(df['LocY'])
```



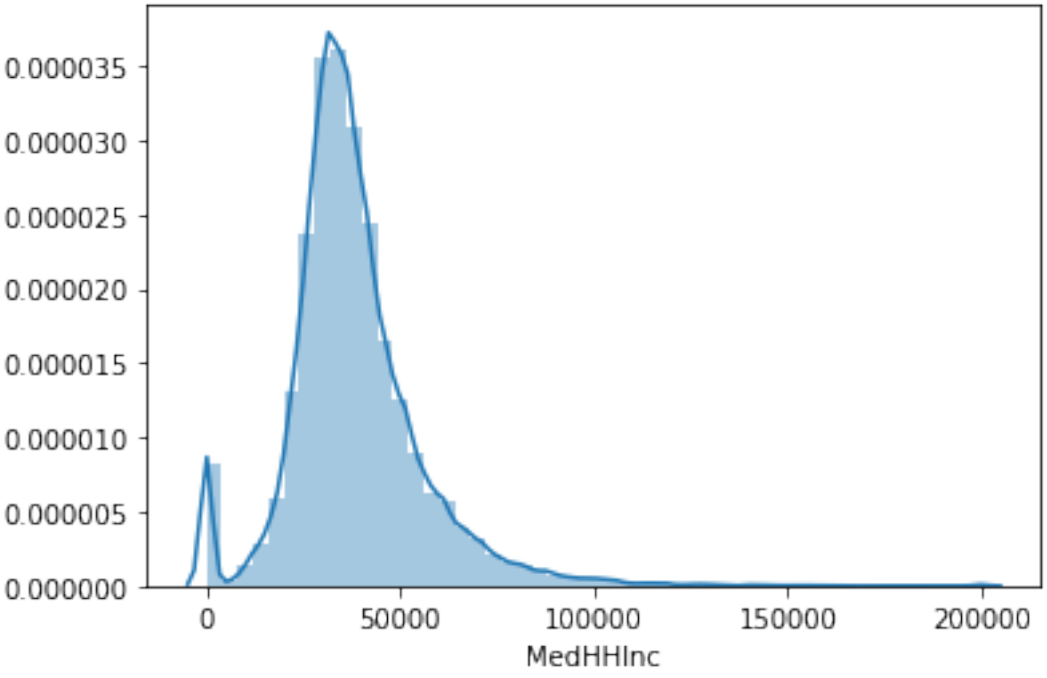
[7]:
```
regdens = sns.distplot(df['RegDens'].dropna())
```



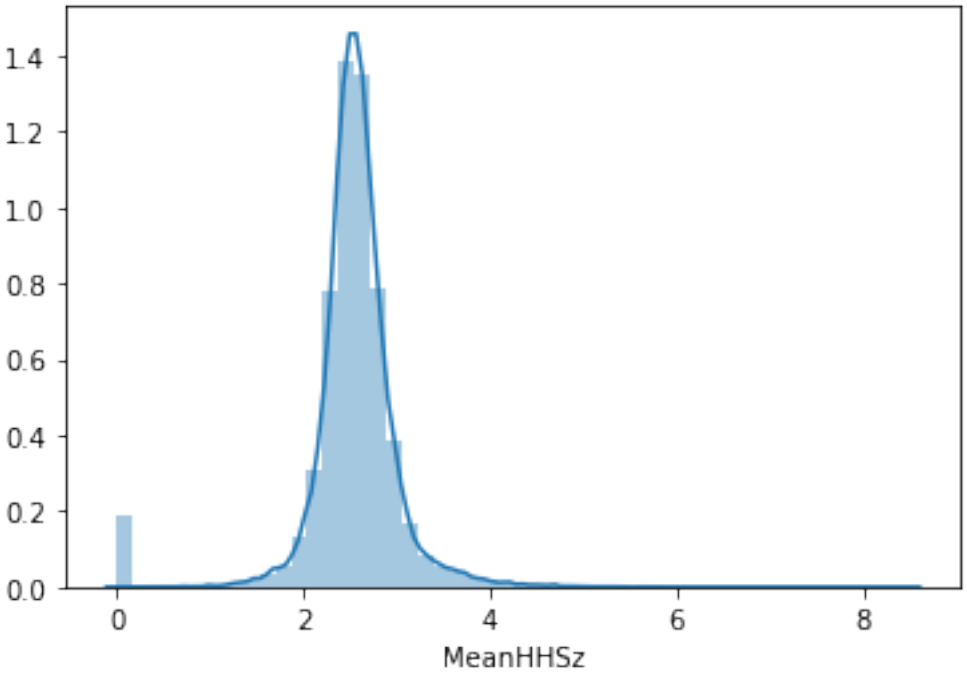
[8]:
```
regpop = sns.distplot(df['RegPop'])
```



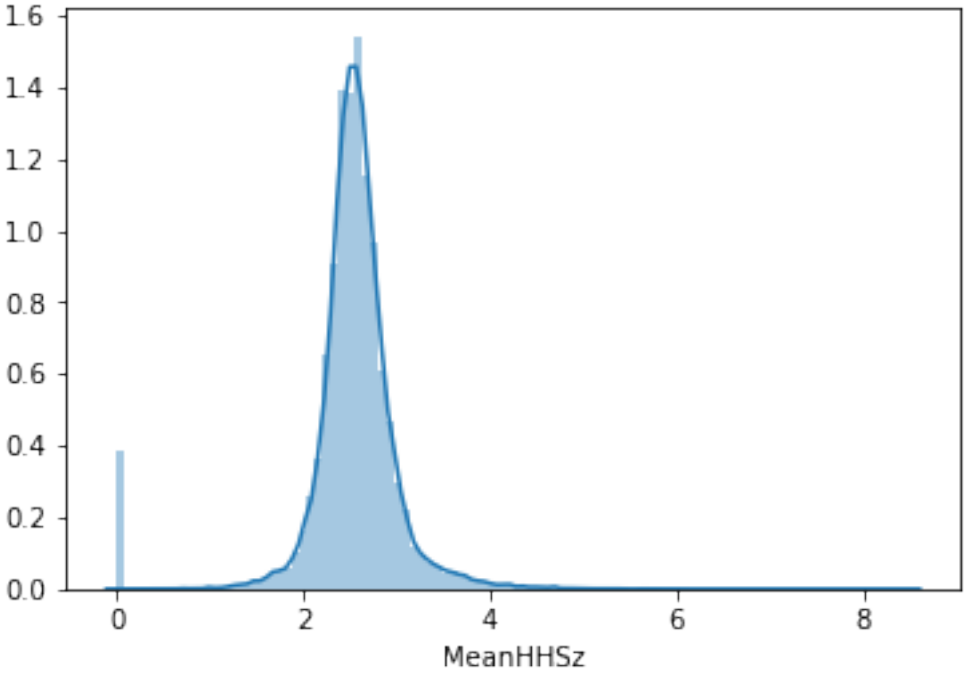
[9]:
```
MedHHInc = sns.distplot(df['MedHHInc'])
```



[10]:
```
MeanHHSz = sns.distplot(df['MeanHHSz'])
