

Distribution Analysis after Clustering

December 16, 2022

0.0.1 Distribution Analysis at a Cluster X MSA level

Sarthak Arora

```
[2]: import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import os
import math as mt
from unidip import UniDip
import unidip.dip as dip
from scipy import stats
import statsmodels.api as sm
import pylab
from scipy.stats import norm
from Common_Functions import add_unique_identifier, data_split
from statsmodels.stats.multitest import fdrcorrection

import warnings
warnings.filterwarnings('ignore')
```

```
[3]: os.getcwd()
```

```
[3]: '/home/lennon_mccartney/Downloads/Prediction-of-commercial-insurance-payments-
for-surgical-procedure-using-DataRobot-main'
```

0.0.2 getting cluster groups we get using only the surgical cost

```
[11]: df_clusters = pd.read_csv("Kmeans_clusters/clusters_only_using_NormCost.csv")
cluster_0 = df_clusters[df_clusters["cluster"] == 0].group.values
cluster_1 = df_clusters[df_clusters["cluster"] == 1].group.values
cluster_2 = df_clusters[df_clusters["cluster"] == 2].group.values
```

```
[12]: # cluster_0 = ["ant_tls_fusion",
# "colorect",
# "femoral shaft fixation",
# "hepat",
```

```

# "hip_fracture_fixation",
# "intracranial_thromb",
# "post_cerv_fusion",
# "post_tls_fusion",
# "prox_tibia_fixation",
# "revision_tha",
# "revision_tka",
# "tha",
# "thoracic",
# "tka",
# "tpa"]

# cluster_1 = ["breast reconstruction",
# "bsp",
# "bunionectomy",
# "cardiac ablation_additional_discrete",
# "cardiac ablation_linear_focal",
# "cardiac_ablaton_anesthesia",
# "cardiac_ablaton_ice",
# "clavicle fixation",
# "fess",
# "hysterec",
# "kidney ablation",
# "lap appendectomy",
# "mastectomy",
# "navigation",
# "orthovisc_monovisc",
# "pnn",
# "robotic_assisted_surgery",
# "rtc_slap_bank",
# "septoplasty",
# "tavr"]

# cluster_2 = [
#     "ankle_fix",
# "ant_cerv_fusion",
# "bariatric",
# "cardiac ablation",
# "hernia",
# "laac",
# "liver ablation",
# "lung ablation",
# "lung ablation",
# "partial shoulder arthroplasty",
# "pka",
# "prostatectomy",
# "proximal humerus",

```

```
# "radius/ulna internal fixation",
# "tsa"
# ]
```

0.0.3 reading the main data and applying preprocessing functions

```
[10]: data = pd.read_csv('Data_Files/JnJ_Files/priv_mcare_f_pay_2022Oct18.csv')
data = add_unique_identifier(data)
model_data, future_data = data_split(data, count_col_name = 'priv_count')
data = model_data
```

```
[13]: ## number of unique procedures in the training data
data["group"].nunique()
```

```
[13]: 42
```

```
[14]: ## total number of missing mcare_median values in the training data
total_mcare_missing = data["mcare_pay_median"].isna().sum()
total_mcare_missing
```

```
[14]: 470
```

0.0.4 adding a new column to the training data for cluster labels

```
[15]: cluster_labels = []
for i in range(len(data)):
    if data["group"].iloc[i] in cluster_0:
        cluster_labels.append(0)
    elif data["group"].iloc[i] in cluster_1:
        cluster_labels.append(1)
    elif data["group"].iloc[i] in cluster_2:
        cluster_labels.append(2)
    else:
        cluster_labels.append("NaN")
```

```
[16]: data["clusters"] = cluster_labels
```

```
[17]: cluster_means = data.groupby('clusters', as_index=False)['mcare_pay_median'].
    ↪mean().rename(columns={'mcare_pay_median': 'mcare_cluster_mean'})
```

```
[18]: fig = sns.barplot(data=data.groupby(by = ["clusters"]).size().
    ↪reset_index(), x="clusters", y = 0)
fig.set(xlabel = "Cluster_Label", ylabel = "Count", title = 'Split of Data Over_
    ↪Clusters')
```

```
[18]: [Text(0.5, 0, 'Cluster_Label'),
      Text(0, 0.5, 'Count'),
      Text(0.5, 1.0, 'Split of Data Over Clusters')]
```



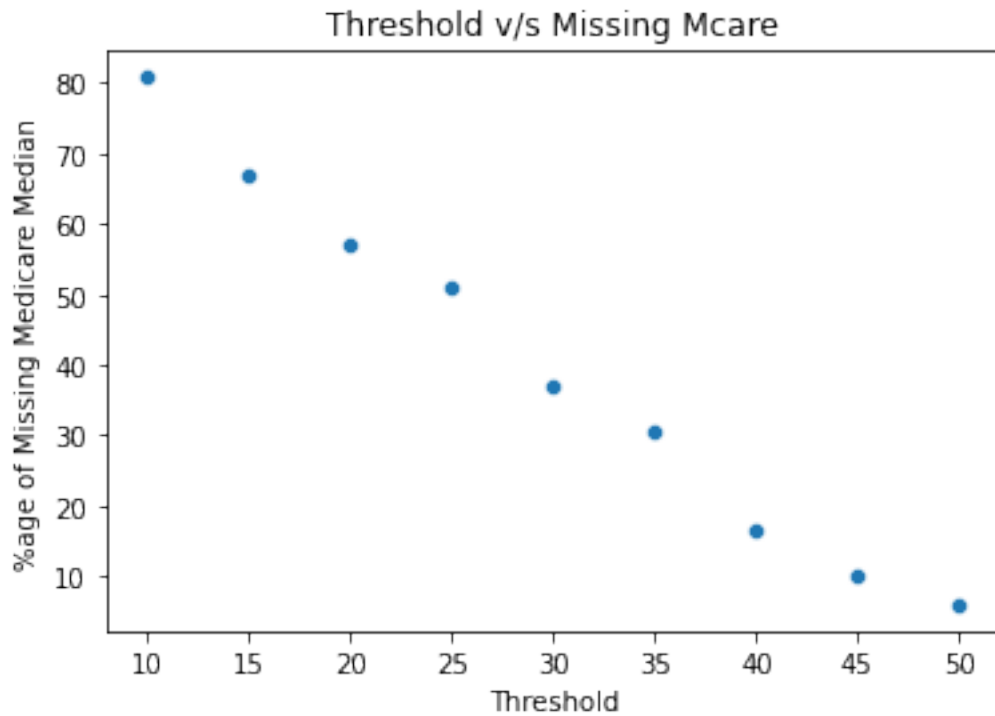
0.0.5 creating a dataframe having number of training examples at an MSA X Cluster Label level.

```
[19]: da_points = data.groupby(by = ['clusters', 'msa']).size().reset_index()
```

0.0.6 Looking at how the number of missing Mcare median values change as we change the threshold (i.e. the minimum number of points we require in a MSA X Cluster distribution)

```
[20]: thresholds = [10,15,20,25,30,35,40,45,50]
missing_count = []
for t in thresholds:
    temp1 = da_points[da_points[0] >= t]
    temp2 = data.merge(temp1, on = ['clusters', 'msa'], how = 'inner')
    missing_count.append(temp2["mcare_pay_median"].isna().sum())
fig = sns.scatterplot(x=thresholds, y = 100*(missing_count/total_mcare_missing))
fig.set(xlabel = "Threshold", ylabel = "%age of Missing Medicare Median", title =
    'Threshold v/s Missing Mcare')
```

```
[20]: [Text(0.5, 0, 'Threshold'),
      Text(0, 0.5, '%age of Missing Medicare Median'),
      Text(0.5, 1.0, 'Threshold v/s Missing Mcare')]
```



```
[21]: da_points = da_points[da_points[0] >= 15]
```

```
[22]: fig = sns.barplot(data=da_points.groupby(by = ["clusters"]).sum().
      ↪reset_index(),x="clusters",y = 0)
fig.set(xlabel = "Cluster_Label", ylabel = "Count", title = 'Split of Data Over_
      ↪Clusters (after thresholding)')
```

```
[22]: [Text(0.5, 0, 'Cluster_Label'),
      Text(0, 0.5, 'Count'),
      Text(0.5, 1.0, 'Split of Data Over Clusters (after thresholding)')]
```



0.0.7 filtering out the MSA X Cluster sets which have more than or equal to 15 training examples

```
[23]: filter_df = data.merge(da_points, on = ['clusters', 'msa'], how = 'inner')
filter_df = filter_df.merge(cluster_means, on = ['clusters'], how = 'left')
filter_df["msa_cluster"] = filter_df["clusters"].astype(str) + "_" +
    ↪filter_df["msa"].astype(str)
filter_df
```

```
[23]:
```

	id	msa	year	site	\
0	26420.0_2018_Inpatient_breast reconstruction	26420.0	2018	Inpatient	
1	26420.0_2020_Outpatient_navigation	26420.0	2020	Outpatient	
2	26420.0_2019_Outpatient_bsp	26420.0	2019	Outpatient	
3	26420.0_2018_Outpatient_bariatric	26420.0	2018	Outpatient	
4	26420.0_2019_Outpatient_bariatric	26420.0	2019	Outpatient	
...	
3080	23104.0_2018_Outpatient_fess	23104.0	2018	Outpatient	
3081	23104.0_2019_Outpatient_hysterect	23104.0	2019	Outpatient	
3082	23104.0_2018_Outpatient_hysterect	23104.0	2018	Outpatient	
3083	23104.0_2019_Outpatient_rtc_slap_bank	23104.0	2019	Outpatient	
3084	23104.0_2018_Outpatient_rtc_slap_bank	23104.0	2018	Outpatient	

```

group  priv_count  priv_pay_mean  priv_pay_median  \

```

0	breast reconstruction	51.0	47327.576470	21408.000
1	navigation	53.0	24278.586230	22610.750
2	bsp	62.0	12194.493390	12292.785
3	bariatric	63.0	8510.499365	8440.050
4	bariatric	65.0	12158.861540	9200.830
...
3080	fess	559.0	11841.383290	10782.000
3081	hysterect	610.0	14291.381590	13581.885
3082	hysterect	726.0	12070.976400	10439.340
3083	rtc_slap_bank	741.0	17471.221130	17544.300
3084	rtc_slap_bank	1034.0	16664.924480	16274.790

	priv_pay_iqr	mcare_count	...	mcare_pay_median	mcare_pay_sd	\
0	23351.715	81.0	...	10395.16	12242.654150	
1	3899.050	427.0	...	10575.60	1806.259876	
2	10401.335	63.0	...	3976.12	1578.030820	
3	11238.265	49.0	...	0.00	1977.703154	
4	13049.110	59.0	...	2181.87	1873.258734	
...	
3080	7816.055	453.0	...	3730.22	990.914736	
3081	7350.695	212.0	...	6129.90	1782.534108	
3082	6875.600	234.0	...	5967.75	1722.511997	
3083	9170.440	1368.0	...	4397.70	1625.875048	
3084	8958.390	1383.0	...	4299.44	1098.442750	

