# Clustering/PCA

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### Data Cleansing/Massaging

```
In [4]: # Basic checks on data
        base_data_df.country.value_counts()
        base_data_df.info()
       base_data_df.isnull().sum()
        <class 'pandas.core.frame.DataFrame'>
        RangeIndex: 167 entries, 0 to 166
       Data columns (total 10 columns):
       country 167 non-null object
       child_mort 167 non-null float64
                     167 non-null float64
        exports
                     167 non-null float64
        health
                     167 non-null float64
        income
                     167 non-null int64
        inflation
                    167 non-null float64
        life expec 167 non-null float64
                   167 non-null float64
                     167 non-null int64
        dtypes: float64(7), int64(2), object(1)
       memory usage: 13.1+ KB
Out[4]: country
        child mort
        exports
        health
        imports
        income
       inflation
       life_expec
        total_fer
       dtype: int64
```

Observations- All columns Non Null. No Need of Dropping any columns/rows

All Columns are Non-Null. Hence no dropping of columns or any Data Infusion Required.

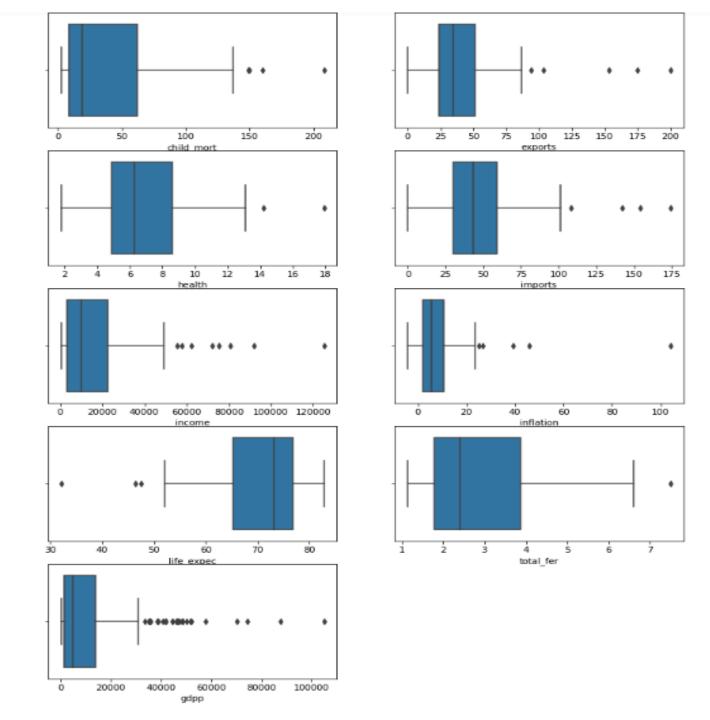
#### **Outlier Treatment**

The number of Outliers are considerably huge in the dataset. In the dataset, each country has single records against itself & dropping any outlier might result in loss of information i.e. records against a country might be eliminated.

- 1) This might cause discrepancies in final analysis, where all the countries are not considered.
- 2) Although PCA is prone to Outliers, the effect of dropping Outliers on Variance, before & after PCA is marginal.
- 3) Since the outliers are huge, they might create a new cluster for further analysis.

Considering the above 3 points,

Outliers have not been eliminated.



