openmp_mpi_k-means

April 13, 2019

1 K-Means Clustering with OpenMP and MPI

1.0.1 Implement the k-means clustering algorithm in OpenMP/MPI, trying to maximize the performance (reduce the execution time) by carefully exploiting the resources within one computing node with multiple processing cores (OpenMP) and across computing nodes (MPI).

Optional: implement the same algorithm in Apache Flink and compare the performance of the two implementations (processing time and scalability) under various workloads.

In [1]:
```
import csv
import random
import sys

import numpy
import os  # We need this module
import matplotlib.pyplot as plt
import seaborn as sns;
from sklearn.datasets.samples_generator import make_blobs
sns.set()  # for plot styling

#Samples
N_SAMPLES = 100000

# Get path of the current dir, then use it to create paths:
CURRENT_DIR = os.path.dirname("__file__")
file_path = os.path.join(CURRENT_DIR, 'dataset_display/dataset.csv')
initial_dataset_path = os.path.join(CURRENT_DIR, 'dataset_display/initialdataset.csv')
initial_centroids_path = os.path.join(CURRENT_DIR, 'dataset_display/initialcentroids.csv
new_dataset_path = os.path.join(CURRENT_DIR, 'dataset_display/newdataset.csv')
new_centroids_path = os.path.join(CURRENT_DIR, 'dataset_display/newcentroids.csv')
objfun_path = os.path.join(CURRENT_DIR, 'dataset_display/objfun.csv')
exectimes_path = os.path.join(CURRENT_DIR, 'dataset_display/exectimes.csv')
results_100_path = os.path.join(CURRENT_DIR, 'dataset_display/results_100/results.csv')
results_1K_path = os.path.join(CURRENT_DIR, 'dataset_display/results_1K/results.csv')
```

```
results_10K_path = os.path.join(CURRENT_DIR, 'dataset_display/results_10K/results.csv')
results_100K_path = os.path.join(CURRENT_DIR, 'dataset_display/results_100K/results.csv'
results_1M_path = os.path.join(CURRENT_DIR, 'dataset_display/results_1M/results.csv')
results_10M_path = os.path.join(CURRENT_DIR, 'dataset_display/results_10M/results.csv')

fig_width = 12
fig_height = 10
```

2 Initial Dataset

2.1 Display the points in the Initial Dataset:

We have an Initial Dataset of 100000 points (later on we'll be using different sizes), randomly generated by a custom Python script. These points are already somehow divided in clusters so that we can more easily test the K-Means Clustering algorithm.

```
In [2]: print('X,Y')
        with open(initial_dataset_path) as csvfile:
            reader = csv.DictReader(csvfile)
            for i,row in enumerate(reader):
                print(row['X'], row['Y'])
                if(i >= 10):
                    break

        print("Total points: %s" % format(N_SAMPLES,'d'))
```

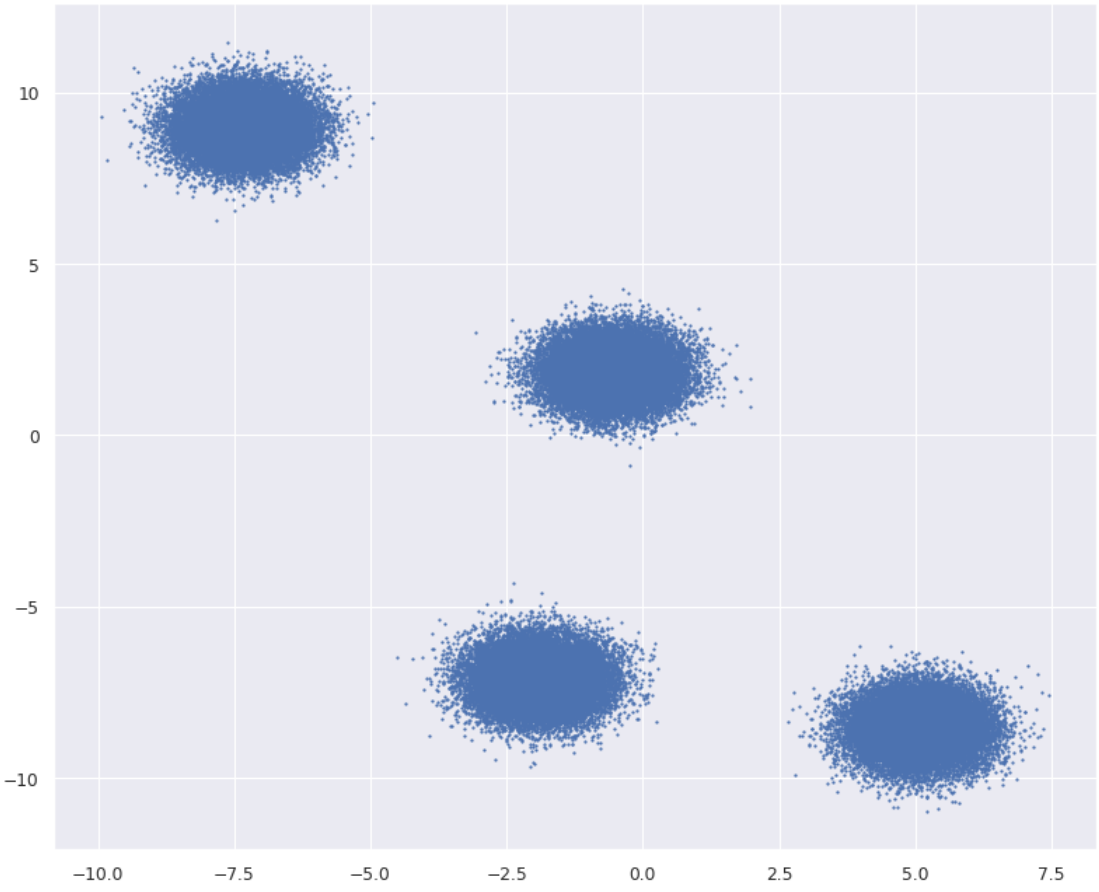
```
X,Y
4.762006 -7.700549
4.490764 -8.202433
-1.384802 2.850730
-1.411994 -6.885759
0.045029 1.578344
-7.419469 9.258043
-6.915910 9.343622
-7.663262 8.672174
-2.618907 -6.364270
-1.369107 -8.103168
-7.965163 9.759896
Total points: 100000
```

2.2 And now we plot the initial dataset:

By plotting the dataset, we can see that is indeed form by 4 clusters easily observable. We'll later test the K-Means Clustering algorithm and see if it can also individuate the clusters.

```
In [3]: x = numpy.zeros(N_SAMPLES)
        y = numpy.zeros(N_SAMPLES)
```

```
#Read the dataset from the CVS file
with open(initial_dataset_path) as csvfile:
    reader = csv.DictReader(csvfile)
    i = 0
    for row in reader:
        x[i] = row['X']
        y[i] = row['Y']
        #print(x[i], y[i])
        i=i+1

#Plot the read dataset
plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
plt.scatter(x[:], y[:], s=1)
plt.show()
```



2.3 Initial Centroids

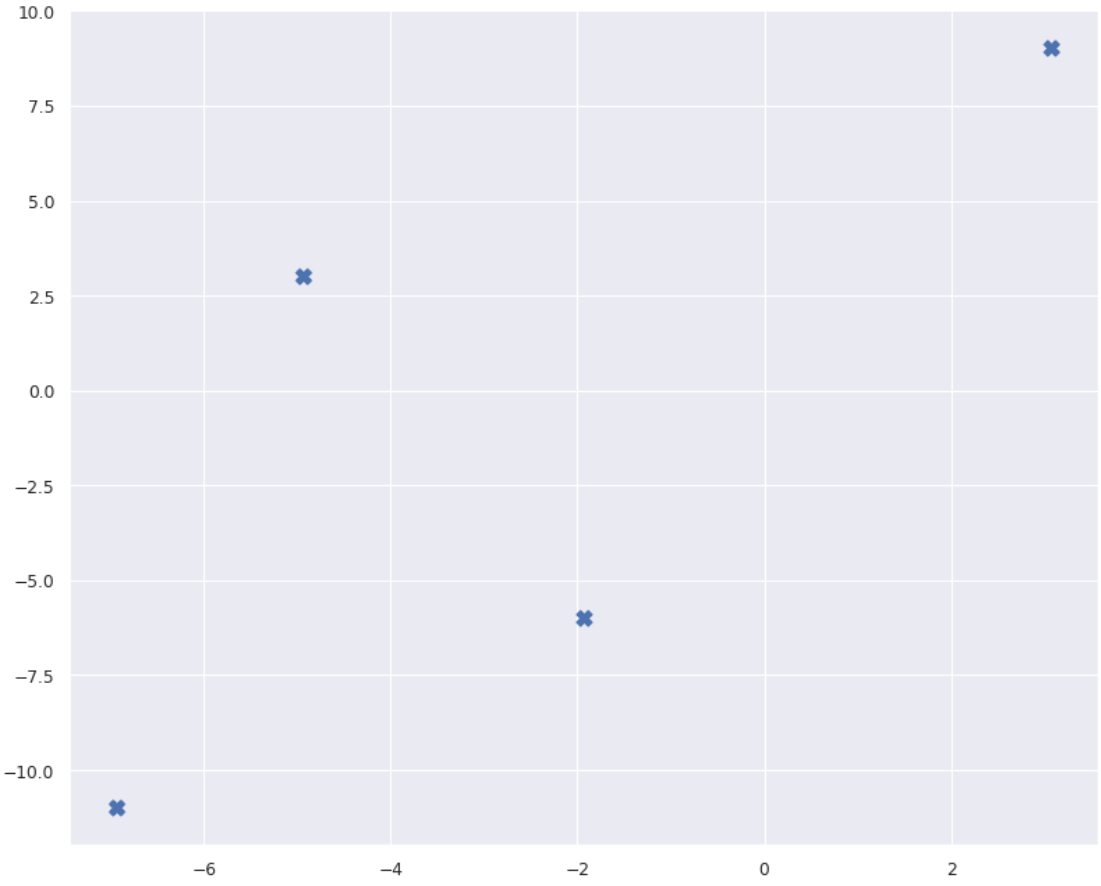
The Initial Centroids are randomly placed at runtime, however a centroids will be recreated if it is too close to another centroid. The initial placing of the centroids is of fundamental importance to the result of the K-Means Clustering algorithm execution on a given dataset. Let's print the centroids:

```
In [4]: print('Cluster,X,Y')
        centroids = 0
        with open(initial_centroids_path) as csvfile:
            reader = csv.DictReader(csvfile)
            for row in reader:
                print(centroids, row['X'], row['Y'])
                centroids = centroids + 1
        print("Total centroids: %d" % centroids)
```

```
Cluster,X,Y
0 3.066931 9.023582
1 -4.933069 3.023582
2 -1.933069 -5.976418
3 -6.933069 -10.976418
Total centroids: 4
```