	CBSA_NAME	State	lon	lat	\
0	Houston-The Woodlands-Sugar Land, TX	Texas	-95.622552	29.598443	
1	Houston-The Woodlands-Sugar Land, TX	Texas	-95.622552	29.598443	
2	Houston-The Woodlands-Sugar Land, TX	Texas	-95.622552	29.598443	
3	Houston-The Woodlands-Sugar Land, TX	Texas	-95.622552	29.598443	
4	Houston-The Woodlands-Sugar Land, TX	Texas	-95.622552	29.598443	
...	
3080	Dallas-Fort Worth-Arlington, TX	Texas	-96.920913	32.707875	
3081	Dallas-Fort Worth-Arlington, TX	Texas	-96.920913	32.707875	
3082	Dallas-Fort Worth-Arlington, TX	Texas	-96.920913	32.707875	
3083	Dallas-Fort Worth-Arlington, TX	Texas	-96.920913	32.707875	
3084	Dallas-Fort Worth-Arlington, TX	Texas	-96.920913	32.707875	

	clusters	0	mcare_cluster_mean	msa_cluster
0	0	48	5221.74077	0_26420.0
1	0	48	5221.74077	0_26420.0
2	0	48	5221.74077	0_26420.0
3	0	48	5221.74077	0_26420.0
4	0	48	5221.74077	0_26420.0
...
3080	0	43	5221.74077	0_23104.0
3081	0	43	5221.74077	0_23104.0

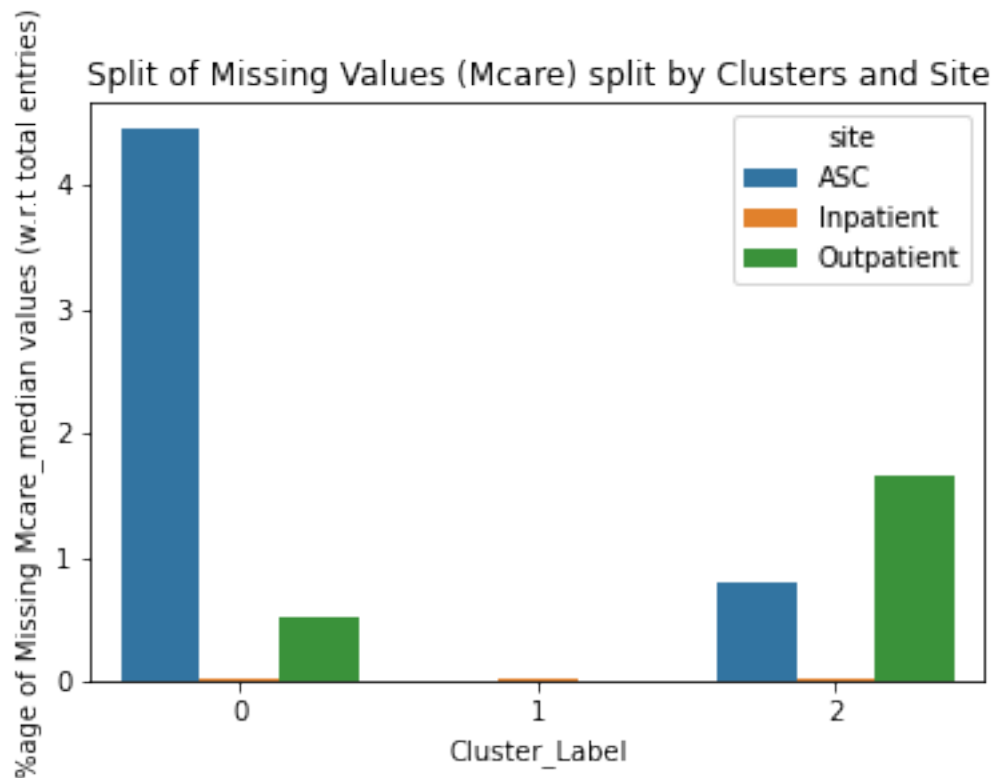
3082	0	43	5221.74077	0_23104.0
3083	0	43	5221.74077	0_23104.0
3084	0	43	5221.74077	0_23104.0

[3085 rows x 22 columns]

0.0.8 How the missing and non missing values are distributed based on the cluster as well as the type of site (Inpatient, Outpatient or ASC)

```
[24]: missing_mcare = filter_df[filter_df["mcare_pay_median"].
      ↳isna()]["msa","clusters","site"]
temp = pd.DataFrame({"msa":[0, 0, 0],
                    "clusters":[1, 2, 0],
                    "site":["Inpatient","Inpatient","Inpatient"]})
x = missing_mcare.append(temp)[["clusters","site"]].groupby(by =
      ↳["clusters","site"]).size().reset_index()
x[0] = (x[0]/data.shape[0])*100
fig = sns.barplot(data=x,x="clusters",y = 0,hue="site")
fig.set(xlabel = "Cluster_Label", ylabel = "%age of Missing Mcare_median values_
      ↳(w.r.t total entries)", title = 'Split of Missing Values (Mcare) split by_
      ↳Clusters and Site')
```

```
[24]: [Text(0.5, 0, 'Cluster_Label'),
      Text(0, 0.5, '%age of Missing Mcare_median values (w.r.t total entries)'),
      Text(0.5, 1.0, 'Split of Missing Values (Mcare) split by Clusters and Site')]
```

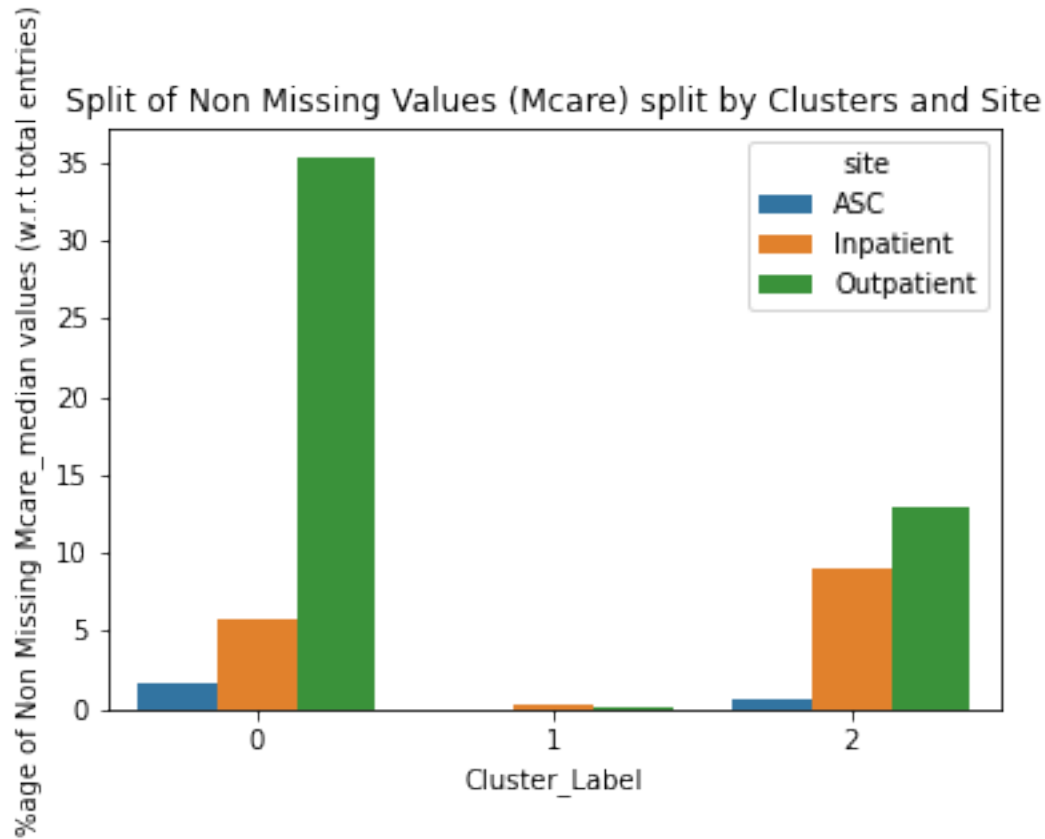
```
[25]: missing_mcare.append(temp)[["clusters","site"]].groupby(by =
↳ ["clusters","site"]).size().reset_index()
x[0] = (x[0]/total_mcare_missing)*100
x
```

```
[25]:   clusters      site      0
0         0      ASC  0.948092
1         0  Inpatient  0.005043
2         0  Outpatient  0.110947
3         1  Inpatient  0.005043
4         2      ASC  0.171463
5         2  Inpatient  0.005043
6         2  Outpatient  0.353013
```

```
[26]: non_missing_mcare = filter_df[~filter_df["mcare_pay_median"].
↳ isna()][["msa","clusters","site"]]
x = non_missing_mcare[["clusters","site"]].groupby(by = ["clusters","site"]).
↳ size().reset_index()
x[0] = (x[0]/data.shape[0])*100
fig = sns.barplot(data=x,x="clusters",y = 0,hue="site")
```

```
fig.set(xlabel = "Cluster_Label", ylabel = "%age of Non Missing Mcare_median_
↪values (w.r.t total entries)", title = 'Split of Non Missing Values (Mcare)_
↪split by Clusters and Site')
```

```
[26]: [Text(0.5, 0, 'Cluster_Label'),
Text(0, 0.5, '%age of Non Missing Mcare_median values (w.r.t total entries)'),
Text(0.5, 1.0, 'Split of Non Missing Values (Mcare) split by Clusters and
Site')]
```



```
[27]: non_missing_mcare[["clusters", "site"]].groupby(by = ["clusters", "site"]).size().
↪reset_index()
```

```
[27]:   clusters      site  0
0         0      ASC  67
1         0  Inpatient 245
2         0  Outpatient 1491
3         1  Inpatient  13
4         1  Outpatient   3
5         2      ASC   30
6         2  Inpatient 379
```

```
[28]: filter_df[(filter_df["msa_cluster"] == "0_26420.0")]["mcare_cluster_mean"].
      ↪unique()[0]
```

```
[28]: 5221.740770207848
```

0.0.9 plotting these distributions using histogram plots and KDE plots (to look for multimodality), we also quantify this multimodality using hartigan's dip test and perform normality tests, t - tests (to check if mean of the distribution is same as the mean of the cluster it belongs to).

```
[29]: uniq_msa_clust = filter_df["msa_cluster"].unique()
      grid = mt.ceil(np.sqrt(len(uniq_msa_clust)))
```