#### PCA- Variance & Scree Plot

```
In [12]: from sklearn.decomposition import PCA
         pca = PCA(svd solver = 'randomized', random state = 42)
                                                                                                                              1.0
         pca.fit(base data df new2)
Out[12]: PCA(copy=True, iterated power='auto', n components=None, random state=42,
             svd_solver='randomized', tol=0.0, whiten=False)
                                                                                                                               0.9
In [13]: #IDentifying Value of Vectors Post PCA
         pca.components
Out[13]: array([[-0.41951945, 0.28389698, 0.15083782, 0.16148244,
                                                                    0.39844111,
                 -0.19317293, 0.42583938, -0.40372896, 0.39264482],
                                                                                                                           Variance
8.0
                [ 0.19288394, 0.61316349, -0.24308678, 0.67182064, 0.02253553,
                 -0.00840447, -0.22270674, 0.15523311, -0.0460224 ]
                [-0.02954353, 0.14476069, -0.59663237, -0.29992674, 0.3015475 ,
                  0.64251951, 0.11391854, 0.01954925, 0.12297749],
                [ 0.37065326, 0.00309102, 0.4618975 , -0.07190746, 0.39215904,
                  0.15044176, -0.20379723, 0.37830365, 0.53199457],
                                                                                                                              0.7
                [-0.16896968, 0.05761584, 0.51800037, 0.25537642, -0.2471496,
                  0.7148691 , 0.1082198 , -0.13526221, -0.18016662],
                [ 0.20062815, -0.05933283,  0.00727646, -0.03003154,  0.16034699,
                  0.06628537, -0.60112652, -0.75068875, 0.01677876],
                [-0.07948854, -0.70730269, -0.24983051, 0.59218953, 0.09556237,
                  0.10463252, 0.01848639, 0.02882643, 0.24299776],
                                                                                                                               0.6
                [-0.68274306, -0.01419742, 0.07249683, -0.02894642, 0.35262369,
                 -0.01153775, -0.50466425, 0.29335267, -0.24969636],
                [ 0.3275418 , -0.12308207, 0.11308797, 0.09903717, 0.61298247,
                 -0.02523614, 0.29403981, -0.02633585, -0.62564572]])
                                                                                                                               0.5
In [14]: # Identifying the Variance Ratio of Components Post PCA
         pca.explained variance ratio
Out[14]: array([0.4595174, 0.17181626, 0.13004259, 0.11053162, 0.07340211,
                0.02484235, 0.0126043 , 0.00981282, 0.00743056])
                                                                                                                                                                                 Number of Coponents
```

From the Above Variance Ratio values & Scree Plot, The first 4 Components describe the Maximum Variance (about 87%). Hence Considering the 4 Components for PCA.

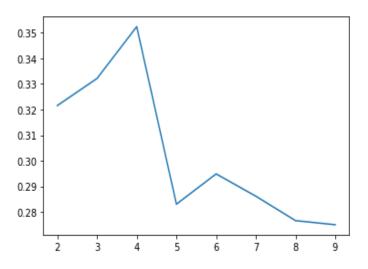
#### K-Means Clustering- Number of Clusters

```
In [67]: #Calculating Hopkins Value
hopkins(pca_df2.drop('ID', axis=1))
#Hopkins Value is Fluctuating between range of 79 & 87. Hence Clustering can be performed on the mentioned dataset.
Out[67]: 0.8392613641113088
```

Hopkins value is Fluctuating between 79% & 87 % .Hence Clustering can be applied on the above dataset.

```
In [23]: #Calculating Silhouette Score
    from sklearn.metrics import silhouette_score
    ss = []
    for k in range(2,10):
        kmeans = KMeans(n_clusters = k).fit(cluster_df)
        ss.append([k, silhouette_score(cluster_df, kmeans.labels_)])
    plt.plot(pd.DataFrame(ss)[0], pd.DataFrame(ss)[1])
```

Out[23]: [<matplotlib.lines.Line2D at 0x1bbdfc2b898>]



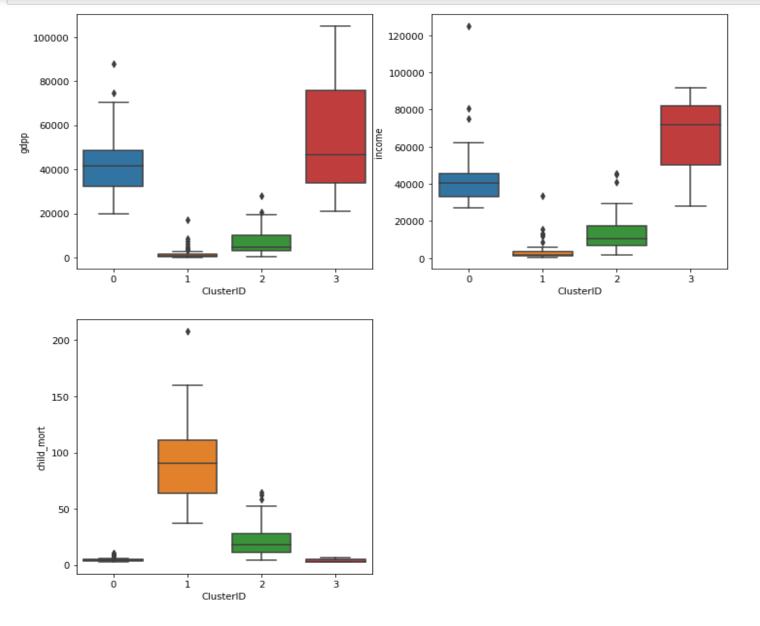
Silhouette Score Drastically Drops Post n=4, hence clustering with n=4

The Silhouette Score increase from n=2 till n=4 & then drastically drops Post n=4.Hence Considering number of clusters=4.