And now we plot them:

```
In [5]: x = numpy.zeros(centroids)
        y = numpy.zeros(centroids)

        #Read the dataset from the CVS file
        with open(initial_centroids_path) as csvfile:
            reader = csv.DictReader(csvfile)
            i = 0
            for row in reader:
                x[i] = row['X']
                y[i] = row['Y']
                #print(x[i], y[i])
                i=i+1

        #Plot the read dataset
        plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
        plt.scatter(x[:], y[:], marker="X", s=100)
        plt.show()
```

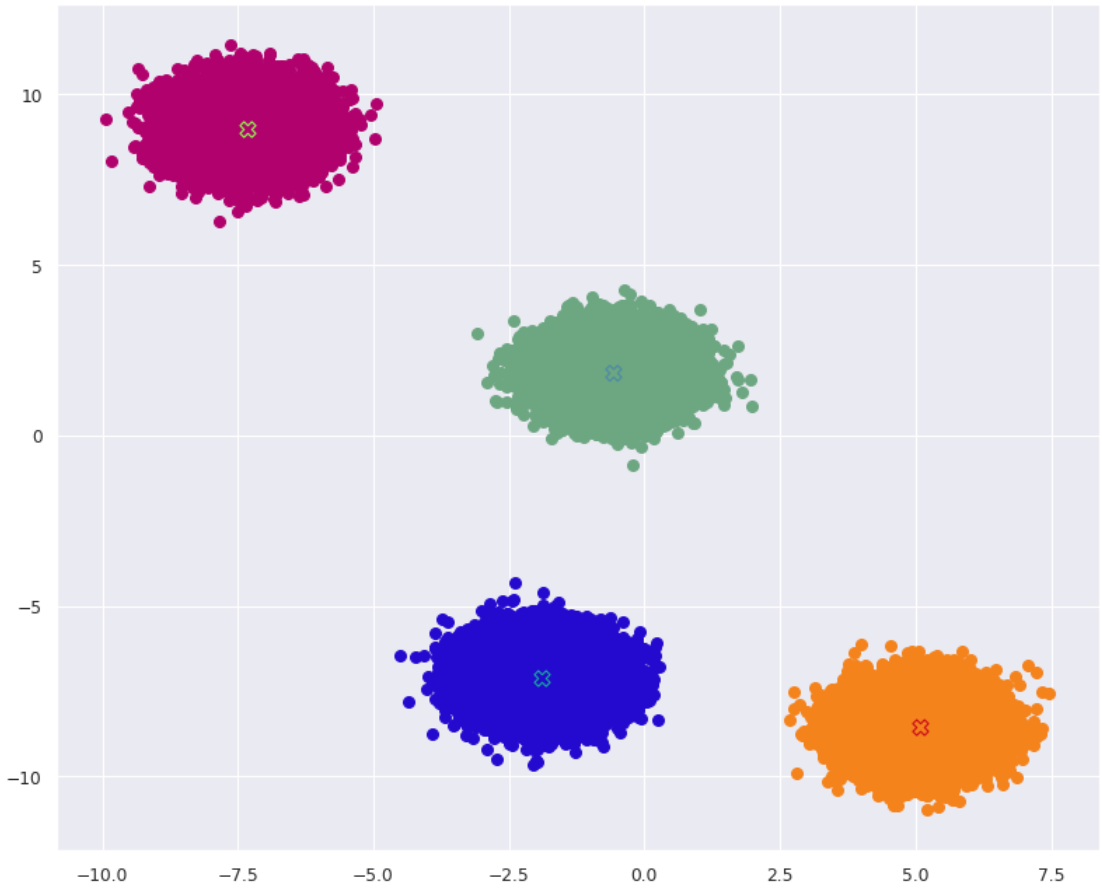


3 Plotting both Dataset and Centroids

We've run the K-Means Clustering Algorithm on the initial dataset and got new centroids each associated to a cluster. So we now plot the resulting clusters separated by a random color and their centroids:

```
In [6]: def random_color():
            return numpy.random.rand(3,)

In [7]: x = numpy.zeros(N_SAMPLES)
        y = numpy.zeros(N_SAMPLES)
        c = numpy.zeros(N_SAMPLES)
        cx = list()
        cy = list()

        plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')

        # Read the new centroids from the CVS file
        with open(new_centroids_path) as csvfile:
```

```
    reader = csv.DictReader(csvfile)
    for row in reader:
        cx.append(float(row['X']))
        cy.append(float(row['Y']))

# Read the new dataset from the CVS file
with open(new_dataset_path) as csvfile:
    reader = csv.DictReader(csvfile)
    i = 0
    for row in reader:
        x[i] = row['X']
        y[i] = row['Y']
        c[i] = row['Cluster']
        # print(x[i], y[i])
        i = i + 1

minK = c.min()
maxK = c.max()
k = (int)(maxK - minK + 1)

# plot the points for each cluster with a different color
for i in range(k):
    x2 = list()
    y2 = list()

    for j in range(N_SAMPLES):
        if c[j] == i:
            x2.append(x[j])
            y2.append(y[j])

    # Plot the read dataset
    color1 = random_color()
    color2 = random_color()
    plt.scatter(x2[:], y2[:], c=color1, s=50)
    plt.scatter(cx[i], cy[i], c=color1, marker="X", edgecolor=color2, s=100)
plt.show()
```



3.1 Running Modes: Normal, OpenMP, MPI, MPI + OpenMP

The program written in C actually executes four different versions of the K-Means Clustering Algorithm. They run sequentially one at a time, but they use the same initial dataset and the same random pair of initial centroids. The initial position of the centroids is of vital importance to the result of the execution so is important that all four versions use the same set of centroids so that we can have a meaningful comparison in performance. All four versions will produce the same result and same objective function value, but they will have different execution times.

We've set the maximum number of cores for the OpenMP version (4 on this PC), and 4 parallel nodes for the MPI (and MPI+OpenMP) version. As expected the OpenMP version perform much better that the sequential version, while with MPI is not always the case, here are the results of a single execution on this dataset:

```
In [8]: print('Execution Times:\n')
        t = numpy.zeros(4)
        with open(exectimes_path) as csvfile:
            reader = csv.DictReader(csvfile)
            for i,row in enumerate(reader):
                t[i] = row['Time']
```

```
        print('Normal Execution --> ' + str(t[0]*1000) + 'ms')
        print('OpenMP Execution --> ' + str(t[1]*1000) + 'ms')
        print('MPI Execution    --> ' + str(t[2]*1000) + 'ms')
        print('MPI + OpenMP Execution    --> ' + str(t[3]*1000) + 'ms')
```

```
Execution Times:

Normal Execution --> 103.364ms
OpenMP Execution --> 107.58800000000001ms
MPI Execution    --> 50.316ms
MPI + OpenMP Execution    --> 219.138ms
```

While the value of the Objective Function is:

```
In [9]: objfun = numpy.zeros(4)
        with open(objfun_path) as csvfile:
            reader = csv.DictReader(csvfile)
            for i,row in enumerate(reader):
                objfun[i] = row['ObjFun']

        print('ObjectiveFunction value --> ' + str(objfun[0]))
```

```
ObjectiveFunction value --> 71883.570312
```

3.2 ——————————————————

4 AmazonAWS Starcluster Results

All the executions and tests explained below were run on a cluster of **four c3.xlarge EC2 Nodes** on Amazon AWS by using the Starcluster open source cluster-computing toolkit. Each node (c3.xlarge) is a powerful machine with 4 cores and 8GB of RAM.