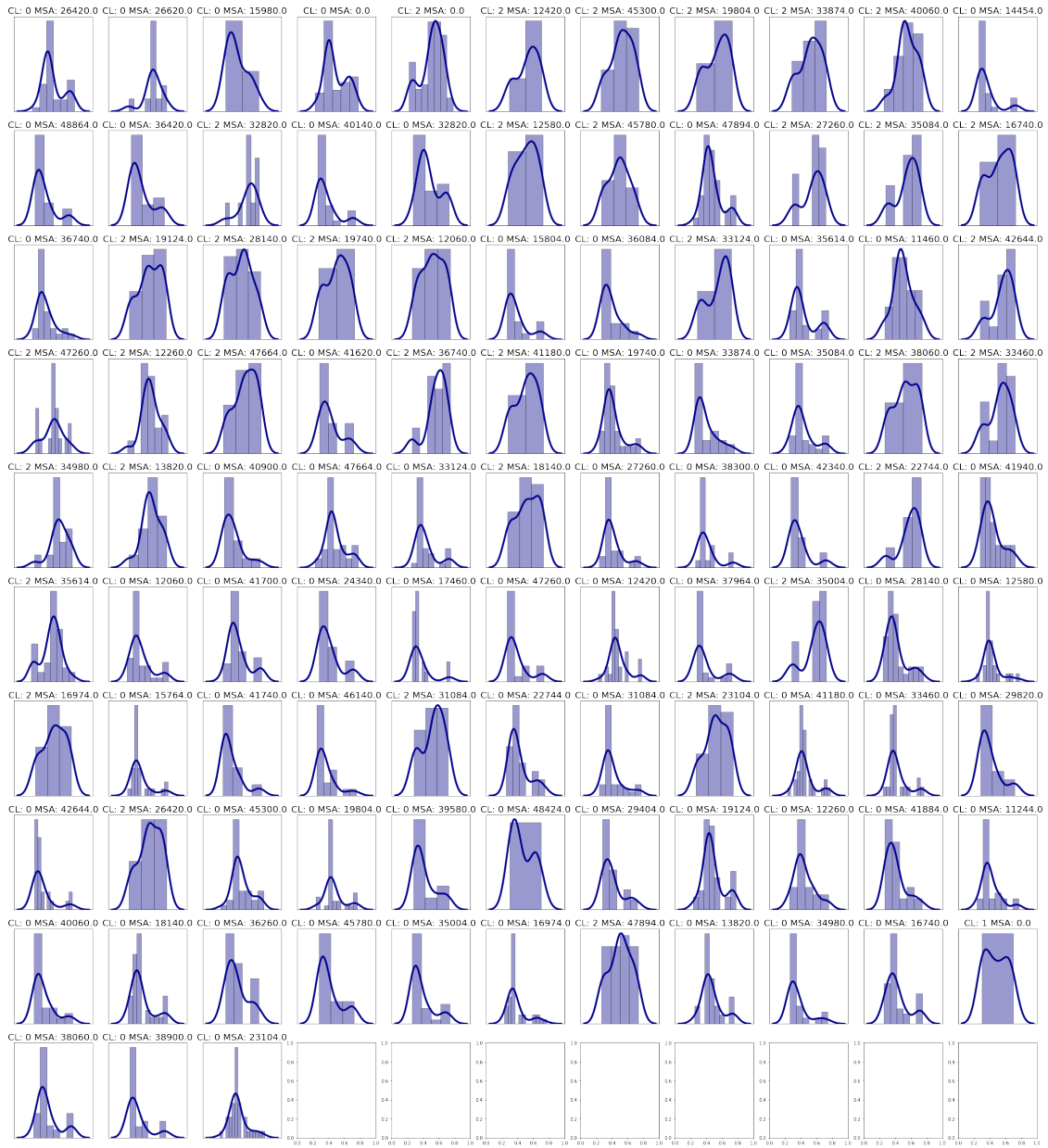
```
[30]: fig, axs = plt.subplots(grid-1, grid, figsize=(40,45))
      normality_test = []
      t_test_p = []
      t_test_st = []
      clusters = []
      msas = []
      interval_list = []
      n_pts = []
      missing_pts = []
      means = []
      sd_list = []
      for i,x in enumerate(uniq_msa_clust):

          dt_pts = filter_df[(filter_df["msa_cluster"] == x)]["mcare_pay_median"]
          clusters.append(int(x.split("_")[0]))
          msas.append(float(x.split("_")[1]))
          k ,p = stats.normaltest(dt_pts,nan_policy="omit")
          # label.append(x)
          normality_test.append(p)
          n_pts.append(len(dt_pts[~np.isnan(dt_pts)]))
          missing_pts.append(len(dt_pts[np.isnan(dt_pts)]))
          gp_stats = dt_pts.describe()
          mu = gp_stats[1]
          std = gp_stats[2]
          means.append(mu)
          sd_list.append(std)
          cl_mean = filter_df[(filter_df["msa_cluster"] == x)]["mcare_cluster_mean"].
          ↪unique()[0]
          t_test = stats.ttest_1samp(dt_pts, popmean=cl_mean,nan_policy='omit')
          t_test_p.append(t_test[1])
          t_test_st.append(t_test[0])
```

```

    Q1 = np.percentile(dt_pts[~np.isnan(dt_pts)], 25, interpolation = ↵
↵ 'midpoint')
    Q3 = np.percentile(dt_pts[~np.isnan(dt_pts)], 75, interpolation = ↵
↵ 'midpoint')
    IQR = Q3 - Q1
    if len(dt_pts) == 0:
        opt_bins = 10
    else:
        bin_width = 2*IQR/np.cbrt(len(dt_pts))
        rng = max(dt_pts[~np.isnan(dt_pts)]) - min(dt_pts[~np.isnan(dt_pts)])
        opt_bins = int(rng/bin_width)
    sns.distplot(dt_pts, hist=True, kde=True,
        bins=opt_bins, color = 'darkblue',
        hist_kws={'edgecolor': 'black'},
        kde_kws={'linewidth': 4},
        ax=axis[int(i/grid),i%grid])
    dt_pts = np.msort(dt_pts)
    intervals = UniDip(dt_pts[~np.isnan(dt_pts)]).run()
    interval_list.append(intervals)
    axis[int(i/grid),i%grid].get_yaxis().set_visible(False)
    axis[int(i/grid),i%grid].get_xaxis().set_visible(False)
    axis[int(i/grid),i%grid].set_title("CL: " + str(int(x.split("_")[0])) + " ↵
↵ MSA: " + str(float(x.split("_")[1])),fontsize = 20)
# plt.savefig("density_plots.png")
#     axis[int(i/grid),i%grid].set_title(intervals[0][1])

```



0.0.10 saving useful metrics from the above distributions and tests in a dataframe

```
[31]: output_df = pd.DataFrame(list(zip(clusters,msas,
    ↪fdr correction(normality_test,alpha=0.1)[1],fdr correction(t_test_p,alpha=0.
    ↪1)[1],t_test_st,interval_list,n_pts,missing_pts,means,sd_list)),columns=["Cluster_Label","M
output_df["msa_cluster"] = output_df["Cluster_Label"].astype(str) + "_" +
    ↪output_df["MSA"].astype(str)
```

```
# print("%age of MSAxCluster groups where we cannot reject the NULL hypothesis
↳ is (90% CI) :",100*len(output_df[output_df["Normality_p_value"] >= 0.1])/
↳ len(output_df))
# output_df.sort_values(by=["Normality_p_value"],ascending=False)
output_df
```

```
[31]:
```

	Cluster_Label	MSA	Normality_p_value	T_test_p_value	T-Statistic	\
0	0	26420.0	0.127812	0.788805	0.620920	
1	0	26620.0	0.013838	0.123862	-2.943756	
2	0	15980.0	0.422595	0.316869	-1.843431	
3	0	0.0	0.031388	0.303299	1.756479	
4	2	0.0	0.080576	0.924204	0.177721	
..	
97	0	16740.0	0.046467	0.648921	-0.947087	
98	1	0.0	0.062180	0.181929	-2.349800	
99	0	38060.0	0.013838	0.924204	0.135872	
100	0	38900.0	0.004533	0.631821	1.061741	
101	0	23104.0	0.016144	0.241226	-2.010111	

	dip_test_interval	no_pts	no_missing_mcare	mean	SD	\
0	[(0, 44)]	45	3	5486.180995	2856.920569	
1	[(0, 11)]	12	3	3945.866667	1501.400623	
2	[(0, 12)]	13	3	4703.731538	1013.170067	
3	[(0, 72)]	73	9	5829.697603	2957.272034	
4	[(0, 81)]	82	13	11668.956890	5658.711046	
..	
97	[(0, 36)]	37	6	4831.688772	2505.147573	
98	[(0, 15)]	16	0	20374.278437	10163.846384	
99	[(0, 38)]	39	3	5275.723344	2481.169257	
100	[(0, 23)]	24	3	5798.572292	2661.559017	
101	[(0, 38)]	39	4	4502.874443	2233.368042	

	msa_cluster
0	0_26420.0
1	0_26620.0
2	0_15980.0
3	0_0.0
4	2_0.0
..	...
97	0_16740.0
98	1_0.0
99	0_38060.0
100	0_38900.0
101	0_23104.0

[102 rows x 11 columns]

```
[32]: output_df[(output_df["T_test_p_value"] > 0.5) & (output_df["no_pts"] > 25)]
```

```
[32]:
```

	Cluster_Label	MSA	Normality_p_value	T_test_p_value	T-Statistic	\
0	0	26420.0	0.127812	0.788805	0.620920	
4	2	0.0	0.080576	0.924204	0.177721	
6	2	45300.0	0.389993	0.790155	-0.568563	
7	2	19804.0	0.116350	0.853197	-0.457147	
18	0	47894.0	0.047050	0.990200	-0.012364	
21	2	16740.0	0.025541	0.788805	-0.618736	
22	0	36740.0	0.012674	0.886566	-0.377989	
23	2	19124.0	0.087106	0.924204	-0.244749	
35	2	47664.0	0.221029	0.942695	0.084182	
39	0	19740.0	0.008259	0.788805	-0.692952	
40	0	33874.0	0.017239	0.853197	0.451613	
41	0	35084.0	0.031388	0.548577	1.234094	
42	2	38060.0	0.062180	0.892486	-0.351189	
47	0	47664.0	0.167777	0.788805	-0.615943	
48	0	33124.0	0.011629	0.788805	0.707992	
49	2	18140.0	0.046467	0.790155	-0.573838	
50	0	27260.0	0.004533	0.537178	-1.283444	
56	0	12060.0	0.012674	0.788805	-0.617792	
57	0	41700.0	0.039443	0.531739	-1.305039	
66	2	16974.0	0.168960	0.924204	-0.130666	
67	0	15764.0	0.003276	0.546821	1.256212	
71	0	22744.0	0.039328	0.857795	0.427354	
73	2	23104.0	0.346953	0.898509	-0.303102	
75	0	33460.0	0.004629	0.931201	0.110398	
77	0	42644.0	0.003270	0.656180	0.931989	
78	2	26420.0	0.256317	0.892486	-0.341462	
79	0	45300.0	0.221029	0.590400	-1.152877	
80	0	19804.0	0.061373	0.898509	-0.299509	
84	0	19124.0	0.092272	0.788805	-0.639812	
87	0	11244.0	0.007252	0.631821	1.009715	
88	0	40060.0	0.009285	0.631821	-1.023471	
89	0	18140.0	0.013838	0.905487	-0.279896	
93	0	16974.0	0.003276	0.853197	0.442169	
94	2	47894.0	0.345591	0.788805	-0.725179	
97	0	16740.0	0.046467	0.648921	-0.947087	
99	0	38060.0	0.013838	0.924204	0.135872	

	dip_test_interval	no_pts	no_missing_mcare	mean	SD	\
0	[(0, 44)]	45	3	5486.180995	2856.920569	
4	[(0, 81)]	82	13	11668.956890	5658.711046	
6	[(0, 30)]	31	1	11054.320806	4931.385112	
7	[(0, 25)]	26	3	11047.795192	5689.699707	
18	[(0, 38)]	39	3	5216.321102	2737.355990	
21	[(0, 33)]	34	2	10975.952136	5484.254439	