```



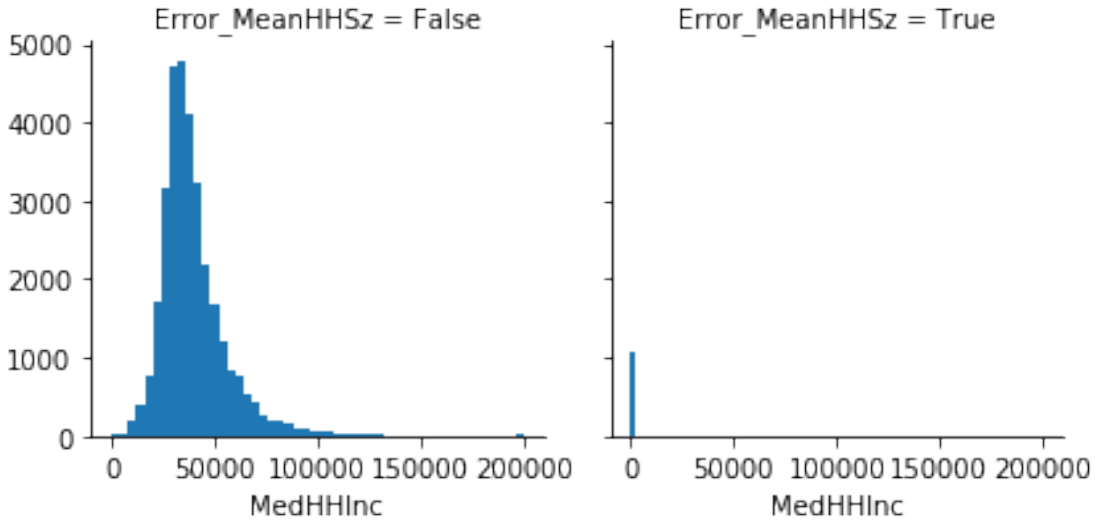
[11]:
```
# zoom in  the bins too 100
ax = sns.distplot(df['MeanHHSz'], bins = 100)
```



[12]:
```
#FacetGrid shows that errorneous data in MeanHHSz are correlated with␣
 ↪errorneous data in other features.
#This serves as a good reason to eliminate all rows with errorneous MeanHHSz.