4.0.1 Cumulative Execution Results

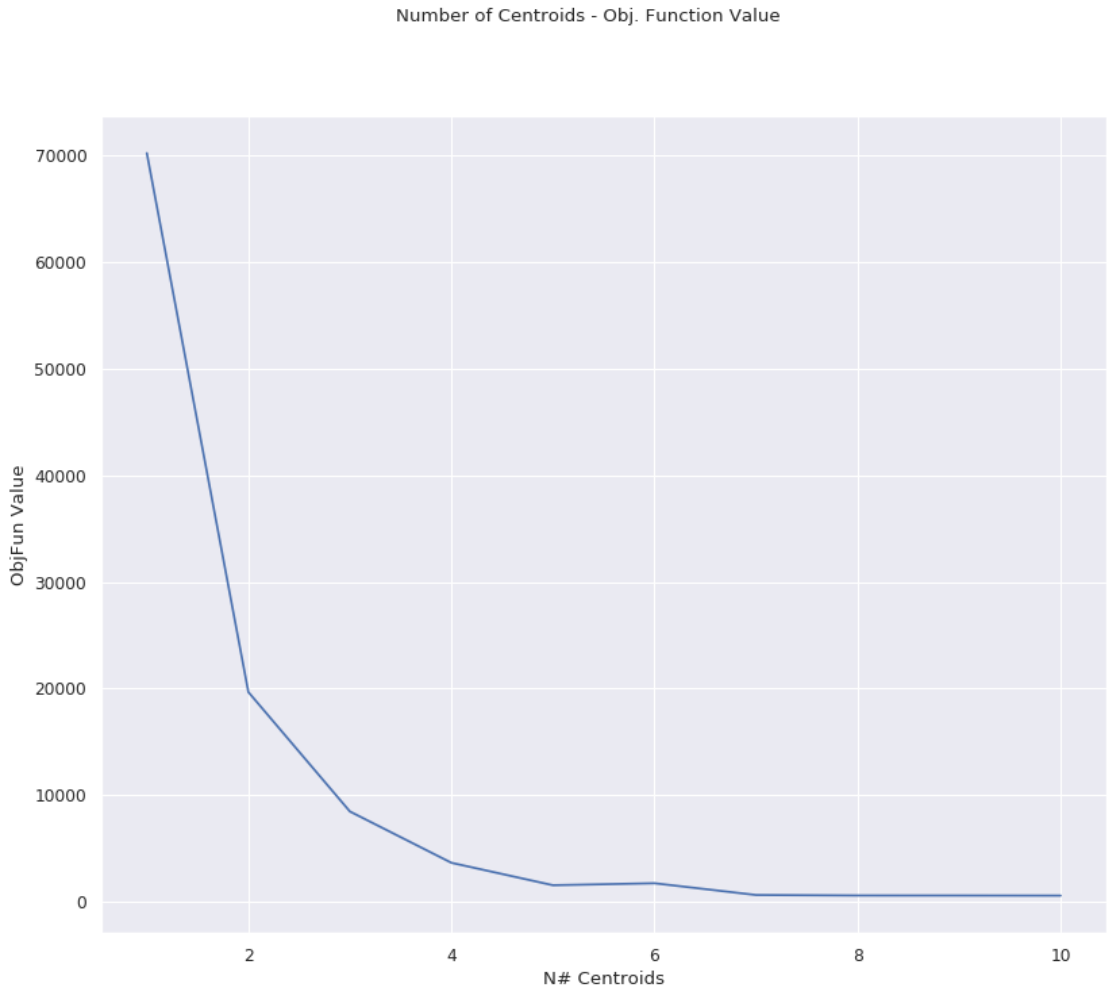
By running a bach script we were able to cumulate a large quantity of execution results (more than 5000 executions). For consistency we've run all four different versions of the K-Means Clustering Algorithm sequentially one at a time on the same initial dataset and the same random pair of initial centroids (changing every cycle). That way the results of each execution can be compared with the executions of the other three versions of the algorithm. For each executions we've stored the number of centroids, the execution mode (algorithm version), the execution time and the obj function result.

4.0.2 1) Relation between number of centroids and obj function value

Let's average the executions results in the large dataset described above and plot the relation between the number of centroids and the obj function value. The execution were made with a number of centroids between 1 and 10.

```
In [10]: def getResultsData(fname):
             row_count = 0
             with open(fname) as csvfile:
                 row_count = sum(1 for line in csvfile)
             print ("Rows in the results file: " + str(row_count))
             EXECUTIONS = int((row_count - 1)/4)

             n_c      = numpy.zeros(EXECUTIONS)
             openmp_c = numpy.zeros(EXECUTIONS)
             mpi_c    = numpy.zeros(EXECUTIONS)
             mpi_mp_c = numpy.zeros(EXECUTIONS)

             n_t      = numpy.zeros(EXECUTIONS)
             openmp_t = numpy.zeros(EXECUTIONS)
             mpi_t    = numpy.zeros(EXECUTIONS)
             mpi_mp_t = numpy.zeros(EXECUTIONS)

             n_of      = numpy.zeros(EXECUTIONS)
             openmp_of = numpy.zeros(EXECUTIONS)
             mpi_of    = numpy.zeros(EXECUTIONS)
             mpi_mp_of = numpy.zeros(EXECUTIONS)

             # Read the new centroids from the CVS file
             with open(fname) as csvfile:
                 reader = csv.DictReader(csvfile)
                 i1,i2,i3,i4=0,0,0,0
                 for i,row in enumerate(reader):
                     mode = int(row['Mode'])
                     #print(mode + "-" + str(i))

                     #Normal Execution
                     if mode == 0:
                         n_c[i1]  = float(row['K'])
                         n_t[i1]  = float(row['Time'])
                         n_of[i1] = float(row['ObjFun'])
                         i1 = i1 + 1
                     #OpenMP Execution
                     elif mode == 1:
                         openmp_c[i2]  = float(row['K'])
                         openmp_t[i2]  = float(row['Time'])
                         openmp_of[i2] = float(row['ObjFun'])
                         i2 = i2 + 1
                     #MPI Execution
                     elif mode == 2:
                         mpi_c[i3]  = float(row['K'])
                         mpi_t[i3]  = float(row['Time'])
                         mpi_of[i3] = float(row['ObjFun'])
                         i3 = i3 + 1
```

```
                #MPI + OpenMP Execution
                elif mode == 3:
                    mpi_mp_c[i4]  = float(row['K'])
                    mpi_mp_t[i4]  = float(row['Time'])
                    mpi_mp_of[i4] = float(row['ObjFun'])
                    i4 = i4 + 1
        return EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c,

    EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR

    x_val = numpy.zeros(10)
    y_val = numpy.zeros(10)

    #Calc the mean values
    for i in range(0,10):
        x_val[i] = i + 1
        #print(str(i))

        #Iterate all the executions for each centroid number
        for j in range(EXECUTIONS):
            if n_c[j] == i+1:
                y_val[i] = y_val[i] + n_of[j]

        #Obj Function values mean
        y_val[i] = y_val[i] / EXECUTIONS
        #print(str(y_val[i]))

    #Plot the between number of centroids and obj function value
    plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
    plt.plot(x_val,y_val)
    plt.suptitle('Number of Centroids - Obj. Function Value')
    plt.xlabel('N# Centroids')
    plt.ylabel('ObjFun Value')
    plt.show()

Rows in the results file: 1209
```



4.0.3 Resulting plot analysis

Given the plot above we can observe the way that the Obj. Function Value (Y-Axis) changes based on the Number of Centroids (X-Asis) used. And we can clearly notice that the Knee value is equal to "4". It's the Knee value because the successive numbers of centroids don't have an Obj. Function Value that decreases greatly. That means that the distances in between the data points and the centroids for each cluster don't decrease much after the value of 4 centroids used. So just by observing the above plot and chosing the knee value we can conclude that the Dataset is composed of 4 clusters witch is correct since we are the ones that generated the datased divided in four clusters in the first place.

4.0.4 2) Relation between Number of Centroids and the Execution Time (by varying the Dataset Size)

Let's now again average the executions results in five different Datasets as described above and plot the relation between the number of centroids and the Execution times. The execution were made with a number of centroids between 1 and 10.

We'll compare the results for each of the four execution modes: **Normal**, **OpenMP**, **MPI**, **MPI + OpenMP**

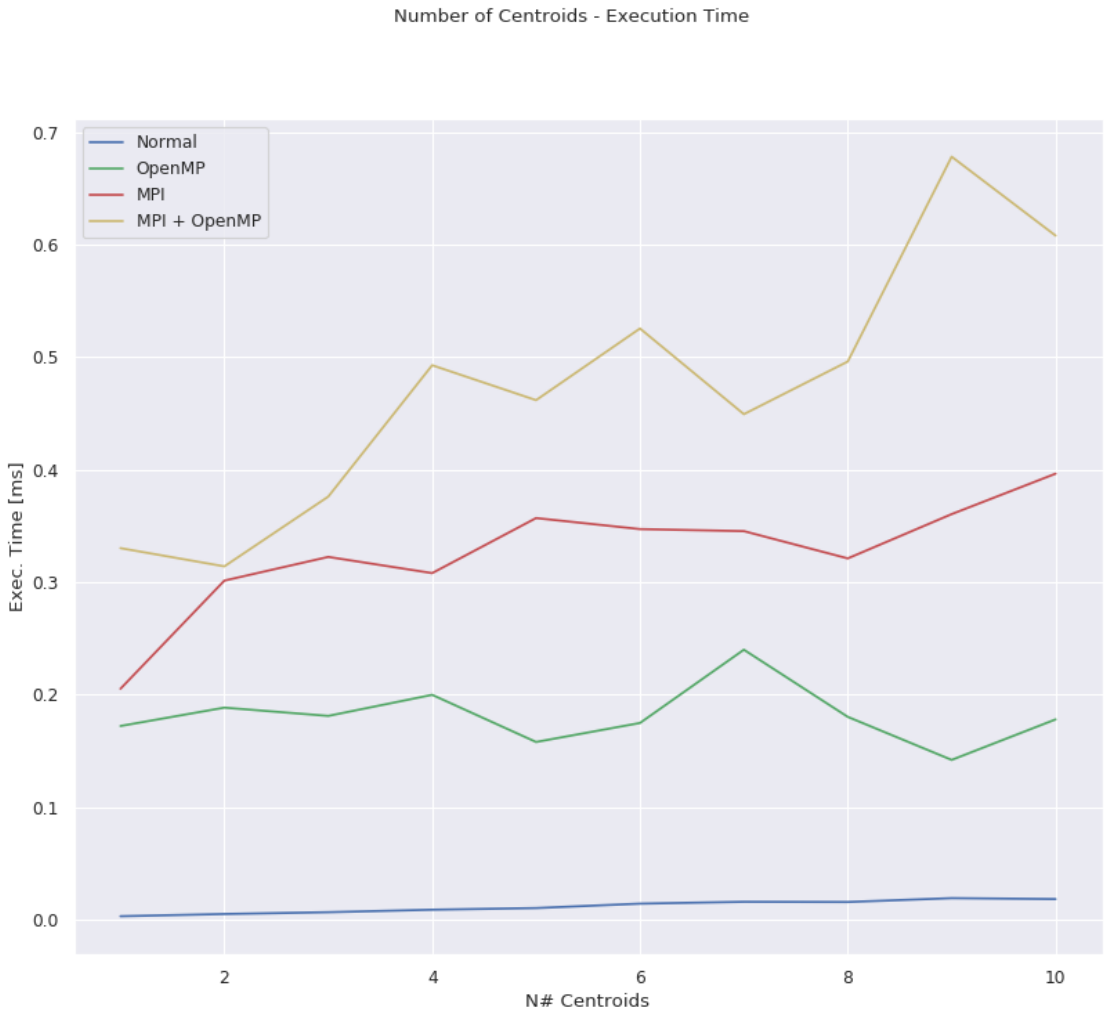
While the datasets that we'll be using have the following sizes: **100, 1K, 10K, 100K and 1M** datapoints (1K=1000 points, 1M = 1000000 points):

4.0.5 2.1) Dataset size: 100

```
In [11]: def plotRealtionCentroidsExecTime():
             x_valc          = numpy.zeros(10)    # Centroids
             y_val_n_et      = numpy.zeros(10)    # Normal Execution Time
             y_val_mp_et     = numpy.zeros(10)    # OpenMP Execution Time
             y_val_mpi_et    = numpy.zeros(10)    # MPI Execution Time
             y_val_mpi_mp_et = numpy.zeros(10)    # MPI + OpenMP Execution Time

             #Calc the mean values
             for i in range(0,10):
                 x_valc[i] = i + 1
                 #print(str(i))

                 #Iterate all the executions for each centroid number
                 for j in range(EXECUTIONS):
                     # Normal Execution
                     if n_c[j] == i+1:
                         y_val_n_et[i] = y_val_n_et[i] + n_t[j]

                     # OpenMP Execution
                     if openmp_c[j] == i+1:
                         y_val_mp_et[i] = y_val_mp_et[i] + openmp_t[j]

                     # MPI Execution
                     if mpi_c[j] == i+1:
                         y_val_mpi_et[i] = y_val_mpi_et[i] + mpi_t[j]

                     # MPI + OpenMP Execution
                     if mpi_mp_c[j] == i+1:
                         y_val_mpi_mp_et[i] = y_val_mpi_mp_et[i] + mpi_mp_t[j]

                 #Execution Time values mean
                 y_val_n_et[i]      = (y_val_n_et[i] / EXECUTIONS) * 1000
                 y_val_mp_et[i]     = (y_val_mp_et[i] / EXECUTIONS) * 1000
                 y_val_mpi_et[i]    = (y_val_mpi_et[i] / EXECUTIONS) * 1000
                 y_val_mpi_mp_et[i] = (y_val_mpi_mp_et[i] / EXECUTIONS) * 1000
                 #print("n " + str(y_val_n_et[i]))
                 #print("mp " + str(y_val_mp_et[i]))
                 #print("mpi " + str(y_val_mpi_et[i]))

             #Plot the relation between number of centroids and obj function value
             plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
```

```
        plt.plot(x_valc,y_val_n_et, '-b', label='Normal')
        plt.suptitle('Number of Centroids - Execution Time')
        plt.xlabel('N# Centroids')
        plt.ylabel('Exec. Time [ms]')
        plt.plot(x_valc,y_val_mp_et, '-g', label='OpenMP')
        plt.plot(x_valc,y_val_mpi_et, '-r', label='MPI')
        plt.plot(x_valc,y_val_mpi_mp_et, '-y', label='MPI + OpenMP')
        plt.legend(loc='upper left')
        plt.show()

    EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
    plotRealtionCentroidsExecTime()
```

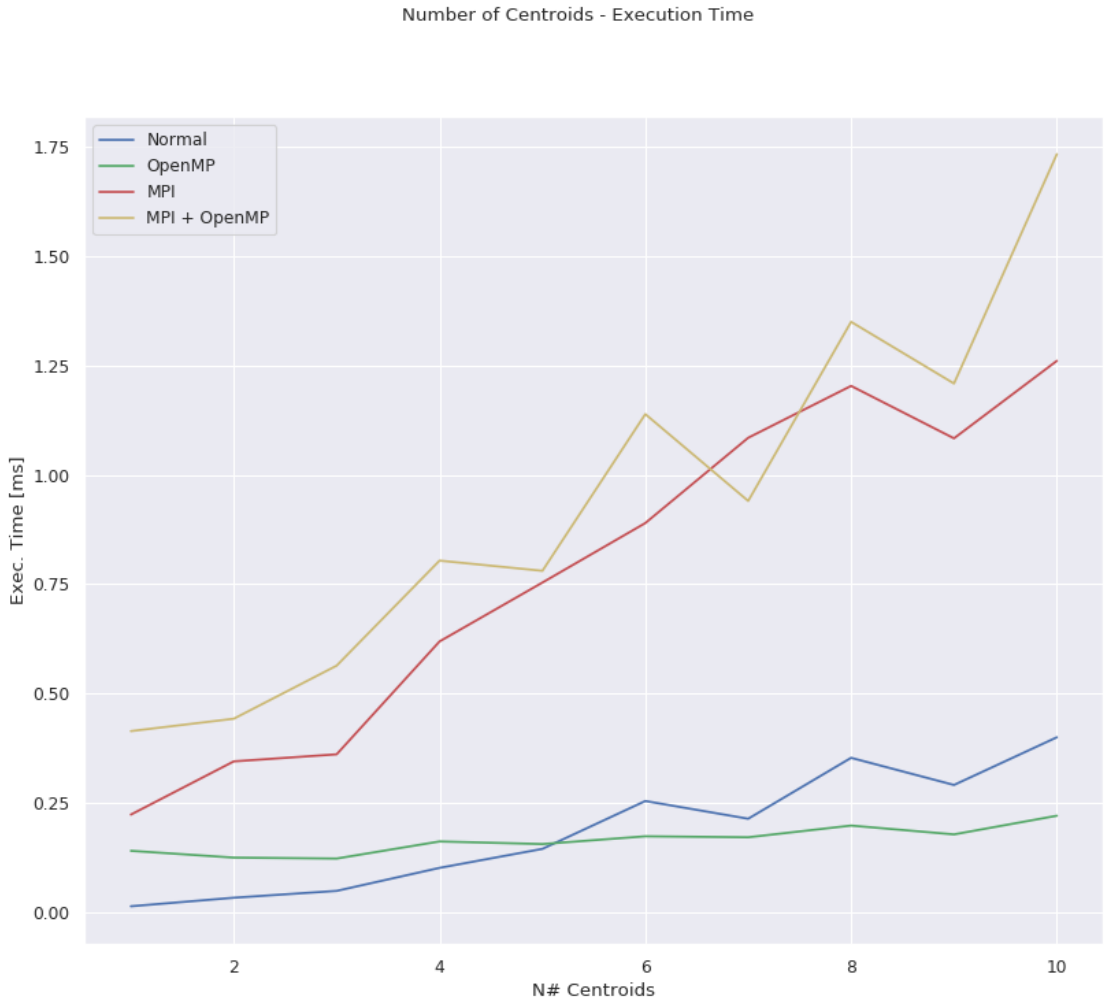
```
Rows in the results file: 1209
```



4.0.6 2.2) Dataset size: 1K

```
In [12]: EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
         plotRealtionCentroidsExecTime()
```

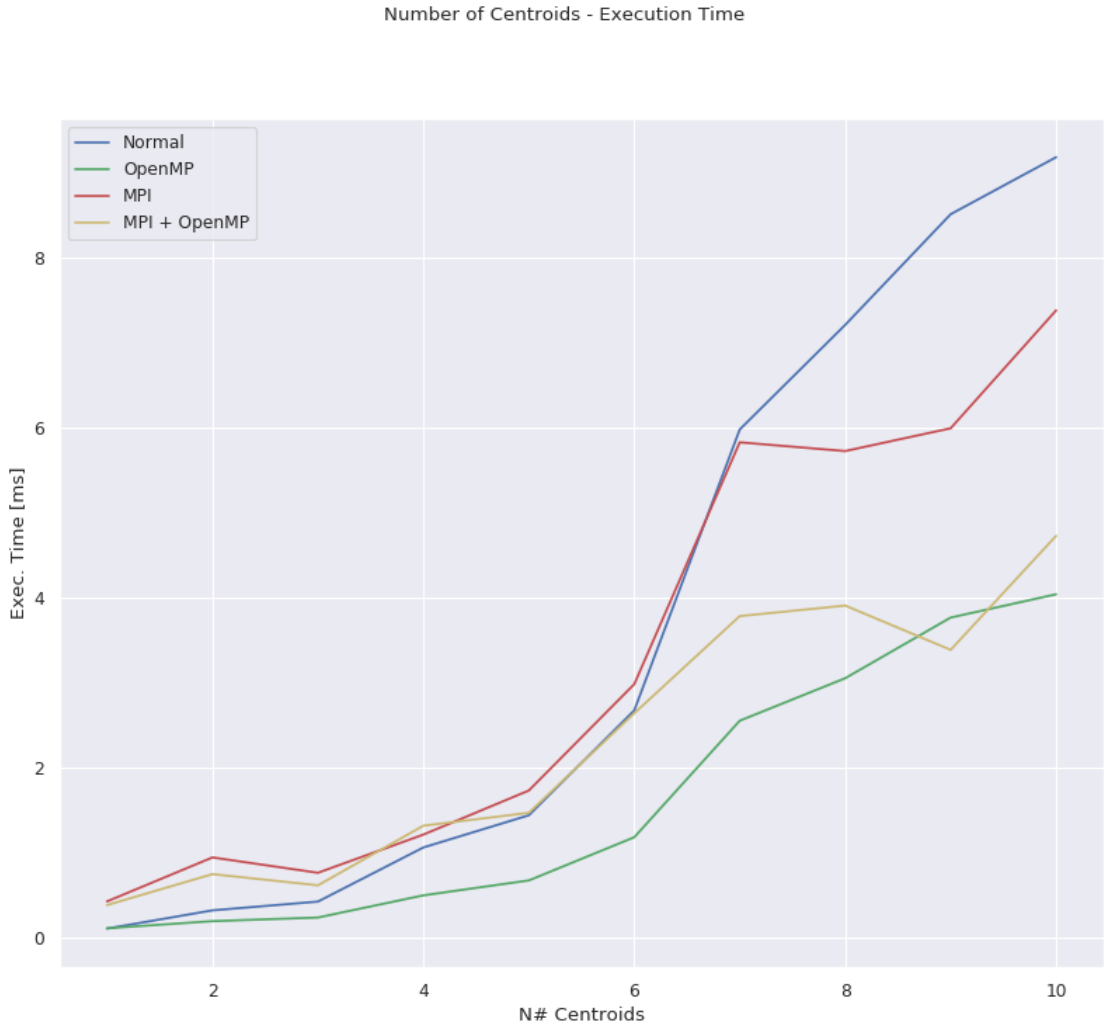
```
Rows in the results file: 1209
```



4.0.7 2.3) Dataset size: 10K

```
In [13]: EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
         plotRealtionCentroidsExecTime()
```

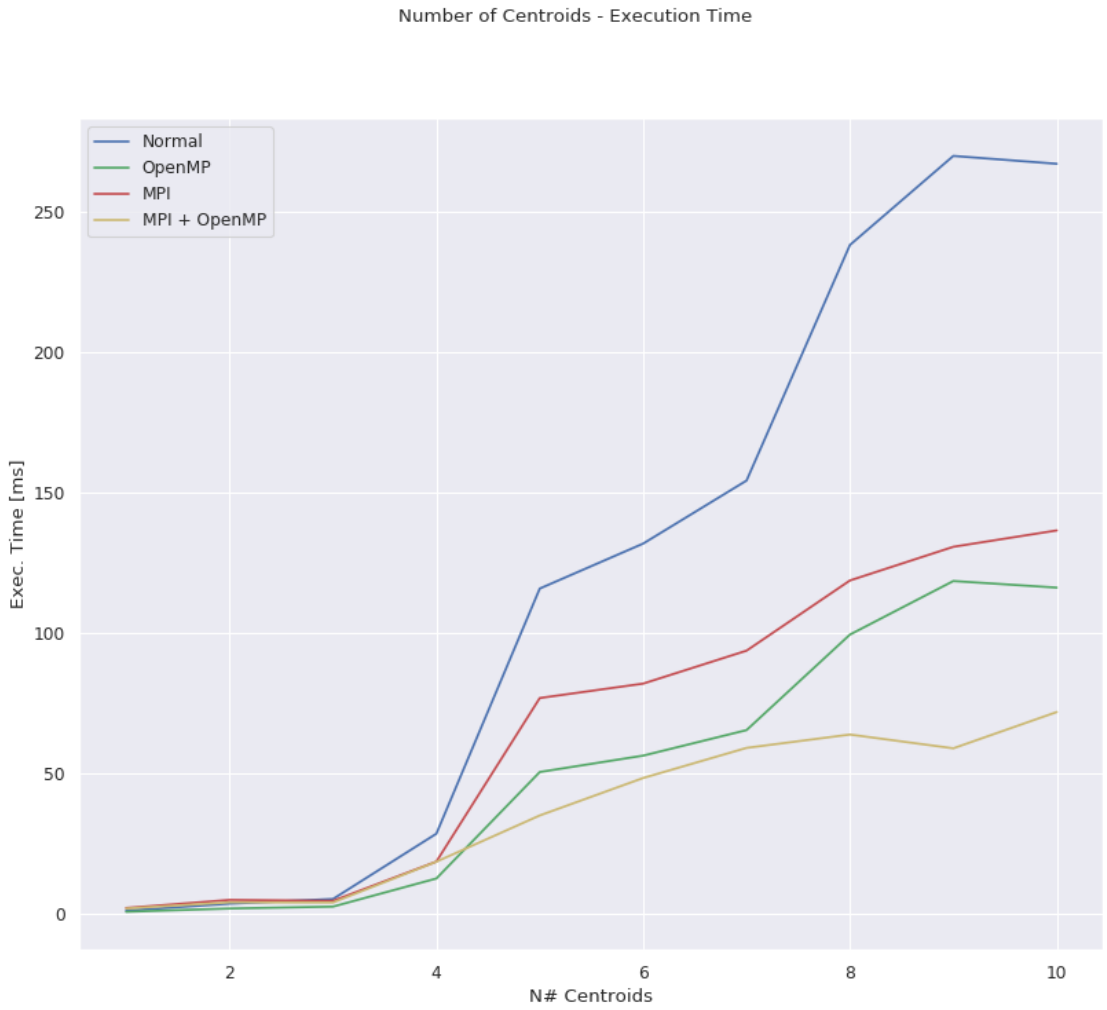
```
Rows in the results file: 1209
```



4.0.8 2.4) Dataset size: 100K

```
In [14]: EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
         plotRealtionCentroidsExecTime()
```

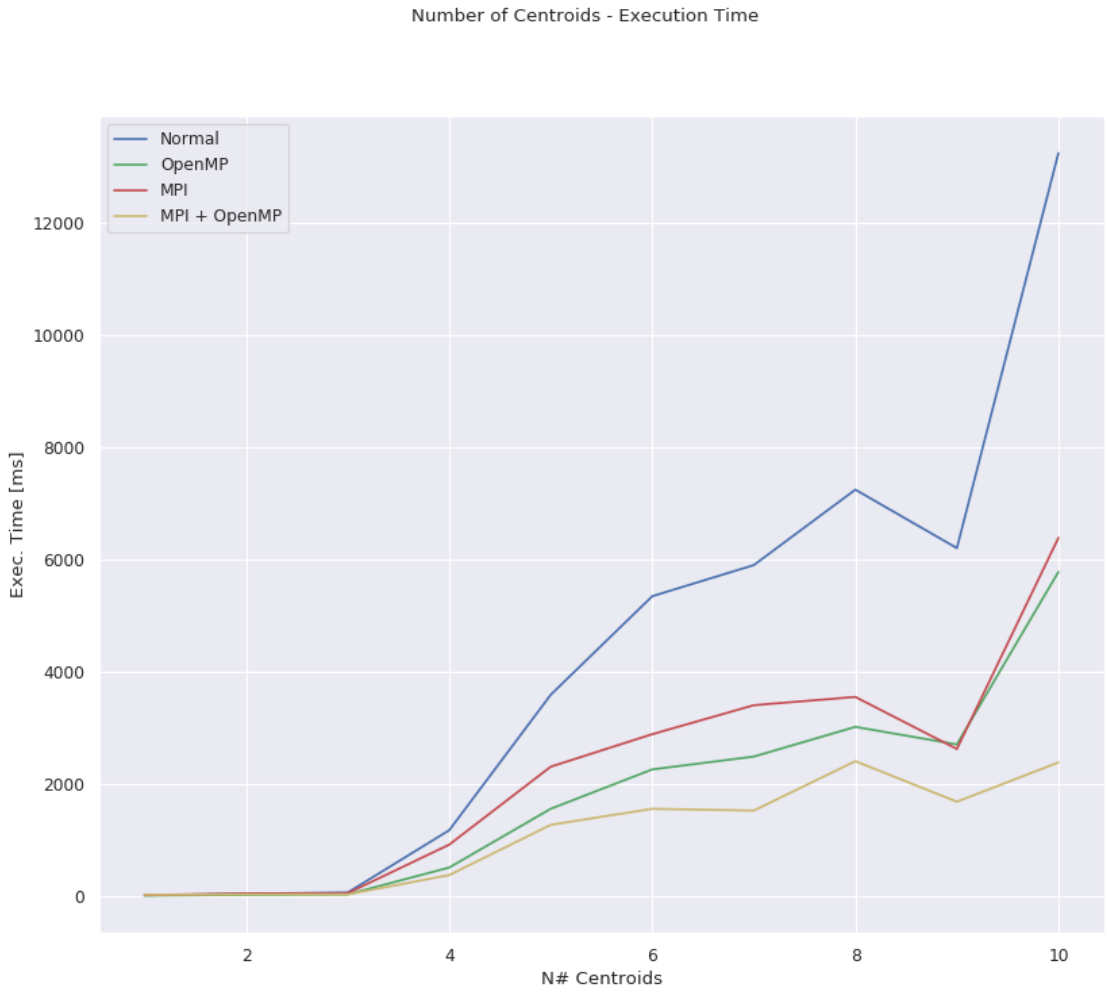
```
Rows in the results file: 1209
```



4.0.9 2.5) Dataset size: 1M

```
In [15]: EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
         n_t_1M, openmp_t_1M, mpi_t_1M, mpi_mp_t_1M = n_t, openmp_t, mpi_t, mpi_mp_t
         plotRealtionCentroidsExecTime()
```

```
Rows in the results file: 609
```



4.0.10 Resulting plots analysis - ExecutionTime

On the above plots we can observe the Execution Times (Y-Axis) for each execution mode base on the number of centroids (X-Axis). The executions were repeated a great number of times for each of the five different datasets dimensions, so that we can test the scalability of the system.

It's immediately clear just by a glance that **OpenMP Mode (Green Line), MPI (Red Line) and MPI+OpenMP (Yellow Line) Modes** outperform the single-core and single-process **Normal Mode (Blue line)** once there is a reasonable big dataset (> 10000 points). On less than 1000 points however none of them performs better than the Normal Mode (as can be seen in the Figure 2.1 - 100points Dataset). This is probably due to all the message exchange between the processes that are necessary for managing the paralellization of the operations and due to the broadcasting/gathering of the data to/from the nodes.

By adding OpenMP to MPI we can see indeed a big improvement, the **MPI+OpenMP (Yellow Line) Mode** not only greatly outperforms the sequential mode but also the OpenMP and MPI Modes. This way, we take advantage not only of the multiple nodes but also of the cores on each node used.

Finally we remind the reader that the above plot is made by averaging the behavior of a large number of executions each with a different initial random centroids placement. And it has been noticed that if the initial placement of the centroids is a good one, then the MPI and MPI+OpenMP Modes perform better, so **by engaging in a more sophisticated algorithms for centroids placement we could improve overall performance**.

4.0.11 3) Relation between the Dataset Size and the Execution Time

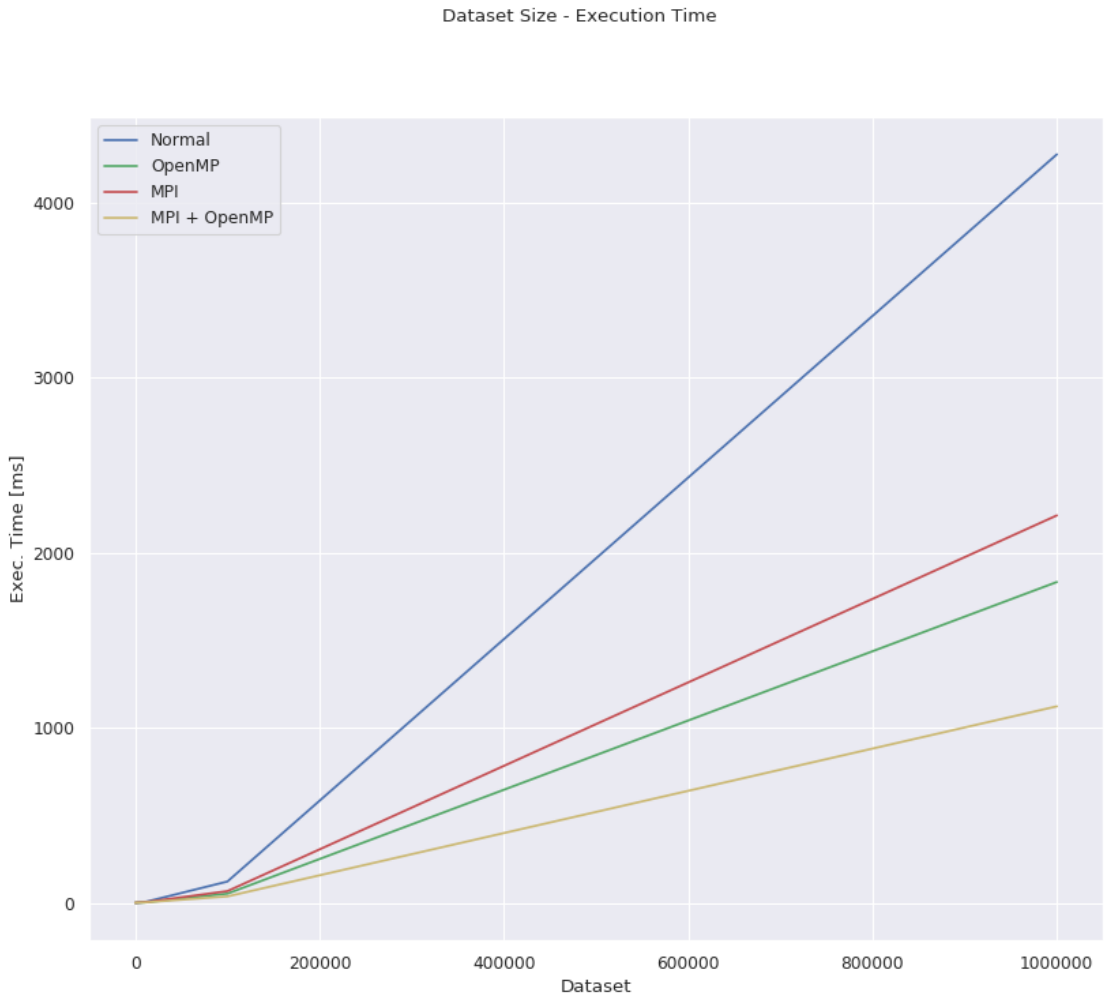
In [16]:

```
def getCentroidsExecTime():
    x_valc          = numpy.zeros(10)    # Centroids
    y_val_n_et      = numpy.zeros(10)    # Normal Execution Time
    y_val_mp_et     = numpy.zeros(10)    # OpenMP Execution Time
    y_val_mpi_et    = numpy.zeros(10)    # MPI Execution Time
    y_val_mpi_mp_et = numpy.zeros(10)    # MPI + OpenMP Execution Time

    #Calc the mean values
    for i in range(0,10):
        x_valc[i] = i + 1
        #print(str(i))

        #Iterate all the executions for each centroid number
        for j in range(EXECUTIONS):
            # Normal Execution
            if n_c[j] == i+1:
                y_val_n_et[i] = y_val_n_et[i] + n_t[j]

            # OpenMP Execution
            if openmp_c[j] == i+1:
                y_val_mp_et[i] = y_val_mp_et[i] + openmp_t[j]

            # MPI Execution
            if mpi_c[j] == i+1:
                y_val_mpi_et[i] = y_val_mpi_et[i] + mpi_t[j]

            # MPI + OpenMP Execution
            if mpi_mp_c[j] == i+1:
                y_val_mpi_mp_et[i] = y_val_mpi_mp_et[i] + mpi_mp_t[j]

        #Execution Time values mean
        y_val_n_et[i]      = (y_val_n_et[i] / EXECUTIONS) * 1000
        y_val_mp_et[i]     = (y_val_mp_et[i] / EXECUTIONS) * 1000
        y_val_mpi_et[i]    = (y_val_mpi_et[i] / EXECUTIONS) * 1000
        y_val_mpi_mp_et[i] = (y_val_mpi_mp_et[i] / EXECUTIONS) * 1000

    return y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et
```

```
x_valds      = numpy.zeros(5)    # Dataset sizes
y_val_n      = numpy.zeros(5)    # Normal Execution Time
y_val_mp     = numpy.zeros(5)    # OpenMP Execution Time
y_val_mpi    = numpy.zeros(5)    # MPI Execution Time
y_val_mpi_mp = numpy.zeros(5)    # MPI + OpenMP Execution Time

def calcMeanExecTime(j):
    for i in range(1,10):
        y_val_n[j]      += y_val_n_et[i]
        y_val_mp[j]     += y_val_mp_et[i]
        y_val_mpi[j]    += y_val_mpi_et[i]
        y_val_mpi_mp[j] += y_val_mpi_mp_et[i]

    y_val_n[j]      /= 10
    y_val_mp[j]     /= 10
    y_val_mpi[j]    /= 10
    y_val_mpi_mp[j] /= 10

EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et = getCentroidsExecTime()
calcMeanExecTime(0)
x_valds[0]=100

EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et = getCentroidsExecTime()
calcMeanExecTime(1)
x_valds[1]=1000

EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et = getCentroidsExecTime()
calcMeanExecTime(2)
x_valds[2]=10000

EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et = getCentroidsExecTime()
calcMeanExecTime(3)
x_valds[3]=100000

EXECUTIONS, n_t, openmp_t, mpi_t, mpi_mp_t, n_c, openmp_c, mpi_c, mpi_mp_c, n_of = getR
y_val_n_et, y_val_mp_et, y_val_mpi_et, y_val_mpi_mp_et = getCentroidsExecTime()
calcMeanExecTime(4)
x_valds[4]=1000000

#Plot the relation between the dataset size and mean executin time for each mode
plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
plt.plot(x_valds,y_val_n, '-b', label='Normal')
plt.suptitle('Dataset Size - Execution Time')
plt.xlabel('Dataset')
```

```
        plt.ylabel('Exec. Time [ms]')
        plt.plot(x_valds,y_val_mp, '-g', label='OpenMP')
        plt.plot(x_valds,y_val_mpi, '-r', label='MPI')
        plt.plot(x_valds,y_val_mpi_mp, '-y', label='MPI + OpenMP')
        plt.legend(loc='upper left')
        plt.show()
```

```
Rows in the results file: 1209
Rows in the results file: 1209
Rows in the results file: 1209
Rows in the results file: 1209
Rows in the results file: 609
```