22	[(0, 28)]	29	3	5060.612045	2295.584796
23	[(0, 36)]	37	2	11345.310382	5283.491647
35	[(0, 31)]	32	7	11641.294203	5603.976773
39	[(0, 31)]	32	6	4957.776087	2154.852929
40	[(0, 32)]	33	3	5380.861515	2024.031903
41	[(0, 33)]	34	4	5818.803129	2821.050857
42	[(0, 35)]	36	3	11226.210943	5666.830722
47	[(0, 41)]	42	3	4979.627948	2547.426171
48	[(0, 31)]	32	4	5558.630786	2691.752250
49	[(0, 32)]	33	5	11015.573819	5429.094858
50	[(0, 26)]	27	3	4744.015741	1934.117228
56	[(0, 43)]	44	3	4991.558520	2471.475014
57	[(0, 26)]	27	4	4729.288408	1960.751466
66	[(0, 29)]	30	6	11425.910033	5532.690456
67	[(0, 27)]	28	1	5795.347857	2416.187603
71	[(0, 25)]	26	3	5456.377433	2799.593927
73	[(0, 30)]	31	3	11284.967097	5013.558166
75	[(0, 26)]	27	3	5268.885514	2218.991225
77	[(0, 25)]	26	3	5665.219231	2426.321132
78	[(0, 32)]	33	3	11241.610606	5321.063152
79	[(0, 35)]	36	3	4800.723448	2191.130885
80	[(0, 34)]	35	3	5075.306000	2892.465696
84	[(0, 44)]	45	3	4972.795809	2610.098853
87	[(0, 26)]	27	3	5681.337734	2365.157247
88	[(0, 25)]	26	4	4857.313846	1815.606184
89	[(0, 35)]	36	4	5100.702750	2594.632371
93	[(0, 39)]	40	3	5426.624379	2930.545850
94	[(0, 28)]	29	3	10848.461704	5268.270167
97	[(0, 36)]	37	6	4831.688772	2505.147573
99	[(0, 38)]	39	3	5275.723344	2481.169257

	msa_cluster
0	0_26420.0
4	2_0.0
6	2_45300.0
7	2_19804.0
18	0_47894.0
21	2_16740.0
22	0_36740.0
23	2_19124.0
35	2_47664.0
39	0_19740.0
40	0_33874.0
41	0_35084.0
42	2_38060.0
47	0_47664.0
48	0_33124.0


```

49  2_18140.0
50  0_27260.0
56  0_12060.0
57  0_41700.0
66  2_16974.0
67  0_15764.0
71  0_22744.0
73  2_23104.0
75  0_33460.0
77  0_42644.0
78  2_26420.0
79  0_45300.0
80  0_19804.0
84  0_19124.0
87  0_11244.0
88  0_40060.0
89  0_18140.0
93  0_16974.0
94  2_47894.0
97  0_16740.0
99  0_38060.0

```

0.0.11

```

[33]: fig = sns.histplot(data=output_df, x="mean", hue="Cluster_Label", palette =_
      ↪ ['tab:blue', 'tab:green', 'tab:orange'])
      fig.set(xlabel = "Distribution_Mean", ylabel = "Count", title = 'Histogram_
      ↪ Showing means of the MSA X Cluster Distributions (Split By Cluster_Label)')

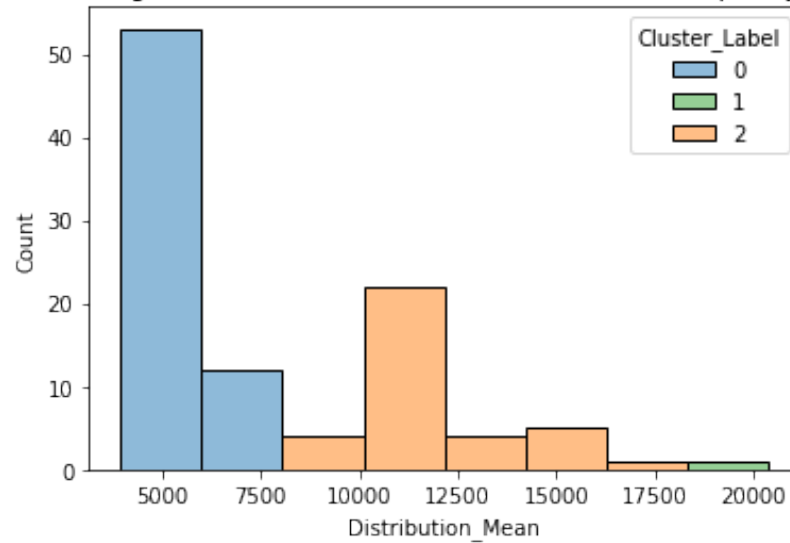
```

```

[33]: [Text(0.5, 0, 'Distribution_Mean'),
      Text(0, 0.5, 'Count'),
      Text(0.5, 1.0, 'Histogram Showing means of the MSA X Cluster Distributions
      (Split By Cluster_Label)')]

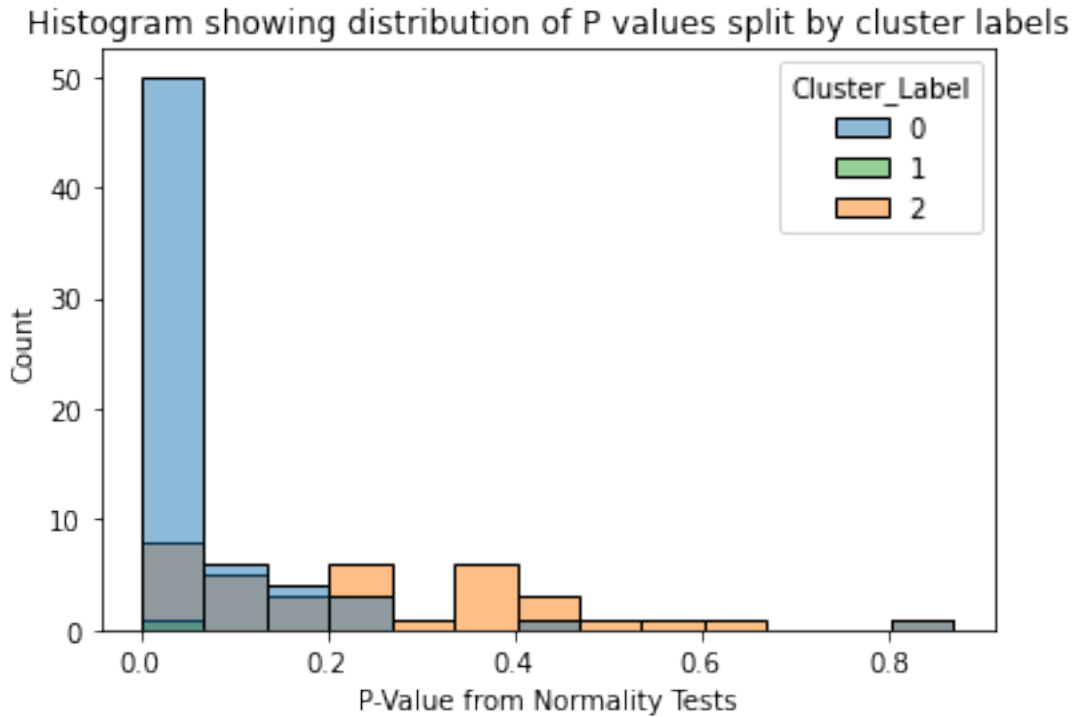
```

Histogram Showing means of the MSA X Cluster Distributions (Split By Cluster_Label)



```
[34]: fig = sns.histplot(data=output_df, x="Normality_p_value",
    ↪hue="Cluster_Label",palette = ['tab:blue', 'tab:green', 'tab:orange'])
fig.set(xlabel = "P-Value from Normality Tests", ylabel = "Count", title
    ↪='Histogram showing distribution of P values split by cluster labels')
```

```
[34]: [Text(0.5, 0, 'P-Value from Normality Tests'),
    Text(0, 0.5, 'Count'),
    Text(0.5, 1.0, 'Histogram showing distribution of P values split by cluster
    labels')]
```



0.0.12 Checking how many missing values do we have for Mcare median where we cannot reject the NULL hyp. in the normality test (i.e. the distributions are normal)

```
[35]: output_df[output_df["Normality_p_value"] > 0.1]["no_missing_mcare"].sum()
```

[35]: 94

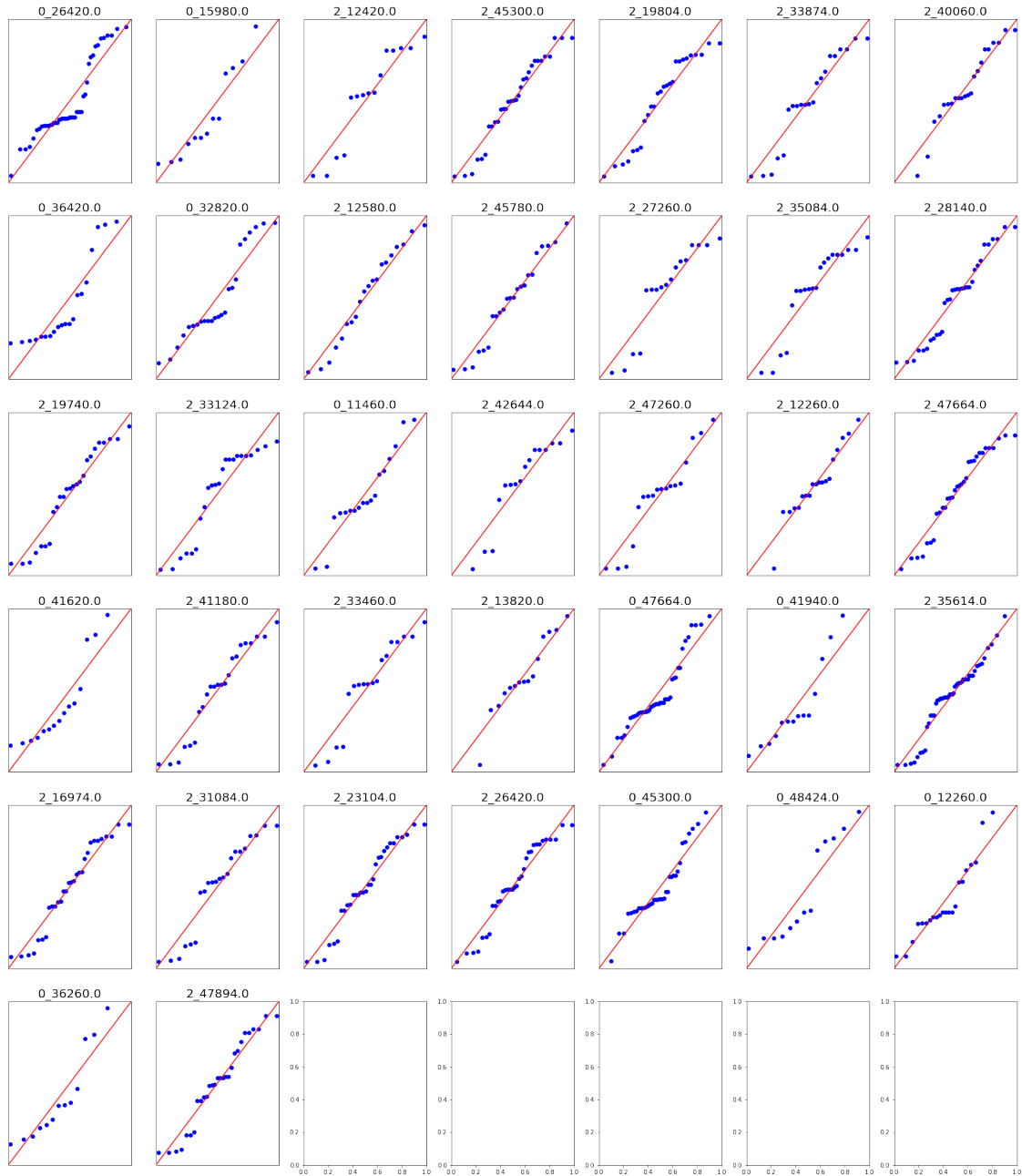
0.0.13 To confirm if these distributions are actually normal, we see their QQ plots

```
[36]: normality_check = filter_df.merge(output_df[output_df["Normality_p_value"] > 0.1], on = ["msa_cluster"], how = 'inner')
      uniq_msa_clust_norm = normality_check["msa_cluster"].unique()
      grid = mt.ceil(np.sqrt(len(uniq_msa_clust_norm)))
      fig, axs = plt.subplots(grid-1, grid, figsize=(30,35))
      for i,x in enumerate(uniq_msa_clust_norm):
          dt_pts = normality_check[(normality_check["msa_cluster"] == x)]["mcare_pay_median"]
          gp_stats = dt_pts.describe()
          mu = gp_stats[1]
          std = gp_stats[2]
          rmv_outliers = dt_pts[(dt_pts > mu - 3*std) & (dt_pts < mu + 3*std)].values
```

```

sm.qqplot(rmv_outliers,dist=norm(mu,std), line ='45',ax=axis(int(i/
→grid),i%grid))
axis(int(i/grid),i%grid).get_yaxis().set_visible(False)
axis(int(i/grid),i%grid).get_xaxis().set_visible(False)
axis(int(i/grid),i%grid).set_title(str(x),fontsize = 20)

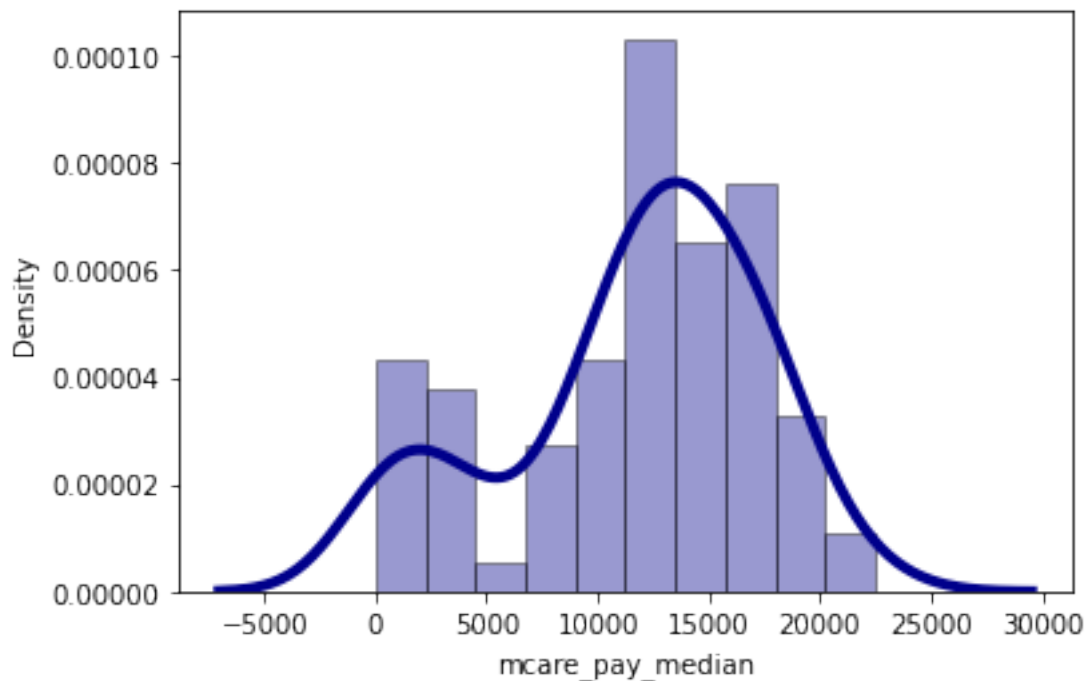
```



0.0.14 trying to remove multimodality by splitting into ASC, inpatient and outpatient (testing this out for one of the examples)

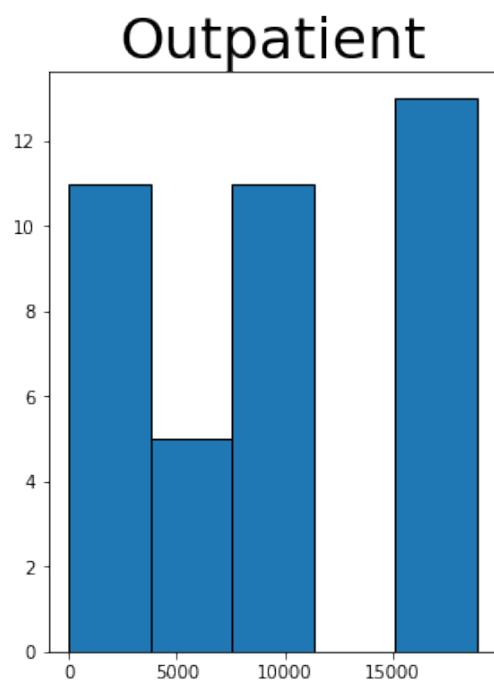
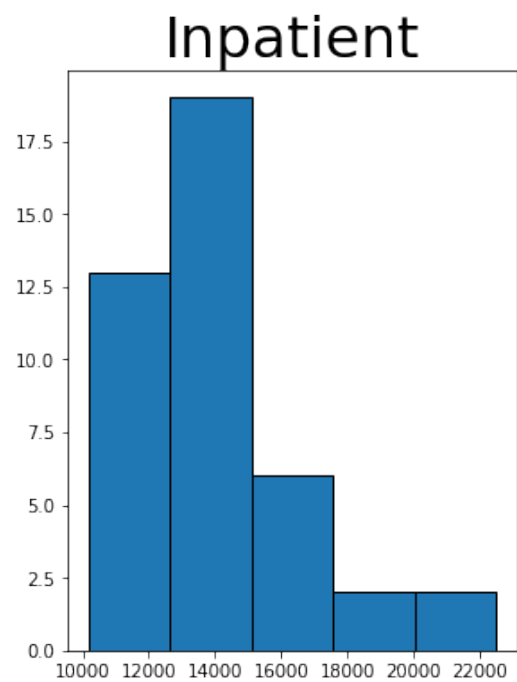
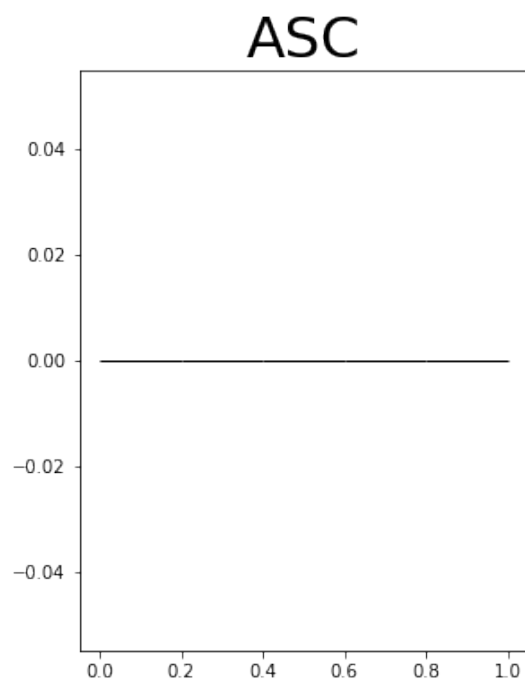
```
[37]: multi_mod_test = filter_df[filter_df["msa_cluster"] == uniq_msa_clust[4]]
sns.distplot(multi_mod_test["mcare_pay_median"], hist=True, kde=True,
             bins=10, color = 'darkblue',
             hist_kws={'edgecolor': 'black'},
             kde_kws={'linewidth': 4})
```

```
[37]: <AxesSubplot:xlabel='mcare_pay_median', ylabel='Density'>
```



```
[38]: fig = plt.figure(figsize = (10,15))
ax = fig.gca()
plt.tight_layout()
fig = (multi_mod_test["mcare_pay_median"]).hist(by = multi_mod_test["site"],
        ↪, bins = 5, ax = ax, ec="k", rot = 0)
[x.title.set_size(32) for x in fig.ravel()]
# plt.savefig("diff_gp_hist.png", dpi = 100)
```

```
[38]: [None, None, None, None]
```