df['Error_MeanHHSz'] = df['MeanHHSz'] < 1
g = sns.FacetGrid(df, col='Error_MeanHHSz')
g = g.map(plt.hist, 'MedHHInc', bins=50)

plt.show()
```



2 2. Building your first K-means clustering

[13]:
```
#data preprocessing
df = df[df['MeanHHSz'] >= 1]

print("Row After preprocessing", len(df))
```

```
Row After preprocessing 32079
```

[14]:
```
# Building your first K-means clustering
clustering_data = df[["MedHHInc", "MeanHHSz", "RegDens"]]
```

[15]:
```
from sklearn.cluster import KMeans

kmeans = KMeans(n_clusters=5, random_state=0).fit(clustering_data)
kmeans.labels_
# add ClusterId
```

```
clustering_data["ClusterID"] = kmeans.predict(clustering_data)
```

```
/Users/liuhongyang/anaconda3/lib/python3.7/site-
packages/ipykernel_launcher.py:6: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-
docs/stable/indexing.html#indexing-view-versus-copy
```

[16]:
```
# how many records are in each cluster
print("Cluster membership")
print(clustering_data['ClusterID'].value_counts())
```

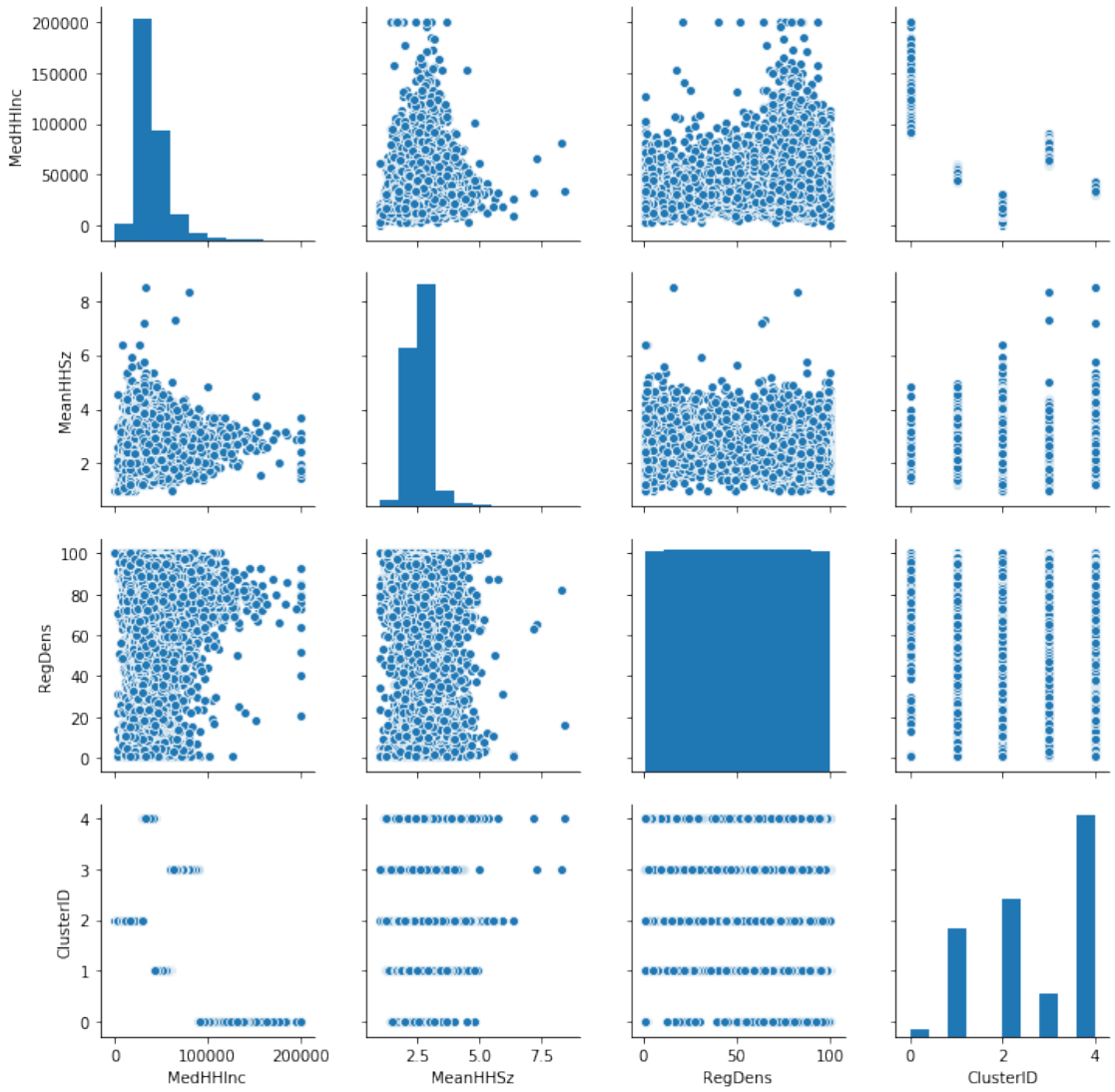
```
Cluster membership
4    13706
2     8502
1     6729
3     2663
0      479
Name: ClusterID, dtype: int64
```

[17]:
```
#values of centroids.
centroids = kmeans.cluster_centers_
print(centroids)
```

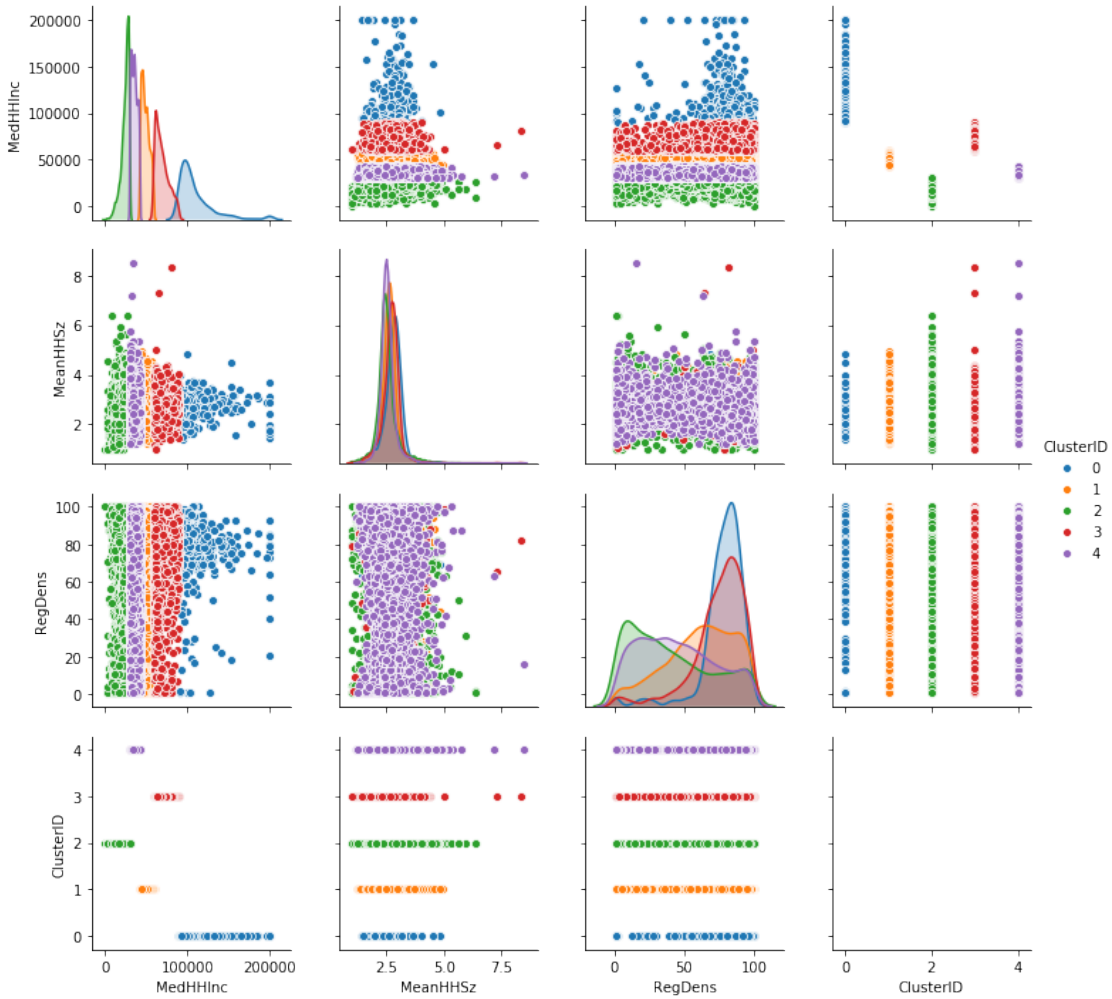
```
[[1.10075038e+05 2.79797071e+00 7.80815900e+01]
 [4.93329196e+04 2.63925837e+00 6.12551005e+01]
 [2.44288485e+04 2.53112519e+00 4.08103954e+01]
 [6.95600849e+04 2.70900413e+00 7.49736941e+01]
 [3.58604695e+04 2.56264195e+00 4.54626332e+01]]
```

3 3. Understanding and Visualising Your Clustering Model

[20]:
```
# use seaborn's pairplot to see how the clusters are spread out
ax = sns.pairplot(clustering_data)
```



[21]:
```
# pairplot the cluster distribution.
cluster_g = sns.pairplot(clustering_data, hue='ClusterID')
plt.show()
```


MedHHInc
MeanHHSz
RegDens
ClusterID
MedHHInc
MeanHHSz
RegDens
ClusterID
ClusterID
0
1
2
3
4

[ ]: