In [1]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
import pandas as pd
from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
from sklearn.cluster import AgglomerativeClustering
from sklearn import metrics
from scipy import stats
```

Question 1

Part 1.1: Work

Read Data

In [2]:
```
PATH_TO_Q1_DATA = 'data/HW1_Q1_Data.csv'
df = pd.read_csv(PATH_TO_Q1_DATA)
```

In [3]:
```
df.head(1)
```

Out[3]:

	S IgG1	RBD IgG1	N IgG1	S IgG2	RBD IgG2	N IgG2	S IgG3	RBD IgG3	N IgG3	S IgG4	...
0	15518.25	11686.5	17408.0	2595.0	2977.5	4418.75	7988.75	10112.75	13740.75	2890.5	...

1 rows × 61 columns

Standardize Data in Columns 1-52

In [4]:
```
'''
 TODO: Standardize columns 1-52 by subtracting off mean of each column a
nd scaling to unit variance
'''
cols = df.columns.values.tolist()[0:52] # get list of columns names for
 columns 1-52

for col in cols:
    if '_zscore' not in col: # to allow re-execution of same cell multip
le times
        col_zscore = col + '_zscore' # add column for zscore
    df[col_zscore] = (df[col] - df[col].mean())/ df[col].std() # z =(x-
μ)/σ  #??std(ddof=??) degrees of freedom
```

Cluster Standardized Data in Columns 1-52

In [5]:
```
# need to choose distance measure, if already choose Euclidean??
# other quality checks if don't know true labels??
kmeans_possible_cluster_nums = [2,3,4,5,6,7,8,9,10] # 1 < k < 11
df_standardized_only = df.iloc[:,61:] # get dataframe with standardized
 columns only

kmeans_cluster_quality_scores = []
for k in kmeans_possible_cluster_nums:
    '''
    TODO: 1. Fit data to k clusters using imported clustering algorithm
          2. Compute quality of results for k clusters using imported
             cluster quality metric and store in a list
    '''
    kmeans = KMeans(n_clusters=k).fit(df_standardized_only)
    labels = kmeans.labels_
    score = metrics.silhouette_score(df_standardized_only, labels) # qua
lity
    kmeans_cluster_quality_scores.append(score)
```

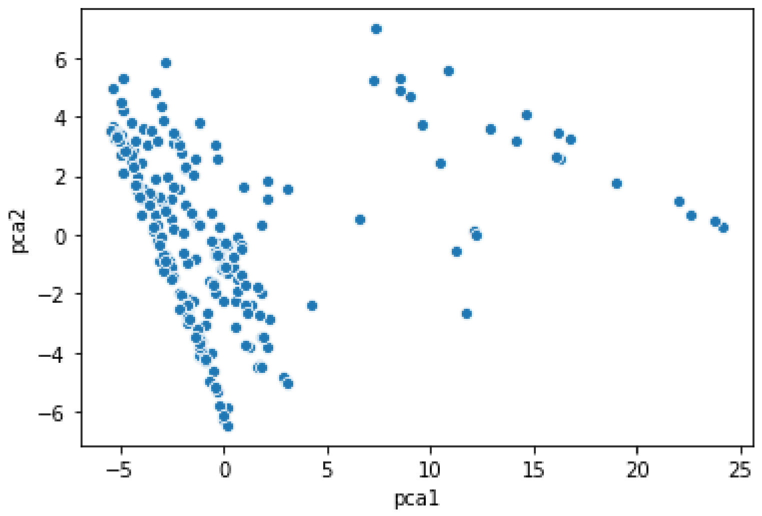
In [6]:
```
kmeans_cluster_quality_scores
```

Out[6]:
```
[0.596020600071851,
 0.2896940008974808,
 0.2947191887383796,
 0.29038266395559587,
 0.2975457234378132,
 0.3211858881637293,
 0.326320973299025 4,
 0.24584952797813056,
 0.2679986168632538]
```

Dimensionality Reduction and Visualization of Data

In [7]:
```
## how to connect true labels to this?? we don't know true labels...
## how to visualize k-means clusters??

pca = PCA(n_components=2).fit_transform(df_standardized_only)
df_pca_plot = pd.DataFrame(pca, columns=['pca1','pca2'])
sns.scatterplot(x='pca1', y='pca2', data=df_pca_plot, legend='full')
```

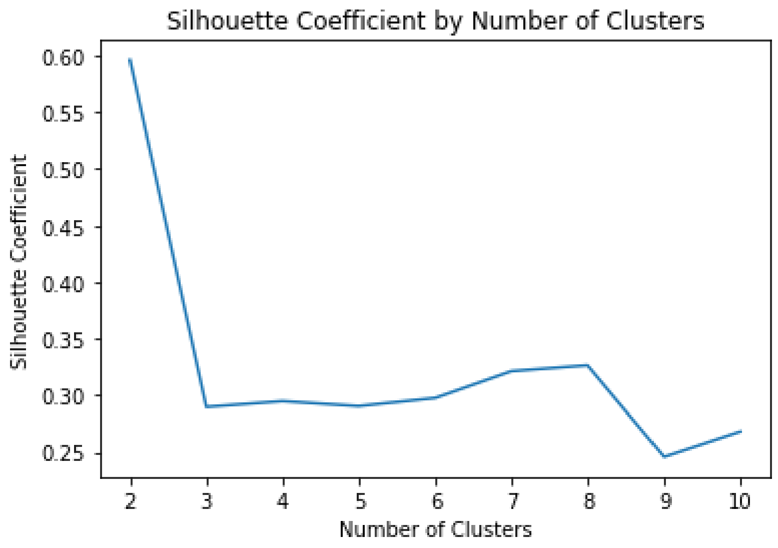
Out[7]:
```
<AxesSubplot:xlabel='pca1', ylabel='pca2'>
```



Visualize Cluster Quality Metrics

In [8]:
```
# Creates line chart to visualize values of cluster quality metric for e
ach possible number of clusters
def plotMetricByK(metric_name, metric_results, num_possible_clusters, PA
TH_TO_SAVE=None):
  '''
  metric_name: Name of cluster quality metric for title and axis label
  metric_results: List containing value of metric, in order, for each
                  possible number of clusters
  PATH_TO_SAVE: Path of file to save plot. If path is not provided, imag
e is not saved
  '''

  plt.clf()

  plt.title(f'{metric_name} by Number of Clusters')
  plt.xlabel('Number of Clusters')
  plt.ylabel(metric_name)
  plt.plot(num_possible_clusters, metric_results)

  if PATH_TO_SAVE:
    plt.savefig(PATH_TO_SAVE)
```

In [9]:
```
'''
 TODO: Plot your choice of cluster quality metric by cluster number to h
elp determine k.

 TIP: If using the above function, place each function call in a separat
e
      cell to visualize multiple cluster quality metrics
'''
plotMetricByK("Silhouette Coefficient", kmeans_cluster_quality_scores, k
means_possible_cluster_nums)
```



Part 1.1: Answer

How many clusters are there in the data? **There appear to be two clusters.**

Explanation: **Good clustering is indicated when the Silhouette Coefficient is close to 1. The Silhouette Coefficient is closest to 1 for two clusters and is much lower for other clustering sizes.**

Part 1.2: Work

Cluster Data

In [10]:
```
'''
  TODO: Cluster data with the number of clusters you determined in part
 1.1 and store resulting labels
'''
kmeans = KMeans(n_clusters=2).fit(df_standardized_only)
kmeans_labels = kmeans.labels_

# add labels as column in original df?? or better to create new df with
 this?
df = pd.DataFrame(df)
df['cluster']=kmeans_labels
```

In [11]:
```
kmeans_labels
```

Out[11]:
```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1,
0,
       1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0,
1,
       1, 1, 1, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0], dtype=int32)
```

In [12]:
```
df.head(1)
```

Out[12]:

	S IgG1	RBD IgG1	N IgG1	S IgG2	RBD IgG2	N IgG2	S IgG3	RBD IgG3	N IgG3	S IgG4	...
0	15518.25	11686.5	17408.0	2595.0	2977.5	4418.75	7988.75	10112.75	13740.75	2890.5	...

1 rows × 114 columns

Univariate Analysis

In [13]:
```
'''
  TODO: Find 4 variables that have statistically significant differences
between values in the clusters (i.e p < 0.05 using pairwise t-tests)
'''
# do I need to split the data into separate dataframes per cluster to do
t-test??
# degrees of freedom??

# split data by cluster
df_cluster0=df[df['cluster']==0]
df_cluster1=df[df['cluster']==1]

# create a dataframe to store test results
cols = df_standardized_only.columns.values.tolist()  # get names of stan
darized columns
df_ttest = pd.DataFrame(columns=['Metric','Statistic','P_value']).astype
(dtype= {'Metric':'object', 'Statistic':'float64','P_value':'float64'})

# Welch's t-test
for col in cols:
    (stat, pvalue) = stats.ttest_ind(df_cluster0[col], df_cluster1[col],
equal_var=False)
    new_row = pd.Series([col,stat,pvalue], index = df_ttest.columns)
    df_ttest = df_ttest.append(new_row, ignore_index=True)
```

In [14]:
```
print(df_cluster0.shape)
print(df_cluster1.shape)
df_ttest.head()
```

```
(207, 114)
(25, 114)
```

Out[14]:

	Metric	Statistic	P_value
0	S IgG1_zscore	-10.536886	1.647515e-10
1	RBD IgG1_zscore	-9.685497	8.688933e-10
2	N IgG1_zscore	-17.543949	2.258925e-15
3	S IgG2_zscore	-16.184907	1.795776e-14
4	RBD IgG2_zscore	-14.480079	2.141806e-13

In [15]:
```
# find metrics with four lowest P-values
df_ttest.nsmallest(4,['P_value'])['Metric'].to_list()
```

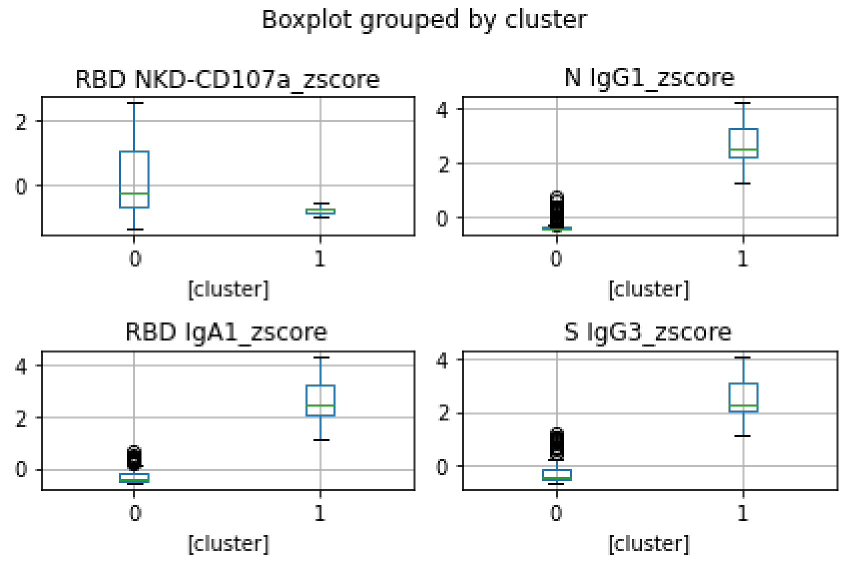
Out[15]:
```
['RBD NKD-CD107a_zscore', 'N IgG1_zscore', 'RBD IgA1_zscore', 'S IgG3_z
score']
```

Part 1.2: Answer

RBD NKD-CD107a, N IgG1, RBD IgA1, S IgG3

Replace the above line with 4 variables that you found from the univariate analysis and output the corresponding box plots in the cells below or as images in this cell

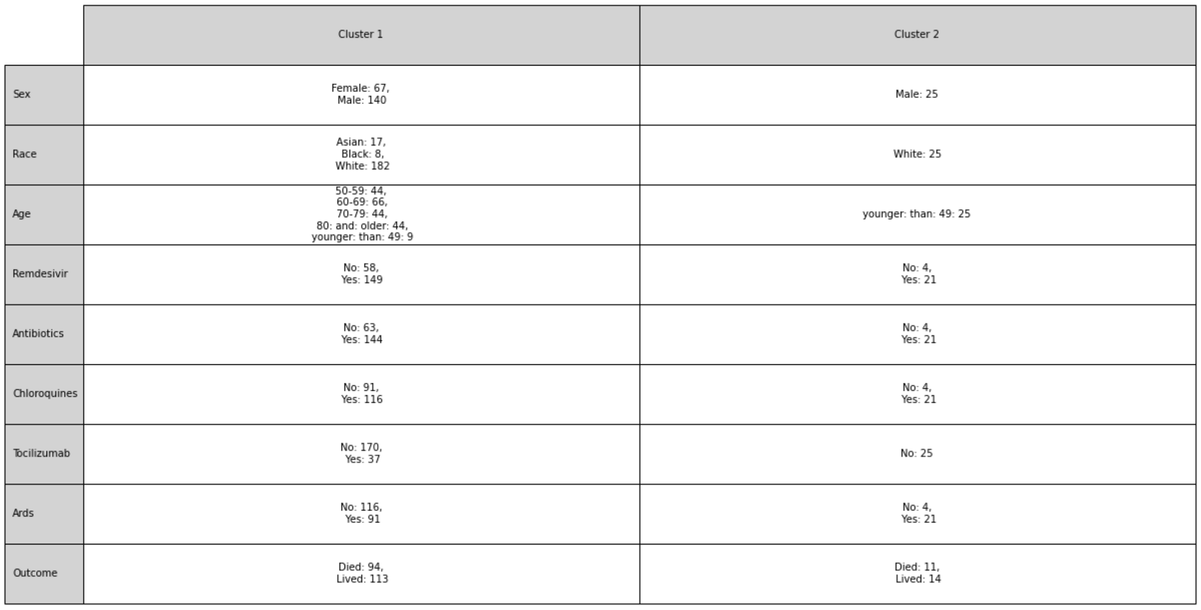
In [16]:
```
'''
  TODO: Create and display boxplots for each of the 4 variables like tho
se in Fig 1. from the paper by Wu et al

  TIP: 1. If you add the cluster labels as an additional column to the d
ataframe, then you can follow the example at https://www.pythonprogrammi
ng.in/boxplot-group-by-column-data.html
       2. If you want to use subplots to put all 4 boxplots in the same
 figure, you can plot the dataframes on a specific subplot using the ax
 keyword. For example,

          fig, axs = plt.subplots(2, 2)

          df.boxplot(column=['Variable'], by=['Cluster'], ax=axs[0,0])
          df.boxplot(column=['Variable'], by=['Cluster'], ax=axs[0,1])
'''

# how to fix labels?
# is this how it should look??
# use standardized data or original??
fig, axs = plt.subplots(2,2)

df.boxplot(column=['RBD NKD-CD107a_zscore'], by=['cluster'], ax=axs[0,0
])
df.boxplot(column=['N IgG1_zscore'], by=['cluster'], ax=axs[0,1])
df.boxplot(column=['RBD IgA1_zscore'], by=['cluster'], ax=axs[1,0])
df.boxplot(column=['S IgG3_zscore'], by=['cluster'], ax=axs[1,1])


plt.tight_layout()
```



Part 1.3: Work

In [17]:
```
# Formats Pandas series to string of form 'index_1: value_1, ..., index_
n:, value_n' w/ indexes alphabetically sorted
def formatValueCounts(value_counts):
  '''
    value_counts: Pandas series
  '''
  count_string = value_counts.to_string()
  formatted_counts = [': '.join(count.split()) for count in count_string
.split('\n')]
  formatted_counts.sort()
  return ',\n '.join(formatted_counts)

# Creates table summarizing data by cluster and categorical feature
def plotSummaryTable(cellText, PATH_TO_SAVE=None):
  '''
  cellText: num_clusters x 9 2D List where cellText[i][j] contains a str
ing summarizing
            the statistics for cluster i and column (53 + j) in the data
  PATH_TO_SAVE: Path of file to save plot. If path is not provided, imag
e is not saved
  '''

  k = len(cellText)
  colLabels = [f'Cluster {i + 1}' for i in range(k)]

  rowLabels = list(df.columns)[52:61]

  cellText = np.array(cellText).T

  plt.figure(figsize=(10,10))
  table = plt.table(cellText,
            colLabels=colLabels,
            colColours=['#D3D3D3'] * len(colLabels),
            rowLabels=rowLabels,
            rowColours=['#D3D3D3'] * len(rowLabels),
            cellLoc='center',
            loc='upper center')
  table.scale(2,5)
  table.auto_set_font_size(True) # was false
#   table.set_fontsize(8)

  plt.axis('off')
  plt.grid(False)

  if PATH_TO_SAVE:
    plt.savefig(PATH_TO_SAVE)
```

In [18]:
```
'''
  TODO: Create a table where the rows correspond to the variables in col
umns 53-61, and the columns correspond to the k clusters you identified.
        For each cell in the table, put summary statistics for that (var
iable, cluster) pair

  TIP: 1. If you create a 2D list, cellText, where cellText[i][j] contai
ns a string summarizing the statistics for cluster i and column (53 + j)
in
          the data, you can pass this into plotSummaryTable (provided ab
ove) to automatically create the table with matplotlib
       2. If you use value_counts() from Pandas, you can pass the result
ing series to formatValueCounts (provided above) to convert it to a form
atted string
'''
#'Sex','Race', 'Age', 'Remdesivir', 'Antibiotics', 'Chloroquines','Tocil
izumab', 'Ards', 'Outcome'

# create 2d list to contain results
rows=2 # 2 clusters
columns=9 # 9 categorical columns
cellText=[[''] * columns for i in range(rows)]


# get summary stats for each categorical column
categorical_cols = df.columns.values.tolist()[52:61]
for i, col in enumerate(categorical_cols):
    for cluster in range(0,2):
        df_one_cluster = df[df['cluster']==cluster] # select data for on
ly one cluster
        formatted = formatValueCounts(df_one_cluster[col].value_counts
())
        cellText[cluster][i]=formatted

output_table = plotSummaryTable(cellText)
output_table
```



	Cluster 1	Cluster 2
Sex	Female: 67, Male: 140	Male: 25
Race	Asian: 17, Black: 8, White: 182	White: 25
Age	50-59: 44, 60-69: 66, 70-79: 44, 80: and: older: 44, younger: than: 49: 9	younger: than: 49: 25
Remdesivir	No: 58, Yes: 149	No: 4, Yes: 21
Antibiotics	No: 63, Yes: 144	No: 4, Yes: 21
Chloroquines	No: 91, Yes: 116	No: 4, Yes: 21
Tocilizumab	No: 170, Yes: 37	No: 25
Ards	No: 116, Yes: 91	No: 4, Yes: 21
Outcome	Died: 94, Lived: 113	Died: 11, Lived: 14

Part 1.3: Answer

Plot the table in one of the above cells or include it as an image in this cell

Are any of the clusters significantly enriched for some particular value? **Yes. One cluster consists entirely of white males younger than 49 who didn't take Tocilizumab. The second cluster is largely white individuals older than 49, but this simply the remainder of the patients so these details are unlikely to be relevant on their own. Roughly half of the patients died in each cluster, so it's not clear if the clusters are clinically relevant.**

Do I need to show statistically significant??

Part 1.4: Work

Clustering

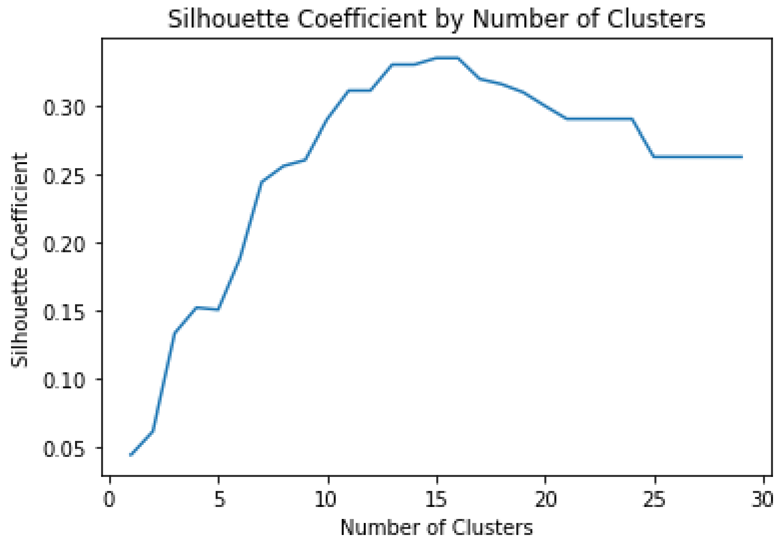
In [19]:
```
'''
TODO: Cluster the numeric variables (Columns 1-52) to find clusters amon
g variables
'''
hier_possible_distance_thresholds = list(range(1,30))

## need to transpose the data first!
df_numeric_variables = df_standardized_only.T
df_numeric_variables

# hierarchical clustering for different distance thresholds
h_quality_scores = []

for d in hier_possible_distance_thresholds:
    hier = AgglomerativeClustering(n_clusters=None, distance_threshold=d
).fit(df_numeric_variables)
    h_labels = hier.labels_
    h_labels
    score = metrics.silhouette_score(df_numeric_variables, h_labels)
    h_quality_scores.append((d,score))
```

In [20]:
```
h_quality_scores
```

Out[20]:
```
[(1, 0.04381498465207157),
 (2, 0.061028385197819564),
 (3, 0.13279712186854872),
 (4, 0.1516855966343379),
 (5, 0.1501262818463638),
 (6, 0.18787001513529739),
 (7, 0.24404908059887112),
 (8, 0.2557911405197007),
 (9, 0.2601938392283203),
 (10, 0.28971297152176684),
 (11, 0.3109277177498267),
 (12, 0.3109277177498267),
 (13, 0.33004434833827606),
 (14, 0.33004434833827606),
 (15, 0.3348582675061609),
 (16, 0.3348582675061609),
 (17, 0.31947491922547433),
 (18, 0.31566997920796314),
 (19, 0.3096641777391753),
 (20, 0.29965051732110354),
 (21, 0.2901239063816258),
 (22, 0.2901239063816258),
 (23, 0.2901239063816258),
 (24, 0.2901239063816258),
 (25, 0.26250368170546834),
 (26, 0.26250368170546834),
 (27, 0.26250368170546834),
 (28, 0.26250368170546834),
 (29, 0.26250368170546834)]
```

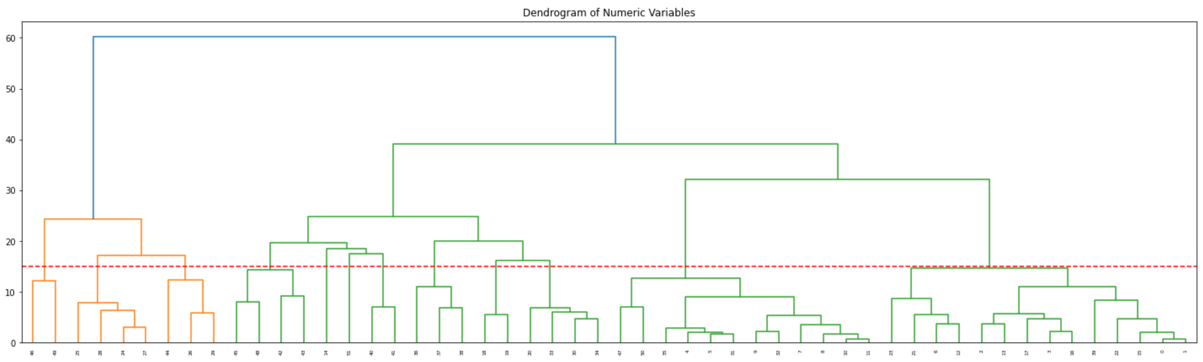
Visualization 1

In [21]:
```
distances,scores = zip(*h_quality_scores)
list(scores)
plotMetricByK("Silhouette Coefficient", scores, hier_possible_distance_t
hresholds)
```



Visualization 2

In [22]:
```
import scipy.cluster.hierarchy as shc

plt.figure(figsize=(25,7))
plt.title("Dendrogram of Numeric Variables")
dend = shc.dendrogram(shc.linkage(df_numeric_variables, method='ward'))
# ward??
plt.axhline(y=15, color='r', linestyle='--')
plt.show()
```



Part 1.4: Answer

How many clusters are there in the numeric variables? **There appear to be 15 clusters of variables.**

Explanation: **When hierarchical clustering is performed, the quality measure (silhouette coefficient) is highest when the distance measure is 15 or 16.**

Part 1.5: Work

In [23]:
```
# determine clusters for variables 1-52
# why don't I have 15 clusters??
hier = AgglomerativeClustering(n_clusters=None, distance_threshold=15).f
it(df_numeric_variables) #?? distance threshold
h_labels = hier.labels_
h_labels

# add clusters to data
df_numeric_variables['variable_cluster']=h_labels
df_numeric_variables.sort_values(by=['variable_cluster'])['variable_clus
ter']
```

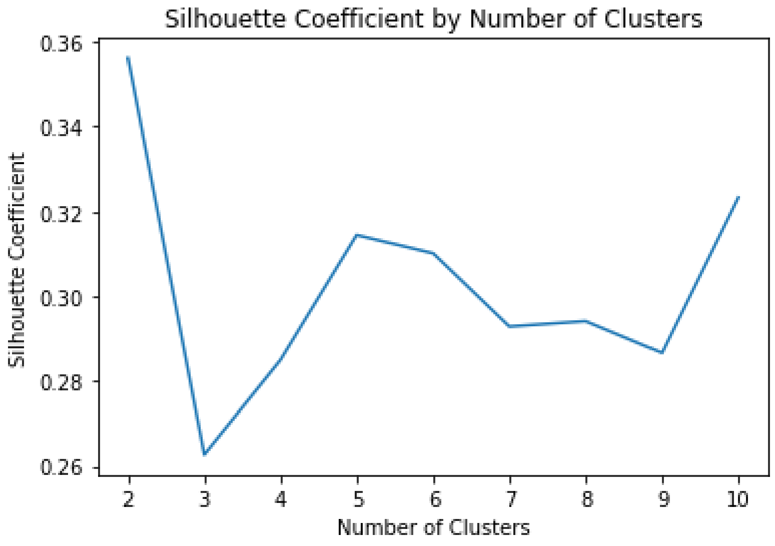
Out[23]:
```
S IgG1_zscore           0
S ADNP_zscore           0
N FcRg2A_zscore         0
RBD FcRg2A_zscore       0
S FcRg2A_zscore         0
N IgA2_zscore           0
RBD IgA2_zscore         0
RBD IgA1_zscore         0
S IgA1_zscore           0
S IgA2_zscore           0
RBD IgG1_zscore         0
S IgG3_zscore           0
N IgG1_zscore           0
S IgG2_zscore           0
S ADCD_zscore           1
RBD ADCD_zscore         1
S NKD-MIP1b_zscore      1
S NKD-CD107a_zscore     1
RBD NKD-CD107a_zscore   2
RBD NKD-MIP1b_zscore    2
N RCA_zscore            3
N NKD-MIP1b_zscore      3
RBD IgG4_zscore         3
S IgG4_zscore           3
N NKD-CD107a_zscore     3
N IgG2_zscore           3
N SNA_zscore            3
RBD IgG3_zscore         3
N IgG3_zscore           3
N IgG4_zscore           3
RBD IgG2_zscore         3
RBD SNA_zscore          3
RBD FcRg2b_zscore       4
S FcRg3A_zscore         4
S FcRg2b_zscore         4
RBD FcRg3A_zscore       4
N IgM_zscore            5
S SNA_zscore            5
S RCA_zscore            5
RBD RCA_zscore          5
RBD ADCP_zscore         6
S ADCP_zscore           6
N ADCP_zscore           6
N FcRg2b_zscore         7
N ADCD_zscore           7
N FcRg3A_zscore         7
N IgA1_zscore           8
NT50_zscore             9
RBD ADNP_zscore        10
N ADNP_zscore          10
RBD IgM_zscore         11
S IgM_zscore           11
Name: variable_cluster, dtype: int64
```

In [24]:
```
'''
TODO: 1. Choose a representative variable from each cluster you determin
ed in Part 1.4
         and create a low-dimensional version of the data using those va
riables
      2. Re-cluster the data using the reduced representation using the
 same
         choices you made for part 1.1.
'''
## same choices??
df_reduced_variables = df.filter(items=['N IgG1_zscore','RBD ADCD_zscor
e','N ADCD_zscore','N IgG2_zscore','RBD FcRg2b_zscore','RBD NKD-CD107a_z
score','NT50_zscore','N ADCP_zscore','N ADNP_zscore','N IgM_zscore','N I
gA1_zscore','RBD IgM_zscore'])
df_reduced_variables.head()


kmeans_possible_cluster_nums = [2,3,4,5,6,7,8,9,10] # 1 < k < 11

cluster_quality_scores = []
for k in kmeans_possible_cluster_nums:
    kmeans = KMeans(n_clusters=k).fit(df_reduced_variables)
    labels = kmeans.labels_
    score = metrics.silhouette_score(df_reduced_variables, labels) # qua
lity
    cluster_quality_scores.append(score)
```

In [25]:
```
cluster_quality_scores
```

Out[25]:
```
[0.35618058945764197,
 0.2626997098346046,
 0.2850013356278675,
 0.3144774292718084,
 0.3101595685593588,
 0.29288257115545946,
 0.29414360100597625,
 0.28666908528572305,
 0.3233422266122763]
```

```
In [26]: # visualize
         # ??quality went way down?
         plotMetricByK("Silhouette Coefficient", cluster_quality_scores, kmeans_p
         ossible_cluster_nums)
```



Select 6 clusters

```
In [27]: # choose k value
         kmeans = KMeans(n_clusters=6).fit(df_reduced_variables)
         labels = kmeans.labels_

         df['low dimension cluster']=labels  # add low dimension clusters
```

```
In [28]: labels
```

```
Out[28]: array([2, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 5, 4, 5, 5, 5, 5, 2, 5, 5, 4,
         5,
                4, 4, 5, 1, 5, 1, 1, 1, 1, 1, 4, 4, 1, 4, 1, 4, 1, 1, 4, 4, 4,
         1,
                4, 1, 1, 5, 1, 4, 1, 1, 2, 2, 2, 5, 2, 2, 5, 2, 2, 2, 2, 5, 2,
         2,
                5, 2, 2, 2, 2, 5, 2, 2, 5, 5, 5, 5, 2, 5, 2, 2, 5, 5, 5, 2, 2,
         5,
                5, 5, 5, 2, 0, 2, 0, 5, 5, 2, 5, 5, 2, 2, 2, 5, 2, 5, 5, 2, 5,
         5,
                5, 2, 2, 5, 2, 2, 2, 2, 2, 5, 2, 5, 0, 2, 5, 2, 0, 5, 5, 2, 2,
         2,
                3, 3, 3, 3, 3, 3, 3, 5, 3, 3, 3, 5, 5, 3, 3, 3, 3, 3, 3, 3, 0,
         0,
                0, 5, 5, 0, 0, 0, 0, 0, 0, 0, 5, 0, 0, 0, 5, 0, 5, 0, 5, 2, 2,
         5,
                2, 2, 5, 5, 5, 2, 2, 5, 2, 5, 2, 5, 2, 2, 2, 5, 0, 0, 0, 0, 0,
         0,
                5, 0, 5, 0, 0, 0, 5, 0, 0, 5, 5, 0, 0, 0, 0, 0, 5, 0, 0, 0, 0,
         5,
                5, 0, 0, 5, 0, 0, 0, 0, 5, 5, 0, 5], dtype=int32)
```

In [29]:
```
df.head()
```

Out[29]:

	S IgG1	RBD IgG1	N IgG1	S IgG2	RBD IgG2	N IgG2	S IgG3	RBD IgG3	N IgG3	S IgG
0	15518.25	11686.50	17408.00	2595.00	2977.5	4418.75	7988.75	10112.75	13740.75	2890.5
1	2226.50	2343.25	3379.75	2444.75	3850.5	4687.00	2404.00	3399.00	4383.00	2214.7
2	2279.75	2450.00	3741.00	2117.00	2321.0	3298.50	2110.75	2256.25	3009.75	2256.7
3	115548.25	93832.00	94973.50	2938.75	2725.0	4380.25	17165.50	14912.00	33445.50	2512.2
4	2645.00	2479.00	4630.00	2256.75	2408.5	3449.50	2086.00	2452.50	3574.75	2127.0

5 rows × 115 columns

Part 1.5: Answer

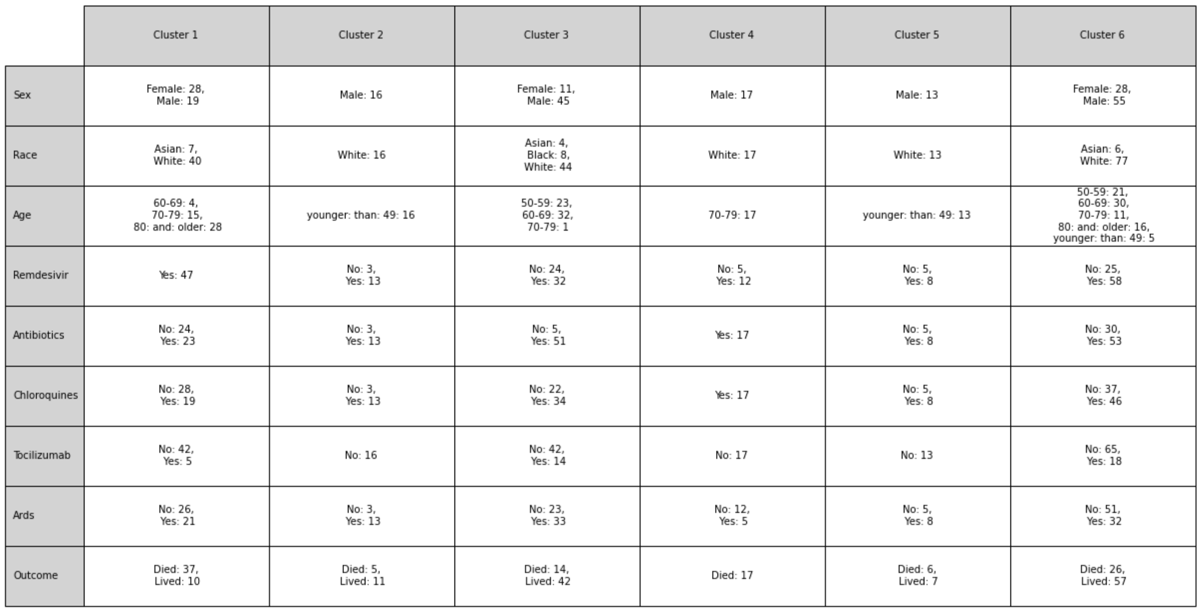
Representative Variables: **N IgG1_zscore, RBD ADCD_zscore, N ADCD_zscore, N IgG2_zscore, RBD FcRg2b_zscore, RBD NKD-CD107a_zscore, NT50_zscore, N ADCP_zscore, N ADNP_zscore, N IgM_zscore, N IgA1_zscore, RBD IgM_zscore**

How many clusters are there in the numeric variables? **Base on the Silhouette Coefficient, there are 2. However, I choose to use 5 clusters.** is that ok??

Explanation: **The Silhouette Coefficient is closest to 1 for two clusters and is lower for other clusterings. There is a spike in the coefficient at 5-6 clusters. Additionally, the difference between the coefficient for 2 clusters and the coefficient for 5-6 clusters is small. Rather than perform the same summary statistic analysis as before, I wanted to explore if anything relevant was found with 5-6 clusters. I performed kmeans clustering and summary statistics for both 5 clusters and 6 clusters. I found that 5 clusters produced clusters that seemed more clinically relevant.**

Part 1.6: Work

In [30]:
```
'''
  TODO: Create a table where the rows correspond to the variables in col
umns 53-61, and the columns correspond to the k clusters you identified.
        in part 1.5. For each cell in the table, put summary statistics
 for that (variable, cluster) pair
'''
# I didn't find a different number...???

# create 2d list to contain results
rows=6 # clusters
columns=9 # categorical columns
cellText=[[''] * columns for i in range(rows)]


# get summary stats for each categorical column
categorical_cols = df.columns.values.tolist()[52:61]
for i, col in enumerate(categorical_cols):
    for cluster in range(0,rows):
        df_one_cluster = df[df['low dimension cluster']==cluster] # sele
ct data for only one cluster
        formatted = formatValueCounts(df_one_cluster[col].value_counts
())
        cellText[cluster][i]=formatted