0.0.15 looking at distributions for mcare_pay_median for outpatient site only

```
[39]: grid = mt.ceil(np.sqrt(len(uniq_msa_clust)))
fig, axs = plt.subplots(grid-1, grid, figsize=(30,35))
t_test_p = []
t_test_st = []
means = []
sd_list = []
clusters = []
msas = []
n_pts = []
missing_pts = []
for i,x in enumerate(uniq_msa_clust):
    dt_pts = filter_df[(filter_df["msa_cluster"] == x) & (filter_df["site"] ==
    ↳ "Outpatient")]["mcare_pay_median"]
    # Q1 = np.percentile(dt_pts[~np.isnan(dt_pts)], 25, interpolation =
    ↳ 'midpoint')
    # Q3 = np.percentile(dt_pts[~np.isnan(dt_pts)], 75, interpolation =
    ↳ 'midpoint')
    # IQR = Q3 - Q1

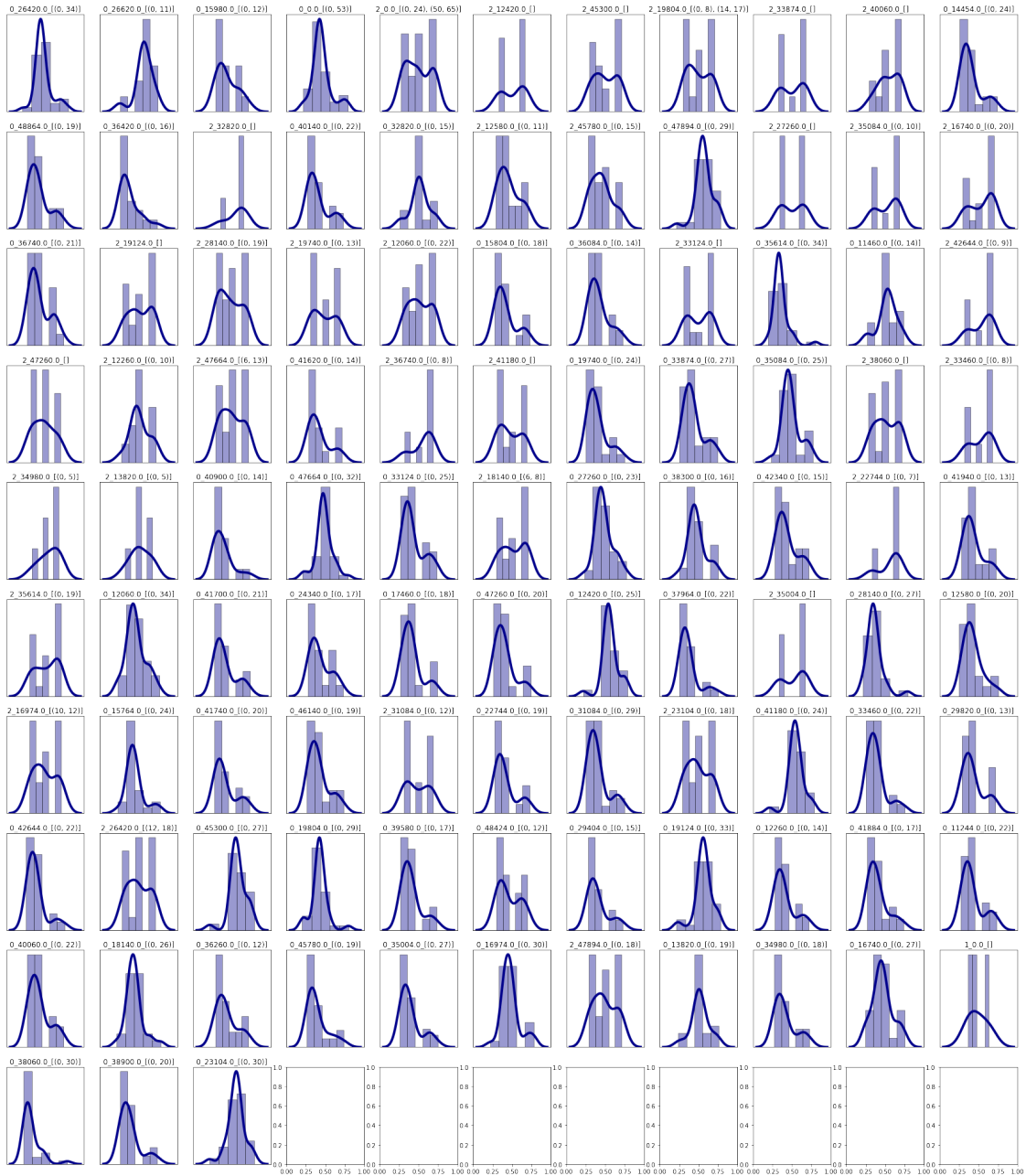
    # if (opt_bins == 0) or IQR == 0:
    #     opt_bins = 10
    # else:
    #     bin_width = 2*IQR/np.cbrt(len(dt_pts))
    #     rng = max(dt_pts[~np.isnan(dt_pts)]) - min(dt_pts[~np.isnan(dt_pts)])
    #     opt_bins = int(rng/bin_width)

    # if opt_bins == 0:
    #     opt_bins = 5
    sns.distplot(dt_pts, hist=True, kde=True,
        bins=5, color = 'darkblue',
        hist_kws={'edgecolor': 'black'},
        kde_kws={'linewidth': 4},
        ax=axs[int(i/grid),i%grid])
    t_test = stats.ttest_1samp(dt_pts, popmean=np.
    ↳ mean(dt_pts), nan_policy='omit')
    t_test_p.append(t_test[1])
    t_test_st.append(t_test[0])
    clusters.append(int(x.split("_")[0]))
    msas.append(float(x.split("_")[1]))
    n_pts.append(len(dt_pts[~np.isnan(dt_pts)]))
    missing_pts.append(len(dt_pts[np.isnan(dt_pts)]))
    gp_stats = dt_pts.describe()
    mu = gp_stats[1]
    std = gp_stats[2]
    means.append(mu)
```

```

sd_list.append(std)
dt_pts = np.msort(dt_pts)
intervals = UniDip(dt_pts[~np.isnan(dt_pts)]).run()
axs[int(i/grid),i%grid].get_yaxis().set_visible(False)
axs[int(i/grid),i%grid].get_xaxis().set_visible(False)
axs[int(i/grid),i%grid].set_title(str(x) + "_" +str(intervals))
# plt.savefig("density_plots.png")
#     axs[int(i/grid),i%grid].set_title(intervals[0][1])

```




```
[40]: output_df = pd.
      ↪DataFrame(list(zip(clusters,msas,t_test_p,t_test_st,n_pts,missing_pts,means,sd_list)),column
output_df["msa_cluster"] = output_df["Cluster_Label"].astype(str) + "_" +
      ↪output_df["MSA"].astype(str)
output_df
```

```
[40]:      Cluster_Label      MSA  T_test_p_value  T-Statistic  no_pts  \
0              0  26420.0              1.0  0.000000e+00      35
1              0  26620.0              1.0  0.000000e+00      12
2              0  15980.0              1.0 -6.473207e-15      13
3              0      0.0              1.0  3.070660e-15      54
4              2      0.0              1.0  0.000000e+00      40
..          ...      ...          ...          ...      ...
97             0  16740.0              1.0  3.995134e-15      28
98             1      0.0              1.0  0.000000e+00       3
99             0  38060.0              1.0 -3.481811e-15      31
100            0  38900.0              1.0  3.743855e-15      21
101            0  23104.0              1.0  1.984632e-15      31
```

```
      no_missing_mcare      mean      SD  msa_cluster
0              0  4766.000571  1985.854460  0_26420.0
1              0  3945.866667  1501.400623  0_26620.0
2              0  4703.731538  1013.170067  0_15980.0
3              0  4541.429444  2176.533544  0_0.0
4              1  9116.143500  6812.260432  2_0.0
..          ...      ...          ...          ...
97             3  4054.546607  1204.613751  0_16740.0
98             0  8983.376667  1047.786119  1_0.0
99             0  4722.290000  1454.372916  0_38060.0
100            0  4892.516429  1113.245254  0_38900.0
101            1  3965.257258  1275.765891  0_23104.0
```

[102 rows x 9 columns]

```
[41]: output_df[(output_df["no_missing_mcare"] != 0)]
```

```
[41]:      Cluster_Label      MSA  T_test_p_value  T-Statistic  no_pts  \
4              2      0.0              1.0  0.000000e+00      40
5              2  12420.0              1.0  0.000000e+00       9
6              2  45300.0              1.0  0.000000e+00      20
7              2  19804.0              1.0  0.000000e+00      17
8              2  33874.0              1.0 -8.215408e-16      12
9              2  40060.0              1.0 -1.244729e-15      13
13             2  32820.0              1.0  0.000000e+00       4
16             2  12580.0              1.0  0.000000e+00      12
20             2  35084.0              1.0  0.000000e+00      11
21             2  16740.0              1.0 -1.348174e-15      21
```

23	2	19124.0	1.0	-2.877737e-15	22
24	2	28140.0	1.0	0.000000e+00	20
25	2	19740.0	1.0	0.000000e+00	14
26	2	12060.0	1.0	2.760690e-15	23
27	0	15804.0	1.0	0.000000e+00	19
32	2	42644.0	1.0	1.591858e-15	10
34	2	12260.0	1.0	0.000000e+00	11
35	2	47664.0	1.0	1.239041e-15	19
37	2	36740.0	1.0	8.800847e-16	9
38	2	41180.0	1.0	-1.107192e-15	14
39	0	19740.0	1.0	0.000000e+00	25
41	0	35084.0	1.0	0.000000e+00	26
42	2	38060.0	1.0	0.000000e+00	22
43	2	33460.0	1.0	-7.509264e-16	9
44	2	34980.0	1.0	0.000000e+00	6
45	2	13820.0	1.0	0.000000e+00	6
48	0	33124.0	1.0	0.000000e+00	26
51	0	38300.0	1.0	3.645283e-15	17
55	2	35614.0	1.0	0.000000e+00	20
57	0	41700.0	1.0	4.835056e-15	22
60	0	47260.0	1.0	0.000000e+00	21
63	2	35004.0	1.0	0.000000e+00	10
64	0	28140.0	1.0	0.000000e+00	28
66	2	16974.0	1.0	-1.225100e-15	18
70	2	31084.0	1.0	0.000000e+00	13
73	2	23104.0	1.0	-2.717326e-15	19
74	0	41180.0	1.0	-3.948769e-15	25
78	2	26420.0	1.0	0.000000e+00	21
81	0	39580.0	1.0	0.000000e+00	18
88	0	40060.0	1.0	0.000000e+00	23
89	0	18140.0	1.0	0.000000e+00	27
91	0	45780.0	1.0	0.000000e+00	20
94	2	47894.0	1.0	0.000000e+00	19
95	0	13820.0	1.0	0.000000e+00	20
97	0	16740.0	1.0	3.995134e-15	28
101	0	23104.0	1.0	1.984632e-15	31

	no_missing_mcare	mean	SD	msa_cluster
4	1	9116.143500	6812.260432	2_0.0
5	3	10928.281111	7253.122933	2_12420.0
6	1	10380.367500	5963.467812	2_45300.0
7	3	9505.459706	6424.323965	2_19804.0
8	1	11622.231667	7669.934125	2_33874.0
9	3	11742.670769	5268.985845	2_40060.0
13	3	12758.817500	7142.368857	2_32820.0
16	3	12655.144583	6949.849871	2_12580.0
20	2	13783.368182	8153.903097	2_35084.0

21	1	11587.624524	6182.923986	2_16740.0
23	2	10993.558182	5929.531110	2_19124.0
24	3	8534.549500	6413.780630	2_28140.0
25	1	9955.000714	6559.401177	2_19740.0
26	3	9555.180000	6319.845081	2_12060.0
27	2	4833.425000	1145.035282	0_15804.0
32	2	13885.312000	7226.961748	2_42644.0
34	3	10248.246364	4459.616477	2_12260.0
35	3	9912.993158	6399.136517	2_47664.0
37	1	12431.855556	6200.503734	2_36740.0
38	3	9202.150714	6147.116359	2_41180.0
39	3	4510.542400	937.357195	0_19740.0
41	1	5083.902885	1316.294008	0_35084.0
42	3	10645.060909	6336.270634	2_38060.0
43	1	13018.604444	7266.981078	2_33460.0
44	2	11156.853333	5615.788611	2_34980.0
45	1	9447.340000	4973.365388	2_13820.0
48	1	4608.896731	994.266088	0_33124.0
51	1	3928.630000	1028.710978	0_38300.0
55	3	13571.593000	7452.955265	2_35614.0
57	1	4115.696591	882.287180	0_41700.0
60	2	4120.448095	850.395665	0_47260.0
63	3	14407.149000	9502.978089	2_35004.0
64	1	4150.861786	1521.238527	0_28140.0
66	3	10531.104444	6299.335089	2_16974.0
70	3	12463.995385	8641.369631	2_31084.0
73	3	10033.610526	5835.730521	2_23104.0
74	1	3933.971000	1151.618145	0_41180.0
78	3	10050.917619	6160.295402	2_26420.0
81	1	4384.711389	914.148235	0_39580.0
88	1	4305.197391	970.036545	0_40060.0
89	1	4275.334444	990.572715	0_18140.0
91	1	4353.415750	1172.377285	0_45780.0
94	3	10312.939474	5982.012846	2_47894.0
95	1	3657.548250	1105.616764	0_13820.0
97	3	4054.546607	1204.613751	0_16740.0
101	1	3965.257258	1275.765891	0_23104.0

```
[42]: output_df[(output_df["no_missing_mcare"] != 0)]["no_missing_mcare"].sum()
```

```
[42]: 92
```