# Scatter Plot of Principal Components- K Means Clustering

```
In [27]: # Scatter Plots - PC1 & PC2
          sns.scatterplot(x = 'PC1', y = 'PC2', hue = 'ClusterID', data = dat_km, palette='Set1')
Out[27]: <matplotlib.axes._subplots.AxesSubplot at 0x1bbe57239e8>
                     ClusterID
          \overline{C}
             -2
                                     PC1
In [28]: # Scatter Plots - PC3 & PC4
          sns.scatterplot(x = 'PC3', y = 'PC4', hue = 'ClusterID', data = dat_km, palette='Set2')
Out[28]: <matplotlib.axes._subplots.AxesSubplot at 0x1bbe57cc400>
          8
                                  -2
                                                      2
                                             0
                                     PC3
```

#### K Means Clustering- Outliers Post PCA



From the Box plots, it is seen that for Cluster 1 Countries Income & GDP is low but Child Mortality is high. Hence these countries require Maximum AID.

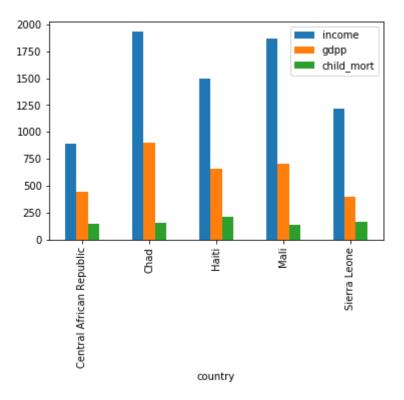
It was observed that the Outlier Behaviour Pre & Post PCA are almost identical. Since the Number of Outliers are large, we are considering not to Drop Any Outlier, as they contain Valuable information.

# K-Means Clustering- Cluster Analysis

```
In [34]: # Cluster Analysis for gdpp,income
          km_clustered_df[['gdpp', 'income', 'ClusterID']].groupby('ClusterID').mean().plot(kind = 'bar')
Out[34]: <matplotlib.axes._subplots.AxesSubplot at 0x1bbe6b6f358>
           60000
                  income
           50000
           40000
           30000
           20000
           10000
                                   ClusterID
In [35]: # Cluster Analysis for child_mort
          km_clustered_df[['child_mort','ClusterID']].groupby('ClusterID').mean().plot(kind = 'bar')
Out[35]: <matplotlib.axes._subplots.AxesSubplot at 0x1bbe6d76358>
                                               ____ child_mort
           80
           60
           40
           20
```

From the Above Charts, for GDP,Income & Child Mortality, it is seen that Countries in Cluster 1 have Low GDP & Income Rate & High rate of Child Mortality. Hence These are the countries that need to be taken in to consideration for HELP.

# K Means Clustering- Identifying Countries

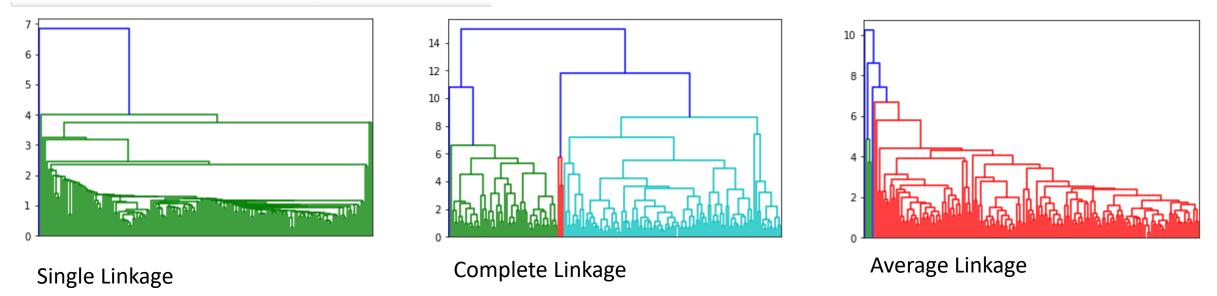


	country	
ClusterID		
0	31	
1	47	
2	86	
3	3	
country	child_mort	
Haiti	208.0	
Sierra Leone	160.0	
Chad	150.0	
Central African Republic	149.0	
Mali	137.0	

From the Above Analysis, using PCA & Kmeans Clustering, there are 47 countries in Cluster 1 that required AID. By Sorting the countries based on Child Mortality, High to Low, above are the Top 5 Countries that require AID at the earliest

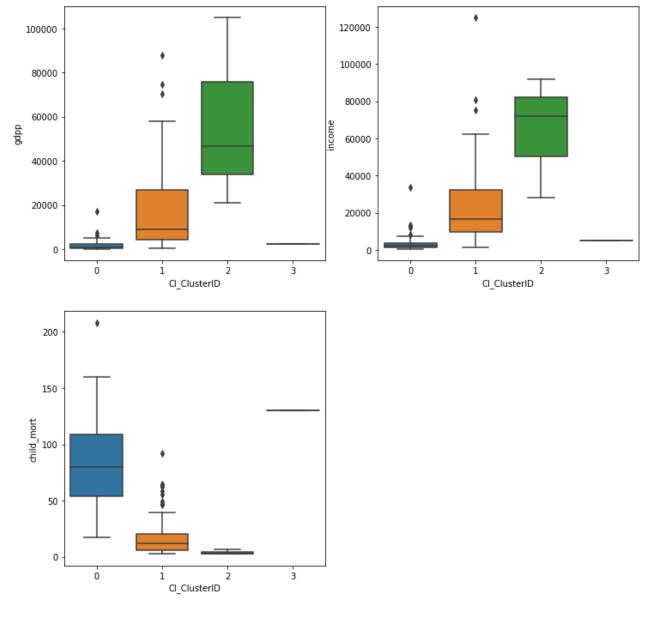
Since Countries in Cluster 1 require Aid on priority, Identifying the countries in Cluster 1.

## Hierarchical Clustering



From the Above Types of Hierarchical Clustering, Considering the Complete Linkage type, we can draw a line @ height=8 and derive 4 clusters. Hence n=4, for hierarchical Clustering.

#### Hierarchical Clustering- Box Plot Analysis



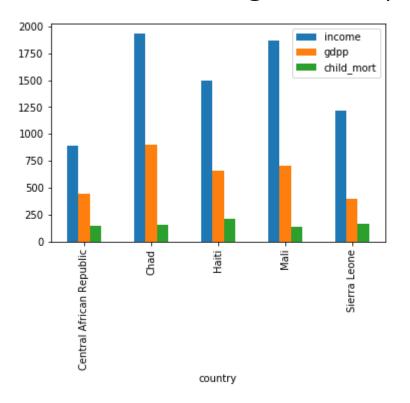
From the Box plots, it is seen that for Cluster 0 Countries Income & GDP is low but Child Mortality is high. Hence these countries require Maximum AID.

#### Hierarchical Clustering – Cluster Analysis

```
In [44]: # Cluster Analysis for gdpp, income for Hierarchical Clustering
          km clustered df[['gdpp', 'income', 'Cl ClusterID']].groupby('Cl ClusterID').mean().plot(kind = 'bar')
Out[44]: <matplotlib.axes. subplots.AxesSubplot at 0x1bbe4a6a278>
                                                        gdpp
           60000
                                                        income
           50000
           40000
           30000
           20000
           10000
                                   CI ClusterID
          # Cluster Analysis for gdpp, income for Hierarchical Clustering
          km clustered df[['child mort', 'Cl ClusterID']].groupby('Cl ClusterID').mean().plot(kind = 'bar')
Out[45]: <matplotlib.axes._subplots.AxesSubplot at 0x1bbe5a918d0>
                   child mort
           120
           100
            80
            60
            40
            20
                                 CI ClusterID
```

From the Above Charts, for GDP,Income & Child Mortality, it is seen that Countries in Cluster 0 & Cluster 3 have Low GDP & Income Rate & High rate of Child Mortality. Hence These are the countries that need to be taken in to consideration for HELP.

## Hierarchical Clustering- Identifying Countries



	country	child_mort
	Haiti	208.0
Sier	ra Leone	160.0
	Chad	150.0
Central African	Republic	149.0
	Mali	137.0
ClusterID	countr	у
54		
109		
		3
		1

From the Above Analysis, using PCA & Hierarchical Clustering, there are 54 countries in Cluster 0 that required AID. By Sorting the countries based on Child Mortality, High to Low, above are the Top 5 Countries that require AID at the earliest

#### Final List of Countries

• Considering Both K-Means Clustering & Hierarchical Clustering, following are the

Top 5 Countries that Require urgent Aid.

- Haiti
- Sierra Leone
- Chad
- Central African Republic
- Mali