output_table = plotSummaryTable(cellText)
output_table
```

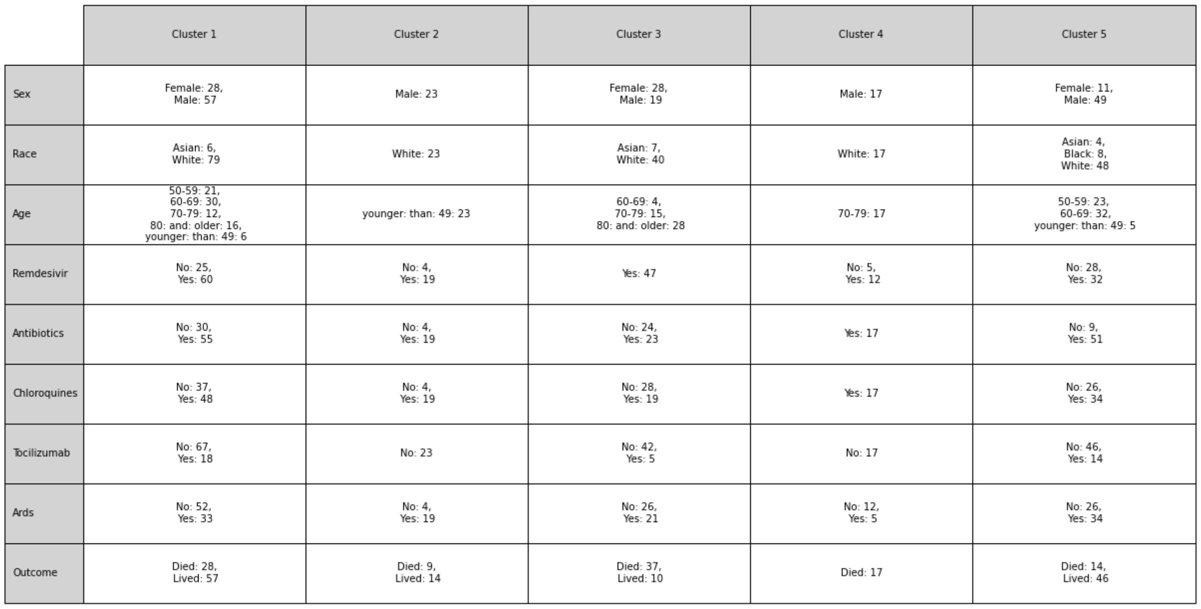


	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Sex	Female: 28, Male: 19	Male: 16	Female: 11, Male: 45	Male: 17	Male: 13	Female: 28, Male: 55
Race	Asian: 7, White: 40	White: 16	Asian: 4, Black: 8, White: 44	White: 17	White: 13	Asian: 6, White: 77
Age	60-69: 4, 70-79: 15, 80: and: older: 28	younger: than: 49: 16	50-59: 23, 60-69: 32, 70-79: 1	70-79: 17	younger: than: 49: 13	50-59: 21, 60-69: 30, 70-79: 11, 80: and: older: 16, younger: than: 49: 5
Remdesivir	Yes: 47	No: 3, Yes: 13	No: 24, Yes: 32	No: 5, Yes: 12	No: 5, Yes: 8	No: 25, Yes: 58
Antibiotics	No: 24, Yes: 23	No: 3, Yes: 13	No: 5, Yes: 51	Yes: 17	No: 5, Yes: 8	No: 30, Yes: 53
Chloroquines	No: 28, Yes: 19	No: 3, Yes: 13	No: 22, Yes: 34	Yes: 17	No: 5, Yes: 8	No: 37, Yes: 46
Tocilizumab	No: 42, Yes: 5	No: 16	No: 42, Yes: 14	No: 17	No: 13	No: 65, Yes: 18
Ards	No: 26, Yes: 21	No: 3, Yes: 13	No: 23, Yes: 33	No: 12, Yes: 5	No: 5, Yes: 8	No: 51, Yes: 32
Outcome	Died: 37, Lived: 10	Died: 5, Lived: 11	Died: 14, Lived: 42	Died: 17	Died: 6, Lived: 7	Died: 26, Lived: 57

Select 6 clusters

In [31]:
```
# choose k value
kmeans = KMeans(n_clusters=5).fit(df_reduced_variables)
labels = kmeans.labels_

df['low dimension cluster']=labels  # add low dimension clusters
```

In [32]:
```
'''
  TODO: Create a table where the rows correspond to the variables in col
umns 53-61, and the columns correspond to the k clusters you identified.
        in part 1.5. For each cell in the table, put summary statistics
 for that (variable, cluster) pair
'''
# I didn't find a different number...???

# create 2d list to contain results
rows=5 # clusters
columns=9 # categorical columns
cellText=[[''] * columns for i in range(rows)]


# get summary stats for each categorical column
categorical_cols = df.columns.values.tolist()[52:61]
for i, col in enumerate(categorical_cols):
    for cluster in range(0,rows):
        df_one_cluster = df[df['low dimension cluster']==cluster] # sele
ct data for only one cluster
        formatted = formatValueCounts(df_one_cluster[col].value_counts
())
        cellText[cluster][i]=formatted

output_table = plotSummaryTable(cellText)
output_table
```



	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Sex	Female: 28, Male: 57	Male: 23	Female: 28, Male: 19	Male: 17	Female: 11, Male: 49
Race	Asian: 6, White: 79	White: 23	Asian: 7, White: 40	White: 17	Asian: 4, Black: 8, White: 48
Age	50-59: 21, 60-69: 30, 70-79: 12, 80: and: older: 16, younger: than: 49: 6	younger: than: 49: 23	60-69: 4, 70-79: 15, 80: and: older: 28	70-79: 17	50-59: 23, 60-69: 32, younger: than: 49: 5
Remdesivir	No: 25, Yes: 60	No: 4, Yes: 19	Yes: 47	No: 5, Yes: 12	No: 28, Yes: 32
Antibiotics	No: 30, Yes: 55	No: 4, Yes: 19	No: 24, Yes: 23	Yes: 17	No: 9, Yes: 51
Chloroquines	No: 37, Yes: 48	No: 4, Yes: 19	No: 28, Yes: 19	Yes: 17	No: 26, Yes: 34
Tocilizumab	No: 67, Yes: 18	No: 23	No: 42, Yes: 5	No: 17	No: 46, Yes: 14
Ards	No: 52, Yes: 33	No: 4, Yes: 19	No: 26, Yes: 21	No: 12, Yes: 5	No: 26, Yes: 34
Outcome	Died: 28, Lived: 57	Died: 9, Lived: 14	Died: 37, Lived: 10	Died: 17	Died: 14, Lived: 46

Part 1.6: Answer

Plot the table in one of the above cells or include it as an image in this cell

Are any of the clusters significantly enriched for some particular value? **When clustering into 5 clusters, all of the patients died in Cluster 4. All were white males in their seventies who had been prescribed antibiotics and chloroquines. None had been prescribed Tocilizumab. Cluster 2 consisted entirely of white males younger than 49 who had not been prescribed Tocilizumab. In Cluster 2, just over half the patients lived, so the outcome doesn't appear clinically relevant at this time.**

```
In [ ]:
```