0.0.16 looking at distributions of mcare_pay_median at a cluster X site level

```
[43]: cluster_site_df = data
cluster_site_df["cluster_site"] = [str(i) + j + z for i,j,z in
↳zip(list(data["clusters"].values), ["_"]*data.shape[0],data["site"].values)]
```

```
[44]: cluster_site_df
```

```
[44]:
```

				id	msa	year	\	
62502	26420.0	2018	Inpatient	breast reconstruction	26420.0	2018		
62503	28660.0	2018	Outpatient	breast reconstruction	28660.0	2018		
62504	37340.0	2018	Outpatient	breast reconstruction	37340.0	2018		
62505	26620.0	2019	Outpatient	breast reconstruction	26620.0	2019		
62506	15980.0	2020	Outpatient	breast reconstruction	15980.0	2020		
...	
66716	0.0	2018	Outpatient	hysterect	0.0	2018		
66717	nan	2018	Outpatient	rtc_slap_bank	NaN	2018		
66718	0.0	2020	Outpatient	rtc_slap_bank	0.0	2020		
66719	0.0	2019	Outpatient	rtc_slap_bank	0.0	2019		
66720	0.0	2018	Outpatient	rtc_slap_bank	0.0	2018		
			site	group	priv_count	priv_pay_mean	\	
62502	Inpatient	breast reconstruction	51.0	47327.576470				
62503	Outpatient	breast reconstruction	51.0	8048.568431				
62504	Outpatient	breast reconstruction	51.0	34211.443140				
62505	Outpatient	breast reconstruction	51.0	6233.098627				
62506	Outpatient	breast reconstruction	51.0	21964.297060				
...		
66716	Outpatient	hysterect	6335.0	14677.391800				
66717	Outpatient	rtc_slap_bank	6910.0	14537.588820				
66718	Outpatient	rtc_slap_bank	7071.0	14769.380650				
66719	Outpatient	rtc_slap_bank	8154.0	14388.208800				
66720	Outpatient	rtc_slap_bank	9895.0	13873.629140				
			priv_pay_median	priv_pay_iqr	mcare_count	mcare_lo	mcare_pay_mean	\
62502	21408.00	23351.7150	81.0	3.54321	14027.076170			
62503	9495.08	6468.6300	72.0	0.00000	4325.565833			
62504	17213.58	24034.8250	68.0	0.00000	5490.479412			
62505	5643.14	3529.6100	70.0	0.00000	5081.383000			
62506	11824.70	17573.6400	71.0	0.00000	6320.088451			
...	
66716	12040.63	11607.0600	2732.0	0.00000	5067.601204			
66717	12213.92	10731.0675	10765.0	0.00000	5460.250379			
66718	12657.14	12031.9000	17493.0	0.00000	4579.359115			
66719	11857.93	11813.4150	20552.0	0.00000	4243.786995			
66720	11897.50	11273.3400	21120.0	0.00000	4124.830504			

	mcare_pay_median	mcare_pay_sd	CBSA_NAME \
62502	10395.16	12242.654150	Houston-The Woodlands-Sugar Land, TX
62503	3609.09	2791.209179	Killeen-Temple, TX
62504	4130.65	3880.597914	Palm Bay-Melbourne-Titusville, FL
62505	3947.27	2657.779225	Huntsville, AL
62506	4640.27	4468.429407	Cape Coral-Fort Myers, FL
...
66716	5491.66	1787.807187	NaN
66717	4843.63	4561.683011	NaN
66718	4554.80	1716.745885	NaN
66719	4259.62	1626.198810	NaN
66720	4166.52	1441.987219	NaN

	State	lon	lat	clusters	cluster_site
62502	Texas	-95.622552	29.598443	0	0_Inpatient
62503	Texas	-97.698227	31.124151	0	0_Outpatient
62504	Florida	-80.721442	28.263933	0	0_Outpatient
62505	Alabama	-86.586104	34.730369	0	0_Outpatient
62506	Florida	-81.872308	26.640628	0	0_Outpatient
...
66716	NaN	NaN	NaN	0	0_Outpatient
66717	NaN	NaN	NaN	0	0_Outpatient
66718	NaN	NaN	NaN	0	0_Outpatient
66719	NaN	NaN	NaN	0	0_Outpatient
66720	NaN	NaN	NaN	0	0_Outpatient

[4219 rows x 20 columns]

```
[45]: uniq_cluster_site = cluster_site_df["cluster_site"].unique()
grid = mt.ceil(np.sqrt(len(uniq_cluster_site)))
```

```
[46]: fig, axs = plt.subplots(grid, grid, figsize=(30,35))
n_pts = []
missing_pts = []
means = []
sd_list = []
labels = []
for i,x in enumerate(uniq_cluster_site):

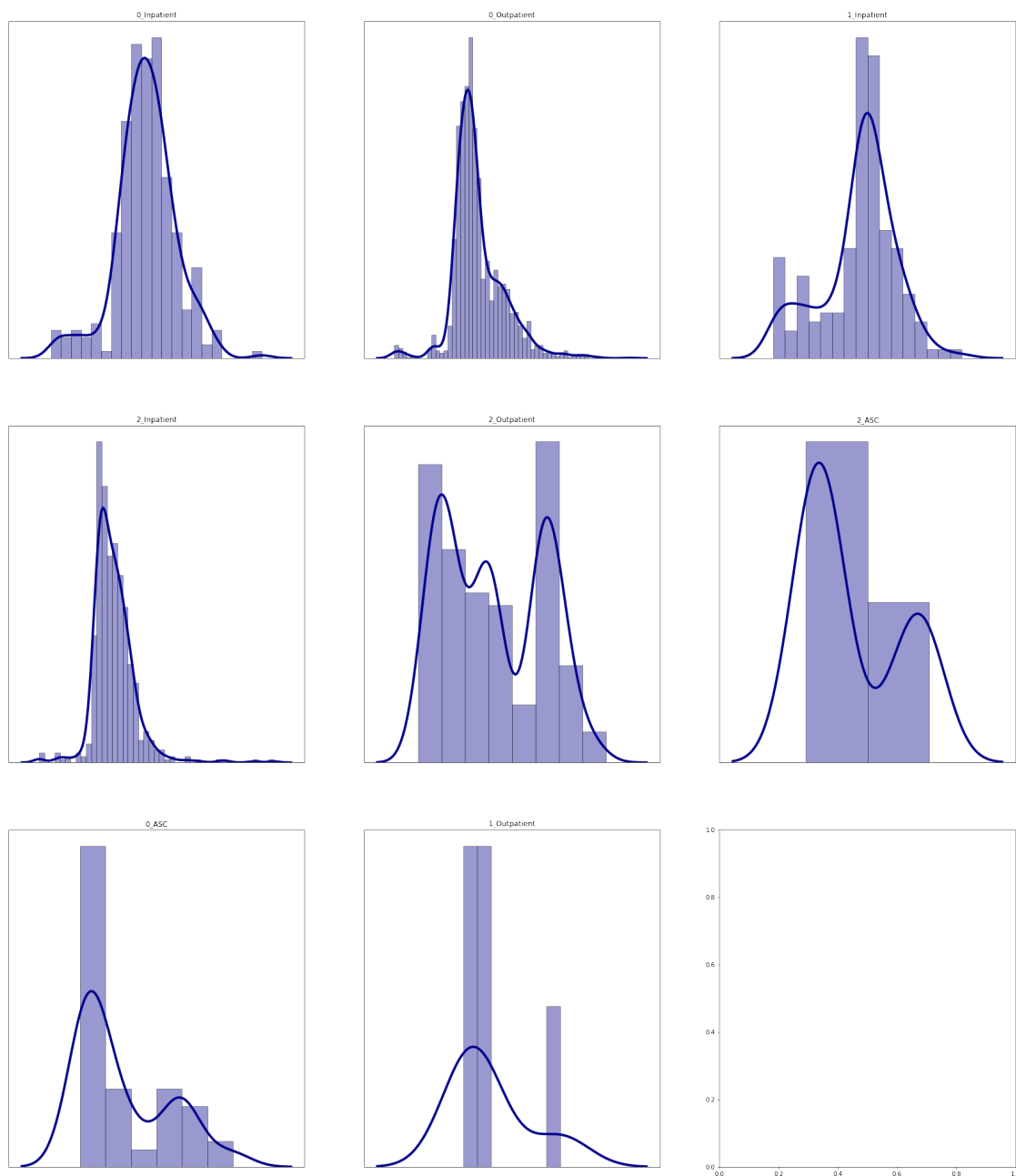
    dt_pts = cluster_site_df[(cluster_site_df["cluster_site"] ==
↪x)]["mcare_pay_median"]
    Q1 = np.percentile(dt_pts[~np.isnan(dt_pts)], 25, interpolation =
↪'midpoint')
    Q3 = np.percentile(dt_pts[~np.isnan(dt_pts)], 75, interpolation =
↪'midpoint')
    IQR = Q3 - Q1
    if len(dt_pts) == 0:
```

```

    opt_bins = 10
else:
    bin_width = 2*IQR/np.cbrt(len(dt_pts))
    rng = max(dt_pts[~np.isnan(dt_pts)]) - min(dt_pts[~np.isnan(dt_pts)])
    opt_bins = int(rng/bin_width)

n_pts.append(len(dt_pts[~np.isnan(dt_pts)]))
missing_pts.append(len(dt_pts[np.isnan(dt_pts)]))
gp_stats = dt_pts.describe()
mu = gp_stats[1]
std = gp_stats[2]
means.append(mu)
sd_list.append(std)
labels.append(x)
sns.distplot(dt_pts, hist=True, kde=True,
              bins=opt_bins, color = 'darkblue',
              hist_kws={'edgecolor':'black'},
              kde_kws={'linewidth': 4},
              ax=axis[int(i/grid),i%grid])
# dt_pts = np.msort(dt_pts)
# intervals = UniDip(dt_pts[~np.isnan(dt_pts)]).run()
# interval_list.append(intervals)
axis[int(i/grid),i%grid].get_yaxis().set_visible(False)
axis[int(i/grid),i%grid].get_xaxis().set_visible(False)
axis[int(i/grid),i%grid].set_title(str(x))
# plt.savefig("density_plots.png")
# axis[int(i/grid),i%grid].set_title(intervals[0][1])

```



```
[47]: output_df = pd.
      ↪ DataFrame(list(zip(labels,n_pts,missing_pts,means,sd_list)),columns=["index","no_pts","no_m
      # output_df["msa_cluster"] = output_df["Cluster_Label"].astype(str) + "_" +
      ↪ output_df["MSA"].astype(str)
      # print("%age of MSAxCluster groups where we cannot reject the NULL hypothesis
      ↪ is (90% CI) :",100*len(output_df[output_df["Normality_p_value"] >= 0.1])/
      ↪ len(output_df))
      # output_df.sort_values(by=["Normality_p_value"],ascending=False)
```