4.0.12 Resulting plots analysis - Scalability

On the above plot we can observe that the scalability of the four modes on the given datasets and cluster of nodes seems to be linear. Moreover, by increasing the size of the datasets the performance gap between the single core and single node mode and the other modes is more pronounced. Note on the figure that with a small dataset the Normal Mode might perform similarly (actually performs better with less than 1000 points). While later on **the best performing mode is OpenMP+MPI Mode followed by the OpenMP Mode and MPI Mode.**

OpenMP+MPI Mode outshines both OpenMP Mode and MPI Mode, while there isn't such a big gap between the latter two. OpenMP performs slightly better than MPI Mode, probably because the message exchange between the local cores impacts less than the message exchange between the nodes.

However, the performance of the OpenMP mode we think that is not going to continue to scale linearly indefinitely by increasing the size of the dataset and the number of clusters. That is because there is a limit on how many cores and computational power a machine can have. At some point the computational power will saturate and the execution time of the OpenMP mode will rise exponentially.

The only modes that will continue scale linearly are the MPI and MPI+OpenMP nodes. That is because you can always add more nodes to your cluster to increase performance. However, that is a supposition since we couldn't actually run tests on much larger datasets and larger clusters of nodes on Amazon AWS because of the large costs and computational time needed for such feat. (for example to run the script on a 10M points dataset would have required approximately a week with the four on demand c3.xlarge nodes)

4.1 ———————————————————————

4.2 ———————————————————————

4.3 OpenMP-MPI vs Flink Comparizon

With the sections bellow we'll be comparing the results from the Flink and OpenMP-MPI projects in terms of processing time and scalability.

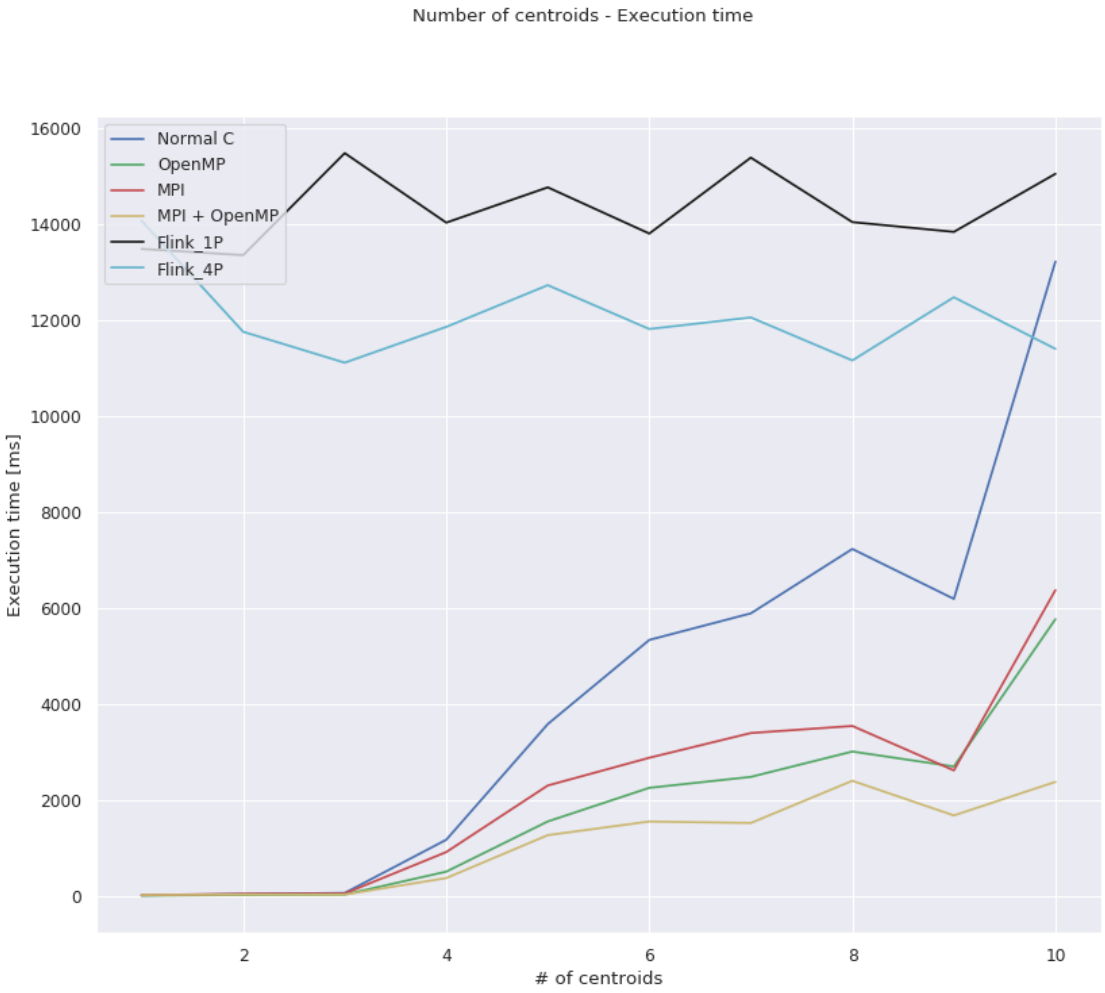
4.3.1 1) Relation between the number of centroids and ExecutionTime

Let's now again average the executions results on a 1M points dataset and plot the relation between the number of centroids and the execution times. The execution were made with a number of centroids between 1 and 10.

We'll compare the results for each mode of both projects: - **Normal C**, **OpenMP**, **MPI**, **MPI + OpenMP** for the OpenMP/MPI Project; - **1P**, **4P** for the Flink Project;

```
In [17]: num_centroids = 10

         #obj_mean_vals = list()
         obj_mean_vals_4p = list() # -p 4
         obj_mean_vals_1p = list() # -p 1
         mink = 1
         maxk = num_centroids+1
```

```
for i in range(mink, maxk):
    fixed_path_objfun = os.path.join(CURRENT_DIR, '../flink-kmeans_clustering/script_re

    objval_iter = list()
    with open(fixed_path_objfun) as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
            iter = int(row['iter'])
            objval = float(row['time'])
            objval_iter.append(objval)

    obj_mean_vals_1p.append([i, numpy.average(objval_iter)])

for i in range(mink, maxk):
    fixed_path_objfun = os.path.join(CURRENT_DIR, '../flink-kmeans_clustering/script_re

    objval_iter = list()
    with open(fixed_path_objfun) as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
            iter = int(row['iter'])
            objval = float(row['time'])
            objval_iter.append(objval)

    obj_mean_vals_4p.append([i, numpy.average(objval_iter)])

x_val = [x[0] for x in obj_mean_vals_1p]
y_val_1p = [x[1] for x in obj_mean_vals_1p]
y_val_4p = [x[1] for x in obj_mean_vals_4p]

plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
plt.plot(x_val,y_val_n_et, '-b', label='Normal C')
plt.plot(x_val,y_val_mp_et, '-g', label='OpenMP')
plt.plot(x_val,y_val_mpi_et, '-r', label='MPI')
plt.plot(x_val,y_val_mpi_mp_et, '-y', label='MPI + OpenMP')
plt.plot(x_val,y_val_1p, '-k', label='Flink_1P')
plt.plot(x_val,y_val_4p, '-c', label='Flink_4P')
plt.suptitle('Number of centroids - Execution time')
plt.xlabel('# of centroids')
plt.ylabel('Execution time [ms]')
plt.legend(loc='upper left')
plt.show()
```



4.3.2 Resulting plot analysis - Processing Time

On the above plot we can observe that for Flink, the execution time does not change too much increasing the number of centroids. The overhead introduced by Flink is much bigger with respect to the increment of time needed to compute the position of more centroids and so we can not observe an increment of time when adding more centroids.

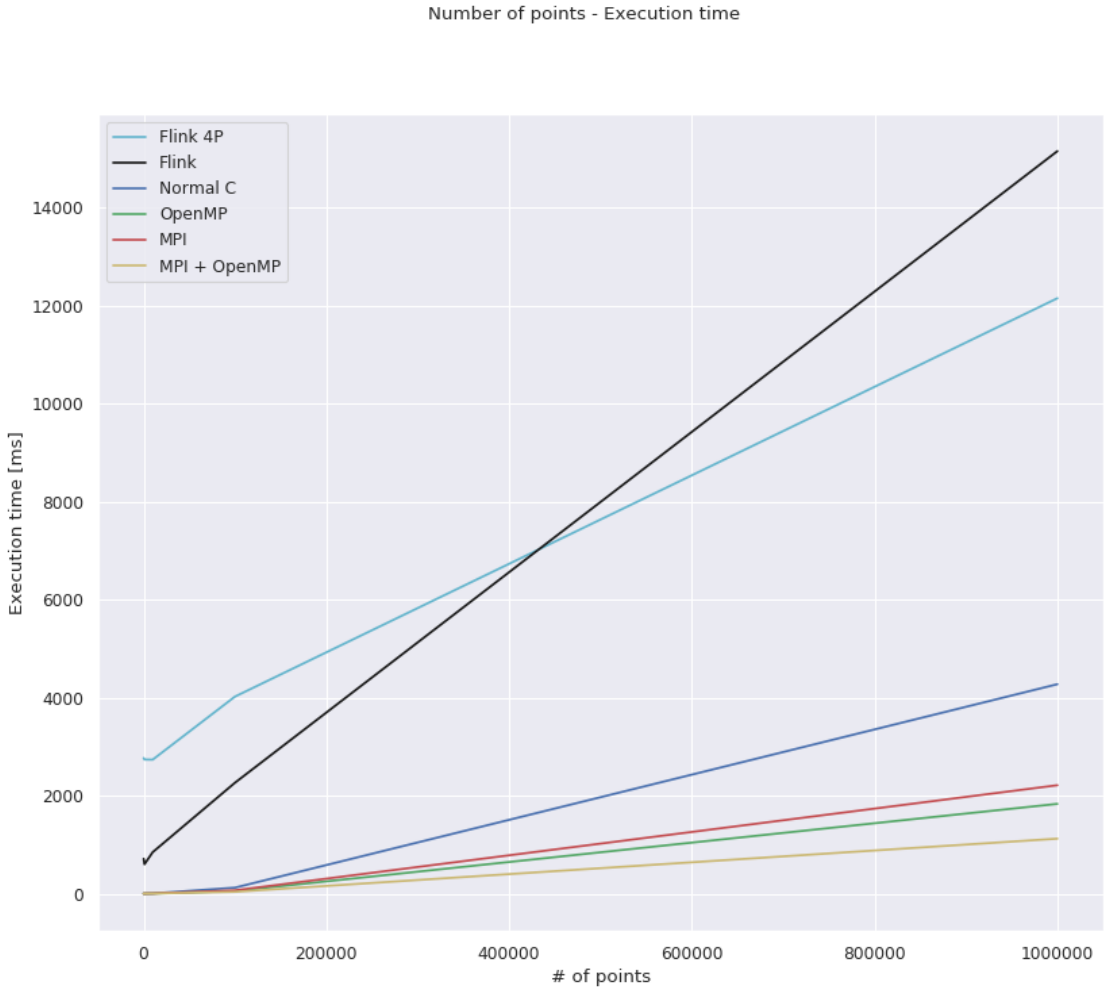
Things are different for the OpenMP/MP Project, where for all four modes we see an increase of execution time by increasing the number of centroids.

That is because MPI and OpenMP are protocols of a lower level compared to Flink, therefore are more efficient and have a smaller overhead. This too is the reason why the OpenMP/MPI project's modes have a smaller execution time compared to he Flink project's modes.

4.3.3 2) Relation between Dataset's number of points and ExecutionTime

```
In [18]: num_of_points = [100,1000,10000,100000,1000000]
         obj_mean_vals_4p = list() # -p 4
```

```
obj_mean_vals_1p = list() # -p 1

mink = 1
maxk = len(num_of_points)+1

for i in range(mink, maxk):
    fixed_path_objfun = os.path.join(CURRENT_DIR, '../flink-kmeans_clustering/script_re

    objval_iter = list()
    with open(fixed_path_objfun) as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
            iter = int(row['iter'])
            objval = float(row['time'])
            objval_iter.append(objval)

    obj_mean_vals_4p.append([i, numpy.average(objval_iter)])

for i in range(mink, maxk):
    fixed_path_objfun = os.path.join(CURRENT_DIR, '../flink-kmeans_clustering/script_re

    objval_iter = list()
    with open(fixed_path_objfun) as csvfile:
        reader = csv.DictReader(csvfile)
        for row in reader:
            iter = int(row['iter'])
            objval = float(row['time'])
            objval_iter.append(objval)

    obj_mean_vals_1p.append([i, numpy.average(objval_iter)])

y_val_4p = [x[1] for x in obj_mean_vals_4p]
y_val_1p = [x[1] for x in obj_mean_vals_1p]

plt.figure(figsize=(fig_width, fig_height), dpi= 80, facecolor='w', edgecolor='k')
line_n, = plt.plot(x_valds,y_val_n, '-b', label='Normal C')
line_mp, = plt.plot(x_valds,y_val_mp, '-g', label='OpenMP')
line_mpi, = plt.plot(x_valds,y_val_mpi, '-r', label='MPI')
line_mpi_mp, = plt.plot(x_valds,y_val_mpi_mp, '-y', label='MPI + OpenMP')
line_4p, = plt.plot(x_valds,y_val_4p, '-c', label='Flink 4P')
line_2p, = plt.plot(x_valds,y_val_1p, '-k', label='Flink')
plt.legend(handles=[line_4p, line_2p, line_n, line_mp, line_mpi, line_mpi_mp])
plt.suptitle('Number of points - Execution time')
plt.xlabel('# of points')
plt.ylabel('Execution time [ms]')
plt.show()
```



4.3.4 Resulting plot analysis - Scalability

On the above plot we can observe that the scalability of both OpenMP/MPI's project modes and Flink's project modes are linear with respect to the linear increase of the dataset size. Moreover, ***we can valuate the scalability of the performances of each mode by the slope of it's curve on the plot***.

As we can see the mode that performs best of all is the OpenMP+MPI Mode followed by OpenMP and MPI Modes. But among these, OpenMP Mode cannot scale indefinitely as there is a limit on how many cores and computational power a node can have.

The only modes that will continue scale linearly are the MPI and MPI+OpenMP nodes in the OpenMP/MPI Project and the Flink with parallelization in the Flink project (although Flink here is not executed on physically different nodes), because you can always add more nodes to your cluster to increase performance. Between these, ***the mode that scale better of all is the OpenMP+MPI Mode***, the reason being that it uses a low level management of a cluster of nodes (with MPI) and also exploits the parallelism within each node (with OpenMP).