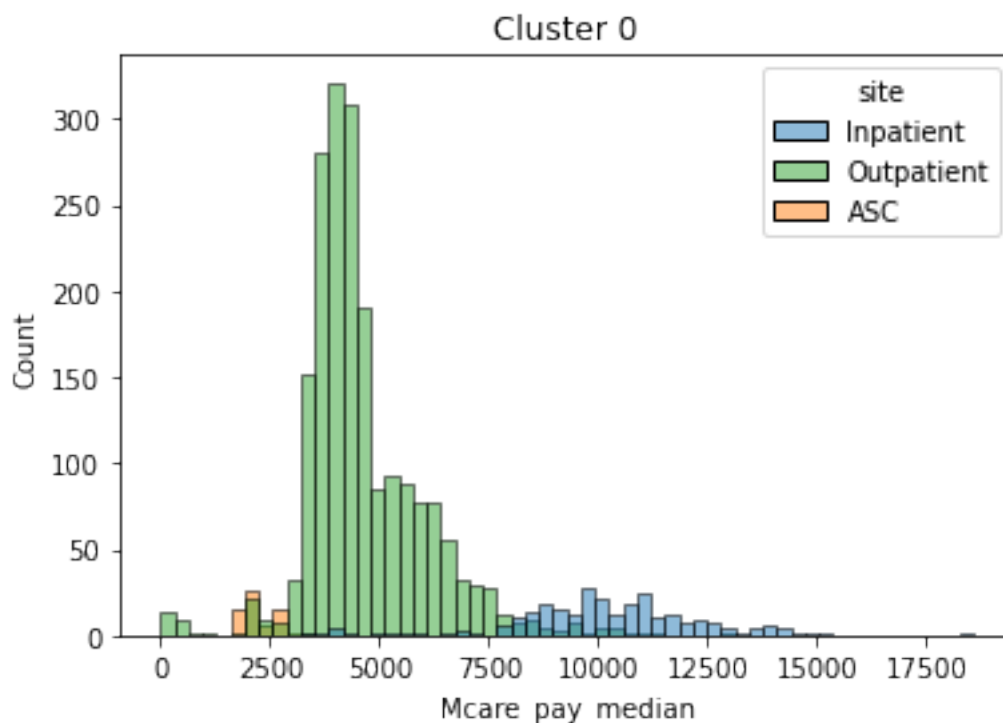
```
output_df
```

```
[47]:
```

	index	no_pts	no_missing_mcare	mean	SD
0	0_Inpatient	277	0	10171.440957	2169.787843
1	0_Outpatient	1975	38	4629.089180	1410.055609
2	1_Inpatient	157	0	26819.030096	8108.833445
3	2_Inpatient	588	1	13401.810723	3762.698828
4	2_Outpatient	650	77	10197.057185	6684.118193
5	2_ASC	30	47	4902.140878	2391.621123
6	0_ASC	67	307	2228.008524	401.101239
7	1_Outpatient	5	0	11461.455000	5021.924998

```
[48]: fig = sns.histplot(data=cluster_site_df[cluster_site_df["clusters"] == 0],  
    ↪x="mcare_pay_median", hue="site", palette = ['tab:blue', 'tab:green', 'tab:  
    ↪orange'])  
fig.set(xlabel = "Mcare_pay_median", ylabel = "Count", title = 'Cluster 0')
```

```
[48]: [Text(0.5, 0, 'Mcare_pay_median'),  
    Text(0, 0.5, 'Count'),  
    Text(0.5, 1.0, 'Cluster 0')]
```

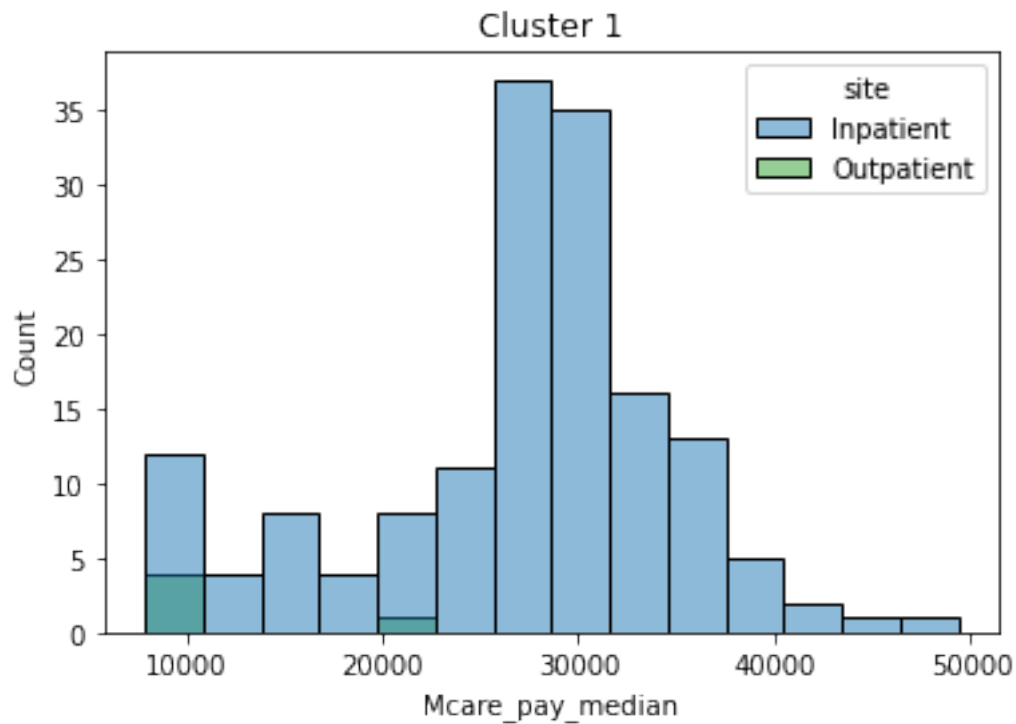


```
[49]: fig = sns.histplot(data=cluster_site_df[cluster_site_df["clusters"] == 1],  
    ↪x="mcare_pay_median", hue="site", palette = ['tab:blue', 'tab:green'])
```



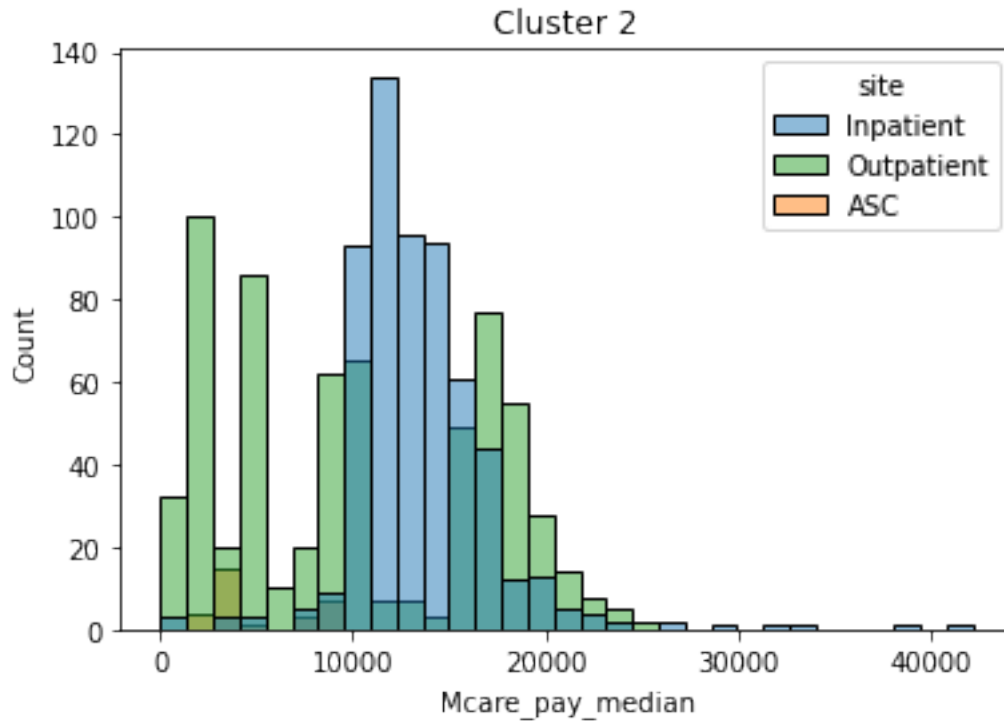
```
fig.set(xlabel = "Mcare_pay_median", ylabel = "Count", title = 'Cluster 1')
```

```
[49]: [Text(0.5, 0, 'Mcare_pay_median'),
      Text(0, 0.5, 'Count'),
      Text(0.5, 1.0, 'Cluster 1')]
```



```
[50]: fig = sns.histplot(data=cluster_site_df[cluster_site_df["clusters"] == 2],
    ↪x="mcare_pay_median", hue="site", palette = ['tab:blue', 'tab:green', 'tab:
    ↪orange'])
fig.set(xlabel = "Mcare_pay_median", ylabel = "Count", title = 'Cluster 2')
```

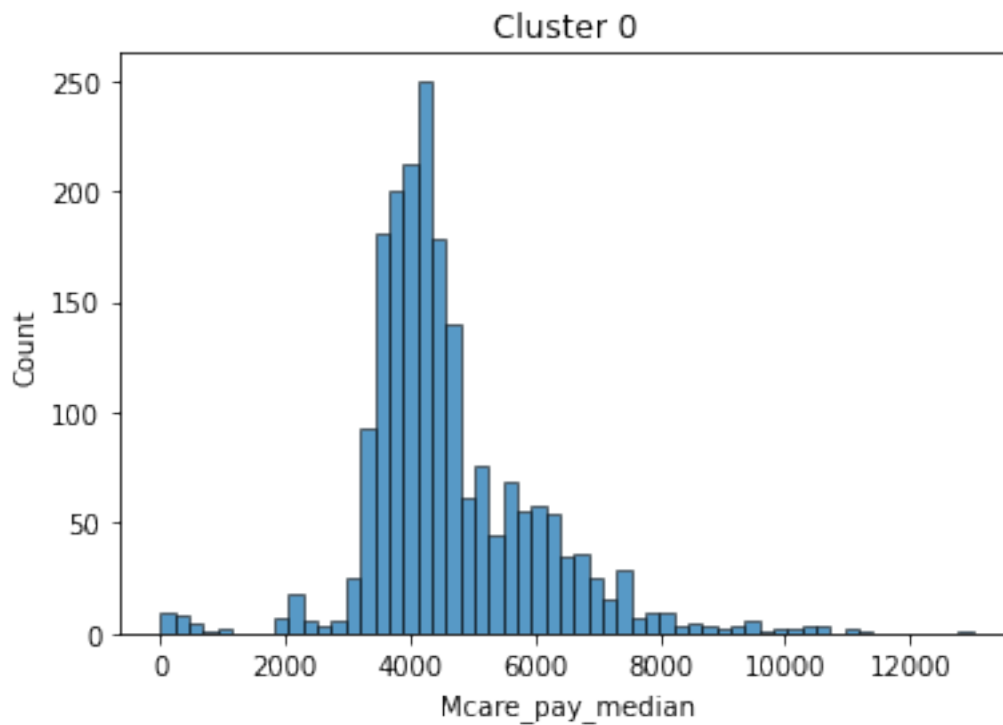
```
[50]: [Text(0.5, 0, 'Mcare_pay_median'),
      Text(0, 0.5, 'Count'),
      Text(0.5, 1.0, 'Cluster 2')]
```



0.0.17 checking for normality in the outpatient category in cluster 0

```
[51]: fig = sns.histplot(data=cluster_site_df[(cluster_site_df["clusters"] == 0) &
→(cluster_site_df["site"] == "Outpatient")], x="mcare_pay_median",palette =
→['tab:blue', 'tab:green', 'tab:orange'])
fig.set(xlabel = "Mcare_pay_median", ylabel = "Count", title = 'Cluster 0')

[51]: [Text(0.5, 0, 'Mcare_pay_median'),
Text(0, 0.5, 'Count'),
Text(0.5, 1.0, 'Cluster 0')]
```



```
[52]: out_0 = cluster_site_df[(cluster_site_df["clusters"] == 0) &
    ↪ (cluster_site_df["site"] == "Outpatient")]["mcare_pay_median"]
gp_stats = out_0.describe()
mu = gp_stats[1]
std = gp_stats[2]
rmv_outliers = out_0[(out_0 > mu - 3*std) & (out_0 < mu + 3*std)].values
sm.qqplot(rmv_outliers,dist=norm(mu,std), line ='45')
```

[52]